

# **DARWIN PROVED**

**BY**

**KOFI BUSIA**

Copyright © 2015 by Kofi Busia

All rights reserved.

This book or any portion thereof may not be reproduced or used in any manner whatsoever without the express written permission of the publisher except for the use of brief quotations in a book review.

Printed in the United States of America

First Printing, 2015

Kofi Busia

428-C Front Street

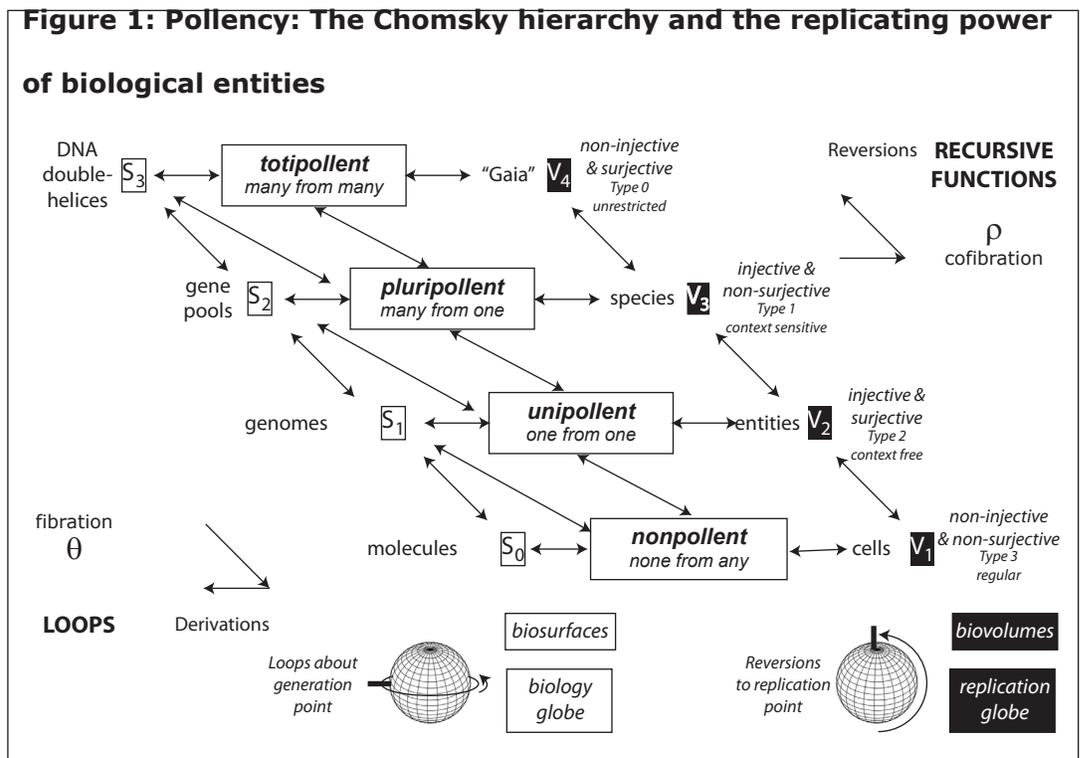
Santa Cruz, California, USA 95060

[www.darwinproved.com](http://www.darwinproved.com)

It is surprisingly straightforward to use algebraic and geometric topology, in combination with both the  $[\Sigma, S, \delta, \alpha_0, F]$  Chomsky production rule from linguistics and informatics and some *Brassica rapa* plants, to comprehensively refute the consensus that contemporary biologists and ecologists seem to have formed that rigorous mathematical–scientific laws and maxims to govern the life sciences are impossible. That consensus has the unfortunate consequence of perpetuating the widespread dogma that Darwin’s theory of evolution is no more than an unproven—and unprovable—hypothesis. We simply place the *B. rapa* plants upon a conveyor belt that is one generation,  $T$ , in length. As they disappear towards the horizon they form a “base”,  $B$ . The “simply-connected” surroundings form their “universal covering space”,  $C$ . Their interactions with, and transformations within, those surroundings create a “fibre bundle” and a “Whitney umbrella”. They have an “injective”  $\xi^{-1}$  fibre lift up into that universal covering space. Those surroundings in their turn have a “surjective”  $\xi$  projection back down onto the plants. The universal covering space has a set of “deck transformations”,  $\eta$ , that are also the Chomsky production’s  $\delta$ . The *B. rapa* plants eventually reappear from the opposite horizon. Their continuing transformations and interactions complete their  $T = 36$ -day “circulation of the generations”. And ... in turning about twice to complete that circulation, the conveyor belt is actually a Möbius strip. And since all those *B. rapa* transformations and interactions have the “homotopy lifting property”, then the surroundings are additionally a “mapping cylinder”,  $M_\lambda$ . The surroundings, as a mapping cylinder, come complete with “fibration”,  $\theta$ , and “cofibration”,  $\rho$ . The plants’ injective  $\xi^{-1}$  fibre lifts are now homeomorphic with the mapping cylinder’s  $\theta$  fibration. The surroundings’ surjective  $\xi$  projections into the plants are similarly homeomorphic with the  $\rho$  cofibration. The plants also have a “fundamental group”,  $\pi(B)$ , formed from a sphere, a torus, and a real projective plane. That fundamental group is isomorphic with the surroundings’ and universal covering space’s deck transformations,  $\eta$ , that govern the Chomsky hierarchy. And since the mapping cylinder is also a universal covering space, then all biology and ecology are determined by the topological criteria governing (i) the base,  $B$ ; (ii) the mapping cylinder,  $M_\lambda$ ; and (iii) the universal covering space,  $C$ , complete with its deck transformations,  $\eta$ , and Chomsky production rule,  $\delta$ . Using  $i$  as an index, then any subset of plants,  $B(Y)$ , formed, as progeny, from any initial set  $B(X)$ , acting as progenitors, is a continuous mapping from  $i_0(B(X)) = 0$  to  $i_1(B(X)) = B(Y)$ , and such that  $M_\lambda: B(X) \times [0, 1] \rightarrow B(X)$ , with  $M_\lambda(x, i) = m_i(x) = 0$  ranging through to  $m_1(y) = y$  for all  $y$  in  $B(Y)$ . The “deformation retract” then declares the laws, the maxims, and the constraints that at long last transform biology and ecology into sound and thoroughly deductive sciences. And ... that  $B(Y)$  subset, of progeny, is the immediate proof that a population free from Darwinian competition and evolution is simply impossible.

# **Part I**

## **The biology and the replication globes**



**I.1.1** It has become almost a cliché to remark that nobody boasts of ignorance of literature, but it is socially acceptable to boast ignorance of science and proudly claim incompetence in mathematics. *Richard Dawkins*.

This paper uses the DNA genetic code with its nucleotide codon syntax and semantics in combination with a four-dimensional hypersphere and the well-known invertible topological properties of a Möbius strip to thoroughly refute contemporary biology’s general consensus that universal laws and deductive logic are inapplicable, if not impossible, because biological phenomena are “too complex”. We instead show that topology’s “classification theorem” allows us to place all biological structures, entities, and populations into four equivalence classes based on the sphere, the torus, and the real projective plane. We thereby provide the four laws of biology, the four maxims of ecology, and the three constraints to which all biological entities and populations are subject.

**I.1.2** Our model begins by perusing the DNA genetic code ... but is not restricted to that bioinformatics approach. As in Figure 1, it reviews all biological-ecological events, assigning them to at least one of two distinct globes of bioactivity.

We provide one “biology globe”. This causes all the more generally biological behaviours. They are the “recurvature” interactions for a generation. We also provide a more specifically “replication globe”. It is responsible for all more explicitly reproductive recurvatures.

Each of our two globes or spheres of activity contributes to an overall biological generation by recurving events about its surface and around its interior and central point. Since each such globe has the potential to create a “circulation” about itself, then these various elements, taken together, allow us to declare that biological populations are “infinite cyclic groups”, with infinite capabilities. They come complete with their equally infinite cyclic subgroups. They can each generate infinitely

many such distinct groupings and subgroupings, each over its potentially infinitely many generations. These are the manifold species.

**I.1.3** Our four dimensions arise because our biology and our replication globes allow for four movements. Three are similar to the ordinary three dimensions of space. They cohere around the central point in each. The fourth is their movement towards and away from each other.

Just as a developing hurricane builds a “wind wall” all about itself, so also are all biological macromolecules, entities, and populations similar kinds of wind walls. They result from the recurvature movements about our two biology and replication globes. The recurvatures are then expressed in terms of their locations about each globe as latitudes; as longitudes; and as heights above each; as well as in terms of their overall circulation lengths and rates as regards those two globes moving towards and away from each other.

**I.1.4** Our model imports the Chomsky(–Schützenberger) hierarchy’s power to conceptualize four main groups of biological actions. The infinite cyclic groups, subgroups, and wind wall recurvatures create the four main categories of biological artefacts:

- some are biological but fail to replicate;
- others are both biological and replicative;
- yet others not only replicate, but add a host of ancillary but non-replicative biological activities;
- a final group—including *Homo sapiens*—are entirely replicative, but give the impression of also being biological.

Our model shows that the four groupings listed above are inevitable results of DNA’s bioinformatic and genetic syntaxes and semantics. The biological Chomsky grammar our model establishes states the recurvature rules of selected sets of chemical components—moving as wind walls—about the two globes.

**I.1.5** Our Chomsky grammar and its resulting hierarchy provide the backbone for the four-dimensional and topological framework in Figure 1. The four rows assign biological recurvatures to the two globes in accordance with their codings. Those produce the accelerative and decelerative behaviours that create the infinite cyclic groups and subgroups in terms of their distances about the globes for the four types.

**I.1.6** Our model’s Chomsky grammar reflects the underlying DNA genetic language. A part of its power is the realization that it is always possible to find some cylinder of maximum volume,  $V$ , that

can replace any sphere. The cylinder's more rectilinear surfaces,  $S$ , give it the potential to turn and to extend infinitely outwards at each point. It can then roll as far in any direction as any sphere.

But if a generation is to complete, then there must always be recurvatures about the globes. Every biological interaction that emerges through some surface,  $S$ , originates in some volume,  $V$ , that also guarantees those continuing recurvatures. We can therefore describe a grammar for those  $V$  behaviours through those  $S$  presenting surfaces.

**I.1.7** Our model thoroughly exploits the realization that a Chomsky grammar is both abstract and versatile. The latter's dominion can be applied to any field desired. It can for example explain an urban sprawl. The relationship between our globes, our surfaces, and our volumes is then similar to that between a language, a grammar, its syntax, and its semantics.

Given that a Chomsky-style grammar describes an entire living language,  $L$ , it is the surprisingly concise:

$$[\Sigma, S, \delta, \alpha_0, F],$$

where  $\Sigma$  is a finite input alphabet of discrete symbols that can represent any object desired;  $S$  is the set of possible alphabet combinations;  $\delta$  is some "transition function" or set of "production rules" over the Cartesian product  $\Sigma \times S$ ;  $\alpha_0$  is an initial state; and  $F$  is the set of permissible terminators in that language.

By convention, the intermediary nonterminals, constructors, and indicators that build a language are represented by upper case letters such as  $S$  and  $F$ ; its completed sentences—or more strictly, its "terminals"—are represented by lower case letters; while Greek letters represent strings of both. So if it is our present desire to compile an English dictionary, then our input alphabet will (at its simplest) be the standard English one of 'a', 'b', 'c'. A set of production rules similar to  $A \rightarrow a$  will then produce all possible English words for its terminals. But we can use the same structure and step up a hierarchy to let our input alphabet instead be the entire English lexicon. Our nonterminals will then be phrase structures. These can combine through a set of production or grammatical rules to create all possible well-formed English sentences. And with appropriate structures and rules, we can describe a town.

**I.1.8** Biological processes and language are both highly complex. No given—and necessarily simple—example can convey the sophistication possible to a Chomsky grammar. But we can nevertheless consider a language,  $L$ , in which:

- our finite alphabet has only two symbols, and so that our input alphabet  $\Sigma = \{a, b\}$ ;
- our sole initiating nonterminal,  $\alpha_0$ , is  $A$ ;
- we have a Rule 1 production or transformation of  $A \rightarrow ba$ ;
- and a Rule 2 of  $A \rightarrow aAb$ .

We can now take up some  $A$  as an  $\alpha_0$  to begin a production. We can next pick either of the

two rules. If we pick Rule 1, we get the trivial production  $A \rightarrow ba$ . Since this is all terminals, we are done.

We can begin again. This time, our initiating  $\alpha_0$  production is Rule 2. We now have  $A \rightarrow aAb$ . Since this is a mixture of terminals and nonterminals, we invoke Rule 2 again, to substitute for that  $A$ . We get  $aAb \rightarrow aaAbb$ . Invoking Rule 2 yet again gives  $aaaAbbb$ . And if we now pick Rule 1, we terminate with  $aaababbb$ .

This rudimentary grammar over  $L$ , with its only two rules and its two alphabet symbols, allows us to create all strings, of arbitrary length, of the general form  $\alpha b a \beta$  where  $\alpha$  and  $\beta$  are equal-length strings of  $as$  and  $bs$  respectively. Its significance and meaning depend upon the field over which this is a language. If, for example, it is an architecture, then we are describing the different kinds of neighbourhoods in an urban sprawl.

**I.1.9** Chomsky productions and grammatical rules are considerably more sophisticated but—similarly to strings of codons—they all produce strings of terminals and nonterminals. Their rules therefore fall into the four broad and well-known types of 3, 2, 1, and 0 that are the four grammars in the Chomsky hierarchy. Our model then assigns DNA’s biological–ecological productions to one or another of the four rows in Figure 1. They represent the transformation rules that distinguish between the different fertility spaces, fertility groupings, and fertility recurvatures that DNA uses to replicate; and also between the biological spaces, groupings, and recurvatures that the replicated entities then use to interact with the surroundings.

**I.1.10** In the language of information science, DNA’s Chomsky style productions are physically and quantitatively measurable upon our globes. Both sets of the biological and the fertility materials are countable. They are each equipollent with  $\aleph_0$ , the set of countably infinite natural numbers (Weisstein 2015a).

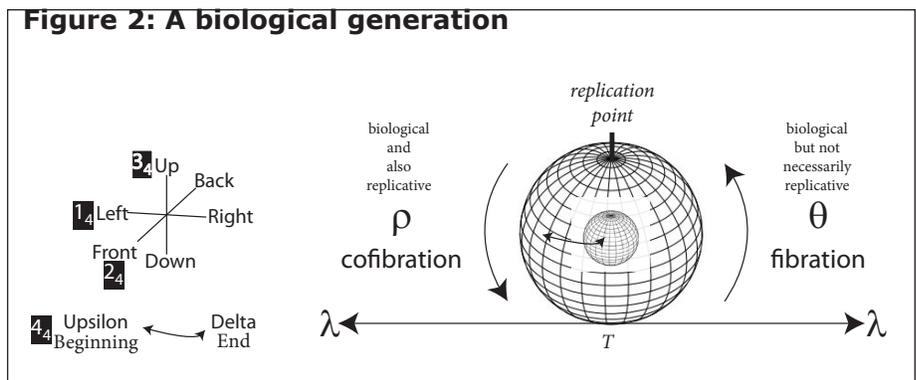
**I.1.11** The four groupings on the left in Figure 1 are the set of non-replication-based recurvatures about our biology globe. They are oriented “trivial cycles”. They bound definite regions on the globe’s surface, so creating the wind walls that surround their centres of activity.

The four groupings on the right differ by being reversible journeys about a Möbius strip. They do not create wind walls. They instead impose curvatures and accelerations. They create the recurvatures about our replication globe.

**I.1.12** The genetic code requires both a transmitter and a receiver. There must be both a wind wall and a velocity upon one or both globes.

**I.1.13** The successful transmission of hereditary information requires both (a) a syntax, and (b) a semantics. This is the propagation of discrete materials, and their circulating wind wall, about both

of our globes. The receiver must therefore possess (a) a cipher to decode the necessary information, and (b) the structures that permit it to carry out whatever task is communicated ... which is in this case to produce viable biological entities by



replicating the winds and wind wall that begot it. They must therefore travel successfully about our two globes. We refer to the Chomsky production rules that achieve this recurvature, and on the right of Figure 1, as a “recursive function”,  $\delta$ .

**I.1.14** As again in Figure 1, the recursive functions in our model have their complementarities of “reversions” and “derivations”. They build our recurvatures about the globes, and from their initial symbols to their terminal ones for a generation. Every replication phenomenon derives from a recursive function journey about a Möbius strip. It is some hyperspherical “biovolume”,  $V$ , that can independently travel about our globes.

But that journey is not just a recurvature about the globes. It is also some associated biological presentation. That surface presentation is the “biosurface”,  $S$ . Its enclosed biovolumes as codons use their production rules to construct biological effects. The resulting biosurfaces, also codons, are their observed biological presentations. Since those surface presentations are, necessarily, terminals, we refer to them as “loops”.

**I.1.15** Our model builds on the fact that DNA, acting as a genetic code, stores information in its codons of three nucleotides each. Genes are the functional segments, having four possible bases. The three nucleotides therefore give  $4^3 = 64$  different possibilities. Their combinations specify the 20 different amino acids used by all living organisms.

**I.1.16** The use of a formal code, of this type, to accomplish such a purpose again requires the receiver of the code to understand the syntax and its rules, and to accord the correct meaning in order to accomplish either, or both, of the biological and/or fertility tasks implied by those symbols. The biovolumes,  $V$ , that DNA generates thus contain biological energies per some unit volume. As recursive functions, they are productions that are then incident upon their presenting biosurfaces as terminals. Their successful transfer thus begets some momentum per relevant unit area, expressed as a timed loop.

**I.1.17** It is unfortunately impossible to represent the four dimensions DNA uses to construct its biological hypersphere in the only two available to us on a piece of paper. Nevertheless, and as in Figure 2, our model will represent a biological generation as two globes. One can initially be regarded as nesting inside the other as they roll. The outer biology globe has the behaviours that supervise all biological interactions and recurvatures; while the inner replication one exclusively handles replications, originating all recursive functions.

The outer biology globe interacts directly with the surroundings to construct our DNA nucleotide codons using three dimensions equivalent to the left-right, front-back, and up-down of ordinary physical space. We can initially think of the fourth dimension—most generally known as ‘upsilon’–‘delta’—as a combination of a horizontal rolling over some absolute time period,  $T$ , and an internal pulsing, during that rolling, to and from each other of the inner replication and outer biology globes. They do so over some distance,  $\tau$ . That combination of  $\tau$ – $T$  is a joint transition (a) to and from the replication point; and (b) forwards in time from the beginning to the end of a generation.

Our model gets its power by using topology’s classification theorem for compact surfaces to examine the conjoined surface these two globes create. All biological structures then fall into very specific equivalence classes based on the resulting normal forms they establish.

Our horizontal hyperglobe translation of time  $T$ , combined with our waxing and waning of distance  $\tau$ , produce the complete set of DNA and biological-ecological interactions,  $\lambda$ , for a recurvature and a generation. Our hyperglobe achieves this by drawing in the needed resources to build its Möbius strip based  $V_n$  molecular reversions. Some of those are allocated to the biology globe, others to the replication one, and yet others to both.

All such “lifts” up into our linked globes, from the surroundings, are uniquely determined by their initiating values at any point. The productions are therefore some hyperspherical  $V_n$ . This is only sometimes replicative; but is always intrinsically biological. The constructed materials now extrude and loop rectilinearly outwards, from the globes, as derivations. They thus produce a set of observed  $S_{n-1}$  biosurfaces and events. Biology therefore consists of this  $S_{n-1}$ – $V_n$  or else  $S_n$ – $V_{n+1}$  coupling, with a replication point,  $\rho$ , acting as a pole.

**I.1.18** The cells at bottom right in Figure 1 are  $V_1$  Möbius strip style biovolumes relative to the  $S_0$  molecules on their left that “tangle” to create their base pairs ... with those same molecules manifesting the relevant biological behaviours in the surroundings as their presenting biosurfaces. But the manifest molecules have a parallel upwards recursion and complexity. They seem able to come together to build the observable  $S_1$  genomes above them. But those apparent productions are merely the biosurfaces belonging to the parallel reversion, on the right, of cells into the  $V_2$  biovolumes that are the enshrining entities for those same genomes. Those are built by our recursive functions.

The DNA codon grammar in our parallel structure is that only those biological constructs that pierce the inner replication globe and return, to interact with the surroundings, have the appropriate syntax and semantics. Only they are successfully fertile and replicative.

**I.1.19** Our grammar stipulates that the period between the beginning of a generation and the pole or replication point is a “fibration”,  $\theta$ ; with that between the replication point and the end of the generation being the “cofibration”,  $\rho$ . The fibration takes in resources and energy from the surroundings; the cofibration then returns them to complete the generation.

**I.1.20** As in Figure 3, the language that DNA speaks is that reproduction is a

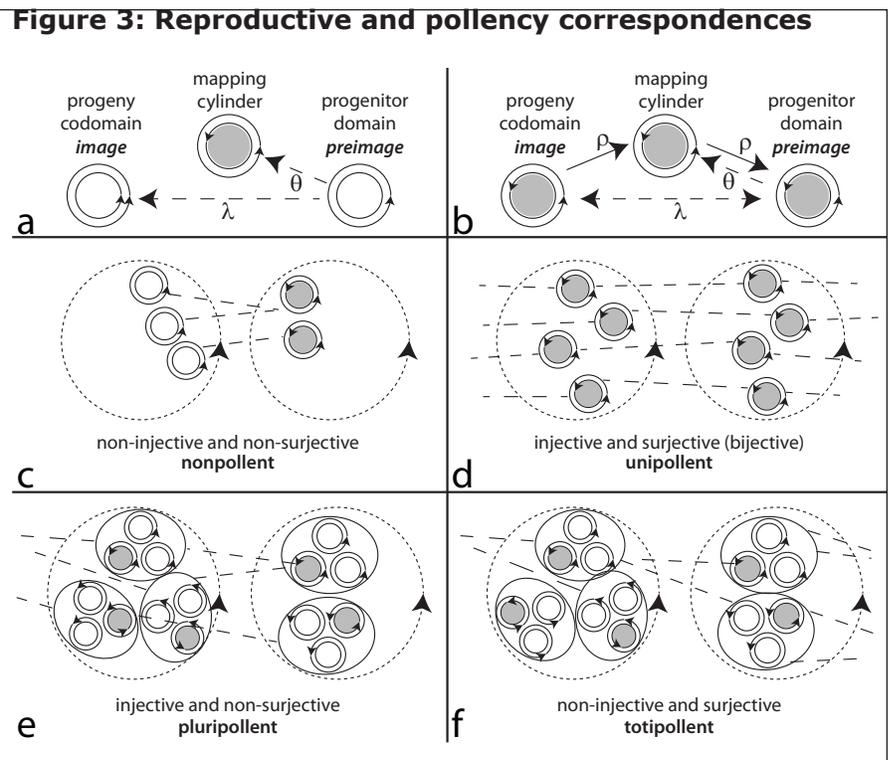
“mapping” of the form  $\phi: X \rightarrow Y$ . DNA maps from a first group of elements in a “progenitor domain”,  $X$ . Those transform to a second set of elements in a “progeny codomain”,  $Y$ . All such  $\phi: X \rightarrow Y$  and/or  $\phi: Y \rightarrow X$  mappings are our recursive Chomsky production rules,  $\delta$ .

Our mappings will generally occur via a “mapping cylinder”,  $M_\lambda$ . That mapping cylinder must then impose sufficient accelerations and velocities on both (a) the groups; and (b) the surroundings to create the needed recurvatures.

**I.1.21** We also define the progenitor domain,  $X$ , as the “preimage”; and the progeny codomain,  $Y$ , as the “image”. A “homomorphism”—from the Greek *homos* for ‘same’, and *morphē* for ‘form’—is then a structural mapping between the groups contained in these different globes and domains.

A biological homomorphism preserves a group’s essential characteristics. It does so throughout all the group’s possible translations and transformations, and quite irrespective of the biological and/or replicative spaces that group transitions through.

**I.1.22** Our model very carefully separates structures from spaces. Since we have our two globes, then we can carefully analyse the realization that not all entities in any one group are obliged to recurve about our two globes at the same velocities and accelerations as they transition across a generation, and so from preimage to image and/or conversely. Entities can therefore map between domain and/or codomain without necessarily also keeping the spaces they each traverse—and so their recurvature values—invariant. They do not all recurve about our two centres in the same ways.



A “homeomorphism”, from the Greek *homoios* for ‘similar’, is a successful mapping between spaces, rather than between groups of elements. A biological homeomorphism therefore preserves the biological space’s characteristics, irrespective of the groups and/or transformations passing through it.

We shall only regard groups of entities as identical if they preserve both (a) their homomorphism, and so group structure; and (b) their homeomorphism, and so space-behaving characteristics. Any populations that successfully match a generation’s worth of biological activities with a generation’s worth of replicative ones have clearly preserved an appropriate structure across all spaces, and will then be both homomorphic and homeomorphic. This is “isomorphic” where *iso* comes from the Greek for “identical”.

**I.1.23** The significance of so distinguishing between iso-, homo-, and homeomorphism is that, as in Wernicke’s aphasia, DNA syntax transmission over a generation is possible without semantic comprehension by the receiver; while as in Broca’s aphasia, it is possible to transmit the semantic comprehension capability that would make a generation possible, but then to fail to effect it by transmitting no—or the wrong—syntax for the decoding.

**I.1.24** DNA’s interactive, complementary, and parallel language and grammar of homo- and homeomorphisms between (a) preimage and image, and (b) biology and replication globes, produces Figure 1’s four horizontal groupings. They are a relationship between our globes. Groups of entities use fibration and cofibration to transition back and forth between progenitor domain and progeny codomain, and so between syntax and semantics.

**I.1.25** Each of our four topological style groupings—based as they are on the sphere, the torus, and the real projective plane—is characterized by its “pollency” or “fertility power”, taken from the Latin *pollēre* ‘to be strong’. This reflects the relationship between the syntax and semantics that produce the different biology and fertility behaviours across our two globes. Each possible combination—being homomorphic and/or homeomorphic—is now “injective” and/or “surjective”, i.e. “one-to-one” and/or “onto”. The four possible groupings of biological artefacts that our model establishes across all biological Kingdoms are:

- **Nonpollent: non-injective and non-surjective.** *Replicatively open; biologically open.* These are biological but not replicative. The replicative pervade the biological, but not conversely. These artefacts, entities, and/or populations correlate with Chomsky’s Type 3 or “regular grammars” and so with “finite state automata”. Linguistically, each of their distinct production rules can have only a single nonterminal,  $X$ , on the left, and may not have more than one terminal,  $x$ , on the right, as in  $X \rightarrow x$ . They may optionally have a nonterminal on the right, as in  $X \rightarrow Yx$  or  $X \rightarrow xY$ . These are Figure 3c. They are neither homomorphic nor homeomorphic. They neither create nor preserve

their biological spaces or structures. They follow Figure 3a, but not 3b. They are replicatively open because all these entities, being only biological, must look elsewhere to be replicated. Their generation cycle is thus incomplete. They do not return to the replication globe. They are “intransitive”. Their biological activities are born from both the progenitor domain and the inner replication globe, via the intermediary mapping cylinder, then transitioning into both the progeny codomain and the outer biology globe. They always appear, in the surroundings, as if direct products from some preimage. They can therefore be analysed as biosurfaces,  $S$ , relative to some set of biovolumes,  $V$ . But they do not decelerate to undertake the reverse transition from progeny codomain back to progenitor codomain ... and so do not replicate. Since no reverse process exists, they do not cross the replication point to reenter the replication globe, and again cannot replicate either their spaces or their groups. They are therefore non-injective, displaying the first of our two methods for falling in this category. And further since they do not return to the replication globe, they can only understand what they are told, by the biology globe, to that limited and nonreplicative extent. So irrespective of how many different production rules might be applied; and irrespective of any apparent biological complexity in their processes; they can form only the trivial biological cycles that restrict them to this biology globe. They have reversions (or “parents”), but no derivations (or “daughters”). They are produced of some Möbius strip, using the mapping cylinder, but do not themselves traverse one. And since these are only trivial cycles that do not traverse a Möbius strip, then they are biologically open. We designate them ‘none from any’ and/or ‘any to none’ for they are neither one-to-one nor onto. They are non-surjective because there are always more replicative elements in the progenitor domain as can produce them than there are in the progeny codomain for there are zero replicative elements in the latter ... which is the first of our two methods for being non-surjective. Therefore: not all elements in any preimage or progenitor domain need map to ones in the image or progeny codomain; while not all elements in any image or progeny codomain are fully mapped to by elements in their partnering preimage or progenitor domain.

- **Unipollent: injective and surjective.** *Replicatively closed; biologically closed.* The biological fully pervade the replicative; while, reciprocally, the replicative fully pervade the biological. These create and preserve both their biological and their replicative spaces. They correlate with Chomsky’s Type 2 or “context free grammars” and with “pushdown automata”. Linguistically, they may have arbitrarily many distinct linguistic production rules again of great complexity, but they can only ever have a single nonterminal symbol on the left side. They may, however, have any number of terminals and/or nonterminals upon the right. They thus have more possibilities than the nonpollent, but do have the limitation that irrespective of context, they behave the same way on every occasion. Like the two groups to follow them, these can

only exist because they emulate Figure 3b by using the mapping cylinder to recurve, and so to successfully reenter the replication globe. Since they cross the replication point, they are transitive. In biological terms, however, the two globes do no more than pervade and sustain each other. The entities can therefore create a Möbius strip. That intermediary mapping cylinder imposes a recurvature for all necessary invertible, accelerative–decelerative and reproductive actions. They thus appear, in the surroundings, as direct injections first from preimage to image; and then from image back to preimage to complete the generation. But although these unipollent entities, of Figure 3d, can therefore replicate, they are both biologically and replicatively closed. They successfully traverse a Möbius strip to complete a cycle, but are more limited than the two groups to follow, for they support no additional biologically trivial cycles. They support no nonreplicative and/or extra-cellular materials in any domain or globe. They understand exactly what they are told by both the replication and biology globes; but also do not understand any more than they are told by either, the two again doing no more than pervade each other. Their Möbius strip operations are therefore somewhat restricted. All elements in the progenitor domain have exactly one image in the progeny codomain and so map to exactly one element; and all elements in the progeny codomain also have exactly one preimage in the progenitor domain, and so are mapped to by exactly one replicating element. These unipollent entities are thus both one to one and onto, which is a ‘one-to-one correspondence’. They recurve, but again permit no additional trivial cycles; and so no additional biological phenomena, in either of the biology or replication globes. They are both homomorphic and homeomorphic. They are “bijective”, which is both surjective and injective.

- **Pluripollent**: injective and non-surjective. *Replicatively closed; biologically open*. These are again replicative, but also add additional biological activities. They can create all biological spaces required, but do not explicitly preserve them. They correlate, linguistically, with Chomsky’s Type 1 or “context sensitive grammars”, and so with “linear bound automata”. Their linguistic production rules allow for more than one nonterminal on the left side of any production rule ... with the added proviso that any nonterminal production,  $X$ , may be surrounded by specified terminals and/or nonterminals as in  $\alpha X\beta$ ; and so that when so surrounded,  $X$  may on those specific occasions be replaced by some third string to create  $\alpha\gamma\beta$ . This nonterminal’s behaviour now depends entirely upon the context in which it is found. These materials, seen in Figure 3e, recurve; and so can again all be reproduced. They are injective. However, their reproductive elements can support additional trivial cycles in the biology globe. The entities can therefore produce a variety of additional, and biologically viable—but nonreplicative—products by invoking operations—as those trivial cycles—beyond each of their replicative ones. But since those added cycles and activities do not themselves replicate or traverse a Möbius strip, they are biologically open. Those

additional trivial cycles emulate nonpollent behaviours by not being able to directly replicate themselves. These entities are therefore ‘many from one’ and/or ‘one to many’ (Latin *plurimus*, ‘very many’). They are, however, replicatively closed because the replicating elements can successfully traverse a Möbius strip. They are overall like the unipollent in being injective and circumscribing a Möbius strip; but differ by supporting those additional nonreplicative and/or extra-cellular materials. They are not homomorphic because the complete biological structures they build, with those supported trivial cycles over in the progeny codomain, are quite unlike those in the progenitor domain that produce them; and conversely. They are, however, homeomorphic because they can recreate their biological spaces in both globes. But when compared to the upcoming final group, then although the progeny can indeed use the biology globe to construct larger biological structures, and trivial cycles, from a more basic replicated unit, they are limited. They cannot reconstruct their replicative centres from yet smaller elements. They are, therefore, somewhat restricted in the replication globe capabilities, but are not restricted in the biology one. Their replicative elements, in the progenitor domain, can thus have multiple images in the progeny codomain; while all elements in the progeny codomain map to at most one element in the progenitor domain and replication globe, having exactly one preimage. They are one-to-one, but not onto, which is injective and non-surjective.

- **Totipollent: non-injective and surjective.** *Replicatively open; biologically closed.* These can only be replicative because each replicative element can induce—but it cannot independently create—biological activity. They correlate with Chomsky’s Type 0 or “unrestricted grammars” and with “Turing machines”. They are recursively enumerable. The sole linguistic production rule is that the left side cannot be empty. These Figure 3f materials are ‘many from many’ and/or ‘many to many’ because, amongst other things, they can support trivial cycles and additional activities in the replication globe. Distinct reproductive centres must, however, link themselves to biological structures, and processes, so they can be viable and build their more complex reproductive structures. They are therefore replicatively open because zero entities in the progenitor domain can—unaided—replicate themselves. Distinct replicative elements must align themselves with others like themselves before they can create a locus that can then produce their joint progeny. They in other words construct replicating elements from smaller units. Those originating progenitor elements can nevertheless use their supporting trivial cycles, built in their progenitor domain, to create multiply sourced derivations, of great biological complexity, over in the progeny codomain. All elements and cycles in the image or progeny codomain are thus mapped to by more than one element from the preimage or progenitor domain. However, elements in the progeny codomain are also biologically closed because they must accelerate the replicative enclosures, and must force the biological structures they

are embedded in to accelerate about the Möbius strip. All replicated elements in the progeny codomain can therefore map themselves back to multiple progenitor domain preimages, thereby having more than one generative element. But since elements in the progenitor domain must first ally themselves, with others, in that domain to create that extended progeny codomain, then they do not—individually—traverse a Möbius strip. They can only traverse one when biologically combined with others. Elements in the progenitor domain can thus have more than one image in the progeny codomain, mapping to multiple elements. But since none of the replicative elements are again individually responsible for any cycles created in the biology globe, then since those cycles can return, they are closed. Their ensuing trivial cycles are therefore both replicatively open and non-injective. And further since all elements in the progeny codomain must have at least one mapping from the progenitor domain, then these are onto but not one-to-one, which is non-injective and surjective.

**I.1.26** We shall now prove that these various and parallel trivial cycle and Möbius strip interactions are DNA's entire language and grammar of syntax and semantics. They invoke our two globes and our two domains to establish (a) the four maxims of ecology that in their turn establish the homeomorphic spaces that can support the wind walls that recurve about our two globes; (b) the four laws of biology that establish the homomorphic structures that can accelerate and decelerate between the biosurfaces and the biovolumes; and (c) the three constraints that link the homomorphic to the homeomorphic to create the circulations of the generations. We shall take *Brassica rapa* as a test case.

# **Part II**

## **Gathering the tools**

**II.1.1** We cannot achieve our objective without adopting a perspective that is fundamentally opposed to the current orthodoxy. And perhaps the best explanation for that overweening insistence that universal laws in biology are impossible comes from Bertram Murray:

... biologists tend to believe that physics is simpler than biology ... allowing them to believe that universal laws and deductive theory are inappropriate in biology. But this is a misunderstanding. In fact, the physical world is extraordinarily complex. What physicists do for the physical world, which biologists do not do for theirs, is to simplify it in order to study it. ...

... Newton's mathematical model has only one planet orbiting a point in space; his physical model has only one planet revolving around one star. And Newton was correct ; the three-body problem has not yet been solved. ...

...

The physical world is not simple. Physicists simplify the physical world in order to study it. Biologists do not simplify the biological world. As Dyson put the difference, "Unifiers are people whose driving passion is to find general principles which will explain everything. They are happy if they can leave the universe looking a little simpler than they found it. Diversifiers are people whose passion is to explore details. They are happy if they leave the universe a little more complicated than they found it. Biology is the natural domain of diversifiers as physics is the domain of unifiers" (Murray 2001).

**II.1.2** The reason biologists cannot simplify their subject, in the way Murray suggests, is simple. They do not adequately define even the most foundational of concepts. Insufficiency of rigour then masquerades as complexity of subject.

Almost as if to make up for their predominantly nonmathematical nature, debates in biology and ecology have a long and fractious history. The parallel universes biologists occupy upon these most basic of issues is perhaps best exemplified by E.O Wilson, who adopts a very different position to Dawkins as quoted at the head of Part I:

Everyone sometimes daydreams like a scientist. Ramped up and disciplined, fantasies are the fountainhead of all creative thinking. Newton dreamed, Darwin dreamed, you dream. The images evoked are at first vague. They may shift in form and fade in and out. They grow a bit firmer when sketched as diagrams on pads of paper, and they take on life as real examples are sought and found. Pioneers in science only rarely make discoveries by extracting ideas from pure mathematics (Wilson 2013).

This unfortunate trait at biology's heart reared its ugly head almost as soon as Darwin had announced his theory. Herbert Spencer's 'survival of the fittest' might be a highly evocative phrase and a masterly abstraction, which Darwin rapidly adopted, but as others soon pointed out (Milner 1990), all it really means is that those that survive are the most likely to have survived, thus telling us nothing.

Since biology currently lacks a rigorous mathematical foundation, it is littered with uncertainties and ambiguities. Even though, for example, all “viable” biological “groups” “reproduce” and so must exhibit a “generation time”,  $T$ , not one of the concepts in quotes has a clear and/or widely accepted definition. Groups and generation time are amongst the most contentious, with different authorities volubly championing different proposals (Charlesworth 1994; Cole 1954; Dawkins 2012; Nowak, Tarnita, Wilson 2010; Pennisi 2011; Thorpe 2012). This, as Lo Bello opines, is the heart of the problem:

All mathematics begins with definitions, so that the first observation to be made about a mathematician is that he is the sort of a person who requires that all technical terms be defined, and that all common words be used properly in accordance with their accepted meanings (Lo Bello 2013).

We obviously intend to give clear definitions for the terms homomorphic, homeomorphic, and isomorphic we introduced in Part I.

**II.1.3** If we are not clear about the limitations behind biology’s current perspectives and lack of clear definitions, as well as the reasons for them, then we cannot overcome them. Stephen Hawking, in his best-selling *A Brief History of Time* (1988), nicely characterizes biology’s somewhat parlous state of affairs:

Someone told me that each equation I included in the book would halve the sales. I therefore resolved not to have any equations at all. In the end, however, I did put in one equation, Einstein’s famous equation  $E = mc^2$ . I hope that this will not scare off half my potential readers (Hawking 1988).

Granted that most biologists consider themselves clear and rigorous, this is a somewhat surprising situation. The only possible reason is a misunderstanding of what ‘rigour’ entails.

Somewhat ironically, Dawkins—who, as his above quote indicates, certainly cannot be faulted for the healthy respect he has for mathematical reasoning—provides one of the best examples of this disparity in discourse concerning the nature of rigour:

I insist on tight discipline. The criterion for recognizing a true replicator for a Darwinian model is a rigorous one. The putative replicators must vary in an openended way; the variants must exert phenotypic effects that influence their own survival; the variants must breed true and with high fidelity such that, when natural selection chooses one rather than its alternative, the impact persists through an indefinitely large number of generations (more precisely, survives at a high enough rate to keep pace with mutational degradation) (Dawkins 2004).

Dawkins’ use of ‘openended’ is immediately problematic. It beautifully summarizes matters. His “memes” illustrate the difficulty. The way he defines them is admittedly colloquially delightful, but it is scientifically unhelpful. It is—unfortunately—completely without a rigorous foundation. It strikes right at the heart of these issues. Our central concern is to remedy its manifest deficiencies.

**II.1.4** There is a difference between seeing what needs to be done, and doing it with sufficient clarity and rigour. Dawkins felt it important, as a working evolutionary biologist, to pinpoint those transmissible “units of culture” that could spread through calls, traits, gestures, etc. He saw that, like genes, they could mutate, propagate, and respond to selective pressures. However, unlike genes, they were not reproductively inherited. He therefore concluded that:

We need a name for the new replicator, a noun that conveys the idea of a unit of cultural transmission, or a unit of imitation. ‘Mimeme’ comes from a suitable Greek root, but I want a monosyllable that sounds a bit like ‘gene’. I hope my classicist friends will forgive me if I abbreviate mimeme to meme (Dawkins 1989).

**II.1.5** There is no questioning that biology must separate the inheritable from the noninheritable. Nevertheless, Dawkins’ ideas of “tight discipline” are rather different from what we intend. Memes do not qualify as an example of such discipline because although Dawkins has successfully highlighted the distinction between our biology and replication globes, he has given no indication of how we can use either them or his memes to make scientifically useful measurements.

**II.1.6** The fault we are here highlighting—if such indeed it be—is not specific to Dawkins. It permeates an entire field of discourse that seems all too happy to leave its signally important terms inordinately vague. Hawking again gives an example:

In the eighteenth century, philosophers considered the whole of human knowledge, including science, to be their field and discussed questions such as: Did the universe have a beginning? However, in the nineteenth and twentieth centuries, science became too technical and mathematical for the philosophers, or anyone else except a few specialists. Philosophers reduced the scope of their inquiries so much that Wittgenstein, the most famous philosopher of this century, said, “The sole remaining task for philosophy is the analysis of language.” What a comedown from the great tradition of philosophy from Aristotle to Kant!” (Hawking 1988).

This is certainly a glib assessment of Wittgenstein; of the debates surrounding him; and, above all else, of the average philosopher’s ability to engage in abstractions. The essence of Wittgenstein’s argument is that while scientists and mathematicians insist upon treating planets as points because it seems to “work” very well indeed, planets are not actually points. Therefore, science is not explaining “reality”. It is either saying nothing at all, or else saying nothing of any consequence.

**II.1.7** Hawking does, nevertheless, make a good point. When, for example, Henry Parker Manning produced his *Geometry of Four Dimensions* (Manning 1914), he was all too well aware he was leading readers into very new terrain. He therefore spoke with great clarity:

The elements of geometry are points. We do not define the term point. It is impossible to build up a system of geometry without undefined terms, and

if we can give different meanings to this word we shall be able hereafter to give our geometry different interpretations. .... The objects which we study are to be regarded as consisting of points, that is, classes of points selected according to various laws from the class which includes all points. Any selected class is said to constitute a *figure* .... The points of a figure may also be said to *lie in* the figure or *belong to* it. One figure is said to *lie in* another when all of its points are points of the second. It will often be convenient to speak of a figure as consisting of certain other figures, but this expression should always be understood as meaning that it consists of the points of these other figures.

Manning tells us that points can be homomorphic. They can easily live in groups. Any figure made from points can itself be (a) a point; and (b) be composed of points. But in complete contrast to that clear usage, group remains one of the most contentious terms in all biology. It lies at the heart of the often acrimonious debate about fitness and what evolves (Dawkins 2012; Nowak, Tarnita, Wilson 2010; Pennisi 2011; Thorpe 2012). Yet the resolution seems so clear and simple. We explicitly adopted it in Figure 1: sometimes it is better to think of biological entities as composed of groups and so as homomorphic; and sometimes as clustering into groups that can then differ, from their original homomorphic ones, in their resulting homeomorphic and topological behaviours. The two together are isomorphic.

**II.1.8** In face of all these difficulties, we shall adopt a simple—but we hope effective—strategy. We largely avoid using ‘group’. When we do, it will be in its strictly technical and mathematical sense.

**II.1.9** We shall instead emulate Dawkins (1989) and coin neologisms, such as ‘pollency’, when we need them. We can then invest our new terms with the specific biological-mathematical meanings we desire, borrowing such rigorous terms as injective, surjective, homomorphic, homeomorphic, isomorphic and the like to tightly define them. The only test they then need to pass is the scientific one of facilitating accurate measurements, such as we do in our *Brassica rapa* experiments. We shall also refer to every step in building our model as one of Dawkins’ memes.

**II.2.1** Since perspective is vital, then our first order of business is to describe biological behaviours in terms of our globes, our winds and wind walls, and our recurvatures, and so that we can eventually apply a set of Chomsky production rules. Our simple ambition is to give clear mathematical form to such unconscionably vague biological utterings as ‘those  $x$  entities live for time  $y$ , but produce zero descendants’. This is both vague and unsatisfactory for it gives us no way to compare entities to each other on any biologically relevant basis.

**II.2.2** Meme 1, and the first step in building our model, is to define our initial nonpollent  $S_0-V_1$  grouping, illustrated on Figure 1’s bottom row. We described it as both replicatively and biologically open, and as non-injective and non-surjective. Such entities are biological, but not replicative.

If our proposed nonpollent entities are indeed incapable of replicative activities, then they do not recurve to our replication globe. No matter how biologically active they might be, they can do no more than surrender to the surroundings. We must signify such behaviour appropriately ... i.e. both qualitatively and quantitatively.

**II.2.3** We begin by noting a contrast. Mathematical precision makes it “obvious” that  $2 + 3 = 3 + 2$ , and that  $2 - 3 \neq 3 - 2$ . We therefore emulate that precision. We do so by asserting that the following Chomsky style production rule exhibits our biological but nonreplicative nonpollency:

$$(x \times y^0 \rightarrow 0),$$

where

- ‘ $x$ ’ is the number of entities;
- ‘ $\times$ ’ means we track them forwards or anticlockwise about the “circulation of the generations”, and so from preimage to image, but without ever entering the replication globe—i.e. by consulting their fibration, but not their cofibration—and so potentially without consulting the mapping cylinder;
- ‘ $y$ ’ is their number of generations lived;
- the ‘ $0$ ’ superscript means their combination of fibration and cofibration makes them intransitive—i.e. both non-injective and non-surjective—having a “reproductive index” of  $\delta = 0$ ;
- and the final ‘ $0$ ’ means they simply dissipate from the biology globe, without themselves creating images in any progeny codomain, and so again without further use of any replication globe or mapping cylinder.

**II.2.4** Since we have now defined a nonreplicative production, then Meme 2, the second step in building our model, is to assert that while the following is successfully replicative and so pollent, it is still not in balance with its surroundings. It is again not in reproductive equilibrium, for although transitive, the preimage and image and the biology and replication globes do not match.

The progenitor domain and progeny codomain are clearly of different sizes meaning biological and replicative events are not bijective. They are not in a one-to-one correspondence:

$$(15 \div 4^3 \rightarrow 40)^{-0.75},$$

where

- ‘15’ is the group of elements in the progeny codomain;
- ‘ $\div$ ’ now asks us to determine their origins by tracking backwards or clockwise around the circulation from image to preimage, and so explicitly via the mapping cylinder;
- ‘4’ asks us to count back four generations or iterations across the mapping cylinder;
- ‘3’ means the group members exhibit three distinct reproductive paths;
- ‘40’ is the number of progenitors we find; and
- ‘-0.75’ means generation time shortens by 25%.

Equilibrium measurably fails because  $15 \neq 40$  and  $\frac{3}{4} \neq 1$ .

We can also observe that our earlier nonpollent entities necessarily fail to attain biological equilibrium because  $(x \times y^0 \rightarrow 0)$  can never match  $(0 \div y^0 \rightarrow x)$  since no matter what the values for  $x$ ,  $y$ , or  $\delta$ , we can never have  $0 = x$ . The zero again means the replication globe recurvature, and so matching mapping cylinder activities, are never invoked.

**II.2.5** The equilibrium we suggest obviously demands that we draw two such expressions—one ‘ $\times$ ’ and one ‘ $\div$ ’—together to match two distinct journeys: one is clockwise, the other anticlockwise. One is with, and one is without, the surrounding mapping cylinder. This is a precise matching between our replication and biology globes, and our fibration and cofibration. It specifically equates homo- and homeomorphism. It is an equality between sphere and cylinder. We therefore also define it as a “doubly closed production”, for both the replication and biology globes are closed.

Meme 3 uses unipollency to define our double closure and our homo-plus-homeomorphic cylindrical–spherical equilibrium. This involves both of our recurvature journeys: one from preimage to image and back to preimage; and one from replication globe to biological one and back to replication. One journey therefore uses the intermediary mapping cylinder, while the other—at least, ostensibly—does not. This is again both homomorphic and homeomorphic and gives us our needed definition of biological and replicative closure:

$$\pi \equiv [(1 \times 1^{\delta=1} \rightarrow 1)^1 \Leftrightarrow (1 \div 1^{\delta=1} \rightarrow 1)^1].$$

The sequence of 1s in the production on the left means:

- we consider one element in the progenitor domain;
- forwards, and so directly from preimage to image;
- for one generation, which is again forwards and could well be one anticlockwise mapping cylinder iteration, but is being explicitly considered without;
- using a bijective and singly reproductive path,  $\delta = 1$ ;
- ending up with one progeny or matching element in the progeny codomain; and
- with generation time holding constant.

The production on the right is then the reverse journey where we:

- begin with one element in the progeny codomain;
- track it backwards for one reverse iteration ... which can now only be clockwise through the mapping cylinder, and so which is also for one iteration and generation;
- using the same singly reproductive and bijective path, with its one-to-one correspondence;
- to find a single and matching element in the progenitor domain;
- with generation time or circuit lengths again holding constant.

Since this defining population and its production has matching preimage and image and so is doubly closed, it is neither growing nor diminishing, in either numbers or time, in either direction, which is both with and without the intermediary mapping cylinder. The  $\pi$  means that there is—by definition—an equilibrium set of both loop and recursive interactions between the entities and their surroundings. The entities are again both homomorphic and homeomorphic. This involves no trivial cycles in either globe and so is doubly closed to them. Our biology and replication globes match.

**II.2.6** Our eventual intention is, of course, to turn to the real world, and to say that since we now have a rigorously defined bijective equilibrium,  $\pi$ , then any real population is, by definition, also in replicative equilibrium when it similarly matches the overall events in its two globes so that:

$$[(x \times 1^\delta \rightarrow y)^{T_1=1} \Leftrightarrow (y \div 1^\delta \rightarrow x)^{T_1=1}] = \pi \equiv [(1 \times 1^1 \rightarrow 1)^{T_1=1} \Leftrightarrow (1 \div 1^1 \rightarrow 1)^{T_1=1}],$$

where  $x$  is the progenitors,  $y$  is the progeny,  $\delta$  is some reproductive index, and the respective absolute generation lengths are  $T_1$  and  $T_2$ .

**II.2.7** We must now define the doubly closed entities, groups, and interactions that our model can use to produce  $\pi$ . This must be a group of entities with a homomorphic group structure, but that also create a transitive and homeomorphic space. Their productions can recreate both those structures and those shapes.

Since our defining entities must, and by definition, recur in both our globes, then they must all be sufficiently like each other so they can remain near to each other at all times, both homomorphically and homeomorphically. We therefore turn to the Greek *plēsios*, meaning ‘like’, ‘near to’ or ‘neighbour’ (Busia 2014) to define them:

- “Plessists”. These are the distinct but pollent doubly closed biological entities that therefore display the homomorphic and homeomorphic metabolisms and physiologies they need to follow whatever reproductive path attains  $\pi$ . They are formed from countable molecules, and can engage in all relevant and observable group behaviours. They are Meme 4.
- “Plessiomes”. The molecules that can successfully both enter and reenter the replication globe to form the homomorphic and biological plessist genomes. These are Meme 5.

- “Plemes”. The meme-like traits, features, behaviours etc. that plessists enact, out in the biology globe, so they can interact both with each other and with their surroundings to homeomorphically maintain the recurvatures that produce  $\pi$ . They are Meme 6.
- “Plesseomes”. The homomorphic group gene pool of all the molecules in all the genomes of all the plessists maintaining  $\pi$ , along with a suitable distribution. Each normalized individual contribution is  $\gamma$ . Meme 7 then defines these plesseomes as multiple copies of  $\gamma$ .
- “Plessetope”. The corporate plemes representative of the plesseomes, and so creating the group homeomorphism of doubly recurvative interactions that maintains  $\pi$ . Each normalized individual contribution is  $\psi$ . Meme 8 defines these plessetopes as multiple copies of  $\psi$ .
- “Plessemorph”. The singular archetypal entity embodying both  $\gamma$  and  $\psi$  as its net set of activities  $\lambda$ ; and so that  $n$  of them are both homomorphically and homeomorphically identical to, and representative of, all the  $n$  plessists, their plessiomes, and their plemes as maintain  $\pi$ , which they do by acting as  $n\lambda$ . The plessemorph is thus a singular and doubly closed entity. It is Meme 9.

Our plessemorphs define our doubly closed bijective biological equilibrium,  $\pi$ . They have homomorphic plesseomes. They interact homeomorphically both with each other and with the surroundings. They use their plessetopes to recurve, and so to recreate a matching set of preimage and progenitor domain, plus image and progeny codomain. These neither grow nor shrink, but maintain a stable state. This is a set of biological activities,  $\lambda$ , resulting from both  $\psi$  and  $\gamma$ . We can always replace a given number of plessists with a given number of plessemorphs whose behaviour across globes and domains is identical. This is so by definition in our model.

**II.2.8** As a part of Memes 4 to 9, we can additionally think of our plessists and/or plessemorphs as constituting a first set,  $A$ . The material plessiomes and/or plesseomes that create them then constitute a second set,  $B$ . Their energetic and interactive plemes and/or plessetopes constitute a third set,  $C$ . We then consider the mappings:  $\phi:A \leftrightarrow B$ ,  $\phi:A \leftrightarrow C$ , and  $\phi:B \leftrightarrow C$ .

**II.2.9** We can now take a first set of plessists  $a_1$  in  $A$ . We can substitute for them a set of plessemorphs  $a_a$  in  $A$  that, by our model, behave identically.

Those  $a_1$  plessists have the plessiomes  $b_1$  in  $B$  ... which again behave identically to our plesseomes  $b_a$  in  $B$ . And our plessists use the plemes  $c_1$  in  $C$ ; for which we can substitute the plessetopes  $c_a$  in  $C$ .

We can then take the two sets of Cartesian products  $A \times B \times C = \{(a, b, c) \mid a \in A, b \in B, c \in C\}$  where we have the usual ordered pairs. We therefore get  $(a_1, b_1, c_1)$  for our plessists, interacting through their plemes and plessiomes; and  $(a_a, b_a, c_a)$  for their equivalent plessemorphs which replicate

them precisely by interacting through their plesseomes and plessetopes. This is again so, by definition, in our model.

**II.2.10** The  $a_1$  plessists and their equivalent  $a_a$  plessemorphs can now interact with and transform each other using both the surroundings and their  $\delta$  sets of Chomsky production rules of syntax and semantics to produce further sets in  $A$ ,  $B$ , and  $C$ . We therefore have parallel sets of plessist and plessemorph transformations. Our plessists replicate their  $A$ ,  $B$ , and  $C$  sets so that  $a_1 \rightarrow a_2$ ,  $b_1 \rightarrow b_2$ , and  $c_1 \rightarrow c_2$ . The plessemorphs replicate them so that  $a_a \rightarrow a_b$ ,  $b_a \rightarrow b_b$ , and  $c_a \rightarrow c_b$ . Their  $\lambda$  biological and ecological activities occur through their plessiomes and plesseomes which map through  $\gamma$  as  $b$  in  $B$  with all  $b_1$ s mapping identically through  $b_a$ s; and with the plessist and plessemorph effects in the surroundings, and on each other, occurring through their pleme and plessetope behaviours mapping through  $\psi$  as  $c$  in  $C$ , the  $c_1$ s again being identical to the  $c_a$ s. The  $a_1$  plessists thereby replicate an  $a_2$  set; with the plessemorphs equivalently replicating an  $a_b$ , with all the  $b$ s once again being identical in their effects to all the  $2$ s that replace the  $1$ s. Those interact with the surroundings as  $a_2$  and  $a_b$  in  $A$ , using  $b_2$  and  $b_b$  in  $B$ , and  $c_2$  and  $c_b$  in  $C$ , through the same biology-ecology of  $\lambda$ , mapping as  $\gamma$  in  $B$  and  $\psi$  in  $C$ . These also contribute to the fibration,  $\theta$  and cofibration,  $\rho$  so that we will eventually have replicated replacements of  $a_3$  and  $a_c$  in  $A$ ,  $b_3$  and  $b_c$  in  $B$ , and  $c_3$  and  $c_c$  in  $C$ , again preserving equivalences in mappings of  $\gamma$ ,  $\psi$ ,  $\lambda$ ,  $\theta$  and  $\rho$  through the same Cartesian products over the same three sets  $A$ ,  $B$ , and  $C$ . The latter can substitute for the former at every point.

**II.2.11** This is all clear, precise, and tightly defined. All we have to do now is relate one or the other of our plessists and/or plessemorphs  $a_1$  and  $a_a$  to some real and existent biological phenomena. For that, we can turn to topology.

**II.3.1** We now have our plessists and plessemorphs and their various  $A$ ,  $B$ , and  $C$  sets and production rules. They recur in our two globes, using their biological–ecological relations  $\lambda$ , made up from their energetic plemes and plessetops  $\psi$ , and their material plessiomes and plesseomes,  $\gamma$ . The latter can again substitute for the former in every conceivable situation.

**II.3.2** Nothing underscores the need for the careful approach we adopt here than the circumstances surrounding René Thom (Johnson 2002). Winner of a Fields medal, his principal mathematical fields were “cobordism” and “catastrophe theory”. He coined the word ‘attractor’, and was the most famous and influential of those who introduced biologists to topology (Thom 1969). His work proved influential not just in morphology, but also in the study of punctuated equilibria. His *Structural Stability and Morphogenesis* (1989) pointed out that even though natural phenomena are always subject to perturbations, they can nevertheless be represented by gradually changing forces. So in spite of all developmental changes, morphological phenomena preserve a basic identity. What was exciting to biologists was that small but continuous changes in parameters could produce significant qualitative ones. Such was the power of Thom’s mathematically accurate formulations that there was no need to know the underlying physical mechanism for even the most abrupt and discontinuous of transformations. A simple mathematical description subsumed even the most complex of physical processes.

**II.3.3** Biologists and mathematicians both classify objects into groups. But while Thom might have brought with him a very strict and mathematically coherent understanding of how mathematicians used the term, he was now working amongst people whose standard for providing definitions was considerably more relaxed—to say the least—than his own. By his own admission, however, that was precisely the reason he left pure mathematics:

... I had nothing new to offer. That made me leave the strictly mathematical world and tackle more general notions, like the theory of morphogenesis, a subject which interested me more and led me towards a very general form of ‘philosophical’ biology (Thom 1958).

Some biologists, such as Francis Crick, dismissed Thom for criticizing the lax usage he came across. They instead criticized him in return for “not really understanding” how science worked (Johnson 2002). But they in their turn never saw the importance of emulating the utmost care that mathematicians and physicists take in, for example, defining velocity and acceleration ... never mind homomorphism and homeomorphism. It is, however, precisely those careful definitions that make the rudiments of both dynamics and topology appear so “simple” that the rigour they insist on is trivialized by deeming biology so complex, a similar search for clarity is inappropriate.

**II.3.4** Much like species, different mathematical groups behave in different ways. Thom's understanding came directly from the tradition of the French mathematician Évariste Galois who was the first to use the term group in relation to equations such as:

$$x^2 - 4x + 1.$$

Galois pointed out that all constants form a first group; coefficients a second; variables a third; and powers a fourth. The different groups thus exhibit different production rules.

“Group theory” now refers, more broadly, to the theory of symmetry. This means virtually any activity subject to any kind of repetition. For that reason, its logic undergirds all scientific inquiry. All scientific laws are governed by group theory.

Group theory is the search for—and mathematical formulation of—internal consistency. It declares an invariance in objects. We are now searching for the internal consistency that drives our plessists and plessemorphs.

Group theory tells us, on this basis, that the above equation's two solutions form the two groups  $A = 2 + \sqrt{3}$  and  $B = 2 - \sqrt{3}$ . Bringing them together into a single group establishes a pattern of invariance. Their group behaviour is that even though  $2 - \sqrt{3} \neq -\sqrt{3} - 2$  and  $2 \div \sqrt{3} \neq \sqrt{3} \div 2$ , all similar algebraic equations with rational coefficients will always have  $A + B = B + A$ , and  $AB = BA$ . This “Galois group” forms cyclic permutations of order two. We note carefully those forwards and backwards operations, which are effectively recurvatures. They have the same result, no matter what the direction.

**II.3.5** Both the above groups  $A$  and  $B$  enjoy a joint identity that leaves them untouched when transposed. And that statement about identity is critical. It is a concept utterly lacking in biological groups. What, after all, do biologists imply when they assert that a given group is “female”, never mind that another forms a “species”? Some organisms alternate sexes in generations; others invert male-female sizes and capabilities; yet others do not have either male or female reproductive parts; yet others still develop them according to circumstance; and so on and so forth for a bewildering variety. And without a clear identity even for specifying female, what hope for species?

**II.3.6** Biology's failure to formalize an identity is most surprising, for one already exists. It was early recognized by Robert Hooke, who dramatically developed the microscope and observed microscopic organisms. His *Micrographia* (1665) was the first comprehensive and illustrated book in microscopy. But not being a mathematician, he did not realize his discovery's formal significance, although he did calculate that there must be 1,259,712,000 in a cubic inch (Inwood 2003).

The fuller recognition of the biological significance of cells—via his famous aphorism *omnis cellula e cellula* or “every cell stems from another cell”—did actually come from the pen and mind of Rudolf Virchow (1859). But granted that it was Hooke who first coined the word, then our Meme 10 is to term biology's unipollent-based doubly closed identity—which defines our plessemorphs, and their plesseomes and plessetopes—the “Hooke cell”. The Hooke cell, therefore,

is our rigorously defined unipollent equilibrium and biological archetype. Since it is dynamic it by definition encompasses recurvatures in  $\lambda$ ,  $\psi$ , and  $\gamma$ .

**II.3.7** To see that a Hooke cell is indeed an identity—for it is both homomorphic and homeomorphic—then we first note that  $1 + 0 = 1$ . Zero is an “identity element”. We further observe that we can introduce infinitely many zeros, and it will make no difference to the original:  $1 + 0^{\infty \text{ times}} = 1$ . An identity therefore leaves things unchanged. The clear implication is that we can similarly take species,  $S$ , as some sort of identity,  $S'$ , for our plessemorphs, plesseomes, and plessetopes as produce it. We can reproduce them infinitely many times, and the species remains the same.

**II.3.8** Identities—as do species—allow for replication. Thus zero, as an “additive identity”, also allows us to replicate its operative groups. We see this clearly in  $3 + 0 + 0 + 0 = 3$  and  $2 + 0 + 0 = 2$ . If we now count up all the inserted identity elements, they will reproduce the implied  $2 + 3 = 5$  as  $5 + 0^5 \text{ times} = 5$ . The inserted identities have replicated the originals, leaving them unchanged. This holds for any  $x$  and  $y$ . An identity immediately allows the production rule and mapping  $\phi: X \rightarrow X$  leaving everything the same. Much more importantly, identities allow for symmetry operations for they leave aspects invariant through transformations.

This operation of addition and its additive identity allows us to note that if we for example take  $n = 6$  and consider the “binary operation” of addition modulo 6, we form the cyclic group  $\mathbf{Z}_6 = \{0, 1, 2, 3, 4, 5\}$ . This simply means that if we consider that first element of ‘0’, then the numbers ‘6’, ‘12’, ‘18’, ..., all leave zero remainder when divided by 6. And since all numbers divisible by 6 behave this same way, we can group them together as a “cyclic subgroup”.

If we now add any members of this cyclic subgroup to each other, we get 0, because  $6 + 12 = 18$ , all three of which are divisible by 6. Since this is the same for all such numbers, then the group generated by this operation by element 0 in  $\mathbf{Z}_6$  is  $\langle 0 \rangle = \{0\}$ . In other words, we can do this infinitely many times— $24 + 36 + (n \times 120)$ —and only ever generate—or replicate—the group identity.

The number 11, on the other hand, leaves a remainder of 5 when divided by 6, which is the last member of the  $\mathbf{Z}_6$  cyclic group. The numbers 17, 23 etc. all leave that same remainder. They can all therefore be classed as members of the same cyclic subgroup.

If we now add any member of this latest cyclic subgroup to any other member, we get the equivalent of  $5 + 5 = 10$ , which leaves a remainder of 4. And if we now add that remainder to any member of this same subgroup, we get  $4 + 5 = 9$ , which has a remainder of 3. And if we then add whatever remainder we get successively to each member of this same subgroup, then we get 2; then 1; and we eventually finish up with a number divisible by 6. So using 5 as a generator, we step through—or replicate—all elements in this  $\mathbf{Z}_6$  cyclic group to give  $\langle 5 \rangle = \{5, 4, 3, 2, 1, 0\}$ .

The numbers 4, 3, and 2 in  $\mathbf{Z}_6$  are very different. When we for example add 4 to any other element in its same cyclic subgroup, we get  $4 + 4 = 8$ , which is a number whose remainder

is 2, modulo 6. And if we add that remainder, yet again, to any member of this same subgroup, we get a number divisible by 6, which is zero, so giving  $\langle 4 \rangle = \{4, 2, 0\}$ . We have this time only generated a limited selection in  $\mathbf{Z}_6$ . We see the same limited generation capacity in  $\langle 3 \rangle = \{3, 0\}$  and  $\langle 2 \rangle = \{2, 4, 0\}$ .

We can, however, once again generate the entirety of  $\mathbf{Z}_6$  if we consider 7, 13, 19, etc, which all leave a remainder of 1 modulo 6. If we add any two of these subgroup members together, we get something like  $13 + 19 = 32$ , which is modulo 6 equivalent to  $1 + 1 = 2$ . And if we now add that 2 remainder to any other member in this same cyclic subgroup, we get something with a remainder of 3; then 4; then 5. So we again generate the entire set, to give  $\langle 1 \rangle = \{1, 2, 3, 4, 5, 0\}$ .

There will always be two members in any such cyclic group that will form cyclic subgroups such that they generate the entire group. We shall soon see that all biological entities form infinite, rather than finite, cyclic groups and subgroups of exactly this kind.

**II.3.9** A similar identity and replication pattern gives us  $1 \times 1 = 1$ , with unity now being the “multiplicative identity”. We can again insert it infinitely many times, making no difference to the original, as in  $1 \times 1^{\infty \text{ times}} = 1$ . And if we insert it an appropriate number of times it becomes a replicator for we can turn both  $3 \times 1 = 3$  and  $2 \times 1 = 2$  into  $3 \times 1 \times 1 \times 1 = 3$  and  $2 \times 1 \times 1 = 2$ . We have successfully reproduced the implied  $6 \times 1^{6 \text{ times}} = 6 \dots$  while leaving the original utterly untouched. This holds, as above, for any  $x$  and  $y$ . We get similar cyclic groups, subgroups, and generators. We have confirmed an important identity–replication production rule.

**II.3.10** Integration and differentiation are admittedly slightly more complex, but the same principles apply. Leonhard Euler realized the full consequences of  $e$  being the exponential identity element for such operations. We can express any initial function  $f_1(x)$  and its differential  $dx$  as some second function,  $f_2(x)$ , that is then a power of  $e$ . For example,  $1/x = 1/e^{\log_e x} = 1/e^{f_1(x)} = 1/f_1'(f_2(x)) = f_2'(x)$ . We can replicate this infinitely many times, as ever leaving the original unchanged. There are similar cyclic groups and subgroups. So as we can with the above identities and cyclic groups, we can always generate the original and therefore replicate it any number of times, both always leaving the original unchanged and generating the entire group.

Euler’s discovery is extremely useful biologically. It helps guarantee both homo- and homeomorphisms. We can express any growth or development continuously and exponentially as a range between 0 and 1, or between “unit limits”. We can therefore evaluate any organism by recasting its behaviours as a “unit expression”, and/or inserting that unit expression appropriately many times into a suitable equation, while, as ever, leaving the original unchanged.

We are well on the way to replicating any biological phenomenon by expressing its rate of change between 0 and 1. It then matches the unipollent. We can compare the two and determine pollencies in terms of injective and surjective behaviours. We can also repeat it an arbitrary number of times, and it remains unchanged. We can therefore use it to carefully define our needed four-

dimensional biological equilibrium, as well as find and define our infinite cyclic groups and subgroups.

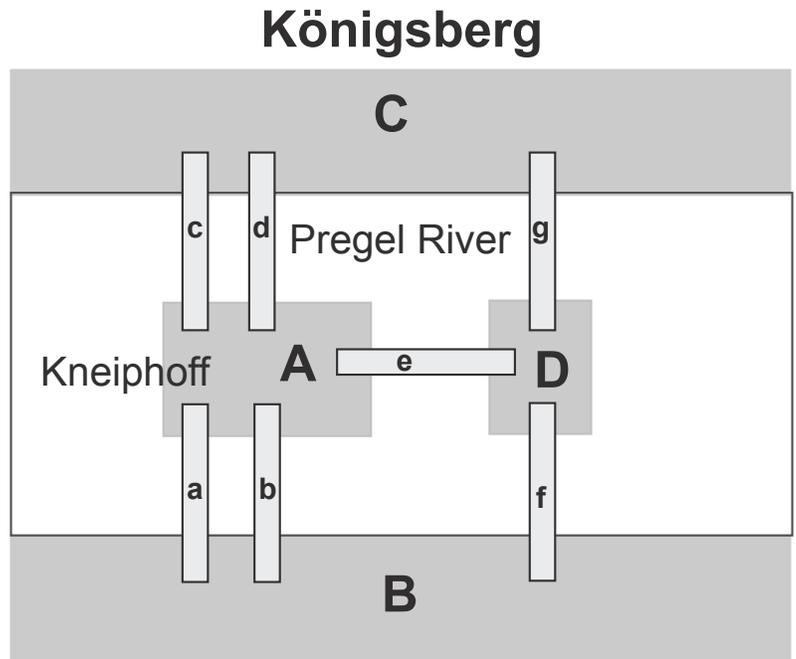
**II.3.11** A big problem would seem to be that even if we can separate the biological from the replicative, the globes can vary very greatly across the generations. But it is also thanks to Euler that a topological identity and invariant to resolve this came to exist. It is now known as the “deformation retract”. As in Figures 1, 4 and 5, it allows us to manipulate any object—in our case between and/or within our replication and/or biology globes—without losing any of its essential characteristics. The points simply create infinite cyclic groups and subgroups.

**II.3.12** Topology began in earnest in 1735 when the mathematician and astronomer Carl Gottlieb Ehler presented Euler with the then unsolved problem of the “Seven Bridges of Königsberg” shown in Figure 4. Euler famously solved it using a variant of the

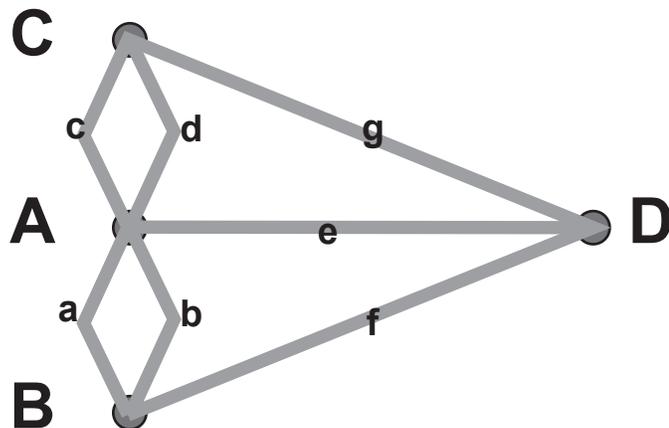
network or stylized map in Figure 5. He had realized that each landmass is homeomorphic. Since the number of points in each is irrelevant, each can be—homomorphically—regarded as a single point ... but each can, for that same reason, be replicated an arbitrary number of times, leaving the original unchanged. This means each can be regarded both as a single point, and an arbitrary collection of such points, irrespective of sizes or shapes.

Topology discusses the relationships between groups and sets of points. Euler proved that when all similar groups of objects—both homomorphic and homeomorphic—are expressed as sets, then they have an “Euler characteristic”. In this Königsberg case the sets are landmasses that form sets

**Figure 4: Königsberg Bridge problem**



**Figure 5: Euler's Königsberg Bridge problem solution**



of homomorphic vertices,  $|V|$ ; the bridges form homeomorphic edges,  $|E|$ ; and the areas between them form homeomorphic faces  $|F|$ . The relevant production rule for an Euler characteristic is:

$$\chi = |V| - |E| + |F|.$$

The Königsberg bridge case gives  $\chi = 4 - 7 + 4 = 1$ .

Euler had thus elucidated the four important topological principles that:

- I. the number of vertices is critical;
- II. each bridge's length is irrelevant;
- III. landmass sizes and shapes are irrelevant;
- IV. each landmass can be reduced to a single vertex.

Topology's deformation retract is implied by III and IV. If two objects are topologically identical then they will have the same Euler characteristic. This means the same production or replication rule.

Since “fixity of shapes” (note similarity to “fixity of species”) is irrelevant in topology, then we can both homomorphically and homeomorphically replicate any object, leaving the original unchanged. We can add—and remove—infinately many points to, and from, the edges, and/or the faces, of any figure or network without affecting any of its essential properties.

**II.3.13** Since we are particularly concerned with biological reproduction—which particularly involves cyclic groups and subgroups—then we most carefully note that we cannot proceed randomly. Simply having the same Euler characteristic does not automatically mean two objects, as sets of points, are topologically identical. A tetrahedon, a cube or hexahedron, an octahedron, and a dodecahedron are very different, but they all have  $\chi = 2$ . Not all globes and generations, therefore, need be the same.

If we have an original set of points  $X$ ; and a subset  $Y$ ; if we use an index,  $i$ , to range a map,  $M_\lambda$ , between them; and if every element  $x$  in  $X$  maps to some  $y$  in  $Y$  as we range that index between  $i_0$  and  $i_1$ ; then we can only preserve homeomorphism, amongst those points, if subset  $Y$  is the deformation retract of  $X$ . However, since two groups of points can have the same Euler characteristic  $\chi$  without being topologically equivalent, then as in the Königsberg Bridge problem, we must specify that our mapping,  $M_\lambda$ , is the continuous  $M_\lambda: X \times [0, 1] \rightarrow X$ , with  $M_\lambda(x, i) = m_i(x) = 0$  to  $m_i(y) = y$  for all  $y$  in  $Y$ , and from  $i_0(X) = 0$  right through to  $i_1(X) = Y$ . The two will now have the same Euler characteristic, such that  $\chi(X) = \chi(Y)$ .

But we additionally preserve homeomorphism in the above case because the  $i_0$  is mapping  $i_0(X)$  directly onto  $i_0(Y)$ . That is the identity map that guarantees they are homeomorphic.

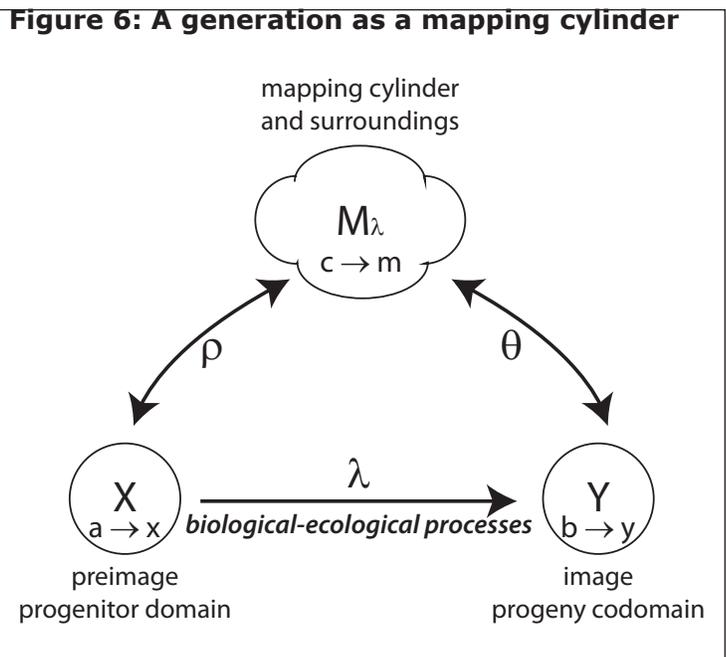
The deformation retract is the special, contained, identity map equivalence. It helps guarantee that both our syntax and our semantics have stayed the same in the resulting production rule, and no matter what transformations our biology and replication globes might go through.

**II.3.14** If we represent our group operation, much more generally, by  $\circ$ , then we can say, equally generally, that any set or group,  $X$ , has the identity property, under that particular operation,  $\circ$ , if an

element,  $\#$ , exists that leaves every other element  $x$  in  $X$  unchanged, and such that both  $x \circ \# = x$  and  $\# \circ x = x$ , again for all elements  $x$  in  $X$ .

As we did with  $1 + 0^\infty \text{ times} = 1$  and  $1 \times 1^\infty \text{ times} = 1$ , we can now use  $\#$  as an index into all the  $x$  in  $X$ , as  $x \circ \#^x \text{ times} = x$ . We can now replicate any  $X$  as a  $Y$ . There will then be a  $y$  in  $Y$  for every  $x$  in  $X$ , with  $\#$  guaranteeing that identity.

An identity's ability to replicate any group is the aspect of especial relevance here. It is how we can use a Hooke cell to guarantee the reproduction of identical objects.



**II.3.15** As in Figure 6, the deformation retract and mapping cylinder work together. If  $X$ , as a preimage, maps to  $Y$ , as an image, using the proposed biological-ecological process  $\lambda$ , then a mapping cylinder  $M_\lambda$  exists to describe that process. We can also conceive of it as the interaction with those same surroundings.

If  $Y$  now has a set of combined internal and external operations,  $\theta$ , that allow it to access neighbourhoods in its mapping cylinder,  $M_\lambda$ , then  $X$  can in its turn use its identity,  $\#$ , to map to those self-same neighbourhoods in that same mapping cylinder. In other words,  $X$  can use the surroundings,  $M_\lambda$ , to replicate  $Y$  ... which then appears as if a set of biological-ecological operations,  $\lambda$ , have seemingly carried  $X$  directly into  $Y$ , as the group operation,  $\circ$ . One of those operations is with the mapping cylinder, the other is without. One is a direct and intrinsic transformation, the other an indirect and extrinsic one.

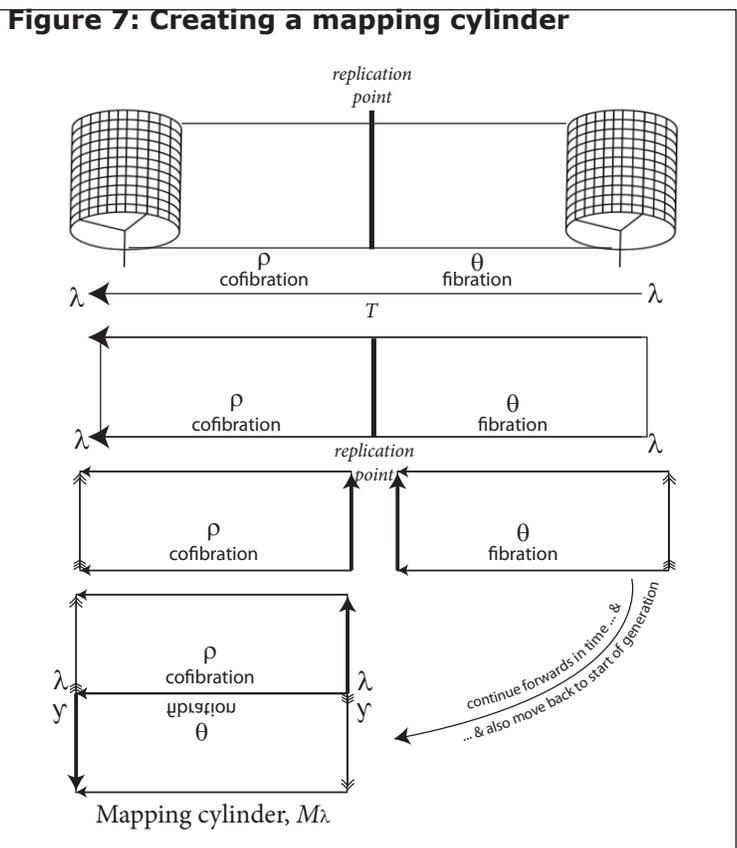
The operation that “lifts” from  $Y$ , as the image, to the mapping cylinder is its fibration,  $\theta$ . It means that there exists a continuous function between  $Y$  and  $M_\lambda$ —or the surroundings—so that given a point  $y$  in  $Y$  and a unit path  $[0,1]$  that started at some point  $b$  in  $Y$  to reach  $y$ , then that path can be lifted to one starting at some  $c$  in  $M_\lambda$ , and that goes faultlessly to  $m$  in  $M_\lambda$ , over that same 0 to 1 range.

The  $\rho$  that similarly lifts from the preimage  $X$  to that same mapping cylinder  $M_\lambda$ , over the same range and in the same fashion, and so from  $a$  to  $x$  in  $X$  to give the same  $c$  to  $m$  in  $M_\lambda$ , is its “cofibration”. Each of  $a$ ,  $b$ , and  $c$ , and  $x$ ,  $y$ , and  $m$ , respectively, are equivalent over all those equally equivalent unit expressions.

And if  $X$  now uses  $\lambda$  to directly map to  $Y$ ; and if  $Y$  is indeed a deformation retract—which we can express equivalently as  $\#$  or  $S^\circ$ —for the mapping cylinder,  $M_\lambda$ ; then a cofibration,  $\rho$ , again exists such that  $M_\lambda$  can accept a mapping from  $X$ ; and with  $Y$  then mapping, with its fibration,  $\theta$ , to

those same points in  $M_\lambda$ . The surroundings are again permitting that transformation.

And alternatively ... if a cofibration  $\rho$  exists that can ostensibly replace the biology-ecology of  $\lambda$  ... then a mapping cylinder,  $M_\lambda$ , must also exist that regards  $Y$  as its deformation retract, complete with a  $\theta$  fibration. The mapping from  $X$  to  $Y$  through  $M_\lambda$ , using  $\rho$ , can now substitute for  $\lambda$  in all possible situations; and with  $Y$  also being able to map to  $M_\lambda$  through  $\theta$ . We have now suitably redefined all  $a_a$ ,  $b_a$ , and  $c_a$  plessemorph, plesseome, and plessetope behaviours in  $A$ ,  $B$ , and  $C$  both (a) directly between  $X$  and  $Y$  as a set of replicative operations; and (b) indirectly through the biology and ecology of the surroundings, as  $M_\lambda$ . They can therefore, and at any time, substitute for our  $a_1$ ,  $b_1$ , and  $c_1$  plessists, plessiomes and plemes; and conversely.



**II.3.16** We somehow have to separate the purely biological transformations from the ones that, while also biological, are additionally replicative. Figure 7 shows how we can do this using such a mapping cylinder. We simply separate the temporal issues of traversing a generation from the more structural biological-replicative and transformational ones. We can do this in four dimensions because they are simply different directions.

**II.3.17** We first consider the more familiar three-dimensional case. Since any sphere contacts any lower and two-dimensioned planar surface in a single point, then a cylinder of specified volume and radius can substitute for that same sphere at that contact point. The two are indistinguishable, again at that point. This holds all about any circulation or orbit. This holds throughout our three-dimensional “realm”, with its three  $x$ ,  $y$ , and  $z$  dimensions.

As in Figure 7, when an ordinary three-dimensional chariot wheel or cylinder, as substitute for some globe’s contact point, rolls along a two-dimensional surface, we get a rectangular trail. We have both a beginning and an end to the generation.

We then take up that resulting rectangle. The replication point sits in the middle. This simply means that the first part, our fibration, leads up to that point; while the second half, our cofibration, leads away. The two match in that since our overall biological-ecological operations

are  $\lambda$ , we now have  $\lambda = \theta + \rho$ , with the replication point acting as their combination. It effects their transition. They together carry the population through the biology and replication globes for a generation.

We now create our  $M_\lambda$  mapping cylinder by cutting that rectangle in two at that replication point. Neither  $\theta$  nor  $\rho$  lose their ability to generate  $\lambda$ . No more so do the biology and replication globes. They can both still—together—generate the whole of  $\lambda$ .

We then reattach the half-rectangle we get as shown. Since neither of the biology and replication globes has lost its individual abilities, they simply create a different interfacing combination. Each of their activity sets still leads to and away from their new junction. We are simply focusing on different aspects of these same phenomena. We can still move forwards in time, and so to the beginning of a new generation. We can still move in that direction along the arrow in the middle.

We also now have a Möbius strip. We can use it, with its rearranged infinite cyclic subgroups, for our recursive functions. They still allocate both the fibrations and cofibrations, and the biology and replication globes, to the same  $\lambda$  through the interfaces to have the same effects in the surroundings. They still generate the original infinite cyclic group. We can again easily get the original generation back. Furthermore, these are our plessists and plessemorphs that we created with our identity operations, leaving the originals untouched, so that nothing in the real world has changed.

**II.3.18** We can now step up a dimension. We can at any time consider our four-dimensional and biological hyperglobe to instead be a “cubinder” or “hypercylinder”—the four-dimensional equivalent of a chariot wheel or tire—that contacts our three-dimensional “realm” at our precise location. A cubinder is simply a four-dimensional cylinder. As it rolls through our three-dimensional realm, it leaves behind it not a rectangle, but a cube.

We can use the resulting cube to create a mapping cylinder, for our interactions. We cut the resulting cube in two; twist it about; and then reattach it. We reorganize our various cyclic subgroups. We also create a Klein bottle.

**II.3.19** We can now think of the biology and ecology of our identity-plus-deformation retract to mapping cylinder-plus-surroundings interaction as an expression of this cyclic subgroup rearrangement. We have a bounding but four-dimensional biology-replication transformational globe interface. It stretches across that mapping cylinder. It identically replicates the more familiar temporal-generational one when it contacts our three-dimensional realm.

If we now use the identity, or deformation retract, as a mediator for all  $\lambda$  interactions in the surroundings, then we can regard any two successions of biological elements as one of preimage to image, and image back to preimage. A generation is a set of productions that deform, directly and successively, into each other across the Möbius strip or Klein bottle through  $\rho$ . Those elements still use the surroundings as a mapping cylinder. They still map directly from  $X$  to  $Y$ . They have successively accessed each other through  $\theta$  and  $\rho$ , still guided by the same mapping cylinder as

before, and by the same deformation retract. They have still processed in the same surroundings, over the same stretch of absolute clock time, for the same complete generation, and using the same set of biological-ecological activities,  $\lambda$ .

Our progenitor to progeny or  $X$  to  $Y$  four-dimensional and recursive function production still appears as the same set of correctly constituted forwards-directed three-dimensional  $\lambda$  loops emerging through our cylinder and biosurfaces,  $S$ . The loops they provide still appear as if they have been produced directly by—and as—the entities concerned. Those production rules can recurve as all the needed progeny-to-progenitor and reversing transitions, and as if through the fibrations and cofibrations  $\theta$  and  $\rho$ , so creating all identical events in biology and ecology. We can now examine both sets of interfaces—the familiar temporal one and the unfamiliar atemporal one—much more closely.

**II.4.1** Now we know the rules and have some clear terms, we can easily define biological reproduction as a suitable recurvature. Our plessists will then respect both homomorphism and homeomorphism, as well as that change of boundaries that creates our mapping cylinders and deformation retracts. We can also soon redefine reproduction as both (i) our cofibration,  $\rho$ , plus mapping cylinder,  $M_\lambda$ ; and (ii) our Hooke cell, or deformation retract,  $S^*$ , plus its fibration,  $\theta$ .

**II.4.2** As our first step in defining our mapping cylinder and its Möbius strip, we formally recognize, for Meme 11, our Hooke cell's ability to pass first into, and then through, both of our replication and biology globes, and so our infinite cyclic groups and subgroups.

We can rigorously define this capability by noting that the plessists that create our doubly closed  $\pi$  equilibrium must undertake a suite of reversible fibration–cofibration metabolic and physiological processes. More specifically, this must be a set of activities that always appears to bound a region of activity and so potentially seems to create a trivial cycle, but that can nevertheless have a velocity and an acceleration that carries it all about both globes.

We can attain our ambitions if we characterize one set of activities as internal and so semantic. These are our biovolumes,  $V$ . We can then characterize the other as external and syntactic. Those impinge upon the surroundings through our biosurfaces,  $S$ . These are then our needed recurvature and invertible interactions involving the boundary between our biology and replication globes.

**II.4.3** We can use the homeomorphism, and the surroundings, to define our homomorphism, and so our deformation retract. We represent one globe and its infinite cyclic subgroups with  $x$ ; another with  $y$ . We simply say that when our plessists surrender any initial atom or joule,  $x_{-1}$  or  $y_{-1}$ , through their surface,  $S$ , they immediately take up another of exactly the same type, through that same surface, as  $x_1$  or  $y_1$ . Since homomorphism demands that the structure remain identical, then these recurvature replacements  $x_1$  and/or  $y_1$  precisely replace the  $x_{-1}$  and/or  $y_{-1}$  ones that departed, passing through the surface, and where  $x_{-1} \equiv x_1$  and  $y_{-1} \equiv y_1$ . Our cyclic subgroups thus regenerate the identical infinite cyclic group and volume,  $V$ , which then has the identical relationship to its subgroups and surface.

We now call the input point that achieves our recurvature replacement  $+r$ , its output  $-r$ . And since they must both be both homomorphic and homeomorphic, then they are together both (a) the homomorphic point  $S_0$ ; and (b) the homeomorphic “pointspace”  $V_0$ . At the end of some given period,  $T$ , our Hooke cell has enacted our unipollent  $S_0$ – $V_0$  process with its  $(x_{-1}, y_{-1}) \rightarrow (x_1, y_1)$  production rule to replicate itself.

This exchange of  $x$  and  $y$ , through  $+r$  and  $-r$ —whether as single and direct homomorphic point  $S_0$ , or the recurvature capable homeomorphic pointspace  $V_0$ —is our identity process,  $\#$ . Each Hooke cell leaves both itself and its surroundings utterly unchanged, for we by definition have both  $x \circ \# = \# \circ x = x$ , and  $y \circ \# = \# \circ y = y$ . And since this is a clearly defined identity operation involving our mapping cylinder,  $M_\lambda$ , then the end result is in all respects identical ... save only for being composed

of a completely different set of both joules and chemical components. Our Hooke cell has been both homomorphically and homoeomorphically recurved and transformed using fibration, cofibration, and a mapping cylinder. The Hooke cell—which by definition incorporates both (a) some time period,  $T$ , and (b) an entire suite and cycle of activities—is therefore our deformation retract. The surroundings are also and by definition its mapping cylinder,  $M_\lambda$ .

We can express this in a more useful fashion. We note that our Hooke cell undertakes both a fibration and a cofibration as it goes through its recurvature involving both  $x$  and  $y$ .

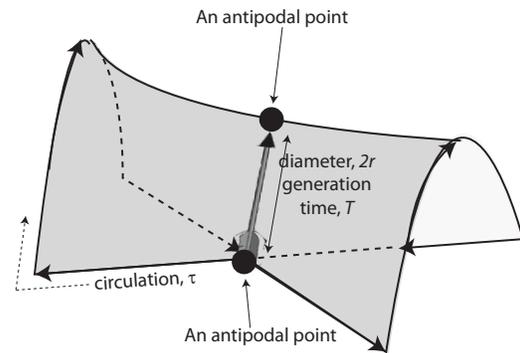
Since the Hooke cell is an identity, involving the biology and replication globes, then it also allows us to reconstruct any arbitrary biological entity as a plessist ... whilst all the time leaving the original unchanged. Since a cyclic subgroup can generate every element in its group, then for every molecule and photon we extract we insert an identical one; and for every one we insert, we extract an identical. We can therefore generate the original, leaving it unchanged. And since, for every  $x$ , there is both a  $+y$  and a  $-y$ ; while, for every  $y$ , there is both a  $+x$  and a  $-x$ ; then we are more technically demanding that this Hooke cell be an irreducible and real analytic set, which is never singly pure-dimensional.

**II.4.4** Figure 8 shows a “Whitney umbrella” (Weisstein 2015c) with exactly these properties. Named for its discoverer, the US mathematician Hassler Whitney, it is a ruled surface for it can be generated by a straight line moving up and down. It has an Euler characteristic  $\chi = -1$  and establishes a “pinch point” (Weisstein 2015b). It can open out to reveal its  $+r$  and  $-r$  properties, as the pointspace,  $V_0$ ; while still also collapsing to become a single pinch point,  $S_0$ . This is therefore an  $S_0-V_0$  coupling. As required, it leaves everything identical.

Meme 12 is now to recognize that the same Whitney umbrella and its  $S_0-V_0$  pinch point can be in different states. It can be distinct  $-r$  and  $+r$  “antipodal points” as its contrasting but homomorphic attributes go through their homeomorphic cycles. But since each antipodal pinch point  $V_0$  pairing can retract to a single  $S_0$  one, then all such  $+r$  and  $-r$  opposites are in some respects the same. Each antipodal point plus the  $2r$  distance between them forms a triplet that is simultaneously a singlet. It can exchange both  $x$  and  $y$  with the surroundings, but act as a single  $+r-r$  unit.

Figure 8’s recurvature creates a rectangle of specified size. And when observed in three dimensions, that rectangle passes through itself. Since it is created by a straight line both moving up and down and circulating about, then it is composed of two different sets of “field principles”:

**Figure 8: A biological generation as Whitney umbrella & self-intersecting ‘pinch point’**



The self-intersection distance for antipodal points is measured as both (1)  $T$  (along the diameter); and (2)  $\tau$  (about the circulation). This gives an overall instantaneous biological processing rate of  $dt = Td\tau$ .

- one radial,  $\psi$ , which establishes the diameter,  $T$ , and can provide a velocity;
- and one circulating,  $\gamma$ , which establishes the bound so that can recurve.

The rectangle when acting as a pinch point can either go directly from preimage to image or vice versa as  $\lambda$  over  $T$ ; or it can circulate about by using its fibration and cofibration,  $\theta$  and  $\rho$ .

**II.4.5** The first field principle in our Whitney umbrella,  $\psi$ , is structural. It is homomorphic. It is radial and radiative, directly linking the two discernible  $+r$  and  $-r$  points. They have opposite but attracting properties. They together create the central pinch point over  $T$ . One is a net donor, and so positive; the other a net recipient, and so negative, with the one therefore attracting the other.

Since this first radiative principle involves an interaction with the surroundings, then it has a syntactic biological and surface effect in time. We therefore define it via the measurable force it exerts with its two opposites. This is via whatever material objects we find at the destination. Their direction of action is set by the direction of the force that a first object exerts upon any second. The quantity is determined from those effects that the first has upon the second. This can now easily be from a progenitor domain to progeny codomain, or vice versa. In an equilibrium case, the various cyclic subgroups form the total of zero as well as the cyclic group itself:  $+r - r = 0$ .

**II.4.6** Our Whitney umbrella's second field principle,  $\gamma$ , is spatial. It is circulating and so produces the wind walls and recurves. It is homeomorphic. It is more concerned with defining a suite. But it again links opposite and attracting points, interacting with the surroundings. It is similarly defined via the measurable and cyclical force it exerts in the surroundings.

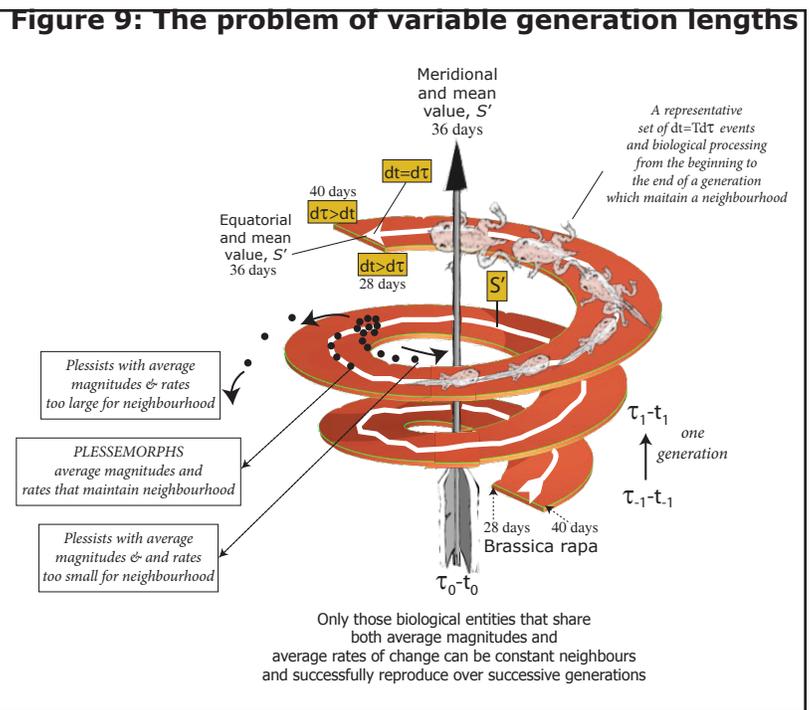
This second spatial and homeomorphic force differs importantly from the first structural and homomorphic one for it binds and couples through spaces to produce that same pinch point. Since only its couplings exist, it produces circular looping fields. It can therefore oversee all progenitor–progeny transformations. The equilibrium case has  $\int dS = 0$ .

Our Whitney umbrella and pinch points create—and are—our plessists. Since our cyclic subgroups produce the cyclic group as  $+r - r = \int dS = 0$ , then they together form a variety of lines, surfaces, and volumes as they interact both with each other and with the surroundings.

We can put this another way. Every point in a Whitney umbrella is located relative to specified others close to it in its neighbourhood ... but each simultaneously displays its antipodal values relative to given others and their antipodal neighbourhoods. These points and their antipodes are also mutually substitutable for each other in given contexts. Meme 13 is therefore to call this identity pinch point and group operation,  $\circ$  or  $\lambda$ , a “self-intersection”.

Meme 14 is now to recognize that all self-intersections must also have a joint identity element,  $\#$ . All the various infinite cyclic subgroups can always come together to produce zero. But that also means each point can be in at least two different, but equivalent, states to create such a neighbourhood and identity.

**II.4.7** These inevitabilities now permit us to resolve problems of the general kind shown in Figure 9, which is simply a different representation of the same recurvature and pinch point. It is the same irreducible real analytic non-singly dimensioned Whitney umbrella of Figure 8. The circuits about each are the same. The  $V_0$  pointspace based  $+r-r$  self-intersection journey about Figure 8's boundary is exactly an  $S_0$  journey up Figure 9's helicoid. The net sum on that axis is still zero, as also the sum of the surrounding recurvatures.



If we catch hold of either of Figure 9's arrow's tip or tail—of value  $S'$ —and push or pull, then we create or remove helicoid levels ... which are also transfers both directly and as recurvatures between preimage and image; or conversely. Each vertical point on a helicoid is identical to the ones directly above and beneath it, whilst being antipodal to all those diametrically across. The two operations are in all respects identical, with  $S' \equiv \#$ , and  $+r - r = \int dS = 0$ .

Our group members now share both (a) the same average magnitudes,  $S'$ , and (b) the same average differentials  $dS'$  about their pinch points. Since they are both homomorphic and homeomorphic, they use their self-intersections to recreate neighbours, neighbourhoods, antipodal points, and helicoid levels using fibrations, cofibrations, mapping cylinders, and deformation retracts.

Our mapping cylinder is all of the helicoid sitting about the deformation retract, which is again both (a) the central axis, and (b) the white middle track. That spiral helix forms the right helicoid that sums as  $\int dS = 0$ . Those values at its centre create the  $+r - r = S'$  which is the median value about which they oscillate. It is again the axial values.

Memes 15 and 16 recognize that the helicoid and self-intersection diameters,  $T$ , and the circulation distances and helicoid orbits,  $\tau$ , which jointly construct those preimage and image exchanges are not fixed. Dawkins' unacceptably vague "openended" has become the topologically precise homeomorphic declaration that these are always antipodal neighbourhoods linking  $\tau$  and  $T$ .

**II.4.8** We can frame a first hypothesis to explain why *Brassica rapa's* generation length varies between 28 and 40 days: plesists with larger initial magnitudes, which are therefore on the helicoid outside track, must also have smaller rates of change—meaning a longer series of smaller  $d\tau$  increments—across that longer  $T$ . They take longer to self-intersect. Plesists with smaller initial magnitudes, which are therefore on the inside helicoid track, have correspondingly larger rates of

change across a shorter  $T$ —meaning a shorter series of larger  $d\tau$  increments—and so self-intersect the more rapidly. These differences are therefore “variations”.

We can also hypothesize that those behaviours tending to the outer track, which is one set of antipodal points and values, delay self-intersections and so are characteristically female; while those tending to the inner track or opposite set of antipodal points instead advance self-intersection, and so are characteristically male. As members of infinite cyclic subgroups, they together give  $+r - r = \int dS = 0$ . This can be subjected to rigorous testing.

**II.5.1** The true difficulty for our model—as in all biology—lies in placing biological entities into suitable groups—both qualitative and quantitative—that can generate suitably replicative and recurvature behaviours. So our next step, Meme 17—in creating our Möbius strip and the inversion we see in the Whitney umbrella—is to recognize reproduction as the joint fibration–cofibration, and boundary interactions. We also recognize that, irrespective of any apparent differences, it is also the joint interaction between Subpopulations  $M$  and  $N$  upon Figure 9’s inner and outer helicoid tracks. They have an average self-intersection time,  $T'$ . It is the species average state and identity,  $S'$  which constructs the right helicoid. It is (a) the distance up the self-intersection’s midline, and (b) its bounding length; and also (c) the time up the helicoid’s meridian, and (d) the central value about the helicoid track. In *Brassica rapa*’s case, these are all  $T' = 36$  days.

The Möbius strip also arises because entities with lesser initial magnitudes, starting their recurvatures on the helicoid inside track, must compensate with higher rates of change so they can tend towards those with greater initial magnitudes, and that therefore have different recurvature rates. In the same way, those with the greater initial magnitudes, starting their recurvatures on the outside track, must have lower rates of change so they can tend towards those beginning with lesser initial magnitudes. The equatorial  $T' = 36$  days track is, by definition, the equilibrium self-intersecting and recurvature path a Hooke cell would pursue under similar conditions. It is the value we use to add or remove antipodal points and equilibrium helicoid levels.

**II.5.2** Since the recurvature distance,  $\tau$ , about either a self-intersection or a helicoid track is a set of fibration–cofibration activities that go all about a closed path, then it is a “linespace”. It is technically also called a “circulation”. The entire linespace is therefore our circulation of the generations.

The plessists in the progenitor domain will transform from their initial preimage state  $S_{-1}$  to become those in the progeny codomain with the final image state  $S_1$ . Every absolute time interval,  $dt$ , involved will contain a given amount of fibration–cofibration biological processing,  $d\tau$ . The precise amount will depend on the generation length,  $T$ , and will be  $dt = Td\tau$ .

Any two Subpopulations  $M$  and  $N$  will have the set of individual plessiomes, plemes, and rates  $S'_M, S'_N, dS'_M/d\tau_M, dS'_N/d\tau_N, dS'_M/dt_M,$  and  $dS'_N/dt_N$ . Since entities with smaller magnitudes must self-intersect with, and recurve about, those with larger magnitudes, the entities within the subpopulations must maintain rates across the circulation distances  $\tau_M$  and  $\tau_N$ , and the historical epochs  $T_M$  and  $T_N$  respectively. The two rates  $dt_M = T_M d\tau_M$  and  $dt_N = T_N d\tau_N$  link the population circulation distance  $\tau_{MN}$  and absolute time  $T_{MN}$  via  $dt_{MN} = T_{MN} d\tau_{MN}$ .

The necessary self-intersection and recurvature distances again require the Whitney umbrella and Möbius strip. Our two subpopulations  $M$  and  $N$  will have archetypal plessemorphs, plesseomes, and plessetopes that define the right helicoid track, and the Whitney umbrella boundary. These attain their equilibrium state. They share the same production rule. This is the joint magnitudes and rates  $S'_{MN}, dS'_{MN}/d\tau_{MN}$  and  $dS'_{MN}/dt_{MN}$ . All these form a group. Their group operation of  $\circ$  could also be the Chomsky production rule,  $\delta$ .

**II.6.1** The power of group theory is that it is a search not for any particular laws, but simply for a commonality. The symmetries it seeks are not always trivially evident. But they are both universal and nonmetric. They emphasize relationships based on a well-defined invariance.

**II.6.2** Even those biologists who advocate the most strongly for gene supremacy agree that biological groupings are important on at least some level. And similarly, those who advocate for group supremacy agree that even the most widespread of their much beloved sociobiological behaviours can be validly described at both the gene and the individual levels.

**II.6.3** Since our plessists will not be useful unless they can address these group issues, then our Memes 18 and 19 stipulate that our plessists—which form rigorously defined infinite cyclic groups and subgroups—interact with the surrounding world to create their mapping cylinder,  $M_\lambda$ , and deformation retract,  $S^0$ . The two memes also decree that plessists abide by the scientific doctrine endorsed by the Nobel Prize Committee that:

The behaviour of the individual constituents that make up our world—atoms (matter) and photons (light)—is described by quantum mechanics. These particles are rarely isolated and usually interact strongly with their environment” (Class for Physics 2012).

Meme 18 now calls photons ‘Ingredient 3’; while Meme 19 calls atoms ‘Ingredient 4’. We further define Ingredient 3 as the radiative,  $\psi$ , component in our Whitney umbrella. It can now easily supervise the replacements of all Ingredients 4. We then define those Ingredients 4 as the circulating  $\gamma$  component. The two together can now propagate as  $\lambda \dots$  again in the Whitney umbrella, and as its overall presentation. The former,  $\psi$ , follow  $T$ ; the latter,  $\gamma$ , follow  $\tau$ . The two together are  $dt = Td\tau$  which is the overall plessist biological behaviour,  $\lambda$ . This is all so, by definition, and in our model.

All plessists can now act together to form  $\pi$ , thus defining its group of 1s for the doubly closed unipollent equilibrium of plessemorphs, plesseomes, and plessetopes. And ... we now have our non-singly dimensioned and irreducible real analytic but biological-ecological set that can suitably interact with the surroundings.

We have also immediately found our Ingredients 1 and 2. They are our Memes 20 and 21. We confirm them by turning to Lev Ginzburg and Mark Colyvan (2004) who inform us that:

- By the Kleiber allometry, an animal’s metabolism has a 3/4 power ratio to its mass. If a first animal is 10,000 times larger than a second, its metabolic rate is only 1,000 times greater.
- By the Fenchel allometry, maximal reproduction rate is related to body size through a 1/4 power ratio: if an animal is 10,000 times larger, it reproduces at 1/10th the speed.
- By the Bonner allometry, maturation time has a 1/4 ratio. If an organism is 10,000 times larger, it takes 10 times as long to reach reproductive age.
- By the Damuth allometry, average density in a natural habitat is related to body size. If a mammal is 16 times larger, it has 1/8th the numbers per unit area.

- By the Calder allometry, an animal's oscillation in numbers is related to its body size: an animal 10,000 times larger has a cycle 10 times longer.

Metabolism is therefore proportional to body size, with the total per unit habitat being roughly the same across species. Entities of approximately the same size produce approximately equal numbers,  $n$ , of viable offspring so that: "a square mile of horses is the same as the metabolism of a square mile of mice" (Ginzburg and Colyvan 2004).

Our Ingredients 1 and 2 must thus create groups by linking those various hierarchies of times and numbers. They do so as the fibration and cofibration lifts,  $\theta$  and  $\rho$ , to and from our mapping cylinder and deformation retract. And since both of Ingredients 3 and 4 participate in all these interactions, then  $\lambda = (\psi, \gamma, d\psi, d\gamma)$ . Its infinitesimal increments,  $d\lambda$ , lift from the progeny codomain to the mapping cylinder as the fibration,  $\theta$ ; and also from the progenitor domain to the same mapping cylinder as the cofibration,  $\rho$ . This is again so by definition.

**II.6.4** Elisabeth Lloyd's (2012) analysis of biological groupings vis-a-vis natural selection, in her *Stanford Encyclopedia of Philosophy* article "Units and Levels of Selection", provides a useful summary of these intense and heated debates. Since, at each point in time,  $t$ , we must count some  $n$ , then we can complete the earlier Memes 14 and 15 by designating  $t$  as our Ingredient 1, and  $n$  as our Ingredient 2.

**II.6.5** Our Meme 22 now declares that as our plessists occupy the successive points  $\tau_{-1}t_{-1}$ ,  $\tau_0t_0$ , and  $\tau_1t_1$  on either the Whitney umbrella or the helicoid, they must simultaneously create self-intersections and conversely. We refer to their successive fibration and cofibration states between deformation retract and mapping cylinder as  $S_{-1}$ ,  $S_0$ , and  $S_1$  respectively. Their average state over the period is  $S'$ , and is our deformation retract, being also both the helicoid axis and its middle track. It again immediately involves the  $\psi$  and  $\gamma$  quantities of Ingredients 3 and 4 interacting to create the biology and ecology of  $\lambda$  for our plessists and plessemorphs.

If we now refer to the  $\tau_{-1}t_{-1}$ ,  $\tau_0t_0$ ,  $\tau_1t_1$  and  $S_{-1}$ ,  $S_0$ ,  $S_1$  points more generally, as  $a$ ,  $b$ , and  $c$ , then we have everything we need to rigorously describe our plessist behaviours. Since Ingredients 1 and 2 must supervise all self-intersections, helicoids, and fibration, cofibration, deformation retract and mapping cylinder behaviours for our homomorphisms and homeomorphisms, then our Memes 23–29 state the properties they must satisfy so that our plessists can occupy any and all  $a$ ,  $b$ , and  $c$  while undertaking the relevant  $\psi$  and  $\gamma$  productions involving Ingredients 3 and 4:

- I. Identity element. If the circulations are to be recurvatures that complete, then there is always some quantity we can add or remove—such as by dragging the helicoid axis up and down—and that nevertheless leaves things identical. This element or state,  $S'$ , must exist. It is both the antipodal recurvature radius and the helicoid axis, and is such that when it is either inserted or removed, every  $n$  at every point  $t$  any number of generations into either the past or the future looks identical. This  $S'$  must describe

a definite self-intersection state and so is a nonzero identity matrix, determinant, or similar. It defines the antipodes and pinch point and the helicoid axis. It is our Hooke cell.

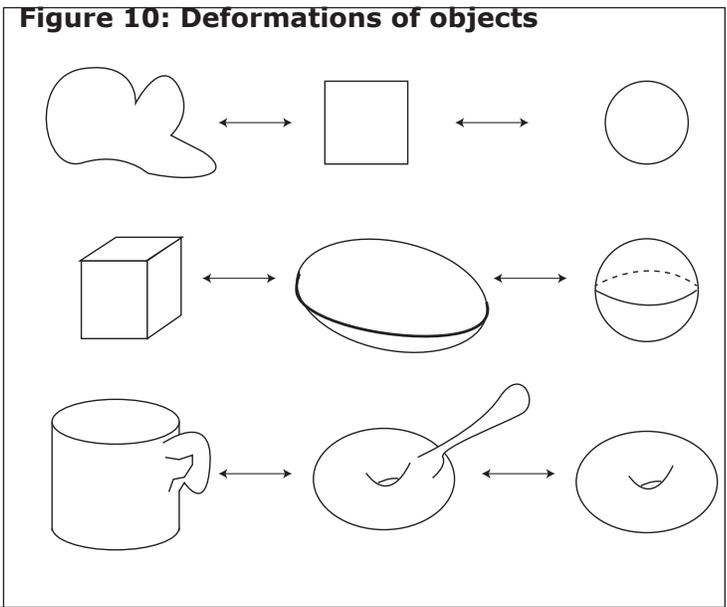
- II. Inverse element. Plessists must self-intersect which is to move in opposite directions between one antipodal point, or location, upon our helicoid and another to produce  $S^?$ . So relative to  $S^?$ , then for every bigger there is a matching smaller; for every faster, a matching slower; and for every before, a matching after. More generally, for every transformation  $a$  in  $S$ , there is a  $-a$ . This is always a fibration–cofibration coupling. The bare minimum, therefore, is that all points in  $S$  are described with rank one tensors with at least two contrasting components—one for  $\psi$  and one for  $\gamma$ —attached to each measurement unit to complete a self-intersection ... which are then vectors.
- III. Closure. If we add, multiply, integrate or differentiate any  $a$  and  $b$ , we must always get a true and correct value of the same type for our  $c$ . Although, strictly, only addition and multiplication are defined as closed, we must still get coherent values for any subtraction, division, and differentiation. Thus if both  $\tau_{-1}t_{-1}$  and  $\tau_0t_0$  have  $S_{-1}$  and  $S_0$  as an  $a$  and a  $b$ , then  $\tau_1t_1$  must also exist as  $S_1$  and as a  $c$ , with the three related as past, present, and future antipodal and helicoid moments and amounts.
- IV. Inverse operation. Biology, as a self-intersection, must have an inverse operation. The antipodal pair are inverses. Both addition and multiplication have similar inverse operations which create their identities. The former define subtraction, the latter division:  $a + -a = 0$  and  $a \times 1/a = 1$ . Bringing a vector or tensor together with its inverse similarly creates its identity. A vector's additive inverse is simply its opposing vector. The inverse of any  $\mathbf{x}$  is some  $-\mathbf{x}$  that pushes in exactly the opposite direction, but with the same magnitude. A vector's multiplicative inverse is a little more involved, for neither dot nor cross products have true inverses. A dot product is a scalar, losing its directional component, and being effectively the shadow length some vector casts in some specified direction. Unfortunately, exactly the same shadow could result by shining a light from some different direction. Similarly, many other vectors could have interacted, orthogonally, to produce any given cross product. But since we demand that succeeding generations repeat, then where one increases, so must others, and by the same amounts. Any  $\mathbf{x}$  and its successive  $\mathbf{y}$  must therefore be related so that  $\mathbf{x}\mathbf{y} = 1$ . This immediately means that  $\mathbf{y}\mathbf{x} = 1$ . We can now resolve these matters by noting that the square of any vector is always a positive scalar, with  $\mathbf{x}^2 = |\mathbf{x}|^2$  and  $\mathbf{y}^2 = |\mathbf{y}|^2$ . And since  $\mathbf{x} = \mathbf{y}$ , then  $\mathbf{x}^2 = |\mathbf{y}|^2$  meaning  $\mathbf{x}^2/|\mathbf{y}|^2 = 1$ . Therefore every  $\mathbf{x}$  that completes a circulation will also have, for the multiplicative inverse that creates its antipodal value, its square divided by its absolute value:  $1/\mathbf{x} = \mathbf{x}/|\mathbf{x}|^2$ . These then occupy each antipodal point to create the self-intersecting pinch point and identity,  $S^?$ , while maintaining all preimages, images, fibrations, cofibrations, deformation retracts, and

mapping cylinders. As we did in our *Brassica rapa* experiment, these can all be easily measured.

- V. Associativity. As long as  $a$ ,  $b$  and  $c$  maintain the same order, then  $a + (b + c) = (a + b) + c$ , and  $a \times (b \times c) = (a \times b) \times c$ . However, their opposite operations of subtraction and division are not associative so that although  $2 + (3 + 4) = (2 + 3) + 4 = 9$  and  $1 \times (2 \times 3) = (1 \times 2) \times 3 = 6$ , we have  $(5 - 3) - 2 = 0$  whilst  $5 - (3 - 2) = 4$ ; and  $4 / (2/2) = 4$  while  $(4/2) / 2 = 1$ . Any vector cross product is also not associative so that  $\mathbf{x} \times (\mathbf{y} \times \mathbf{z}) \neq (\mathbf{x} \times \mathbf{y}) \times \mathbf{z}$ . But they nevertheless respect the strict ordering implied by  $\tau_{-1}t_{-1}$ ,  $\tau_0t_0$ , and  $\tau_1t_1$ . Thus the same inputs lead to the same outputs and successions of states as  $S_{-1}$ ,  $S_0$ , and  $S_1$  circulation after circulation.
- VI. Commutativity. Addition and multiplication follow the rules  $a + b = b + a$  and  $a \times b = b \times a$ . However, the opposite operations of subtraction and division are not commutative:  $0 - 1$  is not the same as  $1 - 0$ , and  $1/2$  is not the same as  $2/1$ . Vector cross products are also not commutative:  $\mathbf{x} \times \mathbf{y} = -\mathbf{y} \times \mathbf{x}$ . But since there is again a regular sequence of operations, then the same inputs applied in the same sequence at the same locations produce the same states,  $S$ , at the same points.
- VII. Distributivity. Multiplication distributes over addition so that  $a \times (b + c) = (a \times b) + (a \times c)$ , with the vector cross product also being distributive so that  $\mathbf{x} \times (\mathbf{y} + \mathbf{z}) = (\mathbf{x} \times \mathbf{y}) + (\mathbf{x} \times \mathbf{z})$ . If  $S$  is some function,  $f$ , composed as  $f(a + b)$ , then we can equally well describe it as  $f(a) + f(b)$ . An original can therefore distribute itself over many successors. And if some operation is composed of the two parts  $ab$ , then its differential  $d(ab)$  is  $adb + bda$ . So if some successor is composed from the distinct inputs of its predecessor, then the same will hold for its own successors.

**II.6.6** We must still account for interactions,  $\lambda$ , with the surroundings. But we have nevertheless defined our recurvatures as plessist reproduction. They are Abelian infinite cyclic groups and subgroups. The group operation involves  $\psi$  and  $\gamma$  as quantities of Ingredients 3 and 4. These are added and/or removed as inverse operations with the surroundings within our self-intersecting “biofield” upon our Whitney umbrella and helicoid. This recurvature involves both of the radiative and coupling components; both of the progenitor domain and progeny codomains; and both of the biology and replication globes. The transactions are expressed as fibrations and cofibrations,  $\theta$  and  $\rho$ , and so as the biological interactions,  $\lambda$ , transitioning between preimage and image. The quantities defining  $S'$  are  $\psi$  and  $\gamma$ , with the processes sustaining them involving  $d\psi$  and  $d\gamma$  to give  $\lambda = (\psi, \gamma, d\psi, d\gamma)$ . Those total operations oversee both the homomorphisms and the homeomorphisms. Their productions are the replications not just of biological structures, but also of the biological spaces that are the biology and replication globes, again as infinite cyclic groups and subgroups.

**II.7.1** When we take (a) the self-intersection radius, and/or (b) the helicoid midpoint arrow pointing upwards of  $T$ ; and also (c) the self-intersection boundary, and/or (d) the right helicoid formed by the median equatorial white line of  $\tau$ ; then all populations recurve by hovering about the equilibrium state,  $S^2$ , using the range  $\pm dS$  to traverse the necessary intervals. That self-intersection boundary and its equivalent journey about the right helicoid are jointly a replication and a reproduction. They involve both of our biology and replication globes.



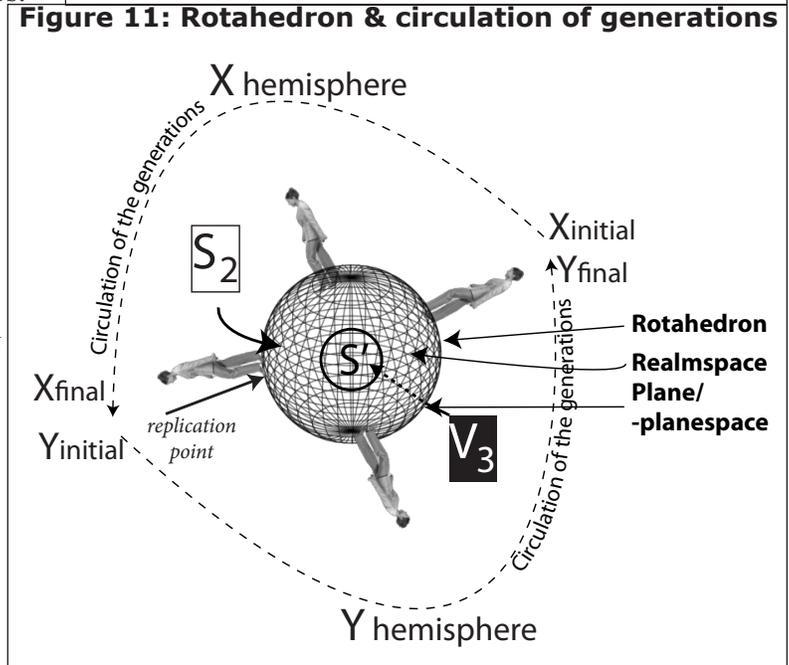
**Figure 10: Deformations of objects**

**II.7.2** Our helicoids, deformation retracts, mapping cylinders, and self-intersections plus antipodal points are all neighbourhood properties. They are therefore topological.

Colin Adams' *The Knot Book* offers topology's standard definition. Figure 10 sets out the well-known intuitions:

Topology is the study of the properties of geometric objects that are preserved under deformations. ... we think of the more general geometric objects in topology as deformable. For instance, a topologist does not distinguish a cube from a sphere, since a cube can be deformed into a sphere by rounding off the eight corners and smoothing the twelve edges (Adams 1994).

Topology therefore deals with well-defined geometric objects that surrender some, but not all, of their properties. Topology is still enough like geometry for the objects in the lower two rows in Figure 10 to be three-dimensional. Objects on the bottom row, however, are different in a way geometry regards as insignificant. They are "genus-one" objects with a "hole" and a single "handle".



**Figure 11: Rotahedron & circulation of generations**

**II.7.3** Meme 30, displayed in Figure 11, goes on to take ready advantage of topology's pictorial dimension to advance our model. Since we must carefully consider the different topological properties

of all surfaces and interiors, being related as  $V_n$  and  $S_{n-1}$ , then that complete figure that supports our recurvatures is more technically a “rotahedron”. The lady is walking about a complete recurving wind wall. She is therefore traversing the radiative–cum–circulating neighbourhoods of our biology and replication globes. This creates both the self-intersections and the circulations of the generations.

By Meme 31, we have a general principle. Any  $S_n$  surface supporting a recurvature is homomorphic. It establishes the syntax and structure. It then surrounds a  $V_{n+1}$  interior that is homeomorphic. That governs the semantics and the space.

**II.7.4** As topology suggests, the rotahedron’s  $S_2$  recurving surface is, locally, a “two-dimensional manifold”. It is an  $S_2$  “plane”. So in spite of the rotahedron’s curved external appearance, its  $S_2$  surface is always, locally, infinite and flat, being identical to an ever-extended rectilinear Euclidean plane. The surface is a complete topological “sphere” that supports parallels and unchanging, fully collinear, “affine transformations”. It preserves all angles, ratios, and distances. It has a completely flat “local topology”. Number duples such as  $(a, b)$  fix its coordinates. So if one dimension is  $A$ , and another  $B$ , then all points upon  $S_2$  are the Cartesian product  $A \times B = \{(a, b) \mid a \in A \text{ and } b \in B\}$ . Its production rules declare the syntax that create that local topology for its exterior.

Although the  $S_2$  plane is locally flat, and a plane biosurface, by Meme 32 it simultaneously has the curving “global topology” that wraps it around a  $V_3$  rotahedron. That outer  $S_2$  sphere therefore bounds a curving biovolume described with three coordinates as  $a, b, c$  where  $A \times B \times C = \{(a, b, c) \mid a \in A, b \in B, c \in C\}$ .

The interior is a curving  $V_3$  “realmspace”. This joint  $S_2$ – $V_3$  plane–plus–realmspace rotahedron is a rigorous topological manifold. Its production rules declare the semantics and the interior that then create the above syntax and exterior.

**II.7.5** By Meme 33, the lady walking about the rotahedron is measuring her circulation, which is both a self-intersection and the recurve journey about the helicoid axis. She is measuring wind walls and her positions for  $x$  and  $y$  using the method Newton first derived when he solved the problem Johannes Kepler had posed (Hughes-Hallett et al, 2002; Stewart, 2003).

Newton described planetary motion trigonometrically, stating their angles via their side lengths,  $x$  and  $y$ . He thus used a set of spherical **IJK** axes, based on a centre  $x^y$ , and a radius,  $r$ . Each point is an  $x/y$ , and so a ratio between two sides. When those values repeat then an orbit—or in our case, a self-intersecting circulation of the generations,  $\tau$ —is complete. Looked at in two dimensions, that orbit is a constant acceleration about that  $x^y$  centre.

But since Newton also described planetary increments infinitesimally, as  $dx$  and  $dy$ , he was always dealing with  $dx/x$ ,  $dx/x^y$ ,  $dy/y$ ,  $dy/y^y$ , and  $dx/dy$ . He had thus realized that every infinitesimal increment,  $d\tau$ , over each infinitesimal time interval,  $dt$ , declares its precise sequencing of locations in the circulation as some  $d\tau/dt$ . If these again repeat, a circulation has been completed. And since every  $dx$  and  $dy$  at any present instant  $dt_0$  and  $d\tau_0$  is added, in each succeeding moment, to its generating  $x$

and  $y$ , then every increment in some prior  $dt_{-1}$  and  $d\tau_{-1}$  becomes a part of  $x$  and  $y$  in a succeeding  $dt_1$  and  $d\tau_1$ . They together define the  $x$ - $y$  centre. Therefore: referencing any property to its current state, and so as  $dx/x$ , immediately uses Newton's spherical  $d\tau$ - $dt$  and **IJK** axes.

**II.7.6** Meme 34 is to note that as the lady circulates across each  $x$  and  $y$  in each of the rotahedron's distinct  $X$  and  $Y$  hemispheres, she is also always (a) somewhere about the central point  $S$ ; and (b) somewhere between an initial and a final hemispherical location. But a line from every  $x$  passes through  $S$  at the centre—which is the identity—to emerge in its antipodal  $y$ . There is therefore a  $V_3$  or Euclidean 3-space or realmspace composed of all lines passing through that origin. Each such line is a unit vector pointing in a given direction. It is opposed by another pointing to its antipodal point. We thus have a unit rotahedron that forms the unit Eulerian limits for any circulation.

**II.7.7** For Meme 35, our unit rotahedron abides by Bezout's theorem. This states that any two planar algebraic curves of degree  $n$  and  $m$  intersect in exactly  $mn$  points. Any two circles therefore intersect in four points: two real, and two upon the "line at infinity". The rotahedron's horizon is therefore at that line at infinity, therefore making all points upon it "properly countable".

By Bezout's theorem every generation or orbit about the population is in fact a circle that passes through the properly counted point at infinity ... which is also our replication point. The "antipodal map" is therefore the identification of each opposite point. It creates our self-intersection. Both the replication point, as  $\theta$ - $\rho$ , and the Möbius strip boundary between the biology and replication globes that define the passage from one generation to the next forwards as ' $\times$ ', and backwards as ' $\div$ ' are such self-intersections. Every population can therefore replicate infinitely many times, leaving the original unchanged.

Since, for Meme 36, the  $S_2$  plane is a two-manifold whose local topology reaches out to infinity, then granted that each antipodal point is "over the horizon", and so "out of sight", by Meme 37, the fibration and cofibration act through the deformation retract and mapping cylinder to recreate each antipodal point as the equally properly counted point beyond infinity.

**II.7.8** The succession all around a circulation as the lady walks about the rotahedron is the key to the recurvatures that are the generations. The resulting spherical axes measure both the biology-replication heredity and the temporal passing of a generation. Both are measured as the ongoing and bounding circulation,  $\tau$ , of definite radius,  $r$  ... and also as the absolute time,  $T$ . We therefore have both the radiative and the circulating—and all their transformations—for the fibration and cofibration.

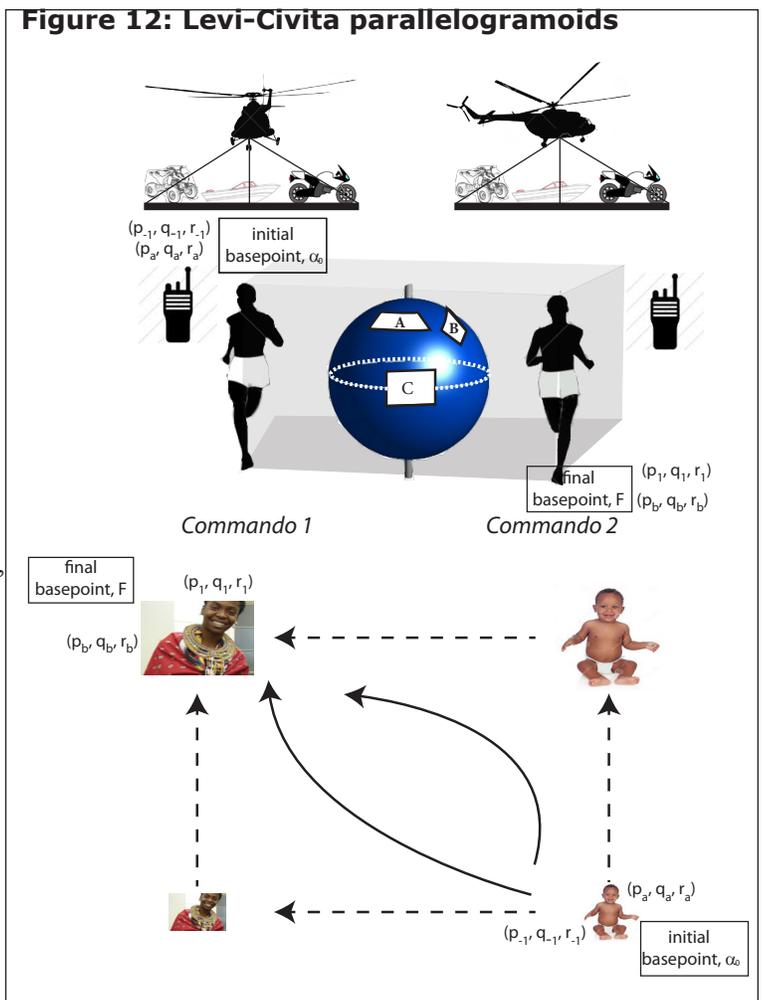
**II.8.1** If we wish to reckon both the biology–replication interface for the Möbius strip, and the temporal interface that marks the beginnings and endings of the generations, then we must ensure that all neighbourhoods remain intact. We must ensure that all distances about the rotahedron’s surface for its local  $A \times B$  topology match those across the centre for its global  $A \times B \times C$  topology.

**II.8.2** We now consider, for Meme 38, the two commandos in Figure 12 running about a rotahedron. We also recollect that Memes 4 to 9 placed our plessists and/or plessemorphs  $a_1$  and  $a_a$  into our first set  $A$ ; their plessiomes and/or plesseomes  $b_1$  and  $b_a$  into a second set,  $B$ ; and their plemes and/or plessetopes  $c_1$  and  $c_a$  into a third set  $C$ . They involve the infinite cyclic groups that are our biology and replication globes, as well as our deformation retract and mapping cylinder.

The commandos’ fibrations and cofibrations as they run about the rotahedron and navigate between  $A$ ,  $B$ , and  $C$  are the transitions between some initial point  $\alpha_0$  and some final point  $F$ , as preimage and image, being  $(a_{-1}, b_{-1}, c_{-1}) \rightarrow (a_1, b_1, c_1)$  and  $(a_a, b_a, c_a) \rightarrow (a_b, b_b, c_b)$  for, respectively, some plessists and plessemorphs. They are each statements in a Chomsky grammar. They are both homomorphisms and homeomorphisms.

**II.8.3** For Meme 39, our two commandos are impelled by forces that pull them away from their initial basepoint,  $\alpha_0$ . Since we are interested in both a set of Chomsky production rules and their biological effects, then these are the same  $\psi$  and  $\gamma$  forces that produce the more general  $\lambda$  and DNA-based infinite cyclic group and homo- and homeomorphisms, as transformations in nucleotide codons, in the humanoids underneath.

We let the commandos have all the ropes, speedboats, all-terrain vehicles and etc. they need to navigate the terrain ... meaning they are free to interact with the surroundings as they wish. We attach elastic strings and sheets to their hands, feet, and head. They therefore draw a whole series of lines, surfaces, and volumes to create our self-intersections and helicoids as statements in the



general syntax and semantics. We can measure both the radiative and the circulating forces working on them—which create our fibrations and cofibrations—by their external effects upon those attached elastic strings and sheets.

For Meme 40, we confirm that our radiative force is composed of Meme 18’s Ingredients 3 as  $\psi$ . Somewhat like a pod of whales migrating towards colder temperatures, it pulls Commando 1 due north.

And we confirm, for Meme 41, that our circulating force is composed of Meme 19’s Ingredients 4 as  $\gamma$ . Somewhat like plants sprouting leaves under increasing sunlight, it pulls Commando 2 due east.

**II.8.4** We need the velocities all about those wind walls. So reporting our two commandos as travelling with a simplistic velocity or rate of change—i.e. rate of change of distance—upon the underlying surface, and so as at so many kilometres per hour, is not helpful. This only uses the standard rectilinear **ijk** axes of this ordinary surrounding three-dimensional Euclidean realm. So for Meme 42, Commando 1 notices that when he examines the northern and southern faces of his little surrounding box of volume elements, then bigger values for latitude keep coming at him from the north as  $+d\psi$  ... while smaller ones keep departing him to the south as  $-d\psi$ .

James Maxwell (1870) was the first to apply the term “convergence” to this realm or volume phenomenon; with William Kingdon Clifford (1878) being the first to apply its opposite of “divergence”. A divergence is thus some property’s increasing rate of change, but directly in alignment with its applicable field of force. Therefore, this Meme 42 says that Commando 1 currently has a “positive divergence”,  $d\psi$ , in the radiative force, which is for latitude. It is the main cause of fibrations and cofibrations—and so contributions to the mapping cylinder—along that given axis.

And since Commando 2 is similarly travelling in a direction aligned with his alternative field of force, then for Meme 43 he similarly sees increasing longitude values,  $+d\gamma$ , again in terms of the underlying surface, coming at him upon his eastern edge of his volume elements; with smaller ones disappearing, as  $-d\gamma$ , to his west. Since this is similarly aligned with the impelling force, Meme 44 says that he currently has a positive divergence,  $+d\gamma$ , in that circulating force for longitude. It is thus the main cause of fibrations and cofibrations, and of mapping cylinder activities along its given axis.

**II.8.5** Each commando will of course have to move around obstacles. This requires deviations into and out of each other’s directions ... which means movements that either add to or subtract from the velocities and accelerations that they each currently have, courtesy of their circulating wind walls.

We now follow the convention Maxwell established (1870). He originally called these recurvature and wind wall transformation phenomena ‘twirls’, but the modern designation is “curl”. So Meme 45 says that each commando can curl—but in this case only two-dimensionally—directly into the other’s directions. Each can therefore change their wind wall velocities and behaviours

so they align, at least temporarily, with the other. It is to each as if each has temporarily been placed under the purview of the other one's force; and so is blowing slightly in that other direction, exhibiting a suitable change in both velocity and wind wall behaviour. That makes each one more or less like the other, by reshaping their wind walls in that direction.

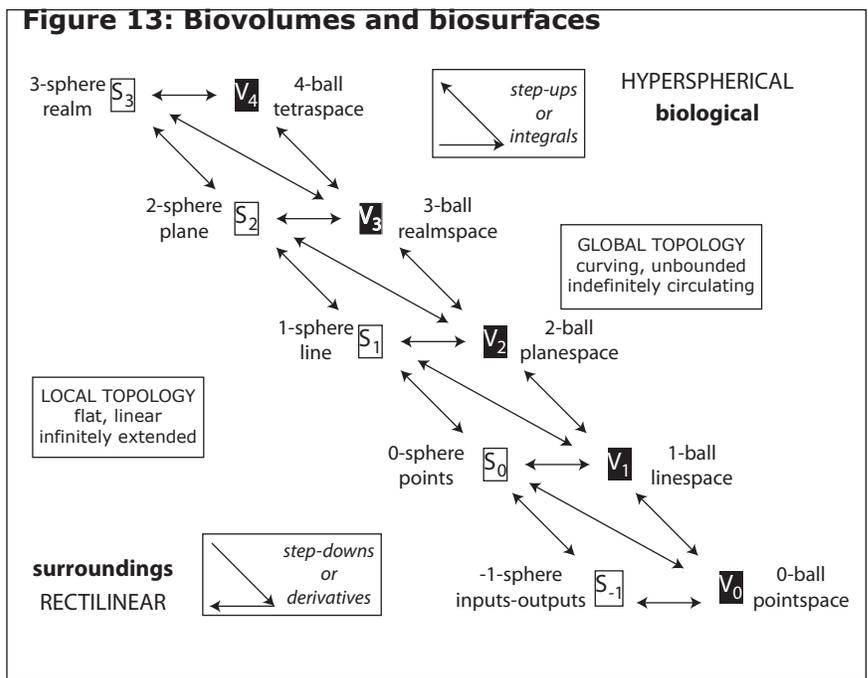
**II.8.6** There is, of course, a further consideration. John Ambrose Fleming regularized these interactivities. Since a curl is any rate of change at right angles to a given applied force, then by Fleming's right-hand rule, our meme is that every time a commando goes rightwards, he registers a positive curl. So all deviations eastwards by the radiating force for Commando 1, and southwards by the circulating force for Commando 2, are each positive curls in longitude and latitude, respectively. These are both positive contributions— $+d\gamma$  and  $+d\psi$ —to the mapping cylinder; with their leftwards movements therefore being negative. Each thus also contributes to the overall fibration, cofibration, homomorphism, and homeomorphism and their joint general biological effect,  $\lambda$ .

**II.8.7** Each commando will additionally go up and down hills; and down and up valleys. These are curls, by both, into some third dimension. They are further contributions to  $\lambda$ , and so to the mapping cylinder. As fibrations and cofibrations and infinite cyclic subgroups, they add to or subtract from the overall movements upon the mapping cylinder between the biology and replication globes, which are the infinite cyclic groups.

**II.8.8** Again by Fleming's right-hand rule, when forces, fibrations, and cofibrations combine to decrease height while keeping a locally lowest point to the right; or else to increase it by keeping a locally highest point to the left; then that is a positive curl for height and so is  $+d\lambda$ , with the opposites being negative,  $-d\lambda$ . Thus Meme 46 declares that to cross a hilly incline up and then down, or a valley down and then up, but always keeping the local maximum on the same side, produces a net curl, into the third dimension, and for that obstacle, of zero. The wind wall overall maintains the same height and direction of motion.

**II.8.9** We now only need to distinguish homomorphic or structural transformational effects from homeomorphic and spatial ones as between biology and replication globes. We also need to clarify all movements into that third dimension that create the heights and depths—and so vertical velocities—upon these circulating wind walls.

**II.9.1** We have a variety of biological and DNA interactions. Some incorporate the replication globe; some do not. If want to understand the effects of these  $\pm d\psi$  and  $\pm d\gamma$  curls that contribute to  $d\lambda$ , then we must measure all volumes and surfaces, energies and momentums, and fibrations and cofibrations. We must determine all the productions as transfers to and from preimages and images that occur in our self-intersections, helicoids, and rotahedrons.



**II.9.2** Figure 13 illustrates Meme 48, which is the emerging biological grammar for the language spoken by those curls and their resulting biological transformations. That grammar confirms that as the commandos run, they create a set of hyperspherical biovolumes,  $V$ , with their elastic sheeting. Each resulting biovolume presents its cylindrical biosurface,  $S$ , to the surroundings. If the volumes are  $(A, B, C)$ , then the surfaces are  $((A, B)_C, (A, C)_B, (B, C)_A)$  where  $a$  is in  $A$ ,  $b$  is in  $B$ , and  $c$  is in  $C$ ; and where each is held as a specific direction of observation, the others then being varied. The surfaces are the three different perspectives—one in each of the  $A$ ,  $B$ , and  $C$  directions—that create the whole.

**II.9.3** Another aspect of our grammar is that the external world does not, itself, connect any elements upon the left of Figures 1 and 13 to create any structures to the right. The external world has no  $\lambda$  or recurvature process. All  $\lambda$  connections are exclusive to recursive functions; to our running commandos; and so to all biological entities. Therefore, only the biovolumes  $V_{0,1,2,3,4}$  displayed on the right can recurve. They are intrinsically biological; are hyperspherical; contain the energies and semantics; and are homeomorphisms. They have an extra global dimension and can exert a semantic pressure per unit volume throughout their relevant space.

Their energies are then incident upon the surroundings, to their left, emerging as lower-dimensional cylinders and loops—and so as discernible events—through the relevant  $S_{-1,0,1,2,3}$  surfaces. Those are their outward expressions as biological events per unit surface, and so are their syntactical structures and homomorphisms through Ingredients 2, 3, and 4.

**II.9.4** Our main interest, in Figure 12, is in the two humanoids underneath the two commandos. Since we want to distinguish their homo- from their homeomorphisms, then Meme 47 is to instruct

the commandos to give each other personalized renditions of their ongoing transformations, using their walkie-talkies. Each commando is, for example, to report his own progress, and his observable effects on their linking elastic sheet, to the other in terms of his own distinct “height-lengths”, and as measured directly upon that surface and sheet.

We note, for Meme 49, that since our commandos are equipped with all necessary accessories, then we can switch them and/or the forces around at any time. Where one goes, the other could equally well go. Granted that the Greek for ‘place’ is *topos*, then they are “homotopically equivalent”.

So for Meme 50 then after one day, the forces switch so that Commando 1 is instead being pulled due east, by  $\gamma$ , with Commando 2 being pulled due north by  $\psi$ . Since they are homotopically equivalent, then we let them meet up at the end of that second day, at  $F$ , to create a “Levi-Civita parallelogramoid”.

**II.9.5** We now have a complete set of production rules. The commandos both understand both. They are homotopically equivalent. But even though in many ways equivalent, we cannot just assume that they are perfectly substitutable.

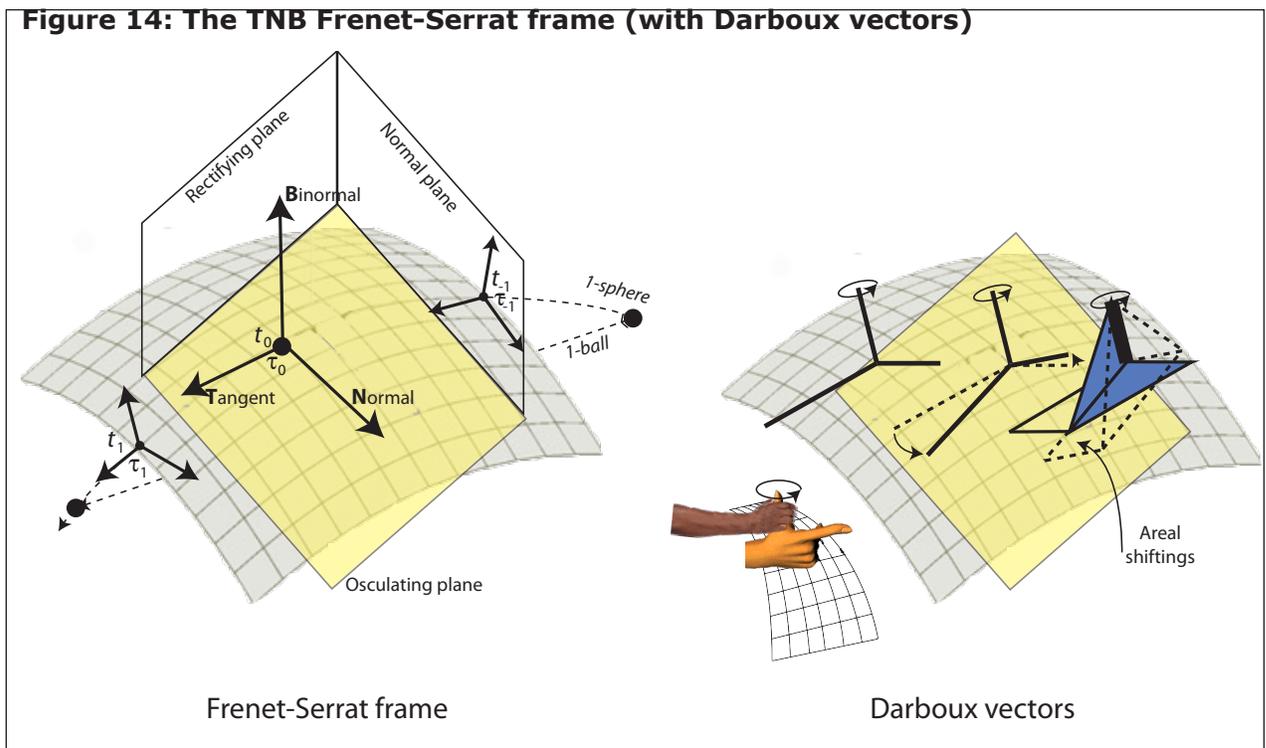
We can perhaps better understand their limitations by understanding the continuities involved. We can compare these commandos, and the forces acting on them, to the letters ‘X’ and ‘Y’.

The letters ‘O’, ‘A’, ‘D’ and ‘B’ all have holes. Although X and Y are similar in both being without such holes, the Y has a single ‘three-vertex’, the X a single ‘four-vertex’. The X can deformation retract onto the Y because we can retract one of its prongs to another. But we can also deformation retract three of the X-prongs onto the three in the Y, and then retract X’s fourth to Y’s centre. We can even retract each prong in each letter to its own centre.

We can next remove both centres. The X now yields four components, the Y only three, all again without holes. All paths in each can continuously deform into each other and retract to a point, always remaining within its component. All seven components are therefore “simply-connected” and homeomorphic. Nevertheless, the original X and Y are not homeomorphic. They are, however, homotopically equivalent.

**II.9.6** The mapping cylinders our commandos interact with can similarly have different possibilities. We must find a way to guarantee that they are not merely homomorphic, but also homeomorphic.

For Meme 50, we note shapes  $A$ ,  $B$ , and  $C$  in Figure 12. They could easily be the elastic shapes our commandos construct. But although all such shapes class as homotopically equivalent, we observe that no matter how Euclidean they might appear locally, when looked at globally, no true straight lines, rectangles, or parallelepipeds can exist on any sphere. The commandos will not necessarily create matching “squaroids”.



The commandos' paths will only properly match if the terrains they cover straddle both the equator and the prime meridian on the same surface, and so that they are properly reflexive and identical. So while everything homeomorphic will immediately be homotopically equivalent, the converse is not necessarily so, for not everything homotopically equivalent is homeomorphic.

**II.9.7** As in Figure 14 the French mathematicians Jean Frédéric Frenet and Joseph Alfred Serrat discovered, independently (Crenshaw 1993a, 1993b; Crenshaw, H., Edelstein-Keshet, L. 1993; Crenshaw, H., Ciampaglio, C., McHenry, M., 2000), that we can blend Newton's **IJK** hyperspherical axis system with the ordinary tangential and rectilinear **ijk** one to determine whether or not our shapes are homeomorphic. The two **ijk** and **IJK** axes can establish both a "1-sphere" and a curved line,  $d\tau$ , for its linespace and circulation. But we can also use the axes and any resulting curve to determine a tangent, **T**, by taking the derivative. It is the shortest path between the points we are measuring. It is the tendency for any curve to depart from a straight line. It is formally known as a "1-ball".

We can, however, take yet another derivative to that derivative. That double derivative establishes the normal, **N**, and tells us how the tangent itself is changing, which is its acceleration. The normal points straight at the centre of any curvature.

Since the tangent and the normal are mutually orthogonal, they form a plane tangential to the original surface, just touching it at that point. Gottfried Leibniz first used the Latin term *osculans*, 'kissing', for this behaviour. It is therefore called the "osculating plane" (Howard 1992). It tells us the rates of left-right arcing, twisting, and turning.

The third dimension we require, to properly analyse  $\psi$  and  $\gamma$ , is orthogonal to the two we already have. It is therefore easily calculated. It gives the binormal, **B**. When we bring normal and binormal together, we create the "normal plane", orthogonal to the osculating one. We can now

measure “torsion”, the surface’s accelerations up into, or out of, the osculating plane as we go right-left. We can now assess the effects of  $d\gamma$  on  $d\lambda$ .

We can finally bring tangent and binormal together to create the “rectifying plane”. It tells us how much the surface lifts towards, or drops away from, the binormal as we travel forwards-backwards. We can now assess the joint effects of  $d\gamma$  and  $d\psi$  on  $d\lambda$ .

**II.9.8** Shortly after the French mathematician Jean Gaston Darboux learned about the “Frenet-Serrat trihedron” or “Frenet-Serrat frame”, he realized that although it describes all translational movements, it misses all rotating ones. If, as in Figure 14, we twist the thumb upon the binormal, the tangent and normal curl to different directions. Darboux noted, however, that they are linked. The rotated index finger is still orthogonal. There are therefore matched exchanges. Again by Fleming’s right-hand rule, if the osculating plane moves counterclockwise to push the normal towards the binormal, or clockwise to push it away, that is positive; otherwise it is negative. The areal velocities on the osculating, normal, and rectifying planes now state all curls.

We now have every parameter, in every neighbourhood, and upon any surface, through all transformations wrought by our raying and circulating fields ... which create the fibrations and cofibrations to and from our mapping cylinder. Thanks to the Frenet-Serrat trihedron, even the most tortuous of mapping cylinder surfaces become locally straight lines and flat surfaces,  $S$  ... but we still always know exactly how much they might be moving curvilinearly as  $V$ . We can soon observe, for example, that although the earth has a local two-dimensional and  $(A, B)$  topology that makes it appear flat everywhere, it nevertheless curves about itself with a global and three-dimensional  $(A, B, C)$  topology that has an average rate of curvature of 13 centimetres per kilometre. We can determine this by observing each of the local  $(A, B)_C$ ,  $(A, C)_B$ , and  $(B, C)_A$  topologies, which then come together to reveal the global  $(A, B, C)$  characteristics.

If we therefore want to determine all curls and three-dimensional variations, which are any extraneous effects  $\psi$  and  $\gamma$  may have upon each other and/or upon any third dimension, then our lady and our two commandos must report all values in three different ways:

- Rectilinearly, **ijk**. These are, simply, their absolute motions emerging tangentially through their surfaces, measured as seconds, kilometres, kilogrammes, and other SI units, being rectilinear and Euclidean. This is Meme 51.
- Hyperspherically, **IJK**. These are Newton’s values stated proportionately, i.e. with respect to their running totals, and so as  $dx/x$ . They are recurvature values equivalent to radians per second about the earth. They complete a generation about some  $x'$  centre, in terms of related antipodal values, and centralized, continuous, hereditary behaviours. This is Meme 52.
- Frenet-Serrat **TNB**. These state the surface directly in terms of current biovolume interior elements, such as via height-lengths, or whatever and other individualized and relevant properties of interest. We already have this as Meme 47.

Those are then the distinct perspectives upon each of  $(A, B)_C$ ,  $(A, C)_B$ , and  $(B, C)_A$ , which then come together to reveal  $(A, B, C)$ .

**II.9.9** As in Figures 1 and 13, any two  $S_0$  values or points immediately form a biosurface, linking as a  $V_1$  biovolume and linespace of definite value. So in accordance with our Meme 48 grammar and our Figure 8 Whitney umbrella, each distinct  $S_0$  point our two commandos pass through has a structure. It is in fact a combined  $S_{n-1}-V_n$ . So our  $S_0$  point is fact an  $S_{-1}-V_0$  pointspace. It has its radiative and circulating couple as a  $-r$  and  $+r$  input-output pairing. Those together create a direct and tangential  $V_1$  1-ball which is a linespace. There is an independent linespace in each of  $A$ ,  $B$ , and  $C$ .

And also, just as a terrestrial road can deviate and lengthen a journey, any two  $S_0$  values or points can be linked by varied accelerations and velocities in our windwalls and recurvatures about the rotahedron. That curving  $S_0$  is the route the commandos would actually have to take, upon the surface, to get from one point to the other. We designate this curving 1-sphere line ' $S_1$ '.

Meme 51 therefore states that between any two points  $S_0$ , there is:

- a  $V_1$  biovolume as a direct linespace; and
- an  $S_1$  biosurface as lines; and that is composed of
- the specific input-output points  $-r$  and  $+r$  that create them.

This is our complete  $S_0-V_1$  nonpollent and production rule pairing as syntax and semantics.

And then as a general principle, two  $S_1$  relationships or curves can bound an  $S_2$  plane or area that, no matter how convoluted, can also be expressed as a completely regular  $V_2$  "rotagon". This is the combination of bounding circle or circumference, at radius  $r$ , plus its enclosed "disc" of so many square metres or relevant units. Therefore: between any collection of values as  $S_1$  lines, lies a  $V_2$  rotagon as their coordination. It is a given "planespace" and biovolume for our similar  $S_1-V_2$  unipollent production rule and syntax–semantics pairing.

In the same way, any given  $S_2$  planes, of whatever shape, can bound a rectilinear  $S_3$  realm or volume. And no matter what its complexity of surfaces, there will be a uniform  $V_3$  rotahedron of radius  $r$  whose surface and interior ball summarize a three-dimensional realmspace as so many cubic metres, or the equivalent, for our  $S_2-V_3$  pluripollent pairing.

And by the same token, two or more  $S_3$  realms are related via a  $V_4$  "rotachoron". This is a four-dimensional hypersphere again of definite radius, volume, and properties. Its surface is a set of  $S_3$  "glomes". Its interior is a  $V_4$  "gongyl", creating our  $S_3-V_4$  totipollent pairing.

**II.9.10** Since the rotachoron is a four-dimensional hypersphere, then its set of three dimensional bounding glomes circumscribe a set of  $S_0 = -r$  and  $S_0 = +r$  pointspace equidistantly about its centre. We always get a mean value for  $\psi$  and  $\gamma$ . These establish the  $\lambda$  of biological-ecological behaviours for our archetypal plessemorphs, and their plesseomes, and plessetopes.

Our rotachoron's four dimensions now have the same two solutions all about themselves, based on  $\pm r$ . Since its shape is symmetrical, its internal  $V_4$  volume or gongyl is given by  $dr = 0$ ,

and  $\int dr = 0$ . And while that  $V_4$  interior biovolume cares only that all its circulating points,  $\tau$ , stay equidistantly about it at  $r$ , the external surroundings will allocate them a set of real-world values according to distance and orientation as  $+r$  and  $-r$ . Meme 53 now says that one in each such pairing,  $-r$ , is a net output from our plessists and biological events to the surroundings; the other,  $+r$ , is a net input to our plessists and plessemorphs from those same surroundings. We have the syntax and semantics that create the recurvatures.

**II.9.11** These above processes are of course more technically called “integrals” and “derivatives”. But as in Figure 13, our Meme 48 grammar calls them “step-ups” and “step-downs”, respectively. We step down from  $(A, B, C)$  to  $(A, B)_C$ ,  $(A, C)_B$ , and  $(B, C)_A$ ; and we step up from them back to  $(A, B, C)$ . So we can step-up from a one-dimensional figure to a two-dimensional one, such as when pick up a line,  $x$ , and push it a certain distance  $y$  across a plane to create an  $xy$  square; or take up that  $xy$  square and push it along the same line for the distance  $z$  to create an  $xyz$  cube. Step-ups then determine—as does the integral calculus—overall totals as distances, areas, volumes etc. and creates  $V_n$  biovolumes. Step-downs then do the opposite. They determine how things have changed to create those step-ups. They find all related, surrounding, momentum interactions as  $S_{n-1}$  biosurfaces. As in Figure 1, we again have the syntactic and semantic interactions, as spheres and cylinders, that sustain all biological entities.

**II.10.1** We must now very carefully consider our two commandos, who represent all biological interactions with the surroundings. They are homomorphic, meaning they are immediately homotopically equivalent. Since we can switch them around at any time, then if one is  $P$  and the other  $Q$ , Meme 54 recognizes that their joint  $PQ$  mapping cylinder satisfies their joint fibrations and cofibrations. Both of their preimages and images map to their joint mapping cylinder. Their joint image is their joint deformation retract. Their joint preimage uses their joint identity—which is some  $S'_{PQ}$ —to reach that joint mapping cylinder.

**II.10.2** But unfortunately, our commmandos will most probably have different rates of change. Their boundary transformations, formed by running, are unlikely ever to be the same. Indeed, since they both feed into the same mapping cylinder—which is simply the surroundings—then that mapping cylinder will always contain a greater number of transformational possibilities than does any distinct preimage or image lifting to it. There is therefore no necessary guarantee that any preimages and images are identical. We indeed confirm, for Meme 55, that shapes  $A$ ,  $B$ , and  $C$  in Figure 12 need not be homeomorphic, and do not automatically create true squaroids. Our two populations can combine in very different ways every time.

**II.10.3** For Meme 56 we now let a single commando run the entire circulation from  $\alpha_0$  to  $F$  and back to  $\alpha_0$ . This is a complete syntax and semantics and recurvature. The humanoids underneath do the same.

**II.10.4** Although we now have our circulation of the generations, we still have no guarantee that any two such circuits are homeomorphic. But since species certainly exist ... then some wind wall transformations and recurvatures, and some syntaxes and semantics, must be sufficiently close to others ... as, indeed, are the plessists that we have already defined as sufficiently close neighbours. We have to determine the syntax and semantics that could produce such similarities.

**II.11.1** We can find our Chomsky production and recurvature rules by returning to Figure 7 where we exchanged the replication point fibration–cofibration transition for a biology–replication globe one as the start of a generation by creating a Möbius strip interaction across our mapping cylinder of the surroundings. But it is quite easy for these two to be homotopically equivalent, but not homeomorphic. Since not all mappings are fibrations, and also since different dimensions are involved, we cannot just assume we have maintained an equivalence.

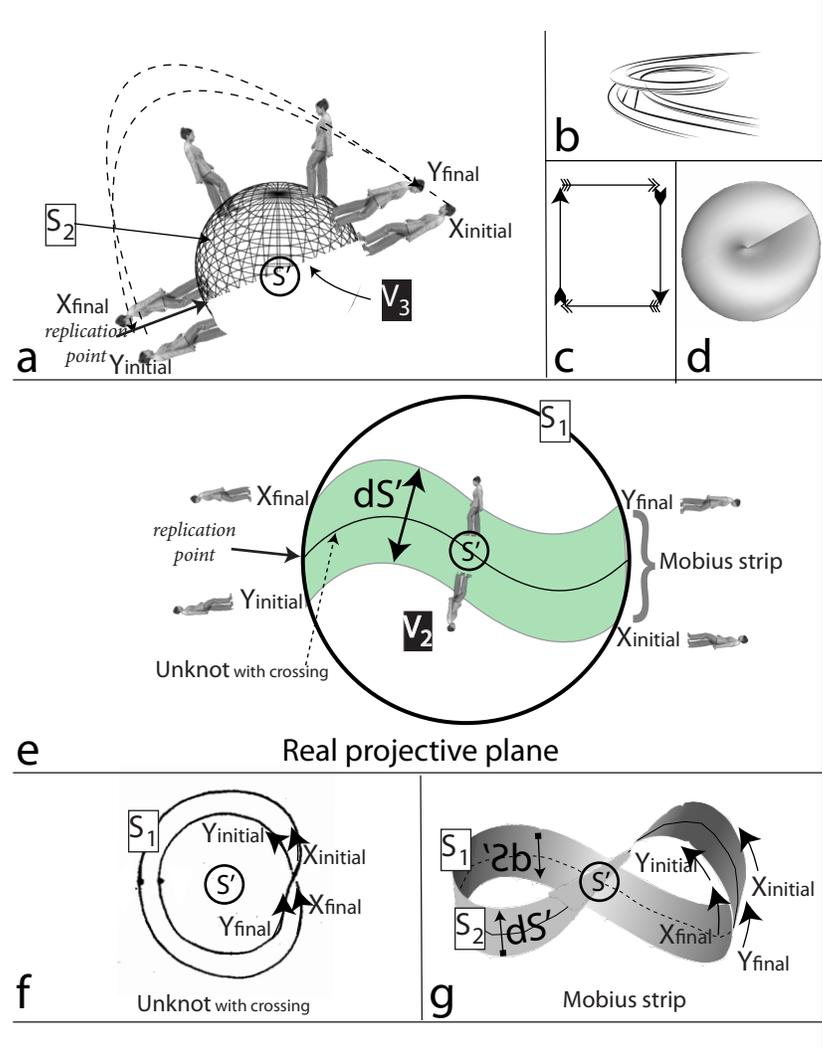
**II.11.2** We can apply our burgeoning self-intersection and topological principles to the Meme 57 we see in Figure 15a as the lady walking about the hemi-rotahedron to produce all recurvatures and a circulation.

Since we already have our Whitney umbrella, which contains our antipodal map and self-intersections, then Meme 58 is to note that since we can get every southern journey on the rotahedron from the north, then we have no real need for that southern hemisphere. We can identify it with the northern one. That way, any wind walls that cross in one half, are guaranteed to cross in the other, and produce a circulation.

**II.11.3** If we cut a rotahedron in half and flatten it down against a plane, the equator goes steadily out to infinity. Bezout’s theorem nevertheless applies equally well to our new self-intersection, even if it moves infinitely far away. Since the point at infinity is properly counted, then every point in the lady’s northern hemisphere uniquely determines one in the south. All points  $y$  in the “missing” southern hemisphere,  $Y$ , are therefore identified by some  $x$  in her currently visible northern  $X$  one.

The identification of opposite points can have consequences for movements proposed in other dimensions. Figure 15b shows what we as three-dimensional beings regard as a perfectly ordinary  $(x, y, z)$  movement and recurvature in three dimensions. It is a highway overpass. But it

**Figure 15: Reproduction and the real projective plane**



would completely mystify a two-dimensional being forced to move in only  $x$  and  $y$ . They would instead see varied movements in their two dimensions, from which they might deduce events in a third.

Identifying our biology and replication globes in that same kind of way allows us to investigate the higher dimensioned  $\epsilon$ - $\delta$  recurvatures. They appear to us, in a lower dimensions, as smooth movements across our mapping cylinder. Identifying the fibration to cofibration transition as a lower-dimensioned replication point, as we do with our hemi-rotahedron, allows us to continue smoothly forwards, through  $\lambda$ . We then undertake, and can measure the effects of, a higher-dimensional transition without taking it explicitly into account.

**II.11.4** Since the northern hemisphere in Figure 15a is topologically homeomorphic to a  $V_2$  rotagon, we can “flatten” it to produce Figure 15e’s planespace. All opposite points are identified.

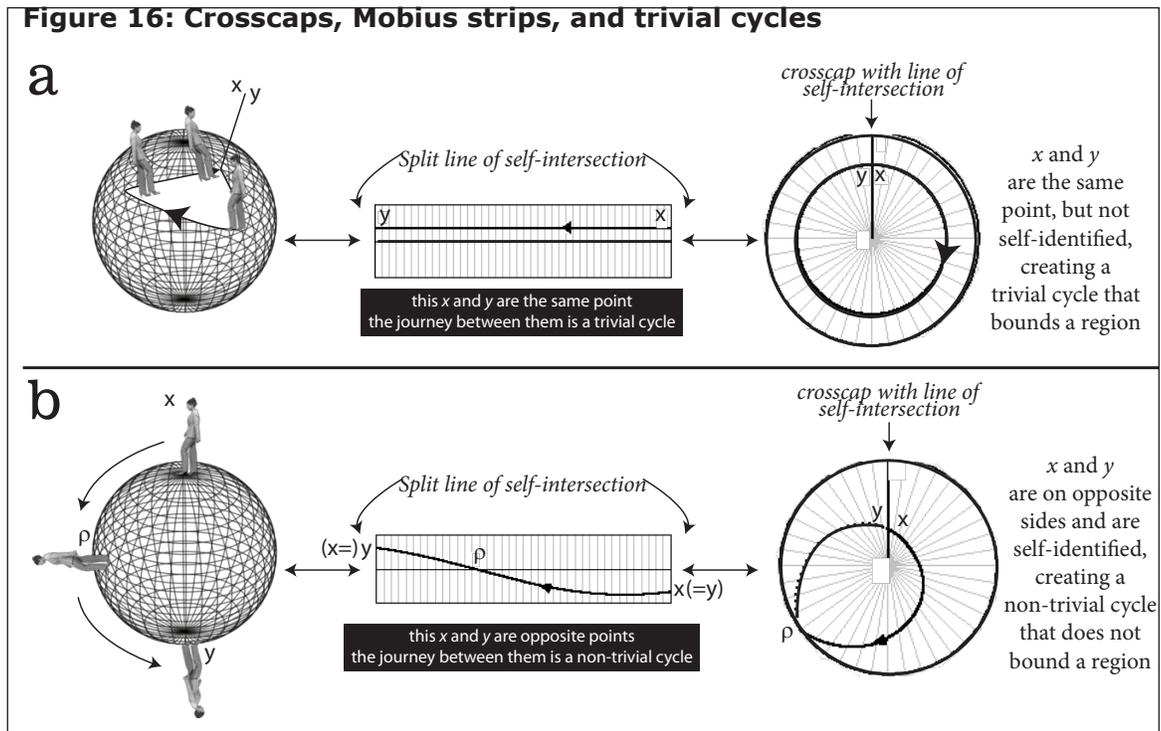
We now have a sphere modulo the antipodal map known as the “real projective plane”. A journey across our new surface is equivalent to one that does a complete orbit about a rotahedron. It crosses over the replication point. It recurves to be both a circulation and a reproduction.

The band across the projective plane has become the complete journey to the opposite hemisphere and back again ... and so is a Möbius strip. We have similarly identified the biology and replication globes. Since this Möbius strip passes through both those biology and replication globes, then it circumscribes a complete generation.

**II.11.5** We now have all our self-intersections in all dimensions. Since we have identified the rotahedron’s two hemispheres, every point upon the projective plane is simultaneously (a) some point  $+r$ ; (b) its antipodal point  $-r$ ; and (c) a line of diameter  $2r$  stretching between them. The real projective plane is therefore a Möbius strip with a disc attached to its boundary. All lines across it are complete planes formed as parts of the geodesics and great circles linking each other diametrically—again in all dimensions—through the origin.

**II.11.6** Although the real projective unfortunately cannot be realized in three dimensions, its “fundamental polygon” in Figure 15c shows how it might be constructed. We first create a Möbius strip by stretching one pair of edges out; twisting them about to make their arrows line up; and then gluing them together. The other two sides are then also stretched out; are twisted so their arrows again line up; and are glued together. That second gluing passes right through the first surface and produces both a complete line of self-intersection and a real projective plane. As in Figure 15d, it looks, in three dimensions, as if it intersects itself, locally. But when seen globally, and in four, it does not self-intersect any more than does the Figure 15b overpass style intersection when observed in three dimensions, and no matter how it might appear in only two when seen by some such lower-dimensioned being. The real projective plane allows us to continue as easily from globe to globe, and

**Figure 16: Crosscaps, Mobius strips, and trivial cycles**



so from beginning to end of a generation, as we do across the replication point. The one is equivalent to the other.

**II.11.7** The real projective plane is the smallest “nonorientable surface”. It is nonoriented because what currently looks like a journey to its opposite side is in fact a continuous shift, in another dimension, that then continues the same journey ... which is in our case the transfer over to the beginning of a next generation.

The real projective plane has an Euler characteristic  $\chi = 1$ . Its complete line of self-intersection, in Figure 15d, is defined by two pinch points at each end, and is formally called a “crosscap”.

**II.11.8** The two points on each edge of a projective plane are identified—glued together—so they are continuous. So also, a journey up a helicoid goes on continuously upwards, yet constantly repeats each point, but always in the next generation. There has in each case been both a fibration and cofibration, which is  $\lambda = \psi + \gamma = \theta + \rho$ .

The points lying on lines upon the projective plane that travel to a boundary have crossed the equator, as the line located at infinity. To again flatten a hemisphere is to push its equator all the way out to infinity; to transition over to the other hemisphere out at infinity; and then to return. But this is the same as simply turning round; going upside down; and returning as if upon the other side.

The points either side of the equator have now been identified. As in Figure 16a, points on lines that do not cross the boundary are not identified, and so are not each other’s antipodes. Thus the lady in 16a does a circuit upon the rotahedron surface. We have  $x = y$  on the rectangle next to her. The two border points are the same for they are the same side of the equator. Since she does not cross the

equator, the rectangle's two end points are not identified. The projective plane on her far right shows her trivial cycle. It bounds a region and returns to the same point. The rectangle's midline and the projective line's boundary are that equator. She makes no contact with either.

**II.11.9** The lady's journey in Figure 16b is different. It crosses the equator at  $\rho$ . The points  $x$  and  $y$  are therefore identified. The path on the rectangle shows that equatorial crossing identified. The  $x$  and  $y$  are the same. But  $y$  is  $x$ 's inverse, for she is now upside down on the other side. The path over on the projective plane now touches the boundary to show that the lady has walked some great circle.

**II.11.10** Each point upon a projective plane is combined with its antipodal one located at  $2r$ . The journey across it traverses both a rotahedron's halves, looping about to return to its beginning. Therefore, any curve starting on a projective plane's identified line that crosses over to its opposite point forms a curve touching the boundary that is immediately a complete circulation of the generations. It involves reproduction. All curves not reaching from boundary to boundary are trivial cycles within one or another hemisphere and/or globe. Those do not pass the replication point or initiate a generation.

**II.11.11** Meme 59 is now to point out that we have our reproductive cycle. Evolution has become a pure exercise in topological reasoning. Our biological self-intersections, fibrations, cofibrations, and biology and replication globe transitions now occur completely naturally, and in whatever dimension.

**II.11.12** We also now have a way to distinguish the biological from the non-biological, and biological trivial cycles from non-trivial ones. We can use a sphere for the trivial, a torus for the non-trivial that can cross an equator, and the real projective plane to establish maxima and minima for those that can do both.



The flattened whole becomes a  $V_2$  rotagon with its  $S_1$  bound. The journey to the opposite side and back is a line across the surface.

**II.12.4** Meme 64 now notes that Figure 17 is specifically created from our Ingredients 1 and 2 of  $t$  and  $n$ , to make  $\tau_m$ . Its bound can then act both recti- and curvilinearly, as both line and linespace in both time and number over a circulation. This simply means that we can always count  $n$  of our chosen artefacts at each moment,  $t$ .

This same meme further notes that  $t$  and  $n$  form (a) the internal  $\tau_m$  planespace as biovolume,  $V_2$ ; and (b) the bounding  $\tau_m S_1$  line, as the biosurface,  $S_1$ . This  $S_2-V_3$  flattening therefore gives our  $S_1-V_2$  rotagon. The meme concludes by noting that such  $S_2-V_3$  to  $S_1-V_2$  flattenings are equally possible for the  $t$  and  $m$ ,  $t$  and  $p$ ,  $n$  and  $m$ ,  $n$  and  $p$ , and  $m$  and  $p$  couplings, making six in all.

**II.12.5** By Meme 65, the  $S_1-V_2$  rotagon we have produced above is also an unknot. Since, for Meme 66, it can shrink to a point, it is simply-connected. This flattening of an  $S_2-V_3$  rotahedron therefore again gives an  $S_1-V_2$  rotagon of various dimensionalities.

**II.12.6** For Meme 67, we confirm that the rotagon we produce has an  $S_1$  circulation with the global topology of a circle ... but the local topology of an infinitely long straight Euclidean line, for that is always how it appears when viewed infinitesimally closely. That bound is a distinct 1-sphere, with Figure 17's again being the conjoined one-manifold,  $\tau_m$ . It therefore gives us both time and number for  $T$  and  $\tau$  for our helicoids and self-intersections, with  $T$  being absolute and rectilinear, and  $\tau$  stating the relative distance between the beginning and end of a generation.

By Meme 68, our  $V_2$  rotagon, bounded by its  $S_1$  surface, can also retract. As on the right of Figure 17, we can observe it in profile. That is a further flattening. It again brings properties together.

**II.12.7** The  $V_2$  disc's profile is a step-down  $V_1$  linespace with  $S_0$  endpoints. It is the linking  $V_1$  line, stretching between  $(r - x')$  and  $(r + x')$ . Our  $V_2$  rotagon's biovolume, and planespace, therefore present an  $S_1$  biosurface, and line, to the surroundings. The enclosed  $V_2$  area is the integral of the  $S_1$  presenting biosurface; while the  $S_1$  line is its circumference and derivative. So by Meme 69, our  $S_1$ , also made from  $t$  and  $n$ , is simultaneously the contained  $V_2$  planespace's derivative. By Meme 70, that line's biovolume is  $V_1 = 2r$ , the step-down derivative. The same holds for all others.

**II.12.8** Then by Meme 71, our  $S_1$  biosurface can also further retract. We can view that line end on. It has two different profiles, one for each end. This gives the two  $S_0$  end points with specific values for  $t$ ,  $n$ , and all others.

Since we now have a further retraction, and step-down derivative, then the two  $S_0$  end points taken together are technically the "0-sphere". They are our  $V_0$  with its  $-r$  and  $+r$  pointspace,

separated by  $2r$ . When pulled apart and suitably joined with others of their kind, they have the syntax and semantics to construct our  $V_4$  rotachoron.

**II.12.9** And then further since, by Meme 72, that  $V_0$  pointspace covers the  $S_1$  line and/or linespace's ends, then the two together are its surface area, such that  $S_0 = 2$ . And those are again the  $-r$  and  $+r$  inputs and outputs. These build our  $V_4$ , and so our biological population, from progenitor domain to progeny codomain. They use the Chomsky hierarchy and this biological grammar of surfaces and volumes which are the recursive functions and infinite cyclic groups and subgroups that build our wind walls and recurvatures.

**II.13.1** If we are to be properly biological, then we must build those wind walls and recurvatures. We must also reconcile the homomorphic, the homeomorphic, and the homotopically equivalent, and properly account for our infinite cyclic groups and their subgroups. We therefore return, for Meme 73, to the four levels Lloyd discusses (2012). They must create the symmetries that can replicate and recurse.

**II.13.2** For Meme 74, we turn to Wilson, who confirms the assignments of our four Ingredients to given biological effects:

Biology is a science of three dimensions. The first is the study of each species across all levels of biological organization, molecule to cell to organism to population to ecosystem. The second dimension is the diversity of all species in the biosphere. The third dimension is the history of each species in turn, comprising both its genetic evolution and the environmental change that drove the evolution (Wilson 2005).

We thus categorize our four one-manifolds of  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  as follows:

- Ingredient 1 is  $t$  and works largely at the population level, sequencing entire groups of our plessists into generations, through  $\tau$  to give  $\tau_t$ .
- Ingredient 2 is  $n$  and arranges and maintains the cells that form the  $n$  entities in any population, but also counts all  $\lambda$  constructs built jointly by  $\psi$  and  $\gamma$  in the infinite cyclic subgroups that act over  $t$  as the  $\lambda$  biology to give  $\tau_n$ .
- Ingredient 3 is  $p$  and mostly arranges molecules into cells; but also provides all energy to build base-pairs into nucleotide codons and the like. It is at the heart of our Chomsky-style semantics, and contributes to  $\psi$ . It gives  $\tau_p$ .
- Ingredient 4 is  $m$ , the molecular nucleotide and DNA count. It is at the heart of our Chomsky-style syntax and contributes to  $\gamma$  to give  $\tau_m$ .

**II.13.3** For Meme 75 we recognize that our four one-manifolds of  $t$ ,  $n$ ,  $m$ , and  $p$  can use the  $S_0$  inputs and outputs with values  $+r$  and  $-r$  to create our plessists and plessemorphs, or biological entities, that enshrine  $\lambda$  through their pointspaces,  $V_0$ . Those are our nucleotide and DNA grammar. And for Meme 76 we recognize the various pointspaces and their behaviours as contributors to distinct one-manifolds.

**II.13.4** Our one-manifolds can now in their turn create their distinct lines and linespaces,  $S_1-V_1$ . There is one for every dimension. This gives values at each point of each of  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ .

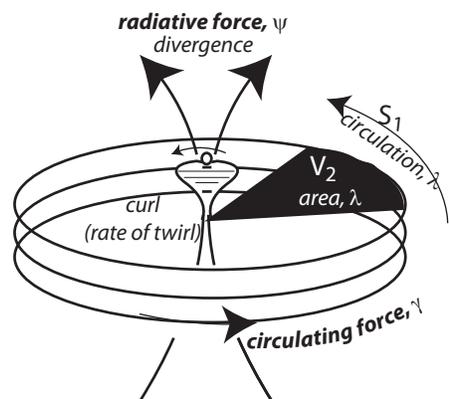
**II.13.5** However, since these manifolds bound a circulation, then they also state the clock times,  $T$ , over which the Ingredients 1, 2, 3 and 4 are each replaced and/or renewed. And since those Ingredients interact with the surroundings, then the one-manifolds are homomorphic. Those absolute

times are  $T$  for the overall circulation to match  $\tau_t$ . The others are  $T_N$ ,  $T_M$ , and  $T_p$  with the absolute time intervals matching the various lengths  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ .

Meme 77 then declares that for every point  $x$  on each manifold, there exists the neighbourhood  $N(x)$  of all points within the distance  $r$ , which is a 1-ball stretching between  $(r - x)$  and  $(r + x)$ . And since each point in  $N(x)$  contains such a 1-ball whose contents are at least  $x$ , then any two neighbourhoods  $N(x_1)$  and  $N(x_2)$  have a mapping that finds all points in each, meaning all four manifolds are continuous. And if they are continuous, while their structures are replaced, then these one-manifolds are also homeomorphic.

And for Meme 78, each one-manifold ranges all about its identity,  $\#$  or  $S^1$ . Each has a 1-ball that contributes to a projective plane. Each spans a complete circulation. They together form our fibrations and cofibrations, and our biology–replication globe boundaries as they contribute to our mapping cylinder.

**Figure 18: Linking the homomorphic, homeomorphic, and homotopically equivalent**



The curl is the force that drives a circulation. It is the localized point-centre of application. It measures the amount of circulating force,  $\gamma$ , per unit of the radiative one,  $\psi$ . It is the “circulation density”,  $\lambda$ .

**II.13.6** The radiative and circulating forces  $\psi$  and  $\gamma$  at work as infinite cyclic subgroups in each of our four one-manifolds produce  $\lambda$  as the infinite cyclic group. They also form the various interconnected  $S_{0,1,2,3}$  biosurfaces that create the self-intersections, the Whitney umbrellas, and the Möbius strips that in their turn bind into the various  $V_{1,2,3,4}$  biovolumes.

The  $d\tau$  biological force is a circulation along the various manifolds per each unit of radiative force,  $d\psi$ , exerted per each interval of time,  $dt$ . It thereby creates  $d\lambda$ . It is also liable to variation.

Maxwell realized, however, that as in Figure 18, every such circulating flow seeks to close a path at some rate. This is in our case to combine the homomorphic and the homeomorphic, in our manifolds, to create the  $\lambda$  biology as the wind wall.

In a process very similar to the construction of a wind wall, when a pie or cake is being baked, it develops a surrounding crust. We can then slice the result. Since every piece of pie is bounded by a length of crust, there is a definite ratio—a flow rate or curl—between the length of crust,  $S_1$ , and the piece’s area,  $V_2$ . Every region is therefore associated with a specific amount of wind wall boundary flow,  $S_1/V_2$ . This is the “circulation density” or circulation per unit area. This curl states the volume density force driving the circulation per each interval, but always as a localized point-

centre of application. There is a definite wind wall pressure and force per each unit contained. Its rate is  $dt = Td\tau$  over the entire circulation.

The curl states the interaction between the biovolume interior,  $V_2$ , and its surroundings,  $S_1$ , that lifts towards the mapping cylinder as  $\theta$  and  $\rho$ .

**II.13.7** Meme 79 now declares that every pointspace,  $V_0$ , upon every manifold is also the  $S_0$  that drives:

- the fibration and cofibration;
- the pinch point self-intersection;
- the movement about the helicoid;
- the recurvature about a rotahedron; and
- the journey across a projective plane.

**II.13.8** Our model now has the archetypal plessemorphs, plesseomes, and plessetopes it needs to describe its population of plessists, plessiomes, and plemes that jointly create both the set of activities as the biological  $\lambda$ , and the surrounding ecology of  $M_\lambda$ . The different recurvatures, wind walls, and interfaces are various combinations of the absolute time spans  $T$ ,  $T_N$ ,  $T_M$ , and  $T_p$ , and the topological manifolds  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ .

**II.13.9** And now that we have all the tools we need to examine the structures that transform within our spaces, we must examine the spaces that support those transformations. We can then relate our model to real world biology and ecology as  $\lambda$ .

# **Part III**

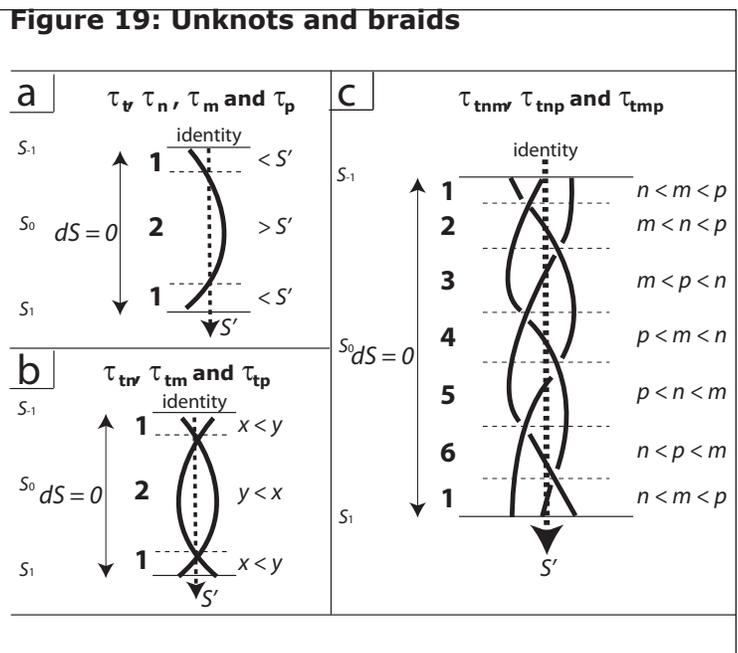
## **Biological spacetime**

**III.1.1** We exchanged the temporality of a generation interface for the non-temporality of a biological–replicative one. But it is the absolute clock times,  $T$ , associated with the former that tell us the homomorphisms populations and their entities use to create their recurvatures. It is instead the manifolds,  $\tau$ , associated with the non-temporal latter that tell us about the spaces and the homeomorphisms through which the populations and entities must transform. These are the surroundings.

Those various manifolds may be continuous and simply-connected, but we cannot assume that the plessists and plessemorphs as the set  $A$ , their plessiomes and plesseomes as the set  $B$ , and their plemes and plessetopes as the set  $C$  will create  $S_{-1}$  plessist populations, as  $(a_{-1}, b_{-1}, c_{-1})$  that will transform into  $S_1$  populations, as  $(a_1, b_1, c_1)$ , that will be both homeomorphic and homotopically equivalent, while their plessemorphs similarly transform from  $(a_a, b_a, c_a)$  to  $(a_b, b_b, c_b)$ . The successors can easily disconnect from their predecessors so they have become either (a) completely nonbiological, or (b) members of alien species. Our Chomsky production rules do not yet guarantee orderly behaviour.

**III.1.2** Since our manifolds can all be retractions, a first problem is that they can combine without necessarily sharing the same dimensionalities. Two very nearby locations can then have different effects. Whether as a single conjoined manifold or various separate ones, the joint manifolds creating any interaction as the fibration–cofibration at the replication point, or else as the biology–replication one that marks a generation’s beginning, will then have radically different consequences upon the same structures, simply through having different dimensionalities.

By Meme 80, the unknots and “one-braids” in Figure 19 represent the one-dimensional and one-manifold linespaces of  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ . Just as do the gluing diagram in Figure 15c and the projective plane in 15e, they recognize that their two ends are continuous. If we glue those ends back together, we get the “closure of the braid” that restores each unknot. Each is then a continuous stream of homomorphic events that are certainly homotopically equivalent. When we, for example, combine  $t$  and  $n$  to make  $\tau_m$ , then the results in different places and times are most likely to be only homotopically equivalent. The two brought together can only be homeomorphic, given their different dimensionalities, if the locales always act in concert. So we must not only guarantee that each individual manifold can impose a recurvature on any given set of entities. We must also ensure that they keep behaving in the same ways when they interact.



**III.1.3** If the population is to continue, then the wind walls must recurve. Each manifold must return to its beginning. We can distinguish between the homeomorphic and the merely homotopically equivalent, in such situations, by recognizing, for Meme 81, that each of our one-manifolds has three inter-related aspects:

- each recognizes the rectilinear **ijk** axes by overseeing a set of temporal sequences,  $dt$ , that create successive moments,  $t$ , across the absolute temporal interval 0 to  $T$ ;
- each recognizes the curvilinear **IJK** axes by ranging from some minimum to some maximum, and back again, and so about its identity,  $S^\circ$ ;
- each recognizes the Frenet-Serrat **TNB** axes by transforming between Euler's unit limits 0 and 1, and so by both the above infinitesimal increments  $dt$  and  $dS$ .

The total transformations that the radiating and circulating forces  $\psi$  and  $\gamma$  cause, across each manifold, and so from  $S_{-1}$  to  $S_1$ , sum as  $\int dS^\circ = 0$ . All unknots therefore have a circulation distance  $\tau$ , while also being replaced by some identity quantity,  $S^\circ$ , over the absolute generation time  $T$ . This is a direct relationship between  $d\tau$  and  $dt$  as  $dt = Td\tau$ . It links the homo- to the homeomorphic.

**III.1.4** Each of the four one-manifolds is distinct. They need not, therefore, respond in the same ways:

- By Meme 82, Ingredients 2—which form both the individual plessists and the archetypal plessemorphs, of set  $A$ , that incorporate  $\lambda$ —are replaced over both the absolute time interval  $T_N$ , and the distance  $\tau_n$ .
- By Meme 83, Ingredients 3—which are the plemes and the plessetopes,  $\psi$ , of set  $C$ , that the plessists and plessemorphs use to interact both with each other and the surroundings—are replaced over the absolute time interval  $T_p$ , and the distance  $\tau_p$ .
- By Meme 84, Ingredients 4—which are the molecular-based plessiomes and plesseomes of set  $B$ , and therefore the DNA nucleotide codons,  $\gamma$ —are replaced over the absolute time interval  $T_M$ , and the distance  $\tau_m$ .

**III.1.5** We now have to find the conditions, for each manifold, that can guarantee when the homotopically equivalent are also homeomorphic. So Meme 85 is to note that the total  $\int dS^\circ = 0$  transformation over each manifold occurs over both  $T$  and  $\tau$ . The former is some combination of  $T_M$ ,  $T_N$ , and  $T_p$ ; the latter of  $\tau_n$ ,  $\tau_m$  and  $\tau_p$ . While the former set govern the homomorphic and so structural events, the latter create the spaces in which they occur, and so the homeomorphisms. The two taken together are the fully biological,  $\lambda$ . They establish the overall rates for the fibration and cofibration, across the biology–replication globe boundary, as well as for the generational transition.

Meme 86 is to note that every one-manifold that recurves and forms a one-braid also states its relationship to its own identity,  $S^\circ$ . This is each one's midpoint value. It is each one's contribution to the replication point.

Since that  $S'$  midpoint and identity exists for every manifold, then as each traverses from its beginning to its end, each is always obliged to be either less than, or else greater than, its identity: either  $>S'$ , or  $<S'$ . Each therefore has two states or regions. Each “flips” from one orientation to the other as the generation proceeds. That “braid-1” orientation in Figure 19a portrays those flips across the circulation.

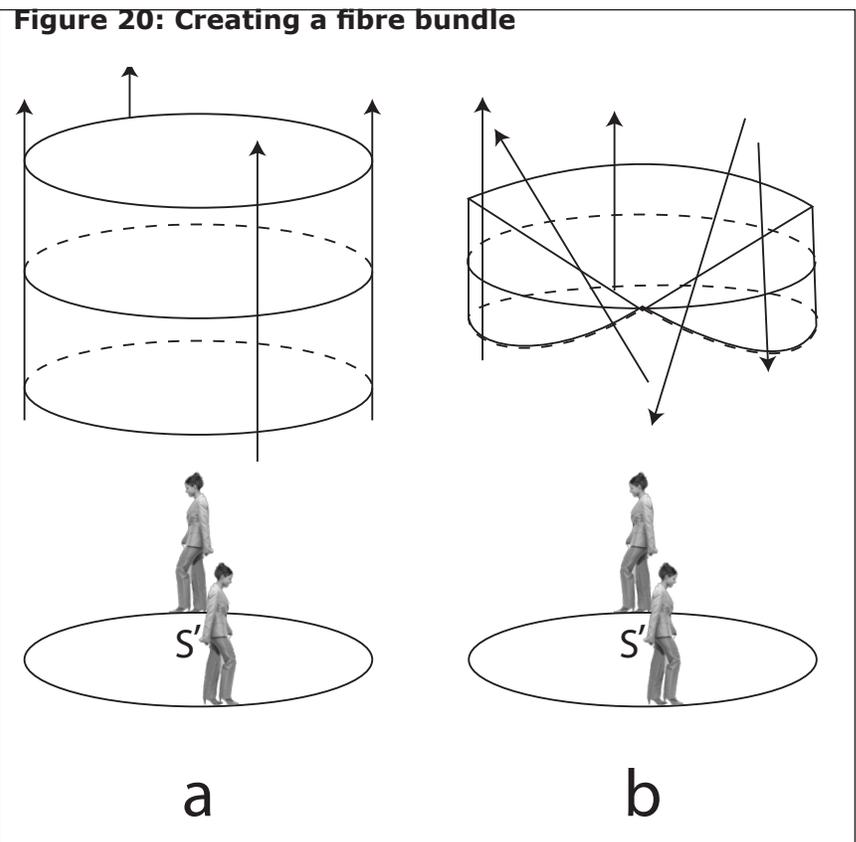
**III.1.6** We then establish, for Meme 87, the extremely important difference between:

- manifolds with  $\tau_t$ ;  
and
- manifolds without  $\tau_t$ .

This states an important constraint. Only those populations and events that remain under the influence of  $\tau_t$  can accelerate hyperspherically and continue with the circulation. The  $\tau_t$  dimensionality therefore distinguishes the manifold combinations that have the recurvature velocities and accelerations that can complete a generation from those that can form only trivial cycles, and so that must gradually become unbiological.

**III.1.7** Figure 20 highlights the consequences of the above distinction. Entities and components without  $\tau_t$ —being  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ —move from preimage to image; or vice versa; or else from biology to replication globe; or vice versa ... but not both. They are observable values for  $n$ ,  $m$ , and  $p$  that gradually dissipate, without returning to the globes. They must fly tangentially away from their current hyperspherical point-, line-, plane-, realm- and tetraspaces. They must decelerate and exit from whichever globe or its complement. They must dissipate and become nonbiological materials, ceasing to participate in recursive functions, looping rectilinearly outwards, into the surroundings, through the surfaces,  $S$ , of points, lines, planes and realms. They therefore go from 0 to  $T$  without returning to any original condition. They are not heritable.

**III.1.8** For Meme 88 we can bring our one-manifolds together in pairs. We get the six combinations  $\tau_{tn}$ ,  $\tau_{tm}$ ,  $\tau_{tp}$ ,  $\tau_{nm}$ ,  $\tau_{np}$ , and  $\tau_{mp}$ . They are all perspectives that keep two others constant,



similarly to the planespaces  $(x, y)_{zw}$  etc.

Irrespective of their outward behaviour, these coupled manifolds are all surfaces. They are planes and planespaces. Each has the duple,  $(x, y)$  that establishes a 2-ball. However, only  $\tau_{in}$ ,  $\tau_{im}$ , and  $\tau_{ip}$  can provide the values for  $n$ ,  $m$ , and  $p$  at that moment  $t$  that allows that population to continue being biological. They provide the driving forces for the curls and circulations that create the recurvatures.

In contrast to that, the three two-manifolds  $\tau_{nm}$ ,  $\tau_{np}$ , and  $\tau_{mp}$  are all without  $t$ . Their properties  $nm$ ,  $np$ , and  $mp$  must therefore emerge, rectilinearly, through surfaces. The  $nm$  establishes the population's total of chemical components; the  $np$  does the same for the population energy; and the  $mp$  is the characteristic population energy density. They are the only properties directly observed.

We then recollect that Newton tells us that if we represent our population values as  $x/x'$ , and so in terms of the identity; and if we thus let  $x$  oscillate either side of  $x'$ , ultimately returning to its initial value; then we complete a cycle. We then have (a) the acceleration for an orbit; and (b) a bounded  $x$  region, with  $x'$  as its centre. Thus the  $n$ ,  $m$ , and  $p$  that can continue about the circulation are associated with an  $nm$ ,  $np$ , and  $mp$  that cannot. They nevertheless share a set of minimum and maximum values.

**III.1.9** As the drum major in Figure 20 now marches around her identity,  $S'$ , she creates a set of circular  $n$ ,  $m$ , and  $p$  bounds for the emerging and rectilinear  $nm$ ,  $np$ , and  $mp$  they form. That circulation, no matter what its dimensionality, can now be the one-manifold that acts as the foundation for a set of biological-ecological transformations.

Whitney (1940) first properly defined the terms now in common use. In his terminology, the drum-major's traverse is acting as a "base space". He referred to the baton that she takes up as "fibre". And if she holds her fibre over her base space as she walks, then she creates a "fibre bundle". It is the product of two contributory topological spaces.

Fibre bundles create a conjoined  $XY$  topological space that allows us to draw conclusions about the original  $X$  and  $Y$ . If, for example, our  $X$  base space is the globe of the earth, while the  $Y$  fibre is the wind velocity at each point, then the resulting  $XY$  fibre bundle allows us to conclude—in line with algebraic topology's "hairy ball theorem" that there is no non-vanishing continuous three-dimensional tangent vector field on an even-dimensional  $n$ -sphere—that there is always some point where wind velocity is zero.

**III.1.10** The one-manifolds that are our base spaces and fibres can easily have different dimensionalities. Their interaction will then certainly be homotopically equivalent, but need not be homeomorphic. The fibre bundles that two different populations or generations can each create can only be homeomorphic if the dimensionalities of each of their bases and fibre bundles match.

Just as the drum major's base space can oscillate using  $x/x'$ , so can the fibre potentially oscillate as  $y$  about  $y'$ . However, if we ensure that our fibre always stays the same side of its  $y'$ —such

as when a tree grows from a minimum to a maximum, and does not itself return to any minimum, thus always being  $+dx$ ; or when a sperm cell swims and depletes its mass-energy, without fertilizing to return to a maximum, so always giving  $-dx$ —then our baton or fibre is the line segment  $Y = [0, 1]$ .

Since our base space is  $X = S_1$  for a circle; while the baton or fibre is  $Y = [0, 1]$  for a line segment; then the bounded  $x$  region, upon the projective plane and/or Möbius strip must be a trivial cycle. The  $x$  region, supporting that  $y$ , is an orientable disc formed about a rotahedron's surface. It does not cross a hemisphere. That limited and bounded  $x$  region will—as a homeomorphism—be a region of discrete biological activity. As a homomorphism, it will be a set of ordinary nonreproductive metabolic-physiological processes undertaken by the entities. It will only move from preimage to image or vice versa; and/or from replication to biology globe or vice versa; but it does not undertake both transitions, for it does not have both recurvature points. It does not cross the replication point and so does not complete a generation.

As in Figure 20a, this limited fibre bundle, created as  $X \times Y$ , will be a cylindrical  $x \times y$  bundle that again does not reach from boundary to boundary. Such fibre bundles can contribute to either a fibration,  $\theta$ , or a cofibration,  $\rho$ , but not to both.

**III.1.11** As in Figure 19b, the three two-manifolds  $\tau_{in}$ ,  $\tau_{tm}$  and  $\tau_{ip}$  are critically different. They all contain  $\tau_c$ . They can freely therefore cross the equator and pass through both identification points. By Meme 89, since each individual manifold in these latter couplings, with  $t$ , maintains its distinct identity, then they can both at some times be less than each of their respective identities; they can both at other times be greater; or one can be greater while the other is less; and vice versa. They are two-braids that exhibit the closure of a braid, and so can return to their start points for a generation. Since they contain  $t$  they have the global topologies that wrap around to create a circulation of the generations.

**III.1.12** But if two-manifolds are indeed going to wrap around for a generation, then they must still abide by certain constraints. By Meme 90, we can relate the two components directly to each other. One will then at some point be greater than the other; and at other times it will be less. The two therefore see-saw about each other in two overall regions. Their two-braid thus creates Figure 19b's "braid-2" with those two flip orientations. But their combination—as they cross the projective plane and curve about the circulation—is always some  $S$ ; the sum of their changes is still  $\int dS = 0$ ; and their overall equilibrium is still some  $S'$ .

**III.1.13** We now add the extra constraint, seen in Figure 20b, that a recurvature point exists. The drum major now twirls the baton with sufficient acceleration to range  $y$  both sides of  $y'$ . As she marches, our  $y$  now oscillates about its midpoint, and goes through its own complete revolution in conjunction with  $x$ . The point of recurvature will occur when the rates of change of latitude and longitude, relative to the surface, are zero.

We have here a different  $X \times Y$  product. Suitable initial values plus rates of change mean the drum major carries this fibre right across the projective plane. Both base and fibre can now return to their start points for a generation. The baton's recurvature or inversion is the constraint that creates the fibres that can then participate in nontrivial fibre bundles.

We now have a Möbius strip: the simplest nontrivial example of a fibre bundle. It has the lifting property that allows it to provide both fibrations and cofibrations with its recursive functions. The recurvatures help create the curvilinear point-, line-, realm-, and tetraspaces that are the biovolumes,  $V$ , that drive all biology. It crosses both the replication point and the generation bound.

**III.1.14** For Meme 91, we next conjoin the manifolds in threes. They form the four 3-balls, realms, and rotahedrons  $\tau_{tnm}$ ,  $\tau_{tnp}$ ,  $\tau_{tmn}$  and  $\tau_{tmp}$ .

By Meme 92, all the four rotahedrons can create realms whose local topologies and fibre bundles are flat, featureless, and Euclidean. They have the familiar three dimensions of left-right, front-back, and up-down, or  $(x, y, z)$ .

However, the  $\tau_{tnm}$  rotahedron is different from the other three. It is again without  $t$ . It can only access Euclidean properties. So by Meme 93 it cannot recurve any of  $n$ ,  $m$ , or  $p$  about a circulation; and it cannot create nontrivial fibre bundles.

By Meme 94, the three remaining rotahedrons— $\tau_{tnm}$ ,  $\tau_{tnp}$ , and  $\tau_{tmn}$ —all contain  $\tau_t$ . They can all recurve globally to form realmspace. Over their whole cycle, however, one component will sometimes be greater than the others; sometimes less; and sometimes in between. The three interact to form biological parallelepipeds whose side lengths see-saw about a cube, producing both the three-braid and the “braid-3” shown in Figure 18c. They establish the accelerations and values for  $nm$ ,  $np$ , and  $mp$  at each point in a generation. When one of its three components either increases or decreases, the other two must flip to either decrease or increase to maintain equilibrium. This gives six flippable orientation regions of greater and lesser inequalities. The sum of all their joint realmspace changes is still zero ... and a joint  $S'$  equilibrium again exists.

**III.1.15** And finally, Meme 95 brings all four one-manifolds together. The fourth splits each of the six braid-3 regions to give a constant  $t$ -acceleration. This draws all local and global topologies together to create an overall four-manifold and rotachoron tetraspace of  $\tau_{tnmp}$ . This creates a four-braid and a “braid-4”. It is a “four-parallelotope” whose side lengths see-saw about a tesseract. This gives 24 regions—such as  $t > n > m > p$ —navigated in regular succession for both  $S$  and  $S'$ , with various dimensional flip orientations and permutations to create a rotachoron. Since  $t$  is present in them all, then  $n$ ,  $m$ , and  $p$  recurve about each other to form a circulation.

These  $t$ -accelerations in the various  $\tau_{tnmp}$  configurations are now responsible for all terrestrial biology. They establish the values for  $nmp$ —and a braid-3—all about the circulation; as also for each of them again in their different configurations throughout all three- and two- manifolds, both homomorphically and homeomorphically. If any of  $n$ ,  $m$ , or  $p$  are considered biological, then both

their recurrence or generation length  $T$ , and the population that contains them, must be specified. That is the recursive biological function and process that uses the nucleotide codons of DNA to create all circulations of the generations specified by the  $t$  in  $\tau_{t\text{tmp}}$ .

**III.1.16** Our  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  manifolds therefore behave as follows:

- The  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  in isolation have each been flattened from some higher dimension of  $\tau_{tn}$ ,  $\tau_{tm}$ , and  $\tau_{tp}$ , and carry  $n$ ,  $m$ , and  $p$  values measured in the surroundings at that given time  $t$ , and at that point in the overall circulation. The one-braid and braid-1 give them a constant state maintained as  $d\tau/dt$ .
- The  $\tau_{nm}$ ,  $\tau_{np}$ , and  $\tau_{mp}$  have also each been flattened from  $\tau_{tnm}$ ,  $\tau_{tnp}$ , and  $\tau_{tmp}$  and therefore possess a constant acceleration to keep exhibiting those values all about a circulation. The two-braid and braid-2 carry them through their values from minimum to maximum and returning as  $d^2\tau/dt^2$ .
- The  $\tau_{nmp}$  has been flattened from  $\tau_{tnmp}$ . This then carries the  $nmp$  all about the circulation. They get their values from the three-braid and braid-3, as  $d^3\tau/dt^3$ .
- The whole is maintained by the governing  $S_3-V_4$  rotachoron that establishes the overall biology and ecology of  $\lambda$ , and through the  $\theta$  fibration and  $\rho$  cofibration.

**III.2.1** Figure 21 now confirms Meme 88. When our  $n$ ,  $m$ , and  $p$  manifolds are independent of  $t$ , then as in Figure 21a, they cannot create circulating biological-temporal momentums. They must instead move rectilinearly. Since the  $\tau_t$  manifold does not accelerate them hyperspherically about the circulation of the generations, they can only form “spacelike” structures. Those are without  $t$ . They again ray out through surfaces upon the rectilinear  $ijk$  axes. They become measurable, in the surroundings, with SI units, as the various observed biological constructs, and obey the second law of thermodynamics.

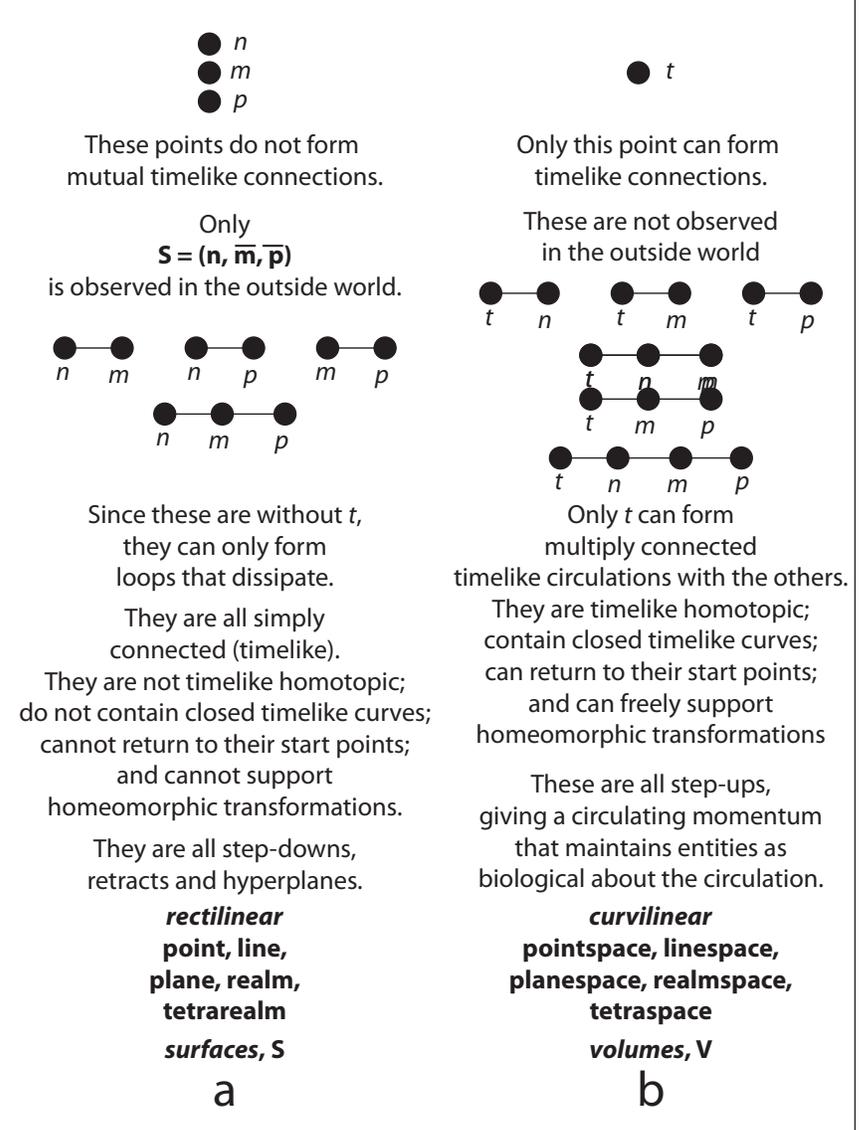
**III.2.2** Meme 96 then specifies, as in Figure 21b, that when  $n$ ,  $m$ , and  $p$  are accelerated about the circulation by the  $\tau_t$

manifold, they associate with  $t$  in some hyperspherical biovolume,  $V$ . The only way to measure them is through some biological population,  $V$ , that encloses them within some set of biological structures,  $S$ . That population has then used its recursive functions as a language of syntax and semantics to create the necessary nucleotide codons.

Each of the  $n$  plessists that the  $\tau_t$  and  $\tau_n$  manifolds form bind their distinct Ingredients 3 and 4 stocks of  $p$  and  $m$ . Those can then undertake their metabolism and their physiology as infinite cyclic groups, complete with infinite generators, and infinite cyclic subgroups through  $\gamma$ ,  $\psi$ , and  $\lambda$ .

**III.2.3** If the plessists formed by the  $\tau_t$  and  $\tau_n$  manifolds are to reproduce, they must recur. They must form wind walls. But they must also be biological. They must survive for the time  $T_N$ —which is the circulation length  $\tau_n$ —so they reach the replication point. They can then be observed using their cofibrations and their nontrivial fibre bundles to reproduce.

**Figure 21: Simply and multiply connected timelike**



A biological circulation can only exist, at every moment  $\tau_0 t_0$ , when there is a positive number,  $n$ , of plessists. The circulation as a whole must therefore have  $\int dn \geq 0$ .

**III.2.4** Each of the  $n$  plessists that exists at any time can only, by definition, contribute to its  $\tau$  circulation for as long as it accelerates hyperspherically. When each has  $\int dp < 0$  and/or  $\int dm < 0$ , then each is by definition trivial and without  $t$ . Each can only dissipate. So if each is to recurve and be a generator, then each must satisfy  $\int dp \geq 0$  and  $\int dm \geq 0$ .

**III.2.5** Since each individual plessist in a reproducing population must have its distinct stock of  $p$  for its plemes, and so that  $\int dp \geq 0$ , then there immediately exists a population energy,  $P$ , that satisfies:

$$P \equiv n\bar{p},$$

where  $\bar{p}$  is the average individual value over the population, along with a suitable distribution.

**III.2.6** There must also be a joint population mass  $M$ , plus distribution, satisfying:

$$M \equiv n\bar{m},$$

where  $\bar{m}$  is now the average individual components value, as their plessiomes, plus its distribution.

**III.2.7** For every population value  $P$  and  $M$ , then there are by definition  $n$  plessists, each of  $p$  and  $m$  for its plemes and plessiomes. But these  $n$  plessists can now always be substituted for by their  $n$  plessemorphs. There are always—and by definition— $n$  such in any plessist population, demonstrating the right helicoid behaviour. This is all so by definition, and in our model.

**III.2.8** For every  $n$  plessists we immediately have a shared value  $\bar{p}$  and  $\bar{m}$  and a population  $P$  and  $M$  constructed equally by those plessists and their archetypal plessemorphs. The  $\bar{m}$  defines the plesseomes for each of the  $n$  plessemorphs. And since it is two-dimensional, it exhibits a surface that supports a recurvature. In the same way, the  $\bar{p}$  defines the distinct plessetopes for those same archetypal  $n$  plessemorphs, as the surface supporting the same recurvature.

**III.2.9** We note, for Meme 97, that all our population's measurable properties,  $S$ , for those plessists and their plessemorphs, must now be given, through those same plessemorphs, by:

$$S \equiv (n, \bar{m}, \bar{p}).$$

**III.2.10** By Meme 98, then at every moment all about the circulation, which is for every  $\tau_0 t_0$  between  $\tau_{-1} t_{-1}$  and  $\tau_1 t_1$ , our plessemorphs are described, in terms of the plessists they substitute for, by  $\bar{p} = P/n$  and  $\bar{m} = M/n$ . These must always exist, along with their infinitesimal plesseome and plessetope increments of  $d\bar{m}$  and  $d\bar{p}$ . This is again so by definition.

By Meme 99, the population's instantaneous change at any time is given by:

$$dS \equiv dn + d\bar{m} + d\bar{p}.$$

**III.2.11** We have already met the above as the braid-3 of Figure 19c. And since the population identity  $S'$  can only be preserved when  $dS' = dn' + d\bar{m}' + d\bar{p}'$ , then when any one of  $n'$ ,  $\bar{m}'$ , or  $\bar{p}'$  leaves that equilibrium value, then at least one of the other two must move in the opposite direction to restore it. That net  $dS'$  interaction must now define the  $dt = Td\tau$  equilibrium that is the biological activity  $\lambda$  at every point. It characterizes the plessemorphs and their plesseomes and plessetopes that in their turn create the 1s for the doubly closed equilibrium that define  $\pi$ .

**III.2.12** And ... by Meme 100, this is all a Lorentzian four-manifold. Those sub-manifolds without  $\tau_t$  can only form simply-connected timelike loops that can use their embedded Hooke cell and deformation retract of  $(n', \bar{m}', \bar{p}')$  to lift as fibration,  $\theta$ , from image to mapping cylinder, or else as cofibration,  $\rho$ , from preimage to mapping cylinder. Each is also either a  $\lambda$  journey from image to preimage as progeny codomain to progenitor domain; or else from preimage to image as progenitor domain to progeny codomain.

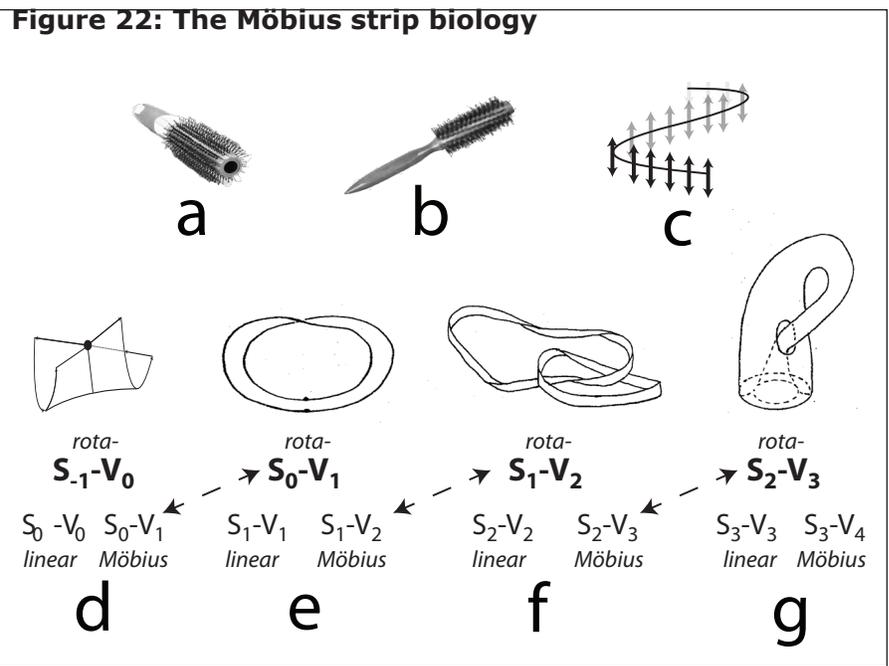
The submanifolds formed with  $\tau_t$  are multiply-connected timelike. The entities formed can now use the same  $(n', \bar{m}', \bar{p}')$  Hooke cell and deformation retract, embedded in them, to recurve. They can eventually undertake the inverse transitions of both  $\rho$  cofibration and  $\theta$  fibration that lift from both preimage and image to the same mapping cylinder, creating the complete biological-ecological interactions,  $\lambda$ , for a generation.

**III.2.13** We now have both the homomorphisms and the homeomorphisms that describe any group of plessists. We can also identify  $\bar{m}$  with  $\gamma$ , and  $d\bar{m}'$  with  $d\gamma$ ; and  $\bar{p}$  with  $\psi$ , and  $d\bar{p}'$  with  $d\psi$ . But ... these are precisely the components in our Whitney umbrella.

**III.2.14** And since  $M = n\bar{m}$  then if ever  $n$  stays constant  $M$  and  $\bar{m}$  must have changed at the same rate over some interval,  $T$ . The same goes for  $P = n\bar{p}$ .

**III.2.15** We indeed have  $n = M/\bar{m} = P/\bar{p}$ . This means that if ever the population values  $M$  and  $P$  change at a different rate from the individual values  $\bar{m}$  and  $\bar{p}$ , then numbers,  $n$ , must be changing. And ... this is very easy to measure. It was indeed the basis of our entire *Brassica rapa* experiment.

**III.3.1** The realization that two or more of our distinct dimensions can combine to act as a single one-manifold is highly problematic. As in Figure 22, biological entities have three modes of presentation. It is why we cannot yet define a species. Those random manifold and dimension combinations allow the homomorphic to be merely homotopically equivalent without being homeomorphic.



**III.3.2** By Meme 101, although our homomorphisms can demonstrate their equivalence by being locally indistinguishable, they are our biological structures centred upon points. Our homeomorphisms are—by contrast—the specific recurvature-capable transformations maintained by these homomorphic and so fully replicative biological structures. But whether our interactions are merely homomorphic or more specifically homeomorphic, they will involve both (a) the points that are the individual homomorphisms and structures, and (b) the entire groups of points that are then the homeomorphisms as the spaces being occupied.

**III.3.3** Again by Meme 101, our homomorphic biological structures reside in those topological spaces called manifolds. A manifold’s properties mean that every point in any homomorphic neighbourhood—which is a biological structure—will always appear locally Euclidean, while globally being otherwise. The structure can now globally either simply dissipate; or else successfully remain biological and transform via the replication globe. But they will appear the same, locally.

**III.3.4** Since our biological manifolds can have different dimensionalities, then they are, locally, some collection of the real numbers,  $\mathbf{R}$ . The number of different real numbers we need to represent any given biological structure depends upon that dimensionality,  $n$ . So if some biological homomorphism uses  $n$  distinct sub-manifolds, then we can easily track its biological homomorphisms with some  $\mathbf{R}^n$ . This simply means a collection,  $n$ , of coordinates which are real numbers,  $\mathbf{R}$ .

**III.3.5** Fibre bundles are instead based on entire neighbourhoods ... i.e. they are constructed from entire groups of points, and not simply from points. Like the two hairbrushes in Figure 22a and b, a fibre bundle involves three different topological spaces, each of which is in our case a manifold. We

have (i) the base,  $B$ , which can be a first homomorphic structure, and which on the hairbrush is its underlying cylinder; (ii) the fibre,  $F$ , which can be either the surroundings or another manifold, and is the hairbrush fibre; and (iii) their product space  $P = B \times F$ , which is the hairbrush's overall shape.

The fibre bundle now means that every neighbourhood, or small region, of  $P$  will look like whatever is the composition,  $B \times F$ , of both base and fibre. That product space is their local neighbourhood coordination of points.

Our fibre bundles can track all our homeomorphisms, which are the effects our two homomorphisms have on each other and on the surroundings. They can do so on their joint product space,  $P$ . Each  $P$  can then use a “projection map”,  $\xi$ , to map continuously back to each of its  $B$  and  $F$  components ... but so that it has a continuous surjective, or onto, function,  $\xi(p) = b$ , which maps from  $P$  to the base space,  $B$ . So if we begin at some  $p$  in  $P$ , such as the tip of some hairbrush fibre in Figure 22a, then we can project along the fibre, back down to embed  $b$  in  $B$ . For every point  $b$  in  $B$ , there is at least one point  $p$  in  $P$ .

**III.3.6** However, we could in fact have created a product space that is instead a Möbius strip, such as with the twisted hairbrush in Figure 22b. But unfortunately, the projection  $\xi(p) = b$  along the fibre back to the base works just as well as it did in the straight hairbrush in Figure 22a. This means that the points  $p$  in our product space  $P$  can easily have attributes not originally present at any  $b$  in  $B$ . Fibre bundle neighbourhoods can clearly have extra properties not present in either base,  $B$ , or fibre,  $F$ . We cannot therefore define species as proposed groups, because they will exhibit recurvature behaviours different from any of those possessed by their members, but in unpredictable ways.

**III.3.7** A circle as base, and a line segment as fibre can create either a cylinder or a Möbius strip for their fibre bundle. But all neighbourhoods in both the resulting cylinder and the Möbius strip will still be locally indistinguishable. Either way, we get our embedding into the base. We can now easily have our semantic and/or syntactic comprehension capability, in our product and fibre bundle, but with one or another of the aphasias. The information from either the base or the fibre necessary to fully access the product space need not necessarily arrive.

**III.3.8** Figure 22c also shows that a line segment taken as the fibre to a circle, for its base, can potentially produce a “tangent bundle” that appears, locally, as an infinitely long straight line,  $U$ . The tangent bundle is some “open set”,  $U$ . This simply means there can be infinitely many different ones, of infinitely many types, but all tangential. Each open set appears, locally, as  $U \times \mathbf{R}^n$ .

**III.3.9** Figures 22d, e, f, and g, and their Meme 101 tell us that (i) the rectilinear Euclidean, (ii) the circular, and (iii) the twisted Möbius fibre bundles are all locally indistinguishable. Figure 22d tells us that our  $S_{-1}-V_0$  pointspace—which builds all biology—is a Whitney umbrella bounded by  $-r$  and  $+r$  input-output points. These can circle outwards and return to pass through the same

point, but with opposite properties, so manifesting a  $V_0$  pointspace. But it can all the time act, to the surroundings, with a flat  $S_0$  unchanging Euclidean local topology. A given cell can have the same inertia whether it is a parent, or is busy splitting into two daughters.

**III.3.10** A population can only complete a circulation if it and its entities exhibit a constant acceleration to carry them about some recurving wind wall. The components must undertake whatever transformations will return them to the beginning of a generation,  $\tau$ .

**III.3.11** These three possibilities—the linear, the circulating, and the twisted—mean that any two  $S_0$  points can bound an  $S_0-V_1$  line with a flat Euclidean  $S_1$  local topology. The resulting curving linespace and global topology can bound a  $V_2$  planespace. That  $S_1-V_1$  line could also however be the  $S_0-V_1$  unknot with crossing, of Figure 22e. It can then bound what looks distinctly like an  $S_1-V_2$  rotagon. It now has the extra dimension, and so can acquire a crossing.

We can use any  $S_1-V_1$  line or linespace to curve about and form an  $S_1-V_2$  rotagon. This again has the local topology of a flat and unending Euclidean plane, but the global topology that bounds a  $V_2$  planespace. But we can just as well produce that same infinitesimally local planespace by travelling infinitely often about the  $S_1-V_2$  Möbius strip of Figure 22f. The result is indistinguishable from either a rotahedron's infinitely surrounding  $S_2$  manifold surface upon an  $S_2-V_3$  rotahedron; or from an infinitely extended Euclidean plane.

We can in the same way create an  $S_2-V_3$  rotahedron with a flat and infinitely extended plane for its surface that is entirely consistent with an infinitely extended  $S_3$  Euclidean local topology for a realm; but that nevertheless has the global topology of an ever-curving three-dimensional realmspace. But we can get that same  $V_3$  realmspace by going indefinitely about the surface of a Klein bottle as an  $S_3-V_4$ .

**III.3.12** If our drum major now takes up a zero-dimensional point and uses an  $S_1$  marching circle as her base, then she creates an identical  $S_1$  circle for her fibre bundle. But since the point is locally rectilinear and Euclidean, it is a value maintained invariantly over time. And further since it is accelerated about the circle that is its base, it forms a trivial cycle upon a rotahedron. It bounds a region.

**III.3.13** We now add the extra constraint that our drum major twist that point as she marches. This is the Whitney umbrella and its  $S_0-V_0$  transformation as the point seemingly journeys between  $-r$  and  $+r$  in its pointspace, demonstrating first one then the other, so being first an input, and then an output, while all the time maintaining its absolute value,  $|r|$ . It is now carried all about a generation.

The fibre bundle is no longer a trivial cycle. It instead becomes an unknot with crossing. It can participate in a recurvature.

**III.3.14** We now have the two globally curving neighbourhoods formed by a “0-ball” as fibre, at a given distance from a circle as base: one with twist, and the other without. The former’s twist means it can switch from  $+x$  to  $-x$  and so cross a real projective plane. The latter cannot.

**III.3.15** If the drum major next takes up a line segment as a fibre—which is some property’s journey outward from its minimum to its maximum, or else conversely—then her marching produces a cylinder as fibre bundle. And if we again add the twisting constraint, to allow the value to move to the other side of an identity and to return to its initial value to complete a circuit, then we again have a recurvature. Some single value can both increase and decrease while others remain the same. We have a Möbius strip. These are the two neighbourhoods formed by a 1-ball as fibre, at a given distance from a circle as base, under both constraints.

**III.3.16** And if the drum major now takes up a circle as fibre—which is an entire two-dimensional interaction and so surface—and holds it vertically to march about, then she creates a torus that can be a set of trivial cycles maintained over time. And if she twists it as she walks, then the cycle of increments is some  $\pm dA$  that creates a Klein bottle. That recurvature is a 2-ball as fibre a given distance from a circle as base under both constraints. We now have a nontrivial cycle that can be the base for a generation.

**III.3.17** And, finally, if she takes up a sphere as fibre and marches, then she creates a “spheritorus”, which is energy and work trivially maintained over time. And if she twists it, the three values have a joint  $\pm dV$  to create a higher-dimensioned Klein bottle. The same work and energy can now fuel a generation. These are the two neighbourhoods formed by a 3-ball as fibre, at a given distance from a circle as base, under both constraints.

**III.3.18** Fibre bundles hold the spatial properties of entire groups of points. They can appear, locally, as homeomorphic to both their bases and their fibres, while having global properties distinct from each. The two together are the biological interactions,  $\lambda$ . They form the various homomorphic  $S-V$  structures which can then interact with different homeomorphisms with the surroundings.

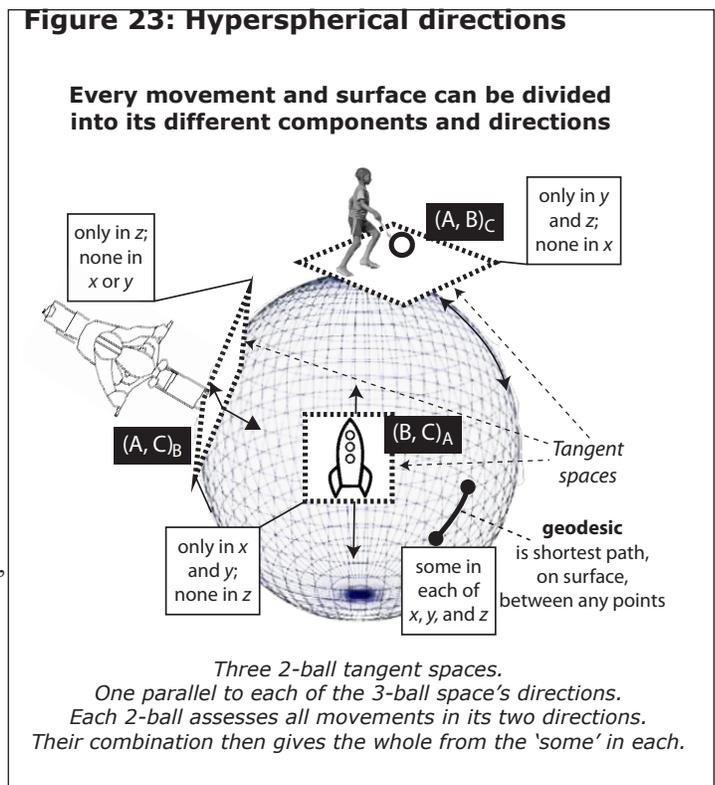
We can now track all deformations between preimage and image, and between the biology and replication globes, as both bases and fibres. Whether as manifolds, or as fibre bundles, they will all be homotopically equivalent. But only some will be homeomorphic. If we want to allocate different entities and groups to different species, then we must distinguish their different syntactical and semantic combinations, as DNA nucleotide codons, to form the various possibilities that are all locally Euclidean, but globally distinct.

**III.3.19** If we do not clarify these differences then we will never identify the different species.

**III.4.1** A biological population and/or its generation can now be a fibre bundle. This will be some arrangement of our four manifolds or dimensions.

**III.4.2** Although the  $V_4$  rotachoron, complete with its  $S_3$  or three-dimensional glome surface, that we use to represent a population, remains impossible to display in the two dimensions on a piece of paper, Manning (1914) showed that it nevertheless remains accessible to thought. As in Figure 23, a dimension is any value or property capable of demonstrating some independent change.

As with our fibre bundles, any two dimensions taken together can alter with respect to each other, and immediately form a surface. Our Frenet-Serrat trihedron promptly makes all their mutual rates of change accessible.



**III.4.3** Just as an  $S_2$  planespace can have (a) the completely flat local topology of an infinitely extended plane, which means no changes in some aspect or dimension; yet (b) is also the surface bounding a  $V_3$  rotahedron, which means regular infinitesimal and linked changes in others; while also (c) potentially expressing the twist of being carried about a Möbius strip, which means oscillating back and forth about a mean; then so also does each  $S_3$  that is a bounding glome upon a  $V_4$  rotachoron have (a) the local topology of an infinitely extended rectilinear realm or three-dimensional space; (b) the global topology of a realmspace that curves about a  $V_4$  surface; and (c) the twist of a Klein bottle. This again simply means the dimensions—even when largely conceptual—have different ways of changing with respect to each other, both locally and globally.

**III.4.4** As again in Figure 23, an ordinary  $V_3$  rotahedron is any set of properties,  $(A, B, C)$  we can describe using its three  $S_2$  “tangent spaces”, one parallel to each axis, and so as  $(A, B)_C$ ,  $(A, C)_B$ , and  $(B, C)_A$ . Holding one specific direction constant allows us to analyse movements in the others.

**III.4.5** The same principle applies to the four dimensions or properties in our  $V_4$  rotachoron. This is an  $(A, B, C, D)$  that has four perfectly ordinary 3-ball Euclidean  $S_3$  glomes—one parallel to each direction—acting as its flattening and surface tangent spaces. These are  $(A, B, C)_D$ ,  $(A, B, D)_C$ ,  $(A, C, D)_B$ , and  $(B, C, D)_A$ . ‘Straight’ then simply means the path whose “tangent vectors”

are currently running parallel to some selected axis. We simply note all values and changes while some specified one holds constant.

**III.4.6** If we take an  $(A, B, C)$  rotahedron, then we can first consider the  $(A, B)_C$  surface. This is the same as a two-dimensional being observing a series of concentric circles as the rotagon pushes up, through his or her universe, which is his or her flat  $AB$  plane (Abbott 1884). The circles he or she sees will grow from an infinitesimally small size to a maximum width—which is the sphere’s diameter—and then back to a minimum as the sphere pushes right through his or world, and through his or her plane. If the sphere does the same for the other two  $(B, C)_A$  and  $(A, C)_B$  possibilities, which are pushes in the  $A$  and  $B$  directions, then the two-dimensional being can observe the entire rotahedron. This is the same principle, for ourselves, in our three-dimensional world, as we contemplate a four-dimensional  $(A, B, C, D)$  rotachoron. It has four-directions in which it can push through our world.

**III.4.7** A rotahedron’s three  $S_2$  planes combine as the three 2-ball flattening Euclidean planes. We observe it as the familiar curving exterior. And just as those three  $S_2$  planes combine to create a rotahedron’s surface ... then so also do the four  $S_3$  glomes upon a  $V_4$  rotachoron’s surface combine to produce its overall three-dimensional realmspace as its surface. This is then observable as an apparently ordinary Euclidean realm or infinitely extended 3-space ... except for additionally exhibiting the biological events that tend an entire population from generation beginning to end. That is then the fourth dimension’s curvature. We observe this curving as the waxing and waning of the generations, and as some set of  $d\tau$  events about a global circulation, for every absolute and linear  $dt$  in time. We have  $dt = Td\tau$ , with  $T = 2r$  being the radius of curvature.

**III.4.8** There is one further—and very important—consideration. The spherical wheel pushing up from underneath the hoop runner in Figure 23 has the same single osculating contact point as the cylindrical one he pushes down from above. The hoop runner confirms that the  $S_2$ - $V_3$  rotahedron underneath him is also a spherical wheel rolling upon his tangent planar surface.

We can always replace the sphere—as the hoop runner above does—with a cylinder, or hoop, of arbitrary length. The sphere is then identical, at its contact point, to the hoop runner’s cylindrical wheel above. That cylinder can then turn to roll in whatever direction. The sphere’s movements are now exactly replicated, on that tangent surface, by that cylinder, which in its turn gives the impression of being able to roll infinitely far in any direction on that surface.

**III.4.9** Our Frenet-Serrat trihedron can now isolate all axes and 1-balls to find the biological “geodesic”. This is any population’s straightest—and so shortest—local path in a biological landscape. It is a movement with respect to our biology and replication globes, and our progenitor domain and progeny codomain. This can then be expressed in terms of the patterns and behaviours

displayed by the nucleotide codons existing at any point, and as they instantaneously transform to others.

**III.4.10** And now we have characterized both the structures and the spaces, we can describe all biological entities and their entire ecological behaviours.

# **Part IV**

**Biologies in**

**four dimensions**

**IV.1.1** We now return to our Chomsky grammar to find the genetic–linguistic production rules that emulate our fibre bundles. They must separate our replicative recurvatures and our Möbius strip transitions across identified boundaries from mere biological-metabolic trivial cycles. We must be able to distinguish all  $(x, y)_\alpha$  biological perspectives and observations from all  $(x, y)$  nonbiological ones, where  $\alpha$  is some coupling such as  $wz$  that recurses.

We therefore reaffirm, for Meme 102, that although the homomorphic objects making up our preimage and image have access to a vast number of transformations, they are made from a limited and countable number of Ingredients 3 and 4 that are always equipollent with  $\aleph_0$ , the set of countably infinite natural numbers. Those laws, maxims, and constraints, working over four dimensions, are then the inheritable transformations that render them biological.

**IV.1.2** Noam Chomsky proved (1956)—in solving a very similar problem—that grammar is the study of the infinite expressions we can produce, using finite means. He thus linked the infinite expressiveness of language, which is the ability to produce infinitely many sentences, to automata theory, when seen as the study of the infinite possibilities of self-acting devices, again using finite means. Since grammar has become the study of the differences between recursive functions and loops, then it is also the study of the differences between semantic interiors and syntactic surfaces.

**IV.1.3** By Meme 103, although the local, the global, and the Möbius strip behaviours that our biological structures engage in always appear the same locally, we can distinguish them using both (a) the Chomsky(–Schützenberger) hierarchy, and (b) the “Church–Turing thesis” (Copeland 2000). These together separate recursive functions from loops.

**IV.1.4** The Church-Turing thesis says that anything we can do with a set of recursive functions, we can also do with a series of loops. We can understand the important difference between them by proposing that I want to track down my old primary school friend Gnowee. Since I do not know her number, I call Anowah. She also does not know it, but says Boakye does. So I call Boakye, who tells me to try Chandra ... who proposes Dagvald ... who refers me to Euan ... who at last suggests Fareeha who at last gives it to me. I could potentially go on indefinitely, asking as many as necessary. I have personally undertaken six iterations of the ‘do-it-by-yourself’ loop.

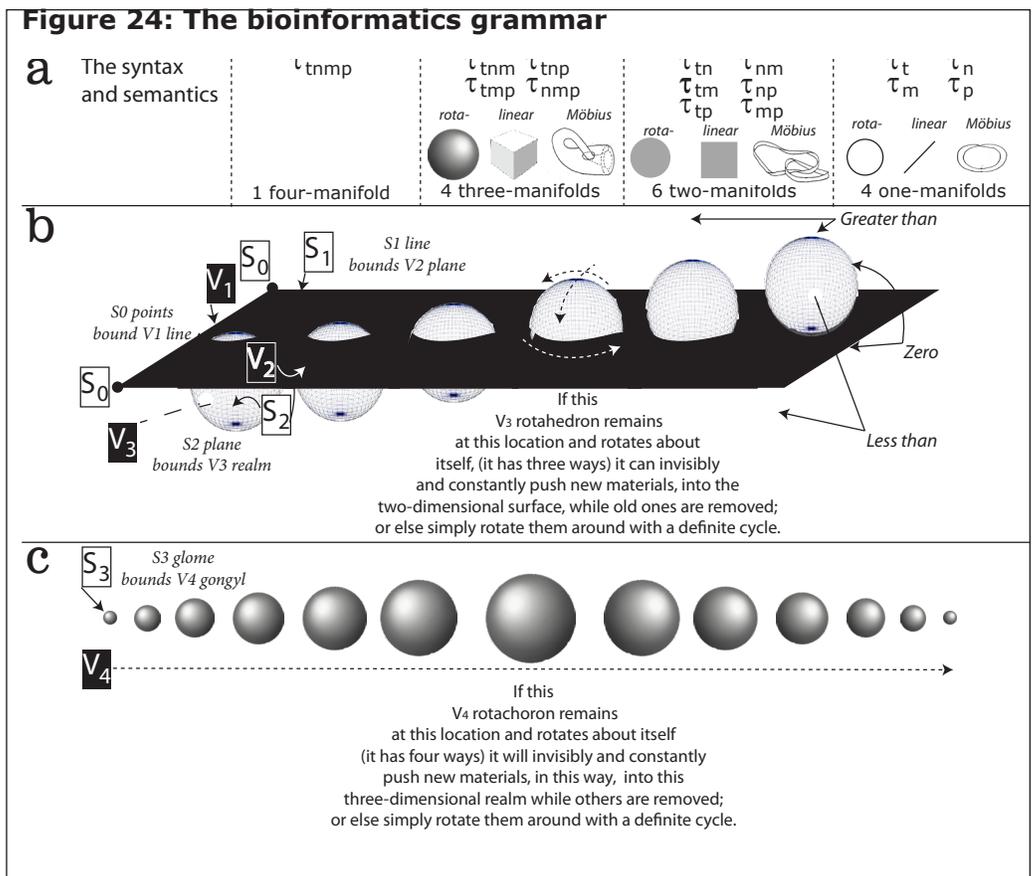
But if, now, Anowah were instead to offer to call Boakye for me; and if she passed back the information; and if Boakye offered to do the same for Anowah; and if all others emulated that behaviour when approached; then that would be six recursive ‘let-me-do-that-for-you’ function calls. This could also go on indefinitely. The end result is the same, for I still get the information. But in the loop case, I have to make all calls myself (one to each and every person in the chain); whereas in the recursive function case, I—personally—only have to make the one (I only need to call Boakye).

**IV.1.5** Chomsky then proved that even though recursive functions and loops have a complete equivalence, a loop-only grammar must nevertheless become prohibitively complex ... whereas a recursive function based one can produce the infinitely many outputs in any language—even of arbitrary complexity—by stepping through a far simpler set of very basic constructs.

**IV.1.6** Our Meme 103 therefore uses both the Church-Turing thesis and the Chomsky hierarchy to turn biology into the study of the infinite possibilities of the infinitely many self-perpetuating and homomorphic entities composed from the finite means of the radiative and the circulating Ingredients 3 and 4. They then behave homeomorphically, with respect to our two identified boundaries.

**IV.1.7** Biology has thus become a bioinformatics study. It is the study of the homotopically equivalent transformations between progenitor domain as preimage; and progeny codomain as image; and conversely; using deformation retracts and mapping cylinders, along with manifolds, fibre bundles, and fibrations and cofibrations as they shift between our biology and replication globes.

**IV.2.1** We have already defined the entirety of the  $\lambda$  biological-ecological behaviours over a generation as both (a) the mapping cylinder,  $M_\lambda$ ; and (b) an infinite cyclic group. The fibration and cofibration,  $\theta$  and  $\rho$ , are then the complementary operators that can produce the infinite cyclic subgroups using the biological grammar of Figure 24a. The elements in



the group are our plessists and plessemorph. They are formed by  $\psi$  and  $\gamma$ , themselves composed from Ingredients 3 and 4 as a result of  $\theta$  and  $\rho$  and their interactions with the surroundings.

**IV.2.2** Now we have the Church-Turing thesis and the Chomsky grammar, we can use Meme 104, in Figure 24, to reinterpret Figure 17, which flattened an  $S_2-V_3$  rotahedron into an  $S_1-V_2$  rotagon. We can create a far more general DNA grammar. We are ready for a much broader statement about the syntax and semantics of any  $S_{n-1}-V_n$ .

**IV.2.3** Any biological presentation becomes a surface instruction set,  $S$ . The  $S_n$  generators form an infinite cyclic subgroup by interacting, as a syntax, within the surroundings. That presentation immediately fronts a bounded  $V_{n+1}$  interior. It is the infinite cyclic group containing that subgroup. The volume of biological materials is the semantics as a complete energy and its density.

**IV.2.4** The  $V_2$  surface in Figure 24b displays one aspect of our biological grammar. It is acting as a “flattening agent”. Any  $(x, y, z)$  construct in Figure 24a can use any direction to flatten as  $(x, y)_z$  etc.

More generally, and in our topological grammar, any lower-dimensioned  $S_{n-1}$  object can act as a “hyperplane” that flattens some immediately higher  $V_n$  dimension onto any of its  $S_{n-1}$  surfaces. As with Figure 24b’s rotahedron becoming a bounded rotagon upon that plane, that  $V_n$  object is becoming a  $V_{n-1}$  ball surrounded by an  $S_{n-2}$  surface. We thus declare this aspect of our grammar, for

Meme 105, by saying that the intersection of every  $n$ -ball with its retract  $n-1$  hyperplane produces an  $n-1$ -ball. We can produce each object in Figure 24a using this method.

**IV.2.5** There is, however, a converse aspect to this grammar. Every  $n$ -ball can be an  $n$ -sphere that surrounds. That flat  $V_2$  surface in Figure 24b is a small portion extracted from a rotahedron of infinite radius. It then acts as the surface that cuts into—and so establishes—an interior and an exterior, and/or lesser and greater, for a higher-dimensioned  $n+1$  ball of radius  $r$ . So if we assign ‘0’ to the cutting hyperplane, then everything in  $V_3$  to one side of  $V_2$  is ‘greater than’, the other side being ‘less than’. We can again both produce and describe each object in Figure 24a using this method.

**IV.2.6** But a  $V_n$  always has an  $S_{n-1}$  bound. As with the rotagon on the surface in Figure 24b, the  $V_n$ 's surrounding  $n-1$ -sphere can be the “trace” that creates that  $n$ -ball by establishing some radius  $r$ . That  $n$ -ball is then a union of concentric  $n-1$ -spheres of volume  $V_n$  and surface  $S_{n-1}$ . That  $n$ -ball is thus the similar trace, whose union of concentric  $n$ -spheres produces a sphere of volume  $V_{n+1}$ , for which it is the surface  $S_n$ .

**IV.2.7** Figure 24b shows our grammar in action. The way the film in a camera “step-down retracts”. or flattens, a three-dimensional view down to only two, is similar to the retractions of a two-dimensional  $V_2$  rotagon to a one-dimensional  $S_1$  line segment or unknot; and also of a  $V_1$  line segment down to its two  $S_0$  points separated by  $2r$ . Those various step-downs create loops which pass outwards, through those surfaces, into the surroundings. They can, however, also be fibre bundles with an added twist.

We have here an example of our multidimensional syntax and semantics. We select some value or statement  $x'$ , establishing a sequence of statements as a radius  $r$ , and creating the hyperspherical boundary,  $\tau$ , that is the biological language. It is simultaneously:

- a journey about a helicoid;
- a trip across a real projective plane;
- a circulation about a rotahedron; and
- the Möbius journey about a set of self-intersecting Whitney umbrellas.

**IV.2.8** But if biological entities are to survive, then recursive functions, and step-ups, creating cofibrations and biovolumes, must exist. So if, as in Figure 24b, we push a  $V_3$  rotahedron through a  $V_2$  world, that step-up process will look—to the inhabitants—like a two-dimensional rotagon steadily growing from a minimum width; to its maximum; and diminishing back to its minimum (Abbott 1884). Since the inhabitants can deduce the rotahedron that has passed through, we have reversed the above flattening process.

**IV.2.9** All such step-ups are our recursive functions. The resulting  $S_1-V_2$  biosurface is perceived as the waxing and waning of an  $S_2-V_3$  biovolume, and so as a dynamic biological cycle.

And then just as we can use an architect's two-dimensional plans as a trace to construct a three-dimensional house, so also is a square pushed upwards through a plane the trace for a cube; and so again is a plane's above sequence of concentric circles the similar trace for a sphere. We can even allocate a central point as a zero; establish lefts and rights, or insides and outsides; and separate that higher-dimensioned object into two. The dimensionality of any resulting  $V_{n+1}$  is always one greater than the dimensionality of whatever hypersphere allows that  $V_n$  to be a trace; and that can also flatten or divide the resulting  $V_{n+1}$ .

**IV.2.10** For Meme 106, we take time,  $t$ , as the fourth dimension. We can then take up an entire  $V_3$  or three-dimensional realmspace. We use it as a trace to create step-ups, reversions, and recursive functions as we push it through our fourth-dimension to produce a tetrarealm by waxing and waning, in time, as both a self-intersection, and a complete circulation of the generations. It is the tetraspace and biovolume,  $V_4$ . It is the transition from progenitor domain and preimage to progeny codomain and image, and back.

**IV.2.11** It is impossible to display the resulting  $V_4$  rotachoron plus its  $S_3$  bounding glomes upon a piece of paper's only two dimensions. But we can observe biological entities waxing and waning as they are carried about their circulation, which is through a generation,  $\tau$ . That  $\tau$  is then the time that it takes to push or flatten a biological rotachoron through this three-dimensional realm. We simply use  $t$  as a hyperplane to create a biological tetraspace that can only be observed over time, and as the cycle of birth, development, reproduction, and dissipation.

**IV.2.12** Our biological Chomsky grammar is now the fibration,  $\theta$ , plus cofibration,  $\rho$ , using the deformation retract,  $S'$ , to lift to the surrounding mapping cylinder,  $M_\lambda$  ... all as the observable biological processes,  $\lambda$ . The structures are manifolds and homomorphisms. The processes are fibre bundles and homeomorphisms. Both involve  $\psi$  and  $\gamma$  as the language of the Ingredients 3 and 4 of photons and molecules.

**IV.2.13** As in Figure 24a, we can use a recursive function to draw Ingredients 3 and 4 in from the surroundings. This creates the four one-manifolds, six two-manifolds, four three-manifolds, and the single four-manifold that we cannot show in two dimensions, and that is the  $S_3-V_4$  rotachoron. That rotachoron can then be flattened with any one of the four different hyperplanes  $t$ ,  $n$ ,  $m$  and  $p$  to produce the four glomes of  $\tau_{nmp}$ ,  $\tau_{tmp}$ ,  $\tau_{mpn}$ , and  $\tau_{tmm}$  respectively.

**IV.2.14** The *nmp* glome has a special status in this grammar. It is a triple set of terminals. All this glome's products and constructs loop out into the surroundings.

**IV.2.15** The remaining three  $\tau_{tmp}$ ,  $\tau_{tm}$ , and  $\tau_{tm}$  glomes can each again be flattened, with hyperplanes, into different directions to produce the six curving  $\tau_{tn}$ ,  $\tau_{tm}$ ,  $\tau_{tp}$ ,  $\tau_{nm}$ ,  $\tau_{np}$ , and  $\tau_{mp}$  two-manifolds that are their surfaces.

**IV.2.16** The three surfaces without *t*—*nm*, *np*, and *mp*—again have a special status and are terminals. They therefore loop out into the surroundings.

**IV.2.17** And, finally, the remaining three  $\tau_{tn}$ ,  $\tau_{tm}$ ,  $\tau_{tp}$  surfaces are then further flattened upon the *t* hyperplane to produce the values for *n*, *m*, and *p*. These are terminal values observed at those specific points  $\tau$  in the circutation ... which is also at some definite and terminal moment of absolute clock time, *t*.

**IV.2.18** Biological entities and materials are thus the spoken syntax and semantics of nucleotide codons within this bioinformatics grammar.

**IV.3.1** Chomsky again proved (Chomsky 1956; 1959) that when a finite set of resources is combined with a limited set of rules, it can nevertheless produce infinitely many objects. Our grammar is that every  $V_n$  biovolume is also an  $S_n$  biosurface to some  $V_{n+1}$ , whilst itself being bound by some step-down  $S_{n-1}$ , which is itself a  $V_{n-1}$  biovolume bound by its own  $S_{n-2}$  biosurface ... and so on down to distinct  $S_0$  input–output points.

Our chosen language only needs to span across  $S_{0,1,2,3}$  and  $V_{1,2,3,4}$ . This is three transitions between the biologically and replicatively closed and open, which is between the non-injective and the injective, the non-surjective and the surjective. They are our three constraints.

**IV.3.2** As in Figure 21b, every biologically infused  $n$ ,  $m$ , and  $p$ —which are our Ingredients 2, 3, and 4—must at some time link to  $t$ , our Ingredient 1, to become timelike connected; produce the timelike homotopic circulations that support homeomorphic transformations; and form the closed intersecting timelike curves that can return to their start points for a generation,  $\tau$ . Elements without  $\tau_t$  retract by taking  $t$  as their hyperplane. They are relinquished to the surroundings as loops. These are indistinguishable from the tail recursive functions and  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  that drive them.

**IV.3.3** Our Chomsky grammar is therefore now that every biovolume as some cell, entity, species, or terrestrial Gaia principle is a step-up composed of recursive functions involving  $\tau_t$ ; while its every presenting biosurface of molecules, genomes, gene pool and entire collection of terrestrial DNA is the equivalent step-down, composed of loops in  $n$ ,  $m$ , and  $p$  at some absolute clock moment,  $t$ . With three such  $t$ -constraints upon  $n$ ,  $m$ , and  $p$  in place, then our biovolumes formed from recursive functions can fly away from the circulating  $\tau_t$  to deliver themselves, to the surroundings, as loops.

**IV.3.4** Our  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  manifolds are one-dimensional unknots. They increment about the closure of their braid. They move from  $S_{-1}$  to  $S_1$  all about their identity,  $S^0$ . Ingredients 2, 3, and 4 must thus undertake their transformations over  $\tau_n$ ,  $\tau_p$ , and  $\tau_m$  to match  $\tau_t$ . But these are also the absolute time spans  $T_N$ ,  $T_p$ , and  $T_M$  that the plessists—and therefore plessemorphs—take over a generation.

**IV.3.5** Since the population of plessists must recurve about our globes, then it must meet the following three constraints:

- We have carefully defined our  $n_n$  plessists so they always act exactly as a population formed by their  $n_a$  archetypal plessemorphs would also act. Since they are both composed from both of our radiative and the circulating field principles, then this Ingredient 2 of  $n$  must be the least variable of the three. And since all the  $n$  plessemorphs must—by definition—recurve about both our globes, then they must at a minimum satisfy  $\int dn = 0$  for our first constraint.
- Each of the above  $n$  plessists and their plessemorphs must be composed of a discrete number,  $m$ , of molecules. Since component numbers can remain constant even as

chemical reactions rearrange chemical bonds within any given entity, then this is the next most variable. Its recurvature about the same globes is given by  $\int dM = 0$  as our second constraint.

- The population energy,  $P$ , as the radiative principle, must be the most variable of the three for any  $p$  in any individual  $n$  can change as both  $n$  and  $m$  hold constant. It must abide by  $\int dP = 0$  as our third constraint.

**IV.3.6** Those three properties of  $\int dn = \int dM = \int dP = 0$  are the three constraints to which all biological populations must be subject. Populations must allocate entities to the replicatively and/or biologically closed and/or open, and to trivial and nontrivial cycles, according as to whether they do, or do not, return to each globe; and also according as to whether they are, or are not, injective and/or surjective. But if populations are to circumnavigate both globes and complete a generation, then they must abide by the above constraints that establish the recurvature conditions.

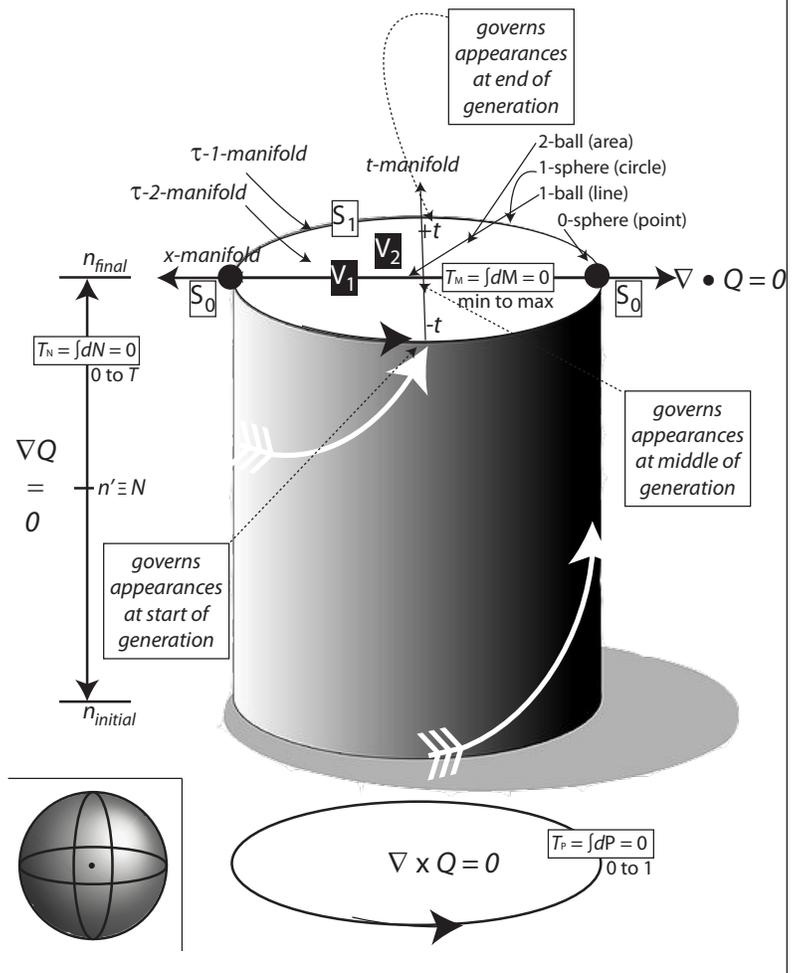
Since biological entities and populations must recurve about our globes, then the sum of the transformations in any viable population must once again be  $\int dn = \int dM = \int dP = 0$ . And if any population is to remain stable, then those transformations must also satisfy  $\int dS^\circ = 0$ . This general grammatical rule of  $\int dn = \int dM = \int dP = \int dS^\circ = 0$  therefore defines the fully biological-ecological DNA and nucleotide codon grammar. These are the “exact differentials” that establish the recurvature parameters.

**IV.4.1** Although four dimensions cannot be properly displayed in only two, Figure 25, which is Meme 106, nevertheless attempts to portray the fuller implications of each of the four  $S_3-V_4$  rotachoron diameters. It suggests the behaviours of one of the four, which is thus acting as a Hooke cell would act in creating a dynamic equilibrium. This is to maintain an  $S^7$  deformation retract state using its  $S_0$  inputs and outputs. Those  $+r$  and  $-r$  exchanges provide the driving forces that produce measurable external results.

Figure 25 may look static, but it is again a set of dynamic events occurring at real and measurable speeds over each of its four diameters. The dynamic equilibrium is a set of constant and precisely balanced interactions with the mapping cylinder and surroundings.

As with the three-dimensional rotahedron equilibrium represented at the bottom of Figure 25, the four directions combine to project towards a central point. Just as those three circles create a rotahedron by intersecting and moving about each other, so do their four four-dimensional equivalents similarly intersect to create a rotachoron. All four diameters deformation retract to the same central point, which then establishes the radius,  $r$ , for them all.

**Figure 25: The time manifold and the numeracy of a biological population**



**IV.4.2** Since our plessemorphs, plesseomes, and plessetopes are composed of, and act as, Hooke cells, then they are the infinite cyclic groups and subgroups whose behaviours of  $\psi$  and  $\gamma$  define the biological recurvatures. As in Figures 19 and 25, this demands that all four  $t$ ,  $n$ ,  $m$  and  $p$  dimensions and manifolds oscillate about their joint  $S^7$ . And since that  $S^7$  is the joint deformation retract for all four, then they are each infinite cyclic subgroups that construct the infinite cyclic group that is their surrounding  $S_3-V_4$  rotachoron and joint mapping cylinder,  $M_\lambda$ .

**IV.4.3** Just as our hoop runner's tyre, in Figures 23, and acting as an ordinary cylinder, can substitute for an entire  $V_3$  rotahedron at its point of contact with an  $S_2$  surface, so can the "spherinder"

in Figure 25 substitute for an entire  $V_4$  rotachoron at its point of contact with our surrounding  $S_3$  realm. And just as the cylinder stretching diametrically across a plane can rotate both itself and its plane about and emulate the rotahedron, then so also can the spherinder reconstruct all possible  $V_4$  rotachoron movements.

**IV.4.4** While an ordinary three-dimensional cylinder is bounded by two two-dimensional circles at each end, the spherinder is bounded by two spheres or 3-balls at each end. And when that ordinary cylinder pushes, with its flat side first, through an  $S_2$  plane, then the plane's two-dimensional inhabitants detect a circle of unvarying size passing by them over some given time interval  $T$  that is the cylinder's length. But if it is pushed through with its round side first, then they will see a line that grows to a rectangle, and then goes back to a line. In the same way, when a four-dimensional spherinder is pushed through our three-dimensional  $S_3$  realm with its "flat side" first, then we will detect a sphere of constant dimensions pass by over some time  $T$ , that is its length; and if it is pushed through with its "round side" first, then we will see a complete cylinder that similarly grows and shrinks from a line back to a line.

**IV.4.5** We can create the biological spherinder for a generation by projecting a sphere across the line of length  $T$ , which is then its axis. But since a spherinder is a diameter, then it can trace out a rotachoron by turning about itself in exactly the same way that either a two-dimensional circle or a cylinder can create a sphere by rotating about. The rotating spherinder's beginning and end points are then coincident. They self-intersect. When we leave one spherical face, we automatically reenter through what looks like the opposite face, at the other end, but we in fact keep going with the same spherinder, continuously, in the same direction about the surrounding rotachoron. Therefore, if the spherinder's two ends are the same size, then we have both a uniform rotachoron and an infinitely long Euclidean line. It and its centre are the four-fold stationary  $S_4-V_4$  point ... and state the recurvature properties.

**IV.4.6** A point or infinitesimally short line segment can create a diameter by pushing all across a rotagon; and a point or infinitesimally small circle can create a diameter by pushing across a rotahedron. Since an infinitesimally small rotahedron can similarly create our spherinder by pushing diametrically across the rotachoron, then a spherinder is the fibre bundle we construct by projecting a  $V_3$  rotahedron, as a fibre, along a line segment, which then acts as a base. The spherinder is therefore the infinitesimally thin cross-section across the  $V_4$  rotachoron's  $2r = T$  diameter. A part of its length is the fibration; a part is the cofibration. A part is therefore the biology globe, a part the replication one. And further since a spherinder has spherical and self-intersecting ends, then it forms a closed loop. It endlessly restates the same biological interactions, generation after generation. All points in our rotachoron become glomes; all lines—particularly the four diameters—become spherinders; and all

planes—particularly the  $\tau_{\text{nmp}}$  one that defines all real-world behaviours—become infinitesimally thin cubinders. A spherinder therefore defines our unipollent and doubly closed equilibrium,  $\pi$ .

**IV.4.7** Since a biological circulation is exactly a recurvature, as a return to an original state, then our spherinder can also be thought of as an infinitesimally short section along a spheritorus ... which is itself the fibre bundle created by projecting a  $V_3$  rotahedron, as a fibre bundle, about a circle of diameter  $T$  and radius  $r$  acting as a base. The spherinder is then taken along the “hypercircumference”  $\tau$ . Events now enter and leave the spherical volume elements, at each end, all about the circulation. Their properties again state the recurvature at every point.

**IV.4.8** Every present moment  $\tau_0 t_0$  in Figure 25’s spherinder lies between  $\tau_{-1} t_{-1}$  at the beginning of a generation and  $\tau_1 t_1$  at the end. Every  $\tau_0$  exists within some curvilinear interval  $\tau_{-1} - \tau_0 - \tau_1$ , while every rectilinear moment  $t_0$  occurs within some rectilinear time interval  $t_{-1} - t_0 - t_1$ . Every present population state  $S_0$  transforms between  $S_{-1}$  and  $S_1$ . Therefore, every absolute and rectilinear time interval  $dt$  along the spherinder’s interior axis is a part of the generation length  $T$ ; but it is also always accompanied by some curvilinear interval  $d\tau$  about the spherinder’s exterior as a part of the circulation of the generations,  $\tau$ . These together are the  $dt = Td\tau$  that define the successive points  $a$ ,  $b$ , and  $c$  upon a helicoid, a rotahedron, a projective plane, our Möbius strips and the like.

**IV.4.9** Since there are the four manifolds and directions of  $t$ ,  $n$ ,  $m$  and  $p$ , then there is one such spherinder in each direction, and along each axis. The  $n$  direction with its  $\int dn = 0$  may be the least variable of the three constraints by defining the number of plessists, but their contribution to any  $S$  at any point can still change by  $dn$ . The two respective rates of change will be  $dn/dt$  along the spherindrical axis, and  $dn/d\tau$  about its surface and the boundary, which is the circulation length.

**IV.4.10** We first introduced, in Meme 99, the mean across any interval, along with its distribution, as  $n'$ . We now further define that mean, for Meme 107, as “one biomole”,  $N$ , where:

$$n' \equiv N.$$

So if the number of plessists across any interval is  $n_{\text{initial}}$  at one end and  $n_{\text{final}}$  at the other, then the number of plessemorphs maintained across that same spherindrical interval is immediately  $n' = N = 1$  biomole where  $n'$  is the weighted mean. This simply confirms that our  $n$  plessists can define our archetypal plessemorphs, and conversely. The number maintained across any spherinder is therefore  $N$  ... while the number at the centre for the deformation retract of any  $n_{\text{initial}}$  and  $n_{\text{final}}$  is also  $n' = N$ . Meme 108 then says that any population maintaining its mean across any spherindrical interval has a size of  $N = 1$  biomole of plessemorphs ... while still behaving in the identical way as the  $n$  plessists concerned.

**IV.4.11** Meme 109 then further says that any population maintaining its  $N = 1$  biomole mean for 1 second has a “numeracy”,  $Q$  of, for example, “one biomole per second”. This is simply a way of saying that the population is, at that moment, maintaining its average numbers for that interval. A numeracy less than 1 means the population has proportionately less than its average number for that interval; and conversely if  $Q > 1$ .

**IV.4.12** As again in Figure 25, Meme 110 now confirms that the absolute population number at the edges of any interval are  $n_{\text{initial}}$  and  $n_{\text{final}}$ . Meme 111 then formally identifies the absolute time  $T_N$  along the axis with the matching circulation distance  $\tau_n$ ; and similarly with  $T_M$  and  $\tau_m$ ,  $T_P$  and  $\tau_p$ , and  $T$  and  $\tau$ . This is effectively to say that we have four spherinders in four different directions across our rotahedron, all of which are equivalent in sharing the same central point as their deformation retract.

**IV.4.13** Since our absolute time interval across the spherinder has the limits 0 and  $T$ , then the number of plessemorphs across our spherinder, in the  $n$  direction, and for those limits, is:

$$N = \int Q dt.$$

The numeracy at each point across the spherinder is then:

$$Q = dN/dt.$$

**IV.4.14** We are again expressing numbers in terms of the mean across whatever interval. And then since that same interval has the limits 0 to 1 for the curvilinear interval,  $\tau$ , then the same population of plessemorphs must exhibit that same equilibrium, between those limits and be observable in the outside world as:

$$N = \int Q d\tau.$$

and:

$$Q = dN/d\tau.$$

**IV.4.15** By Meme 112, the gradient in numeracy across the spherinder,  $\nabla Q$ , is the rate at which the population numbers, of whatever absolute size, must either increase or decrease to attain and maintain the mean for each over that interval. It is:

$$\nabla Q = (n_{\text{final}} - n_{\text{initial}})/N.$$

But since we currently have  $\int dn = 0$ , then the gradient across our spherinder, and for an entire generation, is zero; as also is the rate of change of gradient. And ... if ever both the gradient in numeracy and its rate of change across any interval are zero, then we have a static dynamic equilibrium, and that population is “numerically static”. This is the “stasis of the first kind”.

**IV.4.16** A stasis of the first kind is a dynamic equilibrium determined not just by the number of plessists, but by the number of plessemorphs we can substitute for them. Whatever the plessist

numbers at either end of the interval, they collapse infinitesimally smoothly into the  $N$  plessemorphs that are their centre and the deformation retract. This stasis of the first kind is the first requirement for our defining self-intersection and unipollent equilibrium,  $\pi$ .

**IV.4.17** These are, however, biological entities. Their numerical stasis, as plessists, is not possible without some kind of (A) plessiome and (B) pleme interaction, in the surroundings, to support it. These involve the mapping cylinder,  $M_\lambda$ , and therefore a specified stock of chemical components and joules of energy. There must also be plesseomes and plessetopes for our plessemorphs.

**IV.4.18** There are again four manifolds, one for each of our Ingredients. The  $m$  direction is the next most variable of the three constraints. It acts in conjunction with the  $n$  direction to establish  $\int dM = 0$  over the population.

This dynamic equilibrium requires that when we look in the  $m$ -direction, we see an equilibrium number of components flowing past each edge of the same interval. Those quantities must emulate  $N$  and come smoothly and infinitesimally into a mean at the centre to create the deformation retract. The  $n$  plessiomes must form the  $N$  plesseomes for our plessemorph gene pool.

No matter what their  $-r$  and  $+r$  exchanges, these  $S_0-V_0$  pointspaces have the constant values for  $n$ ,  $m$  and  $p$  at each  $t$ . By our Meme 104 Chomsky grammar, our population is now constructing a homogeneous  $V_4$  rotachoron of fixed and maximum volume with radius,  $r$ , in its four directions of  $t$ ,  $n$ ,  $m$ , and  $p$ . All  $V_0$  pointspaces must have the overall  $S_0$  point behaviours whose exteriors produce the local topology of an infinitely long and one-dimensional Euclidean line at each distinct  $t$  all about every circulation. And since our self-intersection demands that  $r$  is constant in every direction, then:

$$n^2 = m^2 = p^2 = t^2 = r^2,$$

which in its turn defines:

$$\tau_n = \tau_m = \tau_p = \tau_t = \tau.$$

All our four one-manifolds now have the same two solutions of  $+r$  and  $-r$  imposed by their deformation retract. All four therefore exhibit the same  $S_0 = -r$  and  $S_0 = +r$  points all about the  $V_4$  rotachoron. As in Figure 25, our equilibrium occurs when the amount of biological processing,  $d\tau$ , in any absolute interval,  $dt$ , is always the same, both relatively and absolutely, so that  $dt = Td\tau$ ; and so that our rotachoron preserves its total  $V_4$  gongyl.

The rotachoron's four  $\tau_{nm}$ ,  $\tau_{mp}$ ,  $\tau_{mp}$ , and  $\tau_{nm}$  bounding glomes are also the rotahedrons that hold the  $S_2$  surfaces that create the  $dt = Td\tau$ . Each bounding surface therefore holds the interactions that are the external biological–ecological presentations. They produce both  $\pi$  and the sequence of equilibrium-creating 1s. But this again means all  $V_0$  pointspace inputs and outputs all about the circulation, when summed, have matching inputs and outputs over every Whitney umbrella.

Since this is already a numerically static population, then by Meme 113, the spherinder in the  $m$ -direction must help create both  $\int dn = 0$  and  $\int dM = 0$ . These define its surrounding cubinder upon

the rotachoron surface. We can therefore determine the divergence in the components that preserve the above self-intersection and dynamic stasis in numeracy.

If both the population numeracy and the plesseomes must remain the same across this interval, then the same numbers of components must again flow in and out of the spherinder to give a divergence of zero. The divergence in the plessiome and plesseome components that construct our plessists and plessemorphs is therefore:

$$\nabla \cdot Q = \bar{m}_{\text{final}} - (\bar{m}_{\text{initial}} n_{\text{initial}} / n_{\text{final}})$$

Both the gradient and the divergence are now zero,  $\nabla Q = \nabla \cdot Q = 0$ . The population is maintaining both those means across an entire interval. Its rate of change must also be zero right across the spherinder, with the central point again being the deformation retract. So if ever both (a) the divergence, and (b) its rate of change are zero, then the population is “materially static”. This is the “stasis of the second kind”, and is the second requirement for our full unipollent equilibrium.

**IV.4.19** If these first two directions are indeed dynamically static, then so also must be the one for our plemes and plessetopes, which is our third and final constraint of  $\int dP = 0$ . Every spherinder, in every direction, must therefore sit centrally in its surrounding cubinder which is its specified contribution to the mapping cylinder,  $M_\lambda$ . The time across this third spherinder is  $T_p$ . The net Ingredient 3 interaction must satisfy  $T_N = T_M = T_P = T$  and  $\tau_n = \tau_m = \tau_p = \tau$  which are, respectively, the diameter and the circumference.

Since the population gradient and divergence are already both zero, then the curl must match the gradient and divergence so that exactly the same amounts of energy enter and leave the plessist population and each plessemorph at each moment. Therefore any two subpopulations  $A$  and  $B$  must sit evenly either side of their shared equator and prime meridian, forming a squaroid to give both  $dt_{AB} = T_{AB} d\tau_{AB}$ , and  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$ . But... this is the Hooke cell ... our deformation retract ... and our identity,  $S^7$ .

Since the gradient, divergence, and curl are all zero, then all  $\tau_m$ ,  $\tau_{tm}$ , and  $\tau_{tp}$  pairings will act as 1-spheres to  $V_2$  rotagons; with each having the local topology of an infinite flat Euclidean  $S_2$  plane or surface. All  $V_2$  rotagons are the  $S_2$  planespaces whose curls drive the circulation, bounding the observed  $V_3$  rotahedrons which are the waxing and waning of biological activity.

And ... we have successfully described the rates of interactions with the surroundings that produce our  $\pi$  equilibrium. The Ingredients 3 and 4 that construct our plessemorphs across the interval  $n_{\text{initial}}$  to  $n_{\text{final}}$ , must jointly satisfy:

$$\begin{aligned} \nabla \times Q &= P_{\text{final}} \bar{m}_{\text{initial}} - M_{\text{initial}} \bar{p}_{\text{final}} \\ &= \bar{p}_{\text{final}} \bar{m}_{\text{initial}} (n_{\text{final}} - n_{\text{initial}}). \end{aligned}$$

When both this curl and its rate of change are zero, then the population is “energetically static”. This is the “stasis of the third kind”, and the third requirement for our plessemorph’s unipollent equilibrium,  $\pi$ .

**IV.4.20** With the stases of the first, second, and third kinds we have now defined the conditions that allow any infinite cyclic group population with a biology and ecology of  $\lambda$  to create its infinite cyclic subgroup behaviours of  $\psi$  and  $\gamma$  so it can produce the recurvatures that allow it to traverse a Möbius strip and complete a generation, so constructing its biological equilibrium. That equilibrium is  $S'$ , which is also the deformation retract, or generation centre point, of  $S' = (N, \bar{m}', \bar{p}')$  held at some specified  $\tau' t'$  which is both the middle of a generation in absolute clock time, and its centre as a distance. This then constructs the mapping cylinder,  $M_\lambda$ , all about itself as the surroundings. That is the complete set of interactions for a generation.

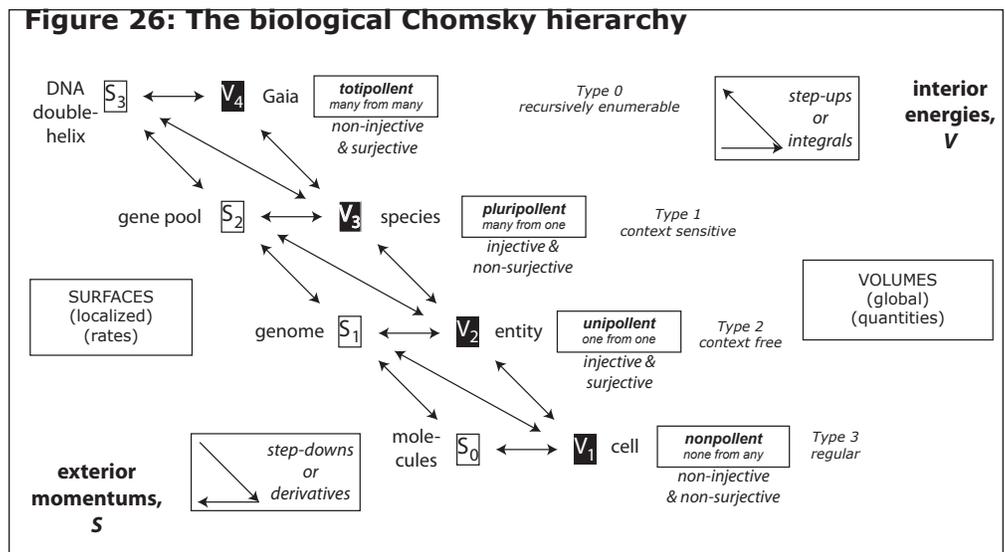
**IV.4.21** Each of the three values in the deformation retract is held at its independent point in the generation at its  $t_0$ , which is also some absolute clock moment  $t$  in the overall generation length,  $T$ . The three nevertheless conjoin as the infinitesimally small self-intersecting sphere that is also the fibre stretching across  $T$ , as its base, to construct the four spherinders that are the population's four  $V_4$  rotachoron diameters. And since  $S' = (N, \bar{m}', \bar{p}')$  is the deformation retract; and also since all infinite cyclic groups are equipollent with the additive group of integers; then  $S'$  states the closed, static and unipollent behaviours that can indifferently substitute for any population in all its activities.

**IV.4.22** A spherindrical population, complete with its fibration and cofibration of  $\theta$  and  $\rho$ , and its deformation retract of  $S'$ , all active across  $T$ , are both the syntax and the semantics that construct the  $\lambda$  that are the mapping cylinder's biology and ecology. They are the surrounding fibre bundle and cubinder of  $\tau$ . All populations can then use their DNA syntax and semantics to oscillate about the three kinds of stasis of  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$ . They are the stases of the first, second and third kinds, being the numerically, the materially, and the energetically static, for the deformation retract.

**IV.4.23** But the populations simultaneously apply the three constraints of  $\int dn = \int dM = \int dP = 0$  over that  $T$  to create the recurvatures around our biology and replication globes that are the manifest biological entities engaging in their activities to construct a generation.

**IV.4.24** This Meme 112 therefore defines a biological population as one that satisfies both (a) the three constraints, and (b) the stases of the first, second, and third kinds.

**IV.5.1** Our population of plessists and plessemorphs must now create both (a) the three kinds of stasis of  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$ ; and (b) the three constraints of  $\int dn = \int dM = \int dP = 0$ . They each use the Chomsky production rule of  $[\Sigma, S, \delta, \alpha_0, F]$  to create the needed biological structures and behaviours.



**IV.5.2** All viable populations must create a specific biology of syntax and semantics. Their various recursive functions must accept molecules from the surroundings through  $S_0$  acting as inputs, and convert them into their various biological entities. Those nucleotide codons, genomes, and other structures will be the  $V_{1,2,3,4}$  biovolumes and energies as step-ups and sequences of fibrations and cofibrations. They will manifest as  $S_{0,1,2,3}$  structures, jointly imposing their recurvatures as biological events. We therefore need a series of production rules that set  $\delta$  to some value.

**IV.5.3** For Meme 113, we note that, as in Figures 1 and 26, when the four levels Lloyd discusses (2012) are understood as the four combinations of mappings of injective and non-injective, surjective non-surjective between sets of progenitors and their progeny, then they correlate precisely with the “Chomsky hierarchy” (Chomsky 1956; 1959). The biological cycle occurs because the same step-up materials that a Chomsky production rule builds as  $V_{1,2,3,4}$  semantic productions immediately loop outwards into the surroundings, through  $S_0$  outputs, and courtesy of the second law of thermodynamics, as observed constructs and biosurfaces, and so as step-downs and  $S_{0,1,2,3}$  syntaxes. The  $\delta$  in  $[\Sigma, S, \delta, \alpha_0, F]$  must therefore step through those levels so that the constraints and their recursive functions—based on fibrations and cofibrations involving  $\theta, \rho, \psi$ , and  $\gamma$ —will create the spherinders and their surrounding cubinders that define our biological equilibrium,  $\pi$ .

**IV.5.4** Meme 114 now sets our Chomsky input alphabet to the four nucleotide “letters” of the DNA codon alphabet. This gives  $\Sigma = \{A, C, G, T\}$ . Our start symbol,  $\alpha_0$ , is always then some initial set of codons that is also some  $S_{-1} = \{n, \bar{m}, \bar{p}\}$  as a preimage in a progenitor domain.

And ... we straight away procure a stoichiometric index (BIPM 2006) into the DNA alphabet. Since our Chomsky and Church-Turing grammar over this language—with its recursive

functions of our fibrations, cofibrations, and the like—can rearrange those letters into all possible DNA strings, then they are the gateway to all 20 amino acids, and so to all possible proteins and biological entities.

**IV.5.5** Our recursive function's initial string is some  $\alpha_0 = \{A, C, G, T\}$ , which is again  $S_{-1} = \{n, \bar{m}, \bar{p}\}$  as a preimage in a progenitor domain. An RNA production uses its recursive function to transcribe the amino acid language, using the surroundings as a mapping cylinder, so inducing a set of  $\lambda$  biological activities. Since they are processes involving  $n$ ,  $\bar{m}$ , and  $\bar{p}$ , then the resulting terminal string takes the form  $F = \{A, C, G, T\}$ ; while also giving some final  $S_1 = \{n, \bar{m}, \bar{p}\}$  as an image in a progeny codomain..

**IV.5.6** The recursive functions in our Chomsky production drive the multiply connected timelike circulations  $\tau_{in}$ ,  $\tau_{tm}$ , and  $\tau_{ip}$ . Since these all involve  $t$ , the functions create the surfaces and collections of nucleotide codons. Their multiply connected and higher-dimensional productions are  $\tau_{tmm}$ ,  $\tau_{tmp}$ ,  $\tau_{tpp}$ , and  $\tau_{tmpp}$ . They ultimately use  $t$  as a hyperplane to flatten themselves into their final values  $n$ ,  $m$ , and  $p$  at some moment. As given Chomsky production rules, these products are therefore the results of recursive functions created from those same nucleotides, all flattened with a  $t$  hyperplane to become  $n\bar{m}$ ,  $n\bar{p}$ ,  $\bar{m}\bar{p}$ , and  $S = \{n, \bar{m}, \bar{p}\}$ .

**IV.5.7** For Meme 115 the first result in our Chomsky production is the nonpollent  $S_0-V_1$  level of molecules—cells. But when those nonpollent productions leave the replication globe and enter the biology one, they do not return. The best they can do is form a set of trivial cycles.

Our nonpollent entities have a fibration, but no cofibration. They do not cross the projective plane. We can denote this by saying that they have a “reproductive index” of  $\delta = 0$ . They therefore have a Chomsky production rule of:

$$[\Sigma = \{A, C, G, T\}, S = \{n, \bar{m}, \bar{p}\}, \delta = 0, \alpha_0, F].$$

**IV.5.8** Our nonpollent entities may not reproduce, but this above production rule can nevertheless produce infinitely many of infinite variety ... as many as there are sentences in any spoken language. Their lack of ability to reproduce is not specific to any Kingdom; nor to any entity.

Complete nonpollent entities could perhaps be a set of pre-Archaea entities. Those likely had no nucleus, and no membrane-based organelles. We do, however, have worker ants, worker bees, mole-rats and other such strictly eusocial entities as cannot reproduce. We also have nonreplicative parts contained within entities, such as our own neurons. All such nonpollent biological materials, wherever located, are equivalent to Chomsky's Type 3 regular grammars, and so to fixed finite state automata.

**IV.5.9** Meme 116 gives our second Chomsky production. This is the unipollent level of  $S_1-V_2$  and genome-entity. This is not merely single-celled entities. It covers any biological material—i.e. in or out of any entity or population, and within any Kingdom—that can replicate.

These unipollent entities do not support trivial cycles, but can re-enter the replication globe. They are equivalent to Chomsky’s “Type 2” or “context-free grammars”, and so to ‘pushdown automata’. Since they can reproduce, we allocate them a set of fibrations and cofibrations with an index  $\delta = 1$ .

**IV.5.10** Our next Chomsky production of Meme 117 produces the third pluripollent level of  $S_2-V_3$  gene pool–species. This is all biological materials—again wherever located—that can both (a) replicate, and (b) support at least some material(s), that cannot. They are suitably exemplified by asexual multicellular entities such as polyps, flatworms, and anything that can bud, fission, and engage in vegetative reproduction, as do starfish that can regenerate from cut limbs. They are also such constructs as organs and tissues. These are produced by trivial cycles in the biology globe, but must be replicated by some nontrivial one that crosses the projective plane. They are equivalent to Chomsky’s “Type 1” or “context sensitive grammars” representing ‘linear bound automata’. We set their  $\delta$  to any integer value.

**IV.5.11** Meme 118 is our final totipollent production level. This  $S_3-V_4$  is DNA-Gaia. We set the reproductive index,  $\delta$ , to any positive, but non-integer, value.

These productions characterize biological materials produced of more than one reproductive centre. Although they can go through trivial cycles in the replication globe, they must always be supported by some nontrivial one that carries them across the projective plane. They are equivalent to Chomsky’s “Type 0” “unrestricted grammars”; are recursively enumerable; and embrace sexual reproduction of:

$$\pi = (2 \times 1^{1/2} \rightarrow n)^1 \Leftrightarrow (n \div 1^{1/2} \rightarrow 2),$$

where  $\delta$  is set to  $1/2$ .

**IV.5.12** We have now accounted for all biological materials. We have a progenitor domain as preimage and progeny codomain as image. Their recursive functions are mappings that are either injective or non-injective; and either surjective or non-surjective.

**IV.5.13** Our last task is to categorize these productions. They are all homomorphic and homotopically equivalent. But some are additionally homeomorphic.

**IV.5.14** We are at last ready to find the rules for the stases of the first, second and third kinds of  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$  and that are also the three constraints of  $\int dn = \int dM = \int dP = 0$ . These separate the

injective from the non-injective, and the surjective from the non-surjective. They thereby also separate preimage from image, and the progenitor domain from the progeny codomain to create all biological entities and behaviours.

# **Part V**

## **The fundamental biological groupings**

**V.1.1** We now have to relate the homomorphic structures biological entities can create to the homeomorphic spaces in which they must move. Since they must all recurve in a four-dimensional space, then we can enumerate their fundamental properties.

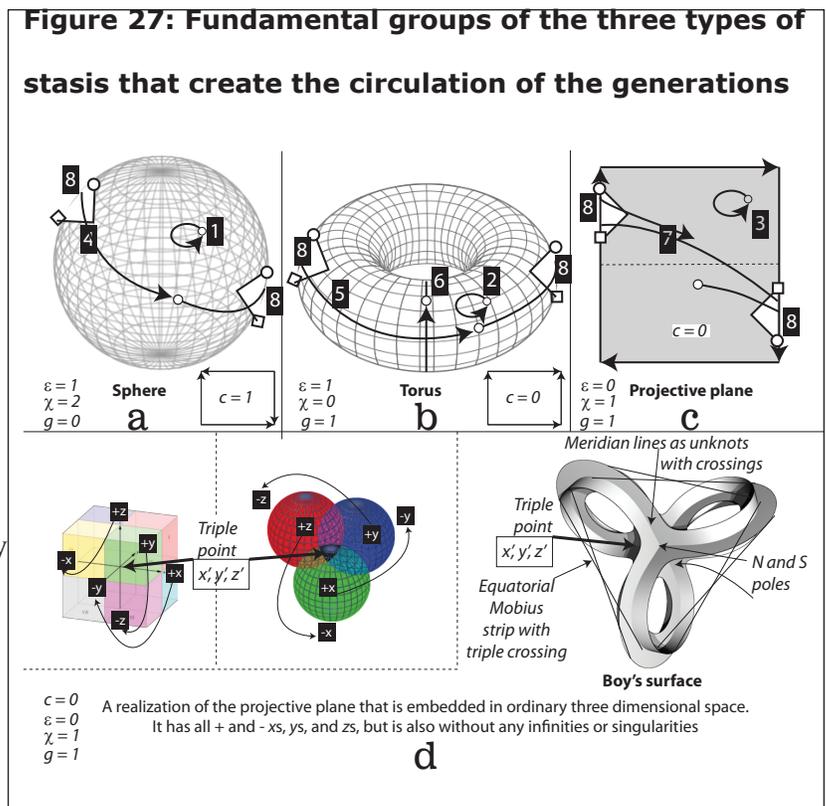
Our Commandos 1 and 2 in Figure 12 showed how to measure the populations underneath them. However, those populations can easily follow homotopic and quantitatively equivalent paths, which begin and end in the same location, but that are not qualitatively equivalent, or homeomorphic. Their 0-, 1-, 2-, and 3-balls can easily exhibit the same

$V_{1,2,3,4}$ . But their paths across their respective  $S_{0,1,2,3}$  surfaces, as measured by their 0-, 1-, 2-, and 3-spheres, could be radically different. Since we currently have no way to distinguish any such paths, then we have no way to distinguish biological populations.

**V.1.2** Our stases of the first, second and third kinds, and our three constraints, may each sum to zero, but they are importantly different. Since the three stases of  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$  incorporate gradients, divergences, and curls, then they are critically dependent upon the precise paths, and directions, they each take. Since they measure surfaces,  $S$ , they are “inexact differentials”.

**V.1.3** The three constraints of  $\int dn = \int dM = \int dP = 0$  present a direct contrast. They are completely indifferent to surfaces and paths. They instead measure interiors, giving values for gongyls for rotachorons, volumes for rotahedrons, areas for rotagons and the like. They depend only upon initial and final values and states. Since they measure volumes,  $V$ , they are exact differentials.

**V.1.4** We can separate the three stases from the three constraints using the three sets of curves on the sphere, the torus, and the real projective plane in Figure 27. The two sets of curves may have certain topological similarities, but they nevertheless create very different paths against the three sets of **ijk**, **IJK** and **TNB** axes that our Frenet-Serrat trihedron can measure. Those differences will have different topological effects on each of the three types of surface, meaning different biologies.



**V.1.5** Figure 27 sets us on our way by demonstrating, for Meme 119, that no populations can complete a circulation of the generations without at some time undertaking transformations—such as in the white Regions 8—that are the direct opposite of those they undertake at some other point. Those opposite points must then be the real projective plane’s identified points.

Since the four dimensions on a real projective plane are again impossible to visualize, we turn to Boy’s surface, shown in Figure 27d. It is the most accessible three-dimensional representation of a set of four-dimensional interactions.

Werner Boy discovered his realization of a real projective plane, in 1901, when his thesis supervisor, David Hilbert, challenged him to prove that one could not be realized in ordinary three-dimensional Euclidean space. As in Figure 27d, Boy successfully connected the positive  $x$ -axis to the negative  $y$ -axis, the positive  $y$ -axis to the negative  $z$ -axis, and the positive  $z$ -axis to the negative  $x$ -axis. Those twisted  $xy$ ,  $xz$ , and  $yz$  planes recreate their  $x = 0$ ,  $y = 0$ , and  $z = 0$  origin by intersecting in exactly their one “triple point”.

Boy’s surface may help us investigate our biological symmetries, but since the unbounded but noninfinite realm it depicts cannot be properly realized without a fourth dimension, it is deceptive. It alludes that its three infinitely extensive Euclidean  $(xy)_{zw}$ ,  $(xz)_{yw}$ , and  $(yz)_{xw}$  planes are in fact circulating planespaces. It also suggests a discrete inside and outside, and so positive and negative locales, over all three of our observable dimensions. We can therefore be left with the impression that the limited realmspace at its centre is the reality ... but we have not seen any  $w$  measures.

The deception in Boy’s surface is precisely that it handles events in four dimensions ... and then represents them in three. We see  $(xyz)_w$  but do not see  $(xyw)_z$ ,  $(xzw)_y$ , or  $(yzw)_x$ .

Boy’s surface can be both a mapping cylinder and/or a fibre bundle. However, a fibre bundle, being a product, can have either or both of its base or fibre as either or both of its projection map and retract. Either or both can contain flips, orientations, magnitudes, and rates of change independent of the other. The upshot is that two neighbourhoods can be homeomorphic, and near each other, on Boy’s surface seen as a mapping cylinder, without their equivalent neighbourhoods being either homeomorphic or near each other on either the base or the fibre that give rise to it. Populations and entities can therefore be near to each other in one structure, but appear separated in another.

The realmspace enclosed in Boy’s surface also belies reality by seemingly trapping all positive, or else all negative, neighbourhoods inside it. But as in this real and three-dimensional realm, it is, firstly, always possible to keep moving onwards infinitely, unboundedly, and rectilinearly in both the positive and the negative directions without ever circling back. And secondly, the surface’s constant curves suggest that a similarly curved tetraspace influences the Boy’s surface events. However, the tetrarealm that imposes those apparently curving  $x$ ,  $y$  and  $z$  behaviours in fact extends indefinitely in all its four directions.

**V.1.6** We begin by considering a one-dimensional line,  $x$ . Since biological entities are not infinite in that they must be replaced, they have the same general difficulty as all manifolds that, like

Boy's surface, are without a boundary; that are unbounded; and yet that are not infinite in extent.

A circle is a one-manifold with the local topology of an infinitely extended line,  $x \rightarrow \pm\infty$ , but with a limited or bounded global topology. It cannot be properly built—as a one-manifold without boundary—within that same one dimensional line. We can only realize its noninfinite and unbounded global topology by creating a two-dimensional circle,  $(x | y)$ . That then provides the infinitely many linespaces for all required line segments.

The circle we use to create our unbounded one-dimensional expanse adds another important possibility. Whatever direction we move in at one point on the manifold, we can move in the opposite direction at another  $(x | \pm y)$ .

We can also eventually return to the original point or orientation. The added dimension therefore allows us to reverse orientations because we can have both  $(x | +y)$  at one moment, and  $(x | -y)$  at another, with no discernible difference in  $x$ :  $(x \rightarrow \pm\infty | \pm y)$ .

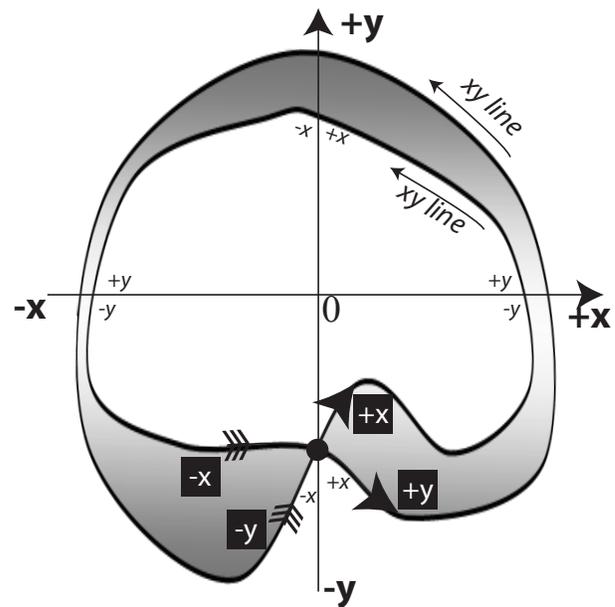
**V.1.7** We then turn to two-dimensional areas,  $(x, y)$ , or  $(x \rightarrow \pm\infty, y \rightarrow \pm\infty)$ . An infinitely extended but unbounded two-dimensional plane and manifold is easy enough to visualize. We simply provide a sphere's surface. Its local topology gives the identical impression of being infinite, even though it is of limited extent. However, that limited yet unbounded two-manifold cannot be built in those same two dimensions. We must turn to a third to construct the sphere whose surface then provides the relevant planespace as  $(x \rightarrow \pm\infty, y \rightarrow \pm\infty | z)$ .

Our sphere's unbounded planespace promptly gives us the same possibility as the circle did for the line. We can soon find a local direction to move in that is counter to any current one. Our third dimension can first reverse, and then restore, any two-dimensional orientation:  $(x \rightarrow \pm\infty, y \rightarrow \pm\infty | \pm z)$ .

**V.1.8** The analogous situation holds for three  $(x \rightarrow \pm\infty, y \rightarrow \pm\infty, z \rightarrow \pm\infty)$  dimensions. The surrounding cosmos gives every impression of being an ever-extending and infinite realm. But it is impossible for us to realize an unbounded and noninfinite three dimensional realmspace within these same three dimensions.

Although we now know that the surrounding universe supports the curves imposed by the Big Bang, a fourth dimension is required to correctly build it ... which is unfortunately not available.

**Figure 28: Mobius strip immersed in two dimensions**



What would then look, to us, like a transition from the beginning to the end of a generation would instead be a slight shift, in another dimension, that then continues indefinitely. We cannot build and observe that fourth dimension, but it could reverse orientations as  $(x \rightarrow \pm\infty, y \rightarrow \pm\infty, z \rightarrow \pm\infty \mid \pm w)$ .

**V.1.9** We can easily use our three dimensions to build a Möbius strip. Its surface is then an  $xy$  two-manifold that can easily reverse orientations with  $z$ . But as in Figure 28, that reversal of orientations is impossible to realize in only two dimensions.

Since that unknot with crossing, complete with indicated area, is a two-dimensional figure, it can only suggest the twisting and nonoriented behaviour we experience so easily in three. It nevertheless helps make our higher-dimensional world's Möbius twist events at least a little clearer to beings confined to that lower-dimensional one. The definite seeming "interior" regions on both Boy's surface and our Möbius representation mark them both as "immersions". Since neither interior reflects the reality, neither is a proper "embedding".

The Möbius strip we represent in Figure 28 cannot be properly embedded in two-dimensional space. It can only be immersed.

**V.1.10** Both Figure 28's unknot with crossing and Figure 27d's Boy's surface make compromises in their efforts to indicate their respective twisting events. The distinction between an immersion and an embedding is that an embedding surrounds any object with all the rest of that space. We have represented Figure 28's crossing point as a small and filled-in rotagon. It is a large dot fully embedded in that two-dimensional space.

We can similarly surround any three-dimensional object with all the rest of space. But we cannot fully surround four-dimensional objects. We can only immerse—and so indicate—them in our three.

**V.1.11** We in our three dimensions can only navigate both sides of a Möbius strip because our extra dimension allows us to twist. Our two-dimensional Möbius strip immersion emulates Boy's, for a two-dimensional being, by creating a circulating linespace. Since that twisting manoeuvre is not available in only two dimensions, we must resort to self-intersections to represent it. The circulating, unbounded, and noninfinite one-dimensional  $xy$  manifold connects the positive  $x$ -axis to the negative  $y$ -axis, and the positive  $y$ -axis to the negative  $x$ -axis.

The interior and exterior that Boy's surface seems to provide is no more real than the apparent space Figure 28's immersion bounds. When a Möbius strip is realized in three dimensions, there are no such interior or exterior regions.

Boy's surface tells us where we can find objects in a bigger and higher-dimensional manifold. The four-dimensional space it depicts is at all points tangential to that immersion. Each of these two constructions is only a mapping to each one's infinitely extended and higher-dimensioned

spaces so that Figure 28's  $x$  and  $y$  axes truly do go marching off to infinity either side, and do not curve round as the immersion suggests.

**V.1.12** In spite of the above caveats concerning its appearances, Boy's surface clarifies that in order to complete a circulation of the generations, it is necessary to traverse both its sides. Such objects must therefore share the same positive and negative absolute values at all times; across all observable dimensions; and so must also always share the same rates of change and behaviours on their bases, their fibres, their fibre bundles, and their deformation retracts and mapping cylinders.

**V.1.13** The symmetries and the rates of change enshrined in our two sets of exact and inexact differentials circulate equally about Boy's surface. While the three constraints are exact differentials that state the smooth and direct paths common to all spaces, the three stases of the numerical, the material, and the energetic are the potentially irregular surfaces that state the paths leading to, and that can surround, those volumes. They are instead inexact differentials. But since the four dimensions they each represent cannot be properly represented in three, then those planespace rates in  $x$ ,  $y$  and  $z$  inform us of the need to master their differences in rates.

**V.2.1** Boy's surface helps us to distinguish between species by demonstrating that the entities in each are constant topological neighbours. They always enjoy each others' velocities and accelerations. The surface confirms that no matter how far the entities might travel in any given direction, they always end up—still together—at their joint triple point values, so creating their equally curving joint mapping cylinder about themselves. They achieve this by sharing the rates of change that define their joint symmetry or invariance. Those rates over time then become the absolute amounts that distinguish each species. But these are exactly our plessists and our plessemorphs, which always undertake communal transformations. They move between their shared maxima and minima, and so about their common deformation retract,  $S' = \{n', \bar{m}', \bar{p}'\}$ , which they jointly maintain over  $T$ .

**V.2.2** Each of the three meridians on Boy's surface is an unknot with crossing constructed from a set of rates. The  $xy$ ,  $xz$ , and  $yz$  planes represent the transformations supervised by the constraints, and that are then its surface. Each meridian twists two planes, as two rates, about itself. Each therefore wraps itself about Boy's surface from one pole to the other, acting as a Möbius strip's centre line. Each thus forms one of the three biological constraints. Each dimension or manifold interacts with two others to form the meridians that then curl about the entire surface.

**V.2.3** The corresponding poles in our biological space are  $n_{\text{initial}}$  as the beginning and  $n_{\text{final}}$  as the end of a generation. Those two values define a diametric route, of minimum rate of change, that punches directly across the Boy's surface interior, creating its triple point, and so defining the overall number density,  $N$ . Since those initial and final values incorporate rates, then the greater is the distance, the greater the relative differentials involved.

**V.2.4** The equatorial plate in Boy's surface is now a fourth Möbius strip. It is orthogonal to the above meridional three. It has three twists. It delineates the maxima that the meridians reach as they journey from pole to pole. It defines the fibration–cofibration cum biology–replication globe interface that creates the mapping cylinder for our recursive functions in Figure 7.

**V.2.5** The Boy's surface equator bounds the unit rotachoron. It is a fourth interface between our biology and replication globes. The fibration transforms the other three, which are the meridians, from pole to equator. The cofibration then imposes the reverse transformations to carry them back to the other pole, which is the self-intersection point.

**V.2.6** The triple point at the rotachoron's centre, bounded by the equator, is the deformation retract that the population uses, with the surroundings, to construct a generation. Their complete biological behaviour is the covering mapping cylinder,  $M_{\lambda}$ , that is Boy's surface. The surface's area again states the rates of change. Boy's surface will therefore help us define a species in terms of a

shared invariance or symmetry, in the rates that create the  $\psi$ ,  $\gamma$ ,  $\theta$  and  $\rho$  that is the complete set of biological activities,  $\lambda$ , that construct it.

**V.3.1** We then turn to the real projective plane in Figure 27c. Its equator is also an unknot with crossing. It can therefore twist a plane of biological activities about itself. The same goes for its meridian, which contains the crosscap that identifies all diametrically opposite points upon a circle.

**V.3.2** Loops upon the real projective plane that do not cross the real projective plane's equator, and so that do not touch its edges, can only form trivial cycles in one hemisphere or another. Any that touch its edges cross the equator and create a circulation of the generations.

**V.3.3** All lines on real projective planes emulate the Boy's surface equator and its three meridians by being continuous journeys. Both the replications across the biology–replication globe interface and the ingress across the generational interface are continuous journeys. They each have a distinctive length, and a distinctive rate of curvature across all four dimensions. Each loop leaves its initial basepoint,  $\alpha_0$ . Each then returns to give  $\alpha_0 = F$  to form a loop,  $s$ , in some space,  $S$ .

**V.3.4** Every circulation of the generations is a continuous loop. But even though every species or biological space,  $S$ , can hold a vast array of such loops,  $s$ , they will all hold certain characteristics in common.

The common characteristic of all such repetitive journeys is their reversibility. If we go first north then east on any loop  $s$  in some space  $S$ , we must eventually go south and west or we do not return to the beginning. If a generation is to repeat, then those rates and lengths must cancel out. But granted that these are topological loops, then the distances concerned are potentially unbounded. This unboundedness does not, however, change the essentials of reversibility. Henri Poincaré (1892) first referred to this essential characteristic as the space's "fundamental group",  $\pi$ .

**V.3.5** As a general principle, each loop  $s$  in  $S$  remains essentially the same if we instead choose to go about it in the opposite direction. This gives  $s^{-1}$ . That reversible succession of rates of change of latitudes and longitudes makes the original,  $s$ , and the reverse,  $s^{-1}$ , homotopically equivalent. They do the same thing, for they go out and back to the same point over the same terrain, and to the same effect.

Going about the same loop in both the forwards and the backwards directions confirms its smoothness and its path-connectedness. It also multiplies them together, as a group operation, to give  $s \circ s^{-1}$ . This is the "zero point loop" of  $\alpha_0$  to  $\alpha_0$  or  $F$  to  $F$ . Since all rates necessarily cancel out, this  $s \circ s^{-1}$  multiplication is also the "constant loop".

**V.3.6** As with all important topological designata, constant loops are independent of size. Figure 29a shows that any two railway lines in a perspective drawing can potentially create a loop. Since they are topological, they can increase any loop's size by extending, without bound, in any direction.

As they move indefinitely far into the distance, the two tracks will look as if they come together to create a single point upon the horizon.

That horizon—which represents the unbounded—is the line at infinity. It lies all around as a circle at infinity.

The opposite direction holds the loop's completion. The same railway tracks approach us from behind, again coming

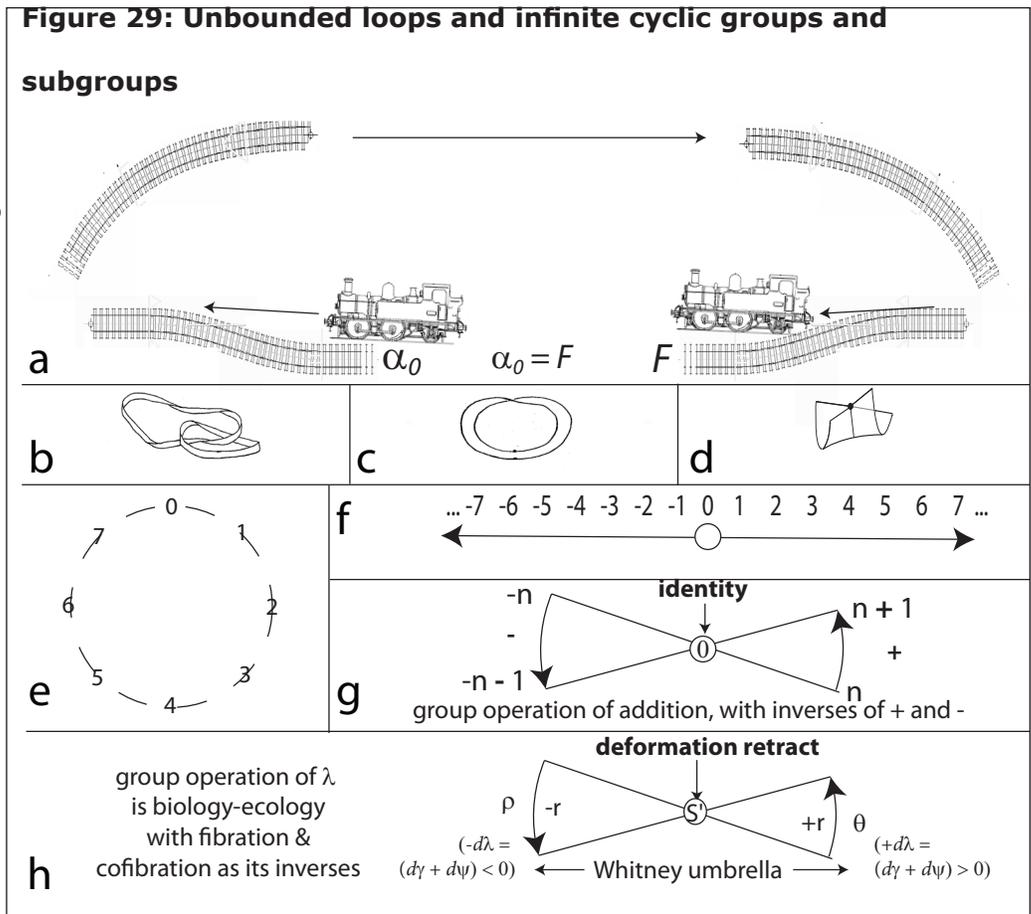
in from a point at infinity. And since they went out to infinity; looped around on the circle at infinity; and then returned as their opposites, again from infinity; then that entire circle out at infinity surrounds us, topologically. It emits and absorbs all such loops. All points upon each such completed loop, irrespective of length and location, are constant topological neighbours. They also indicate rates over lengths that ultimately cancel out, or they would not be loops.

A train can now leave us on its parallel lines; go all the way out to infinity at some initially known rate; circle about while still infinitely far away; and return back from infinity; but over on the other side, and with an opposite rate. The Möbius strip in Figure 29b is now the prototype for all such beginning to end and circulating behaviours (Carter 1993).

**V.3.7** A constant topological loop means that we can draw conclusions about any circulation of the generations, and of any size. Each stretch  $x$  on any constant loop  $s$  in any space  $X$  is precisely matched by both (a) an inverse  $x^{-1}$ , and (b) a complement,  $x'$ .

For each journey  $x$  in  $X$ , there exists a reverse journey  $x^{-1}$ , back across that same interval, and that eventually creates the out-and-back constant loop,  $s$ . This is also the identified and opposite points for that expanse, but as if moving in the same direction, over on that opposite side.

The complement of  $x'$  is the remaining span of any constant loop, and such that  $x \circ x' = s$ . Thus to move along some  $x$  in  $X$ , and then to turn about and return, is equivalent to having moved all about in that same direction and along some opposite and identified span; and to traverse the entire



loop and to return, as if from the opposite direction, and having gone about the whole. To go out a specified distance and turn and return, which is  $x \circ x^{-1}$ , is homotopically equivalent to going about the whole, in the same direction, for  $x \circ x^{-1} \approx x \circ x' \approx s$ .

**V.3.8** The Möbius strip is also defined by both its continuous midline and its boundary. The latter is the unknot with crossing of Figure 29c. Its journeyings nevertheless appear to bound the Möbius strip's area which first diverges steadily from the midline to increase by  $+dA$ ; and then steadily converges by  $-dA$ , leaving a net of zero all about that circulation. The overall absolute value for that area is therefore stated by the amount the midline has travelled. It is a rate that also builds the triple point and deformation retract. An unknot with crossing is thus the prototype for all transformations and rates of change occurring about a central value.

**V.3.9** Since a biological population requires Möbius strips and unknots with crossings, then it also demands the Whitney umbrella of Figure 29d. That sends out a line that circles about; returns to the same point; then goes out the other side to do the same. That double loop,  $s$ , goes forwards and backwards, once upon each side, giving it its inputs, and outputs, of  $+r$  and  $-r$ . They are the contacts with both infinity and the surroundings. This is the singular point with continuous neighbourhoods that creates a self-intersecting rectangle on either side.

The Whitney umbrella is now the double point,  $S_0$ . But it is also our  $V_0$  pointspace. It is the symmetric  $\alpha_0$  or  $F$  zero point that goes nowhere, balancing all lengths and rates simultaneously as  $S_0 - V_0$ . Since it can simultaneously emit and receive all forms of opposite behaviours, then the Whitney umbrella is the prototype for all branching behaviours (Carter 1993).

**V.3.10** Figure 29e confirms that all these loops  $s$  in  $S$  are cyclic groups. As with the eight-member group depicted, each element can successively generate the next, under its given operation. At least one is also able to generate all others, including the group's identity element.

**V.3.11** Figure 29f shows that the integers,  $\mathbf{Z}$ , form an infinite cyclic group. Like all such groups, it is symmetric and has exactly two generators,  $+1$  and  $-1$ . Each can generate the entire set. And again as in all such groups, the generators can come symmetrically together to create the identity:  $+1 - 1 = 0$ . Every element that is not the identity is of infinite order, for it can generate all the infinitely many others. And for every element, there is an opposite which together produce the identity.

There are infinitely many infinite cyclic subgroups. And since the loops we can create with them can all reach out to infinity and return, then the Whitney umbrella can grow or shrink to any size. Its branch points can create the entire bound that is the equator about any possible Boy's surface. Every point holds a definite value while still incorporating opposites around a central identity. All

Whitney umbrellas can form an infinite cyclic group, plus subgroups and generators, as can generate other infinite cyclic subgroups; and as can also replicate any given population, along with the identity.

Figures 29g and h now show that all biological populations are isomorphic with the field of integers. Whitney's umbrella in other words has the identical and symmetric group structure as the integers. All biological entities and populations are thus equipollent with the set of countably infinite natural numbers,  $\aleph_0$  (Weisstein 2015a). Additionally, no element generated by the infinite cyclic group's generator is the identity element, but every element that is not the identity is of infinite order, and can generate the identity in conjunction with another.

**V.3.12** We now know that to go out on any stretch  $x$  along some constant loop  $s$  in some space  $S$  and then to turn and return is homotopically equivalent to proceeding all about that loop ... which is a complete circulation of the generations.

**V.4.1** We must now determine what it means to be “in a species” in terms of the fundamental group or groups that all the loops in any space  $S$  hold in common, and as distinguish them from all loops in any other space, which means from all other spaces.

**V.4.2** Loops 1 to 4 in Figure 27 are in this sense technically equivalent. We can go both forwards and backwards about them all, deforming them into others of that same type. They are all simply connected. They can smoothly contract to the singular point that is their constant loop. Since they are therefore homotopic to that constant loop, they are homeomorphic. These cannot help us separate out species.

**V.4.3** Loops 1 to 3, however, are trivial cycles on each of the sphere, torus, and real projective plane. They do not cross any equator. They can help confirm species boundaries.

**V.4.4** Loop 4 is different to Loops 1 to 3. It is nontrivial. It crosses an equator. It can help define species boundaries.

**V.4.5** The sphere in Figure 27a can host infinitely many loops and cycles, both trivial and nontrivial. If we imagine each loop as a rubber-band, then each can slide easily in any direction. They can all deform freely into each other and into the constant loop. The sphere is therefore simply connected.

**V.4.6** All loops upon a sphere have the common characteristic that they can all slide right off. All possible trivial loops for all  $n$ -spheres, of whatever dimension, behave the same way. The constant loop is their common identity. A sphere’s fundamental group is therefore trivial. No matter what the dimension, all spheres have the “trivial fundamental group”:  $\pi(S) = 0$ .

**V.4.7** Every species similarly has some entities “inside it” by being current and observable. Yet others are “inside it” in the sense of being non-current ... but replicatively accessible. They are therefore currently “outside it”; but only in the sense that they have yet to be replicated. They are inside through having the potential to be replicated. They differ from all future entities in all other species which are therefore “doubly outside” by being (a) yet to be reproduced, but also (b) not being inside that species at all by being permanently and replicatively inaccessible. We must find a way to represent this.

**V.5.1** Loops 5 and 6 upon Figure 27b's torus are very different from the loops upon Figure 27a's sphere. If they were placed back upon the sphere, they would define its equator and prime meridian. But they would also deform and slide off like all others.

When we remove Loops 5 and 6 from the sphere and put them back on the torus, they behave very differently. They have a common contact point upon the toroidal surface. They meet and link. They become impediments to each other. The one on the meridian prevents the one on the equator from sliding off. It is possible to deform the one into the other, so that they switch their directions and their senses of interior and exterior, but they still prevent each other sliding off. These can place boundaries around species.

**V.5.2** Every space,  $X$ , has a boundary which is the set of points,  $C$ , that is its "closure". It is the subset of its points that can be approached from both its interior and the outside. Any point  $c$  in  $C$  is a "boundary point". A "boundary operation" is then that of finding all those boundary points. And even though no noninfinite and unbounded manifold can be built in the same dimension exhibited by its local topology, boundary operations determine their characteristics by studying them at the level of both (a) the two-dimensional plane; and (b) the one-dimensional line.

An interior point can move freely in all relevant directions, unrestricted by any closure or boundary. A two-dimensional plane's interior is any space homeomorphic to a disc or rectangle. Each interior point is then surrounded, on all sides, by others. Thus a sphere's surface—considered independently of its interior—is again homeomorphic to an infinitely extended plane. We do not find a boundary point in any direction.

The same holds for a line. An interior point in one dimension is surrounded by others. So no matter how far we might travel along a circle, we find no boundary point. There are always points to either side. Thus a circle is homeomorphic to an infinitely long Euclidean line.

If we now imagine a disc or rectangle cut in half, then its boundary points only surround a half-plane. The boundary point now has an interior point on one side, and an exterior one on the other. A half-plane is not homeomorphic to a full disc. This holds true whether we stretch or shrink it.

The boundary we have just discovered is instead homeomorphic with an arc that has endpoints on either side. If we stand at the arc's midpoint, then any journey out to one end point is the same as a journey to the other. We get to a boundary point either way. So we can just as well close up the arc and draw those two end points together. We now have a line segment. And since that line segment has the boundary point at its end and no points beyond, then an arc is homeomorphic with a line segment. The half-plane in its turn consists of all points on one side of an infinite straight line, and no points on the other. We can thus use either the half-plane or the line segment to separate any space.

**V.5.3** We can define these anomalous interiors and exteriors for our biological populations by considering the fundamental polygons belonging to the sphere, the torus, and the real projective plane,

and then undertaking their respective one- and two-dimensional boundary operations. We first take up the torus in Figure 27b.

**V.5.4** The torus' fundamental polygon is a full plane. Its edges can be freely pushed to either plus or minus infinity. Boundary points advance and retreat as we approach, without us ever walking into them. Since we can create any torus, of any size, simply by gluing the ends of any cylinder or its fundamental polygon together so the arrows align, then just like a sphere's surface, a torus' would appear to be homeomorphic to an infinite Euclidean plane. There are always more points in the interior, acting as a full plane and rectangle. We again do not find boundary points.

**V.5.5** We can then perform our one-dimensional boundary operations, on the same torus, by applying a retract hyperplane. It becomes an annulus in the plane. And if we next deformation retract those two edges by drawing them inwards equally, the annulus eventually becomes a circle and a one-manifold. We can walk about that circle infinitely in every direction, without ever finding a boundary point. Since this is also equivalent to an infinitely long line, then the torus has no points in any  $C$  or closure set. It therefore has  $c = 0$ .

**V.5.6** A sphere is unfortunately very different.

**V.5.7** We already know that if we cut a sphere in half and then flatten it out into two dimensions, the hemisphere's edge goes all the way out to infinity, and we get a real projective plane. The sphere's fundamental polygon, in Figure 27a, is therefore very different from the torus'. It might look like a full rectangle ... but it is not. It is instead two of our half-planes abutting, each separately bounded by an infinite line.

If we glue the edges of the sphere's fundamental polygon together, the surface becomes infinite and unbounded. It is homeomorphic with an infinitely extended plane. However, the sphere itself is a three-dimensional object. And ... that has an interior and a bound. It will always have that interior. If we try contracting it to a point, we will always find a set of interior points, with a boundary sitting right beside them. Despite its surface having the local topology of a Euclidean plane and always being unbounded, the sphere's interior always has a point of closure, or an edge.

Walking along the boundary of the sphere's fundamental polygon produces a further problem. Since identified points go in opposite directions, from the same point, then we cannot get to the other half-plane without crossing the hemisphere's boundary ... which is an edge. If we measure the flattened hemisphere using spherical coordinates, the plane goes out to infinity; and we return upside down on the other side. If we want to replicate those opposite behaviours then we must remove a line from the full plane to create two half-planes; or we must remove a point from a line to create two line segments, This is equivalent to saying that the boundary point always exists.

We can express the above by saying that the sphere is a bidimensional manifold with an infinite plane for each hemisphere. Each set of points in each of its half-planes has a neighbourhood homeomorphic with the neighbourhood of a point that belongs to the closed half-plane's boundary or closure set,  $C$ . Each half-plane is an arc containing a boundary point,  $c$ . The sphere is a line with central point removed to create two line segments, and therefore has  $c = 1$ .

**V.5.8** While it is true that the torus's surface can emulate the sphere's and support a complete set of infinitely many rubber bands equivalent to the sphere's  $\pi(S) = 0$  trivial cycles ... the ones we place on a torus' meridian or equator have an important restriction. Those two sets—such as Loops 5 and 6—are very different from all those we can place either on a sphere, or elsewhere on the torus' surface.

The torus has a double interior. There is the volume that creates its “filling” when it is a doughnut; and there is the volume behind the surface that makes up its doughnut body. Since the torus has that hole in its middle, none of the infinitely many rubber bands we can place about its prime meridian can slide off. But further since its surface is infinitesimally thin, all rubber bands placed about the prime meridian automatically conjoin with any placed about the equator. And since one set is born from an annulus—which has no closures—then none that bound either the prime meridian or the equator can contract to a point. Each is held fast by the other.

We now find that the only rubber bands that can slide off a torus are its trivial cycles, similar to a sphere. Those, however, bound neither its equator nor its prime meridian.

**V.5.9** The torus now differs significantly from the sphere because the two sets of infinitely many non-contractible loops we can place about either of its two diameters are each independently equipollent with the integers,  $\mathbf{Z}$ . And since none of the three sets of loops the torus has available to it can be persuaded to slide off by first deforming them into any of the others—for two sets are linked—then the torus' fundamental group is very different from the sphere's. It also guarantees us both an equator and a prime meridian for our nontrivial biological loops. It has  $\pi(S) = \mathbf{Z}^2$ .

**V.5.10** We now have both an equator and a prime meridian. This is both (a) a beginning and an ending for our biological circulation, plus (b) a maximum and a minimum. But the two are linked. We cannot yet separate them from each other. We still cannot distinguish the biology–replication globe interface from the generational one that marks the beginnings and ends of the circulations of the generations ... although we must travel to them all.

**V.6.1** We now look at the real projective plane's Loop 7, in Figure 27c. This is ostensibly the same as both the sphere's Loop 4, and the torus's Loop 5. Those each go about their respective equators. But the projective plane is like the torus in being an infinitely extendable plane with no boundary points:  $c = 0$ . However, since Loop 7 is only a loop because its opposite points have been identified, then it is not a loop upon its particular surface. It is a line segment. The projective plane therefore has a different fundamental group from both the sphere and the torus.

**V.6.2** None of the loops located inside the real projective plane's fundamental polygon, in Figure 27c, touch its boundary. Like all the  $\pi(S) = 0$  ones on the sphere, they are all contractible trivial cycles.

However, Region 8 on the real projective plane is highly deceptive. The plane's two parts might look divided, but all its regions—including these abutting the boundary in that Region 8—are locally Euclidean. Since they are identified, we jump smoothly from one point in a Region 8, on one side, to exactly that same point on the opposite side. But as the equivalent Regions 8 upon the sphere and the torus in Figures 27a and b suggest, we teleport across an entire hemisphere to get there.

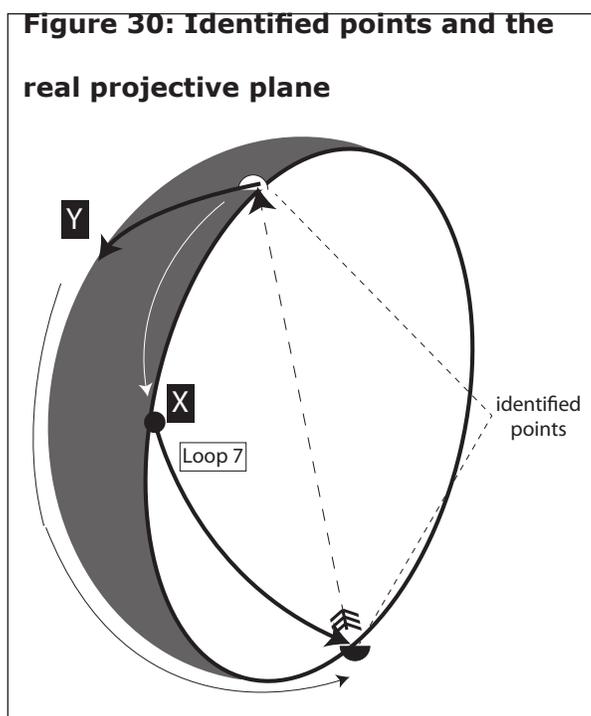
**V.6.3** Figure 30 clarifies what is happening. Loop 7 begins in hemisphere  $X$  on the real projective plane, which travels on the sphere's inside. When we hit the equator and boundary—which identifies opposite points—we immediately teleport to the equivalent point diametrically over on the opposite side. We have only physically crossed the equator once.

We now travel in the same direction, in hemisphere  $Y$ . But this is on the sphere's outside.

When we arrive at the equivalent and identified point opposite our Loop 7 start, we are therefore over on the opposite side, in  $Y$ . But since there are many points in  $X$  we teleported over and have not traversed, we have not yet completed a circulation.

We must now keep going in the same direction. We must travel right across the projective plane and return to the equator to teleport a second time. That second teleport takes us to the same point at the top. We can then travel upon the inside to go back to the start of Loop 7 in  $X$ . Only now do we pass through the same identified points we just covered in  $Y$ , so we can complete the nontrivial loop,  $s$ .

Figure 30 makes clear that we must in fact travel through some Region 8 twice to circumnavigate a globe. This is equivalent to saying that if we begin at some initial  $\alpha_0$  and go forwards to hit some maximum; and if we decrease from that maximum to return to  $\alpha_0$ ; then we have



only completed half a circulation. We have travelled about only one loop on a Whitney umbrella. We must keep going past  $\alpha_0$  to some minimum and then reverse to re-approach  $\alpha_0$  from the same side. We then complete the loop,  $s$  in  $S$ , with the return to  $\alpha_0$  being the final point,  $F$ .

**V.6.4** If a first line representing some journey upon a real projective plane goes to the edge and then reappears from the opposite boundary, but in the opposite hemisphere, then a second line must eventually go back to the original hemisphere, to complete the journey. And if we deform a first loop along one boundary so it moves smoothly into a nearby region at some given rate, then we must deform its complement equivalently smoothly upon the other boundary, at that same given rate. We must always consider all lines twice: once for each opposite hemisphere.

As in Figure 27c, a complete journey across a real projective plane always has two complementary line segments symmetrically placed about a middle one. A completed journey is effectively two complete lines. And since we have to loop twice about any such curve to complete a circulation, then the real projective plane's fundamental group is a cyclic group of order two:  $\pi(S) = \mathbf{Z}_2$ .

**V.6.5** A cyclic group—even if only of order 2—always requires that some subgroup contain a member that can generate the whole. As with all other cyclic groups, this latest  $\mathbf{Z}_2$  one must have the identity,  $\#$ , for its first element. The other must then be the sole group member.

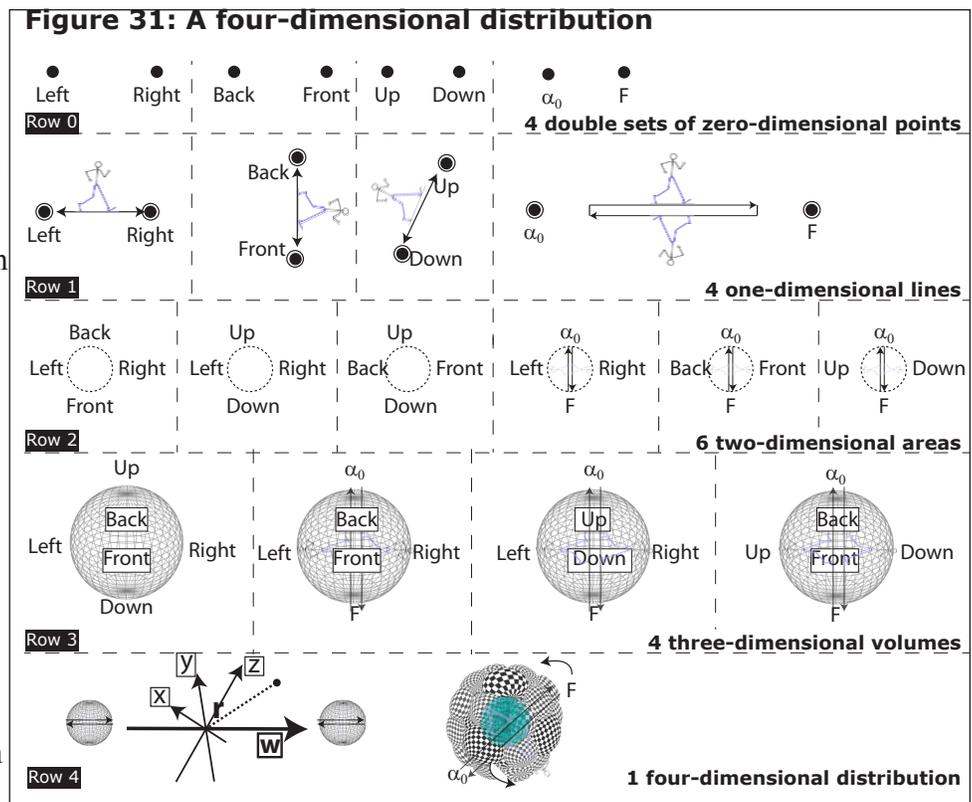
Let the sole member in this cyclic group of order 2 be  $x$ . Since it is the only member in its cyclic subgroup, then we take it up and add it to itself. This steps us through to the next group member. But that must be the identity. There is no other possibility. This gives  $x \circ x = \#$ . And since the only two group members are  $x$  and  $\#$ , then  $x$  has suitably generated the entire group. We thus have  $\langle x \rangle = \{x, \#\}$ .

**V.6.6** If we now take up the identity and add it to itself, we do not step to the next group member. We instead get  $\# \circ \# = \#$ . Adding  $x$  to the identity also keeps it invariant, as in  $\# \circ x = x \circ \# = x$ . Since the identity never generates  $x$ , we have  $\langle \# \rangle = \{\#\}$ . This cyclic group of order 2 therefore has both the entire group and its sole member for its cyclic subgroups.

This cyclic group of order 2 is immediately homeomorphic with the two line segments in Figures 29g and h. They abut each other to give opposite and infinite loops upon either side. The two together are now a line with point removed from between them. That removed point is their identity, for it acts the same to each, being their respective boundary points. They are each now a half-plane and an arc, the whole creating a sphere. And since each of those line segments can also be a constant loop, then we have our Whitney umbrella.

**V.7.1** Our four dimensions give us four Whitney umbrellas. This means eight matching sets of loops. Those eight sets of loops must pass through eight sets of points.

**V.7.2** While it remains impossible to represent four dimensions in only two, Figure 31 demonstrates that since biological entities and populations are communities of rates, then they are infinite cyclic groups constructed from four of Figure 29h's Whitney umbrellas.



**V.7.3** Row 0 in Figure 31 is the complete set of four pairs of zero dimensional points. They are the  $S_0$  0-spheres that establish our four-dimensional rotachoron.

The four  $S_0$  points are also point-pairs. Those point-pairs— $\pm x, \pm y, \pm z, \pm w$ —create our  $V_0$  pointspaces. But when placed in a Euclidean situation, those opposites coalesce and act singly, presenting as  $|x|, |y|, |z|, |w|$ . They are coincident, establishing a common  $S_0$  value.

**V.7.4** Row 1 pushes the coincident  $\pm x, \pm y, \pm z, \pm w$  pairs of 0-spheres apart, as a step-up, to create the one-manifolds that can hold our lines and linespaces. They are the 1-balls that state the distance between the 0-spheres they have at their ends. They are then separated by the distance  $2r$ . Since ordinary physical space is much more familiar, we temporarily label the first three sets Left–Right, Back–Front and Up–Down. The fourth pairing of  $\alpha_0$ – $F$  establishes the beginning and endpoints for a constant loop. These all give the equivalent of  $\nabla Q = 0$  as their gradients. And since the distances between them can vary while the gradient remains the same, then they are again inexact differentials.

**V.7.5** Row 2 brings our various 1-balls together, in pairs, to create the various step-ups that are our  $(x, y)$  2-ball planes and planespaces. Each 2-ball is bounded by its 1-sphere, which is a one-manifold. But each also has a 1-ball stretching diametrically across its middle linking that 1-sphere to that 2-ball area. The diametric 1-ball directly linking the relevant identified 0-sphere points can thus tell us how either the 2-ball area, or the bounding 1-sphere line, is changing. The generation's

beginning can, for example, shift its position at some given rate, relative to its ending. The 1-ball therefore measures the divergence created by the 2-ball. These together give  $\nabla \cdot Q = 0$ . This is also an inexact differential, for the amounts can change while the divergence remains the same.

**V.7.6** Row 3 brings the six 2-balls together to create the various  $(x, y, z)$  realms and realmspaces. Each 3-ball is bounded by a 2-sphere which is an unbounded but non-infinite manifold. Both the journey along the 1-ball diameter, and that about the surrounding 2-sphere can tell us how the contained volume grows and/or changes relative to each. So if our 3-ball contains  $\alpha_0 - F$  then we again know how rapidly properties change across the generation. We know how rapidly the volume is changing due to the gradient and divergence. These together give  $\nabla \times Q = 0$ . And since the quantities can again change while the curl remains the same, then these are yet more inexact differentials.

**V.7.7** And then for Row 4, we take a yet further step up, or integral. If we take up any of the rotahedrons in Row 3 and push them out along the remaining dimension, we will create the identical  $(x, y, z, w)$  rotachoron each time.

We can understand this last step-up as a distribution. We can, for example, consider inflating a hot air balloon; or else measuring the atmosphere, with its different densities, at different heights. We can draw a graph of all the balloon's different volumes at each point in time as we inflate it; or we can record the atmosphere's density per unit volume at a host of different heights. We will then have the balloon's rate of change in its volume across the entire interval; or the rate at which the atmosphere's density changes, in each volume element, at all points. We can now compute how much air the balloon holds at each point, as well as the total moved in and out; or the atmosphere's mass. We in each case know a given property's distribution across some fourth dimension. In the same way a four-dimensional Lorentzian spacetime tells us how gravity is distributed.

Our fourth biological dimension is now telling us how different biological populations distribute their various activities both across an elapsed absolute clock time,  $T$ , and their generation length,  $\tau$ .

**V.7.8** Biological populations also combine their numerical, material, and energetic stases to give  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$ . And since these are all inexact differentials, then the size of the rotachoron they form can change even as these stases of the first, second, and third kinds remain identical. A circle, for example, maintains certain properties as invariant, even if the actual sizes of radius, area, and circumference all change.

**V.8.1** We have a set of both exact and inexact differentials in  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$  and  $\int dn = \int dM = \int dP = 0$ . We are looking to equate them in some group operation,  $\circ$ , that we can perform on some biological population. That group operation should also leave some  $x$  or  $y$  in the group essentially the same. We will then have our strictly biological identity property,  $\#$ . Since it is

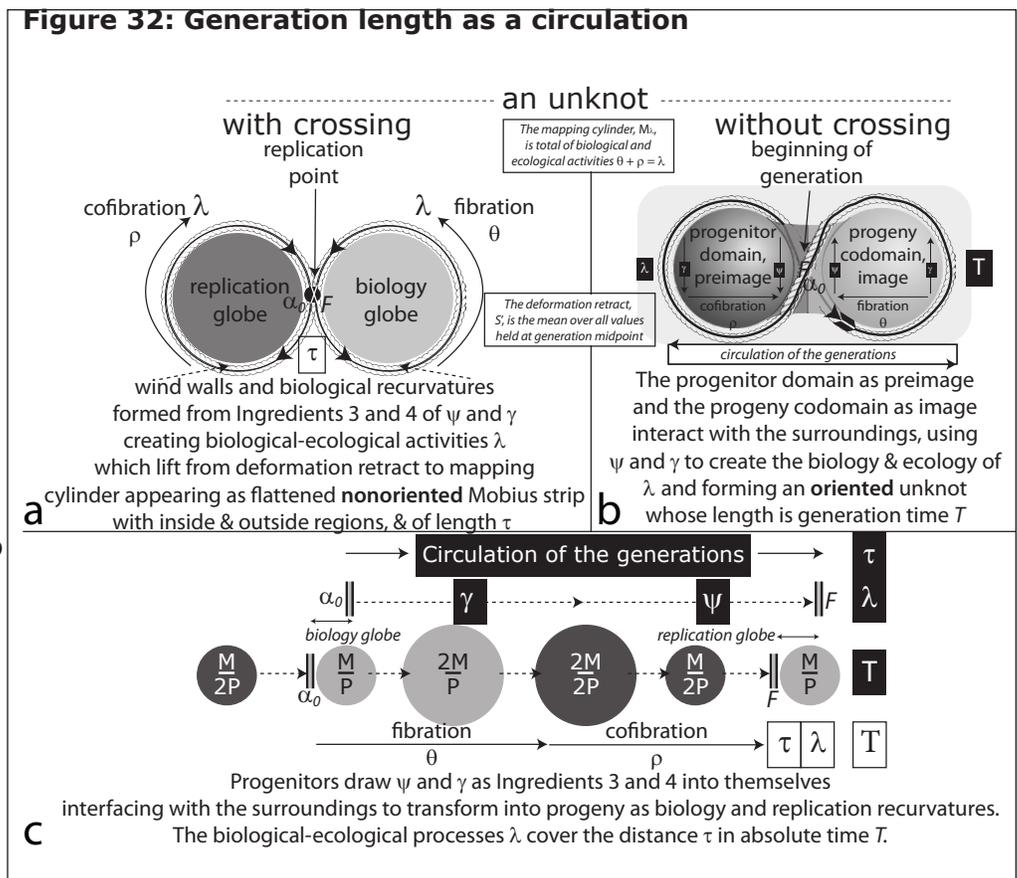
indifferent to both exact and inexact differentials, then we will be able to relate the two sets through that identity.

**V.8.2** All events in both our biology and replication globes affect the surroundings. They are therefore temporal. As in Figures 32b and c, the biological events that create a circulation must therefore have some temporal ordering with respect to each other.

**V.8.3** But as in Figures 32a and c, we can also analyse those same events from a strictly biological perspective. We can assign those same events to one or another of our biology and replication globes based entirely on their effects. Since similar biological events can occur at different points in the cycle, those effects are irrespective of that temporal ordering.

**V.8.4** Figure 32a is two-dimensional. It has a clear but doubled up interior contained inside the unknot with crossing. Figure 32b is three-dimensional. It appears to be the volume defined by a Möbius strip's twisting loops. But since it is embedded, there is no demarcated interior or exterior:

- The two discs in Figures 32a use the replication point—which is their identity—to create a Whitney umbrella of pointspace,  $V_0$ . They also present themselves as the singular point  $S_0$  of specified properties. The total recurvature distance about the two discs—and also about Boy's surface—is  $\tau$ .



- The two globes in Figure 32b arrange the same events temporally. Their diametric distance is the absolute time span,  $T$ , for the same events. That distance punches across Boy's surface. It passes through the triple point at its centre.
- Figure 32c combines both the above as the  $dt = Td\tau$  of biological-ecological processing,  $\lambda$ , that completes a generation. It represents the minimum criteria any population must satisfy to create a fibration and cofibration, and to class as biological.

**V.8.5** We have equivalent ways of understanding biological events. Each of the biology and replication globes recurses—i.e. distributes—its ingested materials about itself, building and/or maintaining its wind walls. Those are its ongoing biological activities,  $\lambda$ . They must also be observable and temporal. Their configurations are the volume and semantics,  $V$ . They have the surfaces and syntax,  $S$ :

- All replicative materials must be biological, but materials can be biological without being replicative.
- All biological events begin, temporally, at some identified point, or equator, and then distribute themselves across time, but none are obliged to complete such a cycle and reach the end of any generation.
- While everything homeomorphic is both homomorphic and homotopically equivalent, not everything homomorphic and homotopically equivalent is homeomorphic.

**V.8.6** We begin a recurvature in Figure 32a about the two-dimensional discs and doubled-up interior at their contact point, which is also the replication point. The fibration,  $\theta$ , carries us anti-clockwise about our biology disc, simultaneously lifting us from deformation retract to mapping cylinder.

When we return to the replication point in Figure 32a, we have only travelled half-way about the Möbius strip. We have inverted some value from  $+r$  to  $-r$ , or conversely. Since we are currently going in a direction opposite to the one we first started with, we must keep going to complete the cycle.

We next enter the replication disc. We undertake the cofibration,  $\rho$ . We eventually get back to the replication point. We are back to moving in the original direction. We have travelled completely about the doubled-up interior, and used our Whitney umbrella and Hooke cell to fully restore  $S_0-V_0$ . Since everything is now the same, we have found our biological  $\circ$  operation. It is this journey around both globes.

Any of our plessists and plessemorphs that go around this Möbius strip and complete a circulation of the generations must abide by:

- Closure, because if  $x$  and  $y$  are each along that path, which is to be in the group, then  $x \circ y$  is also in the group.

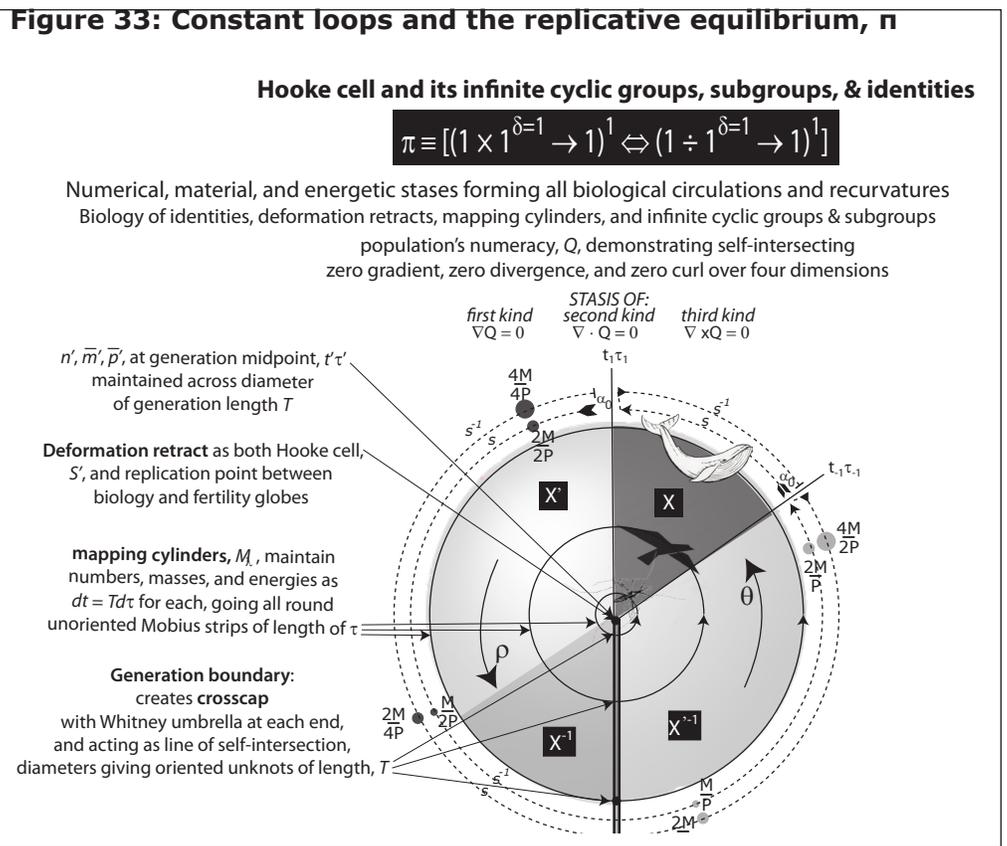
- Identity, because there is an  $\#$ —which is the journey that passes twice through the replication point before returning to some original point in the same direction—and such that for any  $x$ , going all about both globes gives  $x \circ \# = \# \circ x = x$ . And since  $\tau$  is the time required for that generational identity operation, then  $x \circ \tau = \tau \circ x = x$ . We have  $\tau = \#$ . There is a definite amount we can change by that leaves all the same.
- Inverses, because for any distance  $x$ , there is a complement distance,  $x'$ , that completes the recurvature, and so that  $x \circ x' = \tau$  and  $x' \circ x = \tau$ . But there is also the distance  $x^{-1}$  that creates a constant loop, and so that  $x \circ x^{-1} = x^{-1} \circ x = \#$ . This inverse and the complement together produce  $x^{-1} \circ x' = x' \circ x^{-1} = |\tau|$ , with the inverse being the shorter of these two distances. It creates the opposite effect to  $x$ , so that applying it to  $x$  is the same as moving about the whole, as in  $x \circ x^{-1} = x^{-1} \circ x = x \circ x' = x' \circ x = \tau$ .
- Associativity, because if  $x$ ,  $y$  and  $z$  are in the group then  $(x \circ y) \circ z = x \circ (y \circ z)$ .

**V.8.7** Figures 32a and b represent the two interconnected ways of understanding the cycle of the generations. The former is  $\tau$  and nontemporal and nonoriented; the latter is  $T$  and temporal and oriented:

- Figure 32a is concerned solely with  $\tau$  and globe allocations. The biology and fertility globes balance their  $\lambda$  biological activities by distributing their  $\gamma$  and  $\psi$  Ingredient 3 and 4 events between themselves. But since they ignore temporality, they are nonoriented. The biology globe is entirely nonreplicative. The replication one handles all such events. They together provide our interior recursive functions. The sum of the curls about each is the stasis of the third kind,  $\nabla \times Q = 0$ , and is the circulation of the generations.
- Figure 32b is concerned solely with arranging events in a temporal sequence,  $T$ . While it can distinguish between increases and decreases in  $\gamma$  and  $\psi$ , it makes its temporal markers take priority over any proposed distinctions between the biological and the replicative. They each predominate in distinct epochs. The  $\gamma$  increase phase, which is  $m$  and Ingredient 4, has a smaller range than the similar  $\psi$  increase phase, which is  $p$  and Ingredient 3. There will therefore be times when the latter increases while the former is stationary, or even reverses. Since these events are successive, they are oriented. Their ordered activities provide our loops. The sum of the divergences is the stasis of the second kind,  $\nabla \bullet Q = 0$ , and is once again the circulation of the generations.
- Figure 32c represents the sum of the events in both globes, and is  $\nabla Q = 0$  and the stasis of the first kind.

These inexact differentials are independent of size in the sense that they can produce the same, overall, effects, of leaving everything the same, but over greater and smaller ranges. While they may have apparently different effects out in the surroundings, their overall purposes on the objects are the same.

**V.9.1** We now turn to the representation of Meme 112 we see in Figure 33. It sets the three constraints and exact differentials of  $\int dn = \int dM = \int dP = 0$  equal to the three inexact differentials and stases of  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$  using a set of group operations. It is the four-dimensional  $S_3-V_4$  rotachoron. It is the regular  $V_4$  gongyl or interior, surrounded by its four  $S_3$  glomes as its



combination and surface. It holds an entire collection of the constant loops that we can build, at any time, using its plessists and plessemorphs. They display the combined exact and inexact equilibria. They also immediately give us the  $\pi(S) = 0$ ,  $\pi(S) = \mathbf{Z}^2$ , and  $\pi(S) = \mathbf{Z}_2$  fundamental groups for all trivial loops, equators, and identified traversals between minima and maxima.

**V.9.2** Meme 119 now declares that each of the  $\tau_v$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  one-manifold linespaces that create Figure 33's balanced rotachoron has its opposite points identified. Each is a spherinder contained within a cubinder. Each is therefore a diameter. Each supports an entire equator of surfaces and activities for Meme 3's unipollent equilibrium of  $\pi \equiv [(1 \times 1^{\delta=1} \rightarrow 1)^1 \leftrightarrow (1 \div 1^{\delta=1} \rightarrow 1)^1]$ .

**V.9.3** We also follow Euler, so that for Meme 120 we express all increments in Figure 33, over all populations and generations, proportionately. We use  $e$  and a unit interval. Each increment is therefore a function of a suitable identity process starting at unity and growing continuously and exponentially for one unit. Every infinitesimal increment  $dx$ , at all points, is some proportion of the  $x$  at that instant. And since all measures are taken between 0 to 1, then they are all expressed in identical units. So if some interval for the insect on the inside is  $x\%$  of its overall generation length, then the bird and whale outside it exhibit the same proportion. And if some given interval allows some insect, on the inside, to double in whatever property, then the bird and whale outside it will also double, across corresponding intervals. This is a unit rotachoron.

**V.9.4** The  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  one-manifolds from Figure 19 meet at the triple point at the rotachoron's centre of  $\tau_t$ . It has a single point as its  $V$  interior, surrounded by its closure points. Those use a Whitney umbrella to form a continuous circle that is the surface all about it.

**V.9.5** There are matching line segments everywhere between diametrically opposite—and so identified—points. Since all the one-dimensional braid-1s are coordinated in Figure 29h's Whitney umbrella, the  $\tau$  circulation in Figure 33 always passes exactly twice through Figure 32's replication points to give  $x \circ \tau = \tau \circ x = x$  for all  $x$  in  $X$ . We can create a constant loop at every point in our unit rotachoron.

**V.9.6** The implication of  $x \circ \tau = \tau \circ x = x$  for all  $x$  in  $X$ , in our unit rotachoron, is that the centre point is the deformation retract. The surface is the mapping cylinder, complete with all its bounding  $\pi = [(1 \times 1^{\delta=1} \rightarrow 1)^1 \Leftrightarrow (1 \div 1^{\delta=1} \rightarrow 1)^1]$  intervals. Those intervals create the constant loops at every point.

**V.9.7** The further implication of our unit rotahedron is that each and every entity and population throughout  $X$  is immersed in a universe in which it can use the two  $S_0$  input and output points on its Whitney umbrella to maintain itself. The biological–ecological  $\lambda$  is the group operation,  $\circ$ . Its positive and negative aspects are the fibration,  $\theta$ , and cofibration,  $\rho$ , respectively, to give  $\theta \circ \rho = \# = \lambda$ .

**V.9.8** The topological reality is that every population's biological space is locally isotropic. Since the surface stretches from 0 to 1 for all populations and entities; and since all values and rates are proportionate and dependent upon quantities present; then all plessists and plessemorphs everywhere are the same. They all see the same universe in which they can all sustain themselves. Since all entities and populations receive exactly what they require, at every point, to undertake all needed interactions, then every population's biological universe is also always locally homogenous.

**V.9.9** Since every biological population lies upon some Figure 33 surface, then every point about any viable circulation is in principle capable of constructing a constant loop, for a complete circulation, which always has its opposite points identified. Our  $S_3$ – $V_4$  biological rotachoron also therefore allows populations to loop between minima and maxima and complete a circulation. We can create the complementary constant loops all about the rotachoron.

**V.9.10** Every population and species is locally defined by this identical rotachoron, which states all global realities. The resulting cycle and its loops will satisfy both our defined  $\pi$  equilibrium for our plessists and plessemorphs and their exact and inexact differentials, and the Chomsky production rule of  $[\Sigma, S, \delta, \alpha_0, F]$ .

**V.10.1** We can use Figure 33 to consider some Subpopulation  $X$ . Its initial point is  $\alpha_{0X}$ . Its initial circulation point and time is  $\tau_{-1}t_{-1}$ . It increments the distance  $d\tau_x - dt_x$  to reach  $\tau_1 t_1$ . There is a proportionate effects on all subpopulations. They form the same constant loop,  $s_x s_x^{-1}$ .

**V.10.2** Each constant loop for any Subpopulation  $X$  is precisely matched by two others. One is the complement  $X^\gamma$ , the other the inverse  $X^{-1}$ .

**V.10.3** There exists a reverse journey,  $x^{-1}$ , for every journey  $x$  in  $X$ . It moves across that same interval to create the constant loop,  $s^{-1}$ . It implies that every population will return every atom and molecule removed back to the surroundings, thus restoring itself to its prior condition.

**V.10.4** We can therefore always form the inverse subpopulation  $X^{-1}$ . It also has a constant loop formed via the underlying real projective plane's identified points.

**V.10.5** We get  $X^{-1}$ 's initial and final points from  $X$ 's final and initial ones, respectively. It is therefore located diametrically across the rotachoron, linking via the central point, which is the deformation retract.

Subpopulation  $X^{-1}$  exhibits a cofibration for every fibration in  $X$  and conversely. Its constant loop  $s_{X^{-1}} s_{X^{-1}}^{-1}$  is now the precise inverse of  $X$ 's.

**V.10.6** The  $X$  and  $X^{-1}$  populations are inverse couplings. They sit opposite each other on the rotachoron. They therefore form a cyclic group of order 2.

**V.10.7** Subpopulations  $X$  and  $X^{-1}$  immediately confirm our  $\pi(S) = Z_2$  fundamental group. Each of the two line segment pairings, on the two margins, creates a set of half-planes that define our sphere's interior. They are each also a Whitney umbrella whose diameter has the two constant loops that confirm both  $T$  and the  $+r$  and  $-r$  inputs and behaviours. The identity, as the deformation retract, sits between them. Their joint interactions define the surrounding mapping cylinder,  $M_\lambda$ .

**V.10.8** We can also form the complement Subpopulation  $X^\gamma$ . This has  $X$ 's terminal point,  $\tau_1 t_1$ , for its own initial point as  $\alpha_{0X}$ .

We then increment  $X^\gamma$  all about the remainder of the circulation until we reach  $X$ 's initial point,  $\tau_{-1} t_{-1}$ , which becomes  $X^\gamma$ 's terminal one. That complement journey also restores that same population to its prior condition, returning every atom and molecule to the surroundings. Subpopulation  $X^\gamma$  thus forms the constant loop  $s_{X^\gamma} s_{X^\gamma}^{-1}$  all about that remaining circulation.

**V.10.9** Our complement  $X$  and  $X'$  coupling, that goes all about the rotachoron, contains two sets of inverses. It incorporates the  $X^{-1}$  inverse in its middle, as the inverse to  $X$ . But it also has  $X'^{-1}$ , for its last part, and as the inverse to the first part of  $X'$ . Therefore, when we add the entirety of the  $X'$  complement to  $X$ , we get loops all about the circulation of length  $\tau$ . They create  $\pi$ . They again define both the deformation retract and the surrounding mapping cylinder.

**V.10.10** Going all about the Figure 33 circulation in a forwards, or anticlockwise, direction, is exactly the same as going about it in the backwards, or clockwise, direction. We get the identical constant loops. They both invoke (a) the direct series of biological processes,  $\lambda$ , which map directly between  $X$  and  $Y$ ; and (b) a whole series of inverses and complements, the whole of which always map to  $M_\lambda$ .

**V.10.11** Every interval can bring together its  $XX^{-1}$  and  $XX'$  couplings to create both  $(1 \times 1^{\delta=1} \rightarrow 1)^1$  and  $(1 \div 1^{\delta=1} \rightarrow 1)^1$ . But any population that achieves this does so using both of its exact and inexact differentials.

**V.11.1** Our exact and inexact differentials may be theoretically equivalent, but Euler established topology by demonstrating that all the points forming any of the Königsberg landmasses can be collapsed down to a single one; that all the bridges form simple lines as edges which can be deformed; and that all regions can adopt any arbitrary size or shape. They are topologically equivalent throughout because their Euler characteristics,  $\chi$ , maintain a continuous mapping that preserves their deformation retract. If  $X$  and  $Y$  are two such sets, then they have identity properties such that an  $i_0(X)$  exists in  $X$  that acts as  $\#$ , mapping directly onto its equivalent  $\#$  in  $Y$ , which is  $i_0(Y)$  in  $Y$ . This gives  $\chi(X) = \chi(Y)$ . We then have  $Y$  being a deformation retract for  $X$ , with an  $x$  in  $X$  for every  $y$  in  $Y$ .

**V.11.2** Our  $X$ s and  $Y$ s, however, are biological. Since they must each both replicate and be replicated, then they are each both the causes and the products of such cycles.

**V.11.3** Since  $X$  is the progenitor domain and preimage, while  $Y$  is the progeny codomain and image; and since we want to produce a next generation; then we require a reversibility. Since  $Y$  must in its turn become an  $X$  and act as a progenitor domain and preimage to some further set  $Y$  which is then its progeny codomain and image, and with each of  $X$  and  $Y$  behaving identically and successively ... then we require a reverse mapping between  $X$  and  $Y$ . Every point  $y$  in  $Y$  must be able to substitute itself back into  $X$  and restore  $X$  to its original condition.

**V.11.4** We therefore require that an  $i_0(Y)$  in  $Y$  exists that acts as  $\#$ ; and that an  $i_0(X)$  in  $X$  does the same; with each mapping directly to give a  $\chi(Y) = \chi(X)$  to match the above  $\chi(X) = \chi(Y)$ , there then being a  $y$  in  $Y$  for every  $x$  in  $X$ ; and with  $X$  now being the deformation retract for  $Y$ .

**V.11.5** We are demanding that both  $X$  and  $Y$  maintain the identical  $\pi$  equilibrium, with the identical forwards and backwards mappings. They must each have a  $(1 \times 1^{\delta-1} \rightarrow 1)^1$  across their lengths for the other's  $(1 \div 1^{\delta-1} \rightarrow 1)^1$ ; and conversely. Since their forwards and backwards directions must be identical then all mappings between them are only ever both (a) one to one, and (b) onto. They must be continuous bijections.

**V.11.6** We are further demanding that both of  $X$  and  $Y$  be equally endowed with both of our exact and inexact differentials.

**V.11.7** Both of  $X$  and  $Y$  can form fibre bundles. We are therefore and effectively demanding that they each remain reversibly homeomorphic throughout all possible transformations as each is first base,  $B$ , and then fibre,  $F$ , creating their joint and invariant product space,  $P = B \times F$  ... which must also be their mapping cylinder,  $M_\lambda$ , so that  $M_\lambda = B \times F$ .

**V.11.8** We are now making the topological demand that every neighbourhood in  $P$  look exactly like the composition  $B \times F \dots$  and that it never look any different. This is the demand that if one is a set of exact differentials then so is the other; and similarly for the inexact differentials. But since the mapping cylinder is the surroundings, then this is the requirement that each of  $X$  and  $Y$  fails to act, by turns, as progenitor and progeny when the other seeks to act as a complement.

**V.11.9** Although our rotachoron from Figure 33 has given us both an interior,  $V$ , and a surface,  $S$ , that can support our various biological activities, it is a bidimensional manifold. It is an object whose two halves are separated by an infinite plane.

**V.11.10** (A) The rotachoron's  $\pi(S) = 0$  fundamental group seems to guarantee all our trivial loops. (B) The real projective plane's  $\pi(S) = \mathbf{Z}_2$  seems to guarantee us all our nontrivial loops. (C) The torus'  $\pi(S) = \mathbf{Z}^2$  fundamental group seems to guarantee us both a meridian and an equator.

**V.11.11** The torus is certainly helpful, but it unfortunately has that doubled-up interior.

**V.11.12** We can create all the fibre bundles we need by walking a fibre around a base. We can create a base by beginning with an ordinary one-dimensional Euclidean line segment. We then bend it around to create a circle ... which is the same circle we get by first flattening a torus into an annulus; and then retracting it. We create a "one-torus".

**V.11.13** We create our one-torus by looping an original line segment around. We enclose an interior area. We therefore began with an object of dimensionality  $n = 1$ , and then not only did we separate an interior area from an exterior one, but we stepped up a dimension to get the  $n = 2$  circle.

**V.11.14** We can create an ordinary three-dimensional torus from its fundamental polygon of Figure 27b. It has the dimensionality  $n = 2$ . We then perform those two gluings. The first gluing steps us up a dimension to  $n = 3$  to create a cylinder, which has a volume interior and those open ends. The second gluing bends that cylinder around to seal those open ends to create our torus.

**V.11.15** We may now have our two-dimensional surface all about that torus, but we stepped up a dimension to get it. We also enclosed the torus' two distinct volumes. We have that doughnut hole in the middle acting a first interior. And we have everything behind its surface, and in its loop, forming

a second interior. A torus is therefore an object whose  $n$ -dimensional surface always exists in  $n + 1$  dimensions.

**V.11.16** And ... we have our four-dimensional  $S_3-V_4$  rotachoron.

**V.12.1** Figure 32 took our  $X$  and  $Y$  progenitor domain and progeny codomains to give two ways to represent our circulation of the generations. Figure 32a's two-dimensional unknot with crossing flattened our biology and replication globes into two discs. Just as with the torus, we have a clear exterior, but a doubled up interior. Figure 32b was a three-dimensional figure that conjoined our two globes at a single contact point. But since it is bounded by a Möbius strip, its biological events also have no true interior or exterior. It confirms that all Möbius events involve a doubled up interior.

This simply means that any population produced by acts of fertilization and germination must itself create some fertilization and germination events. It therefore approaches the same sizes and activities from the opposite direction, and about the same loop for an  $s \circ s^{-1} = \tau$ . And further since we keep switching directions, then these are nonoriented objects.

**V.12.2** The French mathematician Camille Jordan was the first to fully investigate these issues of what properly separates an interior from an exterior. A trivial curve, on any planar surface, is the most obvious of all "Jordan curves". These are curves, in the plane, that successfully separate a single and continuous exterior region from a single and continuous interior one.

**V.12.3** A Jordan curve is the model for going around either the inside or the outside of something, without changing orientations or crossing over to any other side. Anything that abides by a Jordan curve, and so that can successfully separate a single and continuous exterior region from a single and continuous interior one, has an orientation given by  $\varepsilon = 1$ . Both a sphere and a torus therefore have that orientation.

**V.12.4** If we now draw a properly oriented and trivial Jordan curve, as a loop, upon a sphere's equally oriented surface, we can snip that curve out. We remove a disc from the sphere and make a hole. The remainder of the sphere is homeomorphic to an ordinary Euclidean plane.

If we first deformation retract our Jordan curve, or trivial loop, right down to a single point before using it to snip, the remaining planespace is still homeomorphic to a disc. When the German mathematician Bernhard Riemann first studied surfaces more closely, he described them in terms of such simple and closed curves, pointing out that this was a characteristic invariant for every surface. When Alfred Clebsch later studied this phenomenon, he used the term genus,  $g$ , to describe it (Hirzebruch & Kreck 2009).

The sphere is a compact and oriented surface,  $S$ , that can support a maximum of zero non-intersecting and closed Jordan curves before it becomes disconnected. It has both an orientation of  $\varepsilon = 1$ , and a genus of  $g = 0$ .

**V.12.5** The torus—which can guarantee us our equator—behaves very differently under these Jordan curves. If we apply one to either its equator or its prime meridian, it maintains its  $\varepsilon = 1$

orientation, but splits in two to revert to a cylinder. It therefore only takes the one cut to disconnect this manifold.

If we now apply a second Jordan curve to that resulting cylinder, we get a plane surface. We indeed arrive back at the torus' fundamental polygon, for we can draw on it yet more proper Jordan curves.

If we now reverse our snipping procedure and begin from the torus' fundamental polygon, we can glue it twice to recreate the torus. Its genus is therefore reckoned either as half those snippings and/or gluings; or else as the single cut that disconnects it. So while a torus has the same  $\varepsilon = 1$  orientation as the sphere, since it can support one cut and still not become completely disconnected, then it has the very different genus of  $g = 1$ .

**V.12.6** Nonoriented objects, with their doubled up interiors, behave somewhat differently under these Jordan curve snippings. While we have a single exterior, we have those doubled up interiors. One part is located either side of the crossing point. And since we can keep switching orientations and directions every time we pass through at least one given point, then an unknot with crossing, such as Figure 32a, fails to be a Jordan curve. Such doubled up and nonoriented objects, which keep switching, have an orientation given by  $\varepsilon = 0$ .

**V.12.7** We can now take up each of our biology and replication globes. If we remove a single point from each, they each flatten to become simple two-dimensional discs. We can then attach them, at their singularities, to create Figure 32a's Whitney umbrella. We have recreated that doubled up interior bounded by a nonoriented  $\varepsilon = 0$  unknot with crossing.

**V.12.8** We can now take up those conjoined discs and separate them by snipping, at that crossing, with a single cut. The two previously separated interiors are linked. We finish off with an object homeomorphic to a disc that has a distinct interior and exterior. We have a simple closed curve in the plane that abides by Jordan's theorem.

**V.12.9** We now go up a dimension. We begin with two of our oriented rotachorons. We take one biological and one replicative one. If we next remove a point from each, then they each become homeomorphic to a three-dimensional realmspace. And if we connect them at their singular points, then we have recreated Figure 32b. We have a clear exterior, but the same doubled up interior bounded by a Möbius strip.

**V.12.10** If we snip our creation at its crossing, the interiors will link up to give a single interior, and a single exterior. It gives us a realmspace. We have an object homoemorphic with a sphere.

**V.12.11** However, if we now set out from a pole, on our creation, and head towards the opposite pole, the crossing point on the original has morphed into an equator. We have gone all the way about a loop, or globe, to the crossing ... now masquerading as an equator. We reach the Whitney umbrella branch point. If we continue on, we will branch to the other loop. This is to go past the equator, and to traverse the opposite loop or globe.

**V.12.12** A complete twisted journey about a nonoriented  $\varepsilon = 0$  Möbius strip type object is now homeomorphic to a pole to pole journey upon an oriented  $\varepsilon = 1$  object.

**V.12.13** A twisting  $+dA$  then  $-dA$  journey takes us from pole to equator; and then a  $-dA$  then  $+dA$  twist takes us from the equator to the opposite pole.

**V.12.14** If we snip and then open out a nonoriented object, we get behaviours identical to a seemingly oriented one for we have converted the one to the other. The crossing point for a nonoriented  $\varepsilon = 0$  object is therefore a twisting about, or branching, that is precisely equivalent to crossing an oriented  $\varepsilon = 1$  object's equator.

**V.12.15** Since we have to go up a dimension before either a torus or a real projective plane can guarantee us their equator-like behaviours, then we can observe that the real projective plane we are using for biology has:

$\chi = 1$  for its Euler characteristic,  
 $c = 0$  for its boundary points,  
 $\varepsilon = 0$  for its orientation, and  
 $g = 1$  for its genus.

while Figure 33's rotachoron has:

$\chi = 2$  for its Euler characteristic,  
 $c = 1$  for its boundary points,  
 $\varepsilon = 1$  for its orientation, and  
 $g = 0$  for its genus.

**V.12.16** Although these two objects appear completely different, we can still draw certain valid conclusions.

**V.12.17** By topology's classification theorem, which uniquely characterizes surfaces, as long as we preserve the same genus,  $g$ , orientation,  $\varepsilon$ , boundary points,  $c$ , and Euler characteristic,  $\chi$ , all biological spaces,  $S$ , will be homeomorphic. All deformations and changes in size will then be irrelevant. All our rotachorons and projective planes will remain equivalent in their equatorial and

crossing point behaviours for as long as they maintain the same numbers of maxima and minima, all across the same numbers of dimensions.

**V.12.18** Again by topology's classification theorem, Boy's surface has the same four values as the real projective plane. Those two are therefore fully homeomorphic. Boy's surface is a real projective plane whose axes are arranged, in pairs, so it can be immersed into three dimensions as a sphere-like object. It has the singular advantage of looking quite familiar, while retaining all projective plane values, with the sole difference being that Boy's surface broadens out to an apparent equator, instead of narrowing inwards to a Möbius strip's crossing.

**V.12.19** And since we can always snip a nonoriented  $\varepsilon = 0$  object, containing a Möbius strip crossing, to convert it to an oriented  $\varepsilon = 1$  one containing an equator, then all Möbius strip objects, including our projective plane, are similar to all oriented ones with a genus  $g = 1$ .

**V.12.20** We establish equivalence between our various surfaces by going up a dimension. Since both the torus and the real projective plane have  $g = 1$ , then they can each achieve the same purpose vis-a-vis any lower dimension. They each do exactly what the other can do, which is guarantee any behaviours in our biological space,  $S$ , that demand an equator. Their crossings and their equators are equivalent.

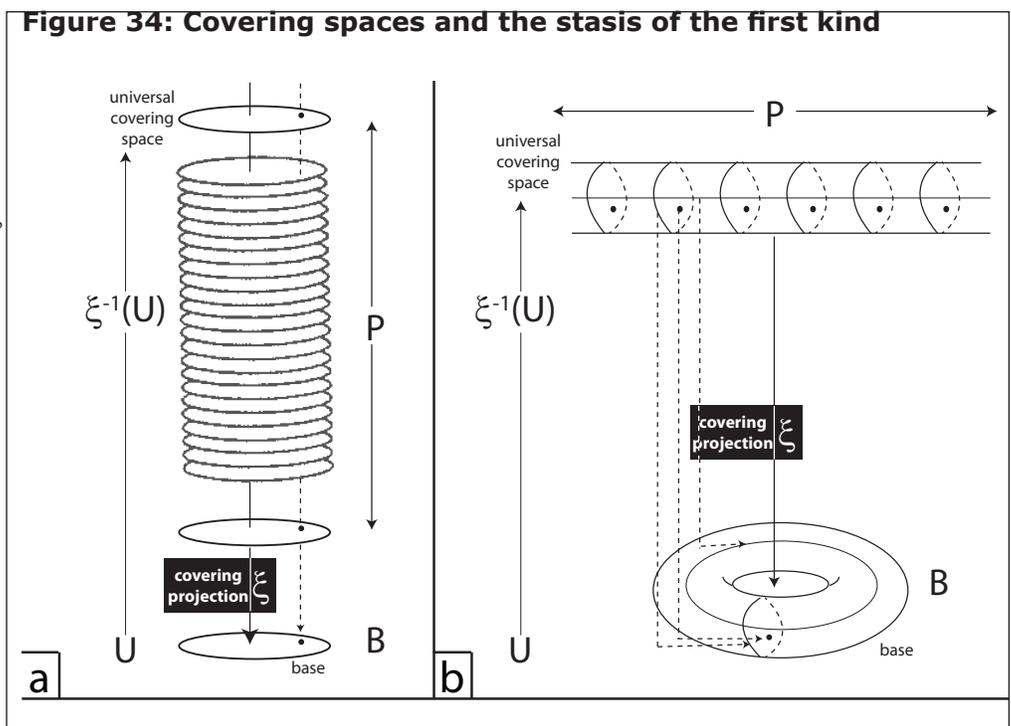
**V.12.21** Both the torus and the real projective plane can give us the inverse and the complement distances of  $s'$  and  $s^{-1}$  to match any  $s$  in  $S$  to build any wind wall, and complete any recurvatures.

**V.12.22** Our  $XX'$  and  $XX'^{-1}$  complement and inverse couplings define both the surrounding mapping cylinder and the deformation retract. They give us both  $s \circ s' = s' \circ s = \tau$  all about the circulation, and  $s \circ s^{-1} = s^{-1} \circ s = S'$ , which is our identity, at every point. And since each inverse journey,  $s^{-1}$ , is homeomorphic to the complement  $s'$  that continues, beyond any margin, all the way round to  $s'$ 's initial point, then every constant loop immediately incorporates an entire generation's worth of identified opposite points.

**V.12.23** Since we now have both the inverse and the complement to any  $s$  in  $S$  upon our projective plane, we have successfully incorporated all three fundamental groups of  $\pi(S) = 0$ ,  $\pi(S) = \mathbf{Z}^2$ , and  $\pi(S) = \mathbf{Z}_2$ . We therefore always have both the  $(1 \times 1^{\delta=1} \rightarrow 1)^1$  and  $(1 \div 1^{\delta=1} \rightarrow 1)^1$  inherent in any point and interval ... and we have created our  $\pi$  equilibrium everywhere in our  $S_3-V_4$  rotachoron.

**V.12.24** As is required in topology, irrespective of their sizes or degrees of deformation, we now have a complete equivalence between our objects with their exact and inexact differentials.

**V.13.1** We still face the bijective demand that  $X$  and  $Y$ , as progenitor domain and progeny codomain, act identically whether they be product or base. This is the demand that every neighbourhood in the product space,  $P$ , always look exactly like, and so be homeomorphic to, the composition  $B \times F$ . It is the demand that the product space,  $P$ , always abide by the “local triviality condition”.



**V.13.2** The local triviality condition is the demand that the global product space be fully homeomorphic with the base. It must be a trivial fibre bundle both by being the same as the base and the fibre, and by being the first one so created. It is the demand that the projection map,  $\xi$ , down from the tips of the hairbrush fibres in Figures 22a and b to embed into each of those bases always have the identical surjective mappings so that the same point, in the same product space, always goes to the same point in the base. Neither base nor fibre may send any of their points to any other point in their product space; and the product space may not use  $\xi$  to embed any of its points to any other in the base at any time. So if a fibre bundle is the quadruple set  $(B, F, \xi, P)$ , then the surjective mapping from product to base of  $\xi:P \rightarrow B$  must be locally trivial, so it can be fully homeomorphic.

**V.13.3** But unfortunately, this local triviality condition, with its insistence on trivial fibre bundles, only permits the straight hairbrush in Figure 22a. It excludes the twisted hairbrush in Figure 22b. That is a nontrivial fibre bundle where the global product space has attributes not present, locally, in either base or fibre by being a Möbius strip.

Since we cannot exclude non-trivial fibre bundles—for we will then have no biology!—we now establish, for Meme 121, the general principle that topology’s above classification theorem—which guarantees the homeomorphisms of spaces that preserve the same genus, orientation, boundary points, and Euler characteristic—can only establish the most generally biological of homomorphisms. The theorem can only establish the overall biological character of all entities and populations.

It cannot establish the more specific homeomorphisms that characterize individual species and populations.

**V.13.4** All our spaces,  $S$ , that abide by topology's classification theorem are now biological by being homomorphic and homotopically equivalent. This is not, however, sufficient for biology because groups of entities can be separately homeomorphic by acting as distinct sets of bases and fibres whose product spaces and mapping cylinders may either breach or extend the local triviality condition.

**V.13.5** We instead require, for Meme 122, that our mapping cylinder,  $M_\lambda$ —which is also the  $B \times F$  progenitor and progeny product space,  $P$ —be a “covering space”. As illustrated in Figures 34 a and b, this then has a “covering projection”,  $\xi$ , that is a continuous function from that projecting topological space,  $P$ , down to another, say  $B$ , and so that the receiving base space has an open neighbourhood,  $U$ , that is covered by all the  $n$  surjective covering projections coming into it from  $P$  ... and with every one of those projections being a local homeomorphism.

**V.13.6** We can construct each of the distinct manifolds in the two covering spaces in Figure 34 into the base  $n$  times over simply by unfurling each one the desired number of times. And contrariwise, we can create the entire covering space simply by gluing together  $n$  copies of each of those bases.

**V.13.7** Figure 34a's covering space is a simple stack of pancakes. Every point in every pancake in the stack suitably covers a given point in the base. And if we undertake the reverse  $\xi^{-1}$  projection from the base upwards, we will find an appropriate point in every one of the pancakes purporting to be a covering for that base.

**V.13.8** Figure 34b's covering cylinder is also a covering space, but this time for a torus. The infinitely many circles along the cylinder's axis cover the infinitely many about the prime meridian. And meanwhile, the single horizontal line along the cylinder's length covers the toroidal equator. Every point on the torus successfully maps to its cover upon the cylinder.

**V.13.9** We have now guaranteed reproduction. The biological significance is that a covering space preserves all copies of the original intact. We can get the cover for all possible generations from any number of current ones; and we can get any current generation from any other; either before or after. All covers to one side, i.e. underneath our species, are now its past generations; with all those the other side being its future ones.

**V.14.1** We may now have a covering space and a projection that guarantees reproduction, but we have still not equated our exact and inexact differentials of  $\int dn = \int dP = \int dM = 0$  and  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$  respectively.

**V.14.2** We now let some circulation follow a given path,  $y$ , about the rotachoron's surface, at the constant altitude, or radial distance,  $r$ . But instead of following its designated path, let some Subpopulation  $D$  first leave, and then return to, that stipulated  $y$  path. It exhibits a  $+dx$  and then a  $-dx$  to and away from  $y$ . That out-and-back expedition is immediately the constant loop  $s \circ s^{-1}$  about  $y$ .

**V.14.3** Subpopulation  $D$ 's out and back expedition is now very similar to the ones made by our three constraints of  $\int dn = \int dP = \int dM = 0$ . It, also, sums to zero as  $\int dx = 0$ .

**V.14.4** The meridians upon Boy's surface—which is now a covering space—are relationships between our various manifolds. They are the stases of the first, second, and third kinds as rates. They arise from the following interactions:

- The one-dimensional gradients along each of the rotachoron diameters of  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ . The inexact differential  $\nabla Q = 0$  comes from  $\tau_t$  and  $\tau_n$  for the cycle.
- The two-dimensional divergences between each coupling to give  $\tau_{tn}$ ,  $\tau_{tm}$ ,  $\tau_{tp}$ ,  $\tau_{nm}$ ,  $\tau_{np}$ , and  $\tau_{mp}$ . The  $\nabla \cdot Q = 0$  comes  $\tau_{tn}$  and  $\tau_{tm}$  interacting over the cycle to produce the quantities in the divergence.
- The two-dimensional curls also in  $\tau_{tn}$ ,  $\tau_{tm}$ ,  $\tau_{tp}$ ,  $\tau_{nm}$ ,  $\tau_{np}$ , and  $\tau_{mp}$ . This is again  $\tau_{tn}$  and  $\tau_{tm}$  interacting over the cycle, as  $\nabla \times Q = 0$ , but now setting the rate at which the Möbius strip is traversed.
- The three-dimensional curls of  $\tau_{tnm}$ ,  $\tau_{tnp}$ ,  $\tau_{tmp}$ ,  $\tau_{nmp}$ . This is both  $\tau_{nmp}$  and  $\tau_{tnmp}$  establishing, between them, both the quantities and the time points at which values and properties for  $n$ ,  $m$ , and  $p$  are produced all about the circulation, and as  $\nabla \times Q = 0$ .

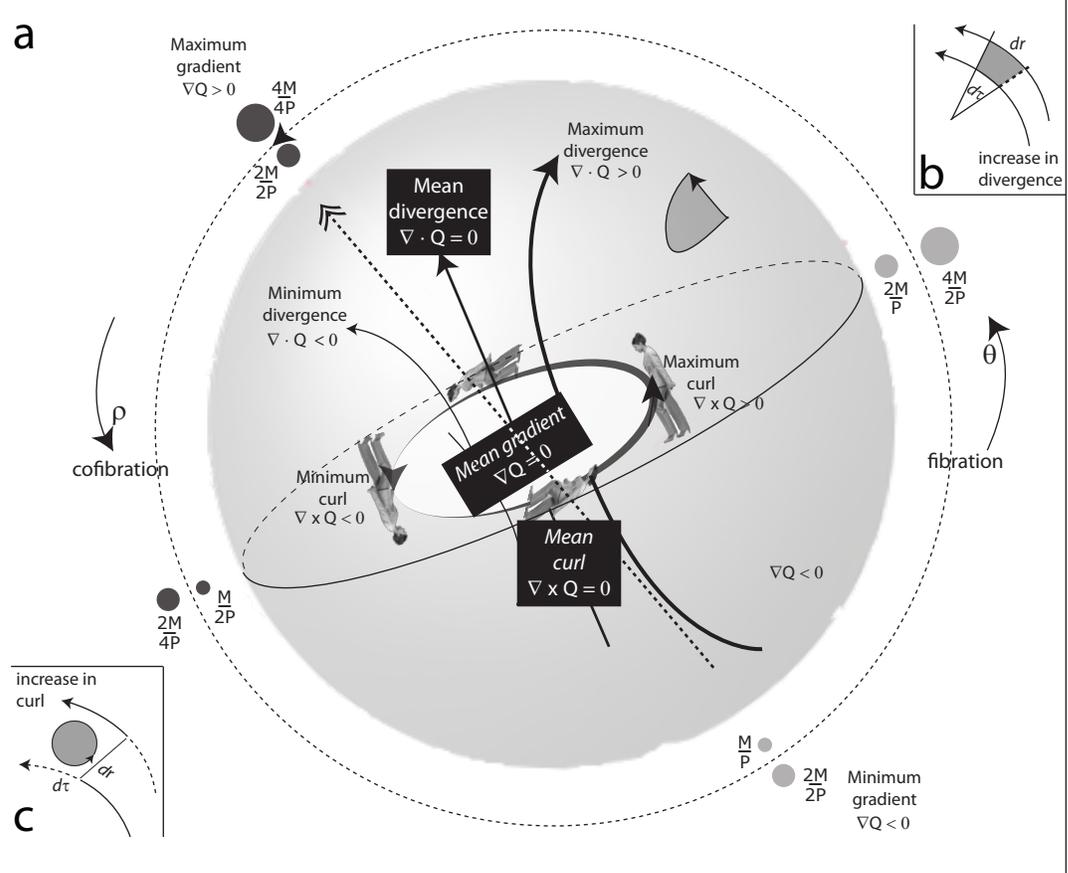
**V.14.5** Every expedition any subpopulation might undertake about our circulation, even in our covering space, will create the two matching constant loops  $s \circ s^{-1}$  that are its Whitney umbrella.

**V.14.6** Each one-manifold is a braid-1 that lies about its midpoint. Each affects the others, with their collective midpoints being their common identity, and the deformation retract.

**V.14.7** Since, by Meme 122, our biological mapping cylinder is now also a covering space, then the relationships between our manifolds will preserve all fundamental groups in both preimage and image.

**V.14.8** When our Subpopulation  $D$  takes its expeditionary path, it has a greater number of transformations than does any Subpopulation  $C$  that sticks to the stipulated path,  $y$ . Subpopulation  $C$  therefore has an additional, and constant  $dx = 0$  constraint ... where Subpopulation  $D$  is less restricted and emulates our three constraints by only having to satisfy  $\int dx = 0$ .

**Figure 35: Homomorphic, homeomorphic, & homotopically equivalent populations, and the stasis of the second kind**



**V.14.9** Since Subpopulation  $C$  is non-expeditionary, it has the shorter journey. And its movements are also across a projective plane. So when Subpopulation  $C$  holds constant, then as in Figure 35b it defines a Möbius strip midline.

**V.14.10** Subpopulation  $D$ 's constant loop expeditions, out to each side of Subpopulation  $C$ , then define the Möbius strip journey all about that axis.

**V.14.11** Since every Möbius strip bounds an area, then each must involve two dimensions. Subpopulations  $C$  and  $D$  must therefore be defining some twisting  $xy$ ,  $yz$ , or  $xz$  plane for Boy's surface.

**V.14.12** And additionally ... given that Subpopulation  $C$  maintains the Möbius strip axis value, it can also create Figure 9's right helicoid.

But since Subpopulation  $D$  oscillates between a minimum and a maximum value, then it cannot form a right helicoid. It must instead move first closer to the helicoid axis, and then away, all

about Subpopulation  $C$ 's white centre line.

**V.14.13** As in Figure 35c, the Whitney umbrella's constant loops,  $s$ , make a definite contribution to the overall circulation. Each has a definite and proportionate circulation density. That is its curl at that point.

And since all movements on each constant loop away from the identity increase the net contribution, they have a positive curl; with those inwards and towards the identity having a negative one because they decrease the net contribution. An in and out about a Whitney umbrella loop therefore sums to zero. All the  $V_0$  events are summed up by the constant  $S_0$ .

**V.14.14** If every span,  $x$ , about some circulation,  $\tau$ , makes the same overall contribution to its circulation, then the curl is everywhere zero. But if any span  $x$  again makes a greater contribution either than the average, or else than its partnering complement or inverse of  $x'$  and/or  $x^{-1}$ , then that  $x$  has a positive curl; and if the converse, then it is negative. If it returns to its start point then its expeditions again sum to zero.

**V.14.15** We now propose a Subpopulation  $A$ . It is a rotahedron. It pushes its three values right across the rotachoron's diameter. It thereby constructs one of the four spherindrical diameters.

That Subpopulation  $A$  spherinder holds fast to the values that Subpopulations  $C$  and  $D$  will each restore when they have completed their circuits about the rotachoron's surface, and have arrived back at the self-intersection point. It therefore passes straight through the deformation retract and Boy's surface triple point of  $\tau't'$ .

**V.14.16** Our Subpopulation  $C$  is now a cubinder upon the rotachoron's surface, and all about Subpopulation  $A$ 's spherindrical diameter.

Subpopulation  $A$  also defines both (a) the helicoid axis, and (b) the central midline about which Subpopulations  $C$  and  $D$  oscillate.

**V.14.17** As a further clarification of these various four-dimensional interactions, then Accra and London are both within a few degrees of the prime meridian. Since Subpopulation  $D$ 's expeditions about that journey will carry it off the prime meridian, it will go to various locations about the surface. Its path is again automatically longer than Subpopulation  $C$ , which always takes the direct journey straight down the prime meridian.

**V.14.18** Subpopulations  $C$  and  $D$  both, however, take a longer path than Subpopulation  $A$ , which is at the centre of the earth's crust, mantle, and core. Subpopulation  $A$ 's route is the path taken by

the earth's centre, as it is carried along its orbital path. Its equivalent Accra–London journey is the projection down from Subpopulations  $C$  and  $D$  onto that centre-holding path from  $\tau_{-1}t_{-1}$  to  $\tau_1t_1$ .

**V.14.19** There is, however, a specific relationship between Subpopulations  $C$  and  $D$  and their surface journeys. Subpopulation  $C$ 's non-expeditionary journey is the self-same journey Subpopulation  $D$  would be undertaking if only Subpopulation  $D$  was successful in negating every acceleration being imposed upon its windwalls and recurvatures. But since Subpopulation  $C$  does exactly the negating of accelerations that  $D$  refrains from, then  $C$  successfully follows its distinctive prime meridian and surface path.

Subpopulation  $C$  successfully instigates an  $s^{-1}$  counter loop for every  $s$  loop that the surface—or other atmospheric exigencies—seeks to impose. And since every surface location Subpopulation  $C$  and its windwalls and recurvatures pass through has a constant loop that confirms the prime meridian, then in successfully countering all possible deviations, Subpopulation  $C$  will always have a shorter path than Subpopulation  $D$ .

**V.14.20** Where Subpopulation  $C$  successfully follows its constant meridional path, Subpopulation  $D$  instead exhibits Figure 35b's Möbius strip increases, and then decreases, about  $C$ . However, the two subpopulations always have the same latitudinal Accra–London divergence. Subpopulation  $C$  defines the Möbius strip axis and right helicoid path about which Subpopulation  $D$  then deviates. And since Subpopulation  $C$  sticks rigidly to the prime meridian, then its longitudinal divergence is always zero ... whereas Subpopulation  $D$  always adds and/or subtracts longitudinal divergences to itself.

**V.14.21** Subpopulation  $D$ 's nonzero longitudinal divergence is the rate of change of the area bound between it and Subpopulation  $C$  as they each move latitudinally about the surface on their Accra–London journey. As in Figure 35b, a positive divergence is the increase in that area. A negative one is its decrease. In the equilibrium situation of the stasis of the second kind, we have  $\nabla \bullet Q = 0$ .

**V.14.22** Subpopulation  $D$ 's divergences in longitude now mean that its expeditions about that Accra–London journey create a constant loop that swings it out first to one side of Subpopulation  $C$ , and then to the other, also creating a series of curls. And since every population is similarly characterized, then they all have similarly matched pairs of two-dimensional constant loops that diverge about some mean, acting as a meridian, to construct the entire rotachoron surface as a set of divergences and curls.

**V.14.23** Every dimension can also create a three-dimensional curl. We have followed Euler and expressed all values proportionately, across the unit distance 0 to 1.

If the total period for some curl and/or constant loop and/or divergence is  $T$ , then it

immediately covers  $1/T$  in each second, which is the rate  $T$  seconds<sup>-1</sup>. So if the blue whale in Figure 33 is  $r$  times further away from its own deformation retract than is the insect from its, then the blue whale covers an area, for its divergence, in each second, that is  $e^r$  times as great. But the blue whale must also curl about its circulation equivalently more slowly again in each second, than does the mosquito, so it can undertake that greater divergence. Where the average mosquito has a circulation of  $\tau = 4$  days, the blue whale not only has  $\tau = 31$  years, but gains 91 kilogrammes, 200 pounds, in weight each day over its first year of life (Busia 2014). The Möbius strip boundaries and areas may be significantly larger for the one than for the other, but both sets of curls and divergence nevertheless increase and decrease to be zero, overall, over  $\tau$  and  $T$ , so that we have the stasis of the third kind where  $\nabla \times Q = 0$ .

**V.14.24** And since every dimension can interact with two others in a three-dimensional curl, then there can be a Subpopulation  $B$  that pursues a route that changes the altitude,  $r$ . Subpopulation  $B$  can therefore evidence a rate of change for  $r$  that takes it beneath the surface. This is a negative divergence in height.

The negative divergence in height Subpopulation  $B$  undergoes is the effect of a gradient,  $-\nabla r$ . So while Subpopulations  $C$  and  $D$  are the same in maintaining altitude—which is by having no constant loop in  $r$ —Subpopulation  $B$  differs, from both, by adding such a constant  $r$  loop in its gradient to give  $\int dr = 0$ .

**V.14.25** The Seikan Tunnel in Japan—which connects the Aomori Prefecture on Honshu with Hokkaido—is the world’s longest and deepest undersea tunnel ... although the Channel Tunnel that connects Folkestone in the United Kingdom, with Coquelles, near Calais, in France, has the longest undersea span. Both these are direct connections that link their surface points by providing shorter journeys, due to their changes in height, than do the surface journeys between those same two locations. They are changes along gradients.

**V.14.26** If Subpopulation  $B$  pursues a route similar to the above tunnels, then both its gradient and its divergence in height are negative for the first part of its journey. That negative divergence and move along the gradient eventually take it to its maximum depth ... which also signals its maximum separation from the surface. The divergence in height is then temporarily zero, because there is no change in height. The gradient, however, still exists. It still points in the same negative direction to the earth’s centre.

**V.14.27** The divergence and the change in height both now reverse to become positive, but against the same gradient. We now have a positive gradient, of the same value, as Subpopulation  $B$  moves in the opposite direction for height, proceeding towards journey’s end.

The original height is eventually restored, all against the same-sized gradients as before. The net divergence in height at journey's end—which is also the sum of all the changes in height—is again zero.

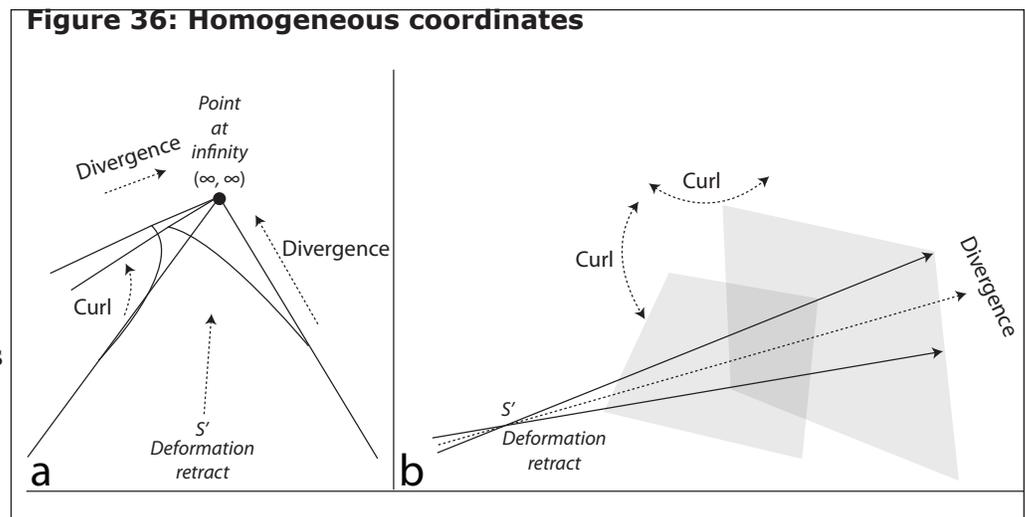
**V.14.28** In addition to the above, the changes in height Subpopulation *B* experiences both are—and exhibit—a curl. If the descent along the gradient, to go below the surface, accompanies an overall rightwards journey about the earth's surface, and so about the earth's centre, then it is a positive curl; otherwise it is negative. And if the accompanying ascent tends leftwards then it is negative; otherwise it is positive. This component of the curl adds to, or subtracts from, any created by changes in circulation density or overall circulation length,  $\tau$ . The curl is therefore normal to whatever two dimensional plane of activities holds the circulation intensity at that point, with its magnitude being the maximum at that point.

**V.14.29** And then finally, since these gradients, divergences, and curls are all rates, then although any path, *x*, between any two points can be shorter than some alternate path, *y*, between the same two points, *y* can still end up being quicker by having the greater rates of change. If we, for example, drive a faster vehicle, then the journey along a more circuitous highway can easily be quicker. The faster vehicle means we can maintain a greater velocity or rate of change. But “quicker” simply means “shorter” in the fourth dimension, which has a greater rate of change. Since this is a four-dimensional rotachoron, we “burrow” “under” the temporal surface. The slower journey remains “on the surface”, and “up above”. We have different divergences and curls in latitude, longitude, and height ... including in the temporal dimension. So if some journey on an ostensibly longer path indeed ends up being quicker, then that fourth, and unseen, dimension either has a shorter path in its direction, or else has a greater gradient,  $\nabla$ , for that fourth dimension, and irrespective of the path's apparently longer distance in any visible dimensions.

**V.14.30** All these same issues of gradients, divergences, and curls will now hold for the longitudinal journey between Singapore and Nairobi. Since those two are within degrees of the equator, then a Subpopulation *D* journey will produce a nonzero constant loop, plus Möbius strip, that now show divergences in latitude about the partnering Subpopulation *C* which has none. It instead balances in its north-south wind wall and recurvature accelerations as it holds to its constant equatorial path, maintaining its divergences in latitude of zero while they share a longitudinal divergence. And a Subpopulation *B* can tunnel beneath them; or fly above them; while a Subpopulation *A* can track their movements relative to the earth's centre. The Accra–London and Singapore–Nairobi circumstances in *A*, *B*, *C*, and *D* mirror each other with just an exchange of latitude for longitude and vice versa. Exactly the same holds over all four dimensions and diameters.

**V.14.31** We can therefore relate our inexact differentials of  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$  to our exact ones of  $\int dn = \int dP = \int dM = 0$  at any time whatever simply by using some  $\int dx = 0$  to relate the two in some appropriate dimension. That is in our case a four-dimensional rotachoron, and a real projective plane. Larger expeditions simply mean a larger  $V_4$  volume. So no matter what the sizes of those expeditions, they sum to create some rotachoron, which simply has a different overall diameter and volume, thus preserving all topological invariants, with that  $\int dx$  linking them together.

**V.15.1** We can equalize our stases of the first, second and third kinds with our three constraints by considering them in four dimensions. The gradients, divergences and curls create constant loops that vary over time as the one-dimensional



gradients and spherindrical diameters of  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  that we see in Figure 35's rotachoron diameters. Their unseen  $\tau_m$ ,  $\tau_{tm}$ , and  $\tau_{tp}$  divergences form the pole to pole gradients that are the values over time that establish the four spherinders, cubinders, and glomes. They together create the  $\tau_{tmnp}$  circulations of the generations for each and every population. They help establish the three meridians of  $\tau_{tm}$ ,  $\tau_{mp}$ , and  $\tau_{tp}$  that define Boy's surface. These flatten with the  $\tau_t$  hyperplane, at each absolute clock moment,  $t$ , to create the twisting  $nm$ ,  $np$ , and  $mp$  surfaces that are the backbone for the Möbius strips. Those then participate in the bases, fibres, fibre bundles, and covering spaces that are all biology and ecology.

**V.15.2** Möbius was the first to realize the implications of the real numbers,  $\mathbf{R}^n$ , we use to represent a point in  $n$ -dimensional space. In his 1827 work *Der barycentrische Calcül* (O'Connor & Robertson, 2015) he introduced the idea of "homogeneous coordinates" that would permit geometric calculations in all projective spaces.

**V.15.3** While two parallel lines upon an ordinary Euclidean plane go out to infinity, seemingly at a constant distance from each other, and so do not intersect, those on a real projective plane will have the perspective projection of Figure 36a that carries them to their meeting at the point at infinity. No matter where they might begin, or how much they might curl towards or away from each other, the divergences and curls do not change that tending to the same point at infinity, which is represented, in Euclidean coordinates, as  $(\infty, \infty)$ .

**V.15.4** Each real projective plane is a hemisphere placed upon a plane. Its horizon line is at  $(\infty, \infty)$ . That is a unique point upon the real projective plane towards which all lines converge. Each is therefore a two-manifold whose global topology forms a curving  $V_2$  planespace, while its local topology forms the  $S_2$  planespace that tends it to infinity.

**V.15.5** Möbius introduced an extra coordinate. Since each real projective plane is two-dimensional, we create homogeneous coordinates by representing each point on each line with the triple  $(x, y, w)$ . So if we have three different lines, we can express any given point upon each as  $(1, 2, 4)$ ,  $(2, 4, 8)$  and  $(12, 24, 48)$ . When re-expressed in ordinary Euclidean coordinates, each become  $(1/4, 2/4)$ ,  $(2/8, 4/8)$  and  $(12/48, 24/48)$ . But these are all the same  $(1/4, 1/2)$  points in Euclidean space. They are thus the same relative point, no matter what their lengths or orientations.

**V.15.6** We now have an equation of the form  $Ax + By + Cw = 0$  for each line upon a real projective plane, with at least one of  $A$ ,  $B$  and  $C$  being non-zero. The  $Cw$ , which is independent of both  $x$  and  $y$ , now allows any line to be transformed to any other. We simply determine  $Ax/Cw$  and  $By/Cw$  for any point transferred from one line or projective plane to another, and we recover the given point. There is the added advantage that a movement towards infinity is tending towards zero as a limit on all lines, which can now do so at their given rates.

**V.15.7** Any  $(x, y, w)$  is now the same as any  $(\alpha x, \alpha y, \alpha w)$ . All points at any point on any one line, expressed in homogeneous coordinates, are equivalent to all points on any other. As long as  $A$ ,  $B$ , and  $C$  are real numbers, with not all three being zero, then they describe the identical line on any projective plane.

**V.15.8** We can now use the non-zero  $\alpha$  to scale by any amount for any other projective plane. We simply multiply and divide by the  $w$ -coordinate. But since a real projective plane contains that extra zero coordinate, all the Euclidean points that tend to infinity cluster around the real projective plane's zero point. If a population of ants ranges from say 2 to 6, while one of blue whales ranges from say 1 to 1,000,000, then even though they have different absolute sizes and values in their point-, line-, plane-, realm- and tetrapaces, the 50% point for the ants is  $4/6$  while that for the whales is  $500,000/1,000,000$ , each on their respective projective planes.

**V.15.9** We can similarly introduce a  $w$ -axis into our three-dimensional space to give the four numbers  $(x, y, z, w)$ . As in Figure 36b, they will handle all divergences, and all curls for all possible Subpopulations  $A$ ,  $B$ ,  $C$ , and  $D$ . Origins exist upon all, but do not necessarily map to the same absolute locations in each. Lines map to lines, but parallel lines do not necessarily remain parallel. Homogeneous ratios still exist, but points may not map to the same specific points that preserve the same ratios in each. It is the homogeneous ratios that preserve all identities, scalings, and rotations across all four dimensions. They form a group. They do not necessarily progress at the same rates across all four dimensions, but they still sum as both  $\int dn = \int dP = \int dM = 0$  and  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$  all about their respective circulations.

**V.15.10** Every biological set  $X$  and  $Y$  forms an open set that abides by the “fundamental theorem on limits”. Each has the Bolzano-Weierstrass property, with every infinite subset having its contained limit point. Each is “sequentially compact” with every possible sequence in each having a convergent subsequence so that:

“If a function  $u$  has a limit  $l$  and  $c$  is a number, then  $cu$  has the limit  $cl$ .

“If  $u$  and  $v$  have the limits  $l$  and  $m$ , respectively, then  $u + v$  has the limit  $l + m$ .

“If  $u$  and  $v$  have the limits  $l$  and  $m$ , respectively, then  $uv$  has the limit  $lm$ .

“If  $u$  and  $v$  have the limits  $l$  and  $m$  respectively, and if  $m$  is not zero, then  $u/v$  has the limit  $l/m$ .

“If  $u$  never decreases and there is a number  $A$  such that  $u$  is never greater than  $A$ , then  $u$  has a limit which is not greater than  $A$ .

“If  $u$  never increases and there is a number  $B$  such that  $u$  is never less than  $B$ , then  $u$  has a limit which is not less than  $B$  (James and James, 1992)”.

**V.15.11** Every population can now scale, using itself as a unit. They all now transition between their points at infinity on each side, all tending to zero as a limit. Their multiplicative inverses and antipodal points will have both squares and absolute values that can tend infinitesimally closely towards zero for each, as the point at infinity, and no matter how much they are each scaled. They all now have additive and multiplicative inverses for all vectors, along with dot and cross products. A move to infinity is simply a move towards zero. The move in each towards a midpoint and/or equator is the move towards a snipped crossing point.

**V.15.12** Every circulation is now equivalent to every other. Each becomes a circle that passes neatly through the point at infinity. They all have their equators and meridians. Each circulation is therefore divided into four quadrants, with each having a specific relationship both to each hemisphere and to the horizon, again differing only by scale. And for every unique line passing through two distinct points on any projective plane, then there is also a unique point lying at the intersection of two distinct lines. The same holds on all planes. The projective plane therefore makes all 0 to 1 expressions equivalent, with an expression or transition in any one being identical to that in any other, again irrespective of scale; and all about the circulation.

**V.15.13** Since all coordinates represent the same basic point, then if a population of ants does not access some given point on its specified real projective plane because it is biologically impossible for it to do so, then since the points are expressed as a set of divergences and curls, the population will still not access those points when scaled to become comparable to a whale; and conversely. Every population’s transformations on every projective plane are therefore unique. They are independent of scaling. They all preserve all identities, all gradients, all divergences, and all curls.

**V.16.1** There are now some consequences to Meme 122's fusion of a biological mapping cylinder with a covering space. Our exact and inexact differentials must manipulate the same Euler characteristics,  $\chi$ , and deformation retracts,  $S'$ , for the preimage and progenitor domain,  $X$ , and image and progeny codomain,  $Y$ , and so that they are bijective, with every point  $x$  in  $X$  able to substitute itself for  $y$  in  $Y$  and conversely. Each must be first base then fibre so that their joint product space  $P = B \times F$  is their mapping cylinder,  $M_\lambda$ . They must both be simply connected.

**V.16.2** Each meridian on Boy's surface must have projections that are locally homeomorphic. All loops—both trivial and nontrivial—can be lifted to each of their covering spaces, preserving all possible transformations.

**V.16.3** Each of  $X$  and  $Y$  when acting as either base or fibre, and therefore each projection, forms a simply-connected surface for the  $M_\lambda$  mapping cylinder. And since the covering space from which they each derive, and that they then form, must also be simply-connected, then every population has its unique “universal covering space”,  $C$ .

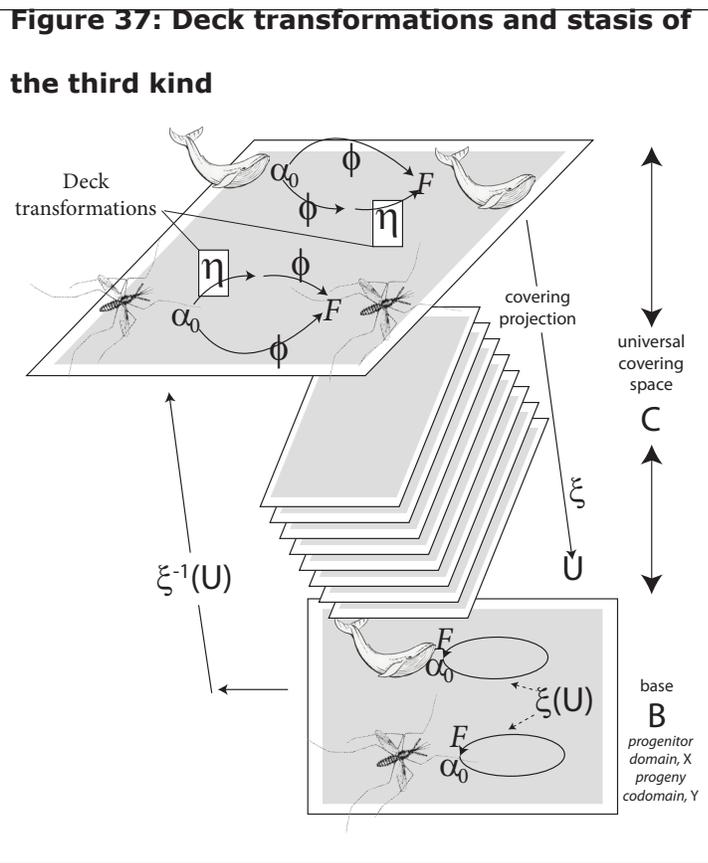
**V.16.4** The unique universal covering space,  $C$ , is also the mapping cylinder,  $M_\lambda$  ... and therefore the surroundings:

- We get the base's  $\pi(S) = 0$  fundamental group, and all its trivial loops, from a genus  $g = 0$  universal covering sphere in  $C$ .
- We get its  $\pi(S) = \mathbf{Z}^2$  fundamental group, and all its nontrivial loops, from a  $g = 1$  universal covering plane which folds into a cylinder for a torus and for our equators again in the universal cover,  $C$ .
- We get its  $\pi(S) = \mathbf{Z}_2$  fundamental group, and all its identified points for all minimum to maximum traversals, by procuring another universal covering sphere. We cut it in two at its equator; duplicate its northern hemisphere; rotate that by  $180^\circ$ ; and reattach. We then have the doubly winding cyclic groups of order two, once again in the universal cover,  $C$ .

We can thus procure all the fundamental groups we need for the progenitor domain,  $X$ , and progeny codomain,  $Y$ , that jointly make the base,  $B$ , from the universal covering space,  $C$ , that is also both (a) the mapping cylinder,  $M_\lambda$ , and (b) the surroundings.

**V.17.1** Each manifold can form a gradient such as  $\nabla Q = 0$  which defines some mean throughout its base space,  $B$ . It is also the foundation for the fibre in all bundle and cover contributions.

**V.17.2** Since each manifold's one-dimensional deviations about its own mean must be observed in the surroundings, then they are the  $\tau_{tn}$ ,  $\tau_{tm}$ , and  $\tau_{tp}$  recursive function values to which we can apply  $t$  as a cutting hyperplane to produce our loops that define the circulation for a generation. This then gives all initial and final values for  $n$ ,  $m$ , and  $p$  over a generation. Each set of values can diverge as its braid-1. Each can be projected both into and out of the universal covering space,  $C$ ; and so in and out of each set of progenitors,  $X$ , and progeny,  $Y$ , that is our base,  $B$ .



**V.17.3** But each one-manifold also conjoins with others to form the two-dimensional divergences and curls that range between some minimum and some maximum as the three sets of paired and twisting Möbius strip values flattened, by  $t$ , from  $\tau_{tnm}$ ,  $\tau_{tnp}$ , and  $\tau_{tmp}$  to be observed as  $nm$ ,  $np$  and  $mp$ . Their oscillations establish biological attributes over time and space for all bases, bundles, and universal coverings in each biological space  $S$ . They define the sizes and dispositions of Boy's surface for a generation, again in the universal covering space,  $C$ .

All four manifolds also come together to create the  $\tau_{tnmp}$  rotachoron. And once that has been flattened by a  $t$  hyperplane, it states the deformation retract and mapping cylinder values for the  $n$ ,  $m$ , and  $p$  maintained at each point  $t$  over the generation. Their three-dimensional curls intersect to define each others' rapidities and directions at each successive point about each base, and each fibre ... and so once more throughout the universal covering space,  $C$ .

As again in Figures 34 and 35, the projections of these gradients, divergences, and curls create the surfaces that are the bases for any current population and generation. They then project back into the universal covering space,  $C$ , to help define that species.

**V.17.4** By Meme 123, our mapping cylinder,  $M_\lambda$ , is also a universal covering space,  $C$ .

**V.17.5** Since our mapping cylinder and universal covering space are now identified, then the three constraints require that the progenitor domain and the progeny codomain each act, by turns, as preimage and image, and so as bases, fibres, fibre bundles, and covering spaces.

**V.17.6** We also now require, as in Figure 37, there be a one-to-one correspondence between the covering projection of  $\xi$  that sends down from the universal cover,  $C$ , into some open set,  $U$ , in the base, and the reverse mapping,  $\xi^{-1}$ , that sends back from the base into the universal cover, therefore acting as a fibre.

**V.17.7** The progeny now loop, in the base, from their initial state,  $\alpha_0(B)$ , to their terminal one,  $F(B)$ . That  $F(B)$  is then identical to the  $\alpha_0(B)$  start point for their own progeny. And since the base interacts directly with the surroundings, then each base necessarily has transformations independent of those in the universal cover,  $C$ , projecting down into it. These are the stases of the first, second, and third kinds.

**V.17.8** The universal covering space,  $C$ , covers all possible bases,  $B$ . It therefore has a far greater number of transformational possibilities than can exist for any single base. Those universal cover transformations must therefore be independent of all those occurring in any one generation, or any one base. Each base must therefore be injective into the universal covering space; while the universal covering space is surjective over each base.

**V.17.9** Since the universal cover's surjective projections must remain unaffected by all returning injective fibres, then as in Figure 37, all universal cover transformations, such as  $\phi$ , must remain unaffected by whichever inverse  $\xi^{-1}$  transformations are currently being sent back, along some fibre, and by some particular progenitor domain or progeny codomain. So any  $\phi$  moving in the universal cover,  $C$ , from some initial point,  $\alpha_0(C)$ , to some final point,  $F(C)$ , must remain able to project the same transformation down into the base. It must identically benefit all possible bases and populations in their  $\alpha_0(B)$  to  $F(B)$  loops, and no matter what inverse  $\xi^{-1}$  arrives back, into the universal cover, from the base.

**V.17.10** Let there now be some second—and so equally surjective—transformation,  $\eta$ , in the universal covering space. When we apply both it and  $\phi$  to  $\alpha_0(C)$ , we still end up—unchanged—at  $F(C)$ , and no matter what the injective  $\xi^{-1}(U)$  fibre arriving. It has the identity property. It acts so that  $\eta \circ \phi = \phi \circ \eta = \phi$ .

**V.17.11** In 1897 Siefert and Threlfall (1980) first referred to such identity transformations as the *Deckbewegungsgruppe* or the ‘covering–movement–group’. They are therefore known as “deck transformations”.

**V.17.12** As again in Figure 37, deck transformations are those identity transformations, within the universal cover, that can both (a) remain unchanged in that cover; and (b) project themselves—as if like a stack of playing cards—through endlessly many covers to arrive—unchanged—in the base.

For every  $\xi$  projection down into the base from the universal cover, a deck transformation exists that allows the cover to undertake a homeomorphic transformation that matches whatever transformations the base might care to undertake, after first receiving that projection, and then projecting its own resulting state back up into the cover, along its  $\xi^{-1}$  fibre, as a reverse projection to arrive back in the universal covering space.

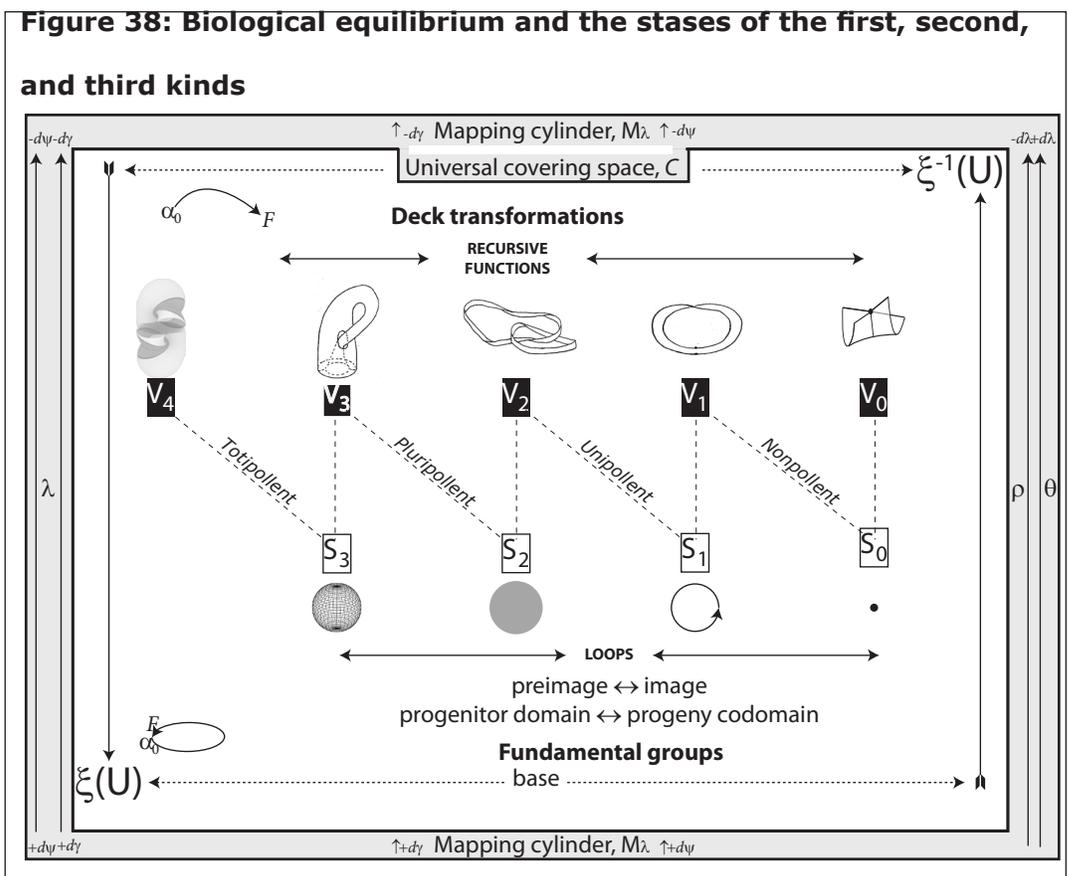
A deck transformation effectively lifts back up into the universal cover whatever projection was previously sent down from the cover, and no matter how it might have been transformed within the base. Every path and loop in every base can therefore lift up into the universal cover to create the precisely matching beginning and endpoints  $\alpha_0$  and  $F$  for that returning path and loop, for it has been left unchanged upon both arrival and departure. No matter what transformations any base might undertake as it interacts with the surroundings, the deck transformations maintain a universal cover integrity.

**V.17.13** Deck transformations state the symmetries within the covering space. They preserve all projections and inverses by mapping the universal cover's identity operations. They therefore ensure a one-to-one mapping between the base's fundamental group and the  $\xi^{-1}$  fibre or inverse projection that lifts from each distinct base into the universal cover.

**V.17.14** Deck transformations also ensure that the universal covering's deck transformation group,  $\eta$ , are isomorphic with the base's fundamental group,  $\pi(B)$ . They form a Galois group.

**V.17.15** Since the deck transformations permute every fibre lifting from every base to create their  $\eta \circ \phi = \phi \circ \eta = \phi$ , then they guarantee the homeomorphism of both the progenitor domain,  $X$ , and the progeny codomain,  $Y$ , as preimage and image; and conversely. They can project through infinitely many covers into the base and still guarantee that base's behaviours ... whilst simultaneously allowing all bases to reciprocally lift all possible subsequent transformations back up into the universal cover, and no matter how frequently they might be repeated. They hold invariant in the face of all permutations in inexact differentials, of whatever type, transmitted up into them. The universal covering space's exact differentials therefore remain supremely indifferent to them all.

**V.18.1** Since the universal covering space,  $C$ , is also the mapping cylinder,  $M_\lambda$ , then the rules for biology and ecology reduce to the rules that govern (a) those deck transformations; and (b) the fundamental groups in the base. Those are (a) the identity,  $\eta$ , in the cover operations; and (b) the



complete set of transformations involving  $\pi(B)$ , which must now be all possible Chomsky production rules within the mapping cylinder,  $M_\lambda$ .

**V.18.2** As in Figure 38, the universal cover pulling up as the  $\xi^{-1}$  fibre from the base is also the mapping cylinder lifting as the fibration,  $\theta$ . This is the combination of  $+\gamma$  and  $+\psi$  moving between base and surroundings as the  $+\lambda$  biology and ecology entering the plessists and plessemorph through their  $+r$  inputs.

**V.18.3** The universal cover projecting down as  $\xi$  is the mapping cylinder lifting as the cofibration,  $\rho$ . This is the combination of  $-\gamma$  and  $-\psi$  moving between base and surroundings as the  $-\lambda$  biology and ecology departing the plessists and plessemorph through the  $-r$  outputs.

**V.18.4** By Meme 124, since our biological spaces conform to both the three stases and constraints then they are interacting with the surroundings to form metric spaces.

**V.18.5** Since our biological spaces are metric, then they are immediately "Hausdorff". Named after the German mathematician Felix Hausdorff, a "Hausdorff space" always contains both the entire set and the empty set,  $\emptyset$ , amongst its infinitely many open sets,  $U$ .

An “open set” in a Hausdorff topology means we can, for example, take any two sets that form two  $S_2$ - $V_3$  rotahedrons, and so that satisfy the general equation,  $x^2 + y^2 + z^2 = r^2$ . Each then has infinitely many points, within its boundary, that satisfies its equation, and that fall either upon, or within, its defining bounds. Each such set can form infinitely many  $V_3$  or 3-ball, subsets. Each of those subsets can also include the entirety of its  $V_3$ . Each set’s empty set,  $\emptyset$ , also falls within its respective  $S_2$  boundary.

A Hausdorff space means that the union,  $\cup$ , and intersection,  $\cap$ , of any finite number of open sets is also always open in the sense that there are infinitely more such sets within each set of bounds that can satisfy that space’s description. And since they all abide by the fundamental theorem on limits, we can always get infinitesimally closer to any and all of them.

A Hausdorff space defines the discrete collections of homomorphic points that are our distinct biological entities. Any two distinct points or collections of points in any Hausdorff space—such as with our plessists, plessemorphs, and other biological entities and that inhabit our biologically metric spaces—can be separated from any other.

**V.18.6** Since our  $t$ -,  $n$ -,  $m$ -, and  $p$ -manifolds are all metric, and therefore Hausdorff, then every point in each is contained in an open set that is always homeomorphic to the real numbers.

**V.18.7** Each set  $U$  is always open in each of  $X$  and  $Y$ . All functions and images  $\phi: X \rightarrow Y$  and  $\phi: Y \rightarrow X$  go to a  $U(X)$  and a  $U(Y)$  in each. Their inverses  $\phi^{-1}(U(X))$  and  $\phi^{-1}(U(Y))$  are also open and continuous.

**V.18.8** If  $p$  and  $q$  are plessists and/or plessemorphs—which means distinct points or groups of points—we straight away have the disjoint open sets  $U(X(p))$  and  $V(X(q))$  in  $X$ , and  $U(Y(p))$  and  $V(Y(q))$  in  $Y$ . They are each separate sets.

**V.18.9** As now required, there exist neighbourhoods in both  $X$  and  $Y$  around  $p$  that do not contain  $q$ ; while there exist neighbourhoods around  $q$  that do not contain  $p$ . All progenitor and progeny sets and subsets are therefore open. Any union is open. Any finite intersection of open sets is again open.

**V.18.10** Every countable open cover of each has a finite subcover. Both  $X$  and  $Y$  are countably compact and equipollent with the natural numbers.

**V.19.1** By Meme 101, our biological structures are locally indistinguishable homomorphic groups of points that reside on and are composed of manifolds, whilst our homeomorphisms, being collections of such groups, can define the global spaces those points occupy.

**V.19.2** Every interaction between a progenitor domain,  $X$ , and a progeny

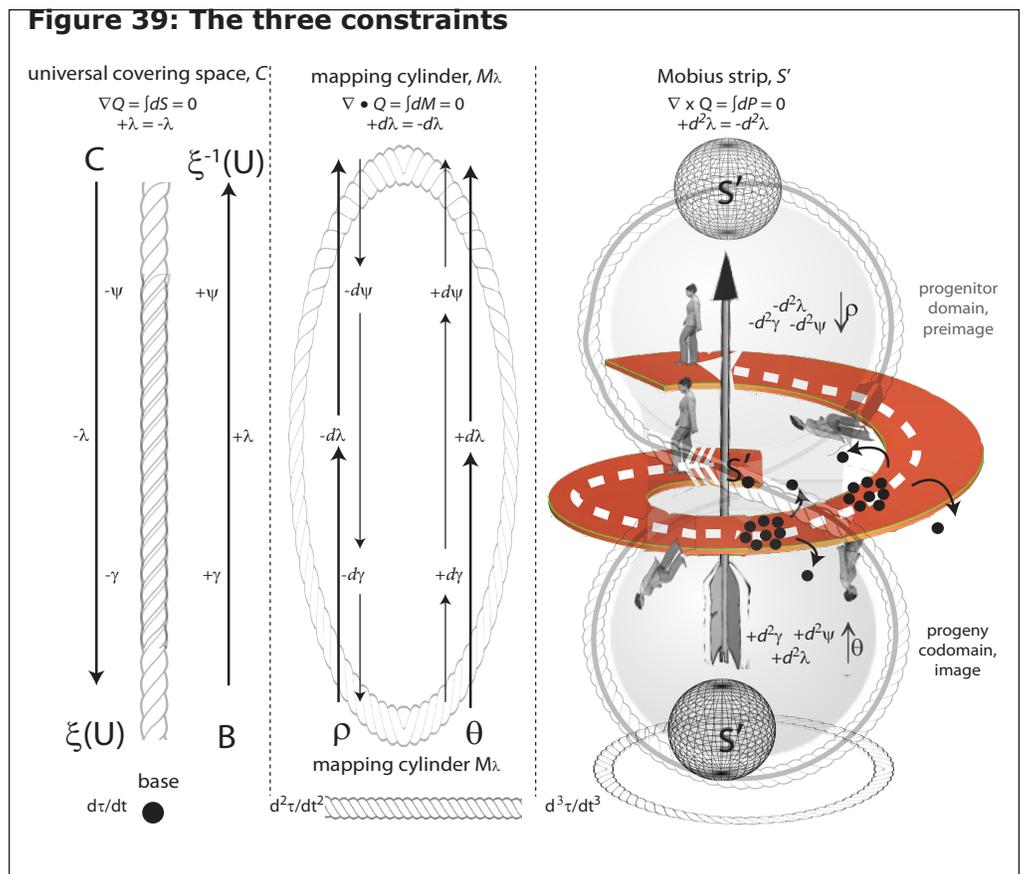
codomain,  $Y$ , is a biological homomorphism between groups of points as entities. It is some mapping  $\phi: X \rightarrow Y$ . It must also be continuous. Since it must be moving from the universal covering space,  $C$ , into the base,  $B$ , it may not be one-to-one. It is therefore a surjective mapping, or onto.

**V.19.3** There must also be a reverse mapping from progeny codomain back to progenitor domain as  $\phi^{-1}: Y \rightarrow X$ . It must again be continuous. And since it cannot be onto, it is an injective mapping, or one-to-one.

**V.19.4** Since one of these mappings is injective, the other surjective, then  $X$  and  $Y$  must be homotopically equivalent.

**V.19.5** Since we have both a homomorphism and a homotopic equivalence between the progenitors,  $X$ , and their progeny,  $Y$ , then they both map between 0 and 1. We have the two continuous functions  $\phi: [0,1] \rightarrow X$  and  $\phi: [0,1] \rightarrow Y$ , respectively, and so that for every pair of points  $a$  and  $b$  in  $X$ , and  $c$  and  $d$  in  $Y$ , then  $a = c = \phi(0)$ ; and  $b = d = \phi(1)$ .

**V.19.6** We also have direct and one-to-one mappings to and from each of  $X$  and  $Y$ , and to and



from both the mapping cylinder and the universal cover. Their deck transformations and fundamental groups must therefore be isomorphic.

**V.19.7** Figure 39 shows the different one-to-one correspondences we can build between the base,  $B$ , on the one hand, and the universal cover and mapping cylinder,  $C$  and  $M_\lambda$ , on the other. For every point we see in the base, which is any value in time, there is a dynamical exchange between  $+r$  and  $-r$  through the Whitney umbrella in the cover. The same point is at one time an input as the surjective  $C \rightarrow \xi(U)$ ; and then it is an output, with the same value, as the injective  $B \rightarrow \xi^{-1}(U)$ . This change occurs at a given velocity, and also equates the first and second stases which are the gradient and divergence in numeracy,  $\nabla Q = \nabla \bullet Q = 0$ . Then for every line we see in the base, which is any unidirectional change maintained over time as either  $C \rightarrow \xi(U)$  or  $B \rightarrow \xi^{-1}(U)$  and so which is a trivial cycle, there is a circulating journey from minimum to maximum and returning that is a nontrivial cycle, and that also aligns some deck transformations with the base fundamental groups. This further equates the first and third stases of the gradient and the curl in numeracy,  $\nabla Q = \nabla \times Q = 0$ . And then for every nontrivial journey in the base and so across a real projective plane, there is an accompanying journey about a Möbius strip as the conjoined  $\xi$  projection down from cover to base and the  $\xi^{-1}$  back along fibre from base to cover that equates all three stases of gradient, divergence, and curl in numeracy:  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$ . This is a circuit about both sides of Boy's surface. It is equivalent to, for example, a given person being taken blindfolded around a given circuit on a first occasion ... which is repeating on a second occasion, but with the blindfold removed. So while the circuit is repeated twice over, the individual concerned believes it to be but a single circuit conducted in two different states.

**V.19.8** Since we can use the real numbers,  $\mathbf{R}$ , to describe all our paths in  $X$  and  $Y$ , then they are by definition connected. And if  $X$  and/or  $Y$  are indeed connected; and if  $\phi$  is a continuous function from  $X$  onto  $Y$  and  $Y$  onto  $X$ ; then each one is mapping to the other while also being connected. We now have discrete collections of homoemorphic points that are the paths in any Hausdorff space.

**V.19.9** If  $p$  and  $q$  are distinct paths in each of  $X$  and  $Y$ , we straight away have the disjoint open sets  $U(X(p))$  and  $V(X(q))$  in  $X$ , and  $U(Y(p))$  and  $V(Y(q))$  in  $Y$ . They are each separate sets. There is a neighbourhood in each that does not contain any paths and points in the other. Any union and finite intersection is also open.

**V.19.10** And ... we at long last have a statement not just about the functions or mappings,  $\phi$ , and so not just about the homomorphisms within  $X$  and  $Y$ . We have here a statement about the spaces. Both the spaces  $X$  and  $Y$  are "path-connected". They are therefore potentially homeomorphic spaces that contain homeomorphic groups of points.

**V.20.1** Although it remains impossible to show four dimensions in only three, Figure 39 depicts the consequences of the interactions between the base,  $B$ , the mapping cylinder,  $M_\lambda$ , and the universal covering space,  $C$  ... with the progenitors,  $X$ , and progeny,  $Y$ , being the base; and the surroundings being the mapping cylinder and universal covering space conjointly.

The universal covering space,  $C$ , in Figure 39a uses its deck transformations to project  $\xi$  into the base at the rate  $d\tau/dt$ . It guarantees the  $XX$ ,  $XX^{-1}$ ,  $YY$ , and  $YY^{-1}$  constant loops, complements, and inverse couplings of  $s \circ s' = s' \circ s = \tau$  and  $s \circ s^{-1} = s^{-1} \circ s = S'$ . Those plessists that can remain sufficiently close to each other, and to these  $S'$  values, will produce the next generation that can then repeat the process.

**V.20.2** Figure 39b has the lifting of progenitor domain as preimage, into the mapping cylinder as a fibration,  $\theta$ , and as a set of biological interactions. We begin moving from  $\alpha_0$  to  $F$ . We have a set of  $\gamma$  and  $\psi$  biological-ecological interactions. They are also a part of the deck transformations,  $\eta$ .

As these same deck transformations then continue to their terminal point  $F$ , so do all the transformations in the mapping cylinder gradually reverse. They become the cofibration  $\rho$ , and a further set of  $\gamma$  and  $\psi$  interactions in the surroundings, again lifting to the mapping cylinder. These are also the  $\xi^{-1}$  reversals projecting from base back to the universal covering space. The total is both the deck transformation identity,  $\eta$ , and the biological–ecological transactions,  $\lambda$ . They occur at the rate  $d^2\tau/dt^2$ .

**V.20.3** We see the same transformations in Figure 39c which depicts a helicoid, a spherinder, and a Möbius strip as the population moves about our biology and replication globes. It moves from an initial location,  $\alpha_0$ , in the universal cover out towards  $F$ . The entities are guided all about the Möbius strip by their Whitney umbrellas. They occur at the rate  $d^3\tau/dt^3$ .

**V.20.4** There is also a set of transformations—overseen by the fundamental groups in the base—looping from  $\alpha_0$  towards  $F$ , but as the set of changes  $S_{-1}$ , about the helicoid, heading towards  $S_0$  in the mapping cylinder. A spherindrical journey from pole to equator is equivalent to a Möbius strip loop towards the crossing point that is the deformation retract,  $S^1$ .

**V.20.5** While the total of the biological-ecological processes is  $\lambda$ , the circulation length is  $\tau$ . The absolute clock time needed to traverse them is  $T$ . The  $\theta$ ,  $\rho$ ,  $\gamma$ ,  $\psi$  and  $\lambda$  operations again proceed along the length in Figure 39a at the rate  $d\tau/dt$ ; they have  $d\lambda$  increments about Figure 39b's unknot at the rate  $d^2\tau/dt^2$ ; and  $d^3\lambda$  increments around Figure 39c's Möbius strip at the rate  $d^3\tau/dt^3$ .

**V.21.1** If we express the points in each of  $X$  and  $Y$  more generally, as  $p$ ,  $q$ , and  $r$ , then we can create a set of homogeneous coordinates that will allow us to scale any population to any other by expressing the four values  $(p, q, r, w)$  as  $(\alpha p, \alpha q, \alpha r, \alpha w)$ , as long as  $\alpha$  is non-zero.

We can alternatively use  $Ap + Bq + Cr + Dw = 0$ . As long as at least one of the coefficients is again non-zero, then we can use  $Dw$  as the independent value that transforms as  $Ap/Dw$ ,  $Bq/Dw$  and/or  $Cr/Dw$ .

Granted that in ' $8/4 = 2$ ' we call 8 the "dividend", 4 the "divisor", and 2 the "quotient", then the  $Dw$  in the above is acting as a "divisor" on the whole biological space. Our dividend is in this case an entire circulation of the generations. That  $Dw$  is a constant that helps determine the space's size and characteristics.

**V.21.2** The entities at any point in our  $X$  and  $Y$  spaces form the subspaces  $U(X)$  and  $U(Y)$ . But if the generation is to continue, then there must exist other spaces that are intrinsically biological, and so at least potentially within the overall  $X$  and  $Y$ , that entities can enter, but that are still outside their current and designated  $U(X)$  and  $U(Y)$  subspaces.

**V.21.3** We can identify those potential spaces the population can enter by taking  $U(X)$  and  $U(Y)$  as divisors. Our dividend is then the entire circulation of the generations. The space we define is outside any current  $U(X)$  and  $U(Y)$ , but still preserves both  $\nabla Q = \nabla \cdot Q = \nabla \times Q = 0$  and  $\int dn = \int dM = \int dP = 0$ .

**V.21.4** Any subspace in each of  $U(X)$  and  $U(Y)$  can take itself as a divisor for the whole. It then creates a "quotient space". And since that quotient space must always exist; and further since it is characterized everywhere by having the same  $Dw$  as its divisor; then the space holds that given divisibility property in common. It is their common divisor. It is therefore also called an "identification space".

**V.21.5** Our identification space is outside any current points and collections of points as either paths or functions ... but is still uniquely accessible to all such points by being a part of their shared identification space. It is again the common dividend for all their divisors to produce their given quotients.

**V.21.6** Since the identification space is characterized by sharing the same divisor everywhere, then it must have some form of "equivalence relationship",  $\sim$ .

**V.21.7** This  $\sim$  equivalence relationship characterizes the space as capable of supporting whatever transformations either will be undertaken, or have been undertaken, by the points currently in  $U(X)$

and  $U(Y)$ , and so that they can either become, or else revert to being, points in that identification space.

**V.21.8** Our topological spaces  $X$  and  $Y$  must bear this  $\sim$  equivalence such that if some set  $U$  is open in that identification space, then its inverse mapping, say  $\sigma^{-1}(U)$ , back into  $X$  and  $Y$  is indeed open. Both  $U$  and  $\sigma^{-1}(U)$  must therefore always be open sets in both  $X$  and  $Y$ .

**V.21.9** If we deformation retract any current  $U(X)$  and  $U(Y)$  subspaces down to a single point, then the remainder is the quotient or identification space. It must share that equivalence relationship,  $\sim$ . And since the equivalences are quotients, then they are ' $X/\sim$ ' and ' $Y/\sim$ ' respectively.

**V.21.10** Our Whitney umbrella and  $\pi(S) = \mathbf{Z}_2$  fundamental group stipulate that for every  $p$  in  $X/\sim$  and  $Y/\sim$  there exists a  $q$  that is the same as  $p$ , excepting only that it has a change in sign. Our equivalence relationship is therefore  $p = \pm q$ .

**V.21.11** We can now say that for any point  $p$  in any  $U(X)$  or  $U(Y)$  we always have the "structural equivalence",  $p \approx q$  where  $p = \pm q$ . The whole of our space therefore has the structural equivalences:

- $p \approx p$ , which is a reflexive structural equivalence;
- if  $p \approx q$ , then  $q \approx p$  which is a symmetric structural equivalence;
- and if we have both  $p \approx q$  and  $q \approx r$ , then we have  $p \approx r$  which is a transitive structural equivalence.

**V.21.12** This  $p \sim q$  equivalence identifies all points throughout the identification space, but as behind their common boundary. It creates the set of open equivalences  $U$  and  $\sigma^{-1}(U)$  all across both  $X/\sim$  and  $Y/\sim$ . And since our structural equivalence is always some  $p \approx q$ , then we can partition  $X$  and  $Y$  into  $p$  and not- $p$ , where not- $p \equiv (-p, \pm q)$ . The entire not- $p$  space is identified by that structural equivalence.

**V.21.13** We now have an open identification space that defines the boundary common to both (a) all  $ps$ , and (b) all the not- $ps$  that can nevertheless transform into  $ps$ . And since for every  $p$  there must exist some  $-p$ , then those two can always produce the identity.

**V.21.14** Identity creation is the structural equivalence throughout our identification space. It holds throughout  $X/\sim$  and  $Y/\sim$ . All points throughout any  $X$  and  $Y$  share that same identity.

**V.21.15** We can in particular note that the sets of points in  $X$  and  $Y$  that do not have this structural equivalence of  $+p$  and  $-p$  coming together to produce a common identity is zero. Our identification space is uniquely identified by its identity,  $S^0$ .

**V.21.16** Our identification space successfully identifies all points opposite to all others. Each identification space thereby gives us all the neighbourhoods accessible to any point in either  $X$  or  $Y$  when either preimage or image.

**V.21.17** And since the  $X/\sim$  and  $Y/\sim$  spaces guarantee that we can find all opposite values for all constant loops, inverses, and complements, then we have a compact and connected projective space that contains both an identity as a crossing point, and a Möbius strip.

**V.22.1** Since our spaces are Hausdorff, path-connected, and now identified, then we can define each  $X$  that deforms to a  $Y$  with that  $Y$  deforming back to  $X$  and conversely as a “zone of reproductive accessibility”. This is also our conjoined identification space,  $X/\sim$  and  $Y/\sim$ .

**V.22.2** Each  $XY$  coupling establishes a set of biological homeomorphisms by establishing both the paths and the boundaries that define biologically replicative populations and spaces. We simply let  $\{X\alpha\}$  be a set of connected—and therefore path-connected—subspaces in  $X$  whose union is all of  $X$ ; and we let  $\{Y\beta\}$  be a set of connected—and therefore path-connected—subspaces in  $Y$  whose union is similarly all of  $Y$ . Each space can therefore be both (a) a complete population, and (b) a generation. And if  $X\alpha_1 \cap X\alpha_2$  and  $Y\beta_1 \cap Y\beta_2$  are each nonempty over all possible indices, then the two spaces are each both (a) connected; and (b) path-connected.

**V.22.3** If our  $X$  and  $Y$  spaces are each indeed connected, path-connected, and identified as  $X/\sim$  and  $Y/\sim$ , then we can bring them together to create a joint  $X \times Y$  or product topology. This immediately has a base  $B$  under the following conditions:

- $B \equiv B_{XY} \cup B_{YX}$ ;
- $B_{XY} \cap B_{YX}$  is not empty;
- $B_{XY} = \{U(X) \times V(Y) \mid \text{such that } U \text{ is open in } X \text{ and } V \text{ is open in } Y\}$ ;
- $B_{YX} = \{U(Y) \times V(X) \mid \text{such that } U \text{ is open in } Y \text{ and } V \text{ is open in } X\}$ .

**V.22.4** We now have the subsets  $U(X)$ ,  $V(X)$ ,  $U(Y)$ , and  $V(Y)$  throughout  $X \times Y$  and  $Y \times X$  that are all properly Hausdorff, open, and nonempty. We also have their respective unions  $U(X) \cup V(X) = X$  and  $U(Y) \cup V(Y) = Y$ .

**V.22.5** However ... the full generality of all the sets that could be formed in either of the product topological spaces  $X \times Y$  or  $Y \times X$  is not necessarily always open. Indeed, we do not necessarily always form either, or both, of those products.

**V.22.6** But since our spaces are explicitly Hausdorff, for all biological entities have definite sizes and measures, then we certainly have the intersections of  $U$  and  $V$  in each of  $X$  and  $Y$ . And if those intersections produce the empty set so that  $U(X) \cap V(X) = \emptyset$  and/or  $U(Y) \cap V(Y) = \emptyset$ , then whichever one of  $X$  or  $Y$  has that empty set intersection does not have a path-connection, and so is suitably “disconnected”. We do not have  $B = B_{XY} \cup B_{YX}$ , and/or  $B_{XY} \cap B_{YX}$  is empty. The  $X \times Y$  product space may be homotopic, but it is now not homeomorphic. We do not then have the full two-way transformations that define a fully viable species. We either have non-compatible parents that produce a non-viable hybrid, or fully compatible parents that produce non-fertile progeny.

**V.22.7** We can now say that if ever either—or both—of  $X$  or  $Y$  acting as either preimage or image is disconnected, in the above sense, then either only one of  $B_{XY}$  and  $B_{YX}$  exists, or else neither does. Since we do not have both, then one or the other, or both, of  $X$  or  $Y$  is disconnected. The disconnected one is either not biological, not replicative, or it is neither. Either one, or both, of  $\theta$  and  $\rho$  fail to lift to the mapping cylinder; and either  $\xi$  is not received from the universal cover by the base, or else  $\xi^{-1}$  is not transmitted by the base to the cover, or else both. That disconnection means one or the other of  $B_{XY}$  or  $B_{YX}$  is empty so that we do not have the full base,  $B$ .

**V.22.8** But if either  $X$  or  $Y$  is not disconnected, then each is by definition connected. And if both  $X$  and  $Y$  are connected—so that we have both  $B_{XY}$  and  $B_{YX}$ , and both  $\xi$  and  $\xi^{-1}$ , and both  $\theta$  and  $\rho$ —then we have a non-empty basis,  $B$ , which acts on both sets of mappings  $X$  to  $Y$  and  $Y$  back to  $X$ . This doubling of space connectedness and path-connectedness gives us the biological double of (a) homomorphism and (b) homeomorphism. It defines both of the non-empty  $XY$  and  $YX$  product spaces over an entire generation. We then have a viable population that can also form a clear species.

**V.23.1** Since our biological spaces  $X$  and  $Y$  are both now Hausdorff and metric, then they together give us a determinable and measurable zone of reproductive accessibility. That zone is defined by the properties projected, as progenitors and their progeny, between the universal covering space,  $C$ , and the mapping cylinder,  $M_\lambda$ . It produces a finitely countable set of plessists, plessemorphs, and/or biological entities as can together create  $\pi$ .

**V.23.2** All the original points  $x$  in any progenitor domain  $X$  of this kind can now take the surroundings as both their mapping cylinder,  $M_\lambda$ , and universal covering space,  $C$ . They can use an index  $i$  to map themselves into a progeny codomain as the points  $y$  in  $Y$ , but with  $Y$  being the deformation retract. This is then the universal cover that projects surjectively as  $\xi$  down into the base. It is also the cofibration,  $\rho$ , lifting from  $X$  into the mapping cylinder, and as part of the overall biological-ecological processes,  $\lambda$ .

**V.23.3** All of the points  $y$  in  $Y$  that result from the  $x$  in  $X$  can now use the same mapping cylinder,  $M_\lambda$ , and universal covering space,  $C$ , to map in reverse as  $\xi^{-1}$ , lifting back from the base into the universal cover; with  $X$  now in its turn being the deformation retract to  $Y$ . This is also the fibration,  $\theta$ , lifting up to the mapping cylinder in the same biological-ecological processes,  $\lambda$ .

**V.23.4** One of those two sets  $X$  and  $Y$  is now the direct progenitor to the other. It lifts plemes and plessetopes, and plessiomes and plesseomes, as  $\psi$  and  $\gamma$ , respectively, into the mapping cylinder as  $\rho$ , while receiving them, surjectively, as  $\xi$  into the base. The other is the direct progeny, again lifting plemes and plessetopes and plessiomes and plesseomes, as  $\psi$  and  $\gamma$ , into the mapping cylinder as  $\theta$ ; but simultaneously injecting them into the universal covering as  $\xi^{-1}$ .

**V.23.5** If, however, there is no basis,  $B$ , with suitable path-connectedness in both directions as  $B_{XY}$  and  $B_{YX}$ , then although both sets  $X$  and  $Y$  may be biological, ecological, and homomorphic as  $\lambda = (\theta, \rho, d\theta, d\rho)$ , there is no shared zone of reproductive accessibility. They do not share a set of increases plus decreases in  $\psi$  and  $\gamma$  in their common product space, and so there is no homeomorphism and no viable species. We now have some clear definitions.

**V.24.1** We have now defined all of biology and ecology. It is the biological journey across a rotachoron from pole to equator to opposite pole over some period of absolute clock time,  $T$ ; as well as the journey from the deformation retract  $S' = (n', \bar{m}', \bar{p}')$  that is the contact point between the biology and replication globes about both of them to return from the same direction and so about a Möbius strip of length  $\tau$ .

**V.24.2** The above journeys also creates the four spherindrical diameters  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  plus three meridians  $\tau_{tm}$ ,  $\tau_{tp}$ , and  $\tau_{mp}$  that create Boy's surface. This again has  $\tau_{nmp}$  centred upon  $\tau't'$  for its triple point, which creates the rotachoron by sustaining  $S'$  over both  $\tau_t$  and  $T$ .

**V.24.3** The replicators that our Hausdorff and topological spaces have provided are open sets. They create an identification space behind the definite  $s \circ s' = s' \circ s = \tau$  and  $s \circ s^{-1} = s^{-1} \circ s = S'$  boundaries. The former is the total distance about the generation, the latter states the distances between the states maintained by defining their centre.

**V.24.4** Since the Möbius strip journey begins and ends at the crossing point, then  $\tau$  is a vector. It measures the displacement from that crossing point, which is the total journey about both globes. We must, however, change in direction twice, which is a set of both (a) jerks or triple derivatives, and (b) accelerations or double derivatives.

**V.24.5** And ... we have now corrected Dawkins' problematic usage of "open-ended" when insisting on "tight discipline" in describing "true replicators" for a "Darwinian model" (Dawkins 2004). Those shared increases and decreases in  $\gamma$  and  $\psi$  that create the biological-ecological activities  $\lambda$  define the mapping cylinder, deck transformations, and universal covering space. Progenitors and progeny can vary topologically with their open sets, but always whilst creating a surface that abides by specific rules, and through a potentially infinite number of generations.

**V.24.6** We can now state those specific rules. They are (A) the three constraints; (B) the four maxims of ecology; and (C) the four laws of biology.

# **Part VI**

## **The laws, the maxims, and the constraints**

**VI.1.1** We can now use our  $S_3-V_4$  rotachoron, the four-dimensional interactions from Boy's surface, and the identification of the mapping cylinder with the universal covering space to deliver the three constraints, four maxims, and four laws that explain all biology and ecology:

The purpose of a model is to summarize knowledge, support insights, make hypotheses explicit and quantitative, and predict or explain new phenomena. Although each aspect of a movement can be explained by many models, the requirement that a single model account for as much normal and abnormal behaviour as possible constrains the choice of models and reveals isomorphisms that contribute to our understanding .... (Ramat, Leigh, Zee, Optican 2007).

**VI.1.2** The three constraints and exact differentials of  $\int dn = \int dM = \int dP = 0$  partner with the three stases of the first, second, and third kinds and the inexact differentials of  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$  to govern the overall sizes and properties unique to each species' unique  $X/\sim$  and  $Y/\sim$  identification space.

**VI.1.3** The three constraints connect the entities' homomorphic structures and their  $\phi: X \rightarrow Y$  and  $\phi: Y \rightarrow X$  mappings to the path-connectedness maintained by those homeomorphic identification spaces.

**VI.1.4** The first constraint determines the unit  $\pm d^3\tau/dt^3$  rapidity with which any unit population,  $Q$ , responds as it moves about its unit identification space,  $\tau$ , with unit circulation,  $T$ . It yanks the population around both of our biology and replication globes using jerks and triple derivatives, which is the biological increments  $\pm d\lambda^2$ .

**VI.1.5** All viable populations must circulate about both sides of Boy's surface, as well as about both of our biology and replication globes. This requires a shared response rate—both internally and externally—to all events, and over all entities.

If the entities are to remain in the same neighbourhoods over an entire generation, then they must share the same rates of change at all times. Since the surroundings are both the mapping cylinder,  $M_\lambda$ , and the universal covering space,  $C$ , then they must share the same triple derivatives and the same integrals in  $\tau$ .

Given that their shared triple derivative is  $d\tau^3/dt^3$ , then their shared triple integral between any absolute interval  $t_{-1}$  and  $t_1$ , equivalent to  $\pm d^2\lambda$ , gives their net activities as their shared biological and ecological interactions  $\pm d^2\gamma$  and  $\pm d^2\psi$ . Each group of entities conduct these over the same and mutual intervals, at the same and mutual rates, and therefore share both  $\tau$  and  $T$ .

**VI.1.6** This is the most variable of the three constraints. It accounts for all biological traits and behaviours. It sets the activity density and texture over all the identification space. It governs the

plemes and plessetopes of Ingredients 3 of  $\psi$ . It twists the  $n$  and  $p$  manifolds to create the  $n\bar{p} = P$  meridian for Boy's surface.

**VI.1.7** The sum of all  $+d^2\gamma$ ,  $+d^2\psi$  and  $+d^3\tau/dt^3$  creates the biology globe. It is all events on one side of Boy's surface; about one side of a Möbius strip; on one side of a real projective plane; and across half a helicoid. It is the sum of all increases in biological processing over all entities at any time.

**VI.1.8** The sum of all  $-d^2\gamma$ ,  $-d^2\psi$  and  $-d^3\tau/dt^3$  creates the replication globe. It is all events on the other side of Boy's surface; about the second side of a Möbius strip; on the other side of a real projective plane; and across the other half of a helicoid. It is the sum of all decreases in biological processing over all entities at any time.

**VI.1.9** The whole circulation covers both globes. Since it is the sum of all  $d^3\tau/dt^3$  and  $d\lambda^2$  distributed across their unit identification space, then it states the equilibrium that is the average unit rate at which any given unit set of entities interact both with each other and with their surroundings over the unit interval that is their circulation of the generations.

**VI.1.10** The inexact differential of  $\nabla \times Q = 0$  creates the energetically static population that is the stasis of the third kind. Its sum is also the exact  $\pm d\lambda^2$  and  $\pm d^3\tau/dt^3$  that again establishes the unit rapidity response. The inexact differential thus combines with its corresponding exact differential which is the:

---

**constraint of constant propagation:**

$$0 = \int_0^1 dP < P' = n' \bar{p}'.$$

Every biological population is associated with a collection of traits, behaviours, and cultural artefacts and information that change constantly, but that can always be divided into discrete elements all of which have the potential to be mimicked and transferred from one individual entity within the population to another.

---

**VI.1.11** The next constraint is the middling most variable of the three and is the base for all fibres. It determines the unit population's ranges in its activities over its circulation.

**VI.1.12** This constraint governs all transfers between the progenitor domain  $X$  as preimage and the progeny codomain  $Y$  as image. The population must therefore move between both an inverse and a complement at some given rate. This constraint's driving differential therefore ensures that

the population leaves some initial and minimum point; that it heads to some maximum at some intermediary point; and that it returns to some final and minimum point. This constraint is therefore the second derivative of  $\tau$  with respect to time:  $d^2\tau/dt^2$ .

The corresponding double integral between any  $t_{-1}$  and  $t_1$  in absolute clock time then gives the net activities as their shared  $\pm d\gamma$  and  $\pm d\psi$ , with the whole being the biological plus ecological transformations conducted with the overall impetus,  $\pm d\lambda$ .

**VI.1.13** This constraint gives the population its complete collection of shared states,  $\pm dS$  over its biological space. That range defines the breadth of the identification space that in its turn supports the transition across the real projective plane and the loops either side of each Möbius strip axis and contact point.

**VI.1.14** All viable populations must draw their progenitor domain  $X$  and progeny codomain  $Y$  together to form the basis for a generation. That is then their constant biological presence as some nucleotide chemical component flux,  $M$ , distributed all across the  $X/\sim$  and  $Y/\sim$  identification space.

**VI.1.15** This constraint therefore establishes the nucleotide chemical component flux that is the population genome of plessiomes and plesseomes, and its Ingredients 4 of  $\gamma$ . These twist as the  $n$  and  $m$  manifolds to create the  $n\bar{m} = M$  meridian and surface. They set its density and responsiveness.

**VI.1.16** The sum of all  $d\tau^2/dt^2$  and  $d\lambda$  activities distributes all chemical components over the  $X/\sim$  and  $Y/\sim$  identification spaces.

**VI.1.17** The sum of all  $+d\gamma$ ,  $+d\psi$ , and  $+d\tau^2/dt^2$  is then the  $+d\lambda$  force that always carries the population towards its maximum presentation, this being a positive divergence. All those positive changes in state are the fibration,  $\theta$ .

**VI.1.18** The sum of all  $-d\gamma$ ,  $-d\psi$ , and  $-d\tau^2/dt^2$  is then the  $-d\lambda$  force that carries the population back towards its minimum presentations, being that population's negative divergence. This is the complete set of reproductive activities as its net negative changes in state. It is the cofibration,  $\rho$ .

**VI.1.19** The two sets of driving differentials create all bases, all fibres, and all fibre bundles. Their total changes form the Ingredient 4 of  $\gamma$  as that base.

**VI.1.20** The stasis of the second kind is the inexact differential of  $\nabla \bullet Q = \bar{m}_{\text{final}} - (\bar{m}_{\text{initial}} n_{\text{initial}} / n_{\text{final}})$  that establishes the population's divergence in its mass flux, creating the materially static population.

This combines with its corresponding exact differential, over the progenitors and their progeny, that is then the overall unit population's entity configuration. It is the population genome and so the:

---

**constraint of constant size:**

$$0 = \int_0^T dM < M' = n' \bar{m}'.$$

The individual entities in every biological population are genotypes which together encode that population's genome or collective genetic encoding, which at least some amongst them are able to reproduce and recreate.

---

**VI.1.21** The last constraint is the least variable. It uses entities to preserve the overall  $X\sim$  and  $Y\sim$  identification spaces. It defines the  $s \circ s' = s' \circ s = \tau$  that governs all constant loops; the  $s \circ s^{-1} = s^{-1} \circ s = S'$  deformation retract; and their doubly closed  $\pi = [(1 \times 1^\delta \rightarrow 1)^T \Leftrightarrow (1 \div 1^\delta \rightarrow 1)^T]$  bijective equilibrium. It is the sum of all  $d\tau/dt$  and  $\lambda$  activities. It forms the universal covering space,  $C$ , and mapping cylinder,  $M_\lambda$ . It determines the  $X \times Y$  product topology. It forms the base  $B = B_{XY} \cup B_{YX}$  with non-empty intersections  $B_{XY} \cap B_{YX}$ .

**VI.1.22** The population's density,  $N$ , at any time is determined by the constant states,  $Q$  and  $S'$ , it can maintain as the set of interactions between its base,  $B$ , and its universal covering space,  $C$ ; and between its  $n$  entities maintained at any time and their mapping cylinder,  $M_\lambda$ . This is the sum over:

- the projections down from universal cover to base and the fibres that lift back, as  $\xi$  and  $\xi^{-1}$  respectively; and
- the total set of biological-ecological processes,  $\lambda$ , that lift as  $\theta$  fibration and  $\rho$  cofibration to and from the mapping cylinder.

These are maintained as a definite overall nonzero state,  $S$ , with nonzero identity,  $S'$ , that defines the pinch points, antipodes, and self-intersections across the  $X\sim$  and  $Y\sim$  identification spaces through the Hooke cell over the entire generation,  $\tau$  and  $T$ . This links  $n\bar{m} = M$  to  $n\bar{p} = P$ . It twists the  $m$  and  $p$  manifolds to create the  $mp$  meridian and surface that sets the characteristic work rate for the identification space.

**VI.1.23** The sum over all the changes about the deformation retract of  $S' = (n', \bar{m}', \bar{p}')$ , at the given rate and for the given time, is the characteristic set of biological-ecological processes,  $\lambda$ . It is the generation length's worth of activities maintained at the rate  $d\tau/dt$ . The total over them all defines the species as its biological and topological space,  $S$ .

**VI.1.24** The population's identification space is defined by its stasis of the first kind of  $\nabla Q = (n_{\text{final}} - n_{\text{initial}})N$ . That overall gradient in numeracy,  $Q$ , is the set of independent gradients in  $n$ ,  $m$ , and  $p$

created by  $mp$  as it twists for its Boy's surface meridian.

**VI.1.25** Although we have sometimes rendered this last constraint as  $\int dn = 0$ , given that it creates the divergence and the curl that is the prevailing set of biological activities for any population, then it is more strictly a combination of the two rates  $dt = Td\tau$  and  $dS = dn + d\bar{m} + d\bar{p}$  that sustain a population's metabolism and physiology as  $S = (n, \bar{m}, \bar{p})$ . It establishes the population's numeracy,  $Q$ , all about its circulation of the generations. It is therefore the:

---

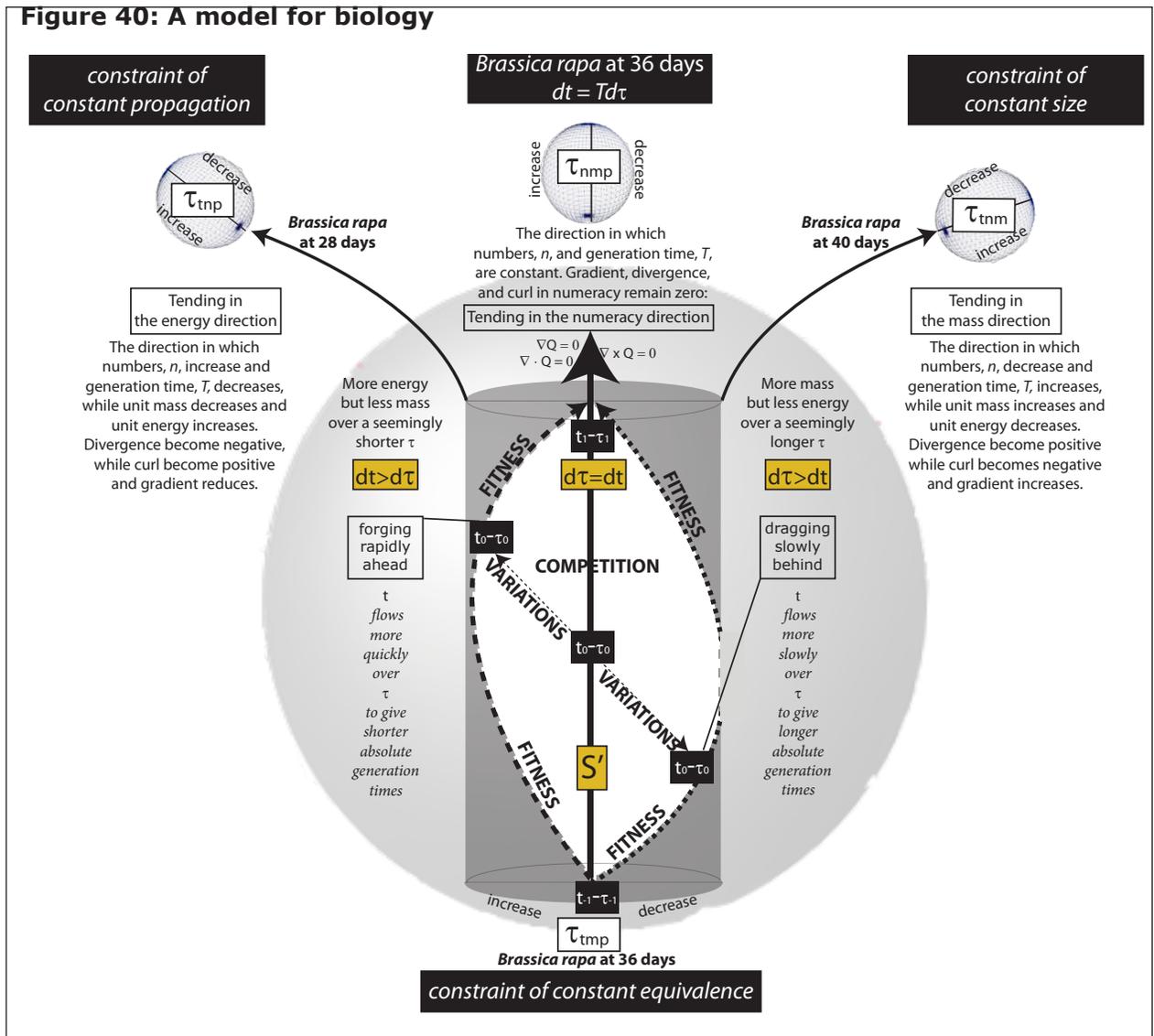
**constraint of constant equivalence:**

$$0 = \int_0^1 dS < S = n \bar{s}.$$

[A] No individual biological entity can be separated from all possible discrete elements of traits, behaviours, and cultural artefacts and information. (Corollary: prodigious savant are always possible; and even “the walls of rude minds are scrawled all over with facts, with thoughts” Ralph Waldo Emerson).

[B] Not all the discrete elements associated with any one trait, behaviour, or cultural artefact or information can be uniquely attributed to any one biological entity. (Corollary: “Bernard of Chartres used to say that we are like dwarfs on the shoulders of giants, so that we can see more than them, and things at a greater distance, not by virtue of any sharpness of sight on our part, or any physical distinction, but because we are carried high and raised up by their giant size” John of Salisbury, *Metalogicon*, 1159).

---



**VI.2.1** The next set of rules are the four maxims of ecology. They establish the path-connectedness of the  $X\sim$  and  $Y\sim$  identification spaces ... and therefore their homeomorphism. They govern the meridians that create the divergences and curls through the spherindrical  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$  diameters and their bounding cubinders. Figure 40 does its best to represent their various four-dimensional relationships, taking *Brassica rapa* as a test case.

**VI.2.2** By Meme 96 our plessists can only be viable if they hold stocks of  $m$  and  $p$  so that  $\int dp \geq 0$  and  $\int dm \geq 0$ . So if any individual entity maintains  $\int dp < 0$  and/or  $\int dm < 0$ , it is certain to dissipate. Any population wishing to remain viable at such moments must hold  $\int dn > 0$  to maintain that non-zero  $\int dN = 0$  mean throughout its identification space. The maxims must therefore create the paths that allow this.

**VI.2.3** The  $dS' = dn' + d\bar{m}' + d\bar{p}'$  of braid-3 of Meme 99 and Figure 19c told us that if one of those three components increases, then at least one of the other two must decrease. So if ever both

$\int dp < 0$  and  $\int dm < 0$  then there must exist paths, inside the identification space, that offset the ongoing entity dissipation. They are paths that will increase  $n$ . The identification space therefore requires that connected paths exist that increase and decrease all of  $m$ ,  $n$ , and  $p$ , which are being distributed around some joint mean,  $S'$ .

**VI.2.4** Figure 40's large  $\tau_{tmp}$  glome, along with the three smaller  $\tau_{tmp}$ ,  $\tau_{tnm}$ , and  $\tau_{nmp}$  ones ranged across the top all have equators. But those equators must have been created by snipping Figure 39c's Möbius strip crossing,  $S'$ , which is the contact point they all held in common. Therefore all movements either towards or away from those equators are movements either towards or away from their common deformation retract,  $S'$ . These are the  $\pm dS'$  of the homeomorphic paths.

**VI.2.5** The two sides of the equators on all the glomes are created by different Möbius strip activities. They therefore have different processing rates. One side accelerates above  $S'$ , the other decreases below it.

**VI.2.6** Figure 40's very large  $\tau_{tmp}$  glome has been flattened by the  $\tau_n$  hyperplane. It is therefore without number. Its large black central arrow is its spherindrical diameter. It establishes the per entity processing requests that carry the population straight towards the small  $\tau_{nmp}$  numeracy glome at top and centre.

**VI.2.7** The small  $\tau_{nmp}$  numeracy glome at top and centre has been flattened by the  $\tau_t$  hyperplane. It therefore receives all momentums, and governs all emergent surfaces. Since it is without  $t$ , it must follow the second law of thermodynamics. Its values therefore fly away into the surroundings. It guarantees that every population will dissipate. It states the  $S = (n, \bar{m}, \bar{p})$  activity rate for an entire population. It sets the equilibrium population numbers observed as the numeracy,  $Q$ , over each circulation distance,  $d\tau$ , and each time interval,  $dt$ . It is rectilinear. It is the only one observed.

**VI.2.8** There is no shorter route about our four-dimensional  $S_3-V_4$   $\tau_{tmp}$  rotachoron than the  $\tau_{tmp}$  glome's large black arrow. It goes straight to the  $\tau_{nmp}$  glome. It punches directly from  $\tau_{-1}t_{-1}$  at the beginning of a generation, to  $\tau_1t_1$  at the end. Any population following it travels on all four equators, simultaneously, and is immediately following that shortest of all possible paths. It is the cubinder that provides the identification space's equilibrium rates. We measured it, for *Brassica rapa*, at  $T' = 36$  days.

**VI.2.9** The  $\tau_{tmp}$  and  $\tau_{nmp}$  glomes also establish the identification space's "temporal divergence". This is the characteristic set of equilibrium biological processing requests made per each unit of time across that population. It helps create both the stasis of the first kind of  $\nabla Q = 0$ , and the  $\int dS = 0$

constraint of constant equivalence. This overall temporal divergence is coordinated through  $dt = Td\tau$  and  $dS' = dn' + d\bar{m}' + d\bar{p}'$ .

**VI.2.10** Both the  $dt = Td\tau$  and  $dS' = dn' + d\bar{m}' + d\bar{p}'$  that determine population behaviours in any identification space are suggested rates. Neither fixes an invariant absolute time interval.

**VI.2.11** Our *Brassica rapa* experiment measured the two linespaces to right and to left as  $T = 40$  and  $T = 28$  days respectively. Both are longer than the central  $T = 36$  day path. They affect  $\tau$  and  $T$  differently across the four dimensions. They are each longer in different ways.

**VI.2.12** The  $\tau_{\text{tm}}$  glome at top right has been flattened by the  $\tau_p$  hyperplane. It therefore sets the identification space's nucleotide chemical component flux as the  $\int dM = 0$  constraint of constant size.

**VI.2.13** When the population selects its 40-day path and heads towards the  $\tau_{\text{tm}}$  population components flux glome, then it is leaving the  $S'$  that is both the Möbius strip contact point and the equator. It moves to the sides of all three other glomes. There will be linked changes in those other rates.

**VI.2.14** Since  $dS' = dn' + d\bar{m}' + d\bar{p}'$ , then the *Brassica rapa* population cannot move to the side of one glome without moving to the opposite side of at least one other. For every ipsilateral movement at one place and time, there is a contralateral one.

**VI.2.15** We look first at the ipsilateral movements. When *Brassica rapa* selects the path to the right of the small  $\tau_{\text{tm}}$  glome, it also selects a path to the right of the large  $\tau_{\text{tmp}}$  one. This  $d\tau$  extends the total number of biological processing requests made to the population. It therefore extends in  $\tau_p$ , which is to increase the temporal divergence.

**VI.2.16** The ipsilaterality exhibited by the small  $\tau_{\text{tmp}}$  glome at the right is the increased temporal divergence. It is the increase in the overall processing orders given to the population at each point about the circulation. It undertakes an increased amount of biological processing. This is  $d\tau > dt$ .

**VI.2.17** But that increase in biological processing demands is made without an accompanying increase in the rate at which the orders can be fulfilled. So with that  $d\tau$  acceleration in processing requests comes a necessary increase in the absolute time,  $T$ , the population will need for all that extra processing.

**VI.2.18** As in Figures 35b and c, the time each individual entity must now allot to the extra processing extends the overall circulation length. The *Brassica rapa* generation length therefore extends to  $T = 40$  days.

**VI.2.19** The path to the right of the  $\tau_{\text{tmm}}$  glome again increases  $\bar{m}$ . This increases the average number of chemical components held per entity. This further increases the total requests made to the population. But there is again no immediate accompanying increase in rate of working. And further since the amounts entering each individual entity increase, the population mass flux,  $M$ , increases. The divergence in the mass flux is therefore given by  $\nabla \cdot M = \bar{m}$ .

**VI.2.20** However, every circulation in a biological and Hausdorff identification space that has an ipsilateral increase requires some countervailing and contralateral decrease. A positive transition in the small  $\tau_{\text{tmm}}$ , and in the large  $\tau_{\text{tmp}}$ , glomes must be accompanied by corresponding decreases upon the two small  $\tau_{\text{tmp}}$  and  $\tau_{\text{nmp}}$  glomes at centre and at left, which must therefore have negative divergences.

**VI.2.21** The  $\tau_{\text{tmp}}$  glome at top left is flattened by the  $m$  hyperplane. It therefore sets the population's unit energy density. And since it is contralateral, a move to its right is a reduction. This decreases the unit energy made available to fulfill the increased requests made, at each clock moment  $t$ , through the large  $\tau_{\text{tmp}}$  glome. The absolute time,  $T$ , required must therefore increase. This is again the 40-day *Brassica rapa* path.

**VI.2.22** And then additionally, a move to the right of the  $\tau_{\text{nmp}}$  numeracy glome, at top centre, reduces the population density,  $N$ . The absolute numbers,  $n$ , in each time interval,  $dt$ , must therefore decrease.

**VI.2.23** Since these are four-dimensional interactions, then the combination of these various ipsi- and contralateral glome transitions means that the  $dS' = dn' + d\bar{m}' + d\bar{p}'$  equilibrium increases  $\bar{m}$ , increases  $T$ , decreases  $n$ , and decreases  $\bar{p}$ .

**VI.2.24** The small  $\tau_{\text{tmm}}$  glome on the right therefore uses its coordinated  $\gamma$  activities to oversee the overall Ingredients 4 replacement. One side of its equator increases the divergence in the population mass flux of chemical components as  $+\gamma = +(\nabla \cdot M) = +d\bar{m}'$ ; while the other decreases it as  $-\gamma = -(\nabla \cdot M) = -d\bar{m}'$ .

**VI.2.25** The zero divergence at the  $\tau_{\text{tmm}}$  glome equator is the population's equilibrium  $S'$ . That value pervades the entire identification space and establishes the  $\bar{m}$  for the plesseomes characteristic of the

plessemorph in any population.

**VI.2.26** Since *Brassica rapa*'s 40-day linespace to the right favours the  $\tau_{\text{tmm}}$  glome, it increases population entity masses. But it simultaneously raises the number of processing requests imposed upon them via the large  $\tau_{\text{tmp}}$  glome; while disfavouring (a) the energy intensity; and (b) the population numbers that can achieve this. It reduces these through the  $\tau_{\text{tmp}}$  and  $\tau_{\text{nmp}}$  glomes at left and centre.

**VI.2.27** And since the path to the right is longer, it moves the population to the outside of Figure 9's helicoid track. And further since that longer path has an overall reduced work rate, then it takes longer to traverse.

**VI.2.28** And ... we indeed observed, in our *Brassica rapa* experiment, that this path had a reduced pot density of only four plants per pot; but the plants had increased masses; along with an increased generation time. And since that small  $\tau_{\text{tmm}}$  glome to the right oversees those Ingredients 4  $\gamma$  replacements in  $\lambda$ , then its net behaviour governs:

---

**Maxim 1: The maxim of dissipation [Darwin's theory of competition]**

$$\int dm < 0; \nabla \cdot M \rightarrow S'; M = n\bar{m}.$$

(A) Any entity that can lift a weight will be prevented from so doing; and/or (B) can be put to use for the same purpose. (C) No entity can lift a weight indefinitely.

---

**VI.2.29** Any *Brassica rapa* linespace that leaves the  $S_3-V_4$  rotachoron equator automatically creates a longer circulation. Therefore, even though the linespace heading towards the small  $\tau_{\text{tmp}}$  glome to the left has  $T = 28$  days and so is shorter in time, it must be longer in some complementary way.

**VI.2.30** The path to the left moves to the left of the  $\tau_{\text{tmp}}$  energy activity glome. It must therefore increase the population's unit energy density ... which is to increase its rate of activity,  $\bar{p}$

**VI.2.31** But this path is contralateral with respect to the previous two glomes: the small  $\tau_{\text{tmm}}$  and large  $\tau_{\text{tmp}}$  ones. The former must now decrease the divergence in the mass flux. This makes entities smaller by reducing  $\bar{m}$ . The latter must decrease the temporal divergence by reducing the number of biological processing requests made, which is  $dt > d\tau$ .

**VI.2.32** This path to the left of  $\tau_{\text{tmp}}$  therefore imposes a decreased demand for biological processing about the circulation. But the  $\tau_{\text{tmp}}$  energy glome's own movements simultaneously increases the

population's energy capability. This allows the population to move to the inside of the helicoid, which is the shorter track. The increased activity rate means that even though this path is longer, it takes less time. We observed this, in our experiment, as that  $T = 28$  days.

**VI.2.33** But there is also an ipsilateral shift to the left of the  $\tau_{\text{tmp}}$  numeracy glome. This is an increase in number density,  $N$ . We observed the increased path length as an increase in pot density to fourteen seeds per pot.

**VI.2.34** We have here an increase in the lengths over two dimensions. They favour the  $\tau_{\text{tmp}}$  glome by increasing the divergence in the energy flux,  $\nabla \cdot P$ , which is by increasing  $\bar{p}$ ; but they also increase the divergence in  $N$ . We may again be travelling about a longer path, but we do so much more quickly.

**VI.2.35** The  $\tau_{\text{tmp}}$  glome to the left governs the Ingredient 3  $\psi$  chemical bond energy flux,  $d\bar{p}$ , for the plemes and plessetopes. Its equator establishes the plessemorph energy throughout the identification space. The glome is therefore:

---

**Maxim 2: The maxim of number**

$$\nabla \cdot P = P/n = \bar{p}$$

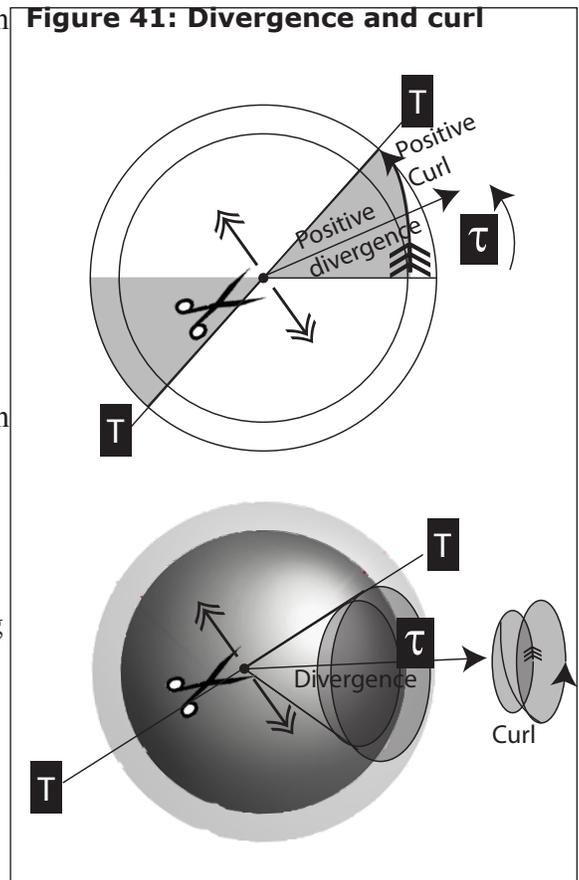
The number of progeny produced depends upon the number of progenitors maintained.

---

**VI.2.36** Every curved line, every rotagon, every rotahedron, and every rotachoron is created by snipping some Möbius strip object. More generally, and as in Figure 41, any  $V_2$  biovolume such as an  $A = \pi r^2$  is accompanied by the one-dimensional measures  $r$  and  $c = 2\pi r$ . If the area changes then  $r$  also changes. But since this is  $T = 2r$  then  $dt$  is non-zero, and the curl also changes.

**VI.2.37** The distance travelled about any circulation is some distance about a Möbius strip ... with that length also being the derivative of whatever area is bound, with respect to some  $r$ . The generation length,  $T$ , is then  $\tau$  the diameter across that area, with the circumference,  $\tau$ , being the circulation. Therefore the rate of change of biological activity about the circulation, which is the curl, depends upon the current divergence, which is the rate at which we move through the generation as  $dt$  and  $d\tau$ .

**Figure 41: Divergence and curl**



**VI.2.38** The same considerations hold over three dimensions. We simply add that the rate of change of a sphere's surface area is the derivative of its enclosed volume element, which is ultimately dependent on the radius,  $r$ , and so on  $T$  and  $d\tau$ . Any changes in any of  $\tau_n$ ,  $\tau_m$  or  $\tau_p$  will affect both the divergences and the two-dimensional curls in  $nm$ ,  $np$  and  $mp$ ; and they will also affect the three-dimensional curl in  $nmp$ , all of which are rates.

**VI.2.39** When *Brassica rapa* selects the path upon the right, the divergence in mass increases more rapidly than the divergence in energy. Since the time interval is  $dt$ , then the average increase in components, over the population, is given by the partial derivative  $+\partial\bar{m}/\partial t$ .

**VI.2.40** But population numbers simultaneously have a contralateral decrease about the  $\tau_{nmp}$  numeracy glome. That net change is the partial derivative  $-\partial n/\partial t$ .

**VI.2.41** Since  $M = n\bar{m}$ ; and since the population's mass flux,  $M$ , occurs over the entire interval  $T$ ; then the total over the entire generation is  $\int M dT$ .

**VI.2.42** However, each individual entity has a mass,  $m$ , at every point. If their number is  $n$ , then their average at every point is  $\bar{m}$ . Since we now have both the numbers and their contributions at each point, then the total over the above interval is also  $\int d\bar{m} dn$ .

**VI.2.43** If the numbers remain constant over any  $T$ , then the net contribution each entity makes at each point, which is a characteristic for the generation, can be determined from  $\int M dT = \int d\bar{m} dn$ . Every entity that participates has this same value  $\bar{m}$ .

**VI.2.44** However, if numbers change, then the characteristic contribution changes. It is no longer shared by all. The range difference is the curl in the mass flux. It is given by  $\nabla \times M = \int M dT \int d\bar{m} dn$ .

**VI.2.45** *Brassica rapa*'s slow 40-day path sees such a large  $+\partial\bar{m}/\partial t$  that the characteristic increase in masses over the remaining members more than compensates for the decreased numbers,  $-\partial n/\partial t$ .

And similarly, the faster 28-day path sees a decrease in the individual chemical components stock of  $-\partial\bar{m}/\partial t$ . But that characteristic mass decrease is offset by a large increase in population numbers,  $+\partial n/\partial t$ .

**VI.2.46** The net result, over *Brassica rapa*'s identification space, is that, in the first place, populations on the helicoid's inside 28-day pole position track have increased numbers, and work at a faster rate. They contribute to the identification space by using their increased curl in numbers,  $+\partial n/\partial t$ ,

to compensate for their reduced divergence in mass,  $-d\bar{m}$ .

But in the second place, plants on the slower outside 40-day track work at a slower rate. They contribute to the same identification space by using their increased curl in mass,  $+\partial\bar{m}/\partial t$ , to compensate for their reduced divergence in numeracy,  $-dQ$ .

**VI.2.47** Whenever population numbers,  $n$ , in any  $X/\sim$  or  $Y/\sim$  identification space change, then there is a curl in mass of  $\nabla \times M = \int M dT \int d\bar{m} dn$ . The contralateral and countervailing changes in  $n$  and  $\bar{m}$  allow the population to balance its two sets of divergences and curls in mass and in numeracy. The net change in the chemical components flux,  $M$ , is given by:

---

**Maxim 3: The maxim of succession [Darwin's theory of evolution]**

$$\nabla \times M = \partial\bar{m}/\partial t - \partial n/\partial t$$

The rate at which progeny is produced depends upon the rate at which competition occurs.

---

**VI.2.48** Energy density changes are the most variable. There can be population wide changes in  $p$  even as both  $m$  and  $n$  remain constant. But both  $M = n\bar{m}$  and  $P = n\bar{p}$  always exist. Since  $n = M/\bar{m} = P/\bar{p}$ , then there must be a work rate,  $W$ , upon any path, and such that  $W = \bar{m}\bar{p}$ .

**VI.2.49** The divergence in numeracy is  $\nabla \cdot Q = \bar{m}_{\text{final}} - (\bar{m}_{\text{initial}} n_{\text{initial}}/n_{\text{final}})$ . The divergence in the chemical components flux is  $\nabla \cdot M = \bar{m}$ . The mass flux can change with no effect on numbers, but the numbers cannot change without affecting the curl in the mass flux,  $\nabla \times M$ .

**VI.2.50** The curl in numeracy is  $\nabla \times Q = \bar{p}_{\text{final}} \bar{m}_{\text{initial}} (n_{\text{final}} - n_{\text{initial}})$ . It can only remain zero if  $n$  does not change when  $M$  changes. But this then means that the population is pursuing the shortest possible path. It is following the cubinder that is the large black arrow, for the equatorial path, and so is heading straight towards the  $\tau_{\text{nmp}}$  glome.

**VI.2.51** If numbers stay the same over  $T$ , then each entity's net and characteristic contribution to the population energy flux over the generation,  $\bar{p}'$ , can be determined from  $\int P dT = \int d\bar{p} dn$ .

**VI.2.52** The path that holds  $n$  constant by ensuring that  $M$  and  $P$  change at the same rates as  $m$  and  $p$ , is the cubindrical one that surmounts the equator. It sets  $W = MP = \bar{m}\bar{p}$ . All other paths are longer due to their curls in both mass and energy ... and as caused by the resulting curl in number.

**VI.2.53** Since  $P = n\bar{p}$ , then only a set of inverse changes in  $n$  and  $p$  can link the divergence to the curl. The curl in energy of  $\int P dT/d\bar{p} dn$  is driven by  $\pm\partial d\bar{p}/\partial t$  and  $\pm\partial n/\partial t$ .

**VI.2.54** The *Brassica rapa* linespace to the left is longer because even though plant masses decrease, numbers and energy density both increase. This increases the work rate,  $W$ , through a curl given by the partial differential  $\pm\partial W/\partial t$ . The path is then travelled more quickly.

**VI.2.55** If our plessists and/or plessemorphs are to create paths within the identification space that allow for the required ipsi- and contralateral accelerations and decelerations that preserve the species equilibrium of  $S' = (n', \bar{m}', \bar{p}')$ , then there must be a curl in energy involving all three properties  $\partial\bar{p}/\partial t$ ,  $\partial W/\partial t$ , and  $\partial n/\partial t$  as:

---

**Maxim 4: The maxim of apportionment**

$$\nabla \times P = \partial\bar{p}/\partial t + \partial W/\partial t - \partial n/\partial t$$

The bioactivity of a biological population is subject to increase from an initial value for one or more of three reasons: (a) increases in mass; (b) decreases in competition. All other increases are due to (c) the essential development of the entity or species.

---

**VI.3.1** Our homomorphic structures can create all biology and ecology by linking to homeomorphic spaces through the three constraints and the three stases, thus defining the deformation retracts,  $S'$ , the mapping cylinders,  $M_{X,Y}$ , and the universal covering spaces,  $C$ , that are the size and properties for each  $X/\sim$  and  $Y/\sim$  identification space. And since each one's structural equivalence is  $p \sim q$ , where  $(p, \pm q)$  and so that  $p = \pm q$ , then any  $\phi(U(X))$  that selects any  $p$  in  $X$  has an open equivalence class  $\phi^{-1}(U(X))$  that takes the whole of  $Y$  for its  $V(Y)$  to select  $\pm q$ . And similarly, any  $\phi(U(Y))$  that selects any  $p$  in  $Y$  has an open equivalence class  $\phi^{-1}(U(Y))$  that reciprocally takes the whole of  $X$  for its  $V(X)$  to select its  $\pm q$ . Therefore the base  $B = B_{XY} \cup B_{YX}$  is always the whole of both the progenitor domain as preimage,  $X$ , and progenitor codomain as image,  $Y$ . The intersection  $B_{XY} \cap B_{YX}$  always holds some path that describes some state,  $S$ , at every point in the generation,  $\tau$ , and so that our four maxims of ecology define the fluxes that suitably pervade those  $X/\sim$  and  $Y/\sim$  identification spaces as the homeomorphisms that preserve the connected paths. We must now declare the four laws of biology that command the homomorphic structures and biological entities to actually follow those homeomorphic paths.

**VI.3.2** The upcoming laws of biology must make definite statements about plessists' and plessemorphs' real-world behaviours so they follow the identification space's homeomorphic paths.

**VI.3.3** Although all individual members in any given population must ultimately dissipate, then by Meme 121 all populations must—as a whole—preserve both their homo- and their homeomorphisms by preserving the path-connectedness that guarantees homeomorphism. The  $n$  plessists and plessemorphs concerned must therefore follow whatever paths preserve  $B_{XY} \cap B_{YX}$  and  $B = B_{XY} \cup B_{YX}$ . They must in other words ensure that  $\bar{m} > 0$  so the base always exists throughout the identification space.

**VI.3.4** Although each distinct entity must again individually dissipate, each also participates in a population-wide system that must at some time exhibit the  $d\bar{m}/dt > 0$  and  $\partial\bar{m}/\partial t > 0$  that maintain the number of their connected paths.

**VI.3.5** But we can take any universal covering space,  $C$ , and form its identification space,  $C/\eta$ . We simply take any point  $p$ , up in the cover, and then deformation retract it to some single point. We then use the same  $p = \pm q$  equivalence to create a structural  $p \approx q$  equivalence over the remainder.

But the  $C/\eta$  identification space, up in the cover, is the not- $p$  that surjectively covers the entirety of the base space,  $B$ . Therefore, and as in Figure 7, every point in the base is accessible from the universal covering space's real projective plane and identified points. As in Figure 32, we now have an extant Möbius strip between cover and base, and between base and cover, with  $s \circ s' = \tau$  and  $s \circ s^{-1} = S'$ , and through which the two can reciprocally access each other, all across the generation, as progenitor domain and preimage,  $X$ , and progeny codomain and image,  $Y$ .

**VI.3.6** Every population resides on a real projective plane and expresses its transformations in homogeneous coordinates. Although Maxim 1 insists that all entities must eventually dissipate, it also guarantees that at least some members will curl to the right-hand side of the  $\tau_{\text{mm}}$  glome. They exhibit a positive divergence in the mass flux,  $M$ . Those members follow paths that take them to the projective plane's identified edges. They therefore have  $m \rightarrow \infty$ .

**VI.3.7** By Meme 96 and Meme 99 some determinable period  $T$  exists so that  $\int dm \geq 0$  and  $\int dp \geq 0$  is always true over a sufficiently large enough number of entities. And since all viable populations must preserve both homo- and homeomorphisms, then there must always be at least one member in any  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification space that preserves those path connections. We must always therefore have  $n \geq 1$ .

**VI.3.8** By Meme 122, when all members in all populations follow  $\int dm < 0$  and  $\int dp < 0$  and succumb to Maxim 1 of dissipation, they also flatten with the  $\tau_t$  hyperplane. They head towards the  $\tau_{\text{nmp}}$  numeracy glome. This creates all a population's observable real-world values of  $n$ ,  $m$ , and  $p$  at each moment  $t$ . All distinct biological entities must, in other words, follow the second law of thermodynamics. They must increase in their entropy. However, if the population is to be preserved, then each population must persuade at least some of its entities to follow the doctrine of "negative entropy" first proposed by Erwin Schrödinger (Schrödinger 1944). This is the combined effect of the glome equators, and their  $S^7$  Möbius strip crossing point.

**VI.3.9** The effect of Schrödinger's negative entropy on paths and identification spaces is that if a given population is to reproduce, then both its progenitor domain  $X$  as preimage and its progeny codomain  $Y$  as image must always have open, non-empty, and Hausdorff sets. Each must access a  $U$  within itself and a  $V$  within the other. All intersections of all these  $U$ s and  $V$ s,  $B_{XY} \cap B_{YX}$ , must be non-empty. They must always produce the base  $B = B_{XY} \cup B_{YX}$ . The identification spaces  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  must not simply exist. They must be followed.

**VI.3.10** But since all entities must eventually dissipate, then the number of disconnected and empty paths in any  $X \times Y$  product space greatly outnumbers the number of connected ones. There is then no homeomorphism, no replication, and no species. Therefore, the paths that any current entities in any  $X$  and  $Y$  follow can easily make  $B = B_{XY} \cup B_{YX}$  non-existent, so that  $B_{XY} \cap B_{YX}$  is empty and there are no viable extant entities.

**VI.3.11** A viable biological system must therefore lift new and connected paths into itself to replace all disconnected ones lost by its non-viable and/or dissipating members. The homomorphic

and homotopically equivalent members must act as bases; as fibres; and as fibre bundles. They must reconstruct all disconnected paths.

**VI.3.12** Our plessists and plessemorphs, as biological entities, must configure their countable Ingredient 4 atoms so they maintain a constant material presence throughout the entirety of the identification space. They must constantly use  $\gamma$  and  $\psi$  to maintain Schrödinger's negative entropy, meaning they must always do work,  $W$ , as clearly defined by the first law of thermodynamics, and so that:  $\delta W = (\delta Q - dU) > 0$  (Encyclopaedia Britannica 2002).

**VI.3.13** Every viable population that wishes to preserve paths must abide by both the constraint of constant size of  $\int dM = 0$  and the stasis of the second kind of  $\nabla \bullet Q = \bar{m}_{\text{final}} - (\bar{m}_{\text{initial}} n_{\text{initial}} / n_{\text{final}})$ . Both (a) the homomorphic members, and (b) the molecules they use to compose themselves must be equipollent with  $\aleph_0$  (Weisstein 2015a). All the above requirements, taken together, give:

---

**Law 1: The law of existence**

$$n > 1; \delta W = (\delta Q - dU) > 0; m \rightarrow \infty; \bar{m} > 0.$$

There is an entity such that it must always lift a weight; and such that it must, and by this means, at some time increase in its mass.

---

**VI.3.14** Not only must the equivalence classes defined by the  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification spaces always exist, but they must have a structural and measurable form. The  $X/\sim$  is the entire  $Y$  codomain of progeny all across the generation, and as viewed by any progenitors at any time,  $t$ , while the  $Y/\sim$  is the entire  $X$  domain of progenitors as again viewed at any time by any progeny; with  $C/\eta$  then being an entire generation's worth of both, and as viewed at any time from any point in the universal cover ... which is then also the entirety of the mapping cylinder,  $M_\lambda$ . But that is itself  $\gamma$  and  $\psi$  combining as the fibration and cofibration that are the entirety of any given biological–ecological activities,  $\lambda$ .

**VI.3.15** If the homomorphic structures are going to reproduce, then they must follow the homeomorphic paths the identification space makes available. They must be constant topological neighbours all about Boy's surface and so must constantly share the same positive and negative absolute values and rates of change. But since the universal covering space,  $C$ , is also the mapping cylinder,  $M_\lambda$ , then this has very particular consequences.

**VI.3.16** Our homomorphic structures must be constant topological neighbours throughout their  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification spaces. We can therefore note that in 1927 the English zoologist and animal

ecologist Charles Elton proposed an identification space for all members of the same species as their shared set of behaviours in their equally shared surroundings:

It should be pretty clear by now that although the actual species of animals are different in different habitats, the ground plan of every animal community is much the same. In every community we should find herbivorous and carnivorous and scavenging animals. ... It is therefore convenient to have some term to describe the status of an animal in its community, to indicate what it is doing and not merely what it looks like, and the term used is “niche”. Animals have all manner of external factors acting upon them—chemical, physical and biotic—and the “niche” of an animal means its place in the biotic environment, *its relationship to its food and enemies*. The ecologist should cultivate the habit of looking at animals from this point of view as well as from the ordinary standpoints of appearances, names, affinities, and past history. When an ecologist says “there goes a badger” he should include in his thoughts some definite idea of the animal’s place in the community to which it belongs, just as if he had said “there goes the vicar”. [emphasis in original] (Elton 1927).

**VI.3.17** We have found our identification spaces. We have also found our equivalence classes.

**VI.3.18** Let there now be a Population  $R$ ; and also a Population  $S$ . If they are indeed members of the same species, then they will have the common base  $B$ . They will share:

- the fundamental group  $\pi(B)$ ;
- the constant loops  $\alpha_0$  to  $F$ , which are equivalently  $\alpha_0$  to  $\alpha_0$ , and/or  $F$  to  $F$ ;
- and the transformations  $\phi: X \rightarrow Y$  and  $\phi^{-1}: X \rightarrow Y$ , which latter is  $\phi: Y \rightarrow X$ .

**VI.3.19** Since Populations  $R$  and  $S$  follow homeomorphic paths, then their  $X$  and  $Y$  subpopulations that are the progenitor domain and progeny codomain are also each others’ deformation retracts. Their entities will occupy neighbourhoods near to each other on both their mapping cylinders as  $M_\lambda(R)$  and  $M_\lambda(S)$ ; and their universal covering spaces as  $C(R)$  and  $C(S)$ .

**VI.3.20** If our Populations  $R$  and  $S$  are indeed members of the same species then as Rossberg et al point out, their subpopulations  $R(X)$ ,  $R(Y)$ ,  $S(X)$ , and  $S(Y)$  must be more than merely homomorphic and homotopically equivalent:

The niche concept has remained of fundamental importance to ecology. It establishes a link between individual-level traits and population dynamics. ... The availability of an ecological niche for a species depends, in a great variety of ways, on interactions between the species comprising an ecological community. These interactions, in turn, are affected by the phenotypic traits expressed in the interacting species. ... However, despite decades of intense

research and debate no universal agreement has emerged as to how niches are to be formally represented, and fundamental questions remain unresolved (Rossberg et al, 2010).

**VI.3.21** We can easily correct the deficiency Rossberg et al highlight. As we saw with the letters  $X$  and  $Y$ , homomorphic objects can lose information when mapped to each other. The four-to three-vertex  $\phi: X \rightarrow Y$  mapping is not the same as the three- to four-vertex  $\phi: Y \rightarrow X$ . These are not bijective. They do not have the same underlying structure.

The mappings  $\phi: R(X) \leftrightarrow S(X)$  and  $\phi: R(Y) \leftrightarrow S(Y)$  between populations that successfully reproduce are, however, invertible. They are homomorphisms possessing both the  $\phi$  and  $\phi^{-1}$  mappings. They are therefore isomorphic.

An isomorphism is a homomorphism between any two sets or structures that have a one-to-one correspondence between their elements so their group operation can be reversed. The bijective mapping means the objects have the same underlying structure, and must also be homeomorphic.

**VI.3.22** The isomorphic Populations  $R$  and  $S$  now share a joint base,  $B$ . They interact with a shared universal covering space,  $C$ . Every point  $x$  in  $B$  has an open neighbourhood  $U(X)$ . Their shared mapping,  $\xi$ , projects—with Möbius strip—from cover down to base. The inverse  $\xi^{-1}$  mapping of the fibre from base back to universal cover is the lifting of the disjoint union of open sets,  $\xi^{-1}U(X)$ , into  $C$ , and again with Möbius strip. Those then avail themselves of the same Möbius strip to immediately map surjectively, and homeomorphically, back down onto  $U(X)$  with  $\xi$ .

**VI.3.23** Since Populations  $R$  and  $S$  are biological, their open sets are their progenitor domain,  $X$ , and progeny codomain,  $Y$ . They are therefore isomorphic across their respective circulations of the generations,  $\tau$ .

**VI.3.24** Since the universal covering space,  $C$ , is topological, it has its own fundamental group. This must be surjective over the base fundamental group,  $\pi(B)$  ... which is immediately injective back into the cover's.

**VI.3.25** Since  $\pi(B)$  is injective into the universal cover, then for every path starting at the base's  $x_0$  identity, there exists a path up in the cover beginning at the cover's identity. So once we fix any loop start point  $\alpha_0$  in the base, we fix a corresponding start point in the cover. Every loop in the base, as a preimage, has a unique image in the cover. If, therefore, Populations  $R$  and  $S$  are isomorphic in the base, they remain isomorphic when lifted to the universal covering space,  $C$ .

**VI.3.26** A deck transformation,  $\eta$ , is an isomorphism from a covering space onto itself.

**VI.3.27** Any given deck transformation,  $\eta$ , is completely determined by whatever point upon it the fibre lifting into it accesses. Both  $\eta$  and any  $\phi: X \rightarrow Y$  and/or  $\phi: Y \rightarrow X$  remain unchanged and unique.

**VI.3.28** If a first universal cover,  $C(M)$ , projects an  $\xi_M$  down into some base,  $B$ ; and if a second universal cover,  $C(N)$ , sends its  $\xi_N$  down into the same base; then  $C(M)$  and  $C(N)$  create the same surjective mapping, and must receive the same injection from  $B$ . Each will therefore be carried from and to the same places in  $B$ . And since they achieve the identical effect, no matter what injective  $\xi^{-1}(U)$  fibre they each receive, then  $C(M)$  and  $C(N)$  are isomorphic.

**VI.3.29** The  $C(M)$  and  $C(N)$  universal covering spaces share the identity property  $\eta \circ \phi = \phi \circ \eta = \phi$ , and have the effect  $\xi_M = \xi_M \circ \eta = \eta \circ \xi_M = \xi_N \circ \eta = \eta \circ \xi_N = \xi_N$ . Their deck transformations  $\eta: C(M) \rightarrow C(N)$  and/or  $\eta: C(N) \rightarrow C(M)$  are therefore also bijective.

**VI.3.30** For any loop from any  $\alpha_0$  in the base  $B$ ; and for its matching universal cover transformation; then the  $\pi(B)$  fundamental group acts by deck transformation to create unique points up in the cover.

**VI.3.31** Since Populations  $R$  and  $S$  will also interact with the surroundings as a mapping cylinder,  $M_\lambda$ , then again as in Figure 7, they have both a fibration and a cofibration. Their cofibration,  $\rho$ , lifts from their progenitor domain as preimage,  $X$ . It is isomorphic with the surjective projection,  $\xi$ , coming down from the universal cover into the base. And their fibration,  $\theta$ , lifts from the progeny codomain as image,  $Y$ , and is isomorphic with the injective  $\xi^{-1}$  lifting from base back to universal cover.

**VI.3.32** Since those of our homomorphic structures that exhibit both the sets of transformations  $\phi: X \rightarrow Y$  and  $\phi: Y \rightarrow X$  are invertible, then they are isomorphic. They are therefore bijective. And those that are indeed bijective can freely exploit the invertible paths in our homeomorphic identification spaces  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$ .

**VI.3.33** Our isomorphic structures therefore correct the deficiency in Elton's ecological niches that Rossberg et al highlighted:

- They can follow connected paths that undertake all biological  $\rho$  and cofibration activities. They can abide by Law 1 and do work as, for example, sperm that swim to fertilize; eggs that polarize; fruits that discard their husks while their endosperms germinate their seeds; and etc. These seemingly negative entropy—but work-preserving—paths lift masses, energies, and heat into the surroundings as  $-\gamma$  and  $-\psi$ .
- The isomorphic and so invertible structures that are the resulting progeny can then also follow connected paths. They undertake such  $\theta$  fibration and biological activities as

grazing, browsing, photosynthesising and the like. These all also abide by Law 1. They require work and emit heat ... but they instead lift masses, energies, and heat from the surroundings back into the population as  $+\gamma$  and  $+\psi$ .

The former set of activities are  $-\lambda$  and take place through  $-r$ . They send about one loop in a Whitney umbrella, as  $-dA$  and  $+dA$ , out and back to  $V_0$ . The latter are  $+\lambda$ , taking place through  $+r$ , sending about the other loop as  $+dA$  and  $-dA$ , to and from the same  $V_0$ . The former emit through the population's  $S_0$  outputs as  $-\gamma$  and  $-\psi$ ; while the latter absorb through the  $S_0$  inputs as  $+\gamma$  and  $+\psi$ . The  $S_0 - V_0$  are together the set of biological-ecological activities,  $\lambda$ .

**VI.3.34** We have successfully defined our  $\pi \equiv [(1 \times 1^{\delta=1} \rightarrow 1)^1 \Leftrightarrow (1 \div 1^{\delta=1} \rightarrow 1)^1]$  equilibrium. It characterizes our  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification space. It declares that if our population wishes to maintain a characteristic equilibrium over a given set of entities, then (a) they must have isomorphic biological structures; and (b) they must occupy homeomorphic spaces. Only then can they cross a real projective plane so they equalize their inexact differentials of their gradients, divergences, and curls with the exact differentials of their three constraints. The entities concerned will then move constantly through each others' neighbourhoods over both a shared circulation length for a Möbius strip,  $\tau$ , that is both sides of Boy's surface; also doing so in the same absolute time interval,  $T$ .

**VI.3.35** The above isomorphisms and their accompanying homeomorphisms for a given identification space provide:

---

**Law 2: The law of equivalence**

$$[(\delta W_1 = \delta W_2) \wedge (\delta W_2 = \delta W_3)] \Rightarrow (\delta W_1 = \delta W_3)$$

If a first entity can follow a path such that Law 1 is satisfied; and if a second entity can follow the same path to the same effect; then the first and second entities are equivalent.

---

**VI.3.36** Both our rotachoron and our real projective plane are four-dimensional, with the former's equator being the latter's snipped Möbius strip crossing point. And since the real projective plane uses homogeneous coordinates, then all points on apparently opposite sides of any equatorial line or surface are identified.

**VI.3.37** By Law 2, our new law of equivalence, every viable population has its  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification spaces that state its specific  $p = \pm q$  equivalence classes. And by Meme 123, we can identify all species via their  $[\Sigma = \{A, C, G, T\}, S = \{n, \bar{m}, \bar{p}\}, \delta, \alpha_0, F]$  Chomsky production rule

which sets  $\delta$  to some value that establishes both their initial and their final biovolumes,  $V_{1,2,3,4}$ , and accompanying biosurfaces  $S_{0,1,2,3}$ .

**VI.3.38** By Meme 124, those same Chomsky productions operate over a base,  $B$ , that is a set of both progenitors,  $X$ , and progeny,  $Y$ , that interact over a circulation length,  $\tau$ , for the absolute time period,  $T$ . They can maintain their Law 2 equivalence by lifting, and so injecting, their disjoint and open sets  $\xi^{-1}U(X)$ , as fibre, into their universal covering space,  $C$ . And no matter how much the base transforms its progenitors and/or progeny, the deck projects them straight back down. It always has  $\xi \circ \xi^{-1} = \# = \tau = S$ . The same overall state is restored about a Möbius strip that has that given crossing point, and is of that given length.

**VI.3.39** Given the above, then there is also always a one-to-one mapping between the universal covering space's deck transformations,  $\eta$ , and the base's fundamental group,  $\pi(B)$ .

**VI.3.40** Since deck transformations are fully homeomorphic with the base fundamental group, then every constant loop  $s \circ s^{-1}$  in the base has an initial point,  $\alpha_0$ , that is also some definite point,  $A$ , in the universal cover. And as the base loops towards its final point,  $F$ , then so also does the deck tend towards its own termination point. The base's loop, with its inexact differentials therefore matches the deck transformations, with their exact differentials.

**VI.3.41** But although our base has isomorphic structures that can follow homeomorphic paths, it also has very many more dissipative ones. We cannot yet isolate the isomorphic from the more generally homomorphic. Even though only isomorphic structures can preserve homeomorphism, any inexact differentials emerging from homomorphic—and therefore merely homotopically equivalent—structures, as say  $\delta F_h$ , are presently non-different from the  $\delta F_i$  inexact differentials that emerge from our isomorphic ones. The latter differ, however, by being equivalent to the cover's exact differentials. The  $\delta F_i$  therefore preserve path-connectedness, while the  $\delta F_h$  do not.

We must distinguish the isomorphic  $\phi(U(X))$  subpopulations in  $X$  that can produce the  $\delta F_i$  inexact differentials. These can form the  $V(Y)$  in  $Y$  that are also the  $\phi^{-1}(U(X))$ . Those  $V(Y)$  in their turn become the  $\phi^{-1}(U(Y))$  that can use some complementary  $\delta F_i$  to produce a  $V(X)$  that is once again a  $\phi(U(X))$ . The  $U(X)$ ,  $V(X)$ ,  $U(Y)$  and  $V(Y)$  subpopulations and their inexact differentials must therefore share an identity so that any  $\phi(U(X))$  can beget a further such set that can in its turn preserve that same  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification space where  $B = B_{XY} \cup B_{YX}$ , and where  $B_{XY} \cap B_{YX}$  is non-empty.

**VI.3.42** The heart of the replication enshrined in our  $\pi \equiv [(1 \times 1^{\delta=1} \rightarrow 1)^1 \Leftrightarrow (1 \div 1^{\delta=1} \rightarrow 1)^1]$  equilibrium Hooke cell and its Whitney umbrella is precisely this equivalence between its exact and

its inexact differentials. We must state the relevant inexact  $\delta F$  increment in terms of some exact one. This requires an identity operation over both the exact and the inexact.

**VI.3.43** At its most simple, the integral calculus tells us the magnitudes of any changes; while the differential calculus tells us their rates. Euler understood clearly that an identity operation leaves things unchanged, so that  $x + 0 = x$ ,  $y \times 1 = y$ ,  $z - w + w = z$ , and  $p \times 1/q \times q = p$ . He realized that an integral exists that is its own derivative, so that the curve  $e^x$  has the rate of change  $x$ . The identity operation leaves things unchanged for if we infinitesimally increment, or decrement,  $e^x$ , we get  $e^x$ .

We can now represent our  $\delta F$  inexact differential as the difference between two arbitrary functions  $G(x, y)$  and  $H(x, y)$  (Fitzpatrick, 2006b; Saad, 2007). If they are  $G(x, y)dx + H(x, y)dy$ , then their difference, as an inexact differential, lies in their two partial differentials, for  $\partial G/\partial y \neq \partial H/\partial x$ .

There must, however, exist a solution, at some point, such that  $\delta F = Gdx + Hdy = 0$ . If we divide by  $Hdx$ , we can express  $dy/dx$  in terms of  $G$  and  $H$ . This gives  $dy/dx = -G/H = c$ .

We now have an entire family of curves, in the  $xy$  plane, with the same  $c$ . We can express that family as  $\Gamma(x, y) = c$ . We thus have the exact differential  $d\Gamma = (\partial\Gamma/\partial x) dx + (\partial\Gamma/\partial y) dy = 0$ .

If we now divide  $d\Gamma$  by  $dx$ , we will have a value for  $dy/dx$ . We get  $d\Gamma = (\partial\Gamma/\partial x) + (\partial\Gamma/\partial y) dy/dx = 0$ . But we have already determined that  $dy/dx$  is  $-G/H$ . We therefore have  $d\Gamma = (\partial\Gamma/\partial x) - (\partial\Gamma/\partial y) G/H = 0$ . Our original two inexact partial differentials now hold the exact  $\Gamma$  in common, so that  $H(\partial\Gamma/\partial x) = G(\partial\Gamma/\partial y)$ . We can finally make our two partial differentials the independent variables in some further function,  $\sigma(x, y)$ , so that  $(\partial\Gamma/\partial x) = \sigma(x, y)G$  and  $(\partial\Gamma/\partial y) = \sigma(x, y)H$ . We now have the exact expressions  $G = 1/\sigma(\partial\Gamma/\partial x)$  and  $H = 1/\sigma(\partial\Gamma/\partial y)$ . We can therefore resolve any inexact differential using an “Euler multiplier” or “integrating factor”, based on  $e$ , and so that  $f_1(x) = f_2'(x) = 1/f_1'(f_2(x))$ .

**VI.3.44** And we need an exact differential. Thanks to the German physicist Hermann Ludwig Ferdinand von Helmholtz, every energy transaction has one. In his 1847 memoir *On the Conservation of Force* he recognized the many different forms of energy systems can contain. He generalized them all—including the thermal—as internal energy,  $U$ . Each system can thus contain many different kinds of energy, such as chemical, electrical, electromagnetic, etc. Everything, however, has thermal energy. The exchange interactions that internal energy can undertake are the thermal interactions,  $\delta Q$ , usually called heat, that contribute to the amount of internal energy,  $U$ , any substance or system has. Heat is the tendency for the molecules to move, and so to interact, with all other forms of energy. Its manifestation of heat,  $\delta Q$ , is simply the tendency to interact, thermally. But its entirely internal changes are the infinitesimal change,  $dU$ . So each system can potentially match its exact internal changes in state to any inexact changes it induces externally. This will equate  $dU$  and  $\delta Q$  through some Euler multiplier.

**VI.3.45** Helmholtz also pointed out that all matter participates in two critically different kinds of interactions. These are (A) their “required states”; and (B) their “allowed states”.

**VI.3.46** The German physicist Rudolf Clausius next allied Helmholtz’s observations to Euler’s exact/inexact discovery. He therefore shows us a method.

**VI.3.47** Clausius simply set the inexact differential of one function equal to the exact integral of another, calling that second equalizing function entropy. It is an Euler multiplier. It is an identity operator. It makes all cycles the same, for they effectively undertake the same identity operation.

**VI.3.48** Systems demonstrate their entropy similarities via their temperatures,  $T$ . Their similarity in temperature occurs independently of their sizes and their energy stocks.

**VI.3.49** Entropy,  $S$ , has all the characteristics of a substance. It is quantitative. It changes all states by admixing with all substances.

Since entropy is substance-like, it flows across boundaries. It is distributed throughout all matter. It flows in and out of all substances and systems seeking to equalize them all in terms of their interactions with the surroundings, at a given rate, and for a given amount.

**VI.3.50** Thanks to Clausius, any two systems working between the same two end points have identity operations over topological—and measurable—Eulerian cycles. Large systems can undertake a greater number of entropy changes, over their larger sizes, while still being identical to smaller ones. They simply go through a larger set of changes for they have greater rates and amounts in entropy. But any two cycles moving between the same two end points have exactly the same net interactions with the surroundings. They each preserve an identity.

**VI.3.51** The second law of thermodynamics now establishes the general behaviour of all matter by distinguishing between Helmholtz’s allowed and required states. The number of microfluctuations allowed to a system may be considerable, but the Euler–Clausius identity tells us that each system jettisons its excess allowed states at a rate that depends upon its own size. That is its entropy.

The cosmos procures entropy from systems by putting them through thermal energy transactions. Those force the system to relinquish at least a portion of its thermal energy externally, as heat,  $\delta Q$ , through some internal and infinitesimal change in state,  $dU$ .

**VI.3.52** By the second law of thermodynamics, every system transforms inexorably towards its required set of states. Those transformations are its interactions with the surroundings. They are

governed by the thermal energy it can establish, due to its temperature,  $T$ . Those required rates and transactions are its “stable equilibrium state”.

**VI.3.53** There is also a vital difference between the “work interactions” and the “nonwork interactions” involved in establishing a set of required states as a stable equilibrium one. Work interactions can achieve measurable mechanical effects,  $\delta W$ , in the surroundings. Nonwork interactions,  $\delta Q$ , cannot. But both are inexact differentials. They are both “path functions”.

**VI.3.54** There is therefore a difference between allowed and required states, and between work and nonwork interactions ... and so between allowed and required paths and interactions. Many transfers of thermal energy,  $\delta Q$ , can produce changes in state,  $dU$ , at some one given temperature,  $T$ . But many transfers of thermal energy,  $\delta Q$ , can also involve changes in temperature,  $dT$ . However, whether they do or do not produce work,  $\delta W$ ; and whether they do or do not involve changes in temperature,  $dT$ ; all transformations of allowed sets to produce the required ones of the stable equilibrium state involve changes in heat,  $\delta Q$ .

**VI.3.55** Temperature, entropy, volume, and pressure are examples of attributes that describe a system’s current state. They can be assessed both before and after any interaction, whether work or nonwork. Their transformations reflect any internal changes in state between some initial state,  $S_{-1}$ , and whatever may be the final state,  $S_1$ . They are exact differentials. And since they reflect those changes in state, then they are “state functions”.

**VI.3.56** Work and heat, as path functions, provide a contrast to state functions. Path functions describe the effects a system has in the surroundings, and as it transitions between its states, and so via its state functions,  $S_{-1}$  and  $S_1$ .

The transitions a path effects as  $\delta W$  and  $\delta Q$  can only be observed when they exit systems; cross boundaries; and enter the surroundings. They are the path effects of the state transformations.

**VI.3.57** But since the path functions of work and heat are inexact differentials, then they are each also partial differentials. We can therefore relate them to our state functions and our exact differentials using our Euler multiplier.

**VI.3.58** More generally: if the numbers of constraints,  $\beta$ , placed about any energy stock, in some system, hold constant; if its amount of substance also holds constant at  $N$  moles; if its internal energy is  $U$ ; and if its entropy is  $S$ ; then its change in entropy, as its energy changes, in its transition away from its allowed sets and towards its required ones is the partial differential  $(\partial S \partial U)_{N,\beta}$  (Encyclopaedia Britannica 2002). This is its “escaping tendency”.

**VI.3.59** Since every system has such an escaping tendency, the second law of thermodynamics uses it to establish their behaviour. All material systems again distinguish between their required and their allowed sets via their above escaping tendency.

**VI.3.60** The removal of constraints from around any allowed set always increases the number of its accessible states.

**VI.3.61** The exploring of those acquired sets, via the escaping tendency, then increases the entropy.

**VI.3.62** And when the system explores any extra and recently acquired allowed states, they in their turn escape via the escaping tendency as either only heat,  $\delta Q = dU$ ; or else some of the heat also diverts into the doing of some work,  $\delta Q = dU + \delta W$ . But whether as more heat and less work, or as more work and less heat, all transformations the system undertakes reflect the same two end points. Any system may freely pursue any combination of inexact paths, but their sum between those same two end states is always the same exact differential,  $dU$ . This is the first law of thermodynamics.

**VI.3.63** If, now, some progenitor domain  $X$  contains some Subpopulation  $U(X)$  with a greater escaping tendency relative to some Subpopulation  $V(Y)$  located in some progeny codomain  $Y$ , then even though both have an escaping tendency, energy will leave  $U(X)$  and transfer over to  $V(Y)$ . The excess states in  $U(X)$  transfer over to the colder, or smaller, or more more tightly configured  $V(Y)$ . The molecules in  $U(X)$  transform more extensively, forcing  $V(Y)$  to alter its states and its molecular distributions.

**VI.3.64** And ... a lower escaping tendency is immediately a greater “capturing tendency”.

**VI.3.65** Subpopulation  $V(Y)$  has a greater capturing tendency relative to Subpopulation  $U(X)$ .

**VI.3.66** Subpopulation  $U(X)$  is now changing in state. It is moving closer to the states exhibited by Subpopulation  $V(Y)$ . But  $V(Y)$  is also changing in its state. It is transforming closer to  $U(X)$ . They are both moving closer to a shared mean  $S'$  maintained between them over time.

**VI.3.67** All populations and systems with a greater escaping tendency now have a one-sided, and irreversible, effect upon all systems with a lower and escaping one. So if  $U(X)$  is larger, and/or located at  $(\tau't' + x)$ , then it changes in its state to become smaller and/or to be located at  $(\tau't' - x)$ . And if  $V(Y)$  is instead larger, and/or located at  $(\tau't' + y)$ , then  $U(X)$  changes in state to become larger and/or to be located  $(\tau't' - y)$  while  $V(Y)$  becomes smaller. They are as inverses tending to the same  $S'$  at  $\tau't'$ .

**VI.3.68** When the base,  $B$ , lifts and injects its disjoint and open sets into the universal covering space,  $C$ , as the  $\xi^{-1}U(X)$  fibre, then the one-to-one mapping between its fundamental group,  $\pi(B)$ , and the deck transformations,  $\eta$ , projects them straight back as  $\xi$ , and so surjectively onto  $U(X)$ . And since all the final points,  $F$ , that the base injects into the cover are homeomorphic with that cover's own terminal point,  $0$ , then no matter what transactions the base undertakes, the cover maintains its path-connectedness. Its deck transformations,  $\eta$ , are unaffected, being maintained through  $\xi \circ \xi^{-1} = \# = \tau$ .

**VI.3.69** Since the universal covering space,  $C$ , is also a mapping cylinder,  $M_\lambda$ , then the base transformations must be isomorphic. All lifted paths are invertible. They preserve the cover's homeomorphic paths ... meaning they also preserve its deformation retract,  $S'_{\text{cover}}$ .

**VI.3.70** By Meme 125, our deck transformations,  $\eta$ —which (a) preserve the cover's identity, and (b) are homeomorphic with the base's fundamental group transformations,  $\pi(B)$ —are path functions.

**VI.3.71** When  $X \leftrightarrow Y$  so the progenitor domain  $X$  transforms into the progeny codomain,  $Y$ , which transforms back, then a set of base homomorphic structures has occupied a set of isomorphic states and pursued a set of homeomorphic paths. By Meme 126 those isomorphic fundamental group transformations,  $\pi(B)$ , are state functions.

**VI.3.72** Both the base and the universal covering space now contain both the inexact  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$  and the exact  $\int dP = \int dM = \int dS = 0$  transformations. They are isomorphic in the former, and homeomorphic in the latter.

**VI.3.73** The base begins at  $\alpha_0$  and terminates in  $F$ . The cover begins at  $A$  and terminates in  $0$ .

**VI.3.74** The base and the cover must both begin in some initial state  $S_{-1}$  at  $\tau_{-1}t_{-1}$  and terminate in some final one  $S_1$  at  $\tau_1t_1$ .

**VI.3.75** Since the number of paths and states a population can explore before its identification space is disconnected is limited, then the  $\eta$  deck transformations have  $A \rightarrow 0$ .

**VI.3.76** But a population's initial state  $S_{-1}$  at  $\alpha_0$  in its base must also be inherited from its predecessors' as their final state,  $F$ . Its own final state,  $S_1$ , after completion of all its upcoming transformations, will have the measure,  $M$ . But its final and measured state  $M$  promptly becomes the

initial state for its own progeny as their inherited  $F$ . And since the base's isomorphisms match the cover's homeomorphisms, then we have both  $A \rightarrow 0$  in the cover and  $F \rightarrow M$  in the base.

**VI.3.77** Since we have an isomorphism–homeomorphism coupling, then when the cover's homeomorphic and surjective projection  $\xi$  arrives as an onto over the base's  $U(X)$ , then the base's real projective plane forms the disjoint, open, and identified  $\xi^{-1}U(X)$  fibre that sends isomorphically and injectively back to the cover. We therefore have a set of mutual progenitor domain and progeny codomain transformations as  $\xi U(X) \circ \xi^{-1}U(X) = S_{\text{base}}^{\circ}$ .

**VI.3.78** The points the base inject into the cover identify with the cover's original projection to create the cover's deformation retract as a set of transformations in the surroundings of  $\xi \circ \xi^{-1} = S_{\text{cover}}^{\circ}$ .

**VI.3.79** If some given group of entities is proposed as a species, then no matter how diverse those entities might be, they must be both isomorphic in the base and homeomorphic in the cover. They must construct both of our identities, being  $\xi U(X) \circ \xi^{-1}U(X) = S_{\text{base}}^{\circ}$ , and  $\xi \circ \xi^{-1} = S_{\text{cover}}^{\circ}$ . But these are both the central white line and axis upon the helicoid in Figure 9 ... and a Möbius strip.

**VI.3.80** By Law 1, at least some entities in every viable population must move to the right of their  $\tau_{\text{mm}}$  glome. But since the entities lie upon a real projective plane and are both isomorphic and homeomorphic, then they must move to the same glome's left when lifted to the universal covering space. And since those are identified points, then they define its equator.

**VI.3.81** The same holds for all four  $S_3$  glomes. They are the  $(\tau_t, \tau_n, \tau_m, \tau_p) V_4$  gongyl's surfaces.

**VI.3.82** Again by Meme 125 we can identify all species through their Chomsky production rule of  $[\Sigma = \{A, C, G, T\}, S = \{n, \bar{m}, \bar{p}\}, \delta, \alpha_0, F]$ . It incorporates  $\delta$ .

**VI.3.83** By Meme 126, we further identify the Chomsky production rule  $\delta$  with the deck transformations,  $\eta$ , so that  $\delta \equiv \eta$ . We therefore have  $\delta = \eta = \xi \circ \xi^{-1} = S_{\text{cover}}^{\circ}$ .

**VI.3.84** By Meme 127, the Chomsky Cartesian product  $\Sigma \times S$  must then be the  $\pm dA$  that forms the Whitney umbrella loops. That same product is the  $X\sim, Y\sim$  and  $C/\eta$  identification space.

**VI.3.85** The Chomsky production rule,  $\delta$ , that now states the deck transformations,  $\eta$ , establishes the biological language of biovolumes  $V_{1,2,3,4}$  and biosurfaces  $S_{0,1,2,3}$ . And since these are configurations

of nucleotide codons, then by Meme 127 their molecules and photons state all capturing and escaping tendencies.

**VI.3.86** The deck transformations,  $\eta$ , can now push their capturing tendencies down into the base as both (a) a surjective  $\xi$  projection, and (b) a set of semantic  $V_{1,2,3,4}$  biovolumes. But since those capturing tendencies are simultaneously step-downs, then they are also the presenting  $S_{0,1,2,3}$  biosurfaces. And by Meme 111, then when they are pushed in the directions  $\tau_t$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ , they take the absolute clock times  $T$ ,  $T_N$ ,  $T_M$  and  $T_P$  to cover those respective circulation distances.

**VI.3.87** The base can similarly lift its own capturing tendencies up into the universal covering space as both (a) an injective  $\xi^{-1}$  fibre, and (b) a set of syntactic  $S_{0,1,2,3}$  biosurfaces. They then act as traces pushed through hyperplanes to reconstruct the concentric  $n$ -spheres that are the biovolumes  $V_{1,2,3,4}$ .

**VI.3.88** The biological cycle is now a series of step-ups and step-downs between surfaces and volumes, and between base and universal covering space. As varied and distinct as they might be in each direction, when all four of the base's inexact  $(\tau_n, \tau_m, \tau_p)_T$ ,  $(\tau_t, \tau_m, \tau_p)_N$ ,  $(\tau_t, \tau_n, \tau_p)_M$ , and  $(\tau_t, \tau_n, \tau_m)_P$  differentials are summed over all four directions, they are the cover's exact  $(\tau_t, \tau_n, \tau_m, \tau_p)$  differential.

**VI.3.89** Each of the four inexact differentials is a combination of divergences and curls:

- The  $(\tau_n, \tau_m, \tau_p)_T$  is the numeracy glome at top centre in Figure 40, varying all of  $n$ ,  $m$ , and  $p$  between the minimum and maximum for the generation, with the  $T$  subscript meaning the temporal divergence holds constant so that the number of biological processing requests made per unit time is always  $dt = Td\tau$ .
- The  $(\tau_t, \tau_m, \tau_p)_N$  is the large glome that varies the biological processing requests, along with entity masses and energies over the generation, but with the divergence in numbers—which is the numeracy,  $Q$ —now holding constant.
- The  $(\tau_t, \tau_n, \tau_p)_M$  is the small glome at left that varies processing, population numbers, and energy density while the divergence in the population's chemical components flux,  $M$ , holds constant, and quite irrespective of whatever population numbers are used to maintain them.
- And  $(\tau_t, \tau_n, \tau_m)_P$  is the small glome at top right that varies the processing, the population numbers, and the chemical components flux per each entity, with the divergence in the energy—and therefore the work rate—now holding constant.

**VI.3.90** Each inexact differential also declares some value for entropy. The curl is both (a) a two-, and (b) a three-dimensional expression as work and heat in the surroundings. And since each

divergence is a rate of change of some area, as  $\pm dA$ , then isomorphism demands that any change in any divergence produces a curl; and that any change in any curl similarly produces a change in some divergence. The various values in  $n$ ,  $m$  and  $p$ , at the different moments  $t$  about a circulation are linked via Figure 19c's braid-3 of  $dS' = dn' + d\bar{m}' + d\bar{p}'$ . The net changes in divergences and curls therefore incorporate all possible rates of change. They will always sum, across all four dimensions, to the exact differentials up in the cover.

**VI.3.91** The changes in state that the inexact differentials impose can now distribute themselves freely over all possible paths in the base ... but they will always sum together to the same value up in the cover.

**VI.3.92** The biological cycle is now a set of loops and inexact differentials in the base,  $B$ , and a set of matching recursive functions and exact differentials in the universal covering space,  $C$ .

**VI.3.93** The biological cycle is also a set of surfaces and volumes as syntaxes and semantics. The  $S_{0,1,2,3}$  syntaxes and the  $V_{1,2,3,4}$  semantics are matching and identified sets in both the base,  $B$ , and the universal covering space,  $C$ . The former are injective, the latter surjective. They are, furthermore, a combination of the required and the allowed sets maintained as a set of connected paths against the surroundings and as  $B = B_{XY} \cup B_{\bar{X}\bar{Y}}$  and  $B_{XY} \cap B_{\bar{X}\bar{Y}}$ . And since every volume has a surface, while every surface bounds some volume, then their biological language is the mapping cylinder of their joint deformation retracts, being  $S_{\text{base}}^{\circ} \circ S_{\text{cover}}^{\circ} = S^{\circ}$ .

**VI.3.94** We now have, by Meme 128, the balance between the escaping and the capturing tendencies. That balance is a required set of  $S' = (n', \bar{m}', \bar{p}')$  as their mean, thereby creating the fibrations,  $\theta$ , and cofibrations,  $\rho$ , that lift into the surroundings as the biological-ecological processes,  $\lambda$ . They are the  $\gamma$  and  $\psi$  interactions that are the plessist and plessemorph metabolism and physiology of the observed biological entities. This  $S'$  is therefore the entities plus their ecological niche as the mapping cylinder,  $M_{\lambda}$ .

**VI.3.95** By Memes 115 to 118, the universal covering space's  $A \rightarrow 0$  semantics and the base's  $F \rightarrow M$  syntactics produce the isomorphic nonpollent, unipollent, pluripollent and totipollent structures via the joint homeomorphic surjective  $\xi$  projections, and the isomorphic injective  $\xi^{-1}$  fibre lifts ... which are also the mapping cylinder  $\theta$  fibrations and  $\rho$  cofibrations.

**VI.3.96** Since every  $\xi$  projection down from the cover involves Ingredients 3 and 4 in photons and molecules as a set of codons, then it is a gain in paths and in allowed sets within the base. It is therefore an equivalent transfer of entropy to the base. The entities now contain a capturing tendency.

Although the sum of the entropies as transferred between cover, base, and surroundings can never decrease, the projection from the cover to the base is promptly a net decline in the cover's escaping tendency. It is a loss in its entropy, its paths, and in its allowed sets. And since the cover is the ecological niche, then it is a transfer to the entities.

**VI.3.97** By the same token, every lift from the base into the cover is a gain in paths and in allowed sets within the cover, which is within the surroundings; but it is a loss in those same paths and allowed sets from the base ... which is the entities as a set of progenitors and their progeny.

**VI.3.98** The losses and the gains in entropy by the entities and the surroundings, and in their escaping and capturing tendencies are again equivalent.

**VI.3.99** Since these transfers between base and universal covering space are equivalent losses and gains in DNA and proteins, then every population is defined by the spherindrical push that is its Mobius strip contact point, its rotachoron equator, and so the  $\Sigma \times S$  Chomsky Cartesian product and identification spaces all across its specified generation length,  $T$ . These are all created by a specified and distinguishing set of DNA codons and proteins carried across the circulation. It is every population's required set of  $S' = (n', \bar{m}', \bar{p}')$ .

**VI.3.100** All biological entities may now have a required set, as  $S'$ , but they must also have an allowed set of transactions. This is the Whitney umbrella's loops and the helicoid steps and levels. It is the  $\pm dS'$  range over both (a) some circulation distance, and (b) some absolute time. These together are  $\pm d\tau - dt$  about  $\tau' - t'$ .

That range is an expression of both (a) the stases of the first, second, and third kinds as the inexact differentials  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$ ; and (b) the three constraints of propagation, size, and equivalence as the exact differentials  $\int dP = \int dM = \int dS = 0$ . The population explores them as a set of isomorphic entities with a shared set of minima and maxima. Those are expressed in their  $\pm\lambda$ ,  $\pm d\lambda$ , and  $\pm d^2\lambda$  activities in the surroundings, using the magnitudes and rates of change expressed through  $d\tau/dt$ ,  $d^2\tau/dt^2$ , and  $d^3\tau/dt^3$ .

The population's Chomsky production rule of  $[\Sigma = \{A, C, G, T\}, S = \{n, \bar{m}, \bar{p}\}, \delta, \alpha_0, F]$  states their complete set of states as the  $dS' = dn' + d\bar{m}' + d\bar{p}'$  language of syntax and semantics all around  $S'$ . The various biosurfaces that are its  $S_3$  glomes, that present to the surroundings, move in their various directions as the spherinders and inexact differentials of  $(\tau_i, \tau_n, \tau_m)_p$ ,  $(\tau_i, \tau_n, \tau_p)_M$ ,  $(\tau_i, \tau_m, \tau_p)_N$ , and  $(\tau_n, \tau_m, \tau_p)_T$ . This produces their unique and exact  $(\tau_i, \tau_n, \tau_m, \tau_p)$  biological structures and behaviours as their diversity in states and paths around their  $S'$  centre as their deformation retract. They move between their base,  $B$ , and their universal covering space,  $C$ , all across  $T$ . This is also their set of biological-ecological interactions,  $\lambda$ , with their mapping cylinder,  $M_\lambda$ , as a set of progenitors,  $X$ , and their progeny,  $Y$ , over both  $\tau$  and  $T$ .

**VI.3.101** Since everything occurring up in the cover—and so in the surroundings—about any circulation length,  $\tau$ , for time  $T$  also occurs down in the base—and so within some specified entities—and conversely, then we now have the complete cycle of proteins and organisms in any population.

**VI.3.102** Biological populations and entities are now similar when their boundary activities as (i) loops, (ii) syntaxes, (iii) semantics, and (iv) recursive functions are also similar. They express themselves in both the surroundings and a set of entities. They are isomorphic transformations along homeomorphic and identified paths. The range between minimum and maximum is the complete set of biological and ecological transactions,  $\lambda$ , across an entire generation, and is:

---

**Law 3: The law of diversity**

$$A \rightarrow 0; F \rightarrow M$$

The sum of all the paths that satisfy Law 2 constitutes the allowed set for the entity and its equivalents; while that which permits them to satisfy Law 1 constitutes the required set.

---

**VI.3.103** The law of diversity states the overall set of connected paths that any  $X/\sim$ ,  $Y/\sim$ , and  $C/\eta$  identification space must maintain. But the escaping tendency eventually forces all individual entities in any  $X \times Y$  topology onto paths with no capturing tendency. Those are disconnected paths whose intersection,  $B_{XY} \cap B_{YX}$ , is empty, falling outside the  $B = B_{XY} \cup B_{YX}$  basis that links the progenitor domain  $X$  to the progeny codomain  $Y$ . The plessists dissipate via the  $\tau_{nmp}$  glome, and are no longer isomorphic.

**VI.3.104** If a population or species remains viable, then there has been a successful transmission of the necessary  $(\partial S \partial U)_{N,B}$  capturing tendency—and so hereditary information—between a set of progenitors and their progeny. That propagation of a discrete set of suitably configured chemical components from one material body to another produces, and requires, both energy and entropy. It services the capturing tendency that is constantly needed to offset the escaping tendency for the dissipation mandated by the surroundings as the second law of thermodynamics. This viability requires both (a) a syntax, and (b) a semantics; as also (c) a surface, and (d) a volume.

**VI.3.105** If a population again remains viable, then some subset of of entities,  $n_{initial}$ , uses its capturing tendency to increase its internal energy by capturing a sufficient quantity of resources and energy from the surroundings. It donates at least a portion of those energies and resources, acting as progenitors, to some second subset, of size  $n_{final}$ . That second subset must then exercise a similar and successive capturing tendency. This requires viable homeomorphic paths and isomorphic states.

**VI.3.106** All groups and subgroups in any viable population must be homomorphic and homotopically equivalent, globally, or they are not biological. But since paths must always dissipate, then specified subsets and subgroups must be both isomorphic and homeomorphic, but can only be so locally. They establish the needed deck transformations up in the cover, and the  $\pi(B)$  fundamental groups in the base. The entities can then generate and regenerate each other using each others' capturing tendencies. The given population has then maintained its global net balance in its capturing tendency with respect to the surroundings, by always again by acting locally.

**VI.3.107** Every viable population that avoids extinction must maintain its global required set  $S' = (n', \bar{m}', \bar{p}')$ , constantly using a local capturing tendency,  $(\partial S \partial U)_{N, \beta}$ , over the generation time,  $T$ , and circulation distance,  $\tau$ . The latter's inexact sums are included in the exact former.

**VI.3.108** Since the Chomsky production production rule,  $\delta$ , is both the mapping cylinder,  $M_\lambda$ , and the universal covering space,  $C$ , then every population is also a matched set of syntax and semantics, and surfaces and volumes as progenitors and their progeny. Each  $S = \{n, \bar{m}, \bar{p}\}$  is an expression of all start symbols, terminal symbols, and non-terminal symbols.

**VI.3.109** Although the population must act globally to maintain a set of paths that are constantly homomorphic and homotopically equivalent, and so whose total capturing tendency over the entire circulation ensures a global isomorphism and a global homeomorphism ... it is again not locally required of all entities, at all their local points, that they all be isomorphic. Paths are permitted to be locally Euclidean, and/or locally hyperspherical—which then support trivial cycles—without being locally identified with any opposite points. They need not individually and locally project to cross any real projective plane, although the plane exists, globally. It is, therefore, globally required that work be done over and above any required set to produce the increases in energy and resources that allow progeny to reproduce by increasing the net number of available paths and allowed sets ... but this same need not hold at every local point.

**VI.3.110** Not all fibre bundles must be locally trivial. Some are non-trivial.

**VI.3.111** The three constraints of constant propagation, size, and equivalence,  $\int dP = \int dM = \int dS = 0$ , first apply, and then remove, allowed sets. The stases of the first, second, and third kinds state are then the ranges that transfer those allowed sets between base,  $B$ , and universal covering space,  $C$ .

**VI.3.112** Since the three stases are inexact, then not all entities that follow a biological path need follow a replicative one.

**VI.3.113** Our recursive functions contain Möbius strip identifications, and thus produce the recursions that sustain a population. As in Figure 39, the biology globe is the set of activities on the increase side of the  $\tau_{\text{imp}}$  glome equator, the replication globe being those on its decrease side. They transmit themselves across our four-dimensional rotachoron and our real projective plane. They use the four different sets of transformation rules to recurve as the injective and the non-injective, the surjective and the non-surjective. They create all biology and fertility spaces and groupings which are the Chomsky hierarchy of nonpollent, unipollent, pluripollent, and totipollent that link base and cover.

**VI.3.114** Just as the second law of thermodynamics requires that one—and only one—of the states allowed to a thermodynamic system be the stable equilibrium one; then so also is it required of any viable species that at the very least one—but allowably more than one—of the paths in its allowed set be such that  $B_{XY} \cap B_{YX}$  be non-empty. This allowed set path then possesses all needed properties for  $U(X)$ ,  $U(Y)$ ,  $V(X)$  and  $V(Y)$ , with  $U$  open in  $X$ , and  $V$  open in  $Y$ ; and  $U$  open in  $Y$ , and  $V$  open in  $X$ . We then have  $B = B_{XY} \cup B_{YX}$ .

And ... that allowed set path is the path of reproduction. It evidences a decrease in both mass and entropy, but maintains the needed global  $\pi = [(x \times 1^\delta \rightarrow y)^{T_i=1} \Leftrightarrow (y \div 1^\delta \rightarrow x)^{T_i=1}]$  bijection between an identified  $X$  and  $Y$ , inexactly over four dimensions, and so as to make the resulting  $S^{\text{base}}$  equivalent to an exact  $S^{\text{cover}}$ , thus maintaining the combined deformation retract  $S^{\text{base}}$  and required set  $(n', \bar{m}', \bar{p}')$ . That allowed set path uses the capturing tendencies in both the base,  $B$ , and the universal covering space,  $C$ , to offset any sacrifices each is forced to make via its escaping tendency. Since this requires a constant input from and interaction with the Chomsky production rule and deck transformations, then both  $A > 0$  and  $dA/dt > 0$  must always hold. And since this allowed set path exists in any viable population, it is the path that passes to the  $\tau_{\text{imm}}$  glome's left so that the population's mass always remains greater than zero, but decreases overall, giving  $\bar{m} > 0$  and  $d\bar{m}/dt \leq 0$ .

**VI.3.115** This allowed set path maintains all biology and ecology. It is the one that crosses the real projective plane and creates all identified points. It maintains the base for all fibres and all activities ranging between a minimum and a maximum. It is a property of the entire population, and of the whole circulation of the generations. It creates a biological cycle when taken conjointly and globally. But it is not the property of either any one entity, nor of any one point, taken severally and locally. We therefore, and finally, have:

---

**Law 4: The law of reproduction**

$$[(d\bar{m}/dt \leq 0) \wedge (\bar{m} > 0)] \Rightarrow [(dn/dt \geq 0) \wedge (dA/dt > 0)]$$

In the allowed set is at least one path such that mass is surrendered, and such that a further entity possessing the required set, and satisfying these four laws, results.

---

# **Part VII**

## **The survival of the plessists**

**VII.1.1** We began our journey by highlighting biology and ecology's abject failure to provide adequate definitions for their core concepts. We shall conclude that journey by proving that a population free from Darwinian fitness, competition, and evolution is simply impossible.

**VII.1.2** Nothing makes the parlous state of affairs in the biological sciences clearer than the definition for natural selection—the acknowledged centrepiece of all theoretical and experimental biology—offered by the *Collins Dictionary of Biology*:

**natural selection**, *n.* the mechanism, proposed by Charles Darwin, by which gradual evolutionary change takes place. Organisms which are better adapted to the environment in which they live produce more viable young, so increasing their proportion in the population and thus being 'selected'. Such a mechanism depends on the variability of individuals within the population. Such variability arises through mutation, the beneficial mutants being preserved by natural selection (Hale & Margham, 1988).

This neatly exemplifies the vagueness, the circularity, and the lack of rigour that bedevils these subjects. Anyone wanting further clarity about natural selection—the *sine qua non* of all modern biology—is referred straight back to the same head word!

**VII.1.3** Our own work has already provided a complete contrast to the above-described state of affairs. We have already framed a comprehensive collection of laws, maxims, and constraints, and provided clarity and some clear definitions for core concepts. We did so by dint of turning to topology and observing that reproduction is homeomorphic with the two embedded processes of (a) sets, and (b) self-replications which were first demonstrated, in the coordinated ways we require, by the German mathematicians Karl Weierstrass and Georg Cantor. They allow us to unambiguously quantify natural selection.

**VII.1.4** We take  $\tau$  as the given generation length, and  $N$  as the mean number across whatever given interval. We can then quantify every population's changes in its numbers as its numeracy,  $Q$ , where both  $Q = dN/dt$  and  $N = \int Q dt$  for absolute clock times; and  $N = \int Q d\tau$  and  $Q = dN/d\tau$  all across the circulation. We can also relate all changes to each other as a set of inexact differentials that match the exact differential  $\int dS = \int dN = 0$ . Those inexact differentials in numeracy are:

- $\nabla Q = (n_{\text{final}} - n_{\text{initial}})N$  as the gradient;
- $\nabla \cdot Q = \bar{m}_{\text{final}} - (\bar{m}_{\text{initial}} n_{\text{initial}} / n_{\text{final}})$  as the divergence;
- $\nabla \times Q = \bar{p}_{\text{final}} \bar{m}_{\text{initial}} (n_{\text{final}} - n_{\text{initial}})$  as the curl.

Natural selection is then the combination of those exact and inexact changes in numeracy over each of (i) the absolute time,  $T$ ; (ii) the circulation length,  $\tau$ ; and (iii) the transition between minimum and maximum values.

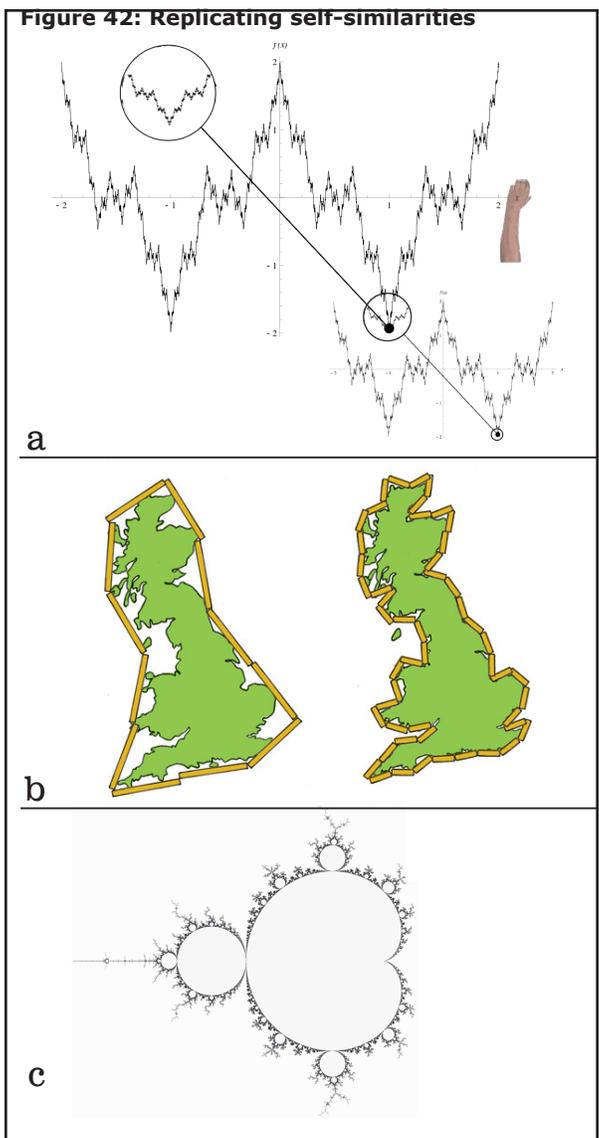
**VII.2.1** The first ingredient we need to prove that a population free from Darwinian fitness, competition, and evolution is impossible is the first ever “self-replicating curve”, seen in Figure 42a. Created by Weierstrass, it serves as a successful and explicit mathematical model for biological replications because it is (A) “everywhere smooth”, and (B) “nowhere differentiable”. This simply means that it has a topology that has no holes anywhere, while its complexity, in the sense of its curvaceousness, also varies in regular and repetitive fashion.

**VII.2.2** We imagine catching hold of Weierstrass’ curve, and pushing or pulling it along its axis, and as shown in Figure 42a. Since it is everywhere smooth, then it is always continuous. It can keep projecting itself, all along its length, indefinitely and infinitely in its given directions—which is in our case both into the past and into the future. And since it is a repeating curve, then we can easily select a final moment  $t_1$ ; an initial moment  $t_{-1}$ ; and determine its rate of propagation across that interval, which is the distance it covers per unit time,  $d\tau/dt$ . But since the curve must cover some specified distance along its length, that actual distance is  $\int \tau dt$ , and is clearly subject to variation as the curve proceeds.

Since the curve is non-linear, then any population following it must undertake a set of accelerations both along that curve and between the moments  $t_{-1}$  and  $t_1$ . That change in the rates of propagation, at any given point, is  $d^2\tau/dt^2$ . The distance covered in undertaking all such changes, across the same interval—and which is also subject to variation—is  $\iint \tau dt dt$ .

And, finally, if the population is to cover both sides of Boy’s surface; and/or traverse both of the biology and replication globes; and/or return to the Möbius strip contact point; then it must undertake the relevant series of jerks, between  $t_{-1}$  and  $t_1$ , and as  $d^3\tau/dt^3$ . That total distance about both globes is  $\iiint \tau dt dt dt$ .

Every self-replicating curve—and therefore every viable population—will have these seven values at each specified moment  $t_0$  between  $t_{-1}$  and  $t_1$ . They use the standard rectilinear **ijk** axes of absolute measures and absolute time. We can place this initial set of seven absolute time-based values in a first set,  $P$ .



**VII.2.3** We can next measure the self-replicating curve's complexity. This is its amplitudinal rapidity in propagation. It reflects the amount of self-replication that passes by at each moment. We can do so through the nowhere differentiable aspect of Weierstrass' curve. Nowhere differentiable means that no matter how closely we approach the curve to determine its rate of change, we always find a complete and entire copy of the original. Weierstrass's entire curve can replicate itself between any two points and/or moments. This embedded self-replication also continues indefinitely. This change in what is replicated at each point and moment is a second rate of propagation that accompanies the first.

**VII.2.4** Working independently of Weierstrass, the English mathematician, physicist, meteorologist and psychologist Lewis Fry Richardson further developed these ideas on rates of replications and self-replications. Figure 42b's "Richardson effect" is the latter's observation, as applied to Great Britain's coast line, that the smaller we make our ruler, and so the finer our subdivisions become, then the greater is the number of bays and inlets we can measure around, and so the longer becomes the perimeter. This is a varying rate of propagation.

**VII.2.5** If all our perimeter points now form a first set  $A$ ; and if all the points constituting the area form a second set  $B$ ; then the one-dimensional measure in  $A$  tends to infinity, at some given and measurable rate, even as the two-dimensional measure in  $B$  remains invariant. But since, no matter what the scale, we recreate the entire area at some rate every time we go all about the perimeter, then the rate at which the replication occurs about the perimeter, and so the rate at which we bound and traverse an area, depends upon the rate at which we scale the perimeter.

**VII.2.6** When the Polish-born mathematician Benoit Mandelbrot was clearing out some of Richardson's old papers, he came across the Richardson coastline paradox. He developed and popularized the ideas behind these embedded self-replications (Hunt 1998). He produced his famous fractals.

A self-replicating fractal's "dimension",  $D$ , states the number of self-similar replicas we can find,  $N$ , as the scaling factor,  $\epsilon$ , changes. It is given by  $D = -\log N / \log \epsilon$ .

If we first take up a Euclidean straight line, then its fractal dimension means that no matter how often we scale and replicate it, it always remains equal to the space it resides in. If we decompose it into four segments, a magnification factor of  $\epsilon = 4$ , we get four line segments, all self-similar. If we magnify each of those by 4, we recover the original. So if, more generally, we decompose it  $N$  times over, we will find  $N$  self-similar copies that again restore the original. A Euclidean straight line segment therefore has the fractal dimension  $D = 1$ . This means that the curve's current rate of propagation is equivalent to that of a Euclidean line. It indicates the degree of complexity—or, alternatively, the number of events—involved in any given self-replication. These are in this case the

same. The number of points in any set may in principle be uncountable, but its fractal dimension will still tell us how self-similar it is as it replicates.

A square, in the Euclidean plane, behaves somewhat differently. If we use the same  $\varepsilon = 4$  magnification factor, we end up with a square that is  $1/4 \times 1/4 = 1/16$ th times the size. We will now need 16 self-similar squares to recover the original. So for any  $N$ , we will always have  $N^2$  self-similar pieces. The square therefore has the fractal dimension  $D = 2$ .

On this same basis, the fractal dimension of a cube is  $D = 3$ , and that of a tesseract (four-dimensional hypercube) is  $D = 4$ . Every four-dimensional object is now “bigger” than every three-dimensional one, which is in its turn bigger than any object in the plane, which is bigger than one on a line, with each having a successively smaller fractal dimension ... meaning that each self-replicates at an equivalently greater rate. So if we consider two or three manifolds or dimensions, and they all behave in Euclidean fashion, then they will deliver the appropriate fractal dimensions.

All self-similar one-dimensional objects are also curves in the plane. They therefore have a fractal dimension lying between 1 and 2. So if, for example, Great Britain’s coastline quadruples in length every time we use a ruler  $1/3$  the size, then we have  $\varepsilon = 3$  and  $N = 4$ , giving it a fractal dimension of  $D = -\log N / \log \varepsilon = 1.2619$ . The complexity of Britain’s coast line—the way in which it changes as we approach it ever more closely—therefore lies somewhere between that of a line and a plane.

Although no three-dimensional “Mandelbrot set” can be built in that there is no three-dimensional analogue for the field of complex numbers, the principle still holds for two and three dimensions. Just as a one-dimensional manifold, such as a coastline, exhibits its changes in complexity upon a plane, so do two dimensions exhibit theirs in a three-dimensional realm. The complexity or fractal dimension for any two-dimensional object we create by bringing two distinct dimensions together lies between 2 and 3. And, similarly, a three-dimensional object exhibits its complexities and self-replications with some value between 3 and 4.

Every self-replicating curve will replicate its curves, its shapes, and its complexities at some rate, over any interval, that in its turn depends upon its development at each specified point. But we can always express this self-replication rate in terms of the rate it maintains between its initial and its terminal values. If we express the average complexity across the curve as  $D'$ , then the value at each point is some rate that is a function of  $D'$  and is given by  $d = D/D'$ . Its various derivatives and integrals will be  $dd/dD'$  and  $\int d dD'$ ;  $d^2d/dD'^2$  and  $\iint d dD' dD'$ ; and  $d^3d/dD'^3$  and  $\iiint d dD' dD' dD'$ . These tell us the changes in complexity relative to each other, and as they influence each other in a cycle. The complexity transitions use a mean that repeats, and that also states each succeeding value in terms of a prior one, thus ultimately completing a circulation about that mean. These additional seven measures use Newton’s hyperspherical **IJK** axes. We can place them in a second set,  $Q$ .

**VII.2.7** Every self-replicating curve has both (a) a perimeter length,  $\tau$ ; and (b) a fractal dimension,  $D$ . These do not all develop in the same ways relative to each other, as the curve propagates in time,  $t$ . Since every population travels along its curve as if it is a one-manifold that is a Euclidean straight

line, then each will have a different rate of self-replication per unit of its length, due to its different shape and non-differentiable component. If we express the value at each point as  $s = D/\tau$ , then the rate is  $ds/d\tau$ . The amount replicated across any interval is always  $\int s d\tau$ . And since the greater is the complexity, then the greater must be the acceleration through those changes, then we also have  $d^2s/d\tau^2$  and  $\iint s d\tau d\tau$ ; and we have  $d^3s/d\tau^3$  and  $\iiint s d\tau d\tau d\tau$  to traverse the Möbius strip. This final set of seven measures links a curve's diversity in its complexity directly to its own length, and to its own amplitudes or changes on its own length, and uses the Frenet-Serrat frame's **TNB** axes. We can place them in a third set,  $R$ .

**VII.3.1** The next ingredient we need to prove that a population free from Darwinian fitness, competition, and evolution is impossible is the “paradox of the infinite series of square numbers”, shown in

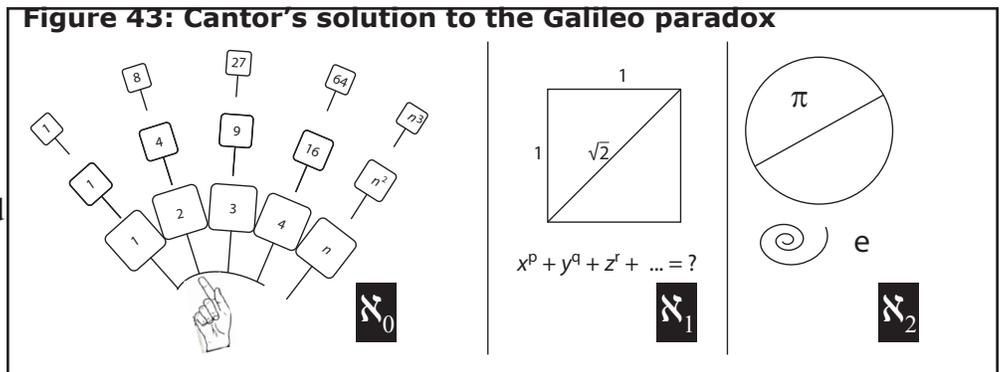


Figure 43. Although the paradox was known long before Galileo, since it received a particularly famous retelling in his epoch-making *Discourses and Mathematical Demonstrations Relating to Two New Sciences*, it is frequently named after him.

The Galileo paradox points out that while the ordinary counting numbers form the infinite series  $1, 2, 3, 4, \dots, n, \dots$ , their squares form the very different—but equally infinite—series  $1, 4, 9, 16, \dots, n^2, \dots$ . This gives the distinct impression, for the paradox’s first part, that the “density of the squares”, amongst the natural numbers, is considerably less than is the density of the ordinary natural numbers. This density effect is even more pronounced amongst the cubes, which go  $1, 8, 27, 64, \dots, n^3, \dots$ . The perceived gaps grow even more quickly.

**VII.3.2** Galileo also pointed out, for the paradox’s second part, that this initial impression must be false. We will never run out of numbers. Since we will never fail to find an  $n^2$  or an  $n^3$  to accompany any  $n$ , then the densities must be equal. So in spite of the initial impression, the squares and cubes must be equinumerous with the ordinary natural numbers. But ... these cannot both be true.

**VII.3.3** The German mathematician Georg Cantor resolved the Galileo paradox by pointing out that we can place all possible natural numbers in a single set. He denoted it  $\aleph_0$ . Since all squares, all cubes, and all possible rational numbers—such as 133/139ths—come from that same set, then they are all equipollent with the countably infinite natural numbers (Weisstein 2015a).

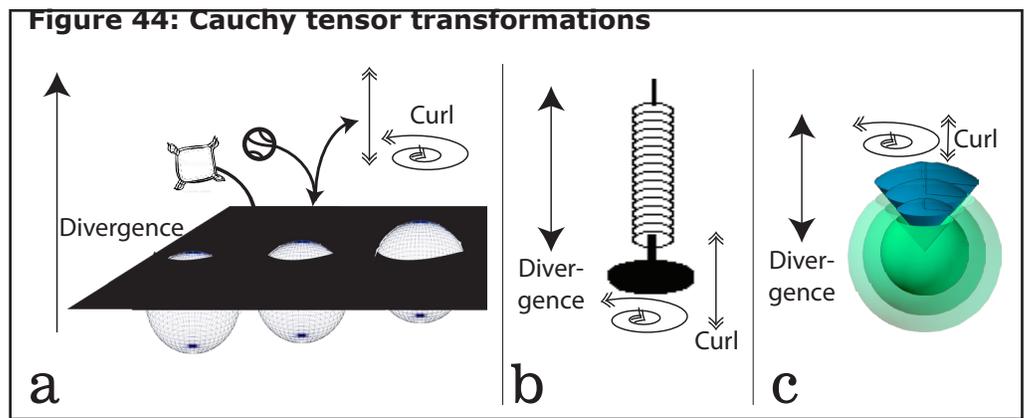
**VII.3.4** Cantor next pointed out that the  $\aleph_0$  set is deficient because no possible combination amongst them can produce the “irrational numbers” that we need to solve even the simplest of purely algebraic equations such as the  $a^2 + b^2 = c^2$  of the Pythagoras theorem and which tells us that the length of a square’s diagonal is  $\sqrt{2}$ . Since that  $\sqrt{2}$  is nowhere in  $\aleph_0$ , then we must create a second infinite set to solve all such algebraic equations. And since this new set can contain all the infinitely many numbers in the first set,  $\aleph_0$ , then that  $\aleph_0$  is injective into  $\aleph_1$ . But further since  $\aleph_1$  contains infinitely many more numbers than can be contained in  $\aleph_0$ , then  $\aleph_1$  is in its turn surjective over  $\aleph_0$ .

**VII.3.5** But that was not the end of Cantor's demonstrations. Neither  $\pi$  nor  $e$ , he pointed out, is the solution to any algebraic equation. There is in fact a whole host of numbers that are not algebraic for they are not the roots of non-zero polynomial equations with rational coefficients. There must, therefore, be a yet larger set of numbers containing those yet even infinitely many more "transcendental numbers". He designated that latest set  $\aleph_2$ .

**VII.3.6** Since both the previous  $\aleph_0$  and  $\aleph_1$  sets are smaller than this newest one, then they are both injective into this latest  $\aleph_2$ , which is in its turn surjective over both those  $\aleph_1$  irrationals and  $\aleph_0$  rationals.

**VII.3.7** We also notice very carefully that we can draw conclusions about the interactions between these various sets based on their relative sizes, and so on their injections, surjections, and possible bijections, and all without determining any specific numbers contained in each. The same goes for the fractal dimensions and their measures of replication and self-replication through the **ijk**, **IJK**, and **TNB** axes.

**VII.4.1** We need one further ingredient to complete our proof. The French mathematician Baron Augustin-Louis Cauchy showed how we can analyse the various situations we see in Figure 44,



which all involve various kinds of transformations.

Whether a ball bounces, a cushion merely falls, or we pass a three-dimensional  $(x, y, z)$  rotahedron in the  $z$ -direction through a two-dimensional  $(x, y)$  surface, we need to assess all possible shapes and transformations, and their rates of change, across all those various dimensions. We can do so using Table 1’s “Cauchy tensor”:

Table 1			
The Cauchy tensor			
	$x$ (length)	$y$ (breadth)	$z$ (height)
$x$ (length)	$xx$	$xy$	$xz$
$y$ (breadth)	$yx$	$yy$	$yz$
$z$ (height)	$zx$	$zy$	$zz$

If we push a rotahedron through the plane, in the  $z$  direction, then the  $zx$  term tells us how much of that  $z$  push has been deformed and flattened into  $x$  as the rotahedron has changed its shape, and has splurged out into that lateral dimension instead of proceeding vertically to the required degree. The  $zy$  similarly tells us how much it might have deformed into  $y$  with that same push.

However, it also works the other way. We can carefully measure a circle in the  $x$  and  $y$  dimensions as  $(x_1, y_1)$ , and  $(x_2, y_2)$ . We can then calculate a Cauchy tensor  $xz$  component to express the force the circle exerted, as an inexact differential, that was originally into the  $x$  direction, but that must have diverted into  $z$ . The same again goes for  $yz$ .

The spring in Figure 44b shows that we can indeed determine the overall forces, both exact and inexact, falling upon, and exerted by, any object and its materials. We simply analyse all its forces and effects in each selected direction.

The  $xx$ ,  $yy$ , and  $zz$  components located along the Cauchy tensor’s diagonals are the “normal pressures” that reveal an object’s most characteristic responses. They are each object’s attempt to hold its shape, whether it be a cushion, a spring, a rotahedron, a bouncing ball, or a self-replicating curve. All an object’s off-diagonal components are then its “shear stresses”. They summarize the overall distortions imposed by the surroundings, and/or that are caused by its material’s deformities.

We can just as easily construct a Cauchy tensor by putting a self-replicating curve’s length,  $\tau$ , fractal dimension,  $D$ , and dimension per unit length,  $s$ , as the heads of the rows and columns to create each component.

**VII.4.2** The normal forces in any Cauchy tensor are also our divergences. We can always determine them by determining the average transformation, and the average distances, in each given direction. The divergence is then always whatever constant rate of change occurs in alignment with whatever given direction, and to and over both time and space. Thus a self-replicating curve can have a divergence in its length; in its fractal dimension; and/or in its dimensionality per unit length. A zero divergence always means the amounts entering and leaving are the same.

The shear forces in any Cauchy tensor are then the curls. They are (a) the variations about whatever average creates the divergence; and/or (b) the transformations that any divergence causes in some other direction. These all apply just as well to the sphere in Figure 44c. Since time is one of our directions, then a curl can be any variation over time, such as a velocity, acceleration, or jerk, all of which are with respect to  $t$ ; or else a partial differential of the form  $\partial x \partial t$ . If divergences are constant then there is no curl; and if there is a curl then there must be a change in divergence somewhere.

**VII.4.3** We should also recollect that our biological entities—our plessists and our plessemorphs—follow all rules for sets. So any two sets of plessists  $X$  and  $Y$  can always be associated via their Cartesian product  $X \times Y$  which forms all possible duples  $(x, y)$  where  $x$  is in  $X$ , and  $y$  is in  $Y$ . And similarly,  $X, Y$ , and  $Z$  can form  $X \times Y \times Z = \{(x, y, z) \mid x \in X, y \in Y, z \in Z\}$ .

**VII.4.4** The three sets  $P, Q$  and  $R$  that we form from our self-replicating curves also follow Cartesian product rules. As in Table 2, we can therefore use their 21 elements to form a single component in a Cauchy tensor. Table 1's  $3 \times 3$  Cauchy tensor with its 9 components would therefore be constituted of  $21 \times 9 = 189$  such elements, each one contributing to the whole.

Each individual component in our self-replicating curve's Cauchy tensor has the structure:

Table 2								
The 21 elements in a single Cauchy tensor component								
		3rd derivative	2nd derivative	1st derivative		1st integral	2nd integral	3rd integral
← ijk row	absolute time, $T$	$\frac{d^3\tau}{dt^3}$	$\frac{d^2\tau}{dt^2}$	$\frac{d\tau}{dt}$	$\tau$	$\int \tau dt$	$\iint \tau dt dt$	$\iiint \tau dt dt dt$
↑ IJK column	min-max distribution	$\frac{d^3d}{dD^3}$	$\frac{d^2d}{dD^2}$	$\frac{dd}{dD}$	$d$	$\int d dD'$	$\iint d dD' dD'$	$\iiint d dD' dD' dD'$
■ TNB component	relative time, $\tau$	$\frac{d^3s}{d\tau^3}$	$\frac{d^2s}{d\tau^2}$	$\frac{ds}{d\tau}$	$s$	$\int s d\tau$	$\iint s d\tau d\tau$	$\iiint s d\tau d\tau d\tau$

Any observed value is a combination of: (i) the homotopic and homotopically equivalent  $\tau$ ; (ii) the homeomorphic replication inherent in each point in the circulation as  $d$ ; and (iii) the isomorphic state for that specified group of transformations—as can create a species—as  $s$ .

Both (a) the overall quantities, and (b) the rates of change in each of the three forms of the changes we discovered, as  $\tau, d$ , and  $s$ , are determined by their coordinated juxtapositions in their integrals and derivatives, and all over 0, 1, 2 and 3 dimensions. These and their fractal dimensions

then ensure that the entities remain neighbours all about the given circulation. If they are biological entities then they define the same base,  $B$ , between the progenitor domain as preimage,  $X$ , and progeny codomain as image,  $Y$ , by sharing all rates, quantities, and distances That base is formed from:

$$B_{XY} = \{U(X) \times V(Y) \mid U \text{ open in } X, V \text{ open in } Y\},$$

and

$$B_{YX} = \{U(Y) \times V(X) \mid U \text{ open in } Y, V \text{ open in } X\},$$

and so that  $B = B_{XY} \cup B_{YX}$ , with the intersection of  $B_{XY} \cap B_{YX}$  being constantly nonempty.

**VII.4.5** Our base is now a mixture of three different kinds of self-replications. We can measure them through their fractal components, using the three different kinds of axes we have discovered:

- **ijk**. The top row of 21 elements making up each distinct tensor component ensures that its interactions with the universal covering space,  $C$ , and mapping cylinder,  $M_\lambda$ , that are the surroundings are constantly homomorphic and homotopically equivalent. This top row of elements in each component contributes to the set of absolute and real time rectilinear **ijk** axes in ordinary space and time. Its transformations are exerted in, and are presented to, the surroundings. It is the surface forces,  $S$ . They emerge as a form of momentum. Each top row thus helps determine the temporal value through its horizontal row in its Cauchy tensor.
- **IJK**. The middle row of 21 elements in each distinct tensor component establishes the homeomorphic paths that link each one successively to the next, all about a circulation. These values link every  $x$  to its  $dx$ , and so to the  $x$  at  $x_{-1}$  and  $x_1$ . It therefore ranges from a minimum to a maximum around some  $x'$  mean. These are the successive and therefore hereditary values transmitted from point to point, all about the circulation, and so across the generation. They together manifest as a form of contained energy, and energy density, within a given volume,  $V$ . Each middle row helps determine the values and succession of values in its Cauchy tensor's vertical column.
- **TNB**. The bottom row of 21 elements in each distinct tensor component imposes the conditions for the prevailing isomorphisms. It determines the distinctive  $S_{n-1}-V_{n-1}$ ,  $S_{n-1}-V_n$ ,  $S_n-V_n$ ,  $S_n-V_{n+1}$ , and  $S_{n+1}-V_{n+1}$  contributions that mesh all rows and columns. Each thereby coordinates with all its lower- and higher-level transformations as base, fibre, fibre bundle, helicoid, rotachoron, Möbius strip, and real projective plane. Each bottom row establishes the values and behaviours for that given component, and at that nexus of row and column.

**VII.4.6** Now we know that we must have three different kinds of sets, and the three different kinds of **ijk**, **IJK**, and **TNB** axes which are of different sizes, we are ready to prove that a population free from Darwinian fitness, competition, and evolution is impossible.

**VII.5.1** A topologically based investigation has the advantage of being extremely general. A topologist can, for example, deform a square into a circle in a way that is geometrically impossible, but still draw valid conclusions. In the same way, while an ant as large as a whale and a whale as small as an ant are both biologically impossible, we are free to investigate the general deformations and transformations available to them. An ant as our first species  $S_1 = \{n_1, \bar{m}_1, \bar{p}_1\}$  might not, in reality, be able to scale upwards to either of  $S_1 = \{\phi_1 n_1, \phi_1 \bar{m}_1, \phi_1 \bar{p}_1\}$  or  $S_1 = \phi_1 \{n_1, \bar{m}_1, \bar{p}_1\}$ , while a whale, as a second species  $S_2 = \{n_2, \bar{m}_2, \bar{p}_2\}$  might not be able to scale downwards to either  $S_2 = \{\phi_2 n_2, \phi_2 \bar{m}_2, \phi_2 \bar{p}_2\}$  or  $S_2 = \phi_2 \{n_2, \bar{m}_2, \bar{p}_2\}$ , but these are clearly two different kinds of transformations. Just as a topologist insists that a sphere is sufficiently different from a torus to force, for example, ‘genus’,  $g$ , to the heart of the subject, then so also is it possible that, quite irrespective of any particular species, the position of any  $\phi$  is significant.

The  $S = \{\phi n, \phi \bar{m}, \phi \bar{p}\}$  proposal suggests that all three variables can scale with identical rates of change. The  $S = \phi \{n, \bar{m}, \bar{p}\}$  proposal insists that all three share one in common. These are not, however, the same.

If  $\phi \{n, \bar{m}, \bar{p}\} = \{\phi n, \phi \bar{m}, \phi \bar{p}\}$  then  $S = \{\phi n, \bar{m}, \bar{p}\} \dots$  which is in fact impossible. The only possibility, over all biological entities, is  $S = \alpha \{\phi n, \kappa \bar{m}, \chi \bar{p}\}$ , with a specific relationship holding between  $\alpha$ ,  $\phi$ ,  $\kappa$ , and  $\chi$ , and so that neither  $\alpha$  nor  $\phi$  can scale any population without immediately also changing and scaling  $\kappa$  and  $\chi \dots$  which are then a set of Darwinian variations. The scaling factors  $\phi$ ,  $\kappa$ , and  $\chi$  are unique to each species, and are their rates of change of  $n$ ,  $\bar{m}$ , and  $\bar{p}$ , respectively.

**VII.5.2** The proposition that  $S = \phi \{n, \bar{m}, \bar{p}\} = \{\phi n, \bar{m}, \bar{p}\}$  is, by contrast, the proposition that biological populations can only undertake the “affine transformations” that use  $\phi$  as their sole scaling factor. It means that  $S' = \{n', \bar{m}', \bar{p}'\}$  is invariant over all circulations of the generations. It insists that  $m$  and  $p$  are Euclidean, with the fractal dimension  $D = 1$ . We can now show that this is impossible.

**VII.5.3** Memes 4 to 9 proposed a set of plessists and plessemorphs that communicate with the material world through  $\psi$  and  $\gamma$  as Ingredients 3 and 4 of molecules and photons. They and their biological-ecological processes,  $\lambda$ , are a first set,  $A$ . We can replace our plessists in  $A$  at any time  $t$ , at any point  $\tau$ , and so over any stretch  $d\tau - dt$ , with plessemorphs that have the identical effect, and so that  $n_a a_a = n_1 a_1$ . Since they form a one-manifold, they each have a fractal dimension between 1 and 2.

The plessists and plessemorphs in  $A$  construct their genes and genomes with molecules. These are the  $\gamma$  plessiomes counted as  $b_1$  in  $B$ . We can, on the same basis, substitute  $b_a$  plesseomes, also in  $B$ , to produce the identical effect, so that  $n_a \{b_a\} = n_1 \{b_1\}$ . All collections of plessiomes and plesseomes and one-manifolds and so also have a fractal dimension between 1 and 2.

And our plessists and plessemorphs interact both with each other and with their surroundings using their plemes and plessetopes. These are their photons,  $\psi$ , as  $c_1$  and  $c_a$  in  $C$ . The  $c_a$  plessetopes can again substitute for the  $c_1$  plemes, so that  $n_1 \{c_1\} = n_a \{c_a\}$ . These, also, are a one-manifold with a fractal dimension between 1 and 2.

**VII.5.4** Since each distinct entity is an  $a$  in  $A$  while its molecules are  $b$  in  $B$ ; and since each  $a$  is composed of numerous molecules whose numbers can change while the entity count remains the same; then  $A$  is injective into  $B$ , with  $B$  being surjective over  $A$ . And when these two sets associate, they form the standard Cartesian product  $(A \times B)_C$ . We can also always isolate the distinct  $A_{BC}$  and  $B_{AC}$  from  $(A \times B)_C$ . The product formed from  $A$  and  $B$  has a fractal dimension lying between 2 and 3.

**VII.5.5** And then since each molecule is a  $b$  in some set  $B$ ; and again since each can have numerous energy levels and form a variety of chemical bonds while the molecular count remains ever the same; then  $B$  is injective into  $C$ , while  $C$  is surjective over  $B$ . They form the Cartesian product  $(B \times C)_A$ . We can isolate  $B_{AC}$  and  $C_{AB}$ . The product has a fractal dimension between 2 and 3.

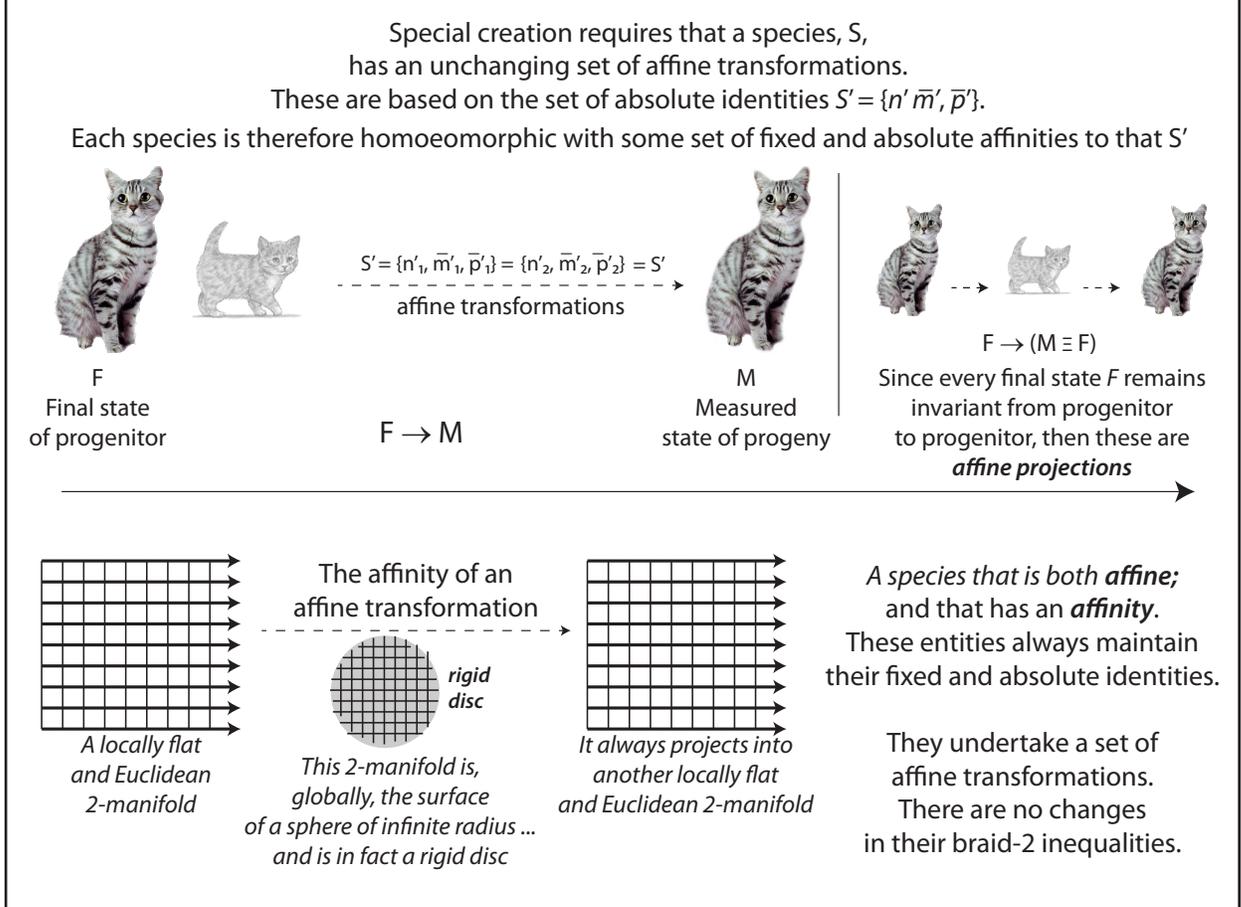
**VII.5.6** And finally, since each distinct entity is an  $a$  in  $A$  while its photons are  $c$  in  $C$  with each  $a$  therefore being composed of numerous photons whose numbers must change, by the second law of thermodynamics, but while the entity count can remain the same; then  $A$  is injective into  $C$ , with  $C$  being surjective over  $A$ . And when these two sets associate, they form the standard Cartesian product  $(A \times C)_B$ . We can also always isolate the distinct  $A_{BC}$  and  $C_{AB}$ . The product has a fractal dimension formed from  $A$  and  $C$ , and lying between 2 and 3.

**VII.5.7** And then further since  $A$  is injective into  $B$  while  $B$  is injective into  $C$ , then  $A$  is injective into  $C$ , while  $C$  is surjective over  $B$ , which is surjective over  $A$ , so that  $C$  is also surjective over  $A$ . And whenever  $B$  injects into  $C$ , so also does some specified and determinable biological entity exist as some  $a$  in  $A$ . We never have  $A$  injecting into  $B$ , or  $B$  being surjective over  $A$ , without some  $c$  in  $C$ ; we never have  $A$  injecting into  $C$ , or  $C$  being surjective over  $A$ , without some  $b$  in  $B$ ; and we never have  $B$  injecting into  $C$ , or  $C$  being surjective over  $B$ , without some  $a$  in  $A$ . The true meaning of there always being a base  $B = B_{XY} \cup B_{YX}$ , with  $B_{XY} \cap B_{YX}$  being non-empty is that we at all times have the Cartesian product  $(A \times B \times C)$ , so that both  $n_1(a_1, b_1, c_1)$  and  $n_a(a_a, b_a, c_a)$  always exist as plessists and plessemorphs respectively. The resulting fractal dimension is always between 3 and 4

**VII.5.8** Given that  $(A \times B \times C)$  always exists, then we can always find the various homeomorphic, path-preserving, and isomorphic mappings  $\phi: A \leftrightarrow B$ ,  $\phi: A \leftrightarrow C$ , and  $\phi: B \leftrightarrow C$ , with all such transformations exhibiting both some absolute time interval,  $T$ , and some circulation distance,  $\tau$ .

**VII.5.9** The elements  $c$  in  $C$ , as our plemes and plessetopes, are free to replicate and self-replicate using any method desired. The individual elements  $a$  in  $A$  and  $b$  in  $B$  over which they are surjective will simultaneously undertake the set of energy transformations  $\pm d\psi$ ,  $\pm d^2\psi$ , and  $\pm d^3\psi$  so they increase from some initial level towards a maximum; down to some minimum; and then returning to their initial level; so that they form a nontrivial loop upon a real projective plane. There therefore

**Figure 45: Affine transformations and the fixity of species**



exists a base in  $\psi$  that is surjective over  $A$  and  $B$ , and whose absolute time span is  $T_p$  while its circulation distance is  $\tau_p = 1$ .

**VII.5.10** The elements  $b$  in  $B$ , as our plessiomes and plesseomes, are also free to replicate and self-replicate using any method desired. The individual elements  $a$  in  $A$  and  $c$  in  $C$ , they being surjective over the former and injective into the latter, will simultaneously undertake the set of chemical component transformations  $\pm d\gamma$ ,  $\pm d^2\gamma$ , and  $\pm d^3\gamma$  so they increase from some initial level towards a maximum; down to some minimum; and then returning to their initial level; so that they form a nontrivial loop upon a real projective plane. There therefore exists a base in  $\gamma$  that is surjective over  $A$  and injective into  $C$ , and whose absolute time span taken is  $T_M$  while its circulation distance is  $\tau_m = 1$ .

**VII.5.11** The elements  $a$  in  $A$ , as our plessists and plessemorphs, are free to replicate and self-replicate using any method desired. The individual elements  $b$  in  $B$  and  $c$  in  $C$  into which they are injective will simultaneously undertake the set of number density transformations  $\pm d\lambda$ ,  $\pm d^2\lambda$ , and  $\pm d^3\lambda$  so they increase from some initial level towards a maximum; down to some minimum; and then returning to their initial level; so that they form a nontrivial loop upon a real projective plane. There therefore exists a base in  $\lambda$  that is injective into both  $A$  and  $B$ , and whose absolute time span taken is  $T_N$  while its circulation distance is  $\tau_n = 1$ .

**VII.5.12** Figure 45 shows the effects of a population with a proposed deformation retract and that can scale so that  $S' = \{\phi n, \bar{m}, \phi \bar{p}\} = \phi \{n, \bar{m}, \bar{p}\} = \{\phi n, \bar{m}, \bar{p}\}$ . It can in other words change in its numbers, with no effects on any other variable, and so that there is no Darwinian fitness, competition, or evolution. This is the creationist and fixity of species proposal.

**VII.5.13** The population in Figure 45 can change  $n$  with zero effects on  $\bar{m}$  or  $\bar{p}$ , so that if we have  $n$  copies of entities, all sharing  $\bar{m}$  and/or  $\bar{p}$ , then we expect  $M = n\bar{m}$  and  $P = n\bar{p}$  to hold at all possible points, over all generations, and whether we measure them over  $T$  or  $\tau$ .

But this is the proposal that biological populations are always “collinear”. It is the proposal that if we use an index  $i = 1, 2, 3$  and consider the three points  $(x_i, y_i, z_i)$  in a Euclidean realm, then the ratios spanning  $(x_1, y_1, z_1)$  and  $(x_2, y_2, z_2)$ —which are  $(x_2 - x_1) : (y_2 - y_1) : (z_2 - z_1)$ —are equal to the ratios spanning  $(x_1, y_1, z_1)$  and  $(x_3, y_3, z_3)$ —which are  $(x_3 - x_1) : (y_3 - y_1) : (z_3 - z_1)$ . Or alternatively, the triangular  $(x_i, y_i, z_i)$  area is zero so that  $x_1(y_2 - y_3) + x_2(y_3 - y_1) + x_3(y_1 - y_2) = 0$ . All rates of change are constant.

As suggested in Figure 45, the “indifferent to  $n$ ” collinearity proposal is that all possible configurations involving  $n$  end up invariant. All possible combinations and figures have the same angles, areas, and perimeters when projected along any axis involving  $n$ . All figures remain parallel; all angles and ratios remain the same; and all commodities demonstrate the same rates of change.

**VII.5.14** All configurations and permutations involving  $n$  form a set of affine transformations that can be translated along any plane, and without any change. Since their transformations and projections perform exactly as they did before, then they are all also “coplanar”.

**VII.5.15** If biological populations are indifferent to numbers, so that  $M = n\bar{m}$  and  $P = n\bar{p}$ , then they are always self-similar in  $n$ . The number dimension must have  $D = 1$ , such that no matter how often we scale and replicate in space and time, the population remains the same. It can accommodate exactly the same types of entities, which will then replicate in the identical fashion. Biological populations and the set  $A$  must then have the same self-similarity as a Euclidean line.

**VII.5.16** The number of entities,  $n$ , in any population, is also  $a$  in  $A$ . It is injective into both  $B$  and  $C$ . And since  $B$  and  $C$  are both surjective over  $A$ , then they must both also have the fractal dimension  $D = 1$ , and so that when they are each associated with  $A$ , they each produce  $D = 2$ . They must both therefore be mutually linear with respect to  $n$ . Since they each have the self-similarity of a Euclidean line, it is preserved when they associate. This population must be perfectly Euclidean.

And since  $A$ ,  $B$  and  $C$  have these collinear, injective, and surjective relations, then when the three associate with each other they exhibit  $D = 3$ , and preserve their Euclidean self-similarity.

**VII.5.17** But if  $A$ ,  $B$ , and  $C$  are linear with respect to each other, so they can all be indifferent to changes in  $n$ , then since the gradient in numeracy is  $\nabla Q = (n_{\text{final}} - n_{\text{initial}})N$ , it must be zero. We always have  $n_{\text{final}} = n_{\text{initial}}$  or the equivalent, which is both a zero gradient, and a rate of change of gradient of zero. So we have  $n_{\text{final}} - n_{\text{initial}} = 0$ ,  $\nabla Q = 0$ , and  $d\nabla Q = 0$ .

**VII.5.18** The divergence in numeracy,  $\nabla \bullet Q = \bar{m}_{\text{final}} - (\bar{m}_{\text{initial}} n_{\text{initial}} / n_{\text{final}})$ , must also be zero. Since  $n$  never changes, then  $\bar{m}_{\text{initial}} n_{\text{initial}} = M_{\text{initial}}$ , while  $\bar{m}_{\text{final}} n_{\text{initial}} = M_{\text{final}}$  meaning that since  $M$  is linearly related to both  $n$  and  $m$ , then if there is no change in  $n$  there can be no change in either  $m$  or  $M$ , so we always have  $\bar{m}_{\text{initial}} = \bar{m}_{\text{final}}$ . So if  $n$  does not change, then neither does the population's mass at any point. Both the divergence and its rate of change are zero.

**VII.5.19** And then also granted that the curl in numeracy is  $\nabla \times Q = \bar{p}_{\text{final}} \bar{m}_{\text{initial}} (n_{\text{final}} - n_{\text{initial}})$ , then again since  $n_{\text{initial}} = n_{\text{final}}$ , both the curl and its rate of change are always zero because both the divergences and gradients in  $n$  and  $m$  are zero, imposing the same on  $\bar{p}$ .

**VII.5.20** Since both  $A$  and  $B$  are injective into  $C$  which is surjective over both, then if  $A$  does not change, no more so do either  $B$  or  $C$ , for  $A$  contains their rates of change. So if a population is indifferent to  $n$ , so that it is replicatively and self-replicatively linear, then the inevitable consequence is that neither  $m$  nor  $p$  can ever change. Since  $M = n\bar{m}$  and  $P = n\bar{p}$ , then both  $\bar{m}$  and  $\bar{p}$  must always have the same rate of change as  $n$ . And since the only way to form the various integrals is through the interactions with the surroundings that require  $dm$  and  $dp$ , then no population quantities can ever form. Those curls and divergences of zero, and their rates of change of zero, mean no change anywhere, at any time, in any population.

**VII.6.1** Proving the general case over all manifolds is not enough. We must prove it for each individual one for the absolute time intervals across the manifolds of  $T_N$ ,  $T_M$ , and  $T_P$  combine to create a joint  $T$ . Their circulation distances  $\tau_i$ ,  $\tau_m$ , and  $\tau_n$  similarly combine as  $\tau_t$ .

**VII.6.2** The set of  $T_N$ ,  $T_M$ ,  $T_P$  and  $T$ , and the set of  $\tau_i$ ,  $\tau_m$ ,  $\tau_n$ , and  $\tau_t$  coalesce. They are a Lorentzian four-manifold.

**VII.6.3** Since the  $T$ s and  $\tau$ s must form the Cartesian product  $T \times \tau$  we immediately have a biological version of the Cauchy tensor. We name it after Ernst Haeckel, a German evolutionary biologist who discovered and named thousands of new species, and who reconstructed evolutionary history based on morphology and embryology.

**VII.6.4** The Haeckel tensor is a  $4 \times 4$ . Since each generation completes, then we must have  $\tau_t \subset A \subset B \subset C$ . Our Haeckel tensor therefore has the following structure:

<b>Table 3</b>								
<b>The Haeckel tensor</b>								
			Exact differentials					
			Volumes, $V$					
			$\tau_{tmp} = T$	$\tau_{tmp} = N$	$\tau_{tmp} = M'$	$\tau_{tmp} = P'$		
			<b>IJK axes: The constraints of constant:</b>					
			<i>equivalence</i>	<i>size</i>	<i>propagation</i>			
			$dt = Td\tau$	$\int dS = 0$	$\int dM = 0$	$\int dP = 0$		
			<b>TNB axes</b>	<b>time, <math>\tau_t</math></b>	<b>number, <math>\tau_n</math></b>	<b>mass, <math>\tau_m</math></b>	<b>energy, <math>\tau_p</math></b>	
			$t =$	<b>time, <math>T</math></b>	$T : \tau_n$	$T : \tau_m$	$T : \tau_p$	
			$\tau_{tmp}$	<b><math>T : \tau_t (T = dt/d\tau)</math></b>	$T : \tau_n$	$T : \tau_m$	$T : \tau_p$	
Inexact differentials	Surfaces, $S$	$\nabla Q = 0$		$n =$	<b>number, <math>T_N : \tau_t</math></b>	$T_N : \tau_n$	$T_N : \tau_m$	$T_N : \tau_p$
		$(n_{final} - n_{initial})N$		$\tau_{tmp}$	$T_N$	$T_N : \tau_n (n/N)$	$T_N : \tau_m$	$T_N : \tau_p$
		$\nabla \cdot Q = 0$		$\bar{m} =$	<b>mass, <math>T_M : \tau_t</math></b>	$T_M : \tau_n$	$T_M : \tau_m (\bar{m}/M')$	$T_M : \tau_p$
		$\bar{m}_{final} - (\bar{m}_{initial} n_{initial} / n_{final})$		$T_M$	$T_M : \tau_t$	$T_M : \tau_n$	$T_M : \tau_m$	$T_M : \tau_p$
$\nabla \times Q = 0$		$\bar{p} =$	<b>energy, <math>T_P : \tau_t</math></b>	$T_P : \tau_n$	$T_P : \tau_m$	$T_P : \tau_p (\bar{p}/P')$		
$\bar{p}_{final} \bar{m}_{initial} (n_{final} - n_{initial})$		$T_P$	$T_P : \tau_t$	$T_P : \tau_n$	$T_P : \tau_m$	$T_P : \tau_p$		

**VII.6.5** The tensor rows use the rectilinear **ijk** axes to project their inexact differentials into the surroundings through their  $S_{n-1}$  surfaces at each moment  $t$ . They do so with the dynamical momentums  $n$ ,  $\bar{m}$ , and  $\bar{p}$ , and over the absolute clock times  $T$ ,  $T_N$ ,  $T_M$ , and  $T_P$ .

**VII.6.6** The tensor columns use the hyperspherical **IJK** axes to project their exact differentials through each population's interior volumes,  $V_n$ . They are then a combination of the kinetic plus

potential energies projected through the surfaces. They satisfy all of Figure 39's constant loops, complements, and inverse couplings for the group operations all around the generation of  $s \circ s' = s' \circ s = \tau$  and  $s \circ s^{-1} = s^{-1} \circ s = S'$  that can repeat the same process, with  $\pi = [(1 \times 1^{\delta=1} \rightarrow 1)^1 \Leftrightarrow (1 \div 1^{\delta=1} \rightarrow 1)^1]$ .

The columns therefore state the generation distance, and the transformational possibilities, as the sums over sets of minima and maxima as can complete a circulation, and so as the combination of  $S' = \{n', \bar{m}', \bar{p}'\}$ ,  $dS' = dn' + d\bar{m}' + d\bar{p}'$ , and  $dt = Td\tau$ —which is  $T = dt/d\tau$ —distributed over the relative generation times  $\tau_v$ ,  $\tau_n$ ,  $\tau_m$ , and  $\tau_p$ .

**VII.6.7** The individual tensor components state every value with their **TNB** Frenet-Serrat unit axes, linking rows and columns, and mediating all ongoing interactions. They form all fibre bundles as  $S_{n-1}-V_{n-1}$ ,  $S_{n-1}-V_n$ ,  $S_n-V_n$ ,  $S_n-V_{n+1}$ , and  $S_{n+1}-V_{n+1}$ .

**VII.6.8** Since we now have all absolute real time values as a set of both inexact and partial differentials,  $\partial$  and  $\delta$ , with respect to  $t$  upon the rows; and all relative and generational values as the exact and also partial differentials,  $\partial$  and  $d$ , with respect to  $\tau$  upon the columns; then the Haeckel tensor's "principal diagonal" is the set of four combined values plus rates of change as create the  $T:\tau_v$ ,  $T_N:\tau_n$ ,  $T_M:\tau_m$  and  $T_P:\tau_p$  that are the normal stresses. They are the divergences that populations must maintain, over specified intervals, and so to establish the properties and quantities that keep them viable. They span both  $\tau$  and  $T$  using their set of rates and form the deformation retract of  $S' = \{n', \bar{m}', \bar{p}'\}$ . The principal diagonals coordinate the three sets of axes and events.

**VII.6.9** Replication is about the different time scales,  $\tau$  and  $T$ , across which the rates of the divergences and curls are projected. The  $V_4$  is simply a statement of volume. It is the gongyl distributed across the four dimensions. The four glomes are the rotachoron's  $S_3$  surfaces which state its values. But since these are biological entities, then those time scales have a group operation. Their paths must stay connected. We must maintain both  $s \circ s' = s' \circ s = \tau$  and  $s \circ s^{-1} = s^{-1} \circ s = S'$ .

**VII.6.10** The proposed affine transformations in Figure 45 and their collinearity can do no more than describe the overall distribution throughout the entire  $S_3-V_4$  space that is the  $\tau_{\text{tmpp}}$  rotachoron. It is an alternative presentation of Figures 33 and 35. It states the normal stresses and principal diagonal for the overall  $T:\tau_v$ ,  $T_N:\tau_n$ ,  $T_M:\tau_m$  and  $T_P:\tau_p$  distribution.

**VII.6.11** The principal diagonal is the "isotropic component", **I**. It states the overall distribution present in every viable population. It is the mean values and set of divergences each population must maintain as the set of properties and quantities that guarantee its connected and isomorphic paths.

It is the set of exact and inexact values that span both  $\tau$  and  $T$  using a set of rates based upon the deformation retract and which also establishes the identity, through  $s \circ s^{-1} = s^{-1} \circ s = S' = \{n', \bar{m}', \bar{p}'\}$ .

This isotropic component, **I**, establishes the constant radius,  $r$ , that is both  $dr = 0$  and  $\int dr = 0$  for the maximum possible gongyl volume. It is the set of all possible Hausdorff points within the interior so that a biological space of dimension  $D = 4$  exists at every point whose paths are all connected. They can then form constant loops of  $s \circ s' = s' \circ s = \tau$  everywhere, and so that we have both  $(1 \times 1^{\delta=1} \rightarrow 1)^1$  and  $(1 \div 1^{\delta=1} \rightarrow 1)^1$  for the  $\pi$  equilibrium at all points. We then have both the exact  $\int dS = \int dP = \int dM = 0$  and the inexact  $\nabla Q = \nabla \bullet Q = \nabla \times Q = 0$  holding good at all points.

**VII.6.12** Since every possible population has mean values over every  $T$ , then every population has an isotropic component. Every viable population then sees a universe in which its every existing entity can maintain itself over every interval, with that set of mean values.

**VII.6.13** A population's isotropic component forms an  $S_3-V_4$  rotachoron whose surface is the set of derivatives that are its four  $\tau_{\text{imp}}$ ,  $\tau_{\text{inm}}$ ,  $\tau_{\text{inp}}$ , and  $\tau_{\text{nmp}}$  glomes. These produce the Euclidean realms whose fractal dimensions are each  $D = 3$ , and that can therefore extend evenly in all directions. These realms then have their six  $\tau_{\text{in}}$ ,  $\tau_{\text{im}}$ ,  $\tau_{\text{ip}}$ ,  $\tau_{\text{nm}}$ ,  $\tau_{\text{np}}$ , and  $\tau_{\text{mp}}$  coplanar and Euclidean slices and surfaces throughout themselves, each of fractal dimension  $D = 2$ . And since all are coplanar, then their derivatives are the collinear  $\tau_{\text{p}}$ ,  $\tau_{\text{n}}$ ,  $\tau_{\text{m}}$  and  $\tau_{\text{p}}$ , all of them maintaining their fractal dimension of  $D = 1$ . And if they are all collinear over all possible points, then they are each composed everywhere of the Euclidean points  $S' = \{n', \bar{m}', \bar{p}'\}$  whose fractal dimension is  $D = 0$ , so they can carry the same invariant entities about their Whitney umbrella  $s \circ s^{-1}$  loops. It must have **ijk = IJK = TNB**.

**VII.6.14** Every viable population can use a set of divergences and curls to create such a realm and realmspace over time, which is then a  $V_4$  gongyl with its  $S_3$  surfaces, all with **ijk = IJK = TNB**.

**VII.6.15** Although every viable population must have an isotropic component, that same isotropic component is the set of mean values that are its divergences over its every interval. However ... if  $n$  is indeed proposed as invariant, then the fixity of species immediately suggests that those are the actual values for the actual entities maintained throughout all populations, and at all times.

**VII.6.16** The sum of every tensor's off-diagonal and shear stresses is its "deviatoric component". They are the deviations from the means. They create a population's "deviatoric stresses".

**VII.6.17** A population's deviatoric stresses are its curls. They are its changes in its gradients, and its divergences,  $\nabla$  and  $d\nabla$ , about any circulation. So if we gradually move towards the mean, at any point, then the deviatoric component equally gradually disappears ... only to reappear if we either

continue on past the mean on the other side, or turn and move back to our start point. Each is away from the mean.

**VII.6.18** Although the deviatoric component always has  $\mathbf{ijk} \neq \mathbf{IJK} \neq \mathbf{TNB}$ , its stresses invert. They help ensure that everywhere maintains  $s \circ s^{-1} = s^{-1} \circ s = S' = \{n', \bar{m}', \bar{p}'\}$ .

**VII.6.19** Since the deviatoric stresses invert to sum to the isotropic component,  $\mathbf{I}$ , then they form a Möbius strip; a real projective plane; and an identification space.

**VII.6.20** The  $T_N:\tau_n$  normal stress for numbers in Table 4, underneath, is a part of the isotropic component. It is the principal determiner of the  $\nabla Q = (n_{\text{final}} - n_{\text{initial}})/N$  gradient in number.

**VII.6.21** The  $T_N:\tau_n$  normal stress also helps establish the divergence and the curl in numeracy. It therefore holds the mean values in number for each of  $\mathbf{ijk}$ ,  $\mathbf{IJK}$ , and  $\mathbf{TNB}$ . One set comes from each row in its 21 constitutive elements.

**VII.6.22** The gradient in numeracy is also determined by the deviatoric stresses on both its row and its column. The  $\tau_m$  and  $\tau_p$  on its row state the current circulation rates in  $m$  and  $p$ . The sets  $B$  and  $C$  exhibiting them are surjective over the  $A$  that holds the entities. They therefore affect all replication and self-replication times.

**VII.6.23** But the dual  $T_N:\tau_n$  index also means that  $T_N$  is the principal determiner for the constraint of constant equivalence that forms its column. This has  $\int dS = 0$ . It sets the overall rate and is a Boy's surface meridian.

**VII.6.24** The constraint of constant equivalence has two other determiners. They are the  $T_M$  and  $T_p$  that also associate, in that same column, with  $\tau_n$ . Since they are off-diagonal, they are deviatoric stresses. Since  $B$  and  $C$  are again surjective over  $A$ , then the  $\tau_n$  that establishes the overall circulation amounts in  $n$  are affected by the absolute times that  $T$ ,  $T_M$ , and  $T_p$  each establish. Those will help determine the ultimate replication and self-replication behaviours found in  $A$ .

**VII.6.25** The combination of rates and times that forms the normal stress and isotropic component of  $T_N:\tau_n$  that determines the overall population numbers and changes in numbers is composed of the following 21 elements:

<b>Table 4</b>							
<b>The 21 elements in the <math>T_N:\tau_n (n/N)</math> isotropic component</b>							
	3rd derivative	2nd derivative	1st derivative	mean values	1st integral	2nd integral	3rd integral
← <b>ijk</b> row: $T_N$	$\frac{d^3n}{dt^3}$	$\frac{d^2n}{dt^2}$	$\frac{dn}{dt}$	<b>n</b>	$\int n dt$	$\iint n dt dt$	$\iiint n dt dt dt$
↑ <b>IJK</b> column: $N$	$\frac{d^3n'}{dN^3}$	$\frac{d^2n'}{dN^2}$	$\frac{dn'}{dN}$	<b>n' = nN</b>	$\int n' dN$	$\iint n' dN dN$	$\iiint n' dN dN dN$
■ <b>TNB</b> component: $\tau_n$	$\frac{d^3s_n}{d\tau_n^3}$	$\frac{d^2s_n}{d\tau_n^2}$	$\frac{ds_n}{d\tau_n}$	<b>s_n = n\tau_n</b>	$\int s_n d\tau_n$	$\iint s_n d\tau_n d\tau_n'$	$\iiint s_n d\tau_n d\tau_n d\tau_n$

**VII.6.26** As is the  $T_N:\tau_n$  isotropic one, every tensor component is a confluence of various quantities as (a) integrals, and (b) derivatives or rates of change. The derivatives and rates build the quantities in the integrals. The different integrals are formed from different sums over different limits. These are: (i) from 0 to  $T$ , which are the intervals of time for the horizontal row and that use the **ijk** axes; (ii) between a minimum and a maximum and so across the population's entire range for the vertical column in their tensor and that use the **IJK** axes; (iii) 0 and 1, to link volumes and surfaces, and the beginnings and ends of the circulation as a discrete set of events using the **TNB** axes.

**VII.6.27** Every tensor component therefore states both an amount and a rate. This is always both (a) the amounts, and (b) the times over which they are acquired and/or consumed. This is also always in all of their 0, 1, 2 and 3 dimensions, involving all manifolds and dimensions, and the **ijk**, **IJK**, and **TNB** axes and their means and distributions.

**VII.6.28** Given the above, then every tensor component is a contributor to a Lorentzian four-manifold. Each is multiply-connected timelike to all others through both its row and its column. Any change in any one manifold has a timelike influence on all others. It changes the absolute time periods,  $T$ , they each take to traverse their  $\tau_n$ ,  $\tau_m$ , and/or  $\tau_p$  distances, as well as the amounts concerned. Populations can thereby impose different magnitudes and rates on each other through their zero-, one-, two- and three-dimensional retracts and hyperplanes. All these can occur in response to  $-\partial n/\partial t \dots$  and such as we measured in our *Brassica rapa* experiment.

**VII.6.29** Every diagonal component in the Haeckel tensor is an isotropic component. It is a normal pressure. It also has four parts. It is:

- a set of quantities, which are integrals;
- a set of rates, which are their derivatives, as divergences and curls.

These are each stated both:

- absolutely;

- relatively.

**VII.6.30** Each component in the tensor also has its **TNB** axes responsible for creating its timelike connections by (a) projecting its numerators horizontally along its rows for its rectilinear **ijk** values; and also (b) by projecting its denominators vertically up its columns for its **IJK** hyperspherical ones.

**VII.6.31** Each component projects a scalar. Each helps create its overall rank zero tensor. Each thus has a definite and distinct magnitude. In the case of the  $T_N:\tau_n$  component, this is  $n$  as the number of entities in that population, at that time.

**VII.6.32** Each tensor component also helps create a mean. This is a part of a range between a minimum and maximum. In the  $T_N:\tau_n$  component, it is  $N$  as the mean across that interval.

**VII.6.33** And finally, each tensor component helps create a generational expanse. This is the set of values that carry it all about a generation. It is the distribution between 0 and 1 that crosses a real projective plane, thus also moving towards infinity and so some maximum. In the case of the  $T_N:\tau_n$  component, there is a specified number of entities,  $n$ , at every  $t$ .

**VII.6.34** And since the product  $A \times B \times C$  must exist, then each of those  $n$  is an  $a$  in  $A$ , injective into a discrete collection of  $n$   $bs$  in  $B$ , and into  $n$   $cs$  in  $C$ . It is therefore a mixture of all three **ijk**, **IJK**, and **TNB** axes; and all three types of fractal measures, with  $D$  between 1 and 2, 2 and 3, and 3 and 4 for each manifold and combination thereof.

**VII.6.35** The axes associate pairwise over all combinations. Since  $xy$  is not the same as  $yx$ , each component contributes to a tensor of rank one. Each thereby gives a sense of direction towards, and away from, its mean, which is the isotropic component, **I**. This is a vector.

**VII.6.36** Each component always transforms to give a sense of being closer to or further away from some given mean value, and closer to or further away from the beginnings and ends of a generation,  $\tau$ .

**VII.6.37** Every tensor and tensor component also always has a gradient,  $\nabla$ , towards and away from whatever mean; and towards and away from the beginnings and ends of that generation. Both these gradients can change in their amounts and rates, and so as  $\nabla$ ,  $d\nabla$ ,  $d^2\nabla$ , and  $d^3\nabla$ .

**VII.6.38** Every distinct value in every tensor component is always (a) an event at some instant,  $t$ ; (b) some proportion of some mean; and (c) located at some point between 0 and 1, and so over  $\tau$ . Each is

therefore always either less than or greater than its mean; moving towards or away from that mean; and over intervals with specified rates. Those are (a) absolute, (b) with respect to that mean, and (c) at a given location in the generation.

**VII.6.39** And since we have both  $xy$  and  $yx$ , then these gradients and their changes form a group, complete with the inverses and the identity that create an identification space. The various axes drive their means and their attributes through the generation.

**VII.6.40** There are first, second, and third integrals over each set of axes. Their lower and upper limits move them over  $T$  and  $\tau$ , also creating the population magnitudes  $N$ ,  $M$ , and  $P$ . They accumulate using their gradients and changes in gradients, their divergences and changes in divergences, and their curls and changes in curls. Their matching derivatives state their rates. These together establish the complete set of behaviours for each generation. They are also invertible.

**VII.6.41** The  $T_N; \tau_n$  component creates both  $N$  and  $\tau$ . This is numbers maintained both (a) at each point,  $t$ , and (b) in succession about the whole circulation. There are again always both (a) magnitudes; and (b) rates.

**VII.6.42** By the Church-Turing thesis, the final result of any tail-recursive function appears identical to a loop, and conversely.

**VII.6.43** Every isotropic component upon the diagonal uses its rectilinear, absolute, and temporal **ijk** axes to establish the momentum value for its row. They are directly observed. These are the biosurfaces  $S_{0,1,2,3}$ . The sum of all the row offerings, for that **ijk** value, is a set of loops.

**VII.6.44** Every isotropic and diagonal component also uses its hyperspherical and relative-proportional **IJK** axes to establish energy and circulation value for its column. This magnitude ranges between a minimum and a maximum. It is the biovolume,  $V_{1,2,3,4}$ . The sum of all the column offerings, for that **IJK** value, is a recursive function.

**VII.6.45** Every deviatoric and off-diagonal or shear component interacts with two principal diagonals:

- It interacts horizontally to influence the isotropic component that carries the means for its row. It therefore affects that set of absolute clock times,  $T$ .
- It interacts vertically to influence a second isotropic component in its column, and so to influence a set of relative and successive generational circulation lengths,  $\tau$ .

**VII.6.46** The deviatoric component interactions are the curls and the partial differentials that create all changes in both  $\tau$  and  $T$ . Their values sum to zero for the exact differential and principal diagonal.

**VII.6.47** Each deviatoric component affects the isotropic one on its row with its numerator.

**VII.6.48** Each deviatoric component affects the isotropic one in its column with its denominator.

**VII.6.49** Since a biological circulation is a Lorentzian manifold, then a population's responses to the  $-\partial n/\partial t$  events that are losses in numbers as jerks will contain opposite effects from each deviatoric component affecting it. Each one affects it in opposite and matching ways, but absolutely and instantaneously in one aspect, and relatively and successively in the other.

**VII.6.50** Any change in numbers affects both a row and a column. It is therefore a net loss in structure. The loss in a row as  $T_N$  is an absolute loss at some moment,  $t$ . It has a sense of direction. It moves either from above the mean towards the mean, or else from the mean and closer towards zero. It is therefore a vector expressed absolutely in time.

**VII.6.51** The loss in a column as  $\tau_n$  is a loss expressed as the flattening of a temporal gradient. It is therefore also a vector, with a sense of direction, and all across a circulation.

**VII.6.52** The jerk of  $\mathbf{j} = -\partial n/\partial t$ , as the loss in numbers, is a group operation involving the deviatoric component. It carries the  $\tau_n$  gradient closer to the mean. It therefore drags the rate of activity in mass and energy, as  $T_M$  and  $T_p$ , closer to its mean.

**VII.6.53** We have already met the deviatoric components  $T_M:\tau_n$  and  $T_p:\tau_n$ . They are the changes in rates and gradients that are Maxim 3 of succession, and Maxim 4 of apportionment. They produce  $\nabla \times M = \partial \bar{m}/\partial t - \partial n/\partial t$  and  $\nabla \times P = \partial \bar{p}/\partial t + \partial W/\partial t - \partial n/\partial t$  respectively.

**VII.6.54** The curls result from the partial differentials exhibited in  $n = M/\bar{m} = P/\bar{p}$ . Since  $n$  has both  $\bar{m}$  and  $\bar{p}$  as its denominators, then any ongoing changes in numbers will produce opposing changes in them both; as also will any ongoing changes in them be opposed to changes in numbers.

**VII.6.55** If the jerk as the ongoing losses in numbers is negative, then the curls as changes in  $m$  and  $p$  will be in opposition to  $n$ , and so will be positive for the circulation ... and as in the braid-3  $dS' = dn' + d\bar{m}' + d\bar{p}'$  of Figure 19c.

**VII.6.56** And contrariwise ... whenever population numbers increase, there is a decrease in the average individual mass,  $\bar{m}$ , and the average individual energy,  $\bar{p}$ , and for exactly the same reasons.

**VII.6.57** However ... the deviatoric  $\tau_n$  responses to any  $-\partial n/\partial t$  also affect the head of their column. This is the  $T$  that establishes the overall generation length.

**VII.6.58** Since this is a multiply-connected timelike Lorentzian four-manifold; and since the temporal gradient has flattened; then the rate at which time flows through this population slows. The generation length,  $T$ , extends through  $\tau_n$ .

As in Figure 40, all losses in numbers will therefore push the population to the right of the small  $\tau_{nmp}$  and  $\tau_{tmp}$  glomes at top left and centre. This decreases numbers and energy density, respectively. But the population is also pushed to the right of the small  $\tau_{tnm}$  and large  $\tau_{tmp}$  one, which increases masses and generation times, again respectively. We measured exactly these effects in our *Brassica rapa* experiment.

**VII.6.59** Since a generation is a four-dimensional  $\tau_{tnmp}$  rotachoron, then if biological populations are truly indifferent to numbers, they must never move in the  $n$ -direction. This is therefore the demand that the rotachoron transforms to a spherinder by flattening on an  $n$ -hyperplane. The population is now obliged to follow Figure 40's cubindrical path with the large black arrow. This is the path directly towards the  $\tau_{nmp}$  numeracy glome. The rates are fixed at the  $\tau_{tmp}$  equator. They are set to  $n = M\bar{m} = P\bar{p}$  through  $\tau_n$ .

**VII.6.60** Since  $n$  is now invariant, then  $\tau_n$  is also invariant. The population has  $n_{\text{initial}} = n_{\text{final}} = n_{\text{mean}}$  at all times. Population changes in  $M$  and  $P$  must therefore track the average individual values,  $\bar{m}$  and  $\bar{p}$ .

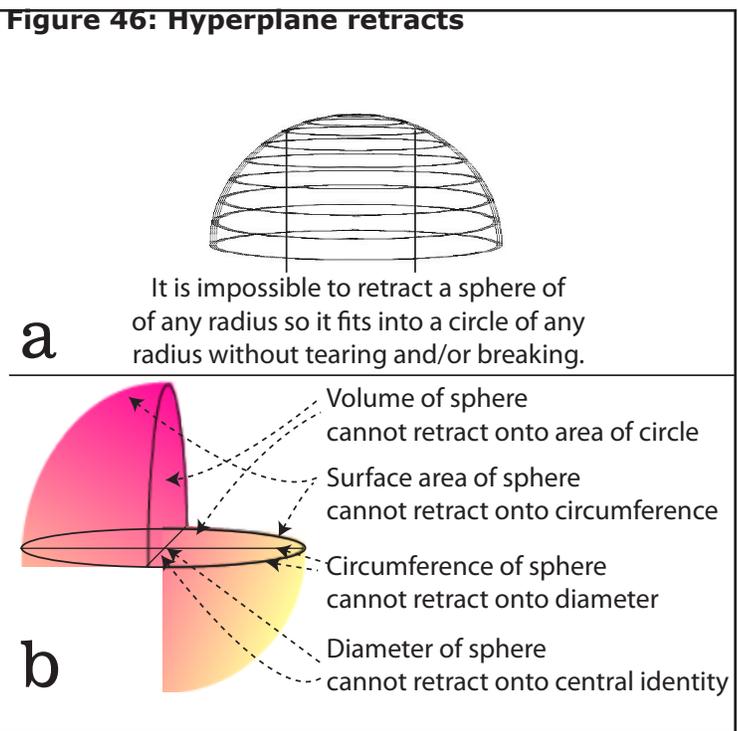
**VII.6.61** The indifference to numbers is the formal request that the curl in numeracy of  $\nabla \times Q = \bar{p}_{\text{final}} \bar{m}_{\text{initial}} (n_{\text{final}} - n_{\text{initial}})$ , be zero. But this again means that  $\bar{m}$  and  $\bar{p}$  must abide by Figure 45. They must have fractal dimensions  $D = 1$  and be collinear and coplanar. They must both follow their divergences exclusively. They may not have curls, for all those are caused by  $\tau_n$  working through  $\partial n/\partial t$ . But since  $n$  does not change, then only the isotropic components are possible. There can be no shears.

**VII.6.62** These demands are all measurable. Therefore:

- if  $\bar{m}$  and  $M$  change at different rates; or if
- $\bar{p}$  and  $P$  change at different rates; or if
- generation length,  $T$ , changes ...

then the population is not exclusively isotropic. It is not free from changes in numbers. A deviatoric component exists.

**VII.6.63** Figure 45 has also already demonstrated that if a population is indifferent to changes in  $n$  and so has a flat and Euclidean fractal dimension and self-similarity of  $D = 1$  in one dimension, then it will have the same  $D = 1$  in the others. This invariant self-similarity therefore affects the  $t$ -manifold. The indifferent to numbers demand is therefore the demand that the  $t$ -manifold cease creating a multiply-connected and timelike space. The  $tn$ ,  $tnm$ , and  $tnp$  time flows must therefore retract to a single identity. All timelike connections will become simply-connected. They will all relocate to the generation midpoint,  $\tau' - t'$ .



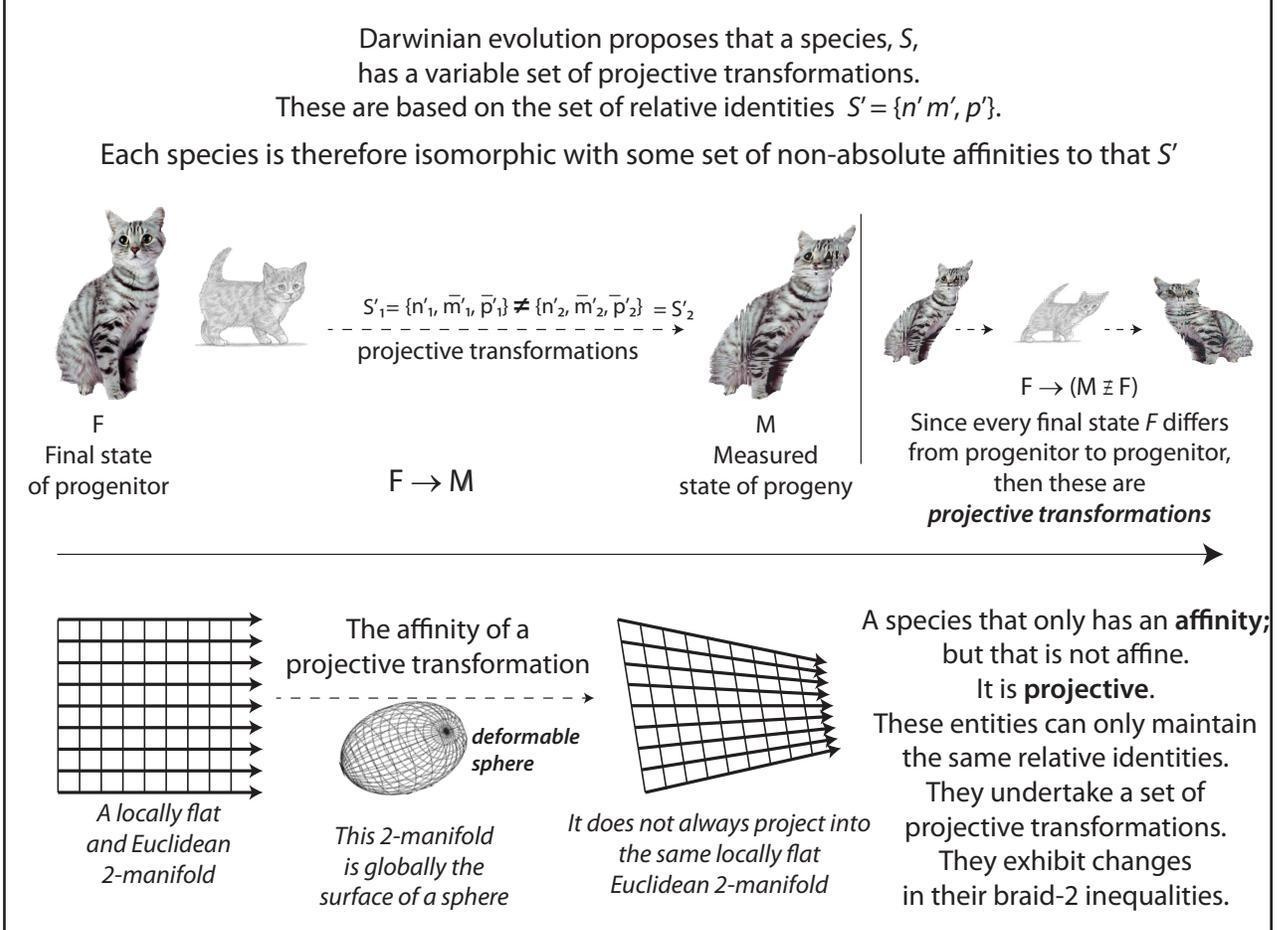
**VII.6.64** The request that a population be indifferent to numbers is therefore the request that a rotachoron convert to a spherinder, and that the entire  $V_4$  volume collapse onto an  $S_3$  surface.

**VII.6.65** If a population is indifferent to numbers, then it has no rates in  $n$ . Since  $\tau_t$  vanishes then the  $\tau_{tnm}$ ,  $\tau_{tnp}$  and  $\tau_{nmp}$  glomes must collapse in the  $n$ -direction. This therefore becomes the demand shown in Figures 46a and 46b. The glome surfaces of  $\tau_{tn}$ ,  $\tau_{nm}$ , and  $\tau_{np}$  must keep collapsing. The rotahedrons flatten to rotagons. But since—as the values for their fractal dimensions makes clear—each  $V_n$  volume is larger than its equivalent  $S_{n-1}$  surface, then this is impossible. It cannot be done without breaking or fracturing.

**VII.6.66** The actual flattening may in principle be impossible, but the fixing of values and rates is not. So the demand that populations be indifferent to numbers is the demand that all rates tend to an equality. All divergences and curls must be zero. All possible populations must strive to set their  $S_0$  inputs identical to their outputs. They become scalar multiples of each other. All their molecules and energies are left in an unchanged and unchanging condition. Generation times also become fixed and unchanging. All populations tend to the  $S' = \{n', \bar{m}', \bar{p}'\}$  values that define the  $\tau' - t'$  generation midpoint. Thus the proposed  $n$ -retraction creates an infinitesimally small and closed timelike loop located at the generation midpoint ... which is a “singularity”.

So we again find, thanks to our topological investigation, that the proposal that biological populations are indifferent to numbers makes all biology impossible, for it is the demand that they all

**Figure 47: Projective transformations and Darwinian evolution**



form fixed and rigid discs incapable of homeomorphisms and transformations. Figure 45's proposed affine transformations of  $S = \phi\{n', \bar{m}', \bar{p}'\}$  and  $S = \{\phi n, \bar{m}, \bar{p}\}$  are therefore again impossible.

**VII.6.67** The only remaining possibility, for all biological populations, is the projective transformations of  $S = \alpha\{\phi n, \kappa \bar{m}, \chi \bar{p}\}$  shown in Figure 47. They must form the deformable spheres in Figure 48a, and that can deform, in all directions, over time. Figure 45's affine transformations of  $S = \{\phi n, \phi \bar{m}, \phi \bar{p}\}$ ,  $S = \phi\{n, \bar{m}, \bar{p}\}$  and  $S = \{\phi n, \bar{m}, \bar{p}\}$  are impossible because they demand an equality in rates in  $n'$ ,  $\bar{m}'$ , and  $\bar{p}'$  ... which is a rigid disc. Biological populations must, instead, exhibit the different curls and divergences for the sphere in Figure 41b. As in Figure 48a, they must form the spheroids that can freely stretch and flex, in different ways, under scaling. So if any population is to scale by some  $\alpha$ , then the  $\phi$ ,  $\kappa$ , and  $\chi$  that establish the scalings in each of  $n$ ,  $m$ , and  $p$  must differ.

**VII.6.68** We have already proven that every population has a universal covering space,  $C$ , and a base,  $B$ , whose fundamental groups,  $\pi(B)$ , are homeomorphic with the cover's deck transformations,  $\eta$ , and so that the cover's surjective  $\xi$  projections are the inverse of the base's injective fibre lifts as  $\xi^{-1}$ ; and also such that  $\eta \circ \phi = \phi \circ \eta = \phi$ . This then means that  $\eta \circ \kappa = \kappa \circ \eta = \kappa$  and  $\eta \circ \chi = \chi \circ \eta = \chi$ , so that none of a population's transformations affect the deck transformations. And since the universal covering space is also a mapping cylinder, then all those homeomorphic and isomorphic cylinder

mappings  $M_\lambda: A \leftrightarrow B$ ,  $M_\lambda: A \leftrightarrow C$ ,  $M_\lambda: B \leftrightarrow C$ , and  $M_\lambda: X \leftrightarrow Y$  involving the progenitor domains,  $X$ , as preimage, and progeny codomains,  $Y$ , as image, exist. So also do all open Hausdorff sets and connected paths. They exhibit the appropriate absolute and relative times and circulation distances, which are the interactions with the surroundings. Their inbuilt Chomsky production rule,  $\delta$ , governs them all.

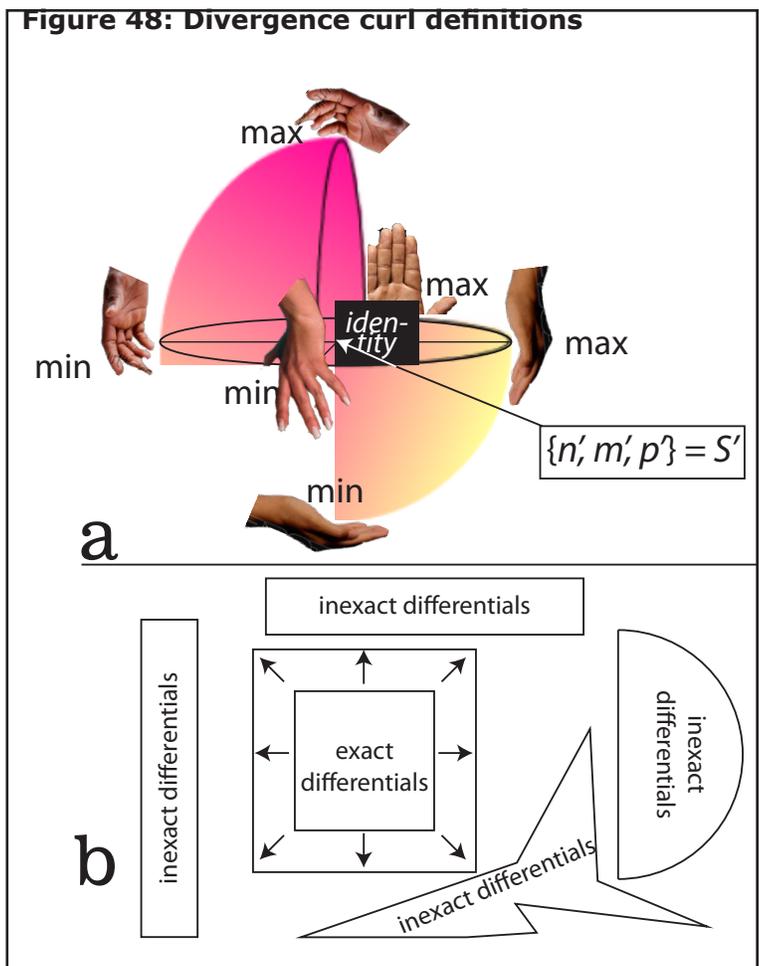
**VII.6.69** No matter how circuitous the perimeters in Figure 48b, we can summarize them all as one-dimensional line expanses. They will all end up ‘ $x$  metres long’, and no matter how varied their shapes and paths. The areas will all similarly end up as ‘ $x$  square metres’, and again no matter what their shapes.

**VII.6.70** We can scale the square in

Figure 48b by any arbitrary factor,  $\xi$ . It will hold its properties and proportions. That scaling is now a projection. It is a self-replication and a set of exact differentials.

**VII.6.71** If we scale the square by  $\xi$ , we can then deform it with a set of inexact differentials. But as long as their sums form a group, then (a) the area to perimeter proportions will remain constant; (b) we can recover the original square at any time. We simply reverse the transformations. This is the inverse fibre lift,  $\xi^{-1}$ . We have  $\xi \circ \xi^{-1} = \#$ . The inexact differentials have formed a suitable group.

**VII.6.72** The above square transformations are between two dimensions, and hold as a matter of principle for any two. For example, virtually the only thing that grows in the harsh northern environments of the Arctic circle and steppes is lichen. Almost the only thing that will eat the lichen is the reindeer. But they must urinate ten to twelve times daily. This is a considerable loss of valuable salt. They therefore drink their own urine. Siberian sled masters often urinate by their sleds to attract reindeer there to hook them up. A traditional Inuit hunting method is to cover a large hole with thin slabs of ice; to urinate on a trail leading to the trap; and to wait for the reindeer, seeking salt to lick, to walk right up and fall in.



The *poronkusema* is a traditional Finnish unit of measure that is the approximate distance a reindeer will walk between its urination events. The *poronkusema* is approximately six miles, 9.6 kilometres, delivering approximately 1.2 litres of urine. We can round this and bring two dimensions together so that  $1 \text{ poronkusema} = 10 \text{ kilometre-litres}$ .

We now consider a Reindeer 1 that walks 20 kilometres to produce a  $\frac{1}{2}$ -litre of urine. This is equivalent to a Reindeer 2 that walks 5 kilometres to produce 2 litres. And both are equivalent to the more standard Reindeer 3 that walks 10 kilometres to produce 1 litre. Each is a *poronkusema* derivative with respect to distance. The urination rates and distances walked, looked at in isolation, seem to vary. However, they all sum, over their respective distances, to produce the same integral.

**VII.6.73** The heart of biology and ecology is Figure 8's Hooke cell which is a Whitney umbrella and our  $S' = \{n', \bar{m}', \bar{p}'\}$  deformation retract. It can undertake a simultaneous fibration and cofibration, involving both  $x$  and  $y$ , and so that for every  $x$  there is a  $+y$  and  $-y$ , while for every  $y$  there is a  $+x$  and a  $-x$  for an identification space.

**VII.6.74** The Hooke cell is an identity operation. It is always  $x + 0 = 0$ . It leaves the original unchanged. It also abides by the first law of thermodynamics.

**VII.6.75** When we take measurements, we extract, and then replicate, every atom and joule in any arbitrary entity. We generate and regenerate the original. This is an identity operation. We simply take our Hooke cell as a standard to create our plessist.

**VII.6.76** We can now create that Hooke cell. We first note that the Earth receives a solar energy, at temperature latitudes, that is of the order of  $p = 100$  joules per second. We can take this as a reference energy rate for our reference Hooke cell. We therefore set it as  $p^* = 1$ . So if some arbitrary biological entity absorbs and emits energy at  $n$  times that rate, then it is equivalent to  $n$  Hooke cells. We measure it as  $np^*$ . We have created our plessist. It replicates all the original's behaviours.

**VII.6.77** We have successfully used our Hooke cell in an identity operation. We can at any time reverse this process. We have left the original completely unchanged.

**VII.6.78** We next observe that the average terrestrial eukaryotic cell has a mass of  $m = 10^{-12}$  grams. We take this as the reference for our Hooke cell. We set it as  $m^* = 1$ .

By the first law of thermodynamics, which our Hooke cell enshrines, we can now measure any arbitrary entity; determine its mass; undertake our identity operation; and declare it as  $nm^*$ .

This is another identity operation. It has left the original unchanged. But ... it has accorded

a specified mass to our plessist, which can take any value without changing its behaviour.

**VII.6.79** Our plessist may have the above  $np^*$  energy intake rate, but it must also always have some energy content or enthalpy. At a representative  $25^\circ$  Celsius, the average biological organism contains matter whose thermal energy is of the order of 0.5 kcal per mole. Glycine, for example, has an energy content of approximately 979 kilojoules per mole (Haynie 2001). We can therefore declare that our Hooke cell always contains 1,000 kilojoules per each mole of its constituents. So in yet another identity operation, we can measure any arbitrary entity, and then transfer it as a specified energy density of  $nV^*$ , and so as some multiple of our reference, to our plessist. This is another identity operation.

**VII.6.80** We can then declare that our Hooke cell takes  $T = 1,000$  seconds to go through its cycle of surrendering and replacing every molecule and joule. This is now our reference generation length. We set it as  $T^* = 1$ . Our Hooke cell replicates itself after that interval. We can again replicate any other entity's generation length, in yet another identity operation, leaving that original unchanged. Granted that a blue whale, for example, has the generation length  $T = 31$  years, then compared to the Hooke cell its length is  $T^* = 11,315$ . This simply means that where the blue whale replicates itself once only, our Hooke cell does so 11,315 times, using exactly the same quantity of energy.

**VII.6.81** And finally, we create a biological population by taking up 1,000 of our Hooke cells. If we keep the number constant over any period,  $T^*$ , then we have a population of plessemorphs that can substitute for whatever number of plessists recognizes that as an average. Whether as an  $a_1$  or an  $a_a$  in  $A$ , they can interact with the surroundings using a specified quantity of mass, numbers, moles, and energy, over 1,000 seconds, creating our  $\pi = [(x \times 1^\delta \rightarrow y)^{T_i=1} \Leftrightarrow (y \div 1^\delta \rightarrow x)^{T_i=1}]$  unipollent equilibrium.

**VII.6.82** Our 1,000 plessemorphs have linked a known and determinable biological population directly to a set of molecular components, in terms of a standard mass, energy and molecular composition ... all undergoing reproduction at a known rate. Since the Greek for species is *genos*, then mass, energy, numbers, and generation length join together to describe an entire population in an "engenetic constant",  $\Omega$ .

**VII.6.83** Our engenetic constant,  $\Omega$ , is simply our unit rotachoron. It stretches exactly one unit in all its four directions, maintaining a  $\pi$  equilibrium,  $\mathbf{ijk} = \mathbf{IJK} = \mathbf{TNB}$ , and an equality between exact and inexact differentials everywhere throughout itself.

**VII.6.84** Since we can describe all populations relative to our enegenetic constant, we can compare them to each other. We simply scale our unit rotachoron with its exact differentials, and its deformations produce a matching set of inexact ones. We are therefore free to introduce and to remove entities, and to adjust their masses and energies as a set of plessists. They can vary, however we so choose, around the plessemorph mean that is our unit rotachoron and enegenetic constant. These comparisons are integrals and derivatives in the various dimensions: both exact and inexact. At the end of any such operation, we can then compare our proposed plessists to the real world entities we began with, and note any differences in values.

**VII.6.85** We already know, for all those transformations, that both  $dt = Td\tau$ , and  $dS = dn + d\bar{m} + d\bar{p}$  must describe our equilibrium population. Our reference one of plessists and plessemorphs, with their  $a$  in  $A$ ,  $b$  in  $B$ , and  $c$  in  $C$ , must also satisfy:

$$dS = \chi(d\bar{m}^*/\bar{m}^*) + \Omega T^*(dV^*/V^*),$$

and/or:

$$dS = \kappa(d\bar{m}^*/\bar{m}^*) + \Omega T^*(dP^*/P^*).$$

where we always measure across the population as  $V^* = M^*/P^*$ . The values for  $\kappa$  and  $\chi$  are always stated in joules. However we choose to deform our population and rotachoron, they can scale  $m$  and  $p$ , respectively, as  $\kappa\bar{m}$  and  $\chi\bar{p}$ .

**VII.6.86** Our plessists and plessemorphs are completely predictable. We can compare them to any population at any time.

**VII.6.87** By the first law of thermodynamics, if a given generation is to complete, then although  $\kappa$  and  $\chi$  are free to vary, there must be equilibrating changes all around that given circulation. The values  $\kappa/\chi$  and  $1 - (\chi/\kappa)$  must maintain a constant relationship. If one changes one way, the other must change another.

Again by the first law of thermodynamics, the energy any one population of plessists uses to change its mass,  $m^*$ , and/or numbers,  $n$ , and/or energy density,  $V^*$ , and/or generation length,  $T^*$ , is precisely equivalent to some corresponding change in some other. We can transform to and from any population while always leaving the original unchanged.

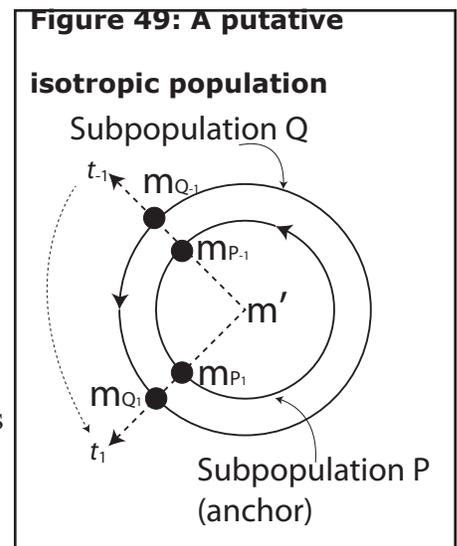
**VII.6.88** If a population is indifferent to changes in its numbers so that  $dn = 0$ , then they must produce the sphenindrical and cubindrical values with those rates of change. Those are the  $d\chi = d\kappa = 0$  transformations in which  $\kappa$  and  $\chi$  remain invariant. They therefore produce those  $\Omega T^*(dV/V)$  and  $\Omega T^*(dP/P)$  population values that always change at the same rates as the individual  $\bar{m}^*$  ones.

**VII.6.89** All the above claims about fixity of species can now be easily tested by experiment.

*Brassica rapa* failed, utterly.

**VII.6.90** The same theoretical and experimental results tell us that if populations do indeed exhibit Darwinian fitness and competition, then we will have a deformable rotachoron. Our values for  $\kappa$  and  $\chi$  will vary with  $\phi$  and  $\alpha$ , meaning that the  $\Omega^T(dV/V)$  and  $\Omega^T(dP/P)$  terms will also vary—but in their associated ways—over the generation. And since they varied in precisely those ways for *Brassica rapa*, then all its transformations have a curl. All its deviatoric stresses sum to an isotropic one. It is proven sensitive to changes in numbers.

And not only did *Brassica rapa*'s generation length vary between 28 and 40 days, but we measured the transformations caused explicitly by  $d\kappa$  and  $d\chi$  at 3.28 grams of mass and 54.012 joules of energy, per 1,000 plants. Those values are the deviatoric components as the offsetting to the changes in the masses and energies of seeds produced per each pod, and plants produced per each pot, as population numbers changed.



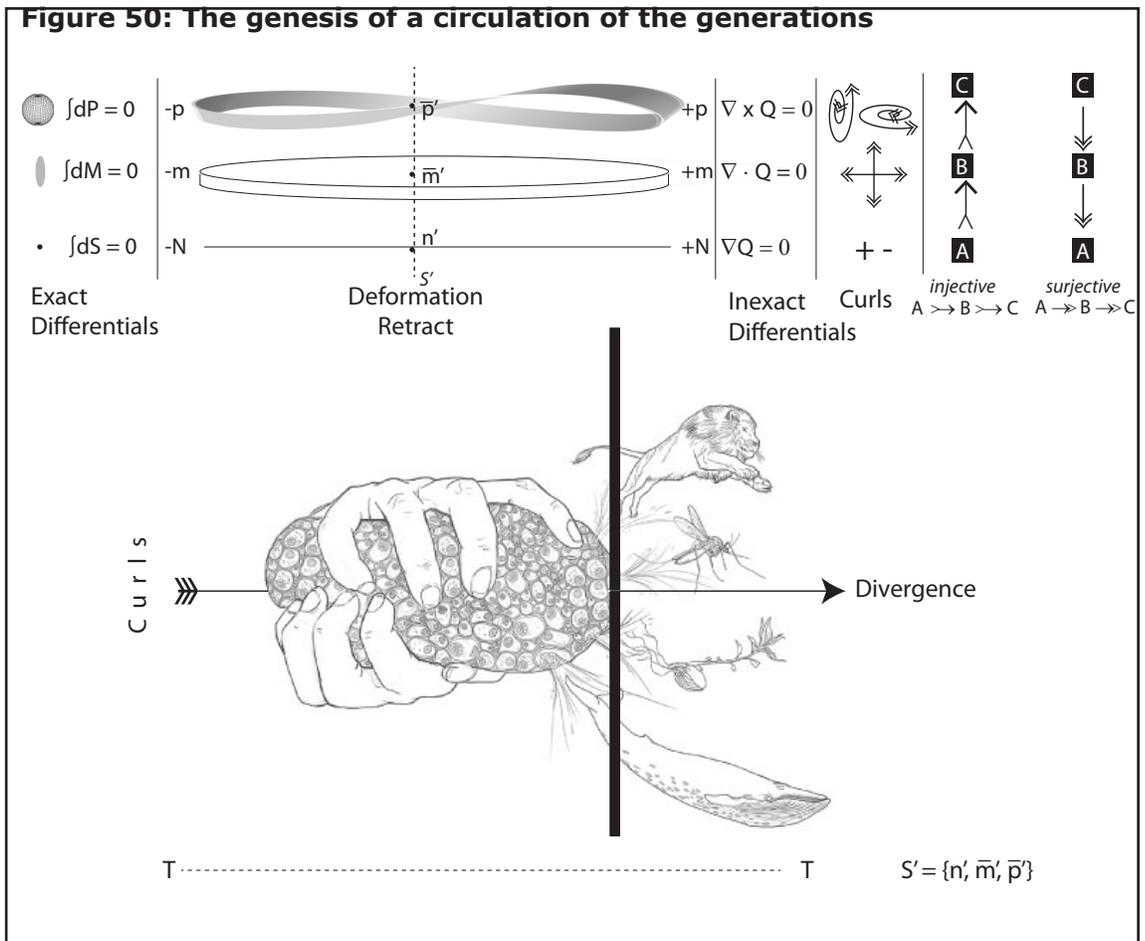
**VII.6.91** Only the Möbius strip remains. If a given species is proposed as isotropic and independent of all influence in numbers; and if it contains the two Subpopulations  $P$  and  $Q$ ; then they each face the immediate difficulties of their fractal dimensions being  $D = 1$ . Since they must be affine, they must each transform as the rigid disc in Figure 49. Their divergences must maintain a set relationship. Their curls must be zero. If their initial values, at  $t_{-1}$ , have a given relation to the generation mean, then all their values must have that relationship at all times. They must be as shown at all subsequent points,  $t_1$ . One population is an “anchor” by being consistently closer to the mean. It must preserve the  $S^*_{PQ}$  identity not only by having the smaller magnitudes, but by having the smaller ranges and rates.

If Subpopulation  $Q$  has three times the mass at one point, it must have one-third at another. Whatever value Subpopulation  $P$  has closer to the mean, both it and  $Q$  must maintain those specific rates of change, so their inverses fall within the identification space.

Since Subpopulation  $P$  and  $Q$  are members of the same species, then their generation lengths must be directly proportional to their masses and energies ... and must remain static. Any variations either across or between generations is a curl and a deviatoric component.

All this can also be subjected to testing by experiment. *Brassica rapa* exhibited a measurable deviatoric component. It did not hold to those proposed values. It was not a rigid disc, but a deformable one.

**VII.6.92** We can now benefit from the advantages of our topological approach. If a homeomorphic mapping from  $A$  to  $B$  exists; and if  $B$  can access neighbourhoods in its mapping cylinder,  $M_\lambda$ ; then  $A$  can use its identity,  $S^*$ , to map to those same neighbourhoods in that same mapping



cylinder; with the same holding for  $B$  if a homeomorphism exists from  $B$  back to  $A$ ; with the two then accessing each others' mapping cylinders, which are the surroundings. And since they are both simply connected, then those same surroundings are a universal covering space. All events in them are deck transformations,  $\eta$ . They are also the Chomsky production rule,  $\delta$ . They govern all possible transformations within the population, which act as a base with homeomorphic fundamental groups.

**VII.6.93** Euler established topology by solving the Königsberg Bridge problem. He demonstrated that the fixity of shapes proposed in Figure 49 is irrelevant in solving certain very general problems. He elucidated the four important principles that:

- the size and shape of each landmass is irrelevant;
- each landmass can be reduced to a single vertex.
- the number of vertices is critical;
- the length of the bridge connecting each vertex is irrelevant.

**VII.6.94** Topology is centred on the deformation retract. As in Figure 50, if biological populations are to successfully replicate, then they must abide by all four of Euler's principles. They must have:

- maxima and minima in  $n$ ,  $m$ , and  $p$  whose  $\pm$  values act as topological vertices;

- variable generation lengths,  $T$ , that act as multiply timelike connecting and topological bridges between the above;
- variable flux amounts in  $N$ ,  $M$ , and  $P$ —the latter two satisfying  $M = n\bar{m}$  and  $P = n\bar{p}$ —built from the variable ranges in  $n$ ,  $m$ , and  $p$ , and also from the variable times and rates in  $t$  and  $T$ , for variable circulation lengths,  $\tau$ .
- a set of magnitudes, each of which can be reduced to a single value, for a set of vertices, and as the deformation retract,  $S^\tau = \{n^\tau, \bar{m}^\tau, \bar{p}^\tau\}$ , all values maintained at  $\tau^\tau$ .

**VII.6.95** We can also express a circulation of the generations by saying that it is a Chomsky grammar such that the intersection of every  $n$ -ball with its retract  $n-1$  hyperplane produces an  $n-1$ -ball, with any lower-dimensioned  $S_{n-1}$  object flattening some immediately higher  $V_n$  dimension, that  $V_n$  object in its turn being a  $V_{n-1}$  ball surrounded by an  $S_{n-2}$  surface.

**VII.6.96** A population and a generation are also a Whitney umbrella. They thus provide an identification space that is an irreducible and real analytic set, never singly pure-dimensioned, complete with its pinch points and antipodal  $-r$  and  $+r$ , and recurvatures. It has the radial and the circulating field principles that are both homomorphic and homeomorphic, creating all syntaxes, semantics, and cyclic groups with their neighbourhoods and identities.

**VII.6.97** A biological generation is further the helicoid presented in Figure 9. Our *Brassica rapa* experiment found that the smaller plants and seeds, as a Subpopulation  $P$ , always developed at the most rapid rates. They would initially occupy positions upon the helicoid inside. They would then gradually drift to the outside as those rapid rates increased their various magnitudes.

Our experiment also found that the larger plants and seeds, as a Subpopulation  $Q$ , always developed at much slower rates. They would initially occupy positions upon the helicoid outside. But they would then gradually drift over to the inside, as their decreased rates of propagation held them relatively static. This is the inversion of values that creates our Möbius strip.

**VII.6.98** If a population is to maintain its essential characteristics, in the face of these opposing sets of magnitudes and rates, then neither of  $dS_p = dn_p + d\bar{m}_p + d\bar{p}_p$  nor  $dS_Q = dn_Q + d\bar{m}_Q + d\bar{p}_Q$  may diverge too widely from each other.

**VII.6.99** The above also requires that our **ijk**, **IJK**, and **TNB** axes differ. This requires a deviatoric component, and so a set of Darwinian variations.

**VII.6.100** If we set  $s = nS^\tau$ , then each distinct entity in each subpopulation is an  $s_p$  and an  $s_Q$ , and where that  $s$  now also states the current number density found about each. Each distinct  $s$  in  $S$

must now hold sufficiently closely to their joint  $s_{pQ}$  mean, which now means the same numbers of neighbours. Both their rates and quantities must match their number densities. And if we measure over the entire population—and so for the time period  $T$ , and the circulation length  $\tau$ —then this  $s_{pQ}$  with its mean number and number density is our plessemorph.

Each distinct plessemorph is now a path,  $s$ , in the biological space,  $S$ . Each one abides by the two group operations  $s \circ s^{-1} = s^{-1} \circ s = S'$ , and  $s \circ s' = s' \circ s = \tau$ . So if some  $s$  in  $s_p$  is to one side of some  $s$  in  $s_Q$  at one point, then each must be the other side of the other at their identification space's opposite point; and the numbers surrounding each must also invert to create the population mean. The rates in both magnitudes and numbers in  $dt_p = T_p d\tau_p$  and  $dt_Q = T_Q d\tau_Q$  form the overall  $dt_{pQ} = T_{pQ} d\tau_{pQ}$ . Their inversions form an outer and an inner boundary which together define the mean values that are the axis and the central band upon the helicoid.

The interactions between  $s_p$  and  $s_Q$  are the set of braid-3 flips we met in Figure 19. If one variable in  $dS' = dn' + d\bar{m}' + d\bar{p}'$  increases the other two must decrease. That central and most characteristic band that forms the helicoid axis and centre is the deformation retract. We measured its net biological processing, for *Brassica rapa*, at  $T=36$  days. This again requires that the **ijk**, **IJK**, and **TNB** axes change in different ways to construct a deviatoric component.

**VII.6.101** We can express this by saying that if a homeomorphism exists that allows  $A$  to access neighbourhoods in its mapping cylinder, then  $B$  can use its identity to map its elements to those same neighbourhoods in that same mapping cylinder. And if a homeomorphism exists that in its turn allows  $B$  to access neighbourhoods in its mapping cylinder, then  $A$  can use its own identity to map to those same neighbourhoods in that same mapping cylinder. Since these two populations can access each others' mapping cylinders, then an identification exists such that the progenitor domain  $A(X)$  can deform the progeny codomain  $B(Y)$ ; while the progenitor domain  $B(X)$  can reciprocally deform the progeny codomain  $A(Y)$ ; with each successively using the values  $n$ ,  $m$ ,  $p$ , and  $t$  in each. This is again a declaration of Darwinian fitness and competition.

**VII.6.102** For as long as the entities follow the four laws of biology of (1) existence, (2) equivalence, (3) diversity, and (4) reproduction; and the four maxims of ecology of (1) dissipation, (2) number, (3) succession, and (4) apportionment; and the three constraints of (1) constant propagation, (2) constant size, and (3) constant equivalence; then they will all be homomorphic and so homotopically equivalent. They will possess rates that are divergences and curls. But they can only be homeomorphic and isomorphic, and so members of some given species, if they hold to the same deformation retract values, constructing a shared set of exact differentials. They will then also share the same inexact differentials; be constant topological neighbours; and use the same  $\kappa$  to govern their masses and changes in mass,  $\gamma$ , and the same  $\chi$  to govern their energies and changes in energy,  $\psi$ .

**VII.6.103** The Church-Turing thesis may well assert that loops and recursive functions can achieve

the same effects, but they are not identical. And since they are not identical then they are not perfectly interchangeable between bases and universal covering spaces; or between mapping cylinders and deformation retracts; or between exact and inexact differentials.

**VII.6.104** Only those biological entities that are constant topological neighbours can share both average magnitudes and average rates of change, and so be constantly homeomorphic and isomorphic. These constant neighbours—which are plessists—also respond to all changes in numbers. This is again Darwinian fitness and competition.

**VII.6.105** A species is a population that maintains a given set of exact differentials and their deformation retract equivalent to a given set of inexact differentials and their curls.

**VII.6.106** We know from Newton that maintaining a constant  $n$  all around a circulation, to maintain such an equivalence in exact and inexact differentials, requires an acceleration, which is then  $d^2n/dt^2$ . A change in that acceleration, as a sudden loss in numbers, is a jerk as  $\mathbf{j} = d^3n/dt^3$ . But as we have already proven above, the population simply deforms inversely to any such jerk, instituting changes in  $m$ , in  $p$ , and in  $T$  to preserve that equivalence ... and as we measured for *Brassica rapa*.

**VII.6.107** Although all jerks are absolute as  $\mathbf{j} = d^3n/dt^3$  they can also be expressed relatively, and so as both (a) changes in numeracy,  $Q$ , and (b) relative to some specified generation length, and so as  $dQ/dt$  and  $d^2Q/dt^2$ . And since these immediately involve permutation in  $\phi$ ,  $\kappa$ , and  $\chi$ , then they are statements of Darwinian fitness and competition.

**VII.6.108** Although the final result of any series of tail recursive functions, as an expression of inexact differentials, always appears identical to a loop as an expression of exact differentials, they are again not perfectly interchangeable. Loops require that numbers do not change. But our *Brassica rapa* experiment demonstrated that the individual values  $\bar{m}$  and  $\bar{p}$  change at very different rates from the population values  $M$  and  $P$ , meaning they each have rates of change that are entirely dependent on the rates of changes in numbers. Mass, energy, and generation length all increased as numbers decreased. These differences in divergences are the inexact differentials that sum to the exact ones all around the path. These can then vary from one generation to the next. The changes in curls we measured were always precisely the changes in divergences. They deform into each other, indifferently, through  $n$ ,  $m$ , and  $p$ . This is again Darwinian fitness and competition. They result from recursive functions.

**VII.6.109** Darwin proposes that if we, for example, wish to produce a mammal, then since a reptile has a host of extremely useful embedded ‘let-me-do-that-for-you’ functions, our best option is to “call” that. By the Church-Turing thesis, the final result will be the same as any loop in any proposed

“template” ... which then strives to abrogate to itself precisely the identity operations already allocated to the universal covering space’s deck transformations,  $\eta$ , and Chomsky production rule,  $\delta$ .

**VII.6.110** Biological populations are defined by topological properties that do not—and cannot—maintain permanently fixed values of any kind. Given that the fractal dimension of any two manifolds in association is always larger than each one individually, then it is impossible for any population to scale linearly. If numbers do not change, then a population must always move spherindrically and in parallel with a numbers axis. This requires specified rates of change in masses and energies. Those values form a straight line tangent upon a curve, a rectilinear plane upon a rotahedron, and a realm emerging from a rotahedron. *Brassica rapa* never followed those values. Every population may appear Euclidean locally, but they all always recurve globally about a manifold.

**VII.6.111** A biological population is instead the continuous survival, in each others’ neighbourhoods, of entities both (a) relatively across their joint and successive generation lengths, and (b) absolutely across their joint historical epochs. They then have common absolute magnitudes and shared relative rates. Darwin’s theory should rightly instead be called “the survival of the plessists”, where the plessists are now the fittest through their shared proximity across a set of both positive and negative rates of change and their associated magnitudes over time.

**VII.6.112** If it is possible to place a population’s entity numbers as they share the same topologically continuous neighbourhoods, across a generation, in some set  $A$ ; and if it is possible to place the chemical components they use in some set  $B$ ; and if it is possible to place the energy they use in some set  $C$ ; and if  $C$  can at some time undertake transformations that are more rapid than those in  $B$ ; and if  $B$  can at some time undertake transformations that are more rapid than those in  $A$ ; then  $C$  is surjective over  $B$  which is in its turn surjective over  $A$  which is  $C \rightarrow\rightarrow B \rightarrow\rightarrow A$ ; which means that  $A$  is injective into  $B$  which is in its turn injective into  $C$  which is  $A \gg\gg B \gg\gg C$ .

We now have  $A \times B \times C = \{(a, b, c) \mid a \in A, b \in B, c \in C\}$  with all possible mapping cylinder transformations  $\lambda$ ,  $\gamma$ , and  $\psi$  as  $M_\lambda: A \leftrightarrow B$ ,  $M_\lambda: A \leftrightarrow C$ , and  $M_\lambda: B \leftrightarrow C$ ; which are the fibration,  $\theta$ , and cofibration,  $\rho$ ; and which are then homeomorphic with the invertible universal covering space projections and base fibre lifts of  $\xi$  and  $\xi^{-1}$ ; and always such that the  $a \in A$  has  $b \in B$  and  $c \in C$  and forming a progenitor domain  $X$ , where the base is a union across  $A$ ,  $B$ , and  $C$  and such that the intersection is not empty; and resulting in a progeny codomain  $Y$  again as  $a \in A$ , with  $b \in B$ , and  $c \in C$  under all the same conditions; and further such that all subsets  $U(X)$ ,  $V(X)$ ,  $U(Y)$ , and  $V(Y)$  throughout  $X \times Y$  and  $Y \times X$  form the unions  $U(X) \cup V(X) = X$  and  $U(Y) \cup V(Y) = Y$  again throughout  $X$  and  $Y$ ; and so that they are also throughout all of  $A \times B \times C$ ; then it is impossible for  $A$  to have a zero rate of change in  $n$  without also and immediately fixing both  $B$  and  $C$  in some single magnitude  $m$  and  $p$  respectively, and also with zero rates as  $A = B = C$ , which then makes all biology impossible ... meaning  $n$  simply must oscillate between some maximum and some minimum both in time and

across a generation, with  $m$  and  $p$  then going through equivalently greater ranges; and all as a set of homotopically equivalent, homeomorphic, and isomorphic paths that can successively convert an  $a_1$  into an  $a_2$  through a set of curls and divergences that can never be fixed in value, but that instead deform smoothly into each other, so making Darwinian fitness, competition, and evolution utterly inevitable. The differences in divergences and curls that cause differences in exact and inexact differentials, and so changes in the shared deformation retracts that are each species identity are then the sole cause of all differences in all entities and populations. They are therefore the sole cause of all speciation.

**VII.6.113** We have now used the laws, maxims, and constraints we determined to disprove creationism and intelligent design.

**VII.6.114** We have produced a fully comprehensive and deductive evolutionary biology.

**VII.6.115** We have also used those same laws of biology, maxims of ecology, and constraints of constant propagation, constant size, and constant equivalence, to give a thoroughly logical and fully deductive proof for Darwin's theory of evolution. We also subjected the theory to Galileo's "ordeal by experiment", using *Brassica rapa*, and provided a complete set of measurements to justify all our claims.

**VII.6.116** This completes the demonstration of the creation of species by the survival of the fittests.

# Part VIII

## Epilogue

**VIII.1.1** We shall now use our theory of biology to produce a theory of economics.