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On the Origin of Taxa

Richard H Zander*

Missouri Botanical Garden, 4344 Shaw Blvd., St. Louis, MO 63116, U.S.A.

Corresponding Author: Richard H Zander, Missouri Botanical Garden, 4344 Shaw Blvd., St. Louis, MO 63116, U.S.A.

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Abstract

The fundamental structure of the Biosphere how taxa resiliently survive millions of years—can be based on principles and laws of physics, particularly through analogy with relationships of classical mechanics and the Pareto alpha index matching a fractal dimension. Like physical conservation laws, these controlling elements survive intact during system change. Arguments are advanced to support the hypothesis of a quadratic origin of taxa based on symmetry breaking and mirror parity, which is extensible from bryophytes to all taxonomic groups. A minimally monophyletic group is one ancestral species with four monothetic immediate descendant species. This relationship is optimized by the Pareto ratio as a pattern constant, which is expressed as an inverse power law at ln(5)/ln(4) or fractal dimension 1.161. Actual species per genus curves are well fitted with the formula $16/x^{1.161}$*, and actual species per genus numbers are modeled by integration of the same curve truncated at 7 species. New species are generated by symmetry breaking of the immediate ancestron (the set of new traits of the single ancestral species shared monothetically by all immediate descendant species). Fractal modeling leads to a quadratic model of evolution, which, because of self-similarity, is applicable to all taxonomic ranks. Models show that control of evolution at least analogically follow first and second differentials of the fitted curve.*

Keywords: Classical Mechanics, Evolution, Fractals, Hollow Curves, Mirror Parity, Pareto Ratio, Symmetry Breaking

1. Introduction

Science melds theory and facts to characterize and predict the existence and effects of natural processes. For instance, in physics, theoreticians impatiently await the discoveries of experimentalists. In macroevolutionary systematics, our great collection-based institutions harbor millions of measurable samples from nature. There are commonly two methods of generating well-supported biological systematics theory. Classical evolutionary taxonomy focuses on grouping and phyletically connecting taxa of various sizes, building on and adding to evolutionary theory. This is a top-down approach. Numerical taxonomy approaches from the other direction in that exact mathematical models attempt to gauge the underpinnings of processes that result in the kinds and relationships of biological diversity [1]. Both methods bracket the complex and chaotic intersections of natural processes we see in nature. Limited by intrinsic constraints of the human psyche and physical capabilities, no one method is adequate, and the two schools of methodology are somewhat estranged. The present paper is deeply based on others preceding it. It attempts to demonstrate that classical and numerical taxonomy reveal the same truths about nature from different but integral methods. This paper uses the consolidative capacities of artificial intelligence to help plumb the deeper aspects of computational and theoretical biology [2]. The mathematical discussion may seem simplistic to physicists, but this paper is intended as a bridge to taxonomists, who are famously innumerate.

1.1. Fractal Evolution

The aim of this paper is to investigate the physical foundations for the discovery in macroevolution that a minimally monophyletic group (here called a "microgenus") of one ancestral taxon has optimally four immediate descendant species, and each of these five species shares the same (optimally) four traits [3-5]. The generation of four descendants resulting in five total species mirroring the same traits allows modeling of this as a fractal process with a dimension of ≈ 1.161, or ln(5)/ln(4) [6]. Note here that logarithmic fractions of a base natural or otherwise give the same result when divided, thus ln(5)/ln(4) = log(5)/log(4). Given the above well-supported fractal nature of evolution in 36 previously studied genera of bryophytes, we examine the possible extension of this feature to other taxonomic groups by modeling relevant physical laws and principles, and operating in all taxonomic ranks by modeling self-similarity.

We will define taxa as, historically, the groups named by evolutionary taxonomists, which model evolutionary trees to reflect descent with modification, as opposed to clades conceived by cladists (most molecular systematists), which reflect analysis by common ancestry. Evolutionary taxonomists preferentially study patterns of origin versus order of origin. Taxa may be modeled as descendant from other

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taxa of the same rank, but clades must include all putative descendants because cladism models evolution on a classification principle, that of holophyly. A back-grounding is necessary for descent-with-modification modeling of macroevolution, the method being fairly new and somewhat at odds with cladistics using common ancestry. The present study is actually a newly developed high-resolution phylogenetics that involves multichotomous dendrograms and multi-order Markov chains using morphological and now standard molecular cladograms that show paraphyly interpretable as an extant ancestor [1,2,7]. Descent-with-modification evolutionary analysis has resulted in minimally monophyletic genera (microgenera) with optimally one ancestral species and four immediate descendant species [6].

The fractal dimension of ln(5)/ln(4) appears in systematics both in the large (Fig. 1) and in the small (Fig. 2). In the large, plots of numbers of species per genus (Figs. 1A and 1B) show that the mass of genera in both vascular plants and reptiles have one to five species. The same concentration of genera per family is showing, in Fig. 1C, more than a hint of self-similarity across scale. The x-axis is tagged at 4 genera to show 20 percent of all genera are when x-axis is to infinity, and 80 percent when truncated at the more realistic 7 genera, to be explained in Results. The same hollow curves are demonstrated with rotifers and in many groups in the Age and Area treatment of Willis [8,9].

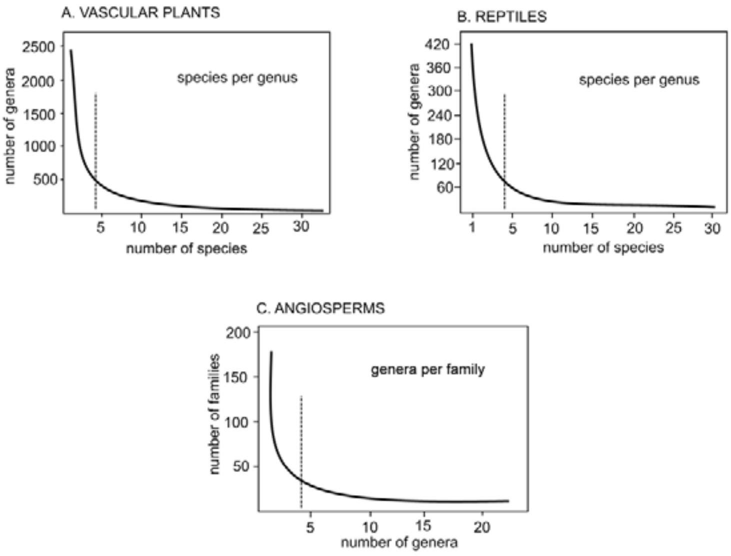

Figure 1: Graphs showing concentration of one to five species or genera. A. Species per genus in vascular plants. B. Species per genus in reptiles. C. Genera per family in angiosperms as a group (after Zander [3]). The hollow curves imply deep processes characterized by formulae involving series, exponents and/or symmetry breaking, expressed, e.g., in the Pareto ratio of 20/80. The number 4 on the x-axis (dotted line) denotes the Pareto boundary of 20:80

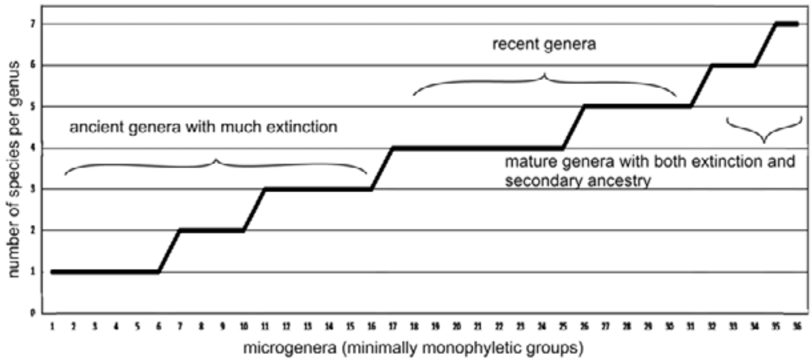

Figure 2: Graph of 36 analyzed microgenera showing numbers of species per genus. Five is optimum, less than five undergoing extinction, more than five have secondary speciation from immediate descendants. More than seven are absent following the Pareto ratio

In the recently segregated family Streptotrichaceae of 10 genera and 26 species, there are an average of 4.04 traits per species and only 2.8 species per genus, but five of the ten genera are monotypic, and, if these are down-played as remnants of larger extinct genera, then there are 4.6 species per genus as reconstructed. Additional microgenera were studied [3,10]. Studies of more recently established genera in the West Indies showed higher numbers of species per genus [6]. Of 36 micro genera total in there were five genera with 6 or 7 species, 15 with 4 or 5 species, and 16 with 1 to 3

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species [11]. The six genera with five species are considered representative of the optimum, while those with fewer species have undergone some extinction, and those few with greater numbers of species include secondary speciation from the immediate descendants. In macroevolution, that which evolves is the immediate ancestron, i.e., the ca. four traits that are new to the ancestral species and transmitted entire to each of the ca. four immediate descendants. It is the immediate ancestron (Fig. 3) that in theory stabilizes each species sympatrically. Balancing the stabilizing effect of the immediate ancestron is the novon, also optimally of four traits, and consists of the newly evolved traits of a descendant species. These traits are state changes of older and probably less important (for survival) characters of the ancestral species.

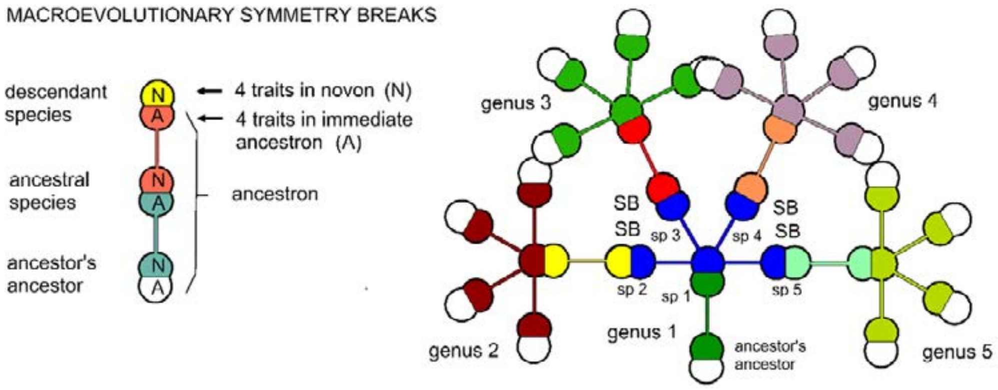

Figure 3: Active elements of macroevolution and symmetry breaking in caulistic diagrams. (Left) A simple three-species caulon. The ancestral species contributes its novon (set of the ancestor's newly evolved traits) entire to the descendant species in which that same set is called the immediate ancestron, while the descendant species generates its own novon from less important characters in the ancestron. (Right) A five-genus caulogram. Five minimally monophyletic genera each of five species in which the shared immediate ancestron is colored the same. Each genus has optimally five identical sets of the immediate ancestron. The change from one genus to the next is an example of symmetry breaking of that immediate ancestron set. Some genera overlap due to crowding in the figure

The generation of four items resulting in five items total (4-gets-you-5) process has a fractal dimension ≈ 1.161or ln(5)/ln(4), which is apparently universal in macroevolution as evidenced in the study of the 36 minimally monophyletic groups (micro genera) in the hollow curves of species per genus and genera per family (Fig. 1), showing self-similar distributions of 5-speciose and 5-genera taxa in many groups [3-5]. Of interest is that he rule-of-four includes traits, where four traits are optimal both in new traits (the novon set) and in the traits shared by ancestral species and its immediate descendants (the immediate ancestron set). This implies that taxonomic ranks are not notional but are based on real, measurable features established by evolution, namely natural selection in the context of deeper processes involving symmetry breaking [12,13]. The edge of chaos evidenced by the logistic map is a candidate for the apparently non-linear process called speciation [14,15]. The Pareto ratio is related to the inverse function $f(x) = A/x^{\alpha}$, where A is 1, and α is about 1. We will examine the probabilistic proportions where α is either 1 or ln(5)/ln(4). ln(5)/ln(4). Moreover, the Pareto principle is self-similar in that, of the above 20% most affluent people, 20% of them receive 80% of the money of the other wealthy folk, 20% of pea pods produce 80% of peas, etc. It seems that the quasi-Zipfian sheaf of evolutionarily important hollow curves presented by Zander may approximate near the number four the Pareto ratio, which is simply but significantly an instantiation of the Pareto distribution $f(x) = Ax–\alpha$ at 20:80, where A = 16 [16,17].

The change from one genus to the next is an example of symmetry breaking in which the unique intersection or overlapping set of the immediate ancestron is broken, being torn away from the ancestral species into different species by the four different novons of the optimally four immediate descendant species (Fig. 3) [18]. This also implies that that the immediate ancestron is basic to the rule-of-four, and provides stasis to the lineage through redundancy of the newly evolved survival traits of the ancestral species. The novons of the immediate descendants and the ancestral species' ancestral traits are all different and provide the new exploratory traits that by organism survival provide adaptability when stasis is challenged by environmental change [6]. It is the balance of preserved and redundant traits of an ancestral species with the about equal number of newly evolved traits that, one hypothesizes, eases speciation through mitigation of competition between allopatric species and coeval descendant species in peripheral areas (peripatry) of the ancestral species [6]. This paper is a first attempt to model this process with fractal trees.

Mirror parity is a feature of nuclear physics that provides an analogy for a similar phenomenon in evolutionary descent with modification. As diagramed (Fig. 4), a narrowly concatenated lineage series of taxa, a caulon (Fig 3a-left), is an alternating set of mirrored traits, the immediate ancestron (traits other than any newly evolved traits) of the descendant being the same as the novon (newly evolved traits) of the ancestor (Fig. 4-right). The symmetry of shared traits in the genus is broken during speciation by natural selection, where new species arise out of sympatry in ancestral niches.

I have suggested a geometric explanation for the four-descendant optimum [17]. Plotting the area outside regular 2D geometric figures inscribed in a circle yields a hollow curve with the area coverage of each cut off portion largest among figures with sides less than five. Thus, hypothetically, the first one to five species originating peripherally around the geographic area of an ancestral species would undergo less competition between co-descendants.

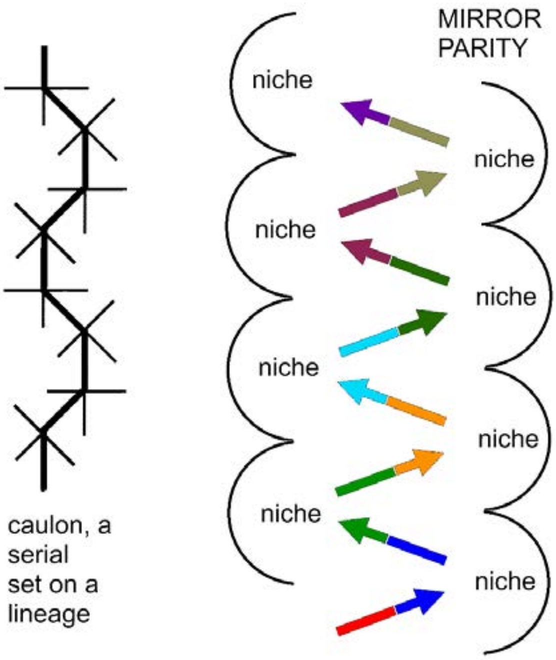

Figure 4: Mirror parity in evolution. (Left) A series of minimally monophyletic genera concatenated serially (without major branching) is a caulon (thick line), being a serial portion of a caulogram. (Right) Arrows show direction of evolution in a caulon. Each arrow is a species. The arrowhead is the novon, the set of new traits obtained by changes of old, little-used ancestron traits, and the arrow base is the immediate ancestron of traits the same of those of the novon (same color) of the ancestor. The novon and immediate ancestron mirror each other sequentially

Given the present fractal context, it is also possible that, prior to competitive exclusion of any more than four or five peripatric descendant species, isolation of populations in the fringes of a fractal ancestral margin (Fig. 5) would restrict swamping of mutational alleles and encourage speciation through localized genetic drift under natural selection. The figure was generated by AI Claude-3.5-Sonnet to create a central mass with fringed margins modeling the geographic range of an ancestral species. It used a fractional Brownian motion algorithm, and consisted of a single enclosing line, with fractal boundary scaling at ln(5)/ln(4) or 1.161, with smooth Catmull-Rom spline interpolation for natural curves. The original output included adjustable roughness and detail controls. Real coastlines have fractal dimensions around 1.2 to 1.3, and actual geographic range peripheries should be similar.

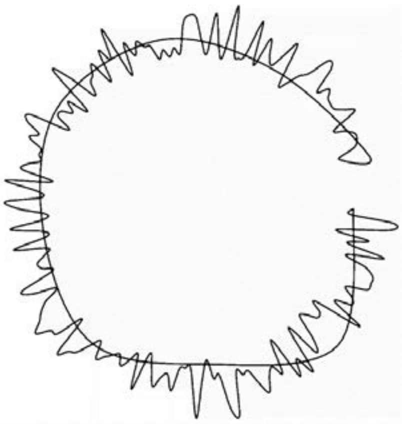

Figure 5: Central ancestral sympatric area with peripatric "shoreline" margin generated fractally at ln(5)/ln(4) demonstrating potential isolation of populations that encourages genetic divergence resulting in speciation

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The fractal dimension (Fig. 5) is scaled by taking an original length L, slicing it into four equal parts, increasing the length to five equal parts, then squeezing it back into the original length by buckling the two inside parts. Thus, a length of five is shortened into a length of four with some portions buckled out of the original dimension. Mainland shoreline periphery is generated following this simple method in (Fig. 6) buckling.

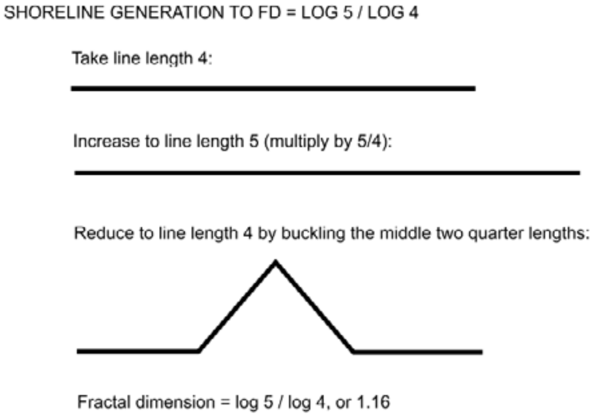

Figure 6: Line that is elongated to 5/4, then buckled back to original length. Smoothing generates a lifelike fractal land-sea margin in Fig. 5

A diagram (Fig. 7) using the equilibrium fixation index p. 100 shows that more than four migrants per generation in an island situation with isolating geography strongly restricts establishment of mutations, but genetic divergence rapidly occurs with fewer migrants per generation [19].

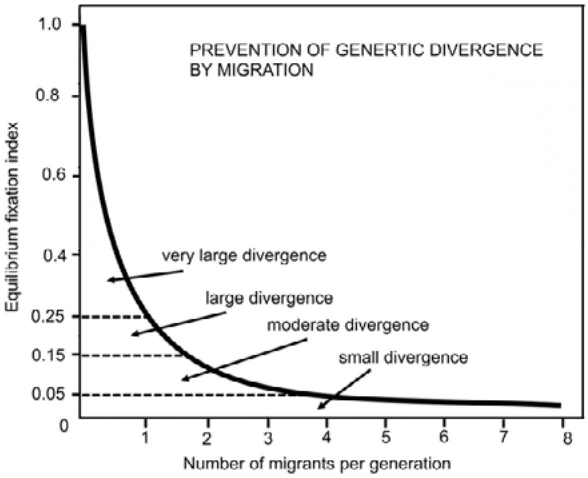

Figure 7: Equilibrium index (y-axis) versus number of migrants per generation in island migration model (adapted from Hartl [19]. This curve is similar to that of 1/x, flattening out at x = 4

Apparently, evolutionary trees do not grow slowly. In a previously published caulogram of the family Streptotrichaceae, the most recent genera are fully beset with descendant species while the genera are reduced in numbers of species as they age, geologically speaking. This implies a kind of punctuated equilibrium or burst of speciation, which is similar to the theoretical avalanches of change associated with self-organized criticality [20]. This is followed by a balanced decay of the lineage through extinction and extension of the lineage terminally by addition of new genera from secondary ancestors. What supports and constrains this lineage and keeps it from going extinct or burgeoning into a massively taxon-rich unit?

2. Materials and Methods

2.1. Data, Models, Analysis

The primary data are from graphs of species per genus and genera per families, and from past analysis of 36 minimally monophyletic groups (microgenera) demonstrating one to four shared recent ancestral traits among the four immediate descendants of one ancestral species. Modeling involved fitting graphs of known formulas to published hollow curves given a previously demonstrated 4-gives-you-5 paradigm, and generation of fractal diagrams representing evolutionary relationships. Interpretation used known physical phenomena and pattern constants as possible explanations, including the logistic map, Pareto distribution and ratio, differential analysis analogous to classical mechanics, Turing patterns,

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and the possibility of Nash equilibria and minimax solutions for balanced long-term survival in a resilient ecosystem. The results encourage analyzing biodiversity and evolution with tools of "hard science," and refute the idea that biological systems may be too complex to describe in terms of universal laws [21].

Standard taxonomic study uses protocols developed over 250 years of native pattern recognition coupled with homology assessment and presently rather well-developed microevolutionary theory to sort specimens into evolutionarily coherent groups as hierarchical sets of taxonomic ranks. These groups provide easily analyzed small data sets that limit mistaken clustering by shared but convergent traits. These smaller groups are examined for minimally monophyletic sets of one ancestral species and a few descendant species. Ancestral species were identified by second-order Markov chains with (1) that species of the small group most similar to an outgroup (most similar species outside the group) and, also (2) being most generalist (least specialized) of the ingroup. This is made more accurate by identifying the few (mostly four) traits shared by all species (among one ancestor and all immediate descendants). Such monothetic traits help define a genus, where a minimally monophyletic genus may be operationally termed a "microgenus." The shared traits are the most newly evolved traits of the ancestor and gifted wholesale to each immediate descendant.

The microgenus is optimally a set of five species radiating from the ancestral species because speciation is rapid as apparently a burst within 22 million years [4,6]. This is followed by speciation from the immediate descendants (secondary descendants may become central ancestors in new genera) and extinction of some of the species. Statistical support for each microgenus is by assigning each of the newly evolved traits (the novon set) of each species one Shannon informational bit, then adding the bits together and interpreting the sum as a Bayesian posterior probability using an odds chart and validated by conjugate priors. The microgenera are strung together by connecting the ancestral species into a branching tree with gradual evolution by concatenation of the novon traits of the ancestral species [11]. This results in a fully monophyletic tree. Molecular data may be used, particularly interpreting paraphyly as data on ancestral species and apophyly as descendant species.

2.2. Artificial Intelligence As Software

The present study used Artificial Intelligence (AI) to model mathematically processes in macroevolution (processes involving species and above) that are apparently random and based on natural selection. This is here considered a significant advance in numerical taxonomy—naming this new method "high-resolution phylogenetics" because complex and calculation-onerous modeling is now possible to clarify fairly simple concepts rooted in heretofore hidden physical processes. An AI is presently most useful in capturing, coordinating, and combining multitudinous known scientific facts and concepts for application to a specific research problem. The Large Language Model is not intended as a calculator, and all mathematical results must be checked with dedicated software. In the present study, AI was mostly used as info-sphere concept consolidation software, in which it excels, and all facts and mathematical results are checked with actual human publications and dedicated software. Interpretations of results by the AI are accepted by the author when consistent with theory, analysis, and data, and are presented as equivalent to human native pattern recognition and reasonable inference. Suggestions by the AI of hypotheses and theoretical postulates were evaluated and some incorporated, after due consideration, in this paper. The author is fully cognizant of the problems on the part of AIs used in in research, including occasional incorrect calculations, confabulation of facts, and misinterpretation of queries.

Most analysis, model building and image generations was done by AI Claude-3.5-Sonnet of Anthropic, Inc., with occasional use of AI Poe Assistant of Quora, Inc. Several other AIs were at first addressed for modeling macroevolution, but it the fractal images they generated were based on Mandelbrot or Julia formulae, and the resulting pretty but context-free images were not interpretable as representing anything in nature. It was Claude-3.5-Sonnet that suggested using iterated function system analysis to generate fractal trees, which proved good models of macroevolution.

Images used by this paper to model processes were generated as HTML files in html Canvas p. 540 by the AI [22]. Iterated function systems generate fractals simply by repeating transformations, usually scaling, recursively, and converging to a fractal attractor [22,23]. Patterns generated are self-similar but complex with only a small set of rules. Mapping is contractive and produces a bounded shape. The Sierpiński triangle is an example, with a fractal dimension of about 1.585, also the well-known Barnsley Fern, Cantor Set, and Koch Snowflake [24-26].

Dendrograms (evolutionary trees) were generated to model the ln(5)/ln(4) tree of four branches per node apparently optimal in actual evolutionary scenarios of 36 previously studied microgenera, including the complete family Streptotrichaceae of 10 genera, to identify possible processes in nature [10]. The number of branches in a microgenus may vary from none or one to four, and immediate descendants may generate secondary descendants. Because the species are monothetic (all share an identical set of traits), the immediate ancestral is easily discerned.

The AI used iterated function analysis to generate trees modeling at fractal dimension ln(5)/ln(4), or1.161, the optimal four branches per node observed in morphology-based taxonomic studies. Such studies suggest that that which evolves is the immediate ancestron of about four species, which provides stasis for the four novons per species that provide variability for adaptation to environmental change. The intent was to find mathematical relationships that may throw light on the underlying processes that support the continued existence of lineages, in the case of Streptotrichaceae for some 88-million years [4].

Support for morphological and molecular methods used for the basic concepts of minimally monophyletic groups include both standard Markov chain Monte Carlo Bayes with molecular data and Turing sequential Bayes with Shannon information for morphological data [3,7]. It is perhaps important how often low integers and 20% and 80% appear in discussions of apparently disparate subjects; although these are doubtless sometimes coincidental [27].

2.3. Alternative Methods

Standard common ancestry analysis using cladistics with dichotomous trees and first-order Markov chains on molecular data can identify the same extant ancestral species if paraphyly and other non-standard clues are used as indicators [7]. Cladistics alone is inadequate in that, because it has been demonstrated rather conclusively that (1) about 80% of ancestral species remain extant, and (2) depending on sampling, an ancestral species can turn up anywhere among its optimally four descendant species on a molecular cladogram, therefore a clade has only a 20% chance of being monophyletic, while (3) lumping different otherwise integral, evolutionarily coherent genera together into a clade, following the cladistic classification principle of holophyly, hopelessly masks the serial, monophyletic organization of minimally monophyletic groups (microgenera). The modern combination of a cluster-analysis form of searching for common ancestry and overemphasis on molecular traits hides information on fundamental evolutionary relationships. The present paper replaces common ancestry with descent-with-modification as a primary investigative tool.

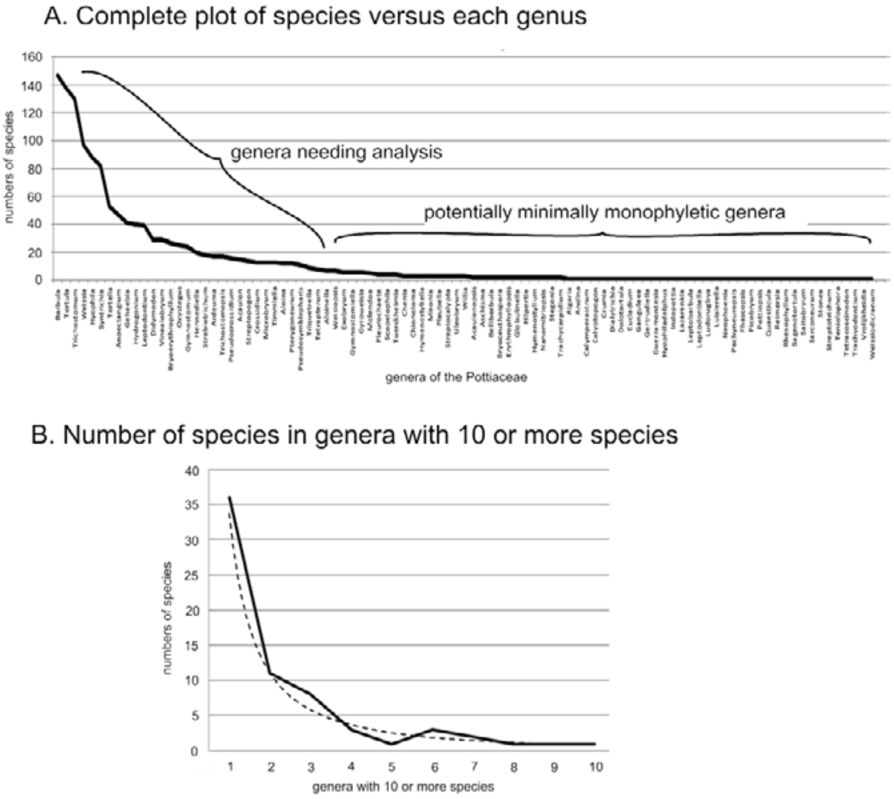

Figure 8: Species per genus of the Pottiaceae (Bryophyta) as of 1993 from Zander [10]. A. All genera (x-axis) graphed against numbers of species per genus. B. Numbers of genera (y-axis) with 10 or fewer species. Dashed line is power curve trendline from Excel spreadsheet

A summary of the species per genus in the 94 genera of Pottiaceae (Bryophyta), including the now segregated Streptotrichaceae (Fig. 8A) shows that large numbers of very small genera are already of a size potentially that of microgenera, yet many large genera remain as evolutionary dustbins. This summary is from 1993, prior to the bloating of the family to about 108 genera by cladistic lumping of long-recognized descendant genera as synonyms of ancestral groups at the same rank by molecular systematists. Most genera have one or very few species, but a graph (Fig. 8B) of just the speciose genera show a power curve in the trendline provided by the Excel spreadsheet. The most speciose genera have 36, 11, 8, 3, and 1 species, approximating the 32, 16, 8 and 2 expected if the curve were generated as powers of 2. The jump to 3, 2 and 1 thereafter may reflect secondary ancestry (descendants of descendants).

3. Results

3.1. Models

The results of this study support the value of informational entropy, particularly the work of Brooks and Wiley as a factor in understanding natural processes [12]. The present study reflects data not available to these authors. Characteristic of how natural processes, including life, survive across time is an equilibrium, a balance between dissolution and elaboration. This is evident across wide scales of space and time. Examples include Edward Tryon's discovery that the exact balance of positive kinetic and potential mass energy

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in the universe with negative potential gravitational energy of all mass; the maintenance of maximum biological diversity through species replacement after loss, that is, Maximum Information Entropy. Pareto ratio amounting to 20% yields 80% in taxonomy, equivalent to a fractal dimension of 1.161 the Lotka-Volterra model for species competition; and adaptations for homeostasis maintaining physiological health in individuals [6,28,29]. This distribution, when an inverse function, results in hollow curves when plotted, and may be operative in inorganic chemistry as the Gazzarrini rule-of-four in inorganic chemistry, and more generally as the Constantin meta-law of physics [30,31].

Given recent work on fractal modeling, it should be considered that the idea of strong forces balancing positive and negative aspects of natural processes is better for stabilizing an internally and externally competitive ecosystem than natural processes that are solely aleatory in response to changing conditions. It is quite possible that fractals model a general distribution of equilibrium-bringing, sustaining processes maximizing informational entropy across scales of space and time by balancing rate and kind of extinction and multiplication of major elements in a lineage. That is, modeling an equilibrium of processes controlling decoherence of lineages by chaotic processes (edge of chaos) with the stabilizing processes of complexity theory (informational redundancy, retention of ancestral new traits in all immediate descendants. As previously suggested evolution is also a process important for lineage survival acting above the species level [11].

Natural phenomena commonly are characterized by hollow curves, initially high on the y axis and tapering off for large values on the x-axis. Excepting a straight line, which is a special kind of curve, all curves are hollow. The curves of Fig. 1 are monotonic, with negative slope, and are typical of simple inverse functions, such as f(x) = 1/x. Changing the exes of a simple graphed inverse function to logarithmic scale creates a straight line, a characteristic of a power law, which includes the power of one in the denominator. A thickened tail, often cited as indicating a power law, is created by decreasing the exponent of the variable in the denominator below 1.0. Power laws are commonly associated with fractal theory, see Mandelbrot and West and Brown [32,33].

3.2. Constants

A physical constant is an experimental quantity that cannot be explained by theory. It is associated with a fundamental aspect of the structure of nature [34]. Numbers identifying patterns emergent in complex systems are very similar to constants differing only in level of predictability in variations, scale of measurement variations, and precision of possible measurement [35]. The latter may be more a matter of categorization than fundamental differences. In this paper, the Pareto ratio is considered sufficiently descriptive of fundamental patterns across scales that it may be considered a "pattern constant." In physics, a conservation law concerns a measurable quantity that does not change as the system changes over time; a pattern constant is much the same. In the function $A/x^{\ln}(5)/^{\ln}(4)$ he exponent ln(5)/ln(4) is a shape parameter that stays the same however the system changes.

Except for occasional horizontal gene transfer, evolution of already speciated groups, that is, higher taxonomic ranks, is not mediated by parallel or coordinated genetic processes similar to those investigated with population biology for microevolution. The present study suggests that the observed similarities affecting survival, resilience, and equilibrium among higher taxa is due to shared and potentially universal physical processes associated with certain physical constants or principles [16,31]. One may identify universally effective but somewhat hidden closely related universals of the macroevolutionary process that may create a balanced combination of adaptation and homeostasis at lineage level.

3.2.1. The Feigenbaum Constant

The Feigenbaum constant 4.669201609..., hereinafter 4.66, rules the logistic graph or nonlinear map in Chaos Theory [36], and is the limiting ratio of bifurcation intervals in the logistic map (Equation 1 and Fig. 9). The value of the variable at the next iteration is x_{n+1}, where x is between 0 and 1, while r is between zero and four, and controls the system. The formula is deterministic but generates complex, chaotic behavior, and is commonly used to model population dynamics, e.g., balancing reproduction and extinction associated with turbulent behavior [37,38]. The initial set of bifurcation intervals for period doubling [39] p. 116 in the logistic map (Fig. 9) , where bifurcations are clearly observable and apparently becoming self-similar and not yet fully chaotic, is the "edge of chaos" [14,40]. It is associated with complex adaptive systems [41] and is here suggested as generative of lineage splitting, which given the shared immediate ancestron, involves symmetry breaking. One should note that the initial bifurcation Fig. 9) results in four to eight distinct paths before rapid dissolution into chaos, possibly reflecting a Pareto ratio (2:8) in this most simple instance of logistic behavior. In addition, random Boolean networks with four or more connections between elements become chaotic [42,43]. The Feigenbaum δ constant is, like ln(5)/ln(4), fixed at various scales.

$$x_{n+1} = rx_n(1 - x_n) \qquad (1)$$

Because even the most recent microgenera have four immediate descendant species extant, speciation is here considered abrupt (in geologic time), as a kind of punctuated equilibrium [44], being modeled by the rapid non-linear degradation of the bifurcations into chaos. If x in the logistic equation (1) represents ln(4) and $1-x$ is ln(5), and r is massive pressure into speciation at the moment of punctuation filling a newly vacated niche, then edge of chaos is a likely model. Adaptation to changing circumstances is enabled by bursts of new species bearing a set of traits originating as character state changes of older, less valuable traits in the ancestral species [6].

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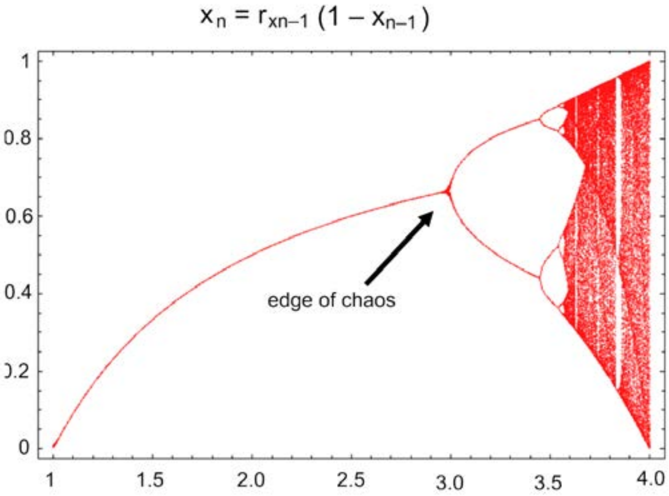

Figure 9: The logistic map. The "edge of chaos" is the beginning of the range of bifurcations leading to the place of total chaos. The symmetry breaking of the set of the immediate ancestron may be due to a similar nonlinear process. Adapted from Weisstein [45]

3.2.2. Zipf's Law

Mathematically, any simple mathematical operation that involves computation with increasing series of numbers (ranks, sequences) is graphically plotted as a hollow curve. The hollow curves that are high at low x values and trail off lower towards higher x values may be somewhat different depending on the mathematical operation. These are commonly generated on linear scales on the x and y axes by various formulae such as: exponential decay functions (Equation 2, where a is initial value, r as a decimal controls decay rate, and x is the period of time),

$$y = a(1 - r)^x \tag{2}$$

or an inverse power law (Equation 3, where the constant $A > 0$ and scales for height, and $\alpha > 0$ is steepness of decay),

$$y = \frac{A}{x^\alpha} \tag{3}$$

or simple logarithmic decay (Equation 4, where the constant $A > 0$ and determines rate of decay or growth, and +1 makes the logarithm defined for $x = 0$).

$$y = A\,(\ln(x) + 1) \tag{4}$$

Zipf's law , involving a harmonic series based on rank (1/2, 1/3, 1/4, etc.), in mathematics, parallels the fractal dimension of evolution when plotting species per genus producing a hollow curve with most area between 0 and 5 on the x axis [16,17]. Zipf's formula (Equation 5, where r is numbered rank and α is a power approximating one) indicates that the rank r of a progressive series approximates the inverse of the numbered rank with a power, α, and with α approximating one. Note the similarity with the inverse power law (Equation 3). Math clue for taxonomists: a negative exponent is equivalent to placing the variable in the denominator, and various authors replace r with x.

$$y \sim \frac{1}{r^\alpha} = r^{-\alpha} \tag{5}$$

A hollow curve [46] illustrates the meta-law of Constantin et al. which plots the frequency (in percent) of symbols and mathematical operators in physics equations [31]. In that, the analysis of numbers of operators (a measure of complexity) in physics equations peaks at 5 in Feynman's work with one-third more data counts than the sets of equations with next highest complexity, and also at 5 in the Wikipedia with more than twice the counts as the next highest; for equations in the Encyclopaedia Inflationaris, equations with complexity 5 were third highest in count, with only equations with 10 and 12 operators in complexity with higher counts. The meta-law for physics formulae of Constantin et al. is governed by Equation 6, where r is rank:

$$x \approx e^{-r/3} \tag{6}$$

A similar hollow curve is present when plotting species per microgenus (Fig. 2 above), and traits per species in micro genera [6,31]. Apparently, this feature of mathematics is closely connected with actual fractal processes in nature, much as set theory models simple arithmetical relationships in nature [6]. Processes in nature that involve growth commonly involve the constant e, for which all constant growth is a scaled version of 2.7182818...., hereinafter 2.72, as a common rate. For instance, periodically more rapidly increasing a unit amount 1 over time (like compounding interest) converges on 1 becoming 2.72. Zipf's law and e are connected by the principle of least effort and natural information optimization. In optimizing information systems (e.g. a branching pattern) e is the optimal base for natural logarithms as it maximizes growth rate for minimal cost. Zipf's law minimizes effort (as entropy). Together Zipf's law and e reflect the principle of maximum information for minimum energy.

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3.2.3. Fractal Representation of Macroevolution

The Pareto ratio constrains the result of the evolutionary process that approximates the universal phenomenon of 4-gets-you-5 (generation of four items results in a total of five items) generalizable to all taxonomic ranks, including that of trait. In other words, 20% of the species generate 80% of the critical shared traits (the immediate ancestron). The Pareto ratio is given by the Pareto distribution with α = 1.161 and is a "pattern constant." The Pareto distribution is essentially the same as Zipf's law, being the fraction $1/x^{\alpha}$.

In that lineages are ultimately connected; the Biosphere is a fractal (Fig. 10). All studied taxa, even including sets of traits, reflect a Pareto fractal dimension of ≈ 1.161, essentially that of the Pareto ratio that 20% of generators create 80% of that which is generated. In this example fractal image (Fig. 10), although based on the optimal fractal dimension of ln(5)/ln(4), here used for scaling, it is not particularly interpretable as representative of things or processes in nature. Mandelbrot did suggest some relationships in his work (but none of the present imaged bulbs, swirls and gyres can be construed to be of theoretic value [47]. Figure 10 is not immediately interpretable as a model of evolution. Only when AI Claude-3.5-Sonnet projected a tree-like image (discussed below), using iterated function system analysis, was modeling possible that reflects lineage change over time.

Figure 10: The Biosphere represented as a fractal image generated with the iterated formula $z = z^2 + c$, where z is a complex number and the complex number c is replaced with ln(5)/ln(4) as scaling factor. Image by AI Poe Assistant

There are many mathematical ways of generating fractal images. The most famous is the Mandelbrot Set (Equation 7 where z_n is a complex number sequentially, c is also a complex number, n is the iteration number, and z_0 initiates the sequence at zero). Complex numbers are generated from pixel coordinates, and include i the square root of minus one (including zero on the imaginary y-axis).

$$z_{n+1} = z_n^2 + c \tag{7}$$

For the Mandelbrot Set, the variable is c, for the Julia Set of fractal images the same general formula is used but the starting variable is z. Polar transformations create the spiral effects. For color effects no divergence results in black, otherwise number of iterations determine the color.

3.2.4. The Fractal Dimension

The fractal dimension is defined in practice as the log of the final number divided by the number generated from an originating number. The originating number is in this case 1, which is multiplied by the number of items generated to get x, while y is the total including the originating umber. The logarithms of these are divided, y by x, to get the fractal dimension in Equation 8. (Logarithms are powers representing, e.g., the dimensions square and cubic.)

$$\text{Fractal Dimension} = \frac{\ln y}{\ln x} \tag{8}$$

Number of branches at a node are limited by crowding. The first recursion is the dendrogram (tree) stem, the second is the first node of four branches. Number of branches in the whole tree increase with the power of the recursion, 1 recursion for 4 branches, 2 for 16, 3 for 64, 4 for 256, etc.

In studied cases of minimally monophyletic macroevolution, the one ancestor generated four descendant species resulting in five species in the group, hence ln(5)/ln(4). The Pareto fractal dimension is ln(5)/ln(4), or 1.160964047..., hereinafter 1.161, also written at log4 5. This controls processes involving self-similar projection of a short list of ancestral traits along a lineage. This universal or pattern constant ensures a complex stasis by preservation of the mostly four newest traits of the ancestor by ensuring their presence in all, mostly four, immediate descendants.

The "1 species generating the shared traits of 4 species" (the generation of the 4-gets-you-5 rule) concept matches the

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ubiquity of Pareto's principle, 20% of items generate 80% of that which is generated, based on the Pareto distribution (Equation 9). Again, 20% of the species generate 80% of the critical shared traits (the immediate ancestron). A is a scaling factor, usually 1; α is shape exponent of 1.161 value for fractal dimension of ln(5)/ln(4). Following Equation 3, if trhe Pareto index α = 1 then the Pareto distribution is the same as the Zipf law, and if α = ln(5)/ln(4) then it gives an inverted Pareto ratio of 80:20 as an integral from 1 to 4 compared to 4 to infinity, which is the key to the proportions of ancestor to descendants in a minimally monophyletic group [48]. Only a cut-off on the x-axis is needed to switch the ratio to 20:80.

$$y = Ax^{-\alpha} = \frac{A}{x^{\alpha}} \qquad (9)$$

A comparison of curves in Fig. 1 with various attempts to fit them using graphing software (Desmos) found that if 16 was substituted for *A* in Equation 3 for "1" in the numerator of Equation 9, and α was ln(5)/ln(4), then there was a good fit in curve shape and position on the x and y axes. This combination preserves the shape of the curve (exponent α) and fits the generally largest number species in the genera. That the numerator is optimum at 16 reflects estimated scaling in numbers of species per genus when calculated as following the formula (9). The Table 1 calculates that, with the Pareto alpha of 1.161, only one or two genera in a family of 36 genera will more than 8 species if the curve is followed, and 5 species per genus is uncommon.

Number of species	Calculation	Number of genera
1	$16/(1^{1.161})$	16
2	$16/(2^{1.161})$	7.16
3	$16/(3^{1.161})$	4.47
4	$16/(4^{1.161})$	3.20
5	$16/(5^{1.161})$	2.47
8	$16/(8^{1.161})$	1.43
10	$16/(10^{1.161})$	1.10

Table 1: Ideal number of genera as a function of number of species calculated with curve-fitting Equation 9, where A = 16 and α = ln(5)/ln(4)

3.2.5. Analogy with classical mechanics

This paper attempts to set plant systematics on a "hard science" footing, which means modeling processes in nature with equations and graphs. Standard mechanics in physics sets x as position, the first differential with respect to time as velocity, and the second as acceleration. Because we have a curve fitting actual data (Fig. 1), the analogy can be instructive. In Fig. 11. The inverse power function is graphed with A at one (the scaling factor does not change the shape of the curve) and α at ln(5)/ln(4) or 1.161.

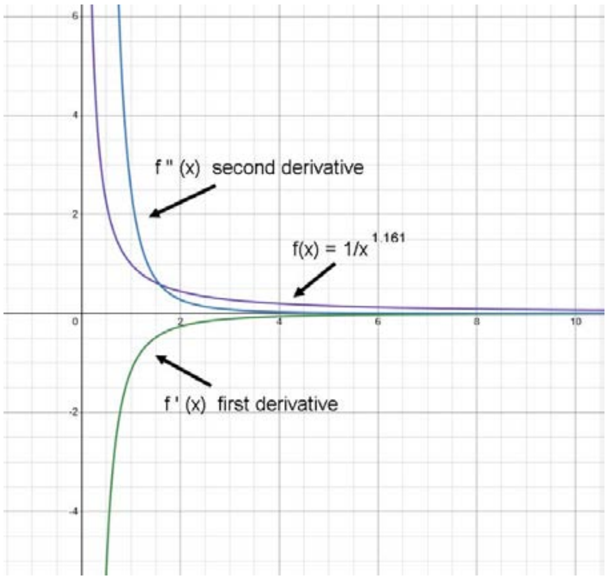

Figure 11: First and second derivatives for a formula fitting species per genus curves. All match at 1.161 on the x (number of species) axis

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The function itself is simply the position in "species-space," a static or equilibrium biodiversity pattern for any one x. The first derivative is analogous to velocity and represents the immediate change (instantaneous rate) in species numbers. The negative slope is the turnover rate in population dynamics and balances survival and extinction. It is analogous to kenetic energy $(f')^2/2$, while potential energy $\int f\, dx$ represents evolutionary potential. Apparently total energy, kinetic plus potential, is conserved across scales, with energy equivalent to conservation of information. The second derivative analogizes acceleration and represents the change in rate of evolution, particularly where evolutionary pressure is most strong and most adaptive. This mathematical structure suggests that speciation follows a universal scaling law where the rate of change (first derivative) and the rate of that change (second derivative) are connected through the ln5/ln4 ratio, producing a self-regulating system that balances diversification with stability. In Fig. 11 the curve of first derivative has positive slope and models punctuational equilibrium. It is mirrored by the second derivative modeling matching loss of evolutionary potential. The three curves nearly merge at x = 4 species, reflecting the Pareto distribution with α index ln(5)/ln(4), which is also the fractal dimension of the evolutionary process in nature. The curves of course changes with the exponent, but the graph is not a solution, it is a model given data from curve-fitting and the rule of four in speciation.

In that exploitation of current resources (x in the denominator) and exploration of new niches (A = 16 in the perfectly fitted curve) is optimal, species cannot improve fitness by changing strategy, which is typical of a Nash equilibrium. The factor 16 acts as a scaling constant that reflects the initial conditions (population size, carrying capacity), while the power law decay on the x axis with exponent ln(5)/ln(4) represents the balanced trade-off between competition and diversification. The rate of speciation (the first derivative) and the rate of competitive exclusion (the second derivative) balance each other leading to the minimax solution and ecological equilibrium. Details of the Nash equilibrium and minimax solution need formal mathematical validation.

3.2.6. The Pareto distribution

The parameter A in Equation 9 acts as a scaling factor that shifts the curve up or down while preserving its shape. It can represent the maximum number of species in a genus (probably less than) four recursions, see Fig. 12) that are possible given constraint of available supportive environment). Because the plots of Fig. 1 are the actual well-sampled data, then they may be treated as probability density curves, that is, summed below some length of the curve. If the fractal dimension is governed by a total of five species per genus, then the probability summed from 1 to 4 compared to that summed from 4 to infinity would give a proportion of numbers of genera with species expected to match the ideal of a minimally monophyletic genus (few species) with numbers of genera with more than 4 immediate descendant species. The areas from 1 to 4 and 4 to infinity under the curve for Equation 9 were calculated with the formula given in Equation 10.

$$f(x) = \int \left(\frac{1}{x^{1.16}}\right) dx \qquad (10)$$

Ln(5)/ln(4) is the fractal dimension of genus origination. For $f(x) = 1/x^{1.161}$, y = 0.20 when x = 4. Integration of the formula to estimate cumulative probability density used both Desmos graphing software and AI. Areas from x = 1 to 4, and 4 to infinity were calculated and normalized (values obtained divided by summed values). For Equation 10, x from 1 to 4 yielded 20 percent, and 4 to infinity 80%. This is the Pareto ratio but the reverse of the expected 20:80 paralleling the clear probabilities of four species being four times as likely as one species. Given that the numbers of species in a genus are not infinite, a truncation of the curve was made. Calculations were made to find what exact number of species allowed 4:1 ratio with exponent ln(5)/ln(4). This proved to be 7 species, with area from 1 to 4 at 0.80 and 4 to 7 at 0.20 (Fig. 12). The area from 1 to 4 ls a probability distribution for the set of immediate descendants, while that from 4 to 7 is the distribution for ancestral species and secondary ancestry (descendants of descendants not themselves ancestors). The immediate descendants appear to be of particular importance in filling the 80 percent slot of the Pareto ratio. The shape of the curve does not change at any scale, implying a fractal self-similarity across taxonomic ranks if, and this is yet to be determined, the number of elements in hierarchical ranks is about the same.

Perhaps unsurprisingly, the largest genus in the Streptotrichaceae has 7 species, matching the prediction of Fig. 12. Following the arguments of Guy, there are only 9 small numbers (1–9) and, when working with small numbers in somewhat unrelated studies, the chance of identity by chance alone is large [27]. Doubtless, there will be variation around these empirical results. Figure 12 reflects the Pareto ratio in only one of three ways. For five species (x = 5) the optimum of 4 descendants to 1 ancestor would imply a probability distribution of 4:1 (80:20), but this is considered optimum. For actual numbers of species per genus (microgenus), the range from 1 to 7 species yields a good theoretical model of evolutionary range. For the Pareto distribution formula for 1 to infinity, the ratio is reversed to 0.20 for 1 to 4 species and 0.80 for more than 4 species; and ratios 26.7 and 72.4 for 1 to 7 and 7 to infinity (the later more different from the Pareto ratio because infinity affects calculation).

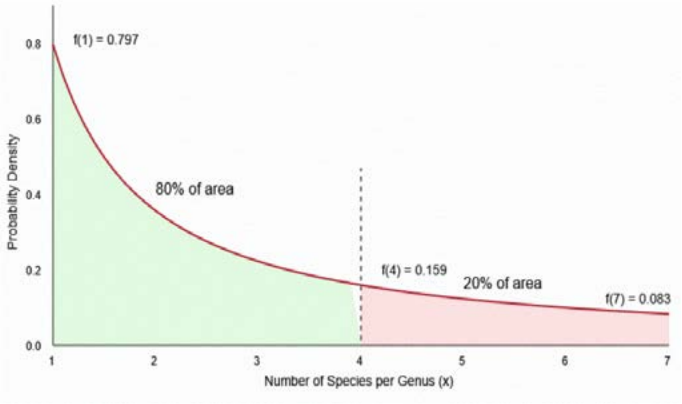

Figure 12: Cumulative probability curve of f(x) = 1/x1.161 for generation of the critical shared traits (the immediate ancestron) for species per genus truncated at 7 species, which is the actual maximum number of species among microgenera of Streptotrichaceae. Probabilities given for various values of numbers of species (x)

The Pareto ratio when described compares two different things, 20% of, say, pea pods generating 80% of peas, yet the probability density is of the 80% of peas compared to 20% of peas generated separately. This is a fractal product, with, say, 5 peas total and with the 4 peas generated by a different process being multiplied by 5/4, a number rendered as a fractal dimension by dividing logarithms.

3.2.7. The Quadratic Model of the Biosphere

The AI used iterative function system to provide a fractal model (Fig. 13) of an evolutionary scenario of four branches at each node, limited to four scales by a recursion depth of four. This reflected the fact that most recent (in a lineage) of actual minimally monophyletic genera in a family lineage were largely of four immediate descendant species, implying an immediate burst of speciation (see also Fig. 11). Genera with fewer descendant species apparently result from gradual extinction over the long term of these optimally 5-speciose genera, implying that four immediate descendants per ancestral species is both strongly encouraged and also strongly constrained by some process in nature, here suggested to be the Pareto pattern constant.

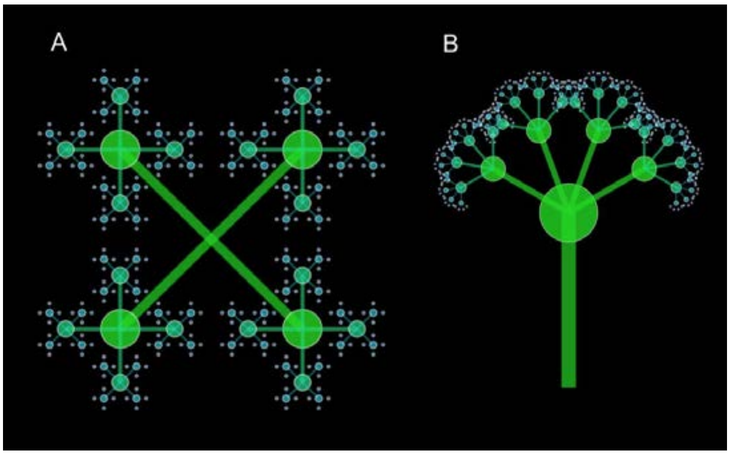

Figure 13: Iterative function system model of the Biosphere as a hierarchically nested taxon, limited to a recursion depth of four. The analogical glue attaching each species to the tree is the set of shared traits of the ancestor. The ln(5)/ln(4) paradigm is applicable at any rank because of self-similarity and scale invariance. A. Quadratic image preserving optimal 90° branching. B. Same model viewed laterally with 60° branching imposed to mimic standard evolutionary tree. Image made by AI Claude-3.5-Sonnet

An example of this fractal in nature (Fig. 14) is the "*Weissia* Probe" of Zander [6] p. 114, which analyzed *Neotrichostomum* and related genera in the West Indies. The genus *Neotrichostomum* is clearly ancestral to four other genera, two of which, *Chionoloma* and *Tainoa*, are microgenera (minimally monophyletic groups), and the other two are part of larger, unstudied groups. In the diagram, numbers refer to new traits evolved in those species (each set is a novon). The numbers of the evolutionarily active features at three different scales are within the range limited by the Pareto ratio of 20:80. Nature, given competition and extinction, does not follow scale invariance exactly [49]. The genus *Neotrichostomum* is ancestral to four other genera. If we fit it to a quadratic taxonomic hierarchy, perhaps it would be classified as a microsupergenus, or maybe just microsubtribus. Whether higher ranks are genuinely governed by the Pareto ratio, even locally, requires more study.

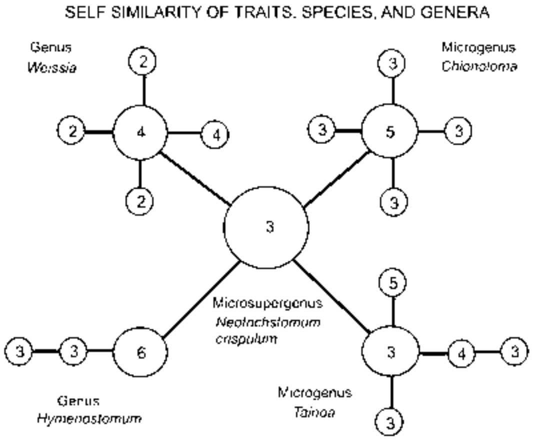

Figure 14: Quadratic evolutionary diagram of genera and species of the Neotrichostomum complex in the West Indies. Species are not named here. The word "Genus" labels larger, unstudied groups. Numbers give size of novon (set of newly evolved traits)

A plot of species per genus for the 36 studied microgenera (minimally monophyletic groups) (Fig. 15) is similar to the expected hollow curve for large classical taxa (Figs. 1 and 8), but is truncated for few numbers of species per genus because only fairly speciose genera were analyzed for the four-gives-you-five fractal character of a microgenus (excepting the family Streptotrichaceae). It was also truncated beyond seven species per genus theoretically by the Pareto pattern constant.

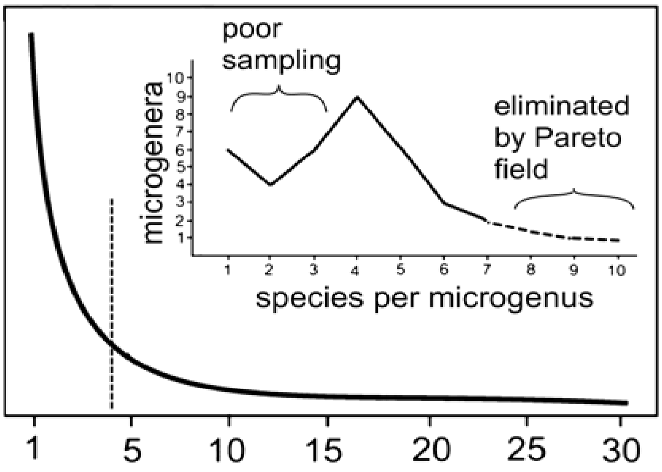

Figure 15: Expected hollow curve for species per genus, with inset species per microgenus (minimally monophyletic group). In inset, cropped curve going up where low on x-axis is due to analysis of only speciose groups (except Streptotrichaceae), and curve absent in the trail high on x-axis (beyond 7) because of truncation by Pareto effect inhibition of multiple descendants from one ancestral species

Darwin's [50] Origin of Species illustrated only one evolutionary tree. It was intended to demonstrate series of extinctions along branching lineages. It was not dichotomous, as is a cladogram, but multichotomous, a caulogram. One feature, in particular, differs from analysis of actual lineages of descent with modification [6]. Darwin assigned the most recent nodes to have fewest branches, implying continued gradual branching of older nodes. The most recent nodes in a real caulogram have fewer branches towards the base. Otherwise the number of branches per node, interestingly, of the two major Darwin branches, one had 22 nodes and averaged 2.9 branches per node (range 2 to 6, with mode of 4), and the other had 15 nodes and averaged 3.5 branches per node (range 2 to 5, mode of 4). Total average branches per node was 3.16. His guesswork on number of branches in speciation was pretty much spot on.

4. Discussion

4.1. Ecological Resilience

Ecological resilience can be defined as the quantity of disturbance that an ecosystem can tolerate without altering self-organized processes and structures [51,52]. Resilience may be modeled as resistance to a regime-shift including extinction through maximizing entropy p. 362 in basins of attraction or alternative states as a low point in a wavy graph or ball-in-cup model [12,53]. Dissipative systems are not Hamiltonian, that is, they are not fully conservative of total energy, and tend to a maximum entropy or equally of Shan-

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non information [54]. In the context of evolutionary taxonomy, resilience is the survival of a nearly complete lineage across rather long time-scales. Modern floras are composed of taxa with at least fossils and often extant genera and species reaching back to the late Cretaceous, as exemplified by a microgeneric (descent with modification) study of the family Streptotrichaceae [3,4]. In the case of the great apes, one can use the Copernican method to predict that the Homininea has at least a small chance of lasting another 200 kiloyears with no changes in its resilience to environmental change, and has a 95 percent chance of lasting another 5,000 years [5,55,56].

4.2. Chaos

The past development of probabilistic methods was a major advance over deterministic formulae and laws in western science, but now chaos and complexity theory have shown that some simple iterative formulae can generate a wide range of complex values that are entirely determined at the outset but show an intrinsic order among highly elaborate and apparently chaotic results. Chaos theory is a vast subject, often well discussed in popular science literature [36,57]. Chaos is easiest exemplified by the logistic map (or quadratic map) generated (Fig. 9) by iteration of a simplified Equation (11):

$$y = rx(1 - x) \tag{11}$$

Solving (1) for y, where y = x_{n+1}, with different values of x between 0 and 1 gives a simple range converging on 0.5, where 0.5 is termed the "attractor," but this is true only below r ≈ 3.449 [37,57,58]. At r ≈ 3.449 continued iteration of Equation 11 gives two values, and with increasingly larger r, say 3.7, a rapid series of essentially random, or chaotic, bifurcations occurs. Above r ≈ 3.7, in the so-called "chaotic regime," the values of y = x_{n+1} are totally irregular and there are no attractors. The formula above is one of the simplest that exhibits chaotic behavior. Following Sheffield p. 277, the formula y = sin(x_{n+1})/4, where y = x_{n+1}, has r initiating bifurcations at r = 3.4 [57]. For all different iterative formulae that exhibit a kind of chaotic graph, a "metric universal" number, ≈ 4.669, the Feigenbaum constant δ, describes the rate at which new states are introduced, that is, the ratio of intervals between bifurcations on a logistic map. Another number, ≈ 2.503..., the Feigenbaum constant α, describes the ratio of the widths of bifurcation intervals at the point of change from simple, periodic bifurcations to when they become chaotic.

The generation of bifurcations in simple single-variable iterative formulae involves a universal connection between all of these formulae. This deep universal may also govern or be implicated in individual ancestor-descendant splitting of a lineage, either at species or genus levels. It may constrain an expressed-trait morphological clock similar to that assumed, and evidenced by fossils, in molecular studies [4]. Lineages do split, and a limited enforced periodicity akin to punctuated equilibrium p. 308 may promote survival of a lineage where chaotic crowding is not adaptive [59]. Rapid diversification may be adaptive because increasing time between speciation events reduces available habitat space logarithmically by competition with other immediate descendants The rule of four in evolution —one ancestral species and four immediate descendant species—is in part derived from the hollow curves of graphs plotted with species per genus and genera per family, these showing a preponderance of species (and genera) in groups of five. The restriction of numbers of species in a minimally monophyletic genus to five may be limited by competition during dispersal of the optimally four descendant species at the periphery of an ancestral range, as illustrated and discussed by Zander [17]. If x in the logistic equation (11) represents the generating function ln(4) and 1–*x* is ln(5) the constraining function, and r is pressure into speciation at the moment of punctuation filling a newly vacated niche, then edge of chaos is a likely model.

4.3. Complexity and Fractals

In addition to deeply hidden universal features of evolution that initiate and constrain splitting of a lineage, another universal process ingrained and powered by natural selection, is the fractal nature of genera with self-similarity at higher and perhaps lower taxonomic ranks. Genetic drift is an important precursor to speciation but only as influencing expressed traits tolerated during natural selection. This conservation under self-similarity is quite like the deep symmetries in physics [60,61]. The fractal pattern of evolution is that generation of four species creates five total, while generation of four genera also creates five total. This is fractal evolution, with a Pareto fractal dimension ≈ 1.161 (or ln(5)/ln(4)). Fractals are complex figures similar to the logistic map but are commonly imaged by formulae with two or more formulae with multiple variables. When these are complex numbers, the quantity *i*, $\sqrt{-1}$, is included. Sheffield [57] p. 278 offered a simple example:

$$y = (w^2 + x^2) + a \tag{12}$$
$$z = 2wx + b \tag{13}$$

Solving for y (in Equation 12) and z (in Equation 13), then replacing w and x with y and z iteratively, creates a phase-space diagram of non-periodic attractors p. 113) associated with the Mandelbrot set of fractal images that preserve structural features across scales [62].

Redundancy of information that allows (1) positive survival of descendant species peripatrically, and in which an ancestral morpho-species in a minimally monophyletic group, through natural selection and genetic drift, invests all (optimally) four descendant species with the (optimally) four newly evolved traits of the ancestor [36,63]. These promote survival sympatrically while the (optimally) four new traits of each descendant have selective advantage in adjacent allopatric ranges. Also, (2) survival of a lineage through geological time intervals is possible due to the rule of four which ensures abundant redundancy through continuance of survival-enhancing traits in all descendants. This taming of chaotic turbulence in evolutionary processes is discussed at length by Zander [3,4].

A theory may be advanced, then, that evolution includes two intertwined processes, (1) the splitting of lineages into an-

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cestor and descendant, which develops newly characterized species to explore and adapt the lineage to changing environments, and (2) the protection of the immediate ancestron (the newest traits of the ancestral species) that preserve the adaptive footprint. The first process is species-based, and may be described by order of origination of species, i.e., a dichotomous tree; the second is genus-based and described by passage of sets of proven traits on a multichotomous tree. The processes are at different levels of interaction of organisms and their environment but proceed as a complex adaptive system, isomorphic with the patterns like the logistic map and fractal imagery.

In summary, decoherence of a lineage may be described by chaos theory, and coherence by complexity theory, together parsimonious of biomass and maximizing informational entropy, i.e., reducing uncertainty while protecting the survival of information through redundancy. This multiplex theory of evolution is apparently controlled by deep universal processes (43,46) at the edge of chaos p. 292ff and governed by resonances and divergences in complexity theory p. 116. It is obtained by numerical methods of analysis of abundant data rooted in taxonomy [59,62,63]. One may ask what causal operation may be involved in the lineage-level evolutionary process and get "a process" as a response. The word "process" in evolution may be likened to the term "field" in physics as mathematical descriptions of actions filling space. Here I advance the Pareto ratio or pattern constant as a rather solidly based equivalent field with α the variable. We can measure gravity and electromagnetic forces and predict results and limitations but what they actually are is as yet beyond mind's reach. We don't even know what "distance" means, given the quantum microcosm and the space-like relativity of the macrocosm, and this not even mentioning the limitations on set theory by category theory and Gödel's theorem [64].

The four-gets-you-five process has a fractal dimension of 1.161, which is apparently universal as evidenced in the hollow curves of species per genus and genera per family, showing self-similar distributions of 5-speciose and 5-genera taxa in many groups. The graph plots exhibit the long and broad asymptotic tail of a power law, which is an exponential curve that exists as a straight line if both graph axes x and y are logarithmic scales [48]. A minimal example is the equation $y = 1/x$, where x has the exponent 1. Decreasing the exponent from 1 towards zero thickens the tail of the curve. All the simple inverse functions have a straight line when graphed with log scales on both axes. Power laws are major sources of the self-similarity in fractal diagrams in that, most simplistically by rescaling the variable (multiply by a constant), proportionality is preserved [39,47].

4.4. Combining the Laws

Various formulae that are associated with fractal evolution and symmetry breaking are variations on a basic identity, the inverse power law, see Equation 14, duplicated here:

$$f(x) = \frac{A}{x^{\alpha}} \qquad (14)$$

A is a scaling factor and does not affect the shape of the curve. If $A = 1$, then the inverse power law is the same as Zipf's law when $\alpha = 1$; and is the same as Constantin's meta-law for physics when $\alpha = 1/3$; and also is the same for Pareto ratio, nearly matched when $\alpha = 1.161$. It is probable that graphs of the results of many processes in nature are simply inverse power laws with α and A as variables, including a hypothetical Pareto field that confines symmetry breaking to the immediate ancestron during speciation [16]. The mathematical connections of α in this context is extensively discussed by Newman, who pointed out that power law distributions are the only distributions that appear the same no matter what scale we use [48]. That is, power laws are scale-free, as are fractals, although it must be pointed out that some distributions are power law only in the tail. Searches for any sign that the Pareto principle is simply an optimized function of some constant in nature went unfulfilled, which indicates that α of 1.161 has a fundamental footprint in nature, also because it is retained as a shape parameter across scales.

4.5. Extinction

The above discussion is limited to speciation, its origin and limits. Speciation is balanced by extinction. The former is apparently caused in bursts, as punctuated equilibrium operating on extant taxa, but the analysis of the family Streptotrichaceae indicates that extinction is gradual except for geologically occasional major catastrophes [20,44,65]. A tentative hypothesis may be advanced that uses the "hot bunk" model, that new niches are simply niches vacated by recently extinct species. At the genus level, it is possible that rapid expansion (Fig. 11) into a newly vacated niche followed by punctuational diversification may fill that niche with descendant species either in fractal shoreline isolated areas (see Figs. 5 and 7) and/or genus-level Turing patterning from inter sibling competition (they share the same ancestral traits) leading to a quadratic dispersal (Fig. 13) of immediate descendant species. As gradual extinction takes place through an increasingly less amenable environment, the ancestral or least specialized species in the genus fills in the niches of the newly extinct descendant species. When the last species of the genus goes extinct, it's now vast niche is exposed for another round of punctuated diversification and gradual trimming of species.

4.6. Common Ancestry Analysis

The present paper does not fit the standard Lakatos Ian Research Programme in that it uses a fairly new method, therefore its fundamentals do have to be defended against the immediate question: "Why don't you use phylogenetics? The differences between the present method, a numerically enhanced evolutionary taxonomy, and cladistics are detailed in recently published papers [4,6,7,11].

The present paper is intended to encourage classical evolutionary taxonomy by offering new numerical methods in the context of descent with modification. This is in opposition to the general deprecation of classical evolutionary taxonomy by cladists as "traditional taxonomy," bringing to mind painted shamans dancing around a smoky fire amid sounds of popping bladders and hoots of supplication to dark and ugly

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gods. Cladists have even published screeds averring the lack of scientific value of the concepts of genera and even species [66-68]. To cladists, taxa, particularly genera, are taken as only notional and anyway unnecessary because common ancestry may be gauged by clades at all levels on a rigorously constrained dichotomous tree of common ancestry [69]. On the other hand, taxa, in descent with modification analysis, are alike in being theoretically invariantly self-similar in construction. Yet they differ in their effect on the ecosystem according to the scales at which they operate, including trait, species, genus, family, kingdom, domain, ecosystem, and biosphere. The hollow curves of cladistic-bloated genera are artificially fattened in the x-axis tail, which does not fit the $16/x^{1.161}$ curve approximating the perceived Pareto effect in evolution (Fig. 1), but, ignoring unexplained lumpiness caused by isolated large groups, instead their generation in cladistics reduces the value of the exponent towards zero. The ln(5)/ln(4) fractal exponent is a fundamental scale-free feature of evolution and this natural attractor should not be changed. Thus, taxonomic rank, as determined in evolutionary taxonomy, is an important differentiation (see also Humphreys and Barraclough and all ranks, given self-similarity, may be modeled as distinct actors in evolution [70].

The core of a taxon is the genus' immediate ancestron as constrained by the Pareto effect, whose symmetry is broken by natural selection and genetic drift, making species and genera very real entities reflecting distinct processes in nature. Suppose we were to use molecular methods with DNA bases for tracking evolution? For a minimally monophyletic group of one ancestral species and, say, four descendant species, there will potentially be five species and 10 evolutionarily informative molecular ancestral variants involved. Searching for paraphyly-apophyly pairs adequately will require more abundant sampling than done at present. It is possible to go beyond simply ascribing ancestor status to a paraphyletic species by using nearest neighbor analysis, but it remains essential that morphological and molecular results are separate and match, and this means a quadratic or at least multichotomous model for both.

5. Conclusions

Some readers familiar with the details of microevolution theory may wonder how evolutionary information is shared without genetic exchange (excepting horizontal gene transfer). In self-similar processes of macroevolution, information is shared by common environmental pressures mediated by physical laws and principles, with ln(5)/ln(4), having a goad for change with ln(5), and a constraint from overgrowth and crowding with ln(4). A research focus on this neglected aspect of macroevolution might be termed "phylophysics."

The "rule of four" theory summarized across several previously cited papers is as follows: Powered by natural selection, a minimally monophyletic unit, the microgenus, maintains an optimizing proportion of character traits that strengthens and sustains the microgenus (and larger context) across millions of years. Microgenera have both novons (new traits unique to the descendant species) and immediate ancestrons (a set consisting of the new traits of the ancestral species shared by all immediate descendant species). The novon provides adaptations for that part of the genus in a similar peripheral or allopatric niche while being fairly neutral sympatric with the ancestor. The immediate ancestron provides initial survival and protect mutations by generating isolation with Turing patterns sympatrically, and give a kind of disguise of shared major traits against overwhelming competition by the ancestor. Turing patterns plus the four-color theorem may allow a possible model explaining the ecological/competition basis for the rule-of-four. In terms of the Lotka-Volterra model, there are only rabbits. No dominance is provided to any one descendant species either sympatric with the ancestral species or when ultimately isolated in a maximally supportive niche. The scenario is thus: A preliminary loading of an empty niche with up to four descendant species, which compete little with each other. Differentiation sympatricially is limited until the four-color theorem enhances isolation and speciation into niches. Additional descendants are limited by crowding and competition. The rule-of-four is maintained by balancing maximum isolation promoting speciation and minimum competition restricting speciation. Competition for area increases as the square while speciation increased as a quadratic.

Peripatric shoreline fractals are the ultimate goal of the descendant species traverse of the ancestral area. Four traits in the novon and four immediate descendants is apparently associated with crowding and the Pareto effect. This is optimum survival for any genus. The "hot bunk" model of punctuated evolution as gradual extinction expanding the range of one species (usually the unspecialized ancestral species) into the ranges of extinct descendants, then revealing a major vacant niche when the last species of a microgenus disappears. A potential ancestral species of another genus expands rapidly into that vacancy with concomitant burst of diversification into a microgenus. Evidence for a rule of four evolutionary theory is: (1) Characteristic hollow curves of fractal dimension 1.161 reflecting the operation of the Pareto effect. (2) All 36 genera examined for minimally monophyletic structure showed the presence of an immediate ancestron as a set of traits identical with the ancestral species' new traits also duplicated in all one to four immediate descendants. (3) Specialized species may be found sym-, peri-, and allopatrically in the ranges of an ancestral generalized species. (4) Mirror parity implies the persistence of a rule of four as a real evolutionary feature. (5) Recent microgenera are larger than more ancient microgenera, seemingly developed rapidly. (6) Evolutionary forces hypothesized here are similar to physical laws in potency and universality.

The ultimate winner of maximized biodiversity is the biosphere (Fig. 10 and 13). The two pattern constants 4.66, being the Feigenbaum δ, and 1.161, as the Pareto fractal dimension, are involved closely with evolution as a timewise sequence of speciation events. These universals, plus the edge of chaos, the latency of the immediate ancestron in the hollow curve, and the restrictions of the Pareto ratio, all effectively balance decoherence and fixation of species-level mutation among descendant species, and coherence and resilience by protecting and banking survival-effective traits.

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One can theorize that complexity processes possibly involving convergence and symmetry breaking of physics in the quasi-Zipfian context provide and control trait redundancy that serves to stabilize lineages and provide resilience over long time spans, while processes of chaos initiate and control lineage splitting. This study in fractal modeling uses accumulated data from prior published taxonomic study that generated evolutionary trees with high statistical support from morphological and molecular analyses including both standard Markov chain Monte Carlo Bayes with molecular data, and Turing sequential Bayes with Shannon information for morphological data [9]. This is new science that presents clearly testable inferences based on data to date not available to or ignored by researchers focused in microevolution, particularly those using analysis by shared ancestry [71-73].

Two fractal images, Figures 10 and 13, represent the ln(5)/ln(4) dimension associated with symmetry breaking of speciation. The first, a rococo image (Fig. 10) based on $z_{n+1} = c + z_n^2$ with $c = \ln(5)/\ln(4)$, do not present any clear analogy or modeling with natural phenomena. The other, a simple four-branching tree (Fig. 13) based on simple recursions at ln(5)/ln(4) in an iterated function system, is a good iconic model fitting macroevolutionary Darwinian theory of descent with modification [74]. What natural causes generate both the object in nature and constrain the model? It has been said that it is possible to deduce the shape of an invisible object by examining the holes left by its passage [75]. The simple tree of Figure 13 may be filed by a Pareto "field" pervading all of evolution (or every process generating an inverse power law) that is no more magical (and no less) than those of electromagnetism and gravity.

One can theorize that complexity processes provide and control trait redundancy that serves to cohere lineages and provide resilience over long time spans, while chaos processes initiate and control lineage splitting. Universally effective but somewhat hidden closely related fundamental constants of the evolutionary process include the Feigenbaum δ constant ≈ 4.66..., ruling the logistic graph in Chaos theory, and the Pareto fractal dimension ≈ 1.161in complexity theory describing self-similar projection of a short list of ancestral traits along a lineage. These two universals are scale-free and effectively balance decoherence and fixation of species-level mutation among descendant species, and coherence and resilience by protecting and banking survival-effective traits. The constant e is not scale-free but doubtless plays a role in limiting growth patterns (e.g. compounding interest) while ln(5)/ln(4) is a discrete power-law scaling. Sustainable branching patterns require a balance of these two processes. The optimal branch scale is $e^{-1/\alpha}$ where $\alpha = \ln(5)/\ln(4)$. The continuous growth rate is limited by e. Together they create stable fractal patterns that efficiently balance growth rate and resources by e and Pareto limitation, respectively [76]. Trees that exceed a certain small size are unstable. According to Bochert and Slade: "As soon as trees surpass a certain, relatively small size, tree structure ceases to be predictable by deterministic branching rules [77]. Extrapolation from small to large branching systems requires the prediction of size-dependent structural changes by stochastic rules which allow for phenotypic variation, yet conserve the specific architectural model of a tree."

Not only does the Pareto principle appear in many natural and social systems as a self-organizing principle, the ratio ln(5)/ln(4) may be a natural optimum for branching structures were more than four branches become inefficient, and the 1.161 scaling factor represents (models) an optimal balance between diversification and resource constraints. Given the facts and above interpretations, it is possible to conclude that taxa are generated by serial symmetry breaking at fractal ln(5)/ln(4). Given self-similarity, this applies to all taxa affected by the Pareto field, including every one of those generating the many similar hollow curves drawn by Willis [9]. The fractal tree (Fig. 13) with four branches per node models the Pareto field, while the size and depth of the branches at fractal dimension 1.161models competition for resources when optimizing exponential growth.

Data on mathematical features of macroevolution allow phylophysical investigations at the intersection of chaos and complexity theory using fractal images that reflect or even reveal certain constants of nature. Results using iterative function system methods with AI software (all arithmetic checked carefully) carrying the mathematical load suggest that Pareto's law operates to ensure a balance of stability and adaptability across taxonomic scales, including traits, species, genera and theoretically higher ranks. Evolution of demonstrably real taxa at levels higher than species is apparently governed by universal processes of constraint and decoherence involving physical constants [3,6]. This paper hypothesizes that new genera are developed in a burst of a few million years as optimally four immediate descendant species from one ancestral species [4]. These share the (optimally) four new traits evolved by the ancestor and parceled out exactly to all optimally four descendant species. This is mirror parity, with the four ancestral traits equally shared and newly evolved traits of each descendant obtained by state changes of old traits unused by the ancestral species. Speciation is, then, through symmetry breaking of the traits shared by all descendants as one or another descendant evolves new traits with mirror parity, but keeps the newest traits of the ancestor. This applies as self-similarity to traits, species, genera, and even families because of self-similarity due to stability across scales of ln(5)/ln(4) exponent. To be investigated in the future is whether speciose groups be deconstructed into microgenera given a limit on the number of traits distributable monothetically, or are large genera major exceptions to the rule, and if so, do polythetic genera share a sustaining but contrary physical principle?

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References

1. Sokal, R. R., & Sneath, P. H. (1963). Principles of numerical taxonomy.
2. Krakauer, D. C., Collins, J. P., Erwin, D., Flack, J. C., Fontana, W., Laubichler, M. D., ... & Stadler, P. F. (2011). The challenges and scope of theoretical biology. Journal of theoretical biology, 276(1), 269-276.
3. Zander, R. H. (2024). Minimally monophyletic genera are the cast-iron building blocks of evolution. Ukrainian Botanical Journal, 81(2), 87-99.
4. Zander, R. H. (2024). Lineages of fractal genera comprise the 88-million-year steel evolutionary spine of the ecosphere. Plants, 13(11), 1559.
5. Zander, R. H. (2025). On the Origin of Taxa.
6. Zander, R. H. (2023). Fractal evolution, complexity and systematics. St. Louis (MO): Zetetic Publications, 1-151.
7. Zander, R. (2024). Integrative systematics with structural monophyly and ancestral signatures: Chionoloma (Bryophyta). Academia Biology, 2(4).
8. Beres, K. A., Wallace, R. L., & Segers, H. H. (2005). Rotifers and Hubbell's unified neutral theory of biodiversity and biogeography. Natural Resource Modeling, 18(3), 363-376.
9. Willis, J. C. (1922). Age and area: a study in geographical distribution and origin of species. The University Press.
10. Zander, R. H. (2018). Macroevolutionary systematics of Streptotrichaceae of the Bryophyta and application to ecosystem thermodynamic stability (pp. 1-237). St. Louis: Zetetic Publications.
11. ZANDER, R. H. (2021). Evolutionary leverage of dissilient genera of Pleuroweisieae (Pottiaceae) evaluated with Shannon-Turing analysis. Hattoria, 12, 9-25.
12. Brooks, D. R., & Wiley, E. O. (1988). Evolution as entropy: toward a unified theory of biology. University of Chicago Press.
13. Ellis, G. F., & Di Sia, P. (2023). Complexity theory in biology and technology: broken symmetries and emergence. Symmetry, 15(10), 1945.
14. Packard, N. H. (1988). Adaptation toward the edge of chaos. Dynamic patterns in complex systems, 212, 293-301.
15. Strogatz, S. H. (1996). Nonlinear dynamics and chaos.
16. Aitchison, L., Corradi, N., & Latham, P. E. (2016). Zipf's law arises naturally when there are underlying, unobserved variables. PLoS computational biology, 12(12), e1005110.
17. Zander, R. H. (2025). Geometric Models of Speciation in Minimally Monophyletic Genera Using High-Resolution Phylogenetics. Plants, 14(4), 530.
18. Krakauer, D. C. (2023). Symmetry–simplicity, broken symmetry–complexity. Interface Focus, 13(3), 20220075.
19. Hartl, D. L. (2020). A primer of population genetics and genomics. Oxford University Press.
20. Plotnick, R. E., & Sepkoski Jr, J. J. (2001). A multiplicative multifractal model for originations and extinctions. Paleobiology, 27(1), 126-139.
21. Fox Keller, E. (2007). A clash of two cultures. Nature, 445(7128), 603-603.
22. Boehm, A., & Ruvalcaba, Z. (2015). Murach's HTML5 and CSS3. Mike Murach & Associates.
23. Barnsley, M. F., & Demko, S. (1985). Iterated function systems and the global construction of fractals. Proceedings of the Royal Society of London. A. Mathematical and Physical Sciences, 399(1817), 243-275.
24. Barnsley, M. (1988). Fractals everywhere Academic press. New York.
25. Barnsley, M. F., & Vince, A. (2011). The chaos game on a general iterated function system. Ergodic theory and dynamical systems, 31(4), 1073-1079.
26. Hutchinson, J. E. (1981). Fractals and self similarity. Indiana University Mathematics Journal, 30(5), 713-747.
27. Guy, R. K. (1988). The strong law of small numbers. The American Mathematical Monthly, 95(8), 697-712.
28. Tryon, E. P. (1973). Is the universe a vacuum fluctuation?. Nature, 246(5433), 396-397.
29. Harte, J., & Newman, E. A. (2014). Maximum information entropy: a foundation for ecological theory. Trends in ecology & evolution, 29(7), 384-389.
30. Gazzarrini, E., Cersonsky, R. K., Bercx, M., Adorf, C. S., & Marzari, N. (2024). The rule of four: Anomalous distributions in the stoichiometries of inorganic compounds. Npj Computational Materials, 10(1), 73.
31. Constantin, A., Bartlett, D., Desmond, H., & Ferreira, P. G. (2024). Statistical Patterns in the Equations of Physics and the Emergence of a Meta-Law of Nature. arXiv preprint arXiv:2408.11065.
32. Mandelbrot, B. (1960). The Pareto-Levy law and the distribution of income. International economic review, 1(2), 79-106.
33. West, G. B., & Brown, J. H. (2004). Life's universal scaling laws. Physics today, 57(9), 36-42.
34. Barrow, J. D. (2002) The Constants of Nature. Pantheon Books, New York.
35. Garrigues-Baixauli, J. (2022). The Origin of the Fundamental Constants.
36. Gleick, J. (2008). Chaos: Making a new science. Penguin.
37. Infeld, E., & Rowlands, G. (2000). Nonlinear waves, solitons and chaos. Cambridge university press.
38. Pimm, S. L. (1984). The complexity and stability of ecosystems. Nature, 307(5949), 321-326.
39. Schroeder, M. (2009). Fractals, chaos, power laws: Minutes from an infinite paradise. Courier Corporation.
40. Hastings, A., & Powell, T. (1991). Chaos in a three-species food chain. Ecology, 72(3), 896-903.
41. Bak, P., Tang, C., & Wiesenfeld, K. (1988). Self-organized criticality. Physical review A, 38(1), 364.
42. Kauffman, S. (1993). Self-organization and selection in evolution. The Origins of Order. Oxford University Press,

Citation: Zander, R. H. (2025). On the Origin of Taxa. *J Theor Phys Math, 3*(1), 1-20.

London.
43. Lewin, R. (1999). Complexity: Life at the edge of chaos. University of Chicago Press.
44. Eldredge, N. (1986). Time frames: The rethinking of Darwinian evolution and the theory of punctuated equilibria. (No Title).
45. Weisstein, E. W., & Problem, C. (2005). From MathWorld–A Wolfram Web Resource http://mathworld. wolfram. com. Collatz Problem. html.
46. Wilkins, A. (2024) The laws of physics appear to follow a mysterious mathematical pattern. New Scientist, 21 October 2024. Viewed 4 March 2025.
47. Mandelbrot, B. B. (1983). The fractal geometry of nature/Revised and enlarged edition. New York.
48. Newman, M. E. (2005). Power laws, Pareto distributions and Zipf's law. Contemporary physics, 46(5), 323-351.
49. Newberry, M. (2025) Art and science illuminate the same subtle proportions in tree branches. The Conversation, 11 February 2025
50. Darwin, C. (1861). On the origin of species by means of natural selection, or, the preservation of favoured races in the struggle for life. J. Murray.
51. Gunderson, L. H. (2000). Ecological resilience—in theory and application. Annual review of ecology and systematics, 31(1), 425-439.
52. Holling, C. S. (1973, November). Resilience and stability of ecological systems.
53. Ludwig, A. K., Barnes, C. D., Fogart, D., Fowler, J. A., Hogan, I. F. E., Johnson, J. E., Twidwell, D. (2020) Ecological Resilience. Plant and Soil Sciences eLibrary Lessons. Accessed Dec. 28, 2025.
54. Weber, B. H., Depew, D. J., Smith, J. D., & Dyke, C. (1990). Entropy, information and evolution: new perspectives on physical and biological evolution. Behavior and Philosophy, 18(2).
55. Gott, J. R. (2002). Time travel in Einstein's universe: the physical possibilities of travel through time. Houghton Mifflin Harcourt.
56. Poundstone, W. (2019). The doomsday calculation: how an equation that predicts the future is transforming everything we know about life and the universe. Hachette UK.
57. Sheffield, C. (1999). Borderlands of Science: How to Think Like a Scientist and Write Science Fiction. Baen Books.
58. Lurie, R. M. (2011) Classic Logistic Map, Heikki Ruskeepää. Wolfram Demonstrations Project. Accessed 2 Feb. 2025.
59. Waldrop, M. M. (1992). Complexity: The emerging science at the edge of order and chaos. London: Penguin.
60. Gross, D. J. (1996). The role of symmetry in fundamental physics. Proceedings of the National Academy of Sciences, 93(25), 14256-14259.
61. Wegsman, S. (2025) How Noether's theorem revolutionized physics. Quanta Newsletter Feb. 7, 2025. Viewed February 27, 2025.
62. Nicolis, G., & Prigogine, I. (1989). Exploring complexity: An introduction.
63. Gleick, J. (2011). The information: A history, a theory, a flood. Vintage.
64. Kline, M. (1982). Mathematics: The loss of certainty (Vol. 686). Oxford University Press.
65. Hughes, B. D., & Reed, W. J. (2002). A problem in paleobiology. arXiv preprint physics/0211090.
66. Stevens, P. F. (1985). The genus concept in practice: but for what practice?. Kew Bulletin, 457-465.
67. Stevens, P. F. (2002). Why do we name organisms? Some reminders from the past. Taxon, 51(1), 11-26.
68. Mishler, B. D. (2021). What, if anything, are species? (p. 168). Taylor & Francis.
69. Humphreys, A. M., & Linder, H. P. (2009). Concept versus data in delimitation of plant genera. Taxon, 58(4), 1054-1074.
70. Humphreys, A. M., & Barraclough, T. G. (2014). The evolutionary reality of higher taxa in mammals. Proceedings of the Royal Society B: Biological Sciences, 281(1783), 20132750.
71. Ferriere, R., & Fox, G. A. (1995). Chaos and evolution. Trends in ecology & evolution, 10(12), 480-485.
72. Minelli, A., Fusco, G., & Sartori, S. (1991). Self-similarity in biological classifications. BioSystems, 26(2), 89-97.
73. Green, D. M. (1991). Chaos, fractals and nonlinear dynamics in evolution and phylogeny. Trends in Ecology & Evolution, 6(10), 333-337.
74. Harré, R. (1985). The philosophies of science.
75. Hughes, M. (2014) The Gist Hunter. Nightshade Books, New York.
76. West, G. B., Brown, J. H., & Enquist, B. J. (1999). A general model for the structure and allometry of plant vascular systems. Nature, 400(6745), 664-667.
77. Borchert, R., & Slade, N. A. (1981). Bifurcation ratios and the adaptive geometry of trees. Botanical gazette, 142(3), 394-401.

Citation: Zander, R. H. (2025). On the Origin of Taxa. *J Theor Phys Math, 3*(1), 1-20.