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The Evolutionary Information Mass-Energy Equivalence of Two-Sigma Bryophyte Lineages

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Abstract

Lineages are conceived as corridors through time of two-sigma exclusion of uncertainty by Bayesian analysis of numbers of morphological traits and species. Methods of structural monophyly constructed evolutionary dendrograms of a family and of a tribe of bryophytes. Shannon informational bits known for speciation events in these groups allow projections of changes into the past. Sampling and relationships in the present imply kinds and rates of origination and extinction of species. Vopson's estimates of the mass of one informational bit is used to calculate total mass of information of two bryophyte lineages from total bits associated with speciation over time. Mass-energy equivalence calculations estimated energy needed for archiving information associated with maintenance of structural and thermodynamic integrity over millions of years. Three levels of observational sampling yield similar information for the two lineages. The Rule of Four is a thermodynamically enforced efficiency limit expending the least free energy to keep error correction active and is a hyper efficient compression processor. Pareto Fractal Dimension allows lineages to maintain a maximum of adaptive variation with minimal energetic overhead. The energetic cost of ongoing structural stability of Streptotrichaceae over 100 million years is about 11.7 megajoules, for Pleuroweisieae about 10.7 megajoules. The entire Biosphere of an estimated one million lineages at 25 species per lineage is stabilized over that time at a cost of about 1.1 × 10^{07} megajoules. The mass-energy equivalence principle may be interpreted as a bound on the structural work done by the Biosphere.

Keywords: Biophysics, Bryophytes, Evolution, Energetic Information Archive, Mass-energy Equivalence Principle, Lineages

1. Introduction

1.1. Synchronicity of view

This paper is one of a series recasting evolutionary systematics in terms of the principles of physics. Here we explore the concepts of discrete time physics as a real-world application. Systematics, the study of organisms and their evolutionary relationships, is a historical science. It is part of the Linnean Endeavor, to discover, classify, describe and explain the diversity of life. This paper evaluates two bryophyte lineages as sums of their information content as that changes over time and reports the calculations as archived mass-energy equivalents. This is a way of evaluating calculated past models of the lineages as they change over a span of about 100 million years. Such change is an important dimension to biodiversity study, and justifies viewing lineages as sets of information in four dimensions. The fundamental value is the thermodynamic cost of such archiving. This is the cost of continued survival and resilience of lineages over millennia against continued resistance of environmental entropy.

The evolutionary lineage of the Streptotrichaceae is rather large in four dimensions, being modeled as branching informational fibers. The limit is the age of the oldest known or well-inferred taxon in the lineage [1], ca. 100 million years ago (mya). The actual least time of existence of some real thing or event is the Planck time, which is quite short. Precision of resolution of the observation is dependent on closeness of the observer in time to what is observed but that is dependent on the availability of event relics upon which position and motion sampling is possible for synchronous calculations, which compare models of lineages as they are calculated to have been constituted at various times. In this paper, observation is equivalent to well-supported inference.

The caulogram (stem-taxon evolutionary tree) of Streptotrichaceae (Fig. 1) gives pertinent information on this bryophyte family for the presently known extant species plus a few inferred extinct taxa. The several caulograms of Figures 2 and 4 estimate numbers of genera extant and extinct for the moss family Streptotrichaceae at about equal spacing (22 my) through time. Genus names are abbreviated (see Fig. 1). Species are estimated to go extinct at about one per genus per ca. 22 million years (Figs. 3 and 5). Progenitor species are designated as round dots, solid if extant, hollow if extinct. Descendant species are numbered by small black squares, the progenitor dots and lineage lines also count as descendant species. Both numbers of species in microgenera (minimally monophyletic groups) and traits between species

are ca. 2 to 5, optimally four [2]. The Streptotrichaceae and Pleuroweisieae are diagramed as tadpole figures (Figs. 3 and 5), where genera, both extinct and extant, are tabulated as increasing with time across 22 my intervals.

Note that these lineages are not the clades of classical phylogenetics. Clades are concatenated dendrogram nodes of calculated unknown common ancestors and are thus mathematical concepts, not taxonomically named or nameable. In cluster analysis on dichotomous trees, there are n – 1 calculated common ancestors (cladogram nodes), in addition to the actual terminal taxa. I have found that about half of all extant species are actually ancestors themselves of one or more other species, cladistic analysis is maximally non-parsimonious in nearly doubling entities involved [3]. Cladistic lineages concatenate these intermediate inferences not actual species. This underscores the difference between analysis by cladistic common ancestry and the more informative use in structural monophyly analysis of serial descent with modification, here.

1.2. Living History

The postulation of "infoentities," as living systems extended through time, is justified in the following fashion: An infoentity is the informational counterpart of a physical system. It is a computer-like instrument that records and makes use of information on observed (impinging) events to continue being self-sustaining, homeostatic, self-perpetuating, renewing, and responsive to environmental exigencies and change over time. It can use calculated inferences, however simplistically including natural selection, to model positions and trajectories affecting its future survival, including data storage in a genome.

2. Materials and Methods

Standard methods for analysis of structural monophyly have been presented and associated statistics well explained [3,4]. They were used for generation of the two evolutionary caulograms (stem-taxon polychotomous evolutionary dendrograms) fundamental for detailing the character state changes that represent informational bits anchoring interpretation of evolution in a lineage. Explained in these prior papers are two fundamental processes: (1) The Rule of Four describes the observed optimum in minimally monophyletic groups (microgenera) of four immediate descendant species per ancestral species and four newly fixed traits per speciation event. (2) The Pareto fractal dimension obtains when a descendant species of one genus generates optimally four descendants in another genus giving them its same own novel traits and yielding a genus of five species of which it is the ancestor (four-generates-five provides a fractal dimension of ln5/ln4, or 1.161); this is the level of "pink noise" characteristic of fractal, hierarchical systems [5]. Other fundamental constraints on living systems have been projected, these may be added. Modeling self-similar, self-organized macroevolution and extinction has been reviewed [6-8].

Critical for retrodiction of past evolutionary patterns is the determination that most genera originate rapidly with about five species within about 22 million years, then may produce secondary descendants from the immediate descendants as evolutionarily unhelpful brown or white noise as somewhat larger fractal dimensions, then gradually decay in number over 88 to 100 my by extinction. Four species or four traits may be viewed each as four informational bits, the uniqueness of which exclude two standard deviations (2 sigma) of uncertainty, each genus maintaining a two-sigma-wide corridor through time [2,5]. We are working with genera that are four-dimensional living structures lasting up to 100 million years or more. Lineages of concatenated genera are the largest self-renewing, evolving, homeostatic structures, and are justly dubbed infoentities held together by the Rule of Four and Pareto Fractal Dimension.

Evolution was modeled by estimating the composition and relationships of species and genera at cross sections of their evolutionary trajectory in time. This kind of analysis is detailed and justified mathematically by Zang et al. [9]. A calculation of past composition of a lineage can be done given the assumption that the ancestor's genus originates as a descendant species of another genus and is distinguished by only a few (about four) traits. A taxonomic lineage is conceptually held together by the fact that most species are so similar (by ca. four trait difference) that there is no room to interpolate another species as a shared ancestor in the concatenated series of species. In addition, all immediate descendant species show the same traits as were newly generated in the ancestral species as an important source of informational reduncancy. Commonly, application of these techniques yields evolutionary diagrams with no immediate reversals in character states (traits). If such a reversal occurred it would counter the probability (subtracting 1 informational bit) of the original assignment of a character state change upon speciation [3]. This is because informational bits are logarithmic and may be added as in sequential Bayesian analysis [2].

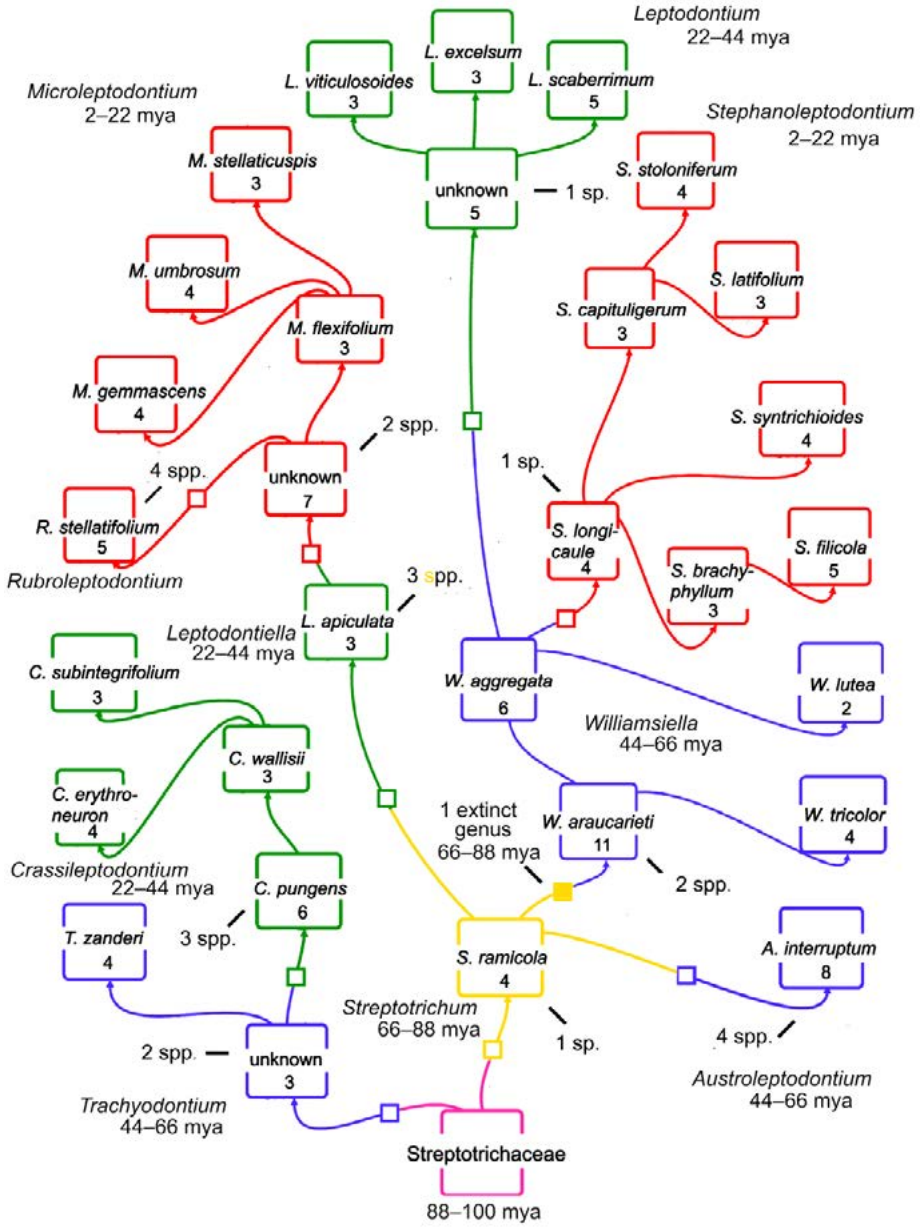

Figure 1: Caulogram of the moss family Streptotrichaceae. Genera are visually separated by different colors. Number of traits in a genus are given in each box. Dates of estimated recency are given with name of genus. The genera are presented as extant in a three-dimensional map, lines connecting extant and extinct genera are inferred timewise branches. The box Streptotrichaceae low in the caulogram represents an Ur group of an unknown number of genera, but at least two. Estimates of the positions of extinct genera (unknowns) are inferred. From Zander [1].

Composing a caulogram using morphological data does not take massive statistical interpretation, as is the case in molecular systematics. Taxonomic groups as classical genera are mostly in the range of one to seven species. The goal in structural monophyly analysis is to identify minimally monophyletic groups, called microgenera but treated nomenclaturally as classical genera. A second-order Markov chain is used to identify one of the species as ancestral to all the others. Ideally, the genus is composed of an expected one ancestral species and four immediate descendant species, each of which may occasionally have a secondary descendant of their own. The two Markov criteria for an ancestral species is that it is most similar to a closely related outgroup species (in a different genus) and also most generalist in adaptations compared to its more highly specialized descendant species. Together with the fact that an ancestral species and its immediate descendants all share the novel traits of the ancestral species, this defines a microgenus as a well-conceived natural group in rank just higher, taxonomically, than a species. This is a unitization of macroevolutionary analysis.

Figure 1 is the fundamental caulogram or stem-taxon dendrogram for the bryophyte family Streptotrichaceae used in recently published studies on lineage evolution, but only the first step in inferential biophysics [1,4]. The synchronous calculations of lineages involves imagining a lineage model moving through time (sectioned in Figs. 2,

3). These changing evolutionary diagrams are explained by three processes. (1) In geologically recent time, genera are originated full-blown, with about four descendants initiated punctuationally within about 22 my [2]. (2) These immediate descendants may have descendants of their own, with some descendants apparently dead ends but others generating up to four descendants and becoming genera in their own right. (3) Species go extinct gradually, with the least-specialized ancestral species hanging on longest. Figures 2 and 4 summarize this evolutionary series back in time, showing presently small genera lower in the caulogram with more species in the past, and showing genera with only the ancestral species extant as simply a descendant species of another genus albeit with the potential of being the ancestor on a new genus in the next newer time segment of 22 my. Figures 3 and 5 show numbers of species calculated for 22 my segments of past time.

The calculations use the values of average numbers of informational bits per species. These values are the evolutionarily significant differences between a species and its one immediate ancestral species, not the total amount of information in a formal taxonomic description of a species. The values are used to calculate the fundamental mass of the information by which the lineage individuates itself. Values are based on Landauer's [10-12] and Vopson's [13-15] discussions of informational mass, particularly that of one bit of information. The idea that information has physical mass is presently unsubstantiated and is rejected with strong arguments by Burgin and Mikkilineni, and Lairez [16,17]. Using the mass of information has been effective, however, in calculation of elements of evolution following the canons of classical mechanics using present-day information [18]. Such information fits the criterion of "functional information" given by Hazen et al. [19]. The purpose of the present paper is to provide a real-world example comparing two information-based processes using, as one factor, total informational mass changing through time.

The information content of a lineage ends at the present and begins as far back in time as there is information to be observed or calculated (inferred) using the same methods. Summaries of how many species are present in a particular segment of time are given with the equitemporal sequential caulograms of Figures 2 and 4. The two sets of caulograms in Fig. 2 and 4 are each an evolutionary synchronogram, which is an informational construct with no one-way arrow of time (these are samples). Calculation of mass for informational living systems (infoentities) are made with data from summaries in Figures 3 and 5.

3. Results

3.1. Observations and their Calculations

Figure 2 is generated be splitting the time-line of the Streptotrichaceeae lineage into five segments using the 22 my figure obtained from analysis of two isolated West Indian microgenera that fully originated during the geological appearance of that area [2]. Working backward, we calculate for each 22 my segment the disappearance of a terminal extant genus and add descendants to internal genera to fill out genera to five species.

3.2. Synchronous Calculations for Streptotrichaceae Lineage

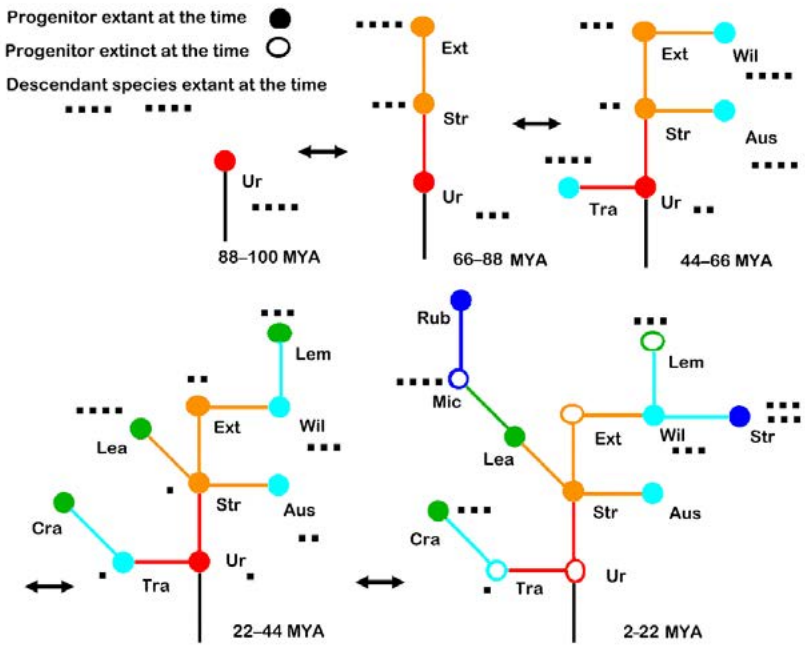

Figure 2: High-resolution phylogenetics showing five sections through Streptotrichaceae at intervals of 22 my in the fourth dimension of time as a synchronogram. Sold dots are extant generic ancestors; hollow dots are presently extinct ancestors or genera. Numbers of immediate descendant species in addition to the ancestor are given by squares. The 2–44 mya diagram is essentially the present, the rest are calculations. Colors distinguish sub-lineages. Double-headed arrows indicate the set of five caulograms is a synchronous information construct with no one-way arrow of time.

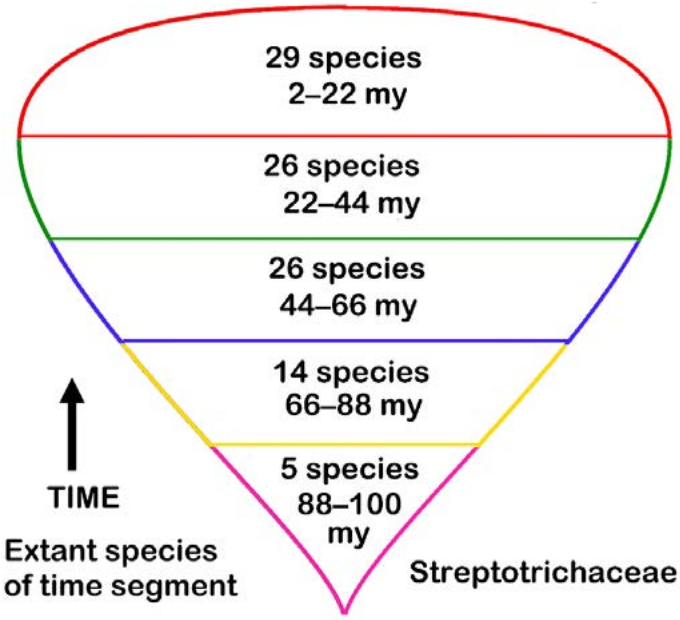

Figure 3: The four-dimension lineage of the moss family Streptotrichaceae sectioned as five segments at 88, 66, 44, and 22 mya, where 2–22 mya is equivalent to the present. Taxa older than 100 my cannot be calculated from available sampling. Estimated extinction of species assumes an initial four descendant species. Colors distinguish time segments.

3.3. Calculation Justifications

A spreadsheet was used for calculations. This paper uses Vopson's formula for the weight of one bit of information, ~ 3.19×10^{-38} kg; in scientific notation, the same is given as 3.19E–18, where E signifies an exponent of 10, that is, a magnitude [13]. Each synchronous calculation of the numbers of species per 22 my time interval in Fig. 3 provides the data for calculation of the mass at one instant or observation for each segment, assuming no or gradual change until the next 22 my segment of time. If there are five observations, then we simply sum the number of species as they evolve (originate and disappear) over 100 my, which turns out to be 100 species as total calculated for 100 my (see Fig. 2), which implies an average of 20 species per observation (synchronous calculation) for Streptotrichaceae.

3.4. Calculations for Steptotrichaceae Lineage

Five segments (Table 1): Five observations match major genusation events in the lineage. For five observations (Fig. 3), we have 100 evolving species, with an average of 20 species reified per observation. Each observation is a potentially synchronous calculable slice across time. The extant species in the family Streptotrichaceae average 4.3 bits per species, thus 4.3 times 19×10^{-38} kg mass per bit times 20 species per observation (time segment) times 5 observations is 1.37×10^{-35} kg. This is the calculated and therefore synchronous informational mass of the lineage from first known origin to present given five observations or synchronous calculations.

Two-cm diameter: Since bryophytes are small, one can resolve them each as a sphere with a radius of one centimeter. How many 2 cm diameter spheres are lined up over 100 million light years? One light year is 299,792.458 m/s. There are 31,557,500 seconds in a year. One light year is then 9.46×10^{17} cm. For a spherical moss with a diameter of 2 cm, there would be half, or 4.73×10^{17} cm such linear mosses, being the same number of observations possible without overlap in one light year. In 100 light years existence of the family, there would be 4.73×10^{15} possible observations. Multiplication of average bits per species (4.3), mass of 1bit, average number of species (20) per segment (any observation at any time is about 20 species), number of observations per light year, and number of light years (100), gives 1.3×10^{-10} kg total potential mass. Sampling throughout time implies the additional observation of no change in traits or taxa. No change is, however, important in that continued existence through conserved momentum is as important as adaptation to exigencies; no change is information.

Planck length: Well, what is the shortest time interval? Planck time is 5.39×10^{-44} seconds is shortest scientifically meaningful time interval, but the shortest time actually measured is a zeptosecond, or 1.00×10^{-21} seconds. But it is the length not the time we need for resolution of synchronous calculations. If two centimeters is the approximate resolution of a moss when sampling for synchronous calculations, what is the maximum resolution possible? The Planck length is 1.6×10^{-35} meters. One light year is about 9.46×10^{15} meters. Dividing one light year in meters by 1 Planck length in meters gives 5.853×10^{50} Planck lengths in one light year. Continuing calculations, 100 million light years is about 9.461×10^{23} meters. Dividing by the Planck length in meters yields 5.85×10^{58} Planck lengths. This is the number of observations possible across 100 my of time when sampling for any object, process or system. Multiplying average bits per species, mass of 1 bit, average number of species observed per segment (which is assumed to apply to all observations at any given

time), number of observations (Planck lengths) per light year, and number of years yields 1.61×10^{23} kg as total mass possible for the Streptotrichaceae. To sum up, the total informational mass of the Streptotrichaceae with a minimal five observations or synchronous calculations is 1.37×10^{-35} kg. This is out of a potential maximal informational mass of 1.61×10^{23} kg. An intermediate and reasonable value is that of 2 cm length of observational sampling, 1.30×10^{-10}.

3.5. Synchronous calculations for Pleuroweisieae lineage

The moss Pottiaceae tribe Pleuroweisieae may be evaluated in the same manner as for Streptotrichaceae for its counterpart as an infoentity (Figs. 4–5). The data is taken from a structural monophyly study by Zander [3], which provides a caulogram of present-day relationships. The average bits per species is 4.54, there are 79 species, summed over four observations. As with Streptotrichaceae, the results are summarized in Table 1. Totals are 1.14×1.14^{-35} kg for four segments slicing the timeline of Pleuroweisieae, 1.19×10^{-10} kg for 2 cm diameter spherical moss, and 1.47 ^× 10^{23} kg for an observation every Planck length.

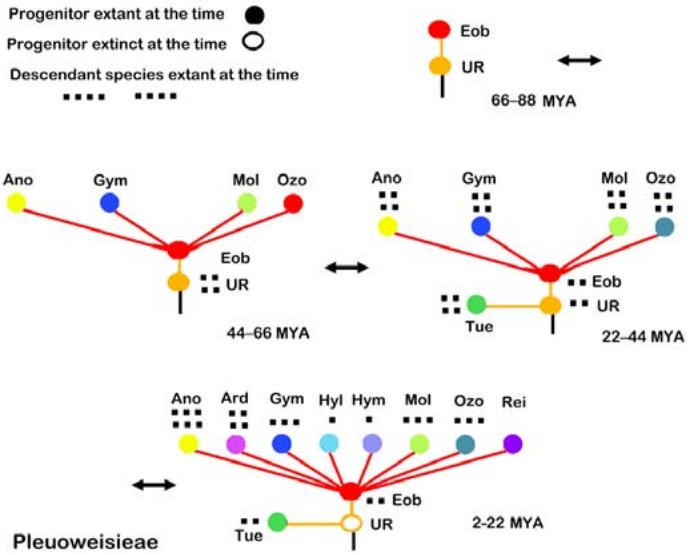

Figure 4: The moss lineage Pottiaceae tribe Pleuroweisieae with appearance calculated for 22 my segments of past time as a synchronogram. Sold dots are extant generic ancestors; hollow dots are extinct ancestors or genera. Numbers of immediate descendant species in addition to the ancestor are given by squares. Colors distinguish sub-lineages. Double-headed arrows indicate the set of four caulograms is a synchronous information construct with no one-way arrow of time.

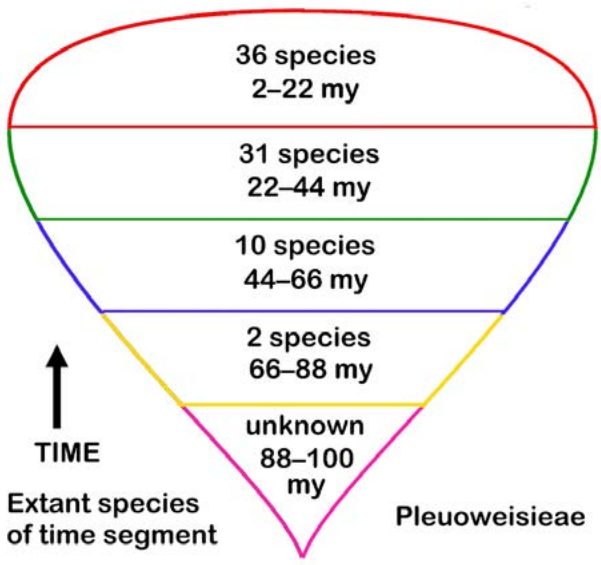

Figure 5: The four-dimension lineage of the moss Pottiaceae tribe Pleuroweisieae sectioned as five segments at 88, 66, 44, and 22 mya, where 2–22 mya is equivalent to the present. Taxa older than 88 my cannot be calculated from available sampling. Estimated extinction of species assumes an initial four descendant species.

3.6. Tabulated Results

We now have the possibility of calculating interactions of discrete informational processes or systems in the past, perhaps even projecting such into the future. Ideally, after calculating the extent and composition of an infoentity's past, simply double the extent to estimate its total past plus future existence. The composition of a future portion of an infoentity is determined with the opposite of analysis of its past. Of course, it is not so simple. The models of past expressions of one informational system shown in Figure 2 are a beginning. The desire to address a mass easily measured by humans, such as one kilogram, is based on an expectation that human-measured objects or processes will interact with the mass of a lineage. Such interactions would necessarily be between "real," solid, palpable objects or fields and the minute mass of information. On the other hand, actual, possible interactions between two elements of informational models similar in size may be calculated synchronous without comparing the effects of huge and tiny masses. Comparison of the masses of different lineages offers an equitable solution. Evolutionary mass-energy equivalents ground this study in thermodynamics.

Comparison of mass and energy bound of lineages (Table 1) depends on the number of synchronous observations. The informational mass of Streptotrichaceae is observed by synchronous calculation with five observations (lineage in five segments), by many observations at 2 cm resolution, and by maximum number of observations at Planck length. Total mass is calculated as total bits × 3.190×10^{-38} kg. Total observed bits is calculated as average bits per species × total/average species observed × number of observations per light-year × number of historical years. The Landauer energy bound (J) is total mass (kg) × c^2 where c = 299,792,458 m/s, assuming room temperature at 300 K. This calculation matches exactly [17] the Landauer' mass-energy equivalence principle of E = N × k_BTln2. Solving for mass yields $m_{bit} = k_B T \ln 2/c^2$.

Given that informational mass is still somewhat speculative, the fallback measure for comparison is simply the number of observations of bits throughout the span of historical time. Total bits observed for the time period may be couched (Table 1, last column) as units of scientific extrapolation of historical reality. The calculation using Planck length seems to be the upper limit on potential observations and depends on an expected convergence to some one value approximated by the initial sampling of four or five segments of calculated evolutionary events based on present day distribution of species and trait changes.

Observed	average bits/sp.	mass of 1 bit in kg	total or average num. spp. observed	num. obs. / light year	num. historical years	total mass in kg	total bits obs.	Landauer energy bound (J)
Streptotrichaceae: 100 species observed over time								
5 segments	4.30	3.190E-38	100	-	-	1.37E-35	4.30E+02	1.23E-18
2 cm diam	4.30	3.190E-38	20	4.73E+17	1.000E+08	1.30E-10	4.07E+27	1.17E+07
Planck length	4.30	3.190E-38	20	5.85E+50	1.000E+08	1.61E+23	5.00E+60	1.44E+40
Pleuroweisieae: 79 species observed over time								
4 segments	4.54	3.190E-38	79	-	-	1.14E-35	3.59E+02	1.03E-18
2 cm diam	4.54	3.190E-38	19.75	4.73E+17	8.800E+07	1.19E-10	3.73E+27	1.07E+07
Planck length	4.54	3.190E-38	19.75	5.85E+50	8.800E+07	1.47E+23	4.62E+60	1.23E+40

Table 1: Calculations of information mass and archiving energy. Observed infoentities; average bits known per species; Vopson's calculation of the mass of 1 informational bit in kg; average number of species observed at one time; number of observations per light year; number of years; total mass in kg of informational bits; total bits observed; Landauer energy bound in joules.

Table 1 presents the results of estimating the total mass-energy equivalents of information of Streptotrichaceae and Pottiaceae tribe Pleuroweisieae. The former taxon is a recent segregate of the Pottiaceae. Figures 2–5 show the composition of these lineages at the present and a few earlier sections through time. The four and five segments calculated for relationships and composition provide an adequate estimate of the composition of each entire lineage whether much or little sampled, such that bits per species and average number of species observed in a segment are transferable to various numbers of observations (sections through the space-time corpus of the lineage, as in Fig. 2 and 4).

Figures 2–5 summarize the results of synchronous calculation of past configurations of probable lineage compositions and relationships for the known existence of the Streptotrichaceae and Pleuroweisieae. The segmentation of the timeline into 22 my durations is a best attempt to capture changes in lineages at the expected rate of origination of new genera, 22 my, given analysis in previous papers [2,4,20]. The two most recent segments have the most species extant, balancing origination and extinction, while extinction gradually overtops origination in the more ancient segments. The caulograms (Figs. 2 and 4) are conceptual sections through lengths of twisted and branching strands of genera surviving through time. The concept of four- dimensional ropes of 2-sigma-wide probabilistic exclusion strands treated as taxa may profitably be addressed in the future through analysis as topological fiber bundles [21].

The results of the study of the mass of informational counterparts of the two lineages are summarized in Table 1. Given the data and Vopson's estimate of the mass of 1 bit of information, the total mass of each lineage infoentity is given for samples of 100 or 88 my at five or four segments (that

is, five or four observations), also for segments only two cm wide (as many observations as there are two cm lengths in 100 or 88 light years), and also for maximum number of segments at Planck's length (as many such lengths as there are in 100 or 88 light years) [13]. The values obtained are very similar in both lineages, probably because (1) the lineages are of similar size in numbers of species, and (2) the Rule of Four obtains for both lineages, constraining the number of bits per species (new traits per speciation) and optimum numbers of immediate descendant species per genus.

Of some significance is that Vopson's estimation of the mass of one bit of information at room temperature is 3.19×10^{-38} kg [13]. This is two magnitudes larger than the maximum estimated mass of the unit of cold (cosmic microwave background temperature) dark matter, the QCD axion, the range of which is 40 to180 μeV (microelectronvolts), or 7.13×10^{-41} to 3.21×10^{-40} kg [22]. However, a bit at similar cold temperature has less mass, about 2.91×10^{-40} kg. The close match of an informational bit and the conjectural axion was suggested by Gasparini and Vopson as evidence in support of the idea that there is a mathematical bridge between cosmology and information theory, that dark matter is actually a physical expression of information [14,23]. If there is indeed some correspondence with informational mass and dark matter, then the present taxonomic paper contributes to the study of cosmology and the role of life as an information generator. On the other hand, a more down-to-earth evaluation of these figures may be had through the mass-energy equivalence principle of Landauer which may be used to measure the energetic cost of archiving actionable information on evolution [10]. Landauer's principle as interpreted by Vopson is simply mass times the speed of light squared, with values in joules [13]. Relevant papers reviewing the use of thermodynamics in the biological context are by Bennett and Kempes [24,25].

The results of the present exercise show that the Streptotrichaceae and Pleuroweisieae have similar informational masses even when measured at different levels of sampling. The number of bits per species is about the same, following the Rule of Four, while the number of immediate descendants per species is similar (although synchronous calculations in part assume this). The Streptotrichaceae lineage goes back in time somewhat farther (100 my) than the Pleuroweisieae (88 my).

The Streptotrichaceae and Pleuroweisieae had 5 and 4 observations respectively have an informational mass of 1.37×10^{-35} and 1.14×10^{-35} kg, respectively. This size is little more than the Planck length of 3.13×10^{-38} and is scarcely comparable in mass to any natural object. The Streptotrichaceae and Pleuroweisieae had one observation per 2 cm (diameter of a "spherical moss") have an informational mass of 1.30×10^{-10} and 1.19×10^{-10} kg, respectively. This is about the mass of a dust mite, which is $1–5 \times 10^{-10}$ kg. The Streptotrichaceae and Pleuroweisieae had one observation per Planck length (smallest distance in theory and therefore the most observations possible) have an informational mass of 1.61×10^{23} and 1.47×10^{23} kg, respectively. This value is about the mass of Jupiter's moon Ganymede at 1.61×10^{23} kg, or Mercury at 3.3×10^{23} kg.

The energy for thermodynamic archiving at the most reasonable sampling size (2 cm) per individual bit is 2.87×10^{-21} joules (at 300 K). The total Streptotrichaceae archiving energy (2 cm diameter) is 1.168×100^{7} joules or 11.7 megajoules. That for Pleuroweisieae is 1.07×100^{7} joules, or 10.7 megajoules. The energy for keeping Streptotrichaceae stable as a lineage over 100 million years is then about 12 megajoules or about the energy released by 1 liter of gasoline. That for Pleuroweisieae is about 10 megajoules, again a miniscule input of energy for massive stabilizing action over time. As fundamental thermodynamic overhead preserving core data the Rule of Four can be considered a hyper-efficient compression processor. In information theory, this constraint minimizes data while maximizing clarity creating a noiseless channel, while clearing a two-sigma conduit restricting uncertainty for environmental fitness. The Rule of Four is a thermodynamically enforced efficiency limit expending the least free energy to keep error correction active. The Pareto Fractal Dimension allows lineages to maintain a maximum of adaptive variation with minimal energetic overhead, conserving information structures over 100 million years.

The Streptotrichaceae generated a calculated 100 species over 100 my, while the Pleuroweisieae generated 79 over 88 my, thus the two taxonomic groups generated species at nearly the same rate over 88 to 100 my.

The average numbers of traits per species in both lineages are nearly the same. The mass results are comparable with the values of resilience for the two lineages obtained by equating resilience with their evolutionary force. Formulae of classical mechanics were used in a previous paper [20] to express numbers of species as mass, and numbers of traits (as informational bits) as velocity. Cumulative numbers of traits of extant species along internal paths of lineages were viewed as evolutionary acceleration or force ($F = MA$). Streptotrichaceae had total resilience of 756 bits, averaging 22.9 bits per speciation event, while Pleuroweisieae had a total of 869 bits, averaging 24.1 bits per speciation event. The proportions of informational mass of Streptotrichaceae to Pleuroweisieae are about 7:5, while for resilience, it is about 9:10. One can state that evaluations of resilience (*as* $F = MA$) match well with similarity of informational mass in the two lineages studied.

4. Discussion

4.1. The Synchronous Concept

Time is here conceived as a linear scale, traversed by informationally massive organisms originating as species, then developing rapidly as small, related groups of species (microgenera) sharing a set of recent isomorphic adaptive traits, then expanding through minor secondary speciation beyond four immediate descendants, then gradually undergoing extinction. A Rule of Four associated with

crowding and resource availability constrains both the number of immediate descendant species to about four, with about four newly evolved traits each. This is a process creating structural monophyly, with about five species per microgenus. One species of a genus generates about four immediate descendants of the next genus, ending up with five species sharing the originating species' novel traits. A genus of five species is an emergent result. This is a fractal process with a dimension of ln5/ln4, which is related to the Pareto law of 20% of one process generating 80% of a different process [24]. The Pareto Fractal Dimension of 1.161 (that is, ln5/ln4) is in the "sweet spot" for "pink noise" associated with emergent, self-similar processes in nature [5].

Vopson's mass-energy equivalence principle of ca. 3.19×10^{-38} kg per bit at room temperature may be interpreted as a bound on the structural work done by the biosphere [13]. The mass-energy equivalent of the weight of a dust mite gives a lineage of plants an efficient, powerful, stable, sustainable, resilient response to the relentless and massive entropic resistance of the biosphere. Life acts as a major thermodynamic generator in the universe. Landauer indicated that the minimum energy required to erase, change or stably archive a single bit of information contra environmental thermal fluctuations is governed by $E = kBT\ln2$, where kB is Boltzmann's constant, and T is ambient temperature (here 300 K) [10]. At this baseline thermal state, preservation of one informational bit is about 2.87×10^{-21} joules. The total energy overhead sustaining a lineage over millions of years is then $Etotal = Itotal \times (kBT\ln2)$. That energy includes all work done by natural selection to establish character states, regulate minimally monophyletic groups, and shield the lineage from entropy.

4.2. Magnitudes of Distribution

The numbers mentioned above are often very large or small and have been concisely reviewed [27,28]. To provide comparison, there are an estimated 10^{82} atoms in the universe. The number of atoms in a gram of hydrogen (Avogadro's number) is 10^{23}. The number of stars in an average galaxy is 10^{11} and that of galaxies in the observable universe is also about 10^{11}. The size of a proton is 10^{-13} cm with a mass of 10^{-24} grams. The size of the observable universe is about 10^{28} cm. There are about 1×10^{80} fundamental particles in it. The mass of ordinary matter in the observable universe is about 1.5×10^{53} kg, and dark matter outweighs ordinary matter 6:1. The range mentioned here stretches across more than 100 magnitudes. If dark matter consists of axions, there would be an estimated 10^{90} axions in the observable universe. Calculation of the number of axions in the observable universe is as follows: total dark matter mass is about 10^{54} kg; estimated axion mass is about 10^{-36} kg; total particles is mass divided by single particle mass, which is 10^{90} axions or bits if one axion massed one bit. This is the limit, apparently, for information based on observation, assuming one axion represented one bit of information by mass.

If axions were homogeneously distributed in a spherical cluster, and 10^{90} is the number of axions at present time and taken as volume, then the radius is a measure of an average linear series or depth in the axion cluster. The volume of a sphere is $V= 4/3\ \pi\ r^3$. Solving for radius, $r = 6.20 \times 10^{29}$ linear axions. Since we are viewing time as a linear series of bit-measured events and assuming one axion per bit, we can get the number of lineages of the size of the Streptotrichaceae that will fit into this average length of possible time measured in axions. One lineage of Streptotrichaceae with 2 cm diameter mosses at 2.03×10^{28} total observed bits is just a little smaller than this length. (We are not using distance or time for comparative measures, instead we are using informational bits.) The measurement using observations at Planck length is far too large (4.62×10^{60} bits). When measured at 5 segments (4.3×10^{2} bits), one can fit 1.41×10^{27} lineages of the informational size of the Streptotrichaceae into the average linear length of axions, rather too many to be significant. The best fit into available axions for a single lineage of 20 species viewed across 100 my of time is that of a series of observations at 2 cm lengths, 2.03×10^{28} bits. This assumes that a single lineage in synchronous calculation is a unique line of information through axion space with the observable universe of different scales for each class of information.

5. Conclusions

The concept of the minimally monophyletic group, or microgenus, has unitized macroevolution such that calculations can be made using species as evolutionary mass and trait changes as evolutionary velocity. The Rule of Four ensures the existence of the two-sigma wide path cleared of uncertainly for a lineage through time; the Pareto Fractal Dimension enforces a time-stable connection between genera; and, since living lineages as the most massive self-organized, self-sustaining, homeostatic, replicating, responsive and evolving systems in the universe, they should generate through time a significant mass-energy equivalent in their informational counterparts that has exerted strong control of the lineage at all times. Gasoline releases about 34 megajoules per liter when burned, or one shot-glass of gasoline per megajoule. The Streptotrichaceae information archiving cost is 11.7 megajoules, that of Pleuroweisieae is 10.7 megajoules. Per lineage, the cost is phenomenally small. There are an estimated 25 million species on Earth. Estimating about 25 species per lineages of minimally monophyletic groups, then there are one million lineages, roughly. If lineages indeed support informational counterparts with a mass-energy equivalent, then the Earth over geologic time of 100million years (the Phanerozoic plus a portion of the Mesozoic), given the measure of 2 cm as one observation, has an accumulated informational mass-energy of a million times the average of 10.7 and 11.7 megajoules, or roughly 11 million megajoules. This is 1.1×10^{13} joules or 1.1×10^{7} megajoules. As chemical energy, this is equivalent to 2.63 kilotons of TNT, about 20% of the Hiroshima atomic yield. Taking advantage of unitization of macroevolution with minimally monophyletic groups under control of the Rule of Four and the Pareto Fractal Dimension, evolution has discovered a very low thermodynamic cost for ensuring the stability of the Biosphere over 100 million years. The

variation in average trait change per speciation event as varying response to levels of environmental resistance should affect such values pr lineage and provide in future research a direct measure of evolutionary effort.

It is possible to interpret elements of the biological historical sciences with concepts and techniques of physics and information science. It is evident that a multidisciplinary approach is needed for continued advancement of evolutionary taxonomy. This paper is a first step in presenting a unitary perspective on biological lineages as very large living information-generating systems across the fourth dimension of time. The informational counterparts of biological lineages are the largest self-sustaining, homeostatic living systems when viewed through time. As in Schrödinger's metaphor, they feed on negentropy and excrete entropy, that is, import free energy available for work, and export heat and otherwise disperse energy. With mass-energy equivalence calculations, they can now be measured and compared. High-resolution phylogenetic analysis using principles of physics with structural monophyly have more clearly delineated such entities. There are eight million specimens in the herbarium here at the Missouri Botanical Garden. Estimating that here are about 50 traits of importance in combination as evolutionary distinguishing features in any lineage, there are then 400 million data points available for study. There is at hand a vast potential for valuable research in the biophysics of macroevolution.

Statement of the Use of Generative AI and AI-Assisted Technologies in the Writing Process

During the preparation of this manuscript, the author used Gemini/Google for literature searches. After using this tool/service, the author reviewed and edited the results, and checked calculations as needed and takes full responsibility for the content of the published article.

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