Punctuated non-equilibrium and niche conservatism explain biodiversity fluctuations through the Phanerozoic

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Abstract

Fluctuations in biodiversity, both large and small, are pervasive through the fossil record, yet we do not understand the processes generating them. Here we use a novel extension of theory from non-equilibrium statistical physics to show that three universal properties of macroevolution, punctuated adaptive radiation, niche conservatism and resultant heterogeneity of diversification rates between taxa, are sufficient to explain previously unaccounted for biodiversity patterns throughout the Phanerozoic. Using this theory, known as super-statistics, we identify taxonomic orders as largely autonomous evolutionary units, each likely experiencing its own unique and conserved adaptive landscape. This indicates that while neutral processes could adequately explain within-order diversification, between-order diversification is likely driven by major evolutionary innovations. Super-statistics, has been successfully used to explain other complex systems including driven turbulent flows and wild stock market fluctuations. Compared to other approaches that have used simple birth-death processes, equilibrial dynamics or non-linear theories from complexity science, super-statistics is superior in its ability to account for both small and extreme fluctuations in fossil diversity. Its success opens up new research directions to better understand the evolutionary processes leading adaptive landscapes to be conserved within orders and undergo punctuated innovations between orders.

1 Background

Biodiversity has not remained constant nor followed a simple trajectory through geologic time[1–6]. Instead, it has been marked by fluctuations in the number of extant taxa, both positive in the case of net origination or negative in the case of net extinction. Major events, such as adaptive radiations and mass extinctions have received special attention[7,8], but fluctuations of all sizes are ubiquitous[2,5,9].

Several approaches have been taken to study the complex trajectory of paleo-biodiversity ranging from the hypothesis that biological systems self-organize to the brink of critical phase-transitions[10,11] to invocations of non-linear environmental perturbations[12] and escalatory co-evolutionary interactions[13]. New data and analyses have not supported any of these hypotheses at the scale of the entire Phanerozoic marine invertebrate fauna[5,14,15]. Other studies have modeled the mean trend in diversity as tracking a potentially evolving equilibrium[2,5,6,16] and yet ignore the potential role of stochasticity and non-equilibrium dynamics in producing observed patterns[4,9,17]. As such, we still lack a synthetic theory of evolving biodiversity through the fossil record. Here we use a simple model of evolution in an abstract niche space derived from universal non-equilibrium processes to predict, with great accuracy, the complex distribution of pervasive diversity fluctuations throughout the marine Phanerozoic.

Despite the heterogeneity of explanations of Phanerozoic biodiversity, consensus has emerged on three properties of macroevolution: *i*) gross ecological and life history attributes of clades (i.e. groups of related species descending from a common ancestor) are often maintained, a phenomenon known as niche conservatism[18,19]; *ii*) long periods of niche conservatism are interrupted by adaptive diversification and exploration of new ecological niche space[19–21]; and *iii*) as a consequence of the interaction between their life history characteristics and the dynamics of the environments they inhabit[22] different clades experience different rates of morphological evolution, speciation and extinction[2,3,23,24].

Observed bursts of adaptive radiation leading to novel morphologies in the fossil record led Eldredge and Gould to their hypothesis of punctuated equilibrium[20]. Here we show that this punctuation is actually akin to the "super statistical theory" of non-equilibrium dynamics in statistical physics[25]. Super-statistics[25] proposes that non-equilibrial systems can be decomposed into locally equilibrial sub-systems. The distribution of equilibria across sub-systems determines the dynamics of the complete system[25]. When these sub-systems are superimposed the resulting system can no longer be described by a single equilibrial model. In the context of macroevolution we propose that a clade with conserved life history characteristics corresponds to a locally equilibrial sub-system. If a certain region of niche space can only contain a finite diversity of taxa[16,23,26,27] then diversity within clades should fluctuate stochastically about this equilibrium due to random origination and extinction. The magnitude of these macroevolutionary rates should be a function of the life history and ecological characteristics that define that region of niche space. Larval type[28], body plan[17], body size[29], range size[29,30] and substrate preference[19] have all been shown to influence such rates. Thus different regions of niche space, and the clades occupying them, will experience different magnitudes of stochastic fluctuation in diversity. As clades occasionally split to fill new regions of niche space their punctuated diversification determines the non-equilibrium nature of the entire biota. Here we show that these properties of macroevolution are sufficient

to explain the complex fluctuations of marine invertebrate diversity through the Phanerozoic.

In statistical mechanics, local sub-systems can be defined by a simple statistical parameter β often corresponding to inverse temperature. In the context of macroevolution we define β as the inverse variance of a homogenous origination-extinction process, which will capture all relevant information about a clade's diversification under such a process. The limit distribution of time averaged fluctuations in clade k's diversity through time should be approximately Gaussian with variance $1/\beta_k$ (Appendix 1). We posit that just as in statistical systems, non-equilibrium dynamics can arise from the mixing of the dynamics of many locally equilibrial subsystems. For marine Phanerozoic diversity this corresponds to mixing the dynamics of many clades, all being described by their unique β_k values. Three exemplar dynamics taken from a bias-corrected (see methods section) aggregation of the Paleobiology Database (PBDB)[5] are shown in Figure 1. To predict the super-statistical behavior of the entire marine invertebrate Phanerozoic fauna we must integrate over all possible local equilibria that each clade could experience. The distribution of β_k values describes the probability that a given clade, chosen at random, will occupy a region of niche space characterized by that inverse variance value. The form of this stationary distribution of β_k values could shed interesting light on the biological processes that lead different clades to different equilibria, as discussed below. Figure 1 shows the shape of this stationary distribution estimated from bias-corrected PBDB[5] data.

To uncover the super-statistical nature of the marine invertebrate Phanerozoic fauna we analyze the distribution of diversity fluctuations using two canonical databased of fossil biodiversity, the PBDB[5] and Sepkoski's compendium[31] of fossil marine invertebrates (results from Sepkoski's compendium are presented in Appendix 2.3). We filter PBDB data to include only well preserved marine invertebrates following previously published collection inclusion criteria[5,6]. We account for detection bias in the PBDB using an extension of the "three timer" correction[5]. "Three timer" correction accounts for the rate of failure to observe a genus, estimated by the number of times a gap occurs in its occurrence history. We extend this correction by also employing a new publication bias correction to help eliminate bias from preferential publication of novel taxa (see methods section). Results obtained from this correction strategy are similar to other published methods (Fig. 2). Fluctuations within a clade are computed as the difference in standing diversity between two time intervals, or equivalently the number of originations minus extinctions in one interval.

Phanerozoic biodiversity can be deconstructed and grouped into clades, or sub-systems, in several different ways. Lacking a full phylogenetic hypothesis for all marine invertebrates we use taxonomic classifications to identify potential sub-systems. Taxa ideally represent groups of organisms that descend from a common ancestor and share similar ecologically and evolutionary relevant morphological traits[32,33]. For Phanerozoic marine invertebrates, Holman[24] has shown that variance in diversity dynamics is less between taxa belonging to the same order than taxa in different orders, indicating that the taxonomic level of orders is a likely candidate for sub-system delineation. To evaluate the optimal taxonomic level for sub-system designation, we test our superstatistical theory using taxonomic levels from order through class to phylum. Additionally we compare our results to randomized taxonomies to confirm that observed patterns are not an artifact of arbitrary classification but instead represent real biologically relevant differences between clades.

2 Methods

2.1 Paleobiology Database data download and filtering

Data were downloaded from the Paleobiology Database (PBDB; www.pbdb.org) on 28 May 2013. Collections were filtered using the same approach as Alroy[5] to insure that only well preserved marine invertebrate occurrences were used in subsequent analysis resulting in 221202 genus occurrences. These were further filtered to exclude those occurrences without order-level taxonomy and those collections with age estimate resolutions outside the 10my default bins of the PBDB resulting in 189516 occurrences left for analysis. To avoid basic sampling concerns we excluded the earliest Cambrian and the Cenozoic.

To focus attention on the variance of fluctuations we center each clade's fluctuation distribution. Because "equilibrium" in the statistical mechanical sense means a system undergoes coherent, concerted responses to perturbation the mean trend line is of less interest than deviations from it. We also note that most clades are already close to centered and so centering has little influence on clade-specific fluctuation distributions.

2.2 Three-timer and publication bias correction

We use a new and flexible method, described below, to correct for known sampling biases in publication-based specimen databases[5,6]. We were motivated to use this method because rarefaction has been shown to under-perform compared to the more data-intensive share-holder quorum subsampling (SQS) method[6]. However, subsampling cannot be applied to small orders (i.e. the majority) because SQS becomes increasingly unreliable as sample size decreases[6]. We therefore develop a simple method based on first correcting for detection bias using the "three timer" correction[5] in which the rate of failure to observe a genus is estimated by the number of times a gap occurs in the occurrence history of each genus. To eliminate further bias due to preferential publication of novel taxa we divide observed number of genera per order per time period by the expected number of genera given publications in that time period. The expected number is calculated by regressing the log-transformed number of genera on log-transformed number of publications. There is a weak trend toward higher diversity with more publications (Fig. 1) meaning that the most important correction comes from the three timer correction.

Our new method effectively re-scales each genus occurrence from 0/1 (absent/present), to a weighted number continuously ranging between 0 and 1. This method achieves similar results to more computationally intensive sub-sampling procedures[5,6]. We directly compare our predicted time series of global genus diversity with results derived from SQS[6] and the raw data (Fig. 2). Our method shows minor differences with the SQS prediction, However, these discrepancies do not have impact the distribution of fluctuations (Fig. 2) and super-statistical analysis on uncorrected PBDB data (see section 2.1) produces a similar result to the analysis on corrected PBDB data presented in the main text.

2.3 Numerical methods

To fit our super-statistical prediction we use the method of least squares instead and maximum likelihood. When building the prediction for $P(x)$ by calculating order-level Gaussian distributions and integrating over them, we use least squares to fit the variance term to each order. We do so because orders potentially show asymmetries in their distribution of fluctuations. Least squares is more flexible in fitting such distributions compared to maximum likelihood which will always estimate the empirical variance as the best-fitting parameters.

We also estimate $P(x)$ directly from the raw data using maximum likelihood to compare the fit of our super-statistical prediction and that of a simple Gaussian distribution using AIC. To calculate a likelihood-based confidence interval on our prediction we bootstrapped the data, subsampling fluctuations with replacement from all orders combined.

3   Results and Discussion

At the order level in both the sampling-corrected PBDB (Fig. 1) and Sepkoski's compendium (Appendix 2.3), fluctuations in genus diversity are well described by a Gaussian distribution (Fig. 1). Gaussian fluctuations would result from a homogeneous origination-extinction process under the condition of independence between orders. Independence could result from neutral-like processes[34], where the dynamics of one taxon are unaffected by those of another, or from dampening mechanisms that stabilize complex networks of interacting taxa[35]. This is in direct contrast to the instability hypothesis underlying the self-organized criticality theory of paleo-biodiversity[10,11].

We estimate the distribution of β_k's simply as the maximum likelihood distribution describing the set of inverse variances for all orders. In both the PBDB and Sepkoski's compendium, Phanerozoic marine invertebrate orders clearly follow a Gamma distribution in their β_k values (Fig. 1). While multiple processes could lead to a Gamma stationary distribution[36], one interesting possibility is a mean-reversion process[36]. Mean reversion could be a consequence of niche conservatism if β_k values are associated with a clade's physiological and life history traits, themselves evolving via Ornstein-Uhlenbeck-like exploration of an adaptive landscape[36,37].

Using the observation of within order statistical equilibrium and Gamma-distributed β_k parameters we can calculate, without further adjusting free parameters, the distributions of order-level fluctuations for the entire marine Phanerozoic, $P(x)$, as

$$P(x) = \int_0^\infty p_k(x \mid \beta) f(\beta) d\beta \tag{1}$$

where $p_k(x \mid \beta)$ is the distribution of fluctuations within an order and $f(\beta)$ is the stationary distribution of inverse variance in the magnitude of order-level fluctuations in diversity. This leads to a non-Gaussian, fat-tailed prediction for $P(x)$ which matches both the PBDB and Sepkoski data closely (Fig. 2 and Appendix 2.3).

To quantitatively evaluate how well the super-statistical prediction matches the data we constructed a 95% confidence envelope from bootstrapped maximum likelihood estimates for $P(x)$. Observed fluctuations fall within this 95% confidence envelope (Fig. 2), indicating

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that the data do not reject the super-statistical prediction. For further comparison, we fit a Gaussian distribution to the observed fluctuations, which corresponds to the equilibrium hypothesis that all orders conform to the same statistics. Using Akaike Information Criterion (AIC) we find that observed fluctuations are considerably better explained by the super-statistical prediction than by the Gaussian hypothesis ($\Delta AIC = 11285.18$). Thus, as expected under the super-statitical hypothesis, the fat tailed distribution of fluctuations arise from the superposition of independent normal statistics for fluctuations within orders.

Computing the distribution of fluctuations using classes instead of orders leads to a substantially poorer fit to the observed data (Fig. 4). We quantify this shift with the Kolmogorov-Smirnov statistic, which changes from 0.041 in order to 0.062 in classes (Fig. 3). However, if super-statistical theory explains the data, this worsening fit with increasing taxonomic scale is expected as the different classes are not well defined subsystems in their fluctuation dynamics. Instead, classes aggregate increasingly disparate groups of organisms, and thus effectively mix their associated Gaussian fluctuations, meaning that one statistic should no longer be sufficient to describe class-level dynamics. Our analysis indicates that orders are evolutionarily coherent and independent entities, with all subsumed taxa sharing key ecological and evolutionary attributes allowing them to diversify concertedly and independently from other orders. Both the good fit at the order level and worsening fit at higher taxonomic levels is confirmed in Sepkoski's compendium, which also allows analysis of phylum-level patterns (Fig. 5).

To further test the evolutionary coherence of orders we conducted a permutation experiment in which genera were randomly reassigned to orders while maintaining the number of genera in each order. For each permutation, we calculated the super-statistical prediction and the Kolmogorov-Smirnov statistic. The permutation simulates a null model in which common evolutionary history is stripped away (genera are placed in random orders) but the total number of observed genera per order is held constant. Repeating this permutation 500 times yields a null distribution of Kolmogorov-Smirnov statistics that is far separated from the observed value (Fig. 3) suggesting the good fit at the order level is not merely a statistical artifact of classification but carries important biological information.

4   Conclusion

Our analysis makes no assumption that orders should correspond to super-statistical subsystems, but identifies them as the appropriate level for marine invertebrates. Holman[24] has also shown that orders are "evolutionarily coherent" in that subtaxa within orders share common diversification dynamics. As we show, orders differ only in the variances of their diversity fluctuations (Fig. 1).

Our study is the first to demonstrate that complex patterns in the sequence of origination and extinction events in the fossil record are the result of a simple underlying process analogous to the statistical mechanisms by which complexity emerges in large physical[38] and social systems[39]. We do so by identifying the biological scale at which clades conform to equilibrial dynamics, which could result from the process of niche conservatism. We then show that punctuated shifts to different equilibria between clades, a consequence of punctuated exploration of niche space by newly evolving clades, leads to a characteristically non-equilibrial

distribution of diversity fluctuations when the marine Phanerozoic fauna is viewed as a whole macro-system.

Our work highlights the importance of both niche conservatism and punctuated adaptive radiation in producing the statistical behavior of the Phanerozoic; our theory thus provides new motivation for identifying the eco-evolutionary causes of innovations between lineages and how those innovations are eventually conserved within lineages. Armed with an understanding of the statistical behavior of diversification we can go on to examine mechanisms underlying additional patterns in the mean trend of biodiversity through the Phanerozoic. In particular, clades have been shown to wax and wane systematically through time[4,9], a pattern that we cannot explain with super-statistics alone.

Super-statistics could also be applied to other areas of evolution and macroecology. For example new phylogenetic models already consider heterogeneous rates of diversification[40]. The super-statistics of clades in adaptive landscapes could provide a means to build efficient models that jointly predict morphological change and diversification. This framework could also provide a new paradigm in modeling the distributions of diversity, abundance and resource use in non-neutral communities. Non-neutral models in ecology are criticized for their over-parameterization**rosindell2011TREE**, yet a persistent counter argument to neutral theory[34] is the unrealistic assumption of ecological equivalency[41] and poor prediction of real dynamics[42]. If ecosystems are viewed as the super-position of many individualistically evolving clades, each exploiting the environment differently and thus obeying a different set of non-equivalent statistics, then diversity dynamics could be parsimoniously predicted while incorporating real biological information on ecological differences between taxa.

Acknowledgments

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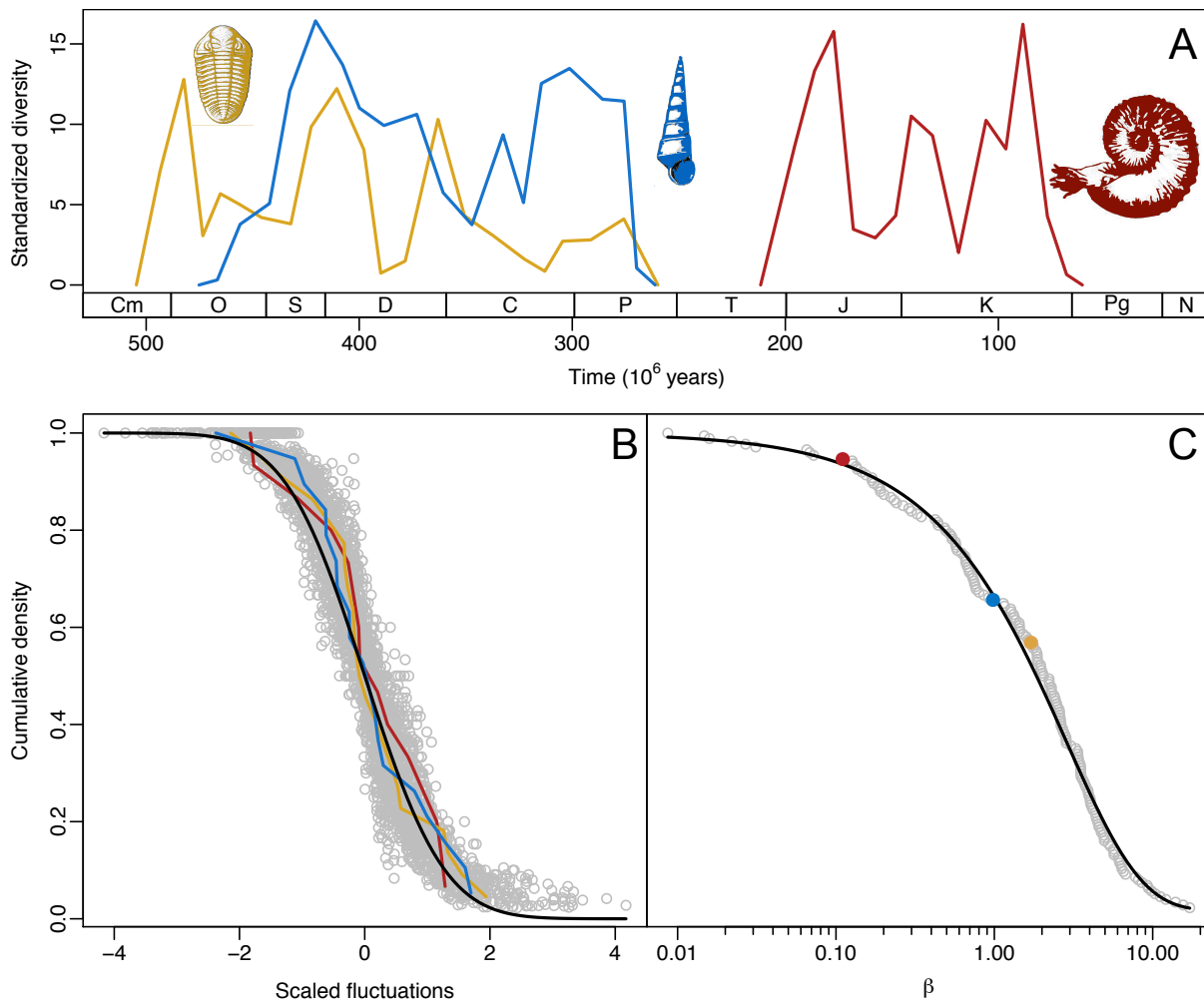
Figures

Figure 1: The distributions of within-order fluctuations in genus diversity shown for the trajectories of three exemplar orders (A) and shown as an empirical cumulative density aggregated across all orders (B). To display all orders simultaneously we simply collapse their fluctuation distributions by dividing by their standard deviations. If orders conform to the Gaussian hypothesis their scaled fluctuations should fall along the cumulative density line of a normal N(0, 1) distribution, as shown in (B). In (C) the distribution of inverse variances β_k across all orders matches very closely to a Gamma distribution (black line); exemplar orders are again highlighted.
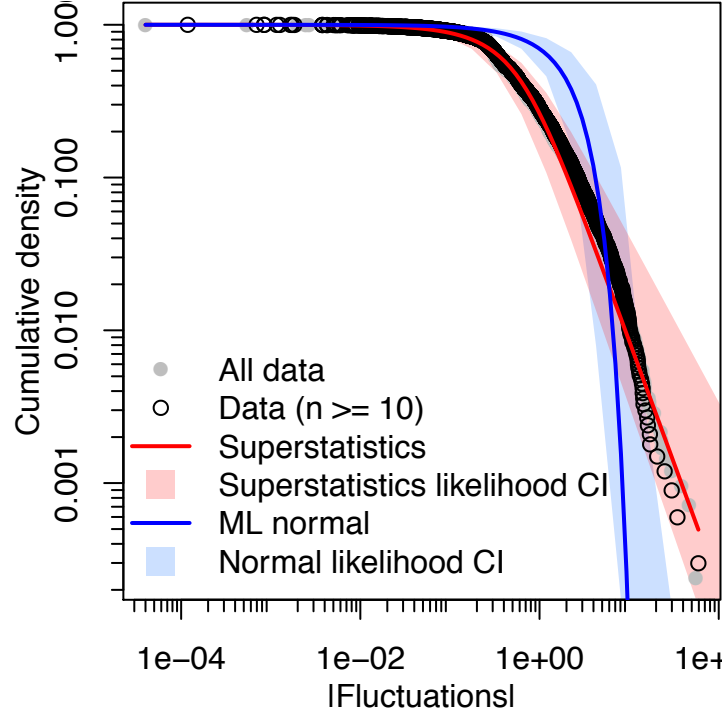
Figure 2: Distribution of fluctuations in genus diversity within orders of marine inverte-brates in the Paleobiology Database[5] after bias correction. The distribution is fat-tailed as compared to the maximum likelihood estimate of the normal distribution (blue line). At the order level the empirical distribution of fluctuations are well described by our super-statistical approach, both when computed from integrating over the distribution of observed variances (red line) and when fit via maximum likelihood (95% confidence interval; red shading).
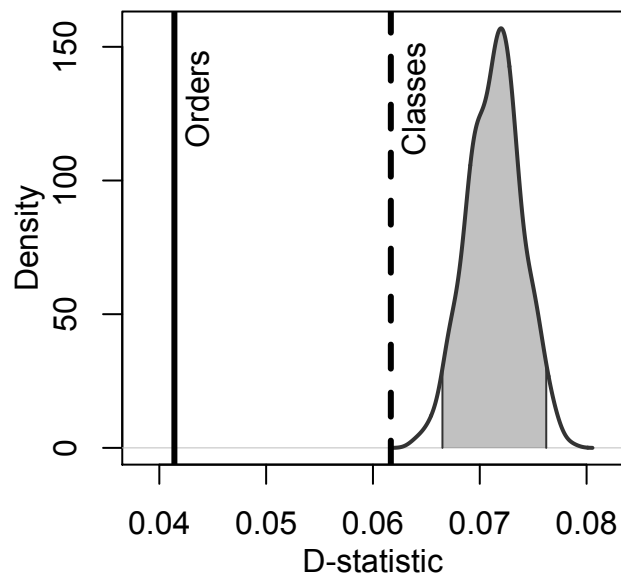
Figure 3: Distribution of Kolmogorov-Smirnov (KS) statistics from randomly permuting genera within orders (gray shading represents 95% confidence interval). Solid black line is observed KS statistic at the order level, while the dashed black line shows the observed KS statistic at the class level.