

# Adaptive landscapes explain fat-tailed fluctuations in marine biodiversity of the Phanerozoic

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1     Fluctuations in biodiversity, both large and small, are pervasive through  
2 the fossil record, yet we do not understand the processes generating them.  
3 Here we use a novel extension of theory from non-equilibrium statistical  
4 physics to show that three universal properties of macroevolution—punctuated  
5 adaptive radiation, niche conservatism and resultant heterogeneity of diver-  
6 sification rates between taxa—are sufficient to explain the previously unac-  
7 counted for fat-tailed form of fluctuations in diversity through the Phanero-  
8 zoic. Using this theory, known as super-statistics, we identify taxonomic or-  
9 ders as largely autonomous evolutionary units, each likely experiencing its  
10 own unique and conserved region of an adaptive landscape. The separation  
11 of timescales between background origination and extinction compared to the  
12 origin of major ecological and evolutionary innovations between orders allow  
13 within-order dynamics to reach equilibrium, while between-order diversifica-  
14 tion is non-equilibrial, driven by major evolutionary innovations. Compared  
15 to other approaches that have used simple birth-death processes, equilibrial  
16 dynamics or non-linear theories from complexity science, super-statistics is su-  
17 perior in its ability to account for both small and extreme fluctuations in fossil  
18 diversity. Its success opens up new research directions to better understand  
19 the universal nature of non-equilibrium dynamics across disparate systems of  
20 interest—from societal to physical to biological. Specifically in the biological  
21 case, research is motivated to understand the evolutionary processes leading  
22 to the stasis of order-level occupancy in an adaptive landscape punctuated by  
23 innovations between orders.

## 24 Introduction

25 Biodiversity has not remained constant nor followed a simple trajectory through geologic  
26 time (1–6). Instead, it has been marked by fluctuations in the number of extant taxa,  
27 both positive in the case of net origination or negative in the case of net extinction. Major  
28 events, such as adaptive radiations and mass extinctions have received special attention  
29 (7, 8), but fluctuations of all sizes are ubiquitous (2, 5, 9). Predicting the magnitude of  
30 these fluctuations continues to elude paleobiologists and biodiversity theoreticians.

31 Several approaches have been taken to study the complex trajectory of paleo-biodiversity  
32 ranging from the hypothesis that biological systems self-organize to the brink of critical  
33 phase-transitions (10, 11) to invocations of non-linear environmental perturbations (12)  
34 and escalatory co-evolutionary interactions (13). New data and analyses have not sup-  
35 ported any of these hypotheses at the scale of the entire Phanerozoic marine invertebrate  
36 fauna (5, 14, 15). Other studies have modeled the mean trend in diversity as tracking a  
37 potentially evolving equilibrium (2, 5, 6, 16) and yet ignore the potential role of stochas-  
38 ticity and non-equilibrium dynamics in producing observed patterns (4, 9, 17). As such,  
39 we still lack a synthetic theory of evolving biodiversity through the fossil record.

40 Despite the heterogeneity of explanations of Phanerozoic biodiversity, consensus has  
41 emerged on three properties of macroevolution: *i*) gross ecological and life history at-  
42 tributes of clades are often maintained, a phenomenon known as niche conservatism  
43 (18, 19); *ii*) long periods of niche conservatism are interrupted by adaptive diversifica-  
44 tion and exploration of new ecological niche space (19–21); and *iii*) as a consequence of  
45 the interaction between their life history characteristics and the environments they in-  
46 habit (22) (conserved through niche conservatism) different clades experience different  
47 rates of morphological evolution, speciation and extinction (2, 3, 23, 24).

Here we show that these simple and well-supported mechanisms are all that are needed to describe pervasive fluctuations in diversity throughout the marine Phanerozoic. These biological mechanisms have a precise correspondence to non-equilibrial theory, known as “superstatistics” derived in statistical mechanics (25) and applied across the physical and social sciences (26, 27). We leverage this correspondence to derive a robust prediction of the distribution of fluctuations in the standing diversity of marine invertebrates preserved in the Phanerozoic fossil record.

Superstatistics (25) proposes that non-equilibrial systems can be decomposed into many local sub-systems, each of which attains a unique dynamic equilibrium. The evolution of these dynamic equilibria across sub-systems evolves more slowly. This separation in time scale allows local systems to reach equilibrium while the system as a whole is far from equilibrium. (25). The superimposition of sub-systems following unique dynamic equilibria determines the nature of the non-equilibrium of the system as a whole. In the context of macroevolution we propose that a clade with conserved life history characteristics corresponds to a sub-system in dynamic equilibrium. We say dynamic equilibrium following MacArthur and Wilson (28) in recognition that while the identity and exact number of taxa will fluctuate stochastically from random origination and extinction, the overall process determining the number of taxa, and by extension, fluctuations in that number, is in equilibrium. Indeed, the different regions of adaptive space occupied by different clades can be conceptualized as different islands with different dynamic equilibria.

Variation in magnitudes of origination and extinction across these islands of adaptive space should correspond to life history and ecological characteristics that define that island or region occupied by a given clade. Larval type (29), body plan (17), body size (30), range size (30, 31) 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.

To uncover the superstatistical nature of the marine invertebrate Phanerozoic fauna we analyze the distribution of fluctuations in the number of genera (the lowest reliably recorded taxonomic resolution) using two canonical databases of fossil biodiversity, the Paleobiology Database (*?, PBDB*) [alroy08] and Sepkoski’s compendium (*32*) of fossil marine invertebrates (results from Sepkoski’s compendium are presented in Appendix 2.3). We define potentially equilibrial sub-systems based on taxonomic hierarchies, as a full phylogenetic hypothesis for all marine invertebrates is lacking. Taxa ideally represent groups of organisms that descend from a common ancestor and share similar ecologically and evolutionary relevant morphological traits (*33, 34*). For Phanerozoic marine invertebrates, the taxonomic level of orders is a likely candidate for equilibrial sub-system delineation (*24*). However, to evaluate the optimal taxonomic level for sub-system designation, we test our superstatistical theory using taxonomic levels from order to phylum. Additionally, we compare our results to randomized taxonomies and confirm that the observed fit of superstatistical theory is not an artifact of arbitrary classification but instead represent real, biologically relevant diversification processes within and between clades.

## Results

In statistical mechanics, local sub-systems can be defined by a simple statistical parameter  $\beta$  often corresponding to inverse temperature. In the context of macroevolution we define the  $\beta_k$  of clade  $k$  as the inverse variance of fluctuations  $x_k$  in the number of genera within that clade. The  $\beta_k$  thus represent the inverse variances of homogeneous origination-extinction processes, which will be approximately Gaussian if clades’ diver-

sification dynamics are independent and in local equilibrium (see Appendix 1). Three exemplar dynamics taken from a bias-corrected (see methods section) aggregation of the Paleobiology Database (PBDB) (5) are shown in Figure 1, and indeed all diversity fluctuations within orders are well characterized by a Gaussian distribution 1.

In independent and dynamically equilibrial dynamics suggested by these Gaussian fluctuations in genus richness could result from neutral-like processes (35), where the dynamics of one taxon are unaffected by those of another, or from dampening mechanisms that stabilize complex networks of interacting taxa (36). This is in direct contrast to the instability hypothesis underlying the self-organized criticality theory of paleo-biodiversity (10, 11).

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 stationary distribution of  $\beta_k$  values describes these possible equilibria, specifying the probability that a given clade, chosen at random, will occupy a region of niche space characterized  $\beta_k$ . The form of this stationary distribution could shed interesting light on the biological processes that lead different clades to explore different regions of adaptive landscapes, and thus different equilibria, as discussed below.

We estimate the distribution of  $\beta_k$ '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  $\beta_k$  values (Fig. 1).

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

$$P(x) = \int_0^\infty p_k(x | \beta) f(\beta) d\beta \quad (1)$$

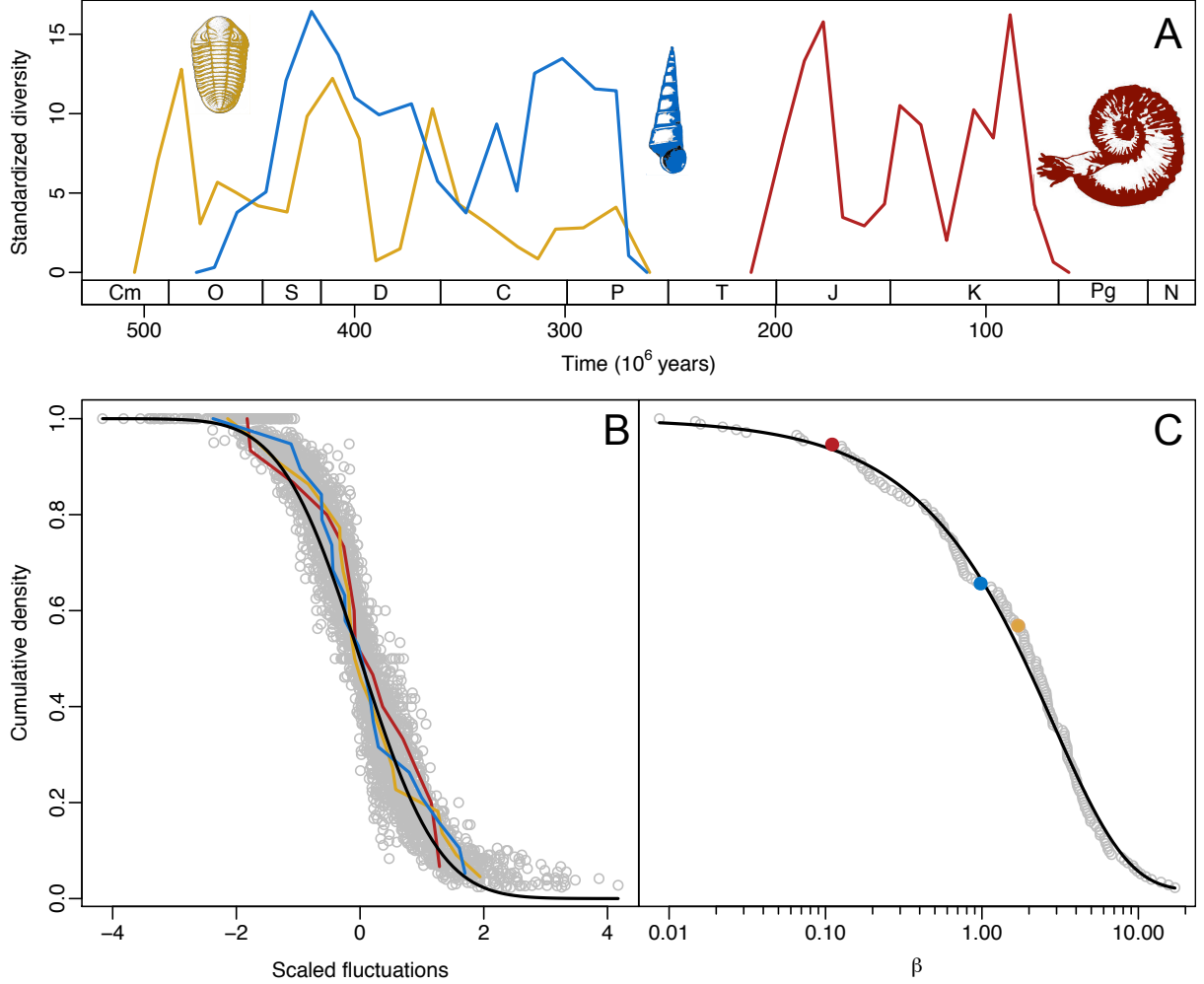


Figure 1: The distributions of within-order fluctuations in genus diversity shown for the trajectories of three exemplar orders (A) and shown as an empirical cumulative density aggregated across all orders (B). To display all orders simultaneously we simply collapse their fluctuation distributions by 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  $\beta_k$  across all orders matches very closely to a Gamma distribution (black line); exemplar orders are again highlighted.

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

124 and Sepkoski data closely (Fig. 2 and Appendix 2.3).

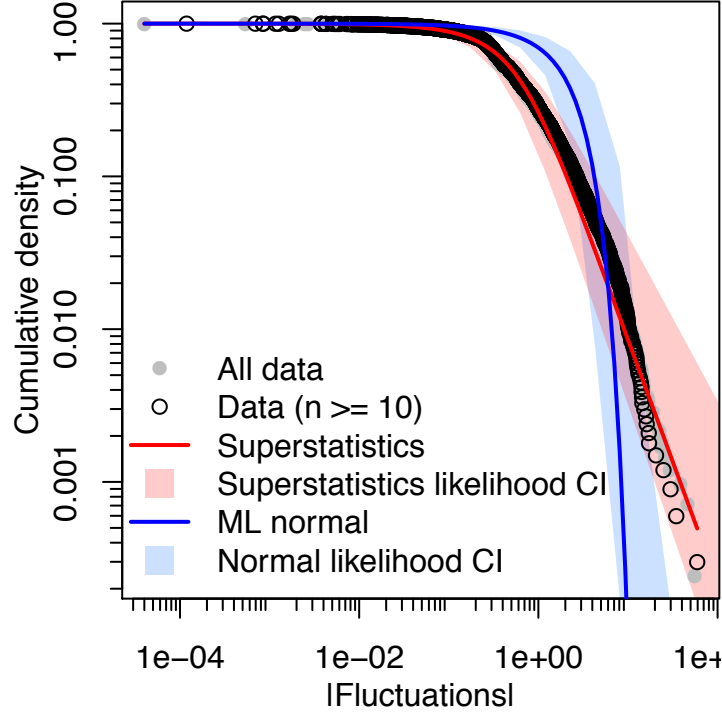


Figure 2: Distribution of fluctuations in genus diversity within orders of marine invertebrates in the Paleobiology Database (5) after bias correction. The distribution is fat-tailed as compared to the maximum likelihood estimate of the normal distribution (blue line). At the order level the empirical 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).

125 To quantitatively evaluate how well the super-statistical prediction matches the data  
 126 we constructed a 95% confidence envelope from bootstrapped maximum likelihood esti-  
 127 mates for  $P(x)$ . Observed fluctuations fall within this 95% confidence envelope (Fig. 2),  
 128 indicating that the data do not reject the super-statistical prediction. For further com-  
 129 parison, we fit a Gaussian distribution to the observed fluctuations, which corresponds  
 130 to the equilibrium hypothesis that all orders conform to the same statistic. Using Akaike  
 131 Information Criterion (AIC) we find that observed fluctuations are considerably better



explained by the super-statistical prediction than by the Gaussian hypothesis ( $\Delta\text{AIC} = 11285.18$ ). Thus, as expected under the superstatistical hypothesis, the fat tailed distribution of fluctuations arise from the superposition of independent Gaussian statistics of 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 for orders to 0.062 for classes (Fig. 3). However, if super-statistical theory explains the data, this worsening fit with increasing taxonomic scale is expected as the different classes should not represent dynamically equilibril sub-systems 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 equilibril and independent entities, with all subsumed taxa sharing key ecological and evolutionary attributes allowing them to reach steady state diversification 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

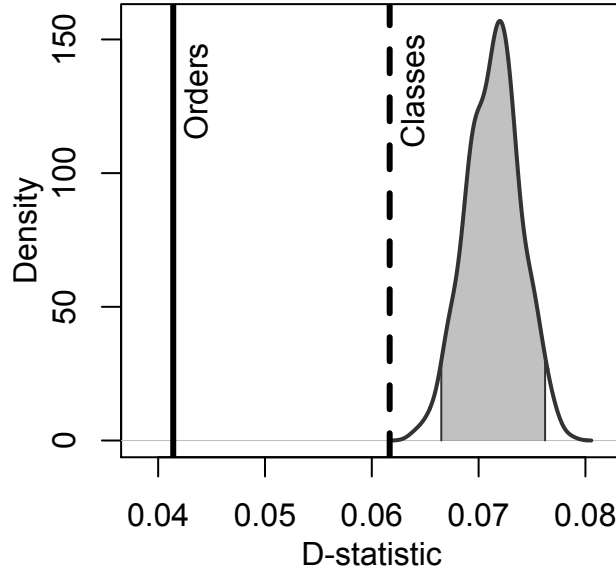


Figure 3: Distribution of Kolmogorov-Smirnov (KS) statistics from randomly permuting genera within orders (gray shading represents 95% confidence interval). Solid black line is observed KS statistic at the order level, while the dashed black line shows the observed KS statistic at the class level.

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.

## Discussion

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 fluctuation of diversity resulting from 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, non-equilibrium physical (26) and social systems (27). We do so by identifying the biological scale at which clades conform to locally independent dynamic equilibria in fluctuations. This scale is determined by the process of niche conservatism (18, 19) within orders. Equilibrium could result from many processes, including neutrality (28, 35), diversity-dependence (16, 37) and processes that dampen—rather than exacerbate—fluctuations in complex ecological networks (38). We then show that punctuated shifts to different equilibria between order, a consequence of punctuated exploration of niche space by newly evolving clades (19–21), leads to a characteristically non-equilibrium distribution of diversity fluctuations when the marine Phanerozoic fauna is viewed as a whole macro-system.

The stationary distribution describing this process of punctuated non-equilibrium is clearly Gamma. A Gamma distribution, while consistent with multiple processes (? , *e.g.*) [cir1985], could result from evolution of diversification rates across an adaptive landscape that promotes niche conservatism and punctuated exploration of niche space. Specifically, if  $\beta_k$  values are associated with a clade’s physiological and life history traits, and those traits evolve via Ornstein-Uhlenbeck-like exploration of an adaptive landscape, the resulting stationary distribution of  $\beta_k$  will be Gamma (39, 40). For macroevolutionary rates to vary across an adaptive landscape, this landscape cannot be flat, and thus niche conservatism punctuated by adaptive exploration is inevitable (21). However, if somehow rate variation could occur in a less peaky landscape, we would expect the distribution of  $\beta_k$  to follow a chi-squared distribution.

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

193 lineages and how those innovations are eventually conserved within lineages. Armed with  
194 an understanding of the statistical behavior of diversification we can go on to examine  
195 mechanisms underlying additional patterns in the mean trend of biodiversity through  
196 the Phanerozoic. In particular, clades have been shown to wax and wane systematically  
197 through time (4, 9), a pattern that we cannot explain with super-statistics alone.

198 Superstatistics could also be applied to other areas of evolution and macroecology.  
199 For example new phylogenetic models already consider heterogeneous rates of diversifi-  
200 cation (2, e.g.) [rabosky2006laser]. The superstatistics of clades in adaptive landscapes  
201 could provide a means to build efficient models that jointly predict morphological change  
202 and diversification. This framework could also provide a new paradigm in modeling the  
203 distributions of diversity, abundance and resource use in non-neutral communities. Non-  
204 neutral models in ecology are criticized for their over-parameterization (41), yet a persis-  
205 tent counter argument to neutral theory (35) is the unrealistic assumption of ecological  
206 equivalency (42) and poor prediction of real dynamics (43). If ecosystems are viewed as  
207 the super-position of many individualistically evolving clades, each exploiting the environ-  
208 ment differently and thus obeying a different set of non-equivalent statistics, then diversity  
209 dynamics could be parsimoniously predicted with superstatistics while incorporating real  
210 biological information on ecological differences between taxa.

211 Superstatistics is a powerful tool to derive macro-scale predictions from locally fluc-  
212 tuating sub-systems whose evolution is driven by interesting, but complex and difficult  
213 to model, biological mechanisms. As such, applications of superstatistics from islands to  
214 populations to clades are ripe for exploration.

## 215 **Methods**

### 216 **Paleobiology Database data download and filtering**

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

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

### 230 **Three-timer and publication bias correction**

231 We use a new and flexible method, described below, to correct for known sampling biases  
232 in publication-based specimen databases (5,6). We were motivated to use this method be-  
233 cause rarefaction has been shown to under-perform compared to the more data-intensive  
234 shareholder quorum subsampling (SQS) method (6). However, subsampling cannot be  
235 applied to small orders (i.e. the majority) because SQS becomes increasingly unreliable  
236 as sample size decreases (6). We therefore develop a simple method based on first correct-  
237 ing for detection bias using the “three timer” correction (5) in which the rate of failure  
238 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.

## 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 com-

pare 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.

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## 322 **Acknowledgments**

323 We thank John Harte, Rosemary Gillespie, Linden Schneider, and Jun Ying Lim for  
324 helpful discussion. We thank the many contributors to the Paleobiology Database for  
325 making data available, and Michael Foote provided a digitized copy of Sepkoski's com-  
326 pendium. AJR thanks funding from Fulbright Chile, the National Science Foundation  
327 Graduate Research Fellowship Program and the Omidyar Program at the Santa Fe Insti-  
328 tute; MAF thanks FONDECYT 1140278; PM thanks CONICYT PFB-023, ICM-P05-002  
329 and FONDECYT 1161023.