**Title:** Empirical abundance distributions are more uneven than expected given their statistical baseline

**Running title:** SADs deviate from statistical baselines

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**Abstract**

Incorporating the emergent properties of ecosystems as complex systems into the search for general processes to explain common ecological patterns is a promising horizon for synthesis in ecology. For example, the ubiquitous hollow-curve form of the species abundance distribution is frequently assumed to reflect ecological processes structuring communities, but can also emerge mathematically from the definition of an abundance distribution. While the hollow curve may be a statistical artefact, ecological processes may induce subtle deviations between empirical species abundance distributions and their statistically most probable forms, which may reflect biological processes operating on top of mathematical constraints and provide new avenues for developing and testing ecological theory. Examining ~22,000 communities, we found that empirical species abundance distributions are highly uneven and dominated by rare species compared their statistical baselines. However, small communities – those with few species or individuals – show deviations less consistently than do larger ones, perhaps because they exhibit poorly-resolved statistical baselines. The extremely uneven nature of most empirical SADs demonstrates a path forward for leveraging complexity to understand ecological processes governing the distribution of abundance, while the issues posed by small communities illustrate the limitations of using this approach to study ecological patterns in small samples.

**Introduction**

Ecological communities are complex systems made of numerous interacting entities subject to a vast array of processes operating in different contexts and at different scales (Levin 1992; Lawton 1999; Maurer 1999; Brown et al 2002; Nekola and Brown 2007; McGill 2019). One strategy for making sense of this inherent complexity is to identify patterns that occur consistently across many communities, and use these common phenomena to develop and test theories regarding general mechanisms that shape community structure (Brown and Maurer 1989; Maurer 1999; Lawton 1999; Gaston and Blackburn 2000; McGill 2019). Distributions describing complex systems, however, can have counterintuitive emergent statistical properties (Frank 2009; 2019). Left unexamined, these properties can interfere with interpreting these distributions in terms of generative mechanism, but, properly understood and accounted for, they can provide leverage for detecting and identifying the processes at work in a system (Jaynes 1957, Harte and Newman 2014). The species abundance distribution (SAD) – the distribution of how all of the individuals in a community are divided among the species in that community – is a leading example of an ecological distribution that is both commonly invoked in the search for general processes, and quite possibly subject to statistical constraints that have thus far complicated efforts to use it in this way (Nekola and Brown 2007; McGill et al. 2007; Locey and White 2013). Investigating and accounting for these statistical considerations may open up new avenues for ecological interpretations of the SAD, in a key illustration of how embracing ecological complexity can bring us closer to ecological insight.

The shape of the SAD is one of the few ecological patterns that is so consistent that it is often considered an ecological law (Preston 1948, 1962a, 1962b, 1980; Lawton 1999, McGill 2003, McGill et al. 2007). Across varied ecosystems and taxa, the species abundance distribution is dominated by a few very abundant species and a larger number of increasingly rare species, generating a distinctive hollow- or J-shaped curve when plotted with species rank on the x-axis and abundance on the y-axis (Fisher et al. 1943; McGill et al 2007). Community ecologists have used the SAD to test numerous theories intended to determine which biological processes are most important for structuring assemblages of species, by comparing theoretical predictions for the SAD to observed SADs (McGill 2003; McGill et al. 2007). However, this approach has proven inconclusive because many theories predict similar shapes for the SAD (McGill 2003; McGill et al. 2007), and even experimental manipulations generate little variation in the shape of the SAD (Supp and Ernest 2014).

The nearly ubiquitous shape of the SAD may actually transcend ecological processes and instead reflect mathematical properties inherent to the definition of an abundance distribution. Many different types of complex systems, ranging from economics to information technology, exhibit empirical abundance distributions with hollow-curve forms similar to ecological SADs (Shockley 1957; Gaston et al. 1993; Nekola and Brown 2007, Blonder et al. 2014; Kiel et al. 2018). This suggests that the hollow curve is a feature of abundance distributions in general and not necessarily an ecological phenomenon. Because the hollow-curve is observed in diverse systems and many theoretical generative processes converge to power-law or log-series abundance distributions (i.e. hollow curves) (Preston 1950; McGill 2003; Nekola and Brown 2007; Frank 2009; Frank 2019), approaches from statistical mechanics and complexity science may best explain the expected emergent shape for the distribution (Preston 1950; McGill 2003; Nekola and Brown 2007; Dewar and Porté 2008). Indeed, recent frameworks grounded in both entropy maximization (i.e. the Maximum Entropy Theory of Ecology (METE); Harte et al. 2008, Harte 2011) and combinatorics (i.e. ‘the feasible set’; Locey and White 2013) generate realistic hollow curves via the random division of the total number of individuals in a community, *N*,into the total number of species present, *S*. If the SAD is statistically inclined to be a hollow curve because of its inherent mathematical features, the hollow-curve in itself may be of limited use for developing and testing ecological theories.

While SADs may be statistically constrained, this does not necessarily mean that they cannot be biologically informative. Biological factors may introduce subtle, but meaningful, deviations between observed SADs and the shapes of the SADs expected due to the mathematical constraints imposed by *S* and *N,* which we hereafter refer to as the “statistical baseline” (Locey and White 2013, Harte and Newman 2014). Thus, it may be possible to use these *deviations* to detect strong ecological processes or evaluate theories (Harte and Newman 2014, Xiao et al. 2016). If the vast majority of mathematically achievable SADs for a community share a similar shape, an empirically observed SAD that deviates even slightly from this statistical baseline is unlikely to have emerged at random (Locey and White 2013). Such a deviation is therefore likely to be the signature of a non-random – i.e., biological – process operating on the relative abundances of species (Harte and Newman 2014). If, over many communities, there are consistent deviations between observed SADs and their statistical baselines, these deviations can help focus and evaluate ecological theories. For example, the high prevalence of rare species in ecological communities has attracted considerable empirical and theoretical attention (e.g. Nee 1991; Magurran 2003), but it is unclear how much of this phenomenon may derive from general mathematical constraints on the SAD rather than ecological processes. Taking into account the statistical baseline, if the prevalence of rare species in observed distributions consistently exceeds what would be expected to emerge from the statistical baseline, this would prompt us to look for ecological mechanisms promoting rarity. The predictions from candidate theories could then be evaluated based on how well they predict specifically the rare tails found in observed distributions instead of the aspects of shape expected given the statistical baseline.

Successfully interpreting SADs in this fashion depends on our capacity to detect and quantify deviations between empirical observations and statistical baselines, which requires metrics and computational approaches that allow us to quantify and interpret whatever deviations may exist. Here, we build upon the combinatoric approach developed by Locey and White (2013) to define and explore statistical baselines for SADs. For a given *N* (total number of individuals) and *S* (total number of species), there exists a finite (but potentially very large) set of possible distributions of individuals into species. Collectively, this set of possible SADs is referred to as the feasible set, with each possible SAD constituting a single element of the set. If an observed SAD is drawn at random from the set of mathematically possible SADs, it is likely to have a shape similar to the shapes most common in the feasible set. The feasible set can therefore be used as a statistical baseline for assessing whether observed SADs deviate from what is likely to occur merely due to mathematical constraints (Locey and White 2013).

The feasible set can also be used to explore how the characteristics of the statistical baseline, and the presence and nature of any deviations that occur, vary over ranges of values for S and N. Although most feasible sets are dominated by generally hollow curves, variation in S, N, and the ratio of N to S modulate more detailed attributes of the SADs in a feasible set (Locey and White 2013). For example, if the ratio of N to S is very low, all possible SADs are mathematically constrained to be fairly even (Locey and White 2013). The feasible set therefore allows us to appropriately calibrate our expectations for what types of observations would be surprising for an SAD given the specific constraints imposed by its S and N. Additionally, accounting for variation in the specificity, or vagueness, of the expectations derived from the statistical baseline may be critically important for disentangling the aspects of the SAD that are likely generated by statistical constraints from those generated by other processes. If the vast majority of mathematically possible SADs are similar in shape – generating a very specific, narrowly defined statistical baseline – then even small deviations between an observed SAD and this baseline can signal the operation of ecological processes. However, if many different shapes occur with more even frequency in the feasible set, the statistical baseline is less specific and less well defined, and our sensitivity for distinguishing biological signal from statistical constraints is greatly reduced. In general, a poorly defined statistical baseline is more likely to occur when the size of the community, in terms of *S* and *N,* is small, because in such cases there may be too fewpossible SADs in the feasible set for a particular shape to emerge as the most common, and therefore most likely, shape. Statistical baselines with broad distributions will therefore impede our ability to assess whether observed deviations ecologically generated or expected to emerge randomly (Jaynes 1957). This general concern has been acknowledged in efforts to compare ecological observations to statistical baselines (Harte 2011, White et al. 2012, Locey and White 2013) but there has not yet been a quantification of these effects for the SAD or an identification of the range of community sizes most strongly affected. Because ecologists study the SAD for communities varying in size from the very small – *S* and *N* < 5 – to the enormous – *S* and *N* >> 1000 – identifying the community sizes for which we can and cannot confidently detect deviations from the statistical baseline is necessary to appropriately contextualize our interpretations.

Here we use the feasible set to define statistical baselines for empirical SADs for 22,000 communities of birds, mammals, trees, and miscellaneous other taxa. We then compare *observed* SADs to their corresponding statistical baselines and evaluate 1) if the shapes of observed SADs consistently deviate from their statistical baseline, 2) how the characteristics and specificity of the statistical baseline varies over ranges of *S* and *N*, and 3) whether this variation appears to be associated with variation in our capacity to detect deviations between observations and the corresponding baselines.

**Methods**

Data and code for all of our analyses can be accessed at [www.github.com/diazrenata/scadsanalysis](http://www.github.com/diazrenata/scadsanalysis).

*Datasets*

We used a compilation of community abundance data for trees, birds, mammals, and miscellaneous additional taxa (White et al. 2012, Baldridge 2015, Baldridge 2016, data from Baldridge 2016). This compilation consists of cleaned and summarized community abundance data for trees obtained from the Forest Inventory and Analysis (Woudenberg et a al 2010) and Gentry transects (Phillipes and Miller 2002), birds from the North American Breeding Bird Survey (Sauer et al. 2013), mammals from the Mammal Community Abundance Database (Thibault et al. 2011), and a variety of less commonly sampled taxa from the Miscellaneous Abundance Database (Baldridge 2015). Because characterizing the random expectation of the SAD is computationally intractable for very large communities, we filtered our datasets to remove communities with more than 40720 individuals, which was the largest community we successfully analyzed. This resulted in the removal of 4 communities from the Miscellaneous Abundance Database. We further filtered the FIA database. Of the 103,343 communities in FIA, 92,988 have fewer than 10 species. Rather than analyze all these small communities, we randomly selected 10,000 small communities to include in the analysis. We also included all FIA communities with more than 10 species, which added 10,355 FIA communities to the analysis and resulted in a total of 20,355 FIA communities. Finally, for sites that had repeated sampling over time, we followed White et al. (2012) and Baldridge (2016) and analyzed only a single, randomly selected, year of data, because samples taken from a single community at different time points are likely to covary. It should be noted that our analyses include data from the Mammal Community Database and Miscellaneous Abundance Database that were collected over longer timescales and cannot be disaggregated into finer units of time. Our final dataset consisted of ~22,000 communities with S and N ranging from 2 to 250 and 4 to 40714, respectively (Figure 1). Details and code for the filtering process can be found in Appendix S1 in Supporting Information.

*Accounting for empirical sampling error*

Because it is logistically impossible to exhaustively catalog all individuals present in most empirical systems, SADs derived from field sampling will inevitably be subject to some degree of sampling error (Bonar et al. 2011). Therefore, in addition to analyzing the raw SADs in our database, we employed two resampling schemes to test if, and how, different forms of observation error affect our results.

First, we explored the possibility that empirical sampling systematically undercounts the true number of rare species in a community (Gotelli and Colwell 2011). Rare species may be more likely to escape detection during sampling, leading to an underestimate of both the total species richness of a community and the proportion of species in the rare tail of the SAD. We used species richness estimators to adjust for this possibility. For each community, we computed the estimated richness using the bias-correct Chao and the ACE estimators (as implemented in the R package “vegan”; O’Hara 2005; Chiu et al 2014; Oksanen et al. 2020), adding one standard deviation of the estimate to each estimate, and taking the mean of the two estimates. This yields a generous estimate of the true number of species in the system. If this estimate exceeded the number of species observed for a community, we added the missing species each with abundance 1, which allowed us to explore the consequences of undersampling rare species while making the smallest possible changes to S and N.

Second, we tested the sensitivity of our results to sampling variability across the entire range of the SAD using subsampling. For each observed community, we constructed subsamples by randomly drawing 60% of the observed number of individuals from the total pool of individuals in the community, without regard to species and without replacement. This introduced substantial room for sampling error between the resampled and observed distributions, but yielded resampled communities that were not trivially small in terms of S and N. We drew 10 resampled communities for each observed community.

We ran our computational pipeline using all raw SADs and all SADs adjusted for undersampling of rare species. Because subsampling increased computational effort up to tenfold, we analyzed all subsampled communities for the Mammal Community, Miscellaneous Abundance, and Gentry databases, but only a random subset of 300 (of 2773) communities from the Breeding Bird Survey and 2000 (of 20179) from the FIA – 1,000 with S < 10, and 1,000 with S >= 10.

*Generating the statistical baseline*

We use the concept of the “feasible set”to establish a statistical baseline for the SAD (Locey and White 2013). For a given number of individuals *N*,there is a finite number of unique ways to partition those individuals into *S* species. The complete set of these unique partitions is the feasible set. Because, in this approach, neither species nor individuals are distinguishable from each other, partitions are unique if and only if they differ in the number of species that have a particular abundance (Locey and White, 2013). Operationally, this means that for *S = 3* and *N = 9*, the species abundances *(1, 3, 5)* and *(2, 2, 5)* count as distinct partitions, but *(1, 3, 5)* and *(3, 1, 5)* are only one element of the feasible set because they each contain one species with an abundance 1, 3, and 5, respectively, and they differ only in the *order* of the numbers. In the absence of justification for additional assumptions regarding the distinguishability of species and/or individuals, we adopted this simple set of assumptions that has previously been shown to generate realistic statistical baselines (Locey and White 2013).

While it is possible to list all possible partitions in the feasible set for small *S* and *N*, the size of the feasible set increases rapidly with *S* and *N*. Therefore, an exhaustive characterization of the statistical properties of the feasible set for large *S* and *N* quickly becomes computationally intractable. This renders it necessary to draw samples from the feasible set, rather than enumerating all of its elements. Previous efforts in this vein (Locey and White 2013) have been constrained by the problem of unbiased sampling of large feasible sets.

We developed an algorithm to efficiently and uniformly sample feasible sets even for large values of *S* and *N*. In brief, the algorithm takes a generative approach to sampling the feasible set for a given combination of *S* and *N*, based on recurrence relations used to calculate the size of the feasible sets for all smaller combinations of *S* and *N*. Let f(S, N) be the number of possible partitions of N individuals into exactly S species, i.e. the size of the feasible set for given values of S and N. Computation of f(S, N) can be achieved without enumerating the entire feasible set through the recurrence relation f(S, N) = f(S-1, N-1) + f(S, N-S) (originally documented in a 1742 letter from Euler to Bernoulli; 1862). For example, consider the feasible set with S = 3 and N = 7. For all possible partitions, either (a) at least one species has an abundance equal to 1, or (b) all of the species have abundance greater than 1. In the case of (a), removing one species with abundance equal to 1 must result in a partition of 6 individuals into 2 species. In fact, all of the unique partitions in (a) must have a corresponding unique partition in the feasible set for S = 2 and N = 6, and vice versa. In the case of (b), removing 1 individual from each species must result in a partition from the feasible set with S = 3 and N = 4. Again, all the partitions in (b) must have a corresponding unique partition in the feasible set with S = 3 and N = 4, and vice-versa. Therefore, f(3,7) = f(2,6) + f(3,4). By storing the values in a lookup table, f(S, N) can be calculated for increasing values of S and N through straightforward summation.

This recurrence relation makes it possible to draw random samples from the feasible set without enumerating all possible partitions of N into S. For the example of S = 3 and N = 7, there are a total of 4 possible partitions (i.e. f(S, N) = 4). Because f(2, 6) = 3 and f(3, 4) = 1, we know that (a) 3 of the 4 partitions must correspond to a partition of the feasible set with S = 2 and N = 6 (but with a species of abundance equal to 1 removed), and (b) 1 of the 4 partitions must correspond to a partition of the feasible set with S = 3 and N = 4 (but with 1 individual removed from each species). Thus, we can determine the probability that a partition drawn at random from the feasible set for S = 3 and N = 4 is in case (a) – probability ¾ - or case (b) – probability ¼. If it is in case (a), we sample a partition for S = 2 and N = 6 and then add a species with abundance equal to 1; if it is in case (b), we sample a partition for S = 3 and N = 4 and then add 1 individual to each species. In this way, we use the recurrence relation to transform the problem of sampling from a large feasible set into the problem of sampling from a smaller, different feasible set, until a partition is uniquely determined, and some back-transformation yields a unique partition for the feasible set of interest. A detailed description of the algorithm we use, based on a slightly different recurrence relation, is available in Appendix S2 and is implemented in the R package feasiblesads available on GitHub at [www.github.com/diazrenata/feasiblesads](http://www.github.com/diazrenata/feasiblesads).

For every community in our database, we drew 4000 samples from the feasible set to characterize the distribution of statistically probable shapes for the SAD. We filtered the 4000 samples to unique elements. For small values of S and N, it can be impossible or highly improbable for the 4000 samples from the feasible set to all be unique, but for large communities, all 4000 are usually unique. We refer to this as the sampled feasible set.

*Comparing observed SADs to their baselines*

For an overall comparison between observed SADs and their statistical baselines, we quantified the degree of dissimilarity between observed SADs and the central tendencies of their feasible sets and compared this to the degree of dissimilarity between random samples from the feasible set and the central tendency (following Locey and White, 2013). If all SADs in a feasible set are equally likely to occur, then observed SADs should not be markedly less similar to the central tendency of the feasible set than random samples from the feasible set. If observed SADs are consistently more dissimilar to the central tendency than samples from the feasible set, strong processes may be at work driving observed SADs away from the central tendency. We defined the degree of dissimilarity between two SADs with the same S and N as the proportion of individuals allocated to species with different abundances between the two SADs, calculated as:

where *n1i* is the abundance at rank *i* for one SAD and *n2i* is the abundance at rank *i* for the other SAD. This value ranges from 0 to 1, with 1 being high dissimilarity. Unlike an R-squared or coefficient of determination, it is never negative and does not depend on which SAD is considered the “reference” or “comparison” sample. To find the central tendency of a given sampled feasible set, we calculated the dissimilarity between every sample drawn from the feasible set and a random set of 500 other samples. We used only a subset of samples because it is computationally impractical to make all pairwise comparisons between large numbers of samples. For each focal sample, we calculated the mean dissimilarity score over the 500 comparison samples, and approximated the central tendency to be the focal sample with the lowest mean dissimilarity. To assess whether an observed SAD was dissimilar to its central tendency, and whether it was so dissimilar as to be statistically unlikely, we calculated the degree of dissimilarity between the central tendency of the corresponding feasible set and all other samples from that feasible set, and between the central tendency and the observed SAD. We then calculated the percentile rank of the observed dissimilarity score relative to the distribution of dissimilarity scores from the sampled feasible set. For a single community, an observed percentile score of 95 indicates that there is a 5% chance of drawing a value greater than the observed value from the distribution of values from the sampled feasible set. After aggregating across communities, if observed SADs reflect random draws from their feasible sets, their percentile rank values should be uniformly distributed from 0 to 100. However, if observed SADs are consistently highly dissimilar from their feasible sets, the percentile values will be disproportionately concentrated at high values. We used a one-tailed 95 confidence interval and tested whether the percentile values for the dissimilarity scores of observed SADs fell above 95 more than 5% of the time. Comparing percentile scores to a one-tailed 95% interval is not meaningful if there are fewer than 20 values in the sampled distribution because, in these cases, it is impossible for an observation to fall above the 95th percentile. We therefore excluded from this analysis communities with fewer than 20 unique SADs in their feasible sets, yielding a total of 22,490 communities. Finally, note that, if the observed dissimilarity scores for individual communities are not systematically higher than the distributions of dissimilarity scores from the corresponding feasible sets, increasing the number of *communities* in the analysis will not increase the frequency of extreme percentile scores.

While the degree of dissimilarity between SADs and the central tendency of the feasible set provides an overall sense of how large and common deviations are, it does not provide very much information about *how* observed SADs differ from their feasible set. We therefore used a set of more targeted, ecologically interpretable metrics to explore how observed SADs compare to their feasible sets in their shape and proportion of rare species. We used three metrics to describe the shape of the SAD - skewness, Simpson’s evenness (1-D), and Shannon’s index. Skewness measures the asymmetry of a distribution around its mean. The Simpson and Shannon indices are commonly used metrics in ecology for assessing how equitably abundance is distributed across species (Maurer and McGill 2011). We also calculated the proportion of rare species (species with abundance = 1) in each SAD, because the proportion of rare species in a community is readily comparable across different community sizes and is of special interest to ecologists. There exists a vast array of possible summary metrics for describing the shape of an SAD, and different metrics emphasize different aspects of the distribution. In this first effort to compare empirical distributions to a statistical baseline, we selected a suite of complementary metrics and explored whether our overall results were consistent between metrics. By calculating these metrics for each of the samples in the community’s sampled feasible set (see *Generating the statistical baseline*,above), we generated a distribution describing the shapes expected from the randomly sampled SADs.

As with the degree of dissimilarity score, to assess whether the shape of an observed SAD was statistically unlikely, we used percentile ranks to compare the values for our summary metrics for the observed SAD to the distributions of values for those metrics obtained from that community’s sampled feasible set. While the actual ranges and values of summary metrics vary widely over large ranges of S and N and thus cannot be used for direct comparisons, percentile ranks are comparable across different community sizes and allow broad-scale assessment across wide ranges of *S* and *N*. We used two-tailed 95% intervals to test whether observed communities’ percentile values for each metric were disproportionately concentrated below 2.5 or above 97.5. In all cases, in testing for unusually high percentile scores, we defined the percentile score specifically as the proportion of values in the sampled distribution strictly less than the observed value, while in testing for low values, we defined it as the proportion of sampled values less than or equal to the observed value. This distinction ensured a conservative estimate of how extreme the observed values were relative to the sampled distribution, even in instances where the sampled distribution had numerous ties. Because it is impossible for an observed percentile score to be above or below the 97.5th or 2.5th percentile if there are fewer than 40 values in the sample distribution, we excluded from these analyses communities with fewer than 40 SADs in their feasible sets. Finally, note that skewness, as implemented in the R package “e1071” (Meyer et al. 2019), always evaluates to 0 for distributions with only two species, and we therefore excluded those cases from analyses of skewness (but included those communities for analyses using the remaining metrics). Our final analysis included 21,395 communities for skewness and 21,403 communities for all other shape metrics.

*The narrowness of the expectation*

of dissimilarity scores and shape metricsFor an overall sense of how tightly elements of the feasible set were clustered around the central tendency, we calculated the mean dissimilarity score between all samples from a feasible set and the approximate central tendency of that feasible set. For a more specific estimate of the narrowness of the distributions of sampled values for the shape metrics, we calculated a breadth index defined as the ratio of the range of values encompassed within a two-sided 95% density interval relative to the full range of values in the distribution (Figure 2). This breadth index for the statistical baseline ranges from 0 (a very narrow distribution and well-resolved baseline) to 1 (a very broad distribution), and is comparable across feasible sets for varying combinations of *S* and *N*. These approaches correspond qualitatively to more computationally-intensive approaches to measuring the self-similarity of the elements of feasible sets (see Appendix S3). We explored how the narrowness of the statistical baseline varies with the number of elements in the feasible set and the ratio of N to S.

**Results**

*Observed SADs compared to their feasible sets*

For four of the five datasets we analyzed – BBS, Gentry, Mammal Communities, and Misc. Abund – observed SADs are dramatically more dissimilar to the central tendencies of their feasible sets than would be expected by chance (Figure 3). Combined over these four datasets, 29% of observed SADs are more dissimilar to the central tendency than are 95% of samples from the feasible set. If observed SADs were simply random draws from the feasible set, we would expect only 5% to be that dissimilar (Table 1). These highly unlikely SADs have dissimilarity scores from 1.5 to 9.7 times greater than the mean dissimilarity between the central tendency and samples from the feasible set, an absolute increase ranging from .04 to .6 on a scale from 0-1 (Figure S4). These datasets also contain highly unlikely observed SADs in terms of their shape metrics. At random, roughly 2.5% of observed percentile scores for these metrics should be very high (>97.5) or very low (<2.5). Instead, these four datasets contain a disproportionate number of communities with very low values for Simpson’s evenness and Shannon diversity, and very high skewness, relative to their feasible sets (Table 1). The Mammal Community, and Miscellaneous Abundance databases also have high proportions of rare species, but this tendency is weaker for BBS and nonexistent for Gentry – in fact, the Gentry dataset has a high representation of sites with *low* proportions of rare species (20% of sites; Table S5). The Gentry dataset also has a disproportionate number of communities with the opposite tendencies to the other datasets for the other shape metrics– that is, an overrepresentation of communities with highSimpson’s evenness and Shannon diversity, and low skewness.

In contrast to the other datasets, percentile scores for sites from the FIA dataset are more uniformly distributed, and the proportions of extreme values are closer to what would be expected by chance (Table 1). Only 7% of FIA communities are highly dissimilar to their feasible sets (compared to a random expectation of 5%). Among the shape metrics, only 2.7% (compared to 2.5% at random) of sites have high values for skewness, 1.3% have high proportions of rare species, 5.7% have low Simpson’s evenness, and 5.4% have low Shannon diversity.

*The narrowness of the expectation*

The ability to detect deviations from the statistical baseline depends in part on the distribution of SADs in the feasible set. Overall, the SADs in a feasible set become more narrowly clustered around the central tendency of that feasible set as the size of the feasible set increases (Figure 4). The sampled distributions for shape metrics also generally become less broad as the size of the feasible set increases. The breadth indices for small communities are highly variable and often very large – approaching 1, meaning that a 95% density interval of the values in the distribution spans nearly the entire range of values – while the breadth indices for larger communities rarely exceed ~.7 for skewness, Simpson evenness, and Shannon diversity, and ~.8 for the proportion of rare species. Among our datasets, the FIA and Mammal Community databases have the smallest communities, in terms of S and N, and tend to be the most dominated by feasible sets with high breadth indices (Figure S6).

*Sensitivity to sampling variability*

In almost all cases, SADs adjusted for the under-observation of rare species are even more extreme relative to their feasible sets than unadjusted SADs (Figure 5; see appendix A7 for complete results of resampling). For all datasets, adjusted SADs have a higher proportion of high values for skewness and the proportion of rare species, and low values for Simpson’s evenness and Shannon diversity, than unadjusted SADs. This is most pronounced for the proportion of rare species for the Breeding Bird Survey: while only 4.5% of unadjusted SADs have very high proportions of rare species, 17.5% of adjusted SADs do. Adjusting for rare species does not appreciably change the proportion of Gentry datasets that feature extremely low proportions of rare species and skewness and high values for evenness and Shannon diversity.

Jackknife resampling consistently reduces the proportion of extreme observations across all datasets and metrics (Figure 5; Appendix A7). In most instances, the proportion of extreme observations still exceeds the proportion that would be expected by chance. However, the proportion of sites with high numbers of rare species observed for the BBS and Mammal Community database drop from 4.5% to 1% and ~13% to 3.5% with resampling. For the FIA dataset, the proportions of sites with high dissimilarity, low evenness and Shannon diversity all drop from 6-8% to 2-3%. Note that, for the FIA dataset, neither the raw nor the resampled SADs have a disproportionate representation of high values for skewness or the proportion of rare species.

**Discussion**

We found widespread evidence that SADs for a range of real ecological communities deviate from the forms expected given the distribution of shapes within their feasible sets. Overall, these deviations may signal that ecological processes operate on top of statistical constraints, thereby driving the SAD away from common shapes generated by purely statistical processes. We also found that whether, and in which specific aspects of the distribution, we detected deviations varied among the datasets we considered. This variability may reflect statistical phenomena related to the size of S and N and their ratio, or it may reflect different biological processes dominating in different contexts. Finally, we note that, althoughThis does not necessarily mean that ecological processes are not operating in these communities, only that be ingGoing forward, testing whether ecological theories or common functional approximations (e.g. the log-normal distribution) accurately predict this range of variation in deviations between observed SADs and their statistical baselines may be much more fruitful than focusing only on the general form of the SAD that emerges from statistical constraints (McGill et al. 2007; Locey and White 2013).

In most cases, and most pronouncedly for the Breeding Bird Survey, Mammal Community, and Miscellaneous Abundance databases, our results suggest that the prevailing processes structuring real communities tend to be those that cause abundance distributions to be highly uneven, rather than those that produce more even abundances across species. For these communities, observed SADs tended to be unusually skewed and uneven, and to have a high proportion of rare species, compared to their feasible sets. Correcting for undersampling of rare species strengthened these effects, while subsampling weakened them – especially for the proportion of rare species, perhaps because subsampling is likely to miss rare species even if it otherwise recaptures the general shape of a distribution. The long rare tail of the SAD has been a consistent focus in SAD research, and our results highlight that the rare tails of observed SADs are extraordinary, even among the hollow-curve shapes that dominate the feasible set. Ecological processes may lengthen the rare tail and decrease the evenness of the SAD, for example by promoting the persistence of rare species at very low abundances (e.g. Yenni et al. 2012). Or, they could drive abundant species to have larger populations than would be statistically expected, without driving other species entirely to extinction (Chesson 2000).

While the Gentry database also exhibits deviations tending towards high unevenness, it exhibits a much stronger tendency in the opposite direction: towards highly even SADs with a lower proportion of rare species than would be expected given their feasible sets. This could indicate that there are biological differences between Gentry and other datasets that result in different forms for the SAD, or that statistical characteristics of the feasible set for these communities modulate the deviations we detect. Compared to the other datasets, communities from the Gentry database tend to have high species richness and low average abundance (the ratio of N to S) (Figure 1). Among these, the communities with high evenness and low proportions of rare species are predominately those with very high species richness and low average abundance (N/S < ~3) (see Appendix A8). These extreme feasible sets constitute an unusual statistical baseline that redefines what attributes in an observed distribution are worthy of note. For example, SADs from these feasible sets have the highest proportions of rare species of any of the feasible sets in our analysis. Although observed SADs for these communities also have high proportions of rare species relative to other communities, taking the statistical baseline into account would suggest that the extraordinary thing about these SADs is actually that they do not have even morerare species. Simultaneously, there may be biological reasons why the species-rich but relatively low-abundance tropical tree communities of the Gentry database differ from those in other datasets. The same mechanisms that promote high diversity, in general, may manifest in high evenness, or ecological features particular to these forests may result in unusual SADs relative to the statistical baseline. Because no communities from our other datasets compare to these Gentry communities in S and N, we cannot disentangle statistical and biological explanations. This is an excellent opportunity to develop additional theoretical and empirical approaches to predict and explain variation in the deviations between SADs and their feasible sets, in particular for species-rich communities from different types of ecosystem.

Unlike the other four datasets, communities in the FIA dataset showed weak or no evidence of deviations from their feasible sets. We entertained two general classes of explanation for why the FIA dataset differs from the others in our analysis: first, that biological attributes of the FIA communities mean that the SADs for these communities differ from the others in our database, and second, that statistical phenomena related to S and N, and specifically community size, may modulate the capacity to detect deviations for these communities. To distinguish between possible biological drivers causing FIA to differ from the other datasets, and factors intrinsic to S and N, we compared a subset of ~300 FIA communities to communities from other datasets with directly comparable S and N. did not find differences in thefor any metrics datasets, conAppendix A9300statistical phenomenadifferences in results between and the other datasets

A second possibility is that these differences reflect statistical phenomena related to community size in terms of S, N, and as a result, the number of possible SADs in a community’s feasible set. The FIA communities are by far the smallest across our datasets (Figure 1), and communities with small values of S and N have smaller feasible sets. When there are relatively few possible SADs, they may be less tightly clustered around their central tendencies, and the distributions for the shape metrics less consistently narrowly peaked, than when there are very large numbers of possible SADs. This variability within the feasible set weakens the statistical distinction between “common” and “extreme” shapes for small, highly variable, feasible sets (Figure 2). Under these circumstances, any deviations – or lack thereof – that we perceive may be less informative than for communities with more strongly defined statistical baselines (Jaynes 1957). The average dissimilarity to the central tendency among elements of the feasible set, and the distributions of breath indices for specific metrics, broadly align with this principle. Across the range of community sizes represented across our datasets, small feasible sets have highly variable, and often very broad, feasible sets, while larger feasible sets have more consistently narrow feasible sets (Figure 4). Very small communities – for example, those with fewer than 2000 possible SADs in their feasible sets, or S ~ 20 and N ~ 40 – exhibit a higher proportion of highly variable feasible sets than large ones, and these small communities tend to show less consistent deviations than larger communities (Figure 6; Appendix A10). Of our datasets, FIA is most dominated by small communities (68% of communities have fewer than 2000 possible SADs), and these small-community phenomena may therefore have the greatest impact on results aggregated over the FIA dataset.

If it is true that the highly variable feasible sets associated with small communities contribute to the weak evidence of deviations observed for the FIA dataset, it means that such considerations may affect our capacity to use this approach to distinguish signal from randomness for a substantial contingent of ecological communities. Because the combinations of S and N represented in our analyses are irregularly distributed among different datasets (Figure 1), and because there is a great deal of variation in our breadth indices not accounted for by the size of the feasible set (Figure 4), we do not interpret these results as showing a threshold for defining problematically small communities. A more systematic exploration of the S and N state space, possibly combined with more nuanced metrics for characterizing the variability of the feasible set, could clarify and refine the relationship between S and N, the size of the feasible set, and statistical power. However, FIA and other small, highly variable communities have on the order of 10-20 species and 30-60 individuals, and these may indicate a general range of values below which we have relatively diminished power to detect deviations from the statistical baseline represented by the feasible set. Communities with on the order of 5 species, or 100s to 1000s of individuals, have previously been identified as “small” in this context (Preston 1948; McGill et al. 2007). To meaningfully draw inferences using deviations in these small communities, we will likely need more sensitive metrics than those used here, and/or theories that generate more specific predictions for the SAD. In the absence of such, we may stand to learn the most by focusing on SADs from relatively large communities.

It is also important to recognize that there are multiple plausible approaches to defining a statistical baseline for the SAD, of which we have taken only one (Haegeman and Loreau 2008, Locey and White 2013). Our approach follows Locey and White (2013) and reflects the random partitioning of individuals into species, with the resulting distributions considered unique if the species’ abundance values are unique, regardless of the order in which the values occur. The philosophy behind the feasible set reflects a longstanding approach in the study of abundance distributions: to focus on the shape of the distribution without regard to species’ identities (McGill 2007). Other assumptions regarding the statistical baseline may be equally valid and generate different statistical expectations, which may alter if, and in what ways, empirical distributions appear unusual. For example, incorporating differences in species order into the statistical baseline – which would imply that identifying *which* species contain the most or least individuals is important for evaluating theory – might reduce the representation of long-tailed, highly uneven SADs within the feasible set, and make the rare tail observed for real SADs appear more unlikely than it does here. Under our assumptions, the SADs (1,2,3,4) and (1, 1, 1, 8) each count as only one unique SAD. Taking species order into account would mean that (1,2,3,4) would count as 24 (4!) unique SADs, because there are 4! ways to assign the abundances to each species. However, an SAD containing species with equal abundances, such as (1, 1, 1, 8), would only count as 4 unique SADs. For SADs, equal abundances are likely most prevalent among rare species. If this is true, then this set of assumptions would generate feasible sets where rare-tailed SADs are relatively scarce, making observed SADs with rare tails seem even more extraordinary. Additional formulations for the statistical baseline exist, including those that approximate exponential, Poisson, or log-series distributions in the limit (Harte et al. 2008, Favretti 2018). Investigating and comparing the results that emerge from different baselines will be an important next step towards reinvigorating the use of the SAD as a diagnostic tool.

Our study demonstrates the utility, and the potential challenges, of applying tools from the study of complex systems and statistical mechanics to the study of ecological communities (Haegeman and Loreau 2008, Harte 2011, White et al. 2012, Harte and Newman 2014)**.** While concepts such as maximum entropy and the feasible set are promising new horizons for macroecology, the small size of some ecological communities may present difficulties that do not occur as often in the domains for which these tools were originally developed (Jaynes 1957, Haegeman and Loreau 2008). When the observed numbers of species and individuals are too small to generate highly resolved statistical baselines, these approaches will be less informative than we might hope – as appears to be the case for the smallest communities in our analysis. In larger communities, where mathematical constraints have stronger effects on the general form of the SAD, our results show that these constraints alone do not fully account for the extremely uneven SADs we often observe in nature – leaving an important role for ecological processes. This ability to detect and diagnose the specific ways in which empirical SADs deviate from randomness can generate new avenues for understanding how and when biological drivers affect the SAD. There are, of course, still many elements to be improved in our ability to distinguish biological signal from randomness, including assessing alternative statistical baselines and calibrating our expected power to detect deviations, especially for small communities. Indeed, more sensitive metrics could also enable identification of processes that operate through time (note that, in this analysis, we sampled only one time point for each community). Continuing to explore and account for the interplay between statistical constraint and biological process constitutes a promising and profound new approach to our understanding of this familiar, yet surprisingly mysterious, ecological pattern.

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