**Introduction**

The species abundance distribution (SAD) has been a major focus of both theoretical and empirical traditions in community ecology, largely because it is one of the very few ecological phenomena to conform to a consistent pattern approaching a law (Lawton, McGill, …). Regardless of the biological specifics of an assemblage, it will almost certainly be dominated by a few very abundant species, with relatively many rare species rounding out the abundance distribution (). Tempted by this remarkably general pattern, we have developed an array of theories to explain the underlying biological processes, as well as methods to divine the internal state of a system based on subtle variations in the SAD (). Ironically, this same generality of form has confounded our efforts to extract biological information from the SAD. There is precious little variation in form among empirical SADs, even in systems subject to experimental manipulations (Supp, ...). Most theories produce similar predictions and perform comparably well when compared to observed distributions, making it difficult to use the SAD to evaluate competing theories (McGill).

Recently, multiple lines of reasoning suggest an explanation and a remedy for this puzzle. The SAD may be subject to a statistical constraint that encourages it to follow a hollow curve, even in the absence of any biological mechanism, and warps our perception of the important aspects of the pattern. Frank () used a statistical mechanics framework to show that a log-series – one of the most common mathematical approximations for empirical SADs – emerges as a statistical by-product of [RMD forgets the precise process and needs to revisit Frank’s stuff]. Harte and associates () used the principle of entropy maximization to find the most-likely form for numerous ecological distributions, given sparse information about broad community properties and minimal assumptions regarding ecological mechanism. They also found that a log-series emerges as the most-likely form for the SAD (). This log-series is an excellent fit to empirical SADs (White et al 2012). Finally, Locey and White (2012) put forward an entirely non-biological derivation for the statistical constraint on the SAD. They leveraged the fact that there are a finite number of ways to divide *N* individuals among *S* species, and used combinatorics to characterize the range of *possible* forms for SADs, or feasible set, for realistic values of S and N. They showed that practically all feasible sets have strong central tendencies towards hollow curves ().

If, as seems apparent, SADs are statistically driven to approximate hollow curves before biology even enters the picture, it is no surprise that we have struggled to interpret the hollow curve in biological terms. But there is hope for a way forward: if we recognize and account for the statistical constraint, we may be able to isolate subtler but more biologically meaningful variation in SADs. Specifically, we can describe SADs not in terms of their absolute shape, but in terms of their shape *relative to what we would expect simply due to statistical constraint* (). If empirical SADs consistently deviate from their distribution of likely forms, these deviations may signal biological processes operating over and above the statistical constraint (). If they instead tend to track their statistically-most-likely forms, there may be little information about biological process to extract from the SAD alone – either because no processes consistently regulate the SAD, or because so many processes operate in various directions that the emergent distribution is indistinguishable from randomness ()

The first step is to characterize how empirical SADs generally compare to their statistical baselines and quantify any consistent deviations. Locey and White ()’s initial efforts along these lines showed that empirical SADs are often more skewed and less even than the central tendencies of their feasible sets. Here, we extend their approach to more specifically quantify the extent and ways in which empirical SADs deviate from (or conform to) their feasible sets. We test whether these deviations correspond to statistical properties, such as overall S and N and the range of variation present in the feasible set, that may further affect detectable patterns. We also test whether deviations vary between communities of different taxonomic [and other?] groups.

Although new conceptual frameworks for interpreting deviations will undoubtedly develop as this approach matures, we can already test one such framework. Borrowing reasoning from statistical physics, Newman and Harte () proposed that systems at “steady state” should more closely resemble random expectations than systems that have recently undergone manipulation or disturbance. At steady state, numerous countervailing processes are in equilibrium, and may cancel each other out at the scale of the SAD. Disturbances may temporarily overwhelm these processes and drive the system into a relatively nonrandom state. Although Supp et al () found that manipulation affected the shape of the SAD only when S and N also changed, their approach focused only on the *overall* shape of the SAD and not changes in the shape of the SAD relative to random expectation. We re-analyze the manipulated animal community data from Supp () to evaluate whether, in keeping with Newman and Harte’s proposition, manipulations induce increased deviations between observed SADs and their statistical constraints.