Biodiversity scales from plots to biomes with a universal species–area curve

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Abstract
Classic theory predicts species richness scales as the quarter-power of area, yet species–area relationships (SAR) vary widely depending on habitat, taxa, and scale range. Because power-law SAR are used to predict species loss under habitat loss, and to scale species richness from plots to biomes, insight into the wide variety of observed SAR and the conditions under which power-law behavior should be observed is needed. Here we derive from the maximum entropy principle, a new procedure for upscaling species richness data from small census plots to larger areas, and test empirically, using multiple data sets, the prediction that up to an overall scale displacement, nested SAR lie along a universal curve, with average abundance per species at each scale determining the local slope of the curve. Power-law behaviour only arises in the limit of increasing average abundance, and in that limit, the slope approaches zero, not ¼. An extrapolation of tree species richness in the Western Ghats to biome scale (60 000 km2) using only census data at plot scale (¼ ha) is presented to illustrate the potential for applications of our theory.

Keywords
Abundance, biodiversity, macroecology, power law, scaling, species–area relationship.


INTRODUCTION
The rate of increase in the number of species with area, or species–area relationship (SAR), is a central focus of ecology (Rosenzweig 1995) and has been a subject of contention despite 230 years of measurement and theoretical analysis (Lomolino 2001). Classic theory suggested that the number of species (S) would scale with area (A) as a power law (S = cAz) with an exponent z = ¼ (Preston 1962; May 1975). The power-law assumption with this value of z has provided a simple, widely used means of estimating both species richness in areas too large to census thoroughly, and future species losses under habitat loss and climate change (May et al. 1995; Brooks et al. 1999; Seabloom et al. 2002; Thomas et al. 2004; Costello & Ward 2006). Nevertheless, empirical evidence indicates a huge variety of SAR shapes, with the reasonableness of the power-law model and the value of the fitted z varying greatly depending on the scale range over which an SAR is analysed, the taxonomic group, and the habitat type (Preston 1962; May 1975; Plotkin et al. 2000a,b; He & Legendre 2002; Drakare et al. 2006). A systematic understanding of this diversity of observed SAR patterns is lacking.

Two broad categories of SAR can be distinguished. Island SAR are constructed from lists of species (within the taxonomic group of interest) found in spatially disjoint patches of habitat of differing area, such as actual islands or different-sized plots scattered throughout a larger mainland ecosystem. Nested SAR are constructed by averaging species richness across the subplots of specified area, using presence–absence data for each species at some finest scale within a larger plot. This work focuses on nested SAR.

The classical derivation of z ~ ¼ was obtained by sampling larger and larger numbers of individuals drawn from the individual pool, and thus at best applies to island, not nested, SAR. Indeed, the abundance distribution alone cannot determine the shape of a nested SAR; that shape will also depend on the degree of aggregation of the individuals within each of the species (He & Legendre 2002; Harte et al. 2008; see Materials and methods). Furthermore, the validity of the power-law model is questionable for many SAR. In particular, when nested SAR data spanning a scale range of several orders of magnitude in area are plotted on log–log axes, the data often clearly exhibit distinct curvature (Rosenzweig 1995;
Plotkin et al. 2000a,b; He & Legendre 2002; Drakare et al. 2006; Harte et al. 2008); such curvature arises even when the $R^2$-values of linear regressions on log–log scales exceed 0.98 as is typical in SAR analyses.

Here we modify and extend a previously developed application (Harte et al. 2008) of the maximum entropy principle from information theory (Jaynes 1982; MaxEnt) to accomplish three closely related goals. We show that: (i) a single quantity, the average species abundance at any specified ‘anchor’ spatial scale, uniquely and accurately predicts the shape of the SAR at larger or smaller scales and thus the theory permits extrapolation to biome scale of species richness from representative small plots nested within a biome; (ii) excluding the trivial case in which each individual is a unique species, exact power-law behaviour for the SAR emerges only in the limit of increasing average species abundance; (iii) in that power-law limit, $\alpha$ approaches 0, not $\frac{1}{4}$. We test these predictions against multiple empirical SAR for plant and bird assemblages. Finally, we provide an application of the upscaling inference procedure by successfully extrapolating tree species richness from 48 4-ha plots in the Western Ghats to the entire 60 000 km$^2$ preserve; although this is only a single test of the upscaling procedure over such a huge spatial scale range, it is presented to encourage other tests, which if successful would lead to eventual applications to biome-scale studies of biodiversity.

The theory developed here differs from that in Harte et al. (2008) in three essential ways. First, that previous work was a top–down theory that allowed prediction of the SAR at smaller scales from knowledge of species richness and total abundance at some largest scale. Thus, it permitted prediction of information that is frequently available (small-scale species richness) from information that is rarely available (biome-scale species richness). Here, we modify the methods developed in the previous paper in such a way so as to allow the maximum entropy principle to be used to upscale knowledge of species richness at a small scale, where it is often available. This difference is consequential because of widespread interest in having reliable predictions of species richness at large spatial scales. Second, we show that a result hinted at in Harte et al. (2008) concerning the limiting case of power-law behaviour for the SAR is stronger than anticipated there. In the previous work we speculated that the power-law limit, in which abundance approaches $\infty$, corresponded to a value of $\alpha \sim 0.16$. In fact, using the revised upscaling methods developed here, we show that the power-law limit corresponds to $\alpha \rightarrow 0$, not 0.16. Third, we use a mix of published and new extensive data sets to demonstrate the universality of the SAR behaviour predicted by our theory.

MATERIALS AND METHODS

Theoretical background

We write the SAR in the form:

$$S(A) = S_0 \sum_{n=1}^{N_0} \left[1 - P(0|n,A,A_0)\right] \phi(n|S_0, N_0).$$

Here $A_0$ is the area at some specified largest spatial scale under consideration, while $S_0$ and $N_0$ are the total number of species and individuals, respectively within $A_0$; $A$ is the area of an arbitrarily selected cell nested within $A_0$ and $S(A)$ is the expected number of species in $A$. Equation 1 states that the expected number of species in a cell of area $A$ located within a larger region of area $A_0$ is the total number of species, $S_0$, in $A_0$ times the sum of the probabilities of the occurrences in $A$ of each of those species.

The term $\phi(n|S_0, N_0)$ is the species abundance distribution, which is the probability that a species picked at random from the species pool in $A_0$ has $n$ individuals. To understand the term $1 - P(0|n,A,A_0)$ in eqn 1, consider the more general function $P(m|n,A,A_0)$, characterizing the individual species. It is a spatial abundance distribution, defined as the probability that a species with abundance $n$ in $A_0$ has $m$ individuals in a census patch of area $A$ nested within $A_0$. The expression $1 - P(0|n,A,A_0)$ is thus the probability that a species with $n$ individuals in $A_0$ is present in such a cell of area $A$. Explicit expressions for $\phi(n|S_0, N_0)$ and $P(m|n,A,A_0)$ were derived in Harte et al. (2008) using methods summarized in Appendix S1.

MaxEnt provides a method for inferring from incomplete knowledge the shape of a probability distribution. In particular, it was proven (Jaynes 1982) that maximizing the information entropy [in its simplest form, information entropy $= -\Sigma P \ln(P)$] of the distribution, $P$, under the available constraints yields the most likely, or least biased, functional form of the distribution. Here, most likely or least biased means the smoothest possible distribution that satisfies the constraints. Maximization under constraint is carried out using the method of Lagrange multipliers (Stewart 2007). In Appendix S1, we provide a very basic explanation of the MaxEnt method.

In applications of MaxEnt, a critical issue is identifying the constraints. In Harte et al. (2008), we assumed an ecosystem characterized by four state variables, in loose analogy with the state variables such as pressure, volume, temperature, and number of moles in thermodynamics. The selected state variables are: ecosystem area ($A_0$), total species richness ($S_0$) within $A_0$, total number of individuals ($N_0$) in the $S_0$ species, and total metabolic rate ($E_0$) of the $N_0$ individuals. Along with a normalization condition, the ratios...
of these state variables provide the needed constraints on a joint probability distribution, \( R(n, \varepsilon) \), over the abundances of the species and the rates of metabolic energy consumption by the individuals in the species (for details, see Appendix S1). Thus, the mean of the species abundance distribution is given by \( N_0/\lambda_0 \) and the mean of the distribution of metabolic rates over the species is \( E_0/\lambda_0 \).

We denote the spatial scale at which state variables are specified as the 'anchor scale'.

By maximizing the information entropy of that joint probability distribution under the constraints imposed from knowledge of the ratios of the state variables, we showed in Harte et al. (2008) that if \( \lambda_0 \) is sufficiently large so that \( e^{-\lambda_0} < 1 \), then the species abundance distribution, \( \phi \), is the Fisher log series,

\[
\phi(n|\lambda_0, N_0) = e_{\phi,0} \cdot e^{-\lambda_0 n}/n, \tag{2}
\]

where \( e_{\phi,0} \), a normalization constant, and \( \lambda_0 \), a Lagrange multiplier, are given by satisfying the constraints that mean of \( n \) over the distribution is equal to \( N_0/\lambda_0 \), and that \( \phi \) is normalized to 1.

These constraints lead to the following determining equations for \( \lambda_0 \) and \( e_{\phi,0} \), and thus the species abundance distribution, at the arbitrary spatial scale \( A_0 \):

\[
\frac{S_0}{N_0} \sum_{n=1}^{N_0} e_{\phi,0} e^{-\lambda_0 n} = \sum_{n=1}^{N_0} e^{-\lambda_0 n}/n \tag{3}
\]

and

\[
e_{\phi,0} = \frac{N_0}{S_0} \left(1 - e^{-\lambda_0} \right) \left( e^{-\lambda_0} - e^{-\lambda_0 N(\lambda_0+1)} \right)^{-1}. \tag{4}
\]

As shown in Harte et al. (2008), while the constraint of total metabolic energy, \( E_0 \) is needed to derive eqn 2, the actual form of the species abundance distribution depends only on \( \lambda_0 \) and \( N_0 \), not on the numerical value of \( E_0 \).

The spatial abundance distribution for each species with known abundance, \( n_i \), in \( A_0 \), can also be derived from MaxEnt. In Harte et al. (2008), we showed that

\[
P(m|n, A, A_0) = e_{\phi,0} \exp(-\lambda_0 pm), \tag{5}
\]

where \( e_{\phi,0} \) and another Lagrange multiplier, \( \lambda_0 \), both depend on \( n_i \), \( A \), and \( A_0 \) and are calculated by satisfying the constraints that \( P \), summed from \( m = 0 \) to \( n_i \), is normalized to 1 and that the mean of \( m \) over the distribution is \( n_i A/A_0 \).

We note that the spatial pattern in the distribution of individuals within species predicted by eqn 5 is not the same as the binomial distribution predicted by the random placement model (Coleman 1981). Relative to the random placement model, eqn 5 predicts aggregation of individuals. Extensive tests of eqn 5 for plant data are presented in Harte et al. (2008).

**Extending the theory to permit upscaling**

At this stage, we depart from Harte et al. (2008). There we used a downsampling procedure for calculating the consequences of eqn 1 for areas smaller than the anchor scale \( A_0 \).

To do that, we fixed the abundance distribution, \( \phi_i \), at the anchor scale \( A_0 \), where the values of \( S_0 \) and \( N_0 \) are presumed to be known, and then to implement eqn 1 we calculated \( 1 - P(0|n, A, A_0) \) from eqn 5 at each scale smaller than \( A_0 \). Here, however, we wish to use eqn 1 to upscale, so that we can predict species richness at scales larger than the anchor scale. The derivations in Harte et al. (2008) can only be used to downscale from the anchor scale, and \( S \) at each scale is presumed to depend solely upon \( S \) and \( N \) at the anchor scale. Now we use eqn 1 in an iterative procedure that allows us to downscale or upscale because it is re-calculated at each scale with new constraint information, the values of \( S \) and \( N \) at the halved or doubled spatial scales.

To illustrate this, consider the simpler case of downsampling first. Now, we require only the special case of eqn 5 that is applicable to a scale halving:

\[
P\left(0|n, \frac{A_0}{2}, A_0\right) = \frac{1}{n+1}. \tag{6}
\]

The apparent discrepancy between eqns 5 and 6 is illusory because for \( A = A_0/2 \), the Lagrange multiplier \( \lambda_0 \) in eqn 5 is identically zero.

Using a notation in which \( \lambda_{0,A} \) is the Lagrange multiplier appearing in the log-series distribution (eqn 2) at anchor scale \( A \), it is straightforward to show that if eqs 2, 4, and 6 are substituted into eqn 1, and the summation in eqn 1 is carried out, then

\[
S(A/2) = S(A)e^{\lambda_{0,A}} - N(A) \frac{1 - e^{-\lambda_{0,A}}}{e^{-\lambda_{0,A}} - e^{-\lambda_{0,A}(N(A)+1)}} \left(1 - \frac{1 - e^{-\lambda_{0,A}N(A)}}{N(A)+1}\right). \tag{7}
\]

If the value of \( \lambda_{0,A} \) determined by eqn 3 is substituted into eqn 7, then \( S(A/2) \) is determined. Because \( N \) scales linearly with area in a nested design, \( N(A/2) = N(A)/2 \), and now with knowledge of \( S(A/2) \) and \( N(A/2) \), this iterative process can be repeated to determine \( \lambda_{0,A/2} \) and \( S(A/4) \), and so forth. In effect, the approach in Harte et al. (2008), in which
the SAD only at the anchor scale is used, discards information whereas this modified approach updates the state variables at each successive scale interval.

More importantly, this modified approach can also be used to upscale species richness data from small plots to allow prediction of biome-scale species richness. In particular, suppose we want to know how many species are in a particular, suppose we want to know how many species are in a sampling unit that has area twice that of the anchor scale $A$ at which $S$ and $N$ are known. We can iterate eqn 7 now to obtain:

$$S(A) = S(2A)e^{\delta_{2A}} - N(2A)$$

$$= \frac{1 - e^{-2\delta_{2A}}}{e^{-\delta_{2A}} - e^{-\delta_{2A}(N(2A)+1)}} \left(1 - e^{-2\delta_{2A}(N(2A)+1)} \right).$$

Here there are two unknowns: $S(2A)$ and $\lambda_{\phi,2A}$. $N(2A)$ is of course equal to $2N(A)$, but a second equation relating $S(2A)$ and $\lambda_{\phi,2A}$ is still needed. Equation 3 provides that second relationship if it is rewritten in the equivalent form:

$$S(A) = \frac{N(2A)}{2A} \sum_{k=1}^{N(2A)} e^{-\lambda_{\phi,2A}} a = \frac{N(2A)}{2A} \sum_{k=1}^{N(2A)} e^{-\lambda_{\phi,2A} a} \frac{n}{N(2A)}. \tag{9}$$

Equations 8 and 9 can be solved numerically for $S(2A)$ and the process can then be iterated up to an arbitrarily large spatial scale that is a multiple of two times the anchor scale area.

**SAR metrics for data comparison**

To characterize the shape of the predicted and observed SAR, we use two measures that can be calculated at every scale from both theory and SAR data: the local slope, $\varepsilon(A) = d \log(S(A))/d \log(A)$, and the local curvature, $\eta(A)$, of $\log(S)$ vs. $\log(A)$. We define curvature in the standard way as:

$$\eta(A) = \frac{(d^2 \log(S(A))/d \log(A)^2)}{(1 + \varepsilon(A))^3/2}. \tag{10}$$

Because our data and our theoretical predictions are for discrete values of area, we calculate $\varepsilon$ and $\eta$ using differences rather than differentials. Hence, $\varepsilon(A) = 0.5[\log(S(A))/S(2A)] + \log(S(2A))/\log(2)$ and $\eta(A) = [\log(S(A))/S(2A)] + \log(S(2A)) - 2\log(S(2A))/\log(2) (1 + \varepsilon^2(A))^{3/2}$.

**Data**

To test our predictions for the shape of the SAR, we examined 41 empirical species–area curves and 194 values of each of $\varepsilon$ and $\eta$ at different $N/S$ values along these curves. These data are from plant censuses in both wet and dry tropical forests, serpentine meadows, temperate montane forest understory, and avian communities in South Africa (details in caption of Fig. 1). They are data sets in which not only are species richness values measured over some range of spatial scales, but also a total abundance estimate is available at the anchor scale. This is essential because knowledge of the state variables, $S$ and $N$, at that scale is needed to predict the SAR at finer scales. Our demonstration of the potential applicability of our theory for upscaling from small plots to biome-scale species richness values uses tree census data from the Western Ghats Preserve in India (details in caption of Fig. 2).

Total abundance census of plants poses certain unique problems. For grasslands, the main problem, resolving what an individual is, is generally resolved by the convention of counting ramets for clonal species. For the tree censuses, a convention is generally adopted to only count trees with a diameter-at-breast-height above some minimal value (e.g., 10 mm) and as long as that convention is consistently adhered to within a given data set, the MaxEnt procedure can be applied.

**Results**

The universal SAR and the power-law limit for the widely applicable case in which $e^{-\varepsilon} << 1$ and $N_i > \delta_i$, it follows from either eqn 7 or 8 that

$$\varepsilon(A) \approx \frac{1}{\ln(2) \ln(\lambda_{\phi,1})}. \tag{11}$$

The curvature at scale $A$, $\eta(A)$, can also be expressed solely in terms of $\lambda_{\phi,1}$. But eqn 9 implies that under those same conditions, the Lagrange multiplier, $\lambda_{\phi,1}$ is a function solely of $N(A)/S(A)$, and hence the shape of the SAR, $S(A)$, is a universal function of the ratio $N/S$, provided that at each scale $e^{-\varepsilon} << 1$. In the limit $N(A)/S(A) \rightarrow \infty$, it follows from eqn 3 or 9 that $\lambda_{\phi,1} \rightarrow 0$. From eqn 11, it follows that in the $N/S \rightarrow \infty$ limit, $\varepsilon \rightarrow 0$. But for all practical purposes, this is also the limit of increasing area because $N$ increases linearly with area in a completely nested census design, whereas $S$ increases more slowly. Thus, the power-law model is predicted to be increasingly valid in the limit in which area increases and $\varepsilon$ decreases towards 0.

Because our theory predicts that the value of $N/S$ at some specified scale determines the shape of the SAR at larger or smaller scales, all SAR have the same shape, differing only in the scale at which they share a common $N/S$ value and the actual number of species at that value. Thus, we predict that all SAR are scale displacements of a universal SAR shape.
Numerical confirmation of universality

To demonstrate this numerically, we use eqns 8 and 9 to upscale \( S \) starting from the values of \( S_0 \) and \( N_0 \) at some ‘anchor’ scale. The solid and dashed lines in Fig. 1a show the predicted \( \zeta \) values for \( N_0/S_0 = 2 \) and 10, respectively. That the curves lie on top of each other is a numerical confirmation that the slope of the SAR is a function of \( N_0/S_0 \) alone. As area increases, \( N \) increases proportionally to area and thus faster than \( S \), and so increasing \( N/S \) corresponds to increasing area. Because the predicted \( \zeta \) decreases with increasing \( N/S \), this implies that SAR should exhibit negative curvature. This is confirmed in Fig. 1b, where the predicted curvatures for the same two anchor values of \( N/S \) as in Fig. 1a (\( N/S = 2 \) and 10) again coincide, indicating dependence solely on that ratio.

From Fig. 1b, we see that theory predicts that the power-law limit for the SAR, which is the limit in which the curvature of a log(\( S \)) vs. log(\( A \)) plot approaches 0, is the limit of increasing \( N/S \). In that limit, Fig. 1a shows that the predicted \( \zeta \) does indeed decrease towards zero.

Tests of theory

The central tendency of the observed \( \zeta \) values plotted against \( N/S \) is in fine agreement with the theoretical prediction (Fig. 1a). Although there is considerable scatter in the observed values of \( \eta \) plotted against \( N/S \) (Fig. 1b), the averages of binned curvature values are well predicted by theory (Fig. 1c). We would expect the relatively small observed variability in \( \zeta \)-values around the central tendency shown in Fig. 1a to result in the large relative variability in observed \( \eta \)-values because curvatures are small differences of relatively large quantities; plotted on the same vertical scale from 0 to 1, the curvature values appear to be tightly clustered as the slopes. Thus, we note that while the predicted SAR curvatures for the South African bird data appear to deviate considerably from the observed values, the slopes themselves for the bird data appear to be in as good agreement as are the slopes for the plant data sets.

An application of upscaling

The predicted shape of the universal SAR is shown in Fig. 2, where the calculated values of species richness (\( X \) in the figure) are obtained by solving eqns 8 and 9 (upsampling) or the equivalent eqns 3 and 7 (downscaling) for the particular case of an anchor value of \( S_0 = 32.5 \) species and \( N_0 = 109 \) individuals, at an anchor scale of ¼ ha. These particular anchor values were chosen because they correspond to census data on tree species richness from the 60 000 km² Western Ghats Preserve in southern India (Krishnamani et al. 2004).
Thus our extrapolation from $0.25$ ha to $60,000$ km$^2$, a scale
for every tree species with
$30$ mm dbh were obtained and
and thus on the constraints.
But in the extreme limit of heterogeneity, in which a
the upscaled total tree species richness.

DISCUSSION

The predicted slope, $z$, of the SAR decreases with increasing
model, the resulting $R^2$ is $0.9956$ and the slope is $0.10.$ But
distinct curvature is apparent in the predicted log–log SAR
over just those 11 data points; with a relatively small number
of data points, even an $R^2 > 0.99$ can be associated with
distinct and systematic curvature.

Many authors (Rosenzweig 1995; Plotkin et al. 2000b;
Fridley et al. 2006; He et al. 2006) have noted that across larger
spatial scale ranges (which tend to correspond to larger
average abundance per species because $N$ increases roughly in
proportion to area and $S$ increases more slowly) fitted $z$ values
tended to drop well below $1/4$. Notably, low slopes ($z < 0.1$)
of the SAR have been reported for microbes (Green et al. 2004;
Horner-Devine et al. 2004, Green & Bohannan 2007); such
low slopes are in accord with our theory because average
abundance per taxonomic unit is likely to be extremely large
for micro-organisms. From Fig. 1a, we predict that the
average abundance per taxon satisfies $\ln(N/S) > 10$ at the
spatial scales at which these data are obtained.

Our MaxEnt-based state-variable theory of macroecology
predicts a universal shape for the SAR, exactly as shown in
Fig. 2. The variable governing the local slope of the SAR at
any scale $A$ is the average abundance per species at that
corresponds to a horizontal displacement of the SAR, and
they can differ in the actual number of species at that value
of $N/S$, which corresponds to a vertical displacement of the
SAR. The data we have examined so far are in reasonable
agreement with this prediction.

Applying our theory to a landscape with two distinct biota
occupying non-overlapping regions will at the very least
require imposition of an additional constraint. But all
habitats are heterogeneous to at least some degree, and so
the question arises as to what influence this has on the
validity of our theory. Because we are looking at completely
nested SAR, habitat heterogeneity is effectively averaged
over and so we speculate that to the extent the theory
reliably predicts SAR, the influence of heterogeneity on the
theory’s predictions is captured by the influence
of heterogeneity on the measured values of the state variables
and thus on the constraints.

But in the extreme limit of heterogeneity, in which a
landscape is occupied by two distinct biota in non-
overlapping regions, the prediction that the slope of the
predicted SAR is a monotonically decreasing function of
area cannot be valid. In such a landscape, a triphasic SAR is
expected. Indeed, it is sometimes observed that at relatively
large, often continental, scales the slope of the SAR steepens
(Rosenzweig 1995; Fridley et al. 2006; Palmer 2007). Is a

We now use these data to demonstrate the potential
usefulness of our upscaling procedure. First, we note that
downscaling from the anchor scale of $1/4$ ha predicts
accurately the species richness data at these smaller scales
(Fig. 2). Then, using eqns 8 and 9, and data only from the
anchor scale of $1/4$ ha, MaxEnt also predicts a total of 1070
tree species in the entire preserve (Fig. 2). Approximately
900 species are currently identified, with several additional
ones being reported each year (Krishnamani et al. 2004), and
thus our extrapolation from $1/4$ ha to $60,000$ km$^2$, a scale
interval greater than $2^{24}$, yields a reasonable prediction for
the upscaled total tree species richness.
MaxEnt approach capable of describing such behaviour? Three possibilities can be identified. First, it is conceivable that if the existence of two distinct biota is incorporated as a new constraint within the MaxEnt framework, the theory might make reasonable predictions. Second, it is possible that even if knowledge of the disjoint species lists is incorporated in the form of an additional constraint, an observed triphasic SAR will still not be predicted by the theory. Finally, at least in some cases it may be that empirical support for a triphasic SAR, at large spatial scales, is a consequence of not using a complete nested design in the construction of the SAR. Further analysis of each of these possibilities is warranted, and in particular we suggest that investigating procedures for incorporating information about non-overlapping species lists between distinct habitats as a constraint is likely to yield interesting insights.

We have not attempted to explain the magnitude of the scatter in the observed $\xi$-values in Fig. 1a around their central tendency. It is possible that considerable information about processes not captured in our purely information-theoretic approach can be mined from the deviations from theory, particularly if they are observed to differ from taxa to taxa, from habitat to habitat, and from scale to scale.

Our theory provides a way of estimating species richness at biome scale from data on species richness and total abundance (summed over species) at a much smaller spatial scale. If further tests of our upscaling procedure continue to validate the technique, opportunity would exist to answer long-standing questions concerning, e.g., Amazonian insect species richness from canopy fumigation studies and large-scale microbial diversity from soil cores or water samples.

Traditional methods of upscaling species richness, using nonparametric estimators (Chao & Lee 1992) or extrapolating collectors’ curves, are not capable of extrapolating reliably over scale intervals as huge as in the Western Ghats (Krishnamani et al. 2004). Indeed only one other previously published method, based on a hypothesized relationship between the dependence of species richness on area and the dependence of a community similarity index on distance between small plots (Krishnamani et al. 2004), has yielded a value in the vicinity of $10^3$ for the number of tree species in the Western Ghats. Because the MaxEnt application that we use here does not predict the species similarity index, we are unable to establish whether or not the agreement between these two methods is accidental.

We note that our results, and specifically the form of eqn 6, reflect the implicit assumption in our application of MaxEnt that the individuals within a species can be considered indistinguishable; in a previous work (Harte et al. 2005, 2008), it was shown that this assumption yields realistically aggregated species-level spatial abundance distributions, whereas the assumption of distinguishability leads to an unrealistic Poisson distribution for the spatial distribution of individuals within species. The implications for spatial structure of the distinction between the assumptions of distinguishability and indistinguishability are discussed in Appendix S1.

The application (Harte et al. 2008) of MaxEnt, on which we based our findings here, is by no means the only possible approach of using MaxEnt to understand scaling patterns in ecology. More generally, the best choice of state variables, the related choices of what constraints to assume, and whether to assume distinguishability or indistinguishability (see Appendix S1) of the individuals in the system can only be determined empirically. We have demonstrated here and in Harte et al. (2008) that with the state variables and constraints described before, and with our choice of indistinguishability, a realistic set of predictions are obtained; we await seeing if other choices and applications of this powerful approach to inference under limited information in the form of constraints can provide comparably realistic predictions.

This raises the question of the generality of our findings about the dependence of the slope parameter on $N/S$ and thus the absence of power-law behaviour for the SAR. Is non-power-law behaviour an inevitable consequence of applying MaxEnt to macroecology? Here it is essential to understand that MaxEnt is simply an algorithm for finding the least-biased shape of a probability distribution subject to known constraints on that distribution. The ecology is all in the constraints, which in our theory arise from ratios of the defining state variables, $A$, $S$, $N_i$, and $E$. Applying MaxEnt to our state variable theory, with the constraints it imposes, does indeed preclude power-law behaviour for the SAR. That is the result illustrated in Fig. 1a or Fig. 2. But applied to different constraints on the two probability distributions, $P$ and $\phi$ in eqn 1, one could obtain quite different results from the MaxEnt algorithm. For example, if one’s prior knowledge of the species abundance distribution happened to be the values of the first and second moments of $\log(n)$, one would obtain a log-normal distribution for $\phi$ from MaxEnt, and for particular values of those moments, one would obtain the canonical log-normal. In addition, using certain prior information about the spatial distribution of individuals within species, one could obtain from MaxEnt a binomial distribution for $P(m)$, as in classical statistical mechanics. In combination, by the results of Preston and May, referred to in the Introduction, a power-law SAR would result. In that case, the predicted slope values in Fig. 1a would follow a horizontal line with $\xi \sim 0.25$, rather than falling as a function of $N/S$. Thus, MaxEnt by itself does not constrain the behaviour of the SAR. Again, the question for ecology is: What set of state variables and constraints derived from them, in combination with MaxEnt, leads to empirically defensible predictions?
Another question arises as to what constitutes the ‘correct’ unit of analysis in a MaxEnt application. For example, we could have carried out our analyses for genera– or family–area relationships instead of SAR. We also could have confined our analysis to just individuals and species satisfying some perhaps arbitrary criteria (e.g. only plants with yellow flowers). Nothing in the logic of MaxEnt would forbid such choices; if the constraints are selected, the procedure should generate testable predictions. Applications of MaxEnt to such taxonomic categories remain to be tested.

We conclude that MaxEnt illuminates simplicity behind the apparent wide variety of SAR observed in nature at subbiome scales. It informs us that the widely used assumption that SAR generally obeys power-law behaviour with c \( \frac{1}{4} \) power exponents is not likely to be useful in ecology, predicting instead that over limited scale ranges nested SAR approximate power-law behaviour in the limits of \( \xi \rightarrow 0 \). At a given scale, a single parameter, the ratio \( N/S \), governs both the slope and curvature of nested SAR. The empirical success of this theory suggests that the hitherto less-than-successful search for a process-based understanding of the SAR might move productively be directed towards the arguably simpler task of finding a mechanistic explanation for observed values of average abundance per species at a specified scale.

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REFERENCES


SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

Appendix S1 The MaxEnt method and its application to ecology.

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