

1 **A new method to analyze species abundances in space using gener-**
2 **alized dimensions**

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Abstract

- Species-area relationships (SAR) and species abundance distributions (SAD) are among the most studied patterns in ecology, due to their application in both theoretical and conservation issues. One problem with these general patterns is that different theories can generate the same predictions, and for this reason they can not be used to detect different mechanisms.
- A solution for this is to search for more sensitive patterns. One possibility is to extend the SAR to the whole species abundance distribution. A generalized dimension (D_q) approach has been proposed to study the scaling of SAD, but there has been no evaluation of the ability of this pattern to detect different mechanisms.
- An equivalent way to express SAD is the rank abundance distribution (RAD). Here I introduce a new way to study scaling of SAD using a spatial version of RAD: the species-rank surface (SRS), which can be analyzed using D_q . Thus there is an old D_q based on SAR (D_q^{SAD}), and a new one based on SRS (D_q^{SRS}). I perform spatial simulations to relate both D_q with SAD, spatial patterns and number of species. Finally I compare the power of both D_q , SAD, SAR exponent, and the fractal information dimension to detect different community patterns using a continuum of hierarchical and neutral spatially explicit models.
- The SAD, D_q^{SAD} and D_q^{SRS} all had good performance in detecting models with contrasting mechanisms. D_q^{SRS} had a better fit to data and a strong ability to compare between hierarchical communities where the other methods failed. The SAR exponent and information dimension had low power and should not be used.
- SRS and D_q^{SRS} could be an interesting addition to study community or macroecological patterns.

Keywords: multifractals, species-rank surface, species-area relationship, multi-species spatial pattern.

Introduction

The species-area relationship (SAR) is considered one of oldest and best-documented patterns, and one of a few fundamental generalizations, in ecology (Crawley & Harral 2001; Šizling *et al.* 2011). The SAR is often characterized through a triphasic curve, with a range of intermediate scales corresponding to power law relationship between the number of species and the area (Preston 1960; Hubbell 2001). Although other quantitative forms could also be appropriate (@Tjorve2003; White *et al.* 2010) this power-law is more widely accepted (Rosindell & Cornell 2007). This relationship implies a self-similar or fractal structure of species distributions for a community across spatial scales (Šizling & Storch 2004).

SARs only give information about the changes of richness with scale, but can be extended by incorporating the species abundances distribution (SAD), using Hill's generalized diversity indexes (Hill 1973). These indexes follow from the definition of generalized entropies used in statistical physics, called Renyi's entropies (Renyi 1970). The scaling of Renyi's entropies is called generalized dimensions, and is used in physics to characterize multifractals (Beck 1990). Multifractals and fractals are related techniques first used in physics to characterize scaling behavior of complex structures (Stanley & Meakin 1988); the difference is that fractals look at the geometry of presence/absence patterns, while multifractals describe the arrangement of quantities such as population density or biomass (Saravia *et al.* 2012a). Multifractal analysis has been applied to ecology in different areas: metapopulation models (Gamarra 2005), analysis of natural landscapes (Kirkpatrick & Weishampel 2005), search patterns in copepods (Seuront & Stanley 2014), and biomass dynamics in microalgae (Seuront & Spilmont 2002; Saravia *et al.* 2012a; Dal Bello *et al.* 2014).

The application of generalized dimensions to extend SAR was first suggested by Ricotta (2000), and the methodology was later developed and applied to Barro Colorado Island forest plots by Borda-de-Água (2002), who estimated generalized dimensions of SAD. Since then, several field studies have characterized species abundance scaling—also called the species diversity-area relationship (DAR)—using generalized dimensions and other multifractal techniques (Yakimov *et al.* 2008, ,). In addition, generalized dimensions have been applied to a spatially explicit neutral model (Yakimov *et al.* 2013) and used in open source software for ecological multifractal analysis (Saravia 2014).

The species abundance distribution (SAD) is another fundamental pattern in ecological communities, and play a major role in ecology and conservation (McGill *et al.* 2007). SADs have been used to compare different communities and to compare models and data, but different mechanisms can produce nearly identical SADs (Chave *et al.* 2002; Rosindell & Cornell 2013). SADs are often presented using rank-abundance diagrams (RADs) in which the log-abundance is plotted against the rank of the species (McGill *et al.* 2007). RADs

are equivalent to cumulative distributions and thus are a robust way to visualize the SAD without losing information (Newman 2005).

Here I propose a new way to analyze the relation of SAD with spatial scale, by attaching the rank of each species to its spatial distribution; in this way the multivariate spatial distribution of species is summarized into a univariate two-dimensional distribution. I call this spatial distribution the species-rank surface (SRS), and it can be analyzed and compared using generalized dimensions. This paper uses simulations of spatial patterns to compare the behavior of generalized dimensions calculated from SRS and SAD. First I use a regular and randomized spatial pattern combined with a uniform and logseries SAD, artificial patterns used to observe the contrast. Then I use a continuum of neutral and hierarchical models to test if generalized dimensions can detect different communities, estimating statistical power and type I error rate. I also compare the performance of generalized dimensions with single dimensional indicators: the SAR exponent and the information dimension.

Methods

Multifractal analysis

Extensive reviews of generalized dimensions and multifractal methods applied to ecology are available (Seuront 2009) and some good introductions have also been published (Scheuring 1994; Borda-de-Água *et al.* 2007). Thus I will only give a brief description. The generalized dimensions technique analyzes the scaling properties of quantities distributed in a space that we assume to be two dimensional (i.e., a plane). This distribution should be self-similar across some range of scales. This is called being multifractal, which can be mathematically represented in different ways (Harte 2001), of which the closest to ecology are the generalized dimensions D_q (Grassberger 1983), also called Renyi dimensions (Renyi 1970). D_q has been used to characterize the probabilistic structure of attractors derived from dynamical systems (Hentschel & Procaccia 1983).

To estimate generalized dimensions I used the method of moments based on box-counting (Evertsz & Mandelbrot 1992). The spatial distribution of quantities μ is covered with a grid, dividing it into $N(\epsilon)$ boxes of side ϵ , allowing us to calculate the value $\mu_i(\epsilon)$ in each. Then the so-called partition function is computed as:

$$(1) \quad Z_q(\epsilon) = \sum_i^{N(\epsilon)} (\mu_i(\epsilon))^q$$

Where q can be any real number and is called *moment order*. The operation is performed for different values of ϵ and q , within a predetermined range. The generalized dimension is then calculated as:

$$(2) D_q = \frac{1}{q-1} \lim_{\epsilon \rightarrow 0} \frac{\log(Z_q(\epsilon))}{\log \epsilon}$$

When $q = 1$, the denominator of the first term in D_q is undefined, so it must be replaced by the following expression:

$$(3) D_q = \lim_{\epsilon \rightarrow 0} \frac{\sum_{i=1}^{N(\epsilon)} \mu_i(\epsilon) \log(\mu_i(\epsilon))}{\log \epsilon}$$

In practical cases as the limit can not be assessed, and the dimensions are estimated as the slope of the $\log(Z_q)$ versus $\log(\epsilon)$ in equation (1) replacing by the numerator in equation (3). This is done for different values of q , provided that it is a real number, which yields a graphs of D_q in terms of q . This is called the spectrum of generalized dimensions.

To be an approximate multifractal, the relationship $\log(Z_q)$ versus $\log(\epsilon)$ should be well described by a linear relationship, but a linear relationship with superimposed oscillations is also acceptable (Borda-de-Água *et al.* 2007). A range of q and ϵ values must be established, and then D_q is estimated using linear regression. Note that D_q is defined as the limit $\epsilon \rightarrow 0$ (equations 2 and 3), and thus to use the method it is sufficient that a scale exists below which a linear relationship applies (Hentschel & Procaccia 1983).

To analyze species-abundance-area relationships with multifractals as Borda-de-Água (2002), the boxes are replaced by species. Thus at each spatial scale ϵ each species holds the quantity of interest: its own abundance. Then the partition function is defined as a sum over the species present $S(A)$ in an area A and the side of the box ϵ is replaced by the area:

$$(4) Z_q(A) = \sum_i^{S(A)} (\mu_i(A))^q$$

where $\mu_i(A)$ is the abundance of species i in an area A . D_q is defined as:

$$(5) D_q = \frac{1}{1-q} \lim_{A \rightarrow \infty} \frac{\log(Z_q(A))}{\log A}$$

When calculating D_q based on species abundances distribution, I refer to it as D_q^{SAD} , and when I calculate them from the species rank surface, D_q^{RRS} ; if I mention D_q without superscript I refer to both. D_q^{SAD}

represents the scaling of the Hill's generalized diversity index (Hill 1973): when the moment order is $q = 0$, then D_q^{SAD} becomes the exponent of the SAR power-law scaling; when $q = 1$, D_q^{SAD} represent the scaling of Shannon diversity index; and when $q = 2$, D_q^{SAD} becomes the scaling of Simpson's index. This is why D_q can characterize diversity-area relationships.

Theoretically D_q must be a non-increasing function of q (Hentschel & Procaccia 1983), which means that if $q_1 \geq q_2$ then $D_{q_1} \leq D_{q_2}$. Some studies have shown small violations of this property for D_q^{SAD} (Borda-de-Água *et al.* 2002; Zhang *et al.* 2006). These violations are related to the way that D_q^{SAD} is defined: the summation of equation 4 is over species, while the summation of the original definition, equation 1, is over boxes, and this changes the way in which the mathematical limits are taken and also the computation method of D_q^{SAD} . A partial solution has been proposed (Yakimov *et al.* 2014), but the anomalies observed may be related to the mathematical assumptions needed for D_q to be non-increasing, in which case a new mathematical proof should be developed for D_q^{SAD} . Thus as long as the linear relationship is reasonable I take D_q^{SAD} as a useful technique of analysis.

In a previous work I proposed a new way to analyze species-abundance-area using multifractals, one that fits more closely to the original definitions of equations 1 - 3: the species-rank surface (Saravia 2014) or SRS. To construct the SRS the spatial distribution of species has to be transformed by assigning to each species position its rank. First I use the species abundances, at the whole plot level, to calculate the species' rank ordering from highest to lowest, assigning a number starting with one. Then the rank is assigned to the spatial position of the individuals of each species, forming a surface. This (mathematical) landscape has valleys formed by the most abundant species and peaks determined by the rarest. Finally the standard multifractal analysis is applied. If sampling was performed using quadrats, without taking the spatial position of individuals, the sum of the ranks of the species in the smallest quadrats can be used to form the SRS.

I use the coefficient of determination (R^2) as a descriptive measure of goodness of fit (Borda-de-Água *et al.* 2002). The C++ source code to perform multifractal analysis is available at <https://github.com/lisaravia/mfsba>.

Generalized dimension relationship with spatial patterns and SADs

I simulated species' spatial patterns with different SADs to demonstrate how D_q is related to them. First I used a uniform SAD, in which all species have approximately the same densities. To generate it I take the number of individuals of each species from a Poisson distribution with the same mean. I distributed them in bands over a spatial grid so they form a regular spatial pattern, in which each grid position is occupied by

exactly one individual. I chose the number of species to exactly divide the side of the grid so all species are strips with approximately the same width (Figure 1). I used square grids with sides of 256 and 512 sites which contain 65536 and 262144 individuals respectively, and 8, 64 and 256 species, and then calculated D_q for the regular pattern, randomizing the positions of species to compare D_q obtained with these two extreme cases. The second SAD I used is a Logseries (Fisher *et al.* 1943) with the same number of species and the same sides as previously. I used the R package `untb` (Hankin 2007) to calculate the density for each species; this basically uses a Poisson distribution with the expected Logseries abundances as means. I then built the regular pattern with strips of species, but as species have different abundances the widths for each species are different (Figure 1). I then estimated D_q for the regular and randomized patterns, simulated 10 spatial patterns for each case, and calculated the mean and standard deviation of D_q .

Spatially explicit model

To simulate more realistic patterns of species-abundance-area relationships I used a stochastic spatially explicit model. I developed a stochastic cellular automata (Molofsky & Bever 2004) model that can switch between neutral or hierarchical competition, representing a continuum between niche and neutral communities (Gravel *et al.* 2006). Under neutral competition individuals do not interact, and all have the same mortality, colonization rates, and dispersal distances; in spite of these gross simplifications neutral models are capable of predicting several real community patterns (Rosindell *et al.* 2011). At the other end of the continuum are niche communities represented by hierarchical competition models [Tilman 1994]. In this case species have differences that imply a competitive hierarchy, in which some species are always better than others, producing competitive exclusion (Chave *et al.* 2002). I added a probability of replacement ρ to the neutral model: when $\rho = 1$ more competitive species always replace less competitive and the model behaves as a pure hierarchical one, and when $\rho = 0$, there is no replacement of species and the model is completely neutral. A more thorough description of the model is given in appendix A, and its C++ source code is available at <https://github.com/lasaravia/neutral> and figshare <http://dx.doi.org/10.6084/m9.figshare.969692>.

Following a classical neutral scheme the model has a metacommunity: a regional collection of communities, from which migration occurs at a rate m . Species can also disperse locally, and I assume an exponential dispersal kernel with average dispersal distance d . Other model parameters are the mortality rate μ , the number of species in the metacommunity and also the size of the community, represented as the *side* of the grid used in the simulations. I use a logseries SAD for the metacommunity, defined by the maximum number of individuals (*side* \times *side*) and the number of species (Fisher *et al.* 1943).

The values of the parameters were in the range estimated for BCI from the existing literature (Condit *et al.*

2002; Etienne 2007; Anand & Langille 2010). I performed 50 simulations for each combination of parameters given in Table 1. To compute the statistical power I made comparisons of communities with different levels of ρ , representing more neutral or hierarchical communities, in which the other parameters were kept constant. I also made comparisons between repetitions with the same ρ to calculate the type I error.

Statistical comparison of methods

I analyzed the performance of two kinds of methods to differentiate communities. The first consists of a set of points or curves: species abundance distributions (SAD), generalized dimensions D_q^{SAD} and D_q^{SRS} . For these I used the Anderson-Darling (AD) test (Feigelson & Babu 2012), a non-parametric test related to the Kolmogorov-Smirnov test. This measures the differences between the empirical distribution functions (EDF) of two datasets as a weighted sum of square deviations between the EDFs. In extensive simulations the AD test has proven more sensitive than the Kolmogorov-Smirnov test (Stephens 1974). I calculated p-values using randomization with 1000 repetitions, using the package kSamples (Scholz & Zhu 2012) in the R statistical statistical language (R Core Team 2014). Scripts for all analyses are available at github (<https://github.com/lisaravia/SpeciesRankSurface>) and figshare (<http://dx.doi.org/10.6084/m9.figshare.1276105>).

The second kind is based on a single dimension or power exponent: the SAR exponent and the information dimension. The SAR exponent is part of the D_q^{SAD} spectra when $q = 0$ (Borda-de-Água *et al.* 2002); an equivalent single number measure from D_q^{SRS} is the information dimension (Ricotta 2000; Chappell & Scalo 2001), that is the D_q^{SRS} when $q = 1$. I calculated the power of these with a T-test using the standard deviation (SD) obtained from the box-counting regressions. These SD are obtained with autocorrelated data because small squares are nested within big squares (see Multifractal Analysis). The consequence is that the SD may be underestimated, but the slopes estimates are still unbiased (Kutner *et al.* 2005). This should result in an increased type I error rate and also in a spurious increase in power.

Calculation of power and type I error

I simulated communities with different degrees of neutral/hierarchical structure, given by the parameter ρ of the model. The power of a test is the ability to reject the null hypothesis (H_0) when it is false. The significance level to reject H_0 was set *a priori* at $\alpha = 0.05$ in all cases, and the rejection rate of each test was calculated as the proportion of P values that less than or equal to α . To estimate power I used independent simulations of communities (50 repetitions) with the same parameters except ρ .

1 The type I error is the probability of rejecting H_0 when it is true (false positive). In our simulations, H_0
 2 is true if two simulated communities have the same ρ (and also are equal in the other parameters). To
 3 estimate type I error I compared independent simulations of communities with the same set of parameters
 4 (50 repetitions) and computed the proportion of rejection.

5 Results

6 A generalized dimension (D_q) can be interpreted like a SAR power law exponent: with larger values, the
 7 change in the number of species is greater when the scale of observation changes to a larger area. D_q express
 8 the change of the quantity under study when scale changes, but is modulated by q . When q is positive the
 9 terms of the sums (equations 2 & 5) with more abundant species have more weight, and become even more
 10 important when q is greater. When q is negative we have the opposite pattern: less abundant species have
 11 more weight in the sum, and so D_q reflects the change of rare species. When q is larger in its absolute value,
 12 D_q is driven by more and more extreme values, and thus D_q will have higher variance. Here I present most
 13 figures with a range of q from -24 to 24, but for statistical comparisons use a smaller range (from -10 to 10)
 14 to avoid large variances.

15 I calculated two versions of D_q : a) the original definition due to Borda-de-Água (2002) where D_q measures
 16 the change in SAD as we change scale (D_q^{SAD}), and b) D_q based on SRS, which measures the change in the
 17 spatial distribution of species' ranks as scale changes (D_q^{SRS}). D_q measures the rate of change with scale
 18 from a baseline that is defined by D_0 . When we study SAD, D_0^{SAD} is the SAR exponent and its value is
 19 around 0.5. A spatial distribution of species that duplicates its number with a duplication of the side of the
 20 area studied has a value of exactly 0.5. When we study SRS the D_0^{SRS} is the fractal dimension of the species
 21 rank surface. Note that in the simulations here, the individuals completely fill the available space, and thus
 22 D_0^{SRS} is equal to 2.

23 For the uniform SAD we expected D_0^{SAD} to be around 0.5, with a symmetric pattern with small deviations
 24 around this value, as all species have the same abundance and occupy the same area. The symmetric pattern
 25 was not observed in the regular cases (Figure 2) because the negative part ($q < 0$) analyzes numbers close
 26 to 0 and the logarithm enhances the differences between small numbers (Laurie & Perrier 2011). Thus the
 27 difference $\Delta D_q = |D_q - D_0|$ is greater for $q < 0$.

28 Theoretically D_q should be decreasing or constant, but this was not observed in D_q^{SAD} for the randomized
 29 spatial patterns with fewer species. This is because when changing scales, there is a point at which no new
 30 species are found, and the scaling relationship breaks. Figure 3 shows an example of D_q fitted using linear

relationships for 64 species and a side=256 sites. The scaling for a randomized pattern D_q^{SAD} breaks at 2.4, equivalent to an area of 256 units. In contrast, the scaling for the regular pattern D_q^{SAD} shows oscillations around the fitted line but no evidence of breaks. When the number of species is higher (256) the D_q^{SAD} is similar to the randomized one (Figure 2); this happens because new species appear in the whole range of scales used.

Histograms of the models' R^2 values (Figure 4) indicate the presence of poor fits or a scaling break. The D_q^{SAD} for randomized patterns and uniform SAD have the lowest R^2 of all cases. Based on all simulations a rule of thumb can be derived: 90% of D_q should have an R^2 of 0.6 or greater, and 50% should have an R^2 of 0.9 or greater (Appendix table 1); if not, one should check the plots of the fits (Figure 3). Several patterns fail to comply this rule—for example, all the uniform randomized patterns, and the logseries randomized with 8 species metacommunity (Appendix table 1 and Appendix figures 2-4).

The D_q^{SAD} for logseries had a more symmetric pattern than for uniform SAD (Figure 2), and exhibited better fits with higher R^2 (Figure 3,4). Comparing regular and randomized spatial patterns, the D_q^{SAD} curves were superposed or inside the SD of the other. Thus it seems that D_q^{SAD} cannot distinguish between such patterns (only considering the cases where the fits are good). Moreover the range of D_q^{SAD} did not change very much with the number of species, as D_q^{SAD} seems to depend mostly on the SAD used to generate the spatial pattern.

For D_q^{SRS} the theoretical decreasing pattern was fulfilled in all cases, and no anomalies were observed (Figure 2). As in the previous case, an asymmetric pattern, was observed with D_q^{SRS} around 2, an asymmetry more pronounced for patterns with uniform SAD than for logseries SAD. This is because logseries SAD have one very abundant species, several less abundant and rare species scattered through the pattern (Figure 1). Thus the abundant species dominated the spatial pattern and in some cases produces a greater $\Delta D_q = |D_q - D_0|$ in the positive side of the plot (Figure 2, 8 Species).

The uniform SAD produced D_q^{SRS} with higher ΔD_q values for regular patterns in the $q < 0$ side. This is because in the regular pattern the species are aggregated, whereas in the randomized pattern there is no aggregation so D_q^{SRS} is closer to two. Thus D_q^{SRS} for regular and randomized are more different on the negative side, and more similar on the positive side. For logseries SAD, the differences in D_q^{SRS} are similar at negative or positive sides of q . In general D_q^{SRS} curves for different spatial patterns and different SADs are distinct, except in some cases for 8 species the curves are inside the SD of a different pattern.

The R^2 values for D_q^{SRS} were all >0.9 and higher than D_q^{SAD} , and all complied with the rule of thumb described above (Appendix table 1). Their linear trends were also better (Figure 3). An example of linear

trends for different number of species and different SADs is shown in the appendix (Appendix figures 2-6). The same qualitative patterns of D_q^{SAD} and D_q^{SRS} are observed for simulations with side=512 (Appendix figure 1).

Simulated Neutral communities

Examples of the patterns simulated by the Neutral/hierarchical model are shown in Figure 5. By definition, hierarchical communities have more competitive species with lower index numbers, and neutral communities have more abundant species with higher index numbers, as determined by metacommunity abundance (see appendix model description). With a greater degree of competitive hierarchy, one or few species dominate and several rare species are scattered over the landscape (Figure 6). This produces a mostly uniform pattern of dominant species with rare species distributed at random. In neutral communities the most abundant species are not so dominant (Figure 6), and leave space for species with intermediate abundances, producing a pattern of several aggregated species. Aggregation is produced in this model only because dispersal is mainly near the parent.

For both estimated D_q the R^2 values were very good: D_q^{SRS} was always $R^2 > 0.9$ and D_q^{SAD} had in almost all cases $R^2 > 0.6$ and a 50% or more of the cases greater than 0.9 (Appendix table 2). Thus both satisfy the rule of thumb described previously.

There are two groups of D_q^{SAD} : one composed of neutral like communities for $\rho < 0.1$ and another composed of more hierarchical ones for $\rho > 0.1$. The curves for hierarchical communities were more separated for negative q than for positive q . In neutral communities this pattern was inverted, with positive q having more different curves. This reflects the patterns in SAD: hierarchical communities have one or few relatively abundant species, resulting in D_q^{SAD} reaching 0 quickly, and no new abundant species are found when changing scale. Neutral communities have more species with intermediate densities, producing $D_q^{SAD} > 0$ on the positive side.

In theory D_q have a constant value when q tends to infinity (negative or positive). Here, D_q^{SAD} spectra quickly reached a constant maximum for negative q and a minimum for positive q , and this pattern was more pronounced with hierarchical communities because they tended to have two types of species: dominant ones reflected on the positive side, and rare species on the negative. When communities are more neutral ($\rho < 0.1$) and there are more species with intermediate densities, D_q^{SAD} tended to reach the asymptotic values more slowly in the negative side.

For D_q^{SRS} a similar groups of neutral or hierarchical communities are also present. We previously saw

that D_q^{SRS} is more related to the spatial pattern than D_q^{SAD} , and thus we can interpret D_q^{SRS} in terms of randomness and aggregation of species. For hierarchical communities, negative-side D_q^{SRS} is very close to 2, that is the dimension of a uniform surface, with rare species exerting a very low influence on uniformly-distributed dominants. For neutral communities there are more species with low to medium densities, and they have greater aggregation, and thus D_q^{SRS} is higher.

When q is positive, lower values of D_q^{SRS} mean more-intense spatial patterns. Communities with $\rho = 1$ are the most hierarchical, with one dominant species and a few very rare species (Figure 6). For these communities D_q^{SRS} is closer to 2, representing the uniform spatial distribution of dominant species. When the metacommunity has more species the local community also has more species (Appendix table 3) and D_q^{SRS} starts to deviate from 2 at lower q . D_q^{SRS} for the intermediate hierarchical case ($\rho = 0.1$) starts higher than neutral at q near 0, but crosses neutral curves and ends in the lowest place. The communities have more species that also are more abundant, but still have few individuals; this forms very sharp peaks in the SRS and produces a D_q^{SRS} farther from 2. The curvature of D_q^{SRS} is thus more pronounced when there are more species. For ρ less than 0.1 communities are more neutral and have more species with similar densities, forming softer valleys and peaks that result in a D_q^{SRS} intermediate between the two hierarchical cases. Simulations with side=512 exhibited similar patterns for D_q (Appendix figure 7).

Statistical Power and type I errors

To calculate the power of the methods I compared communities with different ρ values; in this comparison the alternative hypothesis is true. Rather than estimating type I error, we need to compare different runs of communities simulated with identical parameters. I talk of high power when its value is 0.75 or higher, and low power when it is 0.5 or lower.

For D_q^{SAD} and D_q^{SRS} different ranges of q can be used. High values of q in absolute terms should produce D_q with high variances, resulting in a higher spread of values obtained in different simulation runs. Ranges of q between -10 and 10 or narrower are generally used (Yakimov *et al.* 2008; Laurie & Perrier 2011; Saravia *et al.* 2012a; Wei *et al.* 2013) but sometimes the applied range has been wider (Saravia *et al.* 2012a). I started using a q range of -24 to 24, and found that for this range type I error rates were, in all cases, higher than the nominal significance level $\alpha = 0.5$ (Appendix table 4). As a statistical test is valid if the type I error is lower or equal to α (Edgington 1995), to assure the validity for these methods a narrower range should be used. I thus used a q range between -10 and 10.

Using only one dimension of the spectra (D_0^{SAD} and D_1^{SRS}) resulted in a power generally below 0.5 (Table 2)

and the type I error around 0.4, much greater than α . These high type I error values were expected due to the presence of spatial autocorrelations in the dependent variable (Legendre *et al.* 2002). Parameter estimates can be corrected in different ways [Legendre2012], but these procedures should not increase the power of D_0^{SAD} and D_1^{SRS} .

For communities with lower species numbers (11 species in the metacommunity) the comparisons made with SAD had a constant low power across $\Delta\rho$, so no matter how different the communities are as the points used in the test are the number of species the power is low (Table 3). In contrast, the generalized dimensions D_q^{SAD} and D_q^{SRS} had a high power but Type I error also greater than α . One way to alleviate this problem is to check for a coincidence of the two methods SAD & D_q ; another would be to increase the number of points used inside the q range, because D_q could be calculated for any real number. I used 21 points (Table 3) but that could be increased, as the only restriction is the additional computational time required. In simulated communities with more species (86 & 341 species metacommunity) the type I error fell below α for all the methods and the overall SAD was slightly more powerful (table 3).

Differences between communities ($\Delta\rho$) influence power. Note that with $\Delta\rho < 0.1$, the communities compared are more neutral with a similar number of species and SADs, in comparison with $\Delta\rho \geq 0.1$, which are between neutral and hierarchical (except for 0.9) communities with different numbers of species and SAD. With $\Delta\rho$ less than 0.09 the power in most cases was below 0.5, and thus D_q^{SAD} and D_q^{SRS} could not discriminate communities with ρ from 0 to 0.01. The exception was SAD for neutral communities, when the the metacommunity had 341 species: in this case, the power was near or greater than 0.5. These are comparisons with a higher number of points (circa 100) so this results in a greater power. For differences greater or equal to 0.09, the power was high (over 0.75) in most cases. The exception was $\Delta\rho = 0.9$, but this only happened in comparing two hierarchical communities. In these cases SAD, but particularly D_q^{SAD} , had less (below 0.25 in some cases) power.

Discussion

In this paper I present a new macroecological metric D_q^{SRS} based on generalized dimensions, and use model simulations to compare it with other similar metrics: D_q^{SAD} , SAD, SAR exponent and information dimension. While D_q^{SAD} measures the change in species abundance distribution with scale, D_q^{SRS} represents the change in the spatial distribution of ranks of species. Thus D_q^{SRS} is related to the spatial pattern of species and to its abundance distribution. D_q^{SAD} also reflects changes in spatial pattern; but my results suggest that it

cannot distinguish between regular and randomized spatial patterns. In contrast, D_q^{SRS} curves differ clearly between these patterns.

All D_q curves can be interpreted in terms of q , a parameter that modulates the weight of abundant and rare species in the distribution. D_q for positive q reflects more abundant species or dominance patterns in SAD, while D_q for negative q represents rare species patterns. An alternative way to analyze D_q would be to split species into ranges of abundances and calculate D_0^{SAD} or D_1^{SRS} . This was done for biomass and forest height spatial analysis (Seuront & Spilmont 2002; Kellner & Asner 2009), but for species distributions it has several drawbacks. First, the species' spatial distribution is analyzed as a whole, and it is quite possible that the complete set of species fits very well but one or more single species do not (Šizling & Storch 2004). Second, rare species represent a few points in space, and thus the estimation of D_q will have a high uncertainty. And third, the theory developed for D_q would not be valid (Harte 2001).

In neutral models, the SAR exponent depends on speciation rate (in this case migration from a metacommunity), dispersal distance, and local community size (Chave *et al.* 2002; Rosindell & Cornell 2007; Cencini *et al.* 2012). I did not expect to find high statistical power using the SAR exponent (D_0^{SAD}) because I did not vary migration, dispersal and did not made comparisons between different community sizes. But I found high type I error rates for D_0^{SAD} and the information dimension D_1^{SRS} . This means that the statistical methods should be improved, applying a correction for autocorrelation to lower type I errors, and also a greater number of boxes should be used to increase power. In most cases, a range of different D_q values exists, meaning that the distribution is a multifractal (Stanley & Meakin 1988) and thus will not be well described by only one generalized dimension. To compare communities, D_q^{SRS} and D_q^{SAD} represent an improvement over comparisons made with only one dimension like SAR exponent or information dimension.

The species abundance distribution SAD is the most studied biodiversity pattern in ecology, but it is generally studied at one scale. Here I used the whole simulation area, and at this scale the power of SAD is comarable to that of generalized dimensions. Several studies regard SAD as not very informative because many different models can produce the same patterns, but in my simulations SAD could differentiate models quite well, except for low species communities where its power was low. Generally, the performance of SAD depends on the number of species used in the comparison. When species are around 100, SAD comparison is the only method that can detect differences between very similar neutral communities.

In comparing between competitive hierarchical communities, the number of species was relatively low, and SAD and D_q^{SAD} had a low power, but D_q^{SRS} retained a high power. This highlights the ability of D_q^{SRS} to detect differences in spatial patterns of rare species. Spatial pattern is interdependent with the shape of SAD; for hierarchical communities there are few dominant species that form patches with size similar to

the simulation area, and rare species are scattered. This pattern is enhanced by SRS, and thus different communities can be detected with high power. For neutral communities the SAD is more equitable and there are more species with enough abundances to form species clusters (I do not call them patches because species are intermingled). D_q^{SAD} and D_q^{SRS} thus have a high power to detect differences between neutral communities except where they are very similar. The advantage of D_q over SAD it is that the power should be improved by using a greater number of q values, and this possibility should be the subject of future studies.

When the communities compared had between 3 and 11 species, SAD had low power, D_q^{SRS} had a type I error slightly higher than α , and the D_q^{SAD} type I error was higher. To improve this the number of q used for comparison should be greater than that used in this work ($n=21$).

In summary, D_q^{SRS} always had better fits than D_q^{SAD} and can be applied in all the cases simulated here. It maintained a high power comparing hierarchical communities when the other methods failed. SADs also exhibit good performance with the exceptions already mentioned, although a better approach could be to use both D_q^{SRS} , SAD, and perhaps add other patterns (Münkemüller *et al.* 2012). This new macroecological metric could be a valuable addition to the already established ones and should be used in the study of the scaling of SAD (Borda-de-Água *et al.* 2012; Rosindell & Cornell 2013).

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Manuscript tables

Side	No. Species	μ	d	m	ρ
256	11	0.2	25	0.001	1
512	86				0.1
	341				0.01
					0.001
					0

Table 1: Parameters values used in the simulations of the neutral-hierarchical model

Side	Metacommunity No. Species	Mean No. Species	Type	Power	Type I Error
512	11	5.96	D_1^{SRS}	0.512	0.434
	11	5.96	D_0^{SAD}	0.498	0.494
	86	36.54	D_1^{SRS}	0.521	0.430
	86	36.54	D_0^{SAD}	0.445	0.426
	341	111.31	D_1^{SRS}	0.497	0.342
	341	111.31	D_0^{SAD}	0.494	0.436
256	11	5.90	D_1^{SRS}	0.491	0.408
	11	5.90	D_0^{SAD}	0.471	0.424
	86	32.27	D_1^{SRS}	0.501	0.447
	86	32.27	D_0^{SAD}	0.474	0.388
	341	76.57	D_1^{SRS}	0.490	0.389
	341	76.57	D_0^{SAD}	0.443	0.363

Table 2: Power and Type I error rate for T-test comparison of a single dimension of the generalized spectra: the SAR exponent (D_0^{SAD}) and information dimension of the species rank surface (D_1^{SRS}). The test use the standard deviation obtained in the regressions to fit generalized dimensions. The number of comparisons to calculate the power is n=25000, and for type I error n=6125.

Side	Metacommunity No. Species	Mean No. Species	Type	Power	Type I Error
512	11	5.96	SAD	0.115	0.025
	11	5.96	D_q^{SRS}	0.720	0.102
	11	5.96	D_q^{SAD}	0.568	0.212
	86	36.54	SAD	0.697	0.009
	86	36.54	D_q^{SRS}	0.680	0.014
	86	36.54	D_q^{SAD}	0.616	0.011
	341	111.31	SAD	0.830	0.039
	341	111.31	D_q^{SRS}	0.688	0.000
	341	111.31	D_q^{SAD}	0.609	0.017
256	11	5.90	SAD	0.175	0.000
	11	5.90	D_q^{SRS}	0.654	0.068
	11	5.90	D_q^{SAD}	0.704	0.204
	86	32.27	SAD	0.675	0.019
	86	32.27	D_q^{SRS}	0.657	0.025
	86	32.27	D_q^{SAD}	0.613	0.027
	341	76.57	SAD	0.799	0.035
	341	76.57	D_q^{SRS}	0.670	0.030
	341	76.57	D_q^{SAD}	0.610	0.048

Table 3: Power and Type I error rate of Anderson-Darling statistic to test hypothesis of differences in: species abundance distributions (SAD), generalized dimension based on SAD (D_q^{SAD}) and generalized dimension based on SRS (D_q^{SRS}). The power is calculated testing communities with different ρ and type I error is calculated for communities with the same ρ . The p-values were estimated using 1000 randomizations. The number of points used for SAD comparisons is the number of species found in the communities. The number of points used for multifractal spectra correspond to the q in the range -10 to 10 ($n=21$), according to the following set $q=\{-10,-8,-6,-4,-3,-2.5,-2,-1.5,-1,-0.5,0,0.5,1,1.5,2,2.5,3,4,6,8,10\}$. The number of comparisons for the power calculations were $n=25000$ except for SAD with side=500 & metacommunity species=11, where some comparison with less than 3 species were skipped ($n=23800$). For type I error the comparisons were $n=6125$, and the same exception applies ($n=5846$).

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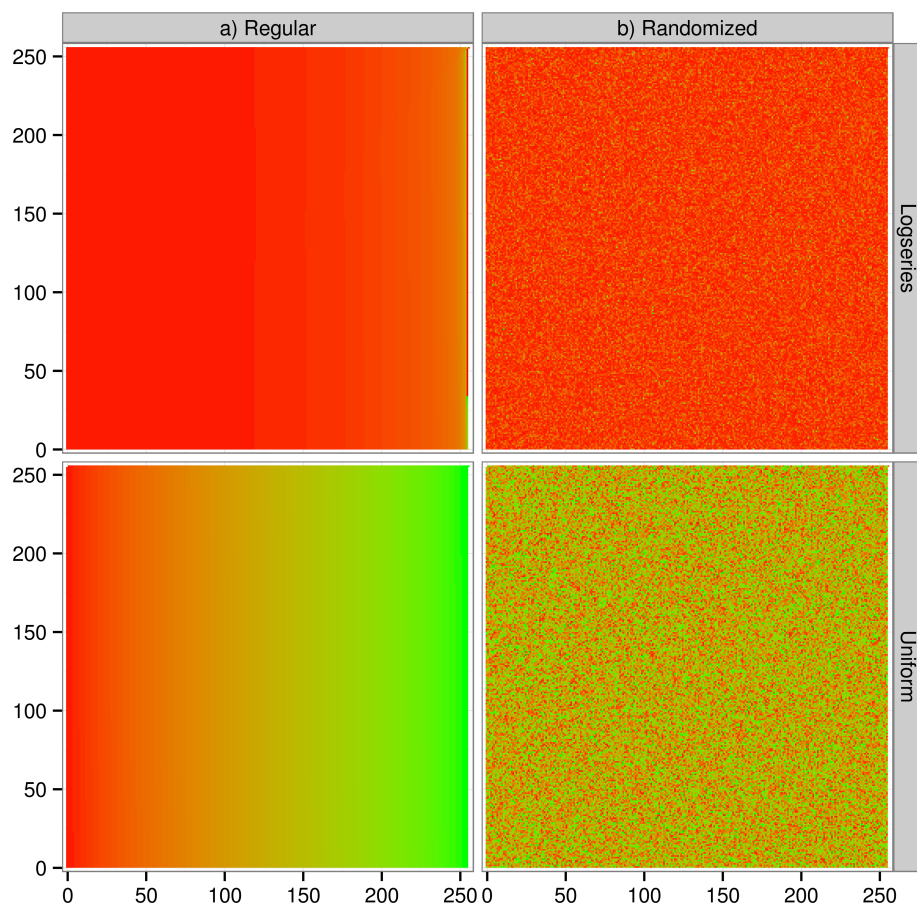


Figure 1: Spatial patterns generated with logseries and uniform species abundance distribution (all species have the same density) with 64 species and a grid with side=256. a) Regular: species are distributed in vertical bands. b) Randomized: the position of species are distributed at random in space.

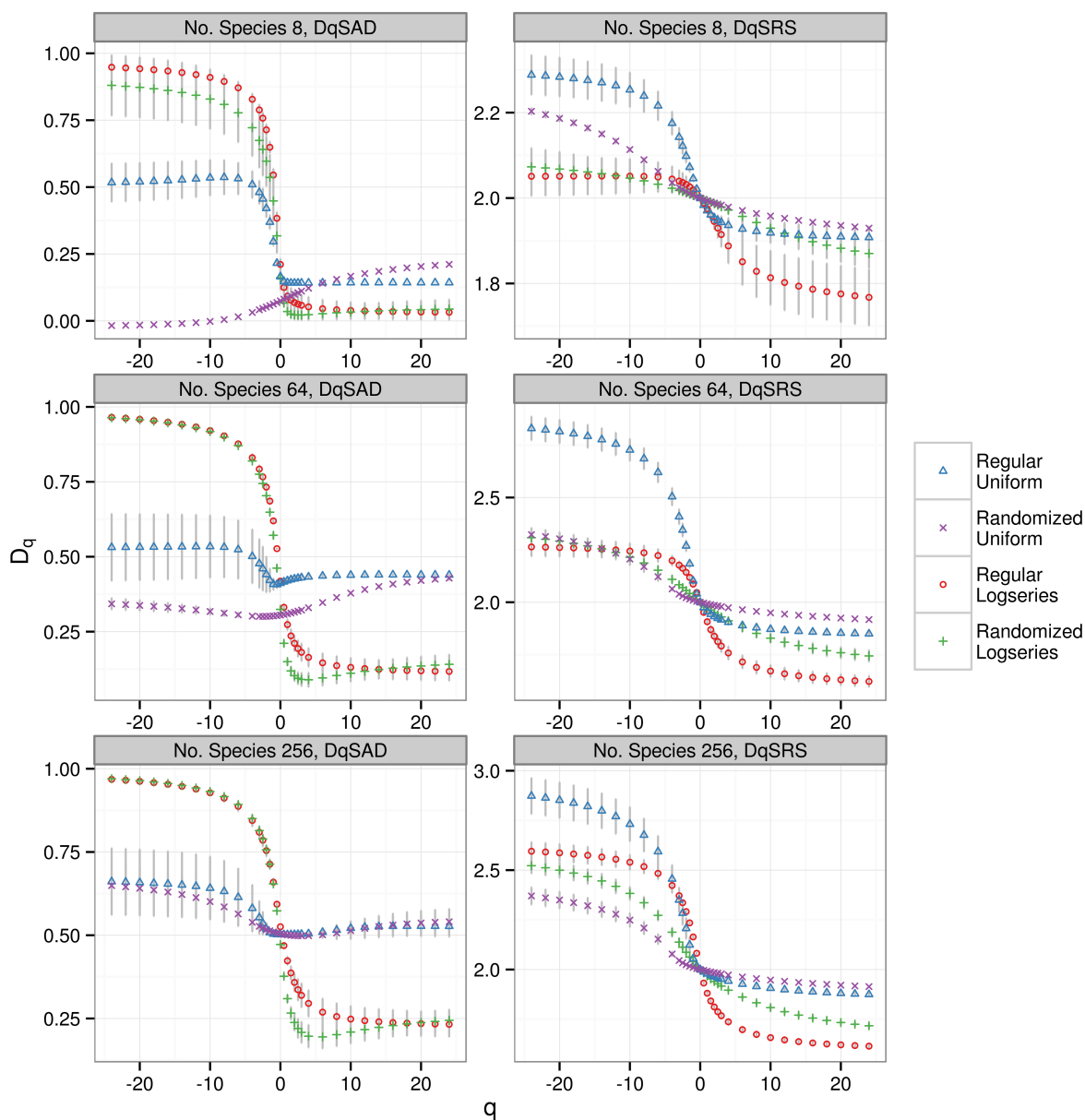


Figure 2: Generalized dimension spectra D_q of simulated species spatial patterns. The points are means of 10 simulated patterns using a spatial grid of side=256. A logseries or uniform species abundance distribution were used, with 8,64 and 256 species. Two forms of generalized dimensions were estimated: DqSRS, from species rank surface D_q^{SRS} . DqSAD, estimated from species abundance distribution D_q^{SAD} . I use two spatial patterns: Regular, the species are distributed in vertical bands, Randomized the spatial distribution of species was randomized.

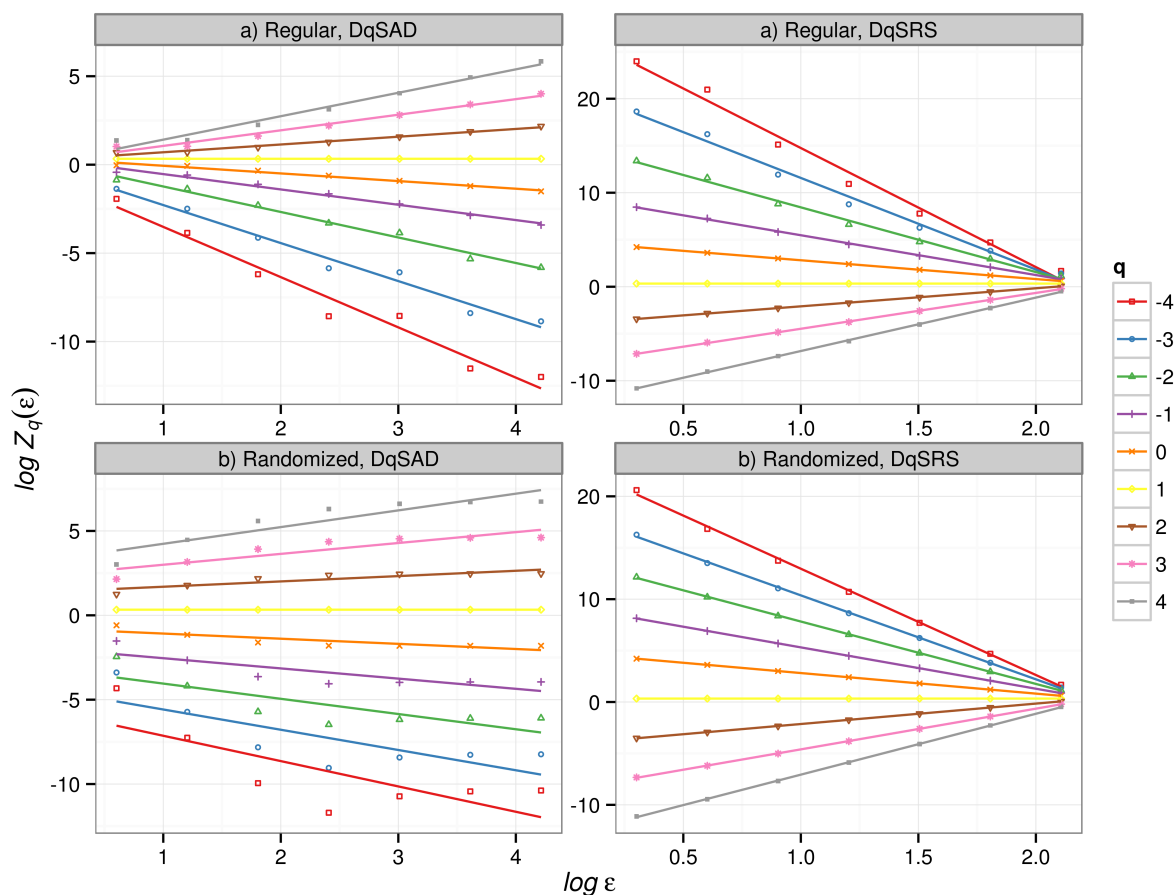


Figure 3: Linear fit from generalized dimension (D_q) estimation showing a range of q from -4 to 4. The spatial grid has a side=256 occupied with 64 species with a uniform abundance distribution. Two different spatial patterns were used: a) Regular, a regular spatial pattern with species distributed in vertical bands of equal width. b) Randomized, the positions of species in the grid are randomized. Two kinds of generalized dimension were estimated: DqSRS corresponds the fit of D_q^{SRS} (see text) and DqSAD is the fit from the estimation of D_q^{SAD} (see text). $Z_q(\epsilon)$ corresponds to the partition function calculated for a box with side ϵ in the SRS case, in SAD case, ϵ represent the area of the box used.

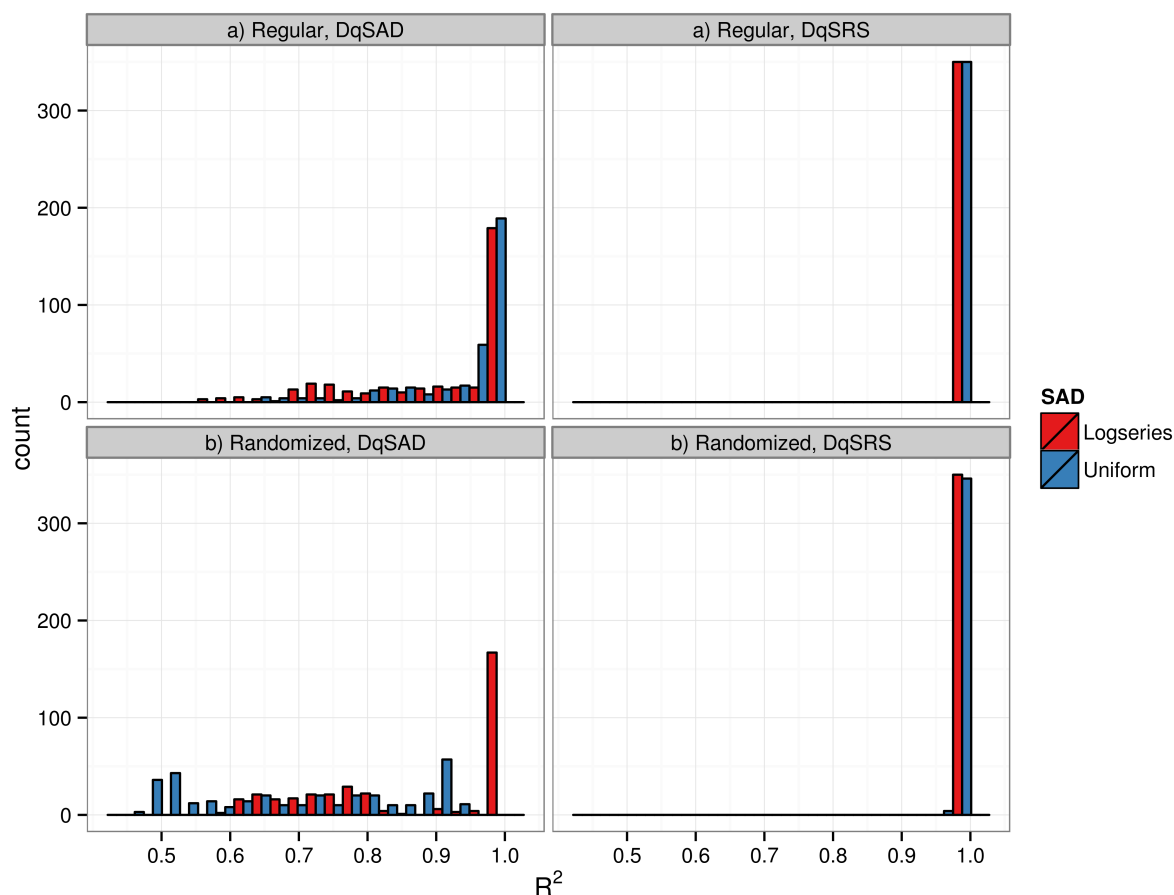


Figure 4: Coefficient of determination R^2 from the regressions to estimate generalized dimension D_q of simulated species spatial patterns. The moment order q is in the range $[-24, 24]$, the simulated pattern use a spatial grid of side=256 and 64 species with a uniform and logseries abundance distribution. Two different spatial patterns were used, Regular: a regular spatial pattern, with species distributed in vertical bands. Randomized, the positions of species in the grid are randomized. Two kinds of generalized dimension were estimated: DqSAD, the R^2 are from the estimation of D_q^{SAD} (see text). DqSRS, the R^2 are from the regressions to estimate D_q^{SRS} (see text).

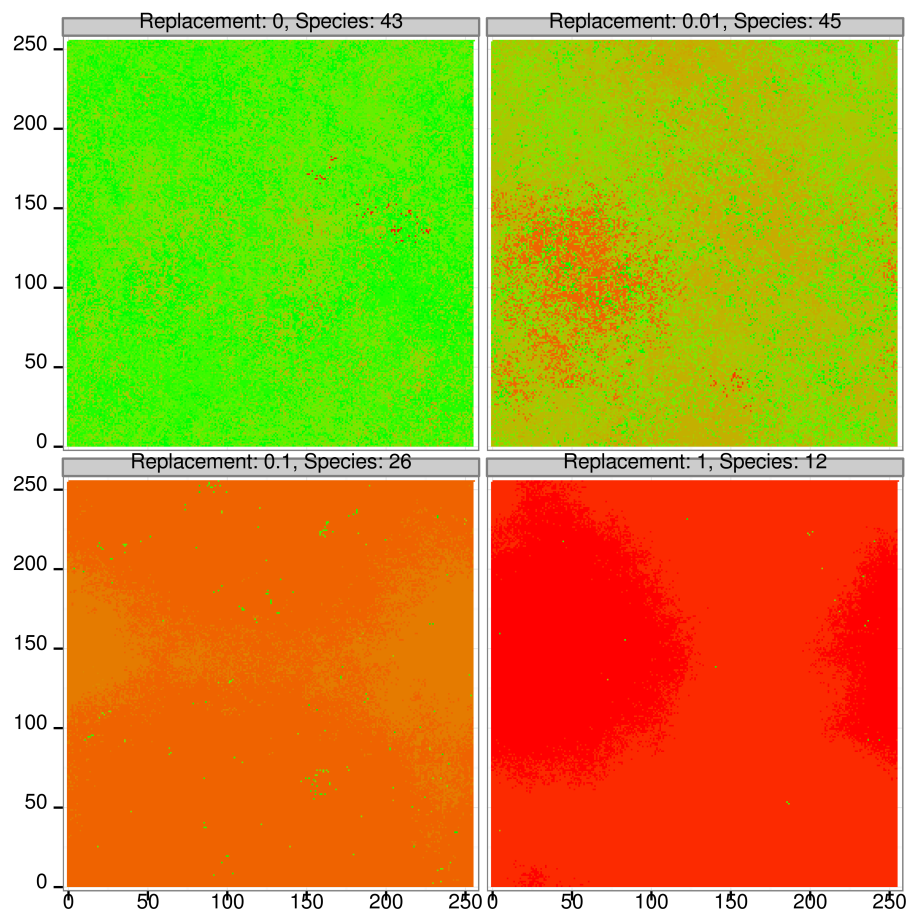


Figure 5: Spatial patterns generated with a spatial neutral/hierarchical model. *Replacement* is the parameter ρ that determines the degree of neutrality. When this parameter is 0 the model is completely neutral and there is no competitive replacement of species. When ρ is 1 competitive superior species always replaces inferior ones and the model is completely hierarchical. The simulations use a metacommunity with a logseries abundance distribution with 86 species and a simulation grid side=256.

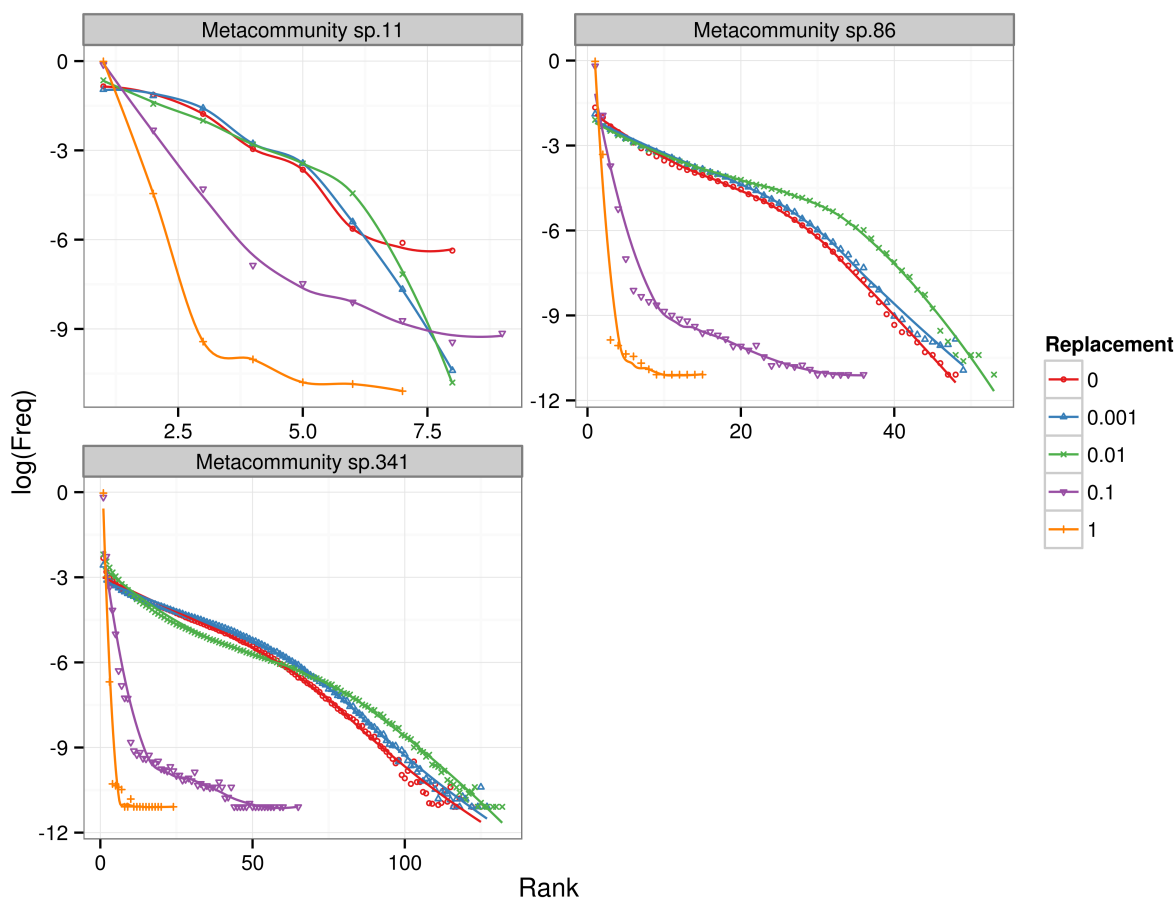


Figure 6: Rank abundance diagrams of communities patterns generated with a spatial neutral/hierarchical model with different number of species in the metacommunity (labelled in each subfigure). *Replacement* is the parameter ρ that determines the degree of neutrality. When this parameter is 0 the model is completely neutral and there is no competitive replacement of species. When ρ is 1 competitive superior species always replaces inferior ones and the model is completely hierarchical. The simulations use a metacommunity with a logseries abundance distribution with 11, 86 and 341 species and a simulation grid side=256, the other parameters used were MortalityRate=0.2, DispersalDistance=0.4 (2.5 grid units), ColonizationRate=0.001.

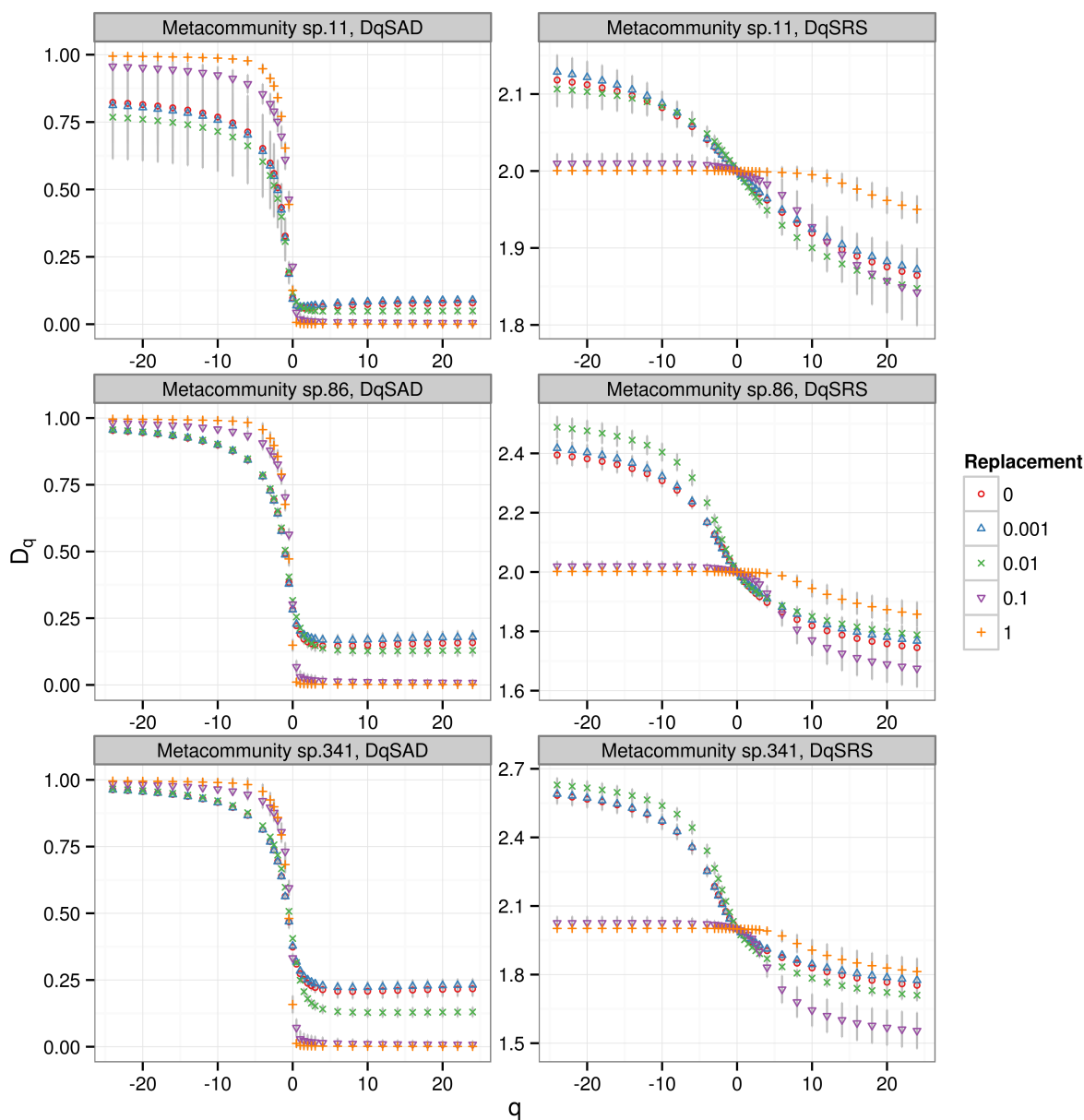


Figure 7: Generalized dimension spectra D_q of spatial patterns generated with a spatial neutral/hierarchical model. *Replacement* is the parameter ρ , that determines the degree of neutrality. When this parameter is 0 the model is completely neutral and there is no competitive replacement of species. When ρ is 1 competitive superior species always replaces inferior ones and the model is completely hierarchical. The points are means and vertical lines are standard deviation of 50 simulated patterns. Simulations use a metacommunity with a logseries abundance distribution with 11,86 and 341 species. The simulation grid side is 256, and the other parameters are given in the main text.

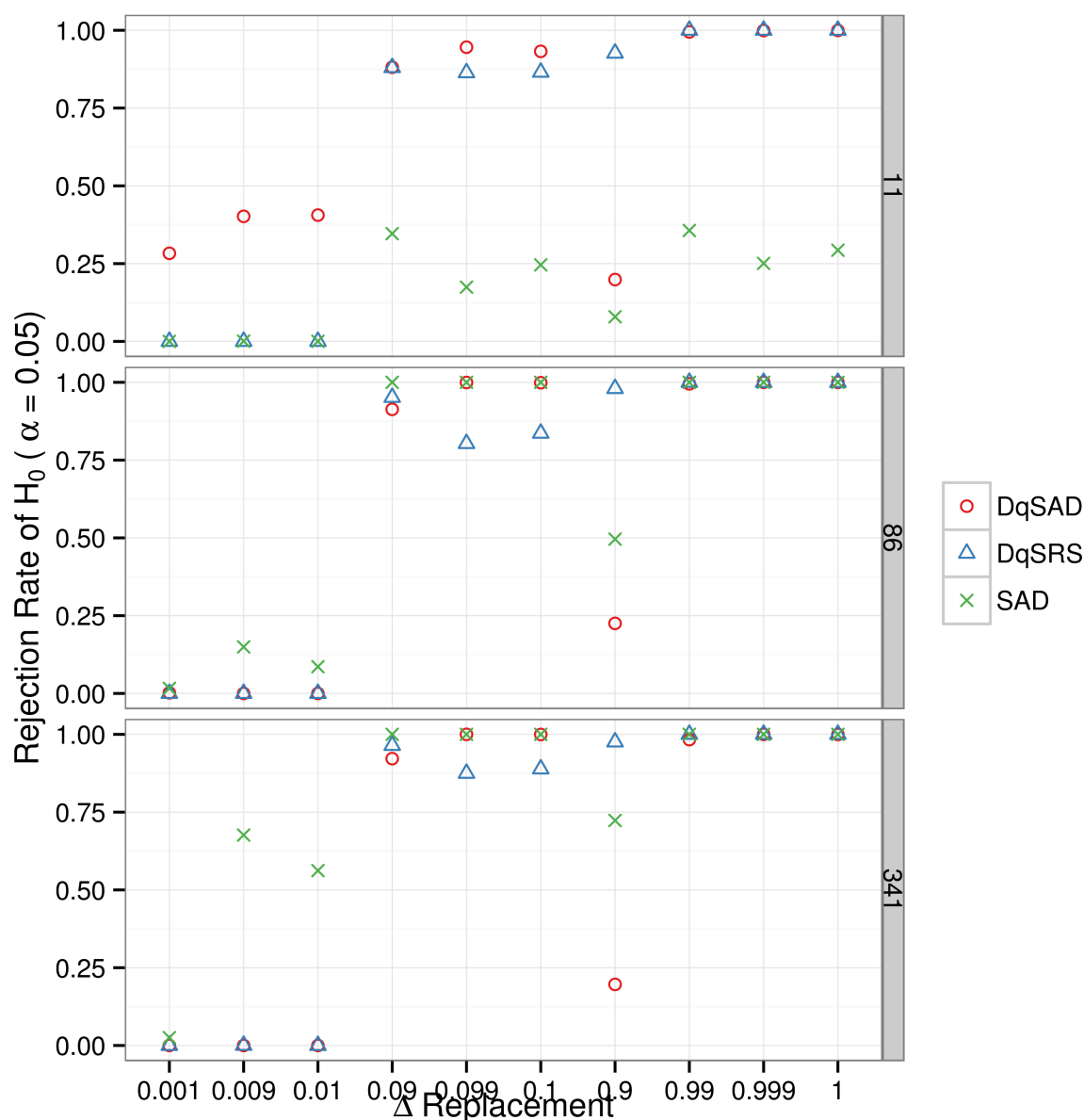


Figure 8: Power of the Anderson-Darling test for the hypothesis that generalized dimensions (D_q) curves and species abundance distributions (SAD) of simulated neutral/hierarchical communities are different. The compared communities differ only in parameter ρ that determines the degree of neutrality/hierarchy. $\Delta\rho$ is the difference in the parameter, when is lower the communities are more similar. DqSAD is the generalized dimension calculated using SAD, and DqSRS is the one calculated using the species rank surface (SRS). The number of comparisons to calculate the frequency is 2500 in all cases. Simulations use a metacommunity with a logseries abundance distribution with 11,86 and 341 species; a grid side of 256 sites, the other parameters are given in the main text.