Chapter 5

The Importance of Scaling in Biodiversity

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Abstract Our main tenet is that biodiversity should be studied as a function of scale. The epitome of a similar approach was that of Mandelbrot in his studies on fractals. Although biodiversity patterns may not necessarily follow the mathematical description of fractals, we argue that much can be learnt if we adopt the perspective of studying biodiversity across scales. A case where the concept of scaling is routinely applied in ecology is the species-area relationship, a relationship describing how the number of species (species richness) changes, i.e. scales, as a function of area. However, the importance of scaling is often neglected in ecology. For instance, it is seldomly applied to another component of diversity, the relative abundances of species, being the latter often described using the proportion of individuals of each species. We exemplify the application of scaling to the species relative abundance with our own work. One of the advantages of studying biodiversity under the framework of scaling is that patterns tend to emerge. These patterns emerge from a myriad of processes and their respective interactions. However, understanding the role of each process individually, or quantifying its role in the community functioning, may be empirically impossible. Thus, we argue from theoretical and practical perspectives, including approaches to conservation problems, that we should concentrate our endeavours on the quantitative description of known patterns, as it is often done in other basic and applied sciences, even if that implies temporarily relegating to a secondary position the detailed analyses of the underlying mechanisms.

Keywords Biodiversity · Patterns · Scaling · Species abundance distributions · Species-area relationship

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5.1 Introduction

Among the several environmental challenges faced by humankind, biodiversity loss looms in the background, with the magnitude of its consequences wrapped in uncertainty. It is then natural that society looks for scientific basis, guidance and solutions in ecology to the present biodiversity crisis. However, ecology is a recently born science (e.g. Worster 1994) and the tools to understand biodiversity at a planetary scale are only now becoming available. In fact, despite the important strides in the nineteenth century by biogeographers such as Humboldt, Darwin or Wallace, the description of biodiversity and biogeography is still very much a piecemeal approach, mainly consisting of data sets of “small” size; “small” is in quotation marks because, though species data sets are indeed small samples of larger communities, they tend to require a tremendous sampling effort in terms of labour and financial costs, as is the case with the censuses of 50 ha plots on tropical tree species regularly undertaken by the Smithsonian Institution (Condit 1998).

Only now one starts to glimpse the possibility of using methodologies enabling sampling at large scales, such as remote sensing (e.g. Asner et al. 2017). But whether these new methods will be sufficiently developed in time to help solve the biodiversity crisis remains doubtful. Moreover, it is not clear if humankind, as a whole, is determined to put a concerted effort to understand biodiversity at a global scale. As S. P. Hubbell (personal communication) has put it, it seems to be easier to raise money to fund astronomy projects than to finance ecology ones, though the latter deal with problems closer to our daily concerns.

Besides the practical aspects faced by ecologists, there are also entrenched attitudes that may hinder progress in ecology. In particular, the tendency to scorn at the “mere” mathematical handling of quantitative patterns when the underlying mechanisms are not fully understood. I contend that this attitude is to be avoided and that much can be learnt from a proper mathematical description of patterns and their interrelationships. Of course, we should not ignore the need to explore the underlying mechanisms, though practical considerations may sometimes require postponing such endeavours.¹

I devote this chapter to the importance of scaling in ecology, and when dealing with scaling patterns often emerge. In particular, we will be interested in biodiversity patterns across spatial scales. When one mentions biodiversity, we tend to think solely of the number of species. Such vision, however, does not fully describe the diversity of life on Earth. Indeed, the notion of biodiversity is far more encompassing. For instance, a common definition by the United Nations Environment Programme Convention on Biological Diversity (UNEP 1992) states that biodiversity

means the variability among living organisms from all sources including, *inter alia*, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part: this includes diversity within species, between species and of ecosystems.

¹This point is also emphasised in Casetta et al., Chap. 1, in this volume.

Similarly, but specifying more clearly the different levels of diversity within a species, it is the definition given by Wilcox (1984) and adapted by the IUCN:

the variety of life forms, the ecological roles they perform and the genetic diversity they contain... at all levels of biological systems (i.e., molecular, organismic, population, species and ecosystem)...

Notice that the latter definition includes also the roles performed by the species in the community, which I identify by what is now referred as functional diversity (e.g. Cernansky 2017). As we will see, when studying communities, ecologists also define diversity not only in terms of number of species (species richness), but also in terms of their relative abundance (e.g. Magurran 1988). This distinction is important. Species richness takes into account only the presence of species; thus, each time an individual of a species not yet recorded is found, the number of species is raised by one, but subsequent individuals of the same species are ignored since that species has already been identified. On the other hand, when collecting information on species abundance all individuals (or some equivalent measure) of a given species have to be recorded since we want to know not simply which species are present but also their relative abundance.

The above definitions imply that we have information on all organisms on Earth. Even at the species level, and disregarding the difficulties of defining “species” (e.g., Coyne and Orr 2004 or Futuyma 2005), quantifying the total number of species is manifestly impossible with our present means. Perhaps for some groups, such as the cetaceans or primates, which have a relatively small number of species and tend to attract a large public and academic interest, it may be possible to identify all the species, but for other groups, such as insects, this is at present completely impossible. This impossibility arises mainly from practical reasons, such as the required labour intensive procedures that it entails or the economic costs involved, not to mention the negative impacts that gathering the data could have on the habitats. Naturally, ecologists have for long devised procedures to circumvent these problems by resorting to carefully devised sampling schemes and by taking advantage of well known patterns (e.g. May 1990). Patterns play a particularly important role in this chapter, as we will now see.

Patterns, by which we mean “regularities in what we observe in nature; that is, [...] ‘widely observable tendencies’” (Lawton 1999), are essential to estimating biodiversity, especially those patterns concerned with how biodiversity *scales* as a function of a given variable. Because the notion of “scaling” is essential to us, we should try to give it a more precise meaning. In general, I will refer to the properties of how a quantity changes as its *scaling properties* or, simply, “*scaling*”. A similar definition is that of Storch et al. (2007) according to whom scaling means “the effort to discover and explain how some state variable or dynamic parameter changes with some other variable”. The relationship between the number of species and area, called the species-area relationship, a mathematical expression that relates how the number of species changes as a function of the size of the area sampled, is one of the best known scaling relationships in ecology (Rosenzweig 1995). Although the exact quantitative formulation of the scaling properties is often disputed (e.g., see

Rosenzweig 1995), my main tenet is that their existence is a fundamental component of studies on biodiversity. Therefore, I argue that the characterization of biodiversity should include not only the quantification of certain variables at one given scale, e.g. the number of species, but also the scaling properties associated with them. In other words, the scaling properties of biodiversity should be seen as an integral part of the biodiversity patterns.

In the previous paragraph, we used the species-area relationship, “one of the boldest and most robust patterns in ecology” as Lawton (1996) put it, as a typical example of a biodiversity scaling pattern. In fact, its application is common practice in theoretical and applied ecological studies. However, most other components of diversity tend to be studied at one single scale, for instance, the relative abundance of species (McGill 2003; Volkov et al. 2003), hence the ideas (and advantages) underlying the concept of scaling are not always explored. This chapter discusses a case study based on my own work concerning the relative abundance of species. Although there are several ways of measuring species abundances, for simplicity we assume that it is measured by the number of individuals.

To realize why it is important to take into account the relative abundance of species, imagine two communities with exactly the same number of species but with very different relative abundances. In one community the individuals are evenly distributed among species (a circumstance that is unlikely to be observed in nature) while in the other community individuals are unevenly distributed among species, with a few species having a large number of individuals and the majority being rare (a circumstance often observed in nature). Given the way individuals are distributed among species, these imagined communities are likely to exhibit very different temporal population dynamics, including the local risk of species extinction, and pose considerably different problems from a conservation perspective.

The relative abundance of individuals is often depicted using histograms called “species abundance distributions”. However, while studies on the species-area relationship emphasize the rate of accumulation of species as area increases, studies on species abundance distributions usually concentrate on a single spatial scale, and efforts are directed towards determining which theoretical statistical distribution provides the best fitting to the empirically distribution. Implicit in this approach is that finding a theoretical distribution that would fit a large number, if not all, of the observed species abundance distributions will provide a pattern that could be used for evaluating theories of species diversity. Although fitting the abundance data at one spatial scale is a worthy endeavour, what has become clear from our studies is that the shape of the distributions depends on the scale at which it is sampled. Here too, as we will see, the concept of scaling may provide a unifying way of describing how the distributions change and reveal possible patterns.

In this chapter I shall argue for the importance of considering questions associated with scaling when dealing with biodiversity issues and associated patterns. But the chapter is in a sense anecdotal, because it deals with my own work on the scaling properties of species abundance distributions, which I use mainly to provide an instance of scaling in biodiversity, and in no way exhausts the topic; for a more complete role of scaling in biodiversity see Storch et al. (2007). But before dwelling

into biodiversity proper, we discuss an example of scaling that has become a classic in fractal studies and that enshrines the basic ideas underlying our approach to the study of biodiversity.

5.2 An Example from Fractals

Richardson (1961) asked what the lengths of the borders between several countries were. Surprisingly, he found that the lengths were considerably different depending on the source of information he looked at. For example, Portuguese sources claimed that the border between Portugal and Spain was 1214 km while Spanish ones specified only a length of 987 km, a 23% difference! A likely explanation for such discrepancy was the size of the “ruler”, that is, the *scale*, used to estimate the length of the border, as pictured in Fig 5.1a. For reasons that we will not speculate about, the Portuguese used a ruler that was smaller, probably half the size, of that used by the Spanish. As we can see from Fig. 5.1a, if we use the “blue” ruler we will obtain an estimate, if we use the “red” ruler, and because its smaller size allows it to follow better the shape of the border, we are likely to obtain a larger estimate. Naturally, we can imagine an even smaller ruler, that will give an even better fit to the border. Since smaller rulers give a better fit, one may be tempted to keep reducing the size of the ruler in the hope that the length would converge to its true value. Such strategy, however, would be self-defeating because the “roughness” of the border, with all its creases, leads to an estimate that keeps changing with the size of the ruler, as we exemplify in Fig. 5.1. Of course, at some subatomic level we would eventually find the true size of the border, but for all practical purposes the border’s length is undefined since it is a function of the ruler’s size (Mandelbrot 1967, 1982). In other words, for borders, and other objects that are fractals, the size is only meaningful when the scale at which it was measured (the size of the ruler, in our example) is also specified. Therefore, it would also not be appropriate to say that the border’s length obtained by the Portuguese is more “correct” than that obtained by the Spanish, since the border does not have a defined length.

For those who seek concrete answers, the question of finding the border’s size may look helpless because there is no numerical invariant characteristic associated with the length; in other words, the length keeps changing. However, if we draw in a double logarithmic plot the length of the border as a function of the ruler’s size, we will see that the points fall approximately on a straight line, as shown in Fig. 5.1b. Because we will make use of logarithms often, a brief digression about its significance is in order. Logarithms are often used when one needs to depict a wide range of values in a single plot. For instance, while in an axis in a linear scale the distance between 1 and 2, 2 and 3, *et seq.*, are equal, in a logarithmic axis of base 10, the “distance” between 1 and 10 is equal to the “distance” between 10 and 100, and then between 100 and 1000, *et seq.* The latter happens because logarithms calculated the power at each a certain base needs to be raised to obtained the observed value. For instance, in base 10, the logarithm of 100 is 2 because $100 = 10^2$,

Fig. 5.1 A schematic representation of a “border” (black line) being fitted with rulers of two different sizes (blue and red “sticks”), plot a, and the hypothetical straight line that would have been obtained after fitting the “lengths” estimated with rulers of different sizes, plot b

and the one of 1000 is 3; or, in typical mathematical notation $\log_{10}(100) = 2$ and $\log_{10}(1000) = 3$. The implication is that logarithms compress the largest values in the axis of a graphic, with the advantage that the smallest ones are then visually better represented. Importantly, double logarithmic scales are used when one wants to identify power laws, and these play a very important role in ecology, as well as, in several scientific disciplines. Power laws are easily identified in double logarithmic plots because in these plots a power law becomes a straight line. To see this, take the general form of a power law, $y = ax^b$, where a and b are constants. If one takes the logarithms on both sides of this equation, we obtain $\log(y) = \log(a) + b \log(x)$. This means that if we plot $\log(y)$ as a function of $\log(x)$, which is what a plot with double logarithm scales does, we observe a straight line with slope b and intercept $\log(a)$.

Returning to the question of the length of the border, we can see from Fig. 5.1b that, although the length of the border changes as a function of the ruler's size, the estimated lengths define a straight line. Therefore, what is invariant, at least for a very large range of ruler's sizes (scales), is the slope of the (approximately) straight line defined by the points; incidentally, the slope is related to what Mandelbrot called the fractal dimension. Observe that, although we could not find any obvious patterns when we measured the borders with different ruler's sizes, a pattern consisting of a straight line emerges when we plot the measurements in a double logarithmic plot. It is now the slope of this line that provides an invariant characteristic that allows a succinct description of the length as a function of the ruler's size. This example shows that, first, it is not enough to study the length of the border at one single scale, since what is relevant is to study how the length changes as a function of the ruler's size, that is, its scaling properties, and, second, a *pattern emerges* when we display the measurements on a double logarithmic scale plot.

5.3 Scaling and the Species-Area Relationship

The above issues associated with the scaling of the borders' length are easily translated into biodiversity studies. Imagine we sample individuals of a given taxon in areas of different size using a nested sampling scheme, that is, a larger area includes smaller ones. When one plots the number of species as a function of the area size, a typical pattern emerges. At the beginning, for small area sizes, the number of species increases fast, but then the rate of accumulation of new species decreases until it reaches an apparent plateau. This is not surprising: first we observe a large number of new species but when the sample size increases, most individuals belong to species already identified, thus the rate of increase of new species progressively decreases. What is surprising is that if we plot the number of species as a function of the area in a double logarithmic plot, the points will fall on an almost straight line, not very differently from what we depicted in Fig. 5.1b but with a positive slope (e.g., Rosenzweig 1995). Because the points follow a linear relationship in a double logarithmic plot, this implies that the number of species scales with area as a power law, $S = cA^z$, where S is the number of species, A is the area, and c and z are constants. Interestingly, a power law species-area relationship is a rather robust pattern since it also arises under other sampling schemes. For instance, if we estimate the number of species in the islands of an archipelago and plot it in a double logarithmic plot as a function of the area of the islands, we will observe that the points fall approximately on a straight line.

The species-area relationship example is important because it represents a biodiversity pattern that exhibits a clear scaling property, with a clear quantitative relationship: a power law $S = cA^z$. Accordingly, ecologists have concentrated on studying the range of the parameter z , the one that controls the rate of increase of the number of species, and how it can be interpreted (e.g. Rosenzweig 1995). In fact, understanding how species change as a function of area has played an essential role in

conservation biology because it (or related relationships) can be used to estimate species extinction due to habitat loss. The basic idea is that if we know how the number of species varies with area, then if part of the original habitat decreases, due to some natural or man-made destructive event, the number of species should also be reduced in accordance with the formula $S = cA^z$. Although simple, this method is not without problems. For instance, Pereira and Daily (2006) pointed out that destroying a habitat and converting it into another, for example, forests into pastures, does not necessarily leads to the extinction of all the species present in the original habitat, since some may still survive in the new one. On the other hand, He and Hubbell (2011) pointed out that the methods to assemble a species-area curve depend on finding the first individual of a new species, while extinction requires finding the very last individual, procedures that are not always equivalent (see also Pereira et al. 2012). In both cases, the consequence is that the number of predicted extinctions is larger than the ones really observed.

5.4 Scaling and Species Abundance Distributions

Species abundance distributions describe not only how many species can be found in a sample but also how the individuals (or other measure of abundance) are distributed among species. Typically, a species abundance distribution is depicted as a histogram where in the y-axis is the number of species and in the x-axis is the number of individuals, usually in a logarithmic scale of base 2. A logarithmic scale of base 2 is used because it is integer base that allows the best discrimination of the species abundances, in particular, it ensures that species with a small number of individuals are well represented in the histograms. Typically, the x-axis corresponds to classes of the logarithm of the number of individuals as follows: 1 individual, 2–3 individuals, 4–7 individuals, *et seq.*, that is, the bins are obtaining by doubling the number of individuals, hence it is called often an octave scale. Accordingly, these histograms contain information on the number of species with a given number of individuals; see Fig. 5.2, for some examples. Although species abundance and species richness are related concepts, the way species abundance distributions have been studied contrasts with that of the species-area relationship. In fact, as we mentioned before, while studies on species area relationships emphasize how species richness change as a function of area, studies on species abundance distributions are often carried at one single spatial scale.

This was not always the case. Some of the original studies on species abundance distributions did focus on how they changed as a function of sample size (Preston 1948, 1962); notice that very often the size of a sample is proportional to the size of the area sampled, therefore in the remainder of this chapter I will use “area size” or “sample size” interchangeably. Preston introduced the concept of *the veil line*, a line that would move to the left of the distribution as more data are gathered, progressively revealing more species and the full shape of the distribution. In particular, using data on birds, Preston showed that, once enough data had been collected, a maximum

Fig. 5.2 The species abundance distribution for four different sizes of area within the BCI 50 ha plot. The x-axis corresponds to classes of the logarithm of the number of individuals as follows: 1 individual, 2–3 individuals, 4–7 individuals, *et seq.*

appeared for intermediate abundance classes (like in Fig. 5.2b–d), in contrast with the distribution observed for small sample sizes that were monotonically decreasing functions (like in Fig. 5.2a). The latter shape had been previously reported by Fisher et al. (1943) for data on Lepidoptera (moths and butterflies) who fitted the distribution using a logseries distribution. Because the histograms observed by Preston for large samples had a bell shape when plotted in a logarithmic scale, Preston suggested that a lognormal distribution rightly described the data. We now know that the concept of the veil line is not appropriate (Dewdney 1998; Green and Plotkin 2007) and computer simulations and empirical work suggest that the lognormal is not the distribution for very large sample sizes (ter Steege et al. 2006; Borda-de-Água et al. 2007).

While Preston did pay attention to scale, some of the most recent studies on species abundance distributions have focused on determining which theoretical distri-

bution gives the best fit to an empirical observed distribution at a specific scale (Hubbell 2001; McGill 2003; Volkov et al. 2003). (I suspect this approach may partially reflect Preston's attempt to describe species abundances by assuming the lognormal to be the limiting distribution.) The problem with this approach is that the shape of the distributions keeps changing for a wide range of scales (cf. Fig. 5.2), and reaching a sample size that is representative of the community may not be practical or economically feasible; for example, collecting data for the first census on tree species in a 50 ha plot in Barro Colorado Island, Panama, (the data used to draw Fig. 5.2) took approximately 2 years (S. P. Hubbell, personal communication) but of course this is a very small part of the entire forest of which the plot is part of. Moreover, not only the shape of the distributions changes considerably, even for shapes that are visually similar, given the stochasticity inherent to any natural process and sampling procedure, it is very likely that a theoretical distribution that gives the best fitting at one scale may not give the best fitting at another.

Although it is undeniable that for a ecological community a specific instant in time there is a species abundance distribution, our experience based on empirical and computer simulations has shown that from a practical perspective all we can aim for is to understand how the species abundance distribution changes as a function of area. Therefore, we have developed an approach that, instead of analysing the species abundance distribution at one single scale, describes how the distributions change as a function of a given scale (typically the area size) using non-parametric descriptors, namely, the moments of the distributions (Borda-de-Água 2012, 2017).² The important finding was that, though the original motivation was partially due to impracticalities of obtaining large samples on large areas, there is also relevant information on the description of how the distributions change as a function of a scale, that is, on the patterns associated with the scaling properties of the distributions. Such information can be used in two ways, first, it provides patterns that can be used to checked whether theoretical models of species diversity predict the scaling for the species abundance distributions, as those empirically observed, and, second, the same patterns can be used to predict the species abundance distributions for larger scales.

The technical aspects of describing the change in the distributions by using their moments are easy. If a species i has X_i individuals, and we call the logarithm (usually of base 2) of this quantity $x_i = \log_2(X_i)$, then the n th moment, M_n , is calculated using

the formula $M_n = \frac{1}{S} \sum_{i=1}^S x_i^n$, where S is the number of species; when $n = 1$, the previ-

ous expression is simply the formula of the mean. Thus, in order to describe the change in the distributions, we calculate several moments (e.g. the first 10) for each area and then plot each of the moments as a function of area. For instance, assume that we have information on the location of the individuals of all tree species in a given area, then we can apply the moments' formula for several sub-areas of different sizes and plot the result as a function of area. This is what was done to obtain Fig. 5.3, that shows the evolution of the moments as a function of area size for the

²For a complete description of diversity indices see Crupi, Chap. 6, in this volume.

Fig. 5.3 The logarithm of moments from order 1 up to order 11 as a function of the logarithm of areas between 1 and 50 ha using data on tropical tree species from the 50ha plot in Barro Colorado Island, Panama, using all stems with diameter at breast height larger or equal to 10 cm. The order of the moments increases when we go from the bottom to the top lines. The dashed lines added to each moment are the curves of best fit obtained from linear regressions of the logarithm of the moments versus the logarithm of the area between 8 and 50 ha

tree species in a 50 ha plot in Barro Colorado Island, Panama. An important result of this exercise is that the moments are approximately linear in a double logarithmic plot; a point to which we will return soon.

Our approach to deal with the scaling of species abundance distributions is similar to the one underlying the species-area relationship. The species-area relationship describes how the number of species change as a function of the area, and, accordingly, it is a single curve. On the other hand, being a distribution, the information on the species abundance cannot be summarized in a single number. Although sometimes we use a single descriptor, such as the mean, the variance, the skewness or the kurtosis (which are in fact related to the moments), each of these reveals only one aspect of the distribution (e.g. Press et al. 1996). To fully describe a distribution we need all these descriptors (and in fact more). In the same way, we need several

moments of the species abundance distribution. As a consequence, for a given area, instead of a single point (the number of species), we have several points (the moments). Therefore, to describe the scaling properties of the species abundance we need several curves, one for each moment. Nevertheless, besides the multiplicity of curves, this approach is essentially the same as that of the species-area relationship.

One of the advantages of using the moments of the distributions is the possibility of extrapolating the species abundance distributions for larger areas (Borda-de-Água et al. 2012). Naturally, to extrapolate the species abundance distributions several assumptions need to be met, in particular, it is implicit that the extrapolation is being performed to a habitat that is not too dissimilar from the habitat where the data were collected. However, instead of dwelling into technical details, I prefer to emphasise the importance of having observed what seems to be a general pattern relating the moments with area size. In fact, the linear behaviour of the moments observed in Fig. 5.3 for tropical tree species was also observed for arthropods from the Azorean archipelago (Borda-de-Água et al. 2017). This observation suggests that the scaling properties of the moments of the species abundance distributions may be a general property for several taxa and, that being the case, there is the prospect that this is a biodiversity pattern. Of course, more studies are required to assert the generality of this observation.

5.5 Final Remarks

The existence of unchanging properties is not given much weight by most statisticians. But they are beloved of physicists and mathematicians, like myself, who call them invariances and are happiest with models that present an attractive invariance property (Mandelbrot 1999).

I do not think it is fair to say that biologists fit the above quote (or statisticians, for that matter). After all, biology has one of the great examples of generalizations in science: Darwin and Wallace's theory of evolution by natural selection. However, I personally find easy to marvel over the diversity of species, and study diversity for its own sake, without looking for the underlying patterns or processes. As Lawton (1999) put it, there is "an almost suicidal tendency for many ecologists to celebrate complexity and detail at the expense of bold, first-order phenomena." I also agree with Lawton (1996) when he stated "[w]ithout bold, regular patterns in nature, ecologists do not have anything interesting to explain." However, it is my impression that often patterns, or attempts to identify them, are not given their due importance (see also Lawton 1992). For instance, we often hear that patterns are important but explaining the underlying mechanisms is what really matters. I am sympathetic with this view; in fact, it merely expresses natural curiosity and the desire to have a deeper understanding of the observed phenomena. However, patterns may emerge from a myriad of causes and have several equally valid explanations. Often, all these causes translate into a simple formula, like the species-area relationship, that combines the action of multiple inextricable causes. These causes occur at different

levels of organization in the community, whose effects we can only hope to describe (at least at the moment) from an upper (macro) level of description, and by ignoring the subtle (micro) details occurring at the lower levels.

The existence of theories at different levels of complexity is common in other fields, such as physics, as it is illustrated by thermodynamics and statistical mechanics. The former deals only with macroscopic variables, such as pressure, temperature and volume, while the latter explicitly acknowledges the existence of atoms and tries to derive the laws of thermodynamics from considerations of the statistical properties arriving from a large number of particles (e.g. Reif 1983). For instance, Boyle's law merely states that the product of the pressure and volume of a gas, at a given temperature and (low) density, is constant. This law was obtained based solely on experimental observations, and in itself did not provide any explanation for why that should be the case. Later on, the kinetic theory of ideal gases provided an explanation based on the idealization of a gas as a set of particles with specific (idealized) properties (e.g. Resnick et al. 2001). However, this new development did not remove the practical importance of Boyle's law, but it helped understand its underlying mechanisms and, importantly, its limitations. From a historical perspective we can now realize that having ignored Boyle's law, because it lacked an underlying explanation, would have probably been rather detrimental by hindering a pattern and, hence, the motivation to develop the kinetic theory of gases, and could have delayed the development of practical applications. Furthermore, although we may have the mechanisms that connect the different scales from the microscopic (statistical mechanics) to the macroscopic level (thermodynamics), in some applications researchers and engineers may operate solely within the realm of thermodynamics without need to resort to a more complicated description based on statistical mechanics.

I would like to reiterate with another example the importance of being practical, that is, using what has been firmly experimentally established even if there is not a deeper knowledge of the concerned phenomena. The development of the electromagnetic theory may be the epitome of this approach (e.g. Kraus 1984). Indeed, Maxwell's equations, that still provide the theoretical foundations for electromagnetism, were introduced in the second half of nineteenth century when there was not even the concept of the electron. Still, relevant technological developments in electrical engineering, such as those by Edison and Tesla on the production and transmission of DC and AC currents, were largely independent of the developments in physics that led to the discovery of the electron (for an interesting account of the developing of electrical engineering see Bodanis (2006) or Meyer (1971)). Physicists did not stop at Maxwell's equation and further discoveries on more basic aspects of the structure of matter led to the quantum theory that now provides a model for how electric currents operate. But notice that these latter achievements in physics were often obtained thanks to the parallel developments in electrical engineering that experimentalists used to construct their apparatus. Interestingly, and as a final note, the difference between the models first idealized by physicists and engineers and the physical reality that was later uncovered led to a peculiar convention still in use today. Modelling the electric current as due to the displacement of electrons with their negative charge within a

metal was not something that the first physicists and engineers knew, therefore it is no wonder that current was modelled as a fluid moving from the positive to the negative potentials, which is a perfectly natural model if one thinks of the electric current as the flow of a liquid, such as water, that moves from regions of higher to lower potentials. The convention of the electric current flowing from the positive to the negative potentials is the one still in use, because from a practical perspective it does not really matter, but, I suspect, it is unlikely to have been adopted had the researchers been aware of the negative charge of the electrons.

The important point is: we should not think less of a science because it lacks at present a deeper knowledge of its established patterns, nor shall we ignore these patterns because we do not have a clear understanding of their mechanisms. Ignoring, as a first approximation, the details of all ecological interactions was our approach to the study of species abundance distributions. In fact, we did not dwell into the explanations of the patterns observed, although in some cases they may have a simple interpretation in terms of dispersal ability or habitat diversity. Instead, we focused on strategies to obtain the patterns, and the advantages that may result from their identification; for instance, the possibility of forecasting species abundance distributions to hitherto unsampled areas.

Finally, our approach may have seemed unambitious. The reader did not find explanations or attempts to develop explanatory theories. Instead, I discussed only patterns that arose from our studies. This is because I think that patterns are the building blocks of the natural sciences and, as such, I believe that revealing patterns is a first step towards developing or testing theories, as in the previous examples from physics. The analysis of the scaling properties of the species abundance distribution described in this chapter fits in this general scheme, by suggesting a new biodiversity pattern associated with the scaling properties of the moments of species abundance distributions. In this regard two consequences of having detected a scaling pattern are important. First, and from a theoretical perspective, having detected a scaling pattern can be used as a benchmark criterion for evaluating the performance of the models that attempt to recreate patterns of relative species abundance. Second, and from a practical perspective, the pattern associated with the moments can be used to forecast species abundance distributions for areas that are too large to be sampled with our present technology; with obvious applications whenever the knowledge of the species abundance is required, such as in conservation studies. In summary, uncovering another pattern is important because enable us to take action in situations that cannot be postponed, even if the “microscopic” details are not fully understood. Such approach has worked well in physics and engineering, as the examples above illustrated; it remains to be seen if it works equally well in ecology and its practical applications.

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