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Biodiversity in a Rapidly Changing World: How to Manage and Use Information?

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1. Introduction

Biodiversity science has been evolving quickly and moved from a focus on systematics and taxonomy in the 1970–80s, to a more dynamic view of biodiversity's role in ecosystem functioning throughout the 1990s. The early 2000s have placed biodiversity within the context of ecosystem services and human well-being, and some efforts are currently focusing on putting this concept into practice, and on valuing and mapping ecosystem services in order to shed light on economic and environmental consequences of decisions (Larigauderie and Mooney, 2010a).

Ecosystem services are defined as the benefits that humans obtain from ecosystems (Seppelt et al., 2011). The Millennium Ecosystem Assessment (MA, 2005) contributed substantially to pose the ecosystem services concept as a policy tool to achieve the sustainable use of natural resources bringing a broad research approach, where ecological, economic and institutional perspectives are integrated to produce insights into human impacts on ecosystems and the welfare effects of management policies.

In December 2010, the United Nations Environment Programme (UNEP) was asked to convene a meeting to determine modalities and institutional arrangements of a new assessment body to track causes and consequences of anthropogenic ecosystem change (Perrings et al., 2011). This was an important step to the foundation of the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES) that works closely with UNESCO, FAO, UNDP and other relevant organizations (Larigauderie and Mooney, 2010b). The establishment of IPBES provides an important link with international policy, proposing a relationship between key scientific organizations, environmental policy bodies, and research funding organizations, which is a critical feature to address both scientific capacity and the policy relevance of research aiming to build capacity for and strengthen the use of science in policy making.

As pointed out by Mooney et al. (2009), the capacity of ecosystems to deliver essential services to society is already under stress and it is urgent to track the changing status of ecosystems, deepen the understanding of the biological underpinnings for ecosystem service delivery and develop new tools and techniques for maintaining and restoring resilient biological and social systems. Additionally, solving problems posed by global change requires coordinated international research, and as much attention to social science as it does to natural science (Carpenter et al. 2009).

Pollination is considered as a key element of ecosystem services (Daily, 1997). Ollerton et al. (2011) estimated that the proportion of animal-pollinated species is near 78% in temperate-zone communities and 94% in tropical communities and that the global number and proportion of animal pollinated angiosperms is 308 006, which means 87.5% of the estimated species-level diversity of flowering plants.

The decline of pollinators has received attention since the 1990 decade (Buchmann e Nabhan, 1996; Kearnes et al., 1998). Recently, multiple drivers were suggested as the main causes to this decline (Schweiger et al., 2010; Potts et al., 2010) such as loss and fragmentation of habitat, aggressive agricultural practices, pathogens, invasive species and climate changes.

In order to achieve a better understanding about pollinator species threats it is necessary new research approaches, especially considering the necessity to build useful public policies to protect them. Here, we discuss new approaches to research on pollinators, especially bees, based mostly on Information Technology tools, such as, Biodiversity Databases, DNA Barcode, Morphometric Analysis and Species Distribution Modeling. At the end, a study case is presented, considering some Brazilian bee species and the potential impact of climate change on their distribution.

2. Digitization and sharing of biological collection data

According to Chapman (2009) the Earth's biodiversity is estimated to comprise approximately 11.3 million species, from which less than 2 million have been formally described by science. These figures reveal the limited knowledge we have which is a key issue for the preservation and sustainable use of biodiversity and ecosystem services. In order to fill that gap more field data is necessary to discover and map the biodiversity before it is gone. Nonetheless a lot can be done with the existing data, if it becomes more available and if other techniques are applied to analyze the data.

Traditionally biodiversity primary data are hosted in biological collections distributed around the world. They vary broadly in relation to size and organization, ranging from large, structured, well-documented and maintained museum collections to small sets of specimens kept by individual researchers with limited resources. Both data sources are important as they may cover different gaps – taxonomic and geographic - in our quest to know life on Earth.

The most traditional users of biological collections have been taxonomists and systematists that use them for identifying, naming and classifying species, for studying the diversity of species and the relationships among them through time (Baird, 2010). However, while these studies are essential for the development of other disciplines, such as ecology, biological collections are also essential data sources to help answer questions that interest and may involve many more individuals and knowledge areas including basic biology, human economics, and public health.

Typically they help address questions on natural resource inventories, on the occurrence and distribution of species over space and time; on the reasons for changes that may have occurred; the effect of environmental change – including climate change - on biodiversity (Scoble, 2010). This applies to native (wild) species, to economically important species, to infectious disease vectors, and to invasive species for which distribution prediction can be very helpful.

Despite the broad use already in place, biological collection data still has a great potential to be used in research, on natural and agricultural resources management, on education and on sustainability science (Scoble, 2010).

A broader, more open and easier access to specimen data is vital to distribute information and in turn create knowledge (Canhos et al., 1994; Baird, 2010). However for this to become effective it is necessary to digitize data and make it available on the web. Only then we will be able to make plain use of the wealth of data and information which is hardly accessible in many cases in collections throughout the world and which, in many cases, only integrated can provide a better picture of a species scenario.

The digitization of collection data is in itself a challenge. It implies an important effort in terms of cost and time, which sometimes competes with other demands on those who digitize. The cost-effectiveness of data digitization is not easy to prove, especially when resources are scarce, although its scientific value can be agreed upon. In cases where an economically important question can directly benefit from the data, this can be less of a problem. Since both volume and quality of data are essential, digitization in a larger scale demands the effort to be prioritized, focused and sustained, according to Scoble (2010). The author also mentions the difference in digitization efforts that is required for different taxa, such as plants and insects, as a result of the methods used for mounting the specimens and the labels that contain the data to be digitized.

Currently biological data digitization is a global effort which is led by institutions such as GBIF and TDWG. The Global Biodiversity Information Facility (GBIF, www.gbif.org) was created in 2001 after a recommendation from a working group of the Megascience Forum of the Organization for Economic Cooperation and Development (OECD), and is open to participation of any country or international organization that agrees with its purpose of making scientific biodiversity information freely available. Its three core services and products are: "1. an information infrastructure – an Internet-based index of a globally distributed network of interoperable databases that contain primary biodiversity data; 2- Community-developed tools, standards and protocols – the tools data providers need to format and share their data; and 3 - Capacity-building – the training, access to international experts and mentoring programs that national and regional institutions need to become part of a decentralized network of biodiversity information facilities". Besides developing tools to be used by itself and by others, such as a data portal, GBIF provides access to more than 276 million occurrence registers (including specimens and observations) integrating in a single access point data of data providers from all over the world.

Other regional and national initiatives have collaborated and participated actively on the global effort towards digitizing and standardizing biological data: in Europe (ENHSIN – European Natural History Specimen Information Network, and EDIT - European Distributed Institute of Taxonomy), in America (IABIN – InterAmerican Biodiversity Information Network, with data from many countries in the continent – www.iabin.net).

The Biodiversity Information Standards (TDWG – www.tdwg.org), also known as the Taxonomic Databases Working Group, was originally formed to establish international collaboration among biological database projects. It now focuses on the development of standards for the exchange of biological data, having as mission also the promotion of the standards. Maybe the most important existing standard is Darwin Core (DwC), a standard for exchange of biological information. It is primarily based on taxa and their occurrence in nature as documented by observations, specimens, and samples, and related information. Other important standard is a protocol for data exchange, TAPIR - TDWG Access Protocol for Information Retrieval (www.tdwg.org/standards), which allows data to be exchanged among different systems, using agreed upon standards, such as DwC.

Currently one trend within the community of biodiversity informatics is to develop new standards for other contents, expanding from the current specimen/observation focus to other aspects of biodiversity, such as genomic data, interaction data (Saraiva et al., 2009) and species data, and multimedia data, such as images. The new contents will broaden the scope of the data networks and offer new possibilities for data analysis hopefully allowing address issues that are even closer to societal needs, cross-cutting different disciplines.

Specimen and observation data are fundamental to develop distribution models using ecological niche concepts. Molecular data and images are key to identify a specimen and to study the relationship between individuals and populations.

3. DNA barcode

One of the biggest problems faced today by researcher is the lack of specialized personnel to identify biodiversity. In times of a rapidly changing world and fast loss of habitats and biodiversity, it is almost impossible to measure the existing species in the ecosystems. There is a lack of identification keys and genera revisions. The taxonomists are few and normally have more complexes problems to focus the simple species identification for the general public or to scientists from other science areas. The development of alternative tools to assess biodiversity other than traditional taxonomy is an urgent need.

At this point, the astonishing development of molecular biology in the last years has indicated new alternatives that can be used to identify species. Since the final of the last century, mitochondrial DNA (mtDNA) has been used as a very interesting and powerful alternative tool. This molecule has an enormous potential due to extremely peculiar and unique characteristics, like being a small circular genome, with high evolutionary rates but well conserved in animals (Arias et al., 2003). In neotropical stingless bees, it has been largely used in populational studies and in the evaluation of genetic diversity (Francisco et al., 2001; 2008; Brito & Arias, 2005; May-Itzá et al., 2010).

Although very controversial, the use of this molecule to identify species was proposed in 2003. Based on the principle that differences on the sequence of the genes are greater between species than within species, the proposition consists in sequencing approximately 650 base pair from the beginning of the Cytochrome Oxidase I (CO-I) gene and comparing it among the species (Herbert et al., 2003). According to recent revisions, the studies show the efficiency of these genic regions to discriminate species and it is working well in the vast majority of the animal cases studied until that moment (more than 95%) (Vogler and Monaghan, 2007; Waugh, 2007).

In fact, the use of a mtDNA sequence to identify cryptic species is constantly reported in literature. However, the standardization of the procedures and the establishment of some guidelines are the novelty in the DNA barcode proposition (Brown et al., 1999; Mitchell and Samways, 2005). Briefly, the following sequence is proposed in this procedure:

- the standardization of the region to be used;
- the possibility of an operation to be largely used, since the sequencing methodologies are becoming more and more accessible;
- the obligatory deposition of vouchers in entomological collections, in order to facilitate future studies of combined morphological + molecular studies;

- an accurate organization of large data bank available to the general public at the CBOL (Consortium for the Barcode of Life) website (Mitchell, 2008).

In bees, some studies are corroborating the effectiveness of the technique in species identification. The complete bee fauna of a taxonomically well resolved region was tested and the 150 species were correctly identified. Together with these results, they also identified some cryptic species and joined individuals from different sexes in the same species. In this last case, most of these species description was based in individuals from only one gender (Sheffield et al., 2009).

Another example is the use this approach, combined with traditional morphological analysis, in a study of a taxonomically extremely difficult group of bees, the subgenus *Dialictus* (family Halictidae; genus *Lasioglossum*). In this case, DNA barcoding proved essential for the delimitation of numerous species that were morphologically almost indistinguishable. The main conclusion of these studies is that DNA barcoding is efficient at the detection of cryptic species, associating the sexes of dimorphic species, associating the castes of species with strong queen-worker dimorphism and as a generally useful tool for basic identification (Gibbs, 2009). (For a revision of successful cases see Packer et al., 2009).

A global campaign to barcode the bees of the world has been initiated (see the website at: www.bee-bol.org).

4. Morphometric analysis

The first attempts to classify bee subspecies of *Apis mellifera* was based mainly in differences in color and body size. However, since there is a great superimposition in these parameters, most of the classification systems based in these characteristics failed in correctly identify the individuals (Ruttner, 1988). In 1940, Goetze proposed a large number of measures, to be taken from several parts of the bee body in order to better differentiate the geographical ecotypes present all over its wide geographical distribution that encompasses Africa, Europe and parts of Asia.

However, all the analysis used until the moment were based in uni-variate statistics, which takes into consideration only one measure at a time and the range of the measures often overlap and turn more difficult to achieve a precise identification. It was only after the works of DuPraw (1964, 1965a; b) that the usage of multivariate statistics was proposed and, with help of Principal Component Analysis and Discriminant Analysis that the identifications became more precise. An important advance is also proposed in this series of works, where DuPraw (1965a) indicated the use of measures that are independent of size, like angles between vein junctions in the wings, avoiding the environmental effects, like food availability, parasites and others.

After these propositions and a series of small studies, it is published a guide to discriminate the subspecies of *A. mellifera* (Ruttner et al., 1978). In this work, the authors propose approximately 40 measures to be taken from several parts of at least 20 bees per colony to achieve a good confidence in the classification. It was based on morphometric results that the existence of evolutionary branches in *A. mellifera* (Ruttner et al., 1978) that were later confirmed by mitochondrial DNA (Franck et al., 2000), microsatellites (Estoup et al., 1995) and SNPs (Withfield et al., 2006). In spite of being very informative and confident, this kind of analysis is often very time consuming.

More recently, allied to the development of computational methods, the analysis became faster and some of them completely automated as ABIS (Automated Bee Identification

System) (Schröder et al., 2001). The first step in this process was the construction of a semi-automated system based on features extracted from the images of the forewings, in which the user had to plot landmarks in the wing vein intersections (Schröder et al., 1995). A full automated version of the software was developed with some modifications, like the automated identification of the landmarks and the implementation of a non-linear discriminant analysis, which improved the identification rates of the individuals (Schröder et al., 2001). In this process, ABIS extract more than 300 features related to create a "fingerprint" of each species. This pattern is stored in a databank and each new wing loaded in the software is compared to the databank in order to identify the species. It was very efficient in discriminating the European species of the genus *Andrena, Colletes* and *Bombus* (Schröder et al., 2001), Africanized honey bees (Drauschke et al., 2007; Francoy et al., 2008) and also *Euglossa* species (Francoy et al., unpublished data).

Another morphometric technique that is presenting very interesting results concerning shape variation is geometric morphometrics (Bookstein, 1991). While studies with standard morphometrics analyze shape variation using co-variation of pairs of linear measures, geometric morphometrics is based on the variation of the relative positions of the landmarks and therefore, is able to describe more clearly any changes in shape and also to graphically reconstruct these differences (for a detailed description of the method, see Rohlf and Marcus, 1993).

The first attempt to use this methodology in the patterns of wing venation to differentiate bee groups was done in Africanized honey bees and in the subspecies that formed this hybrid. The relative warps analysis of the landmark positions in the wing was able to correctly classify 85% of the individuals in the correct group and the higher error rates were found in two subspecies that belong to the same evolutionary branch (Francoy et al., 2008). It is important to state that these bees are not easily distinguishable even for the well established standard morphometric methods. Another interesting result from this work is the possibility of correctly identify 99.2% of the Africanized sample, which is always a concern in areas newly occupied for these bees. Additionally, the usage of these methods allows a quicker identification than the traditional methods, once it can be done in a few minutes while the identification through standard morphometrics is more time consuming, around a few hours per colony. Still in honey bees, it was already demonstrated that other European subspecies (Tofilsky, 2008) can be identified using this methodology as well as different species from the genus *Apis* (Rattanawannee et al., 2010).

In stingless bees, the first work using this methodology demonstrated the power of the technique to identify cryptic biodiversity (Francisco et al., 2008). Colonies from two distinct populations of *Plebeia remota* kept in the same apiary for more than 10 years do not presented any gene flow. Until that moment, the populations were considered as the same species. This result was reinforced by other molecular markers, like mitochondrial DNA and cuticular hydrocarbons, which pointed in the same direction of the morphological data. It was also very informative to discriminate species with very little or no external morphological differences, like species from the genus *Eubazus* (Villemant et al., 2007), *Bombus* (Aytekin et al., 2007) and *Euglossa* (Francoy et al., unpublished results). Other works also indicated the efficiency of the technique in stingless bees. When working with bees from the same genus, studies showed 93.4% of success in the discrimination of 6 species of *Plebeia* (Francoy et al., unpublished results). It was also demonstrated the discrimination of sub-populations of *Nannotrigona testaceicornis* (Mendes et al., 2007), differences between the wings of males and workers in stingless bees (Francoy et al., 2009) and in honey bees

(Rattanawannee et al., 2010), and also the efficiency in discriminating the species when large datasets are used at the same time, as the correct identification of 93% of the individuals into the respective group for 34 different species of stingless bees (Francoy et al., unpublished results).

Together with the efficiency in identifying species based only in the patterns of wing venation, perhaps one of the most important applications of this kind of analysis is the possibility of mapping intra-specific variability within a species and consequently, tracking the geographical origin of samples. It allows the researchers to evaluate this variability in several geographic scales. The stingless bee *Melipona beecheii* has a geographical distribution that ranges from Mexico to Costa Rica, where it inhabits the most varied environments. An analysis of the patterns of wing venation of bees from Mexico, Nicaragua, El Salvador, Guatemala and Costa Rica indicated marked differences among the populations, correctly re-assigning 87% of the individuals to the respective group (Francoy et al., 2011). It was also demonstrated that it is valid for other examples, like bees from the genus *Peponapis* in North America (Bischoff et al., 2009), *Apis florea* (Kandemir et al., 2009) and *Apis mellifera* populations (Özkhan and Kandemir, 2010) and *Nannotrigona testaceicornis* sub-populations (Mendes et al., 2007).

Another geometric approach that is very promising is the outline of wing cells. It has already been demonstrated that features extracted from a single wing cell can discriminate *Apis mellifera* subspecies (Francoy et al., 2006). Based on this principle, it was proposed that people already knew how to manage colonies to transportation around 3000 years ago. In an archaeological excavation in the middle of the Jordan valley in Northern Israel it was found what appears to be a well-organized apiary. Two of the hives contained charred honey comb remains with many honey bee body remains. Although most remains were damaged, two wings with clear cells were of sufficient quality to perform morphometric measurements comparable to those available for present-day subspecies over the entire distribution range of *A. mellifera*. However, as only small parts were available, only feature extracted from single wing cells were compared. It was determined that the wings belonged to the subspecies currently living in parts of Turkey, instead of the one living in Israel. Since the climatic data indicated no extreme climate and vegetation change in the last 3000 years, the authors concluded that the beekeepers already knew how to transport colonies across long distances and kept importing bees from Turkey because of the more suitable behaviour of the *A. m. anatoliaca* bees rather than the original *A. m. siriaca* (Bloch et al., 2010).

Despite effective species discrimination from application of landmark or outline-based methods used independently, the combined results of these two methods is only now being investigated. In an exploratory study, five species of *Euglossa* were analyzed using landmark and outline based methods in order to compare the efficiency of both. Regarding the landmark analysis, 18 landmarks were used and achieved 84% of correct identifications. In the outline based analysis, a complete exploratory characterization of all wing cells was made and the wing cells that better discriminated the five species correctly re-assigned 77% of the individuals to the respective group. However, when using the features extracted in both analysis in a combined matrix, the correct classification rates achieved 91% (Francoy et al., unpublished results).

In order to improve the process and to make the analysis faster and more precise, new tools are being developed for a complete automation of the system like algorithms to automatic identification of the landmarks (Bueno, 2010) and new processes of features extraction that make the entire process more reliable and efficient (Buani, 2010). The automated identification system uses two computational algorithms to complete the recognition and classification of bee species. The first algorithm, named kNN (k-Nearest Neighbour), is used to select and extract morphometric features related to the distances between the landmarks plotted in the wing veins intersections from the pictures. The second algorithm, named FkNN (Fuzzy kNN) implements a variation of the Fuzzy Logic for species classification. For an optimized result, the features selection involves a statistical analysis which evaluates the better landmarks for the classification process and only the most informative are used in the species characterization in the Fuzzy Logic (Buani, 2010).

The morphometric analysis of forewing is a very powerful tool to describe species variation and also to identify species based on landmark and outline morphometric methods. Allied to that, morphometric analysis is a fast, inexpensive and informative method to be used in the characterization of species and its variation.

5. Modeling species distribution

Innovative techniques are urgent to understand species geographic distribution, especially considering the impact of global changes. A computation technique was developed to model species distribution. This tool received different names, which will be considered here as synonymous, e. g., species distribution modeling, ecological niche modeling, and recently, habitat suitability modeling.

Species distribution modeling (SDM) can combine georeferenced occurrence data points (latitude x longitude) with different data sets that characterize the environment where the focal species occur. These sets are combined and analyzed aiming to build a representation of ecological requirements of the focal species or, in other words, a representation of their ecological niche. The final result can be projected in the geographic space, indicating the areas that are suitable to the focal species and can be potentially occupied by it.

Usually, these data sets are comprised by abiotic features, such as temperature, precipitation and altitude, which describe the environment where the species occur. But SDM can include data about occurrences of interacting species (biotic features) that are also responsible for shaping geographical distribution, such as other species involved with the focal species on mutualism, competition or parasitism. And finally, it can include data about the species dispersal capacities, in order to estimate their capability of occupying new environments. These features are the base of modelling and its conceptual framework can be found mainly in Soberon (2010) (but also see Elith and Leathwick, 2009). Nowadays, abiotic, biotic and dispersion capacities can be integrated in BIOMOD (Thuiller, 2003) a computational system developed to R (The R Foundation for Statistical Computing) that can be used to model species distribution.

Considering the relationship between bees and plants, interactions are key aspects to include in SDM and have been considered its main challenge (Elith and Leathwick, 2009). Interactions are also of special concern when considering scenarios of global change (Schweiger et al., 2010). Mismatches between the correspondences of geographic areas of obligate interacting species due to climate change were already suggested (Stralberg et al., 2009). Besides, the relationship between pollinators and their host plants includes a temporal correspondence, in which plants synchronize the flowering period with their pollinators' activity, and this correspondence can also be changed due to climate changes (Hulme, 2011)

Interacting species are closely related to their geographic areas of distribution (Giannini et al., 2010; Giannini et al., 2011). For example, when characterizing the flower visitors' composition at the whole range of their host plant distribution, Espíndola et al. (2011) found geographically structured variability of the prevailing visitor. They suggested that climate is driving the specificity of this interaction, by potentially affecting the phenology of one or both interacting species, providing an example of the direct effect that the abiotic environment can have on the plant–insect interaction.

This is in accordance with Thompson (2005) who suggested a geographic mosaic theory of coevolution stating that interspecific interactions commonly exhibit geographic selection mosaics and trait remixing among populations. From this view, the form and trajectory of coevolutionary selection vary across landscapes. In addition, gene flow and metapopulation dynamics continually shift traits among populations, thereby continually altering the structure of local selection.

Laine (2009) reviewed 29 studies that support this theory, concluding that natural coevolutionary selection produces genetic differentiation among populations and may be an important mechanism promoting diversity in nature given how different types of interactions show divergence, and how variable the causes promoting such divergence are. One of the remarkable results of this review is the spatial scale over which it is possible to find divergent coevolutionary trajectories. Variation was detected in populations separated by some hundreds of kilometers highlighting the potential for the environment to create geographically variable selection trajectories. For example, analyzing a rare and endangered solitary bee (*Colletes floralis*), Davis et al. (2010) found an extremely high genetic differentiation among populations at the extreme edges of the species range. Also, Pellissier et al. (2010) analyzed how the traits of different pollination syndromes influence the distributions of plant species in interaction with pollinators. They used a combination of environmental descriptors and found a potential effect of the pollinator on the spatial distribution of plant species. Also, analyses of a system involving the Japanese camellia and its obligate seed predator, found that the sizes of the plant defensive apparatus (pericarp thickness) and the weevil offensive apparatus (rostrum length) clearly correlated with each other across geographically structured populations (Toju and Sota, 2006).

Therefore, intermingled with environmental (abiotic) and interaction (biotic) features, geographical distribution is also related to species evolutionary trends, determining patterns of genetic diversity and trait variation across space. New approaches are necessary to analyze the importance of these complex features. Recently, Pavoine et al. (2011) suggested a framework based on a mathematical method of ordination to analyze phylogeny, traits, abiotic variables and space in a plant community. Another example can be found in Diniz Filho et al. (2009) proposing an integrated framework to study spatial patterns in genetic diversity within local populations, coupling genetic data, SDM and landscape genetics. Also, Kuparinen and Schurr (2007) developed a framework to link the spatio-temporal dynamics of plant populations and genotypes, and a similar approach was suggested for modeling the variation of geographical distribution of animals in a climate change scenario (Kearney and Porter, 2009).

To analyze the multiple drivers shaping the species geographical distribution is a challenge that will be met by integrating different fields of research. In order to attain the objective of predicting impacts on species distribution due to global changes, it is necessary to consider that species are genetically heterogeneous entities and, in order to protect them, it is necessary to protect its genetic diversity. As species diversity might act as insurance against environmental changes, genetic diversity should also have the potential to protect communities from environmental variability (Lavergne et al., 2010). Taubmann et al. (2011)

analyzed the genetic population structure of the endangered mayfly (*Ameletus inopinatus*) in its European range genotyping hundreds of individuals from different populations. They found variations in genetic diversity and also projected the distribution of species through SDM for the year 2080 finding some areas of regional habitat loss. By relating these range shifts to the population genetic results, they were able to identify conservation units that, if preserved, would maintain high levels of the present-day genetic diversity and continue to provide long-term suitable habitat under future climate change scenarios.

Most ecological forecasting of future species ranges is based on models that generally ignore evolution and assume that the mechanistic relationship between species abundance and environmental characteristics is unchanged at the timescale of the projection (Lavergne et al., 2010). But there is accumulating evidence that evolution can proceed fast (Hairston et al., 2005) and genetic variation for adaptation - and more generally for traits defining species ecological niches - is common both between and within populations, suggesting a high level of local adaptation to climate at a fine scale (Pearman et al., 2008). Adaptation and dispersal are often presented as alternative mechanisms whereby a population can respond to changing environmental conditions playing a crucial role in tracking favorable environmental conditions through space (Pease et al., 1989). Thus migration of different genotypes could have important consequences for the evolution of geographical distribution limits (Davis et al., 2005).

Addressing the main aspects discussed here about distribution of species, it was suggested that the new trends on SDM, regarding the impacts of global changes on species diversity, are niche evolution, phylogeographic and phylogenetic research (Zimmermann et al., 2010). As pointed out by Gilman et al. (2010), the key question is not the effects resulting from global change on individual species, but the stability of the system as a whole. Integrated fields of research will allow novel analysis of both historical and contemporary drivers of species ranges, and will likely provide new possibilities to understand present day species distributions and project them to the future.

Species distribution modeling presents some steps and requires expertise knowledge about the focal species and also ecology, geography and clime. The following summarized steps are suggested.

5.1 Occurrence points

It is necessary to prepare a database with presence and absence points of the focal species. This step can include the georeferencing of points (latitude x longitude) and the exclusion of doubtful or inaccurate information. Occurrence data can be obtained from biodiversity data providers such as Global Biodiversity Information Facility (GBIF) and The Inter-American Biodiversity Information Network (IABIN). Also, to search occurrences in the literature or perform new local surveys can provide additional information.

5.2 Environmental data sets

This step aims to obtain the environmental layers to be used. Usually, they must be on 'raster' format, in which a matrix of cells is used to build the image. Generally, a Geographic Information System (GIS) software is necessary, such as ArcGIS (ESRI Inc.) or DIVA GIS (LizardTech, Inc. and University of California) to prepare them for SDM. Climate data sets can be found in the WordClim (Hijmans et al., 2005) and in the International Center of Tropical Agriculture (CIAT) websites. Categorical data sets can be found in World Wild Life

Fund (WWF) (Terrestrial Ecorregion - Olson et al., 2001) and Global Land Cover database (Bicheron et al., 2008).

5.3 Algorithm

Algorithms are finite sequences of instructions for calculating a function. There are lots of algorithms for SDM. Two important ones are Maxent (Maximum Entropy - Phillips et al., 2006) and Genetic Algorithm for Rule set Production (GARP - Stockwell and Peters, 1999) that have been successfully applied to small data sets with presence-only occurrence points (Wisz et al., 2008). GARP and other algorithms can be found in openModeller (Santana et al., 2008), a computational system to perform SDM. Another system available to SDM is BIOMOD (Biodiversity Modelling – Thuiller, 2003) developed to R (The R Foundation for Statistical Computing) that presents nine algorithms.

5.4 Model evaluation

Generating an independent data set is necessary to evaluate the model accuracy. This data set can be obtained through new surveys on supplementary areas or dividing the original data set in two. One of the data sets will be used to generate the models (train data) and the other to test it (test data). Usually, it is suggested to divide the original data set randomly and without reposition in 70% of the data to generate the model, and 30% to test it (Fielding and Bell, 1997; Hirzel and Guisan, 2002). It is also possible to divide the data considering their spatial pattern (Peterson et al., 2008). The area under the receiver operating characteristic curve (AUC) is usually used to evaluate the models. Values of AUC range from 0.5 for models with no predictive ability, to 1.0 for models giving perfect predictions (Swets, 1988). Some authors discussed the use of AUC to evaluate the model accuracy (Peterson et al., 2008) but nowadays, it is the most important method to this end (but see other alternatives on Thuiller, 2003). It is also possible to check the model accuracy conducting new surveys on the areas suggested as potential areas of occurrence by modelling.

6. Example of tools' integration using pollinators

Preliminary analyses regarding some Brazilian pollinators and species distribution modeling were recently done. We chose some species of *Melipona* and *Centris* bees (Apidae; Hymenoptera) to forecast the impact of future climate changes (Saraiva et al., in press; Giannini et al., in press).

Melipona genus is comprised by eusocial bees that are mainly associated to Atlantic Forest, an endangered moist forest of Brazil. This genus was suggested as an important pollinator to this ecosystem by Ramalho (2004). On the other hand, *Centris* is comprised by solitary species that are especially important to plants that produce floral oil, on which they depend to build their nest and feed their offspring (Simpson 1989).

The analyzed species of *Melipona* were also reported as pollinators of some fruit crops, as açai (*Euterpe oleracea*), avocado (*Persea americana*) and guava (*Psidium guajava*) (Castro, 2002; Venturieri *et al.*, 2008). The *Centris* species were reported as pollinators of acerola (*Malphighia punicifolia*), murici (*Byrsonima crassifolia*), cashew (*Anacardium occidentale*) and tamarind (*Tamarindus indica*) (Castro, 2002; Freitas *et al.*, 2002; Vilhena and Augusto, 2007; Rego *et al.*, 2006; Ribeiro *et al.*, 2008; Siqueira, 2010). Recently, Nunes-Silva et al. (2010) also demonstrated the importance of *M. fasciculate* on performing buzz pollination on tomatoes.

Some of these crops are cultivated regionally, and in this case, the loss of native pollinators can cause a potentially higher impact on local economy.

To forecast the future distribution of some species pertaining to these two genera, we used a moderate scenario of climate change to the years 2050 and 2080 and we find an alarming decreasing of potential areas of occurrence to all species. *Melipona* species presented the highest decrease, but *Centris* species presented a remarkable fragmentation on future suitable habitats. For genetic reasons, bees are particularly sensitive to the effects of small population size through the production of sterile males (Zayed and Packer, 2005; Alves *et al.*, 2011). Therefore, small fragmented areas could not be able to maintain viable population.

Nevertheless, some areas were highlighted as possible areas of conservation to these bees, because they are suitable now and will remain like this in the future. These areas can be considered as important areas in a large scale study about pollinators' conservation. Another interesting approach to conserve genetic diversity of these organisms is to associate the genetic variability of the populations with the future distribution maps and check if the populations with larger genetic variability are found in the possible remaining refuge areas. As discussed previously, this genetic variability can be measured by morphometric or molecular methods. The comparison of the current distribution of the genetic variability with the future scenarios for species distribution is of fundamental importance to verify if this variability will be naturally preserved or if other public actions will be necessary to a more effective conservation.

7. Acknowledgment

To FAPESP (04/15801-0), CNPq (575069/2008-2) and Research Center on Biodiversity and Computing (BioComp).

8. References

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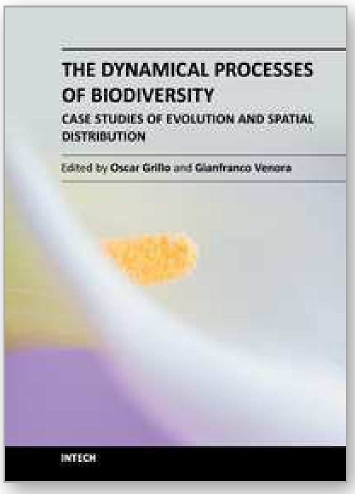

The Dynamical Processes of Biodiversity - Case Studies of Evolution and Spatial Distribution
Edited by PhD. Oscar Grillo

ISBN 978-953-307-772-7
Hard cover, 366 pages
Publisher InTech

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