MARCO ANTÔNIO DE AMORIM PEIXOTO

BIOGEOGRAFIA E CONSERVAÇÃO DA ANUROFAUNA NO COMPLEXO SERRANO DA MANTIQUEIRA, SUDESTE DO BRASIL

Dissertação apresentada à Universidade Federal de Viçosa como parte das exigências do Programa de Pós Graduação em Biologia Animal, para obtenção do título de *Magister Scientiae*.

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Aprovada em: 23 de Março de 2016

Ubirajara de Oliveira

Renato Neves Feio
(Coorientador)

Pedro Seyferth R. Romano
(Orientador)

Ao povo de Santa Constância, que, apesar dos enormes desafios que a vida

lhe impõe, ainda transmite alegria todos os dias!

“Life is for the stubborn and if to drown look for me upstream!"

João Corrêa.

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RESUMO

PEIXOTO, MARCO ANTÔNIO DE AMORIM. M. Sc,. Universidade Federal de Viçosa, Março de 2016. **Biogeografia e conservação da anurofauna no Complexo Serrano da Mantiqueira, Sudeste do Brasil.** Orientador: Pedro S. R. Romano. Coorientador: Renato Neves Feio.

A busca por padrões de distribuição, diversidade e riqueza de espécies são os principais objetivos da Biogeografia. Enquanto que, em uma escala global ou continental, os padrões de distribuição de espécies são bem documentados e conhecidos, o mesmo não se aplica a escalas menores. O Complexo Serrano da Mantiqueira é um grande complexo montanhoso que se ocorre ao sul do estado do Espírito Santo, se estende pelo estado de Minas Gerais e alcança o planalto de Poços de Caldas, no limite entre Minas Gerais e São Paulo, passando ainda pelo estado do Rio de Janeiro na altura do Planalto do Itatiaia. Aqui, nós realizamos o primeiro estudo sobre riqueza e padrões de distribuição biogeográfica da anurofauna do CSM, utilizando a análise de elementos bióticos, em dois bancos de dados: um com todas as espécies, e outro com apenas as espécies endêmicas. Adicionalmente nós discutimos a conservação das áreas de endemismos baseados nas espécies de anuros que compõe as unidades biogeográficas naturais encontradas. Um total de 208 espécies foi registrado para o CSM, sendo que 78 são espécies endêmicas. A região de Santa Tereza foi a mais rica em número de espécies, com 88 espécies. O modelo de vicariância aplicado aos anuros do CSM atendeu a predição de que os anuros não estão homogeneamente distribuídos ao longo do CSM. A análise de elementos bióticos, utilizando todas as espécies que ocorrem na CSM, reconheceu sete áreas de endemismos. Utilizando o banco de dados endêmico também reconhecemos sete elementos bióticos para o CSM. A taxa de perda de habitat para os sete elementos endêmicos alcançou uma média de 64%. Além disso, cinco dos sete elementos endêmicos foram apenas parcialmente cobertos por alguma área de proteção integral. Este foi o primeiro estudo biogeográfico com anuros no CSM. Duas das áreas de endemismos encontradas para anuros já tinham sido reconhecidas também para outros grupos. Dos sete elementos bióticos, cinco deles foram reconhecidos com base em espécies que se encontram em áreas de altitude. Isso se deve principalmente a pequenas regiões estáveis durante os ciclos climáticos do Pleistoceno. Além disso, algumas dessas áreas estão sobre formações rochosas bem distintas do encontrado no CSM, o que levanta questões sobre a existência de relação entre as duas variáveis. Perda de habitat e fragmentação são duas variáveis descritas como a maior ameaça a biodiversidade, mesmo assim altos níveis de perda foram detectados. Nós recomendamos a criação e ampliação de Unidades de conservação em áreas relacionadas aos elementos endêmicos, com o intuito de conservar as unidades biogeográficas naturais encontradas.

ABSTRACT

PEIXOTO, MARCO ANTÔNIO DE AMORIM. M. Sc,. Universidade Federal de Viçosa, March, 2016. **Biogeography and conservation of anurans from Mantiqueira Mountain Range, southeastern Brazil.** Advisor: Pedro S. R. Romano. Co-advisor: Renato Neves Feio.

The search for distribution patterns, diversity and species richness are the mainly goals of the biogeography. In a global or continental scale, the patterns of species distributions are well-know, whereas in a smaller scales is not the same. The Mantiqueira Mountain Range (MMR) is a complex of mountains and occurs in the Espirito Santo State, extends from Minas Gerais State and ended in boundaries of Minas Gerais and São Paulo State, in the region of Poços de Caldas plateau, having a small portion inside the Rio de Janeiro State, in the Itatiaia plateau. Here, we explore, to the first time, the richness and the biogeographical patterns of anurans in the MMR using the biotic element approach. We use two datasets: all species of the MMR and only endemic species. In addition, we discuss about the conservation of areas of endemism based on the species that formed the natural biogeographical units found. A total of 208 species was recorded to the MMR, been 78 endemic species. The hot region was indicated as Santa Teresa region, in the north of Serra da Boa Vista. The vicariance model, apply to the anurans from CSM didn’t reject the prediction of heterogeneous distribution of the anurans through the MMR. The analysis of biotic elements indicated the presence of seven endemism areas based on both, endemic and all species dataset. The habitat loss had an average of 64%, in the seven endemic biotic elements. Moreover, five of the endemic elements were only partially covered by any protected area. This was the first biogeographical study of anurans in the MMR. Two of these seven endemism areas is recognized to others groups. Five endemic elements were formed based on species that are typically from high altitudes. These regions are indicated as stable areas through the Pleistocene cycles, explaining this singular biota. In addition, we speculate the influence of the geomorphological of MMR might have affected anurans evolution and endemism, once that some endemic elements were related with areas with singular geomorphological history. Habitat loss and fragmentation have been described as a major threat to the maintenance of biological diversity in the tropical forests. Therefore, the endemic biotic elements achieved high rates of habitat loss and miss effective protection. Then, we emphasize the importance of creating and increase protected areas covering the regions of these areas of endemism.

1. INTRODUÇÃO GERAL

1.1 Apresentação e contextualização da proposta

Os primeiros trabalhos sobre a distribuição dos táxons indicaram uma distribuição não homogênea da biota sobre a terra (e.g.: Bufon, 1761; von Humboldt, 1806; de Candolle, 1855; Scatler, 1858; Wallace, 1876). Estudos mais recentes (e.g.: Kreft & Jetz, 2013; Morrone, 2014) confirmam tal padrão heterogêneo de distribuição da biota, o que reflete a complexidade sobre processos históricos e limites ecológicos que restringem e explicam a distribuição das espécies. Além disso, padrões gerais de distribuição biogeográfica são identificados. As regiões zoogeográficas propostas por Wallace (1894), por exemplo, ainda são parcialmente reconhecidas atualmente, mesmo após a inclusão de diferentes grupos de organismos e o acúmulo de mais de 100 anos de pesquisas mais abrangentes sobre tais áreas (Kreft & Jetz, 2013). Tal constatação demonstra que em larga escala, os padrões são robustos e bem documentados. Em menor escala, no entanto, os problemas na delimitação de unidades biogeográficas se tornam mais evidentes, devido, principalmente, (1) à falta de simpatria estrita entre espécies co-distribuídas, (2) aos papéis da dispersão e da extinção e (3) aos incompletos conhecimentos taxonômico e sistemático – os chamados déficits Lineano e Wallaceano. (Cracraft, 1994; Morrone, 1994; Hausdorf, 2002; Whittaker et al., 2005).

Em biogeografia, informações básicas são as localidades de ocorrência conhecidas para um determinado conjunto de espécies (Nihei, 2008). A coleta desses dados é o primeiro passo para a inferência sobre a real área de distribuição. Nessa etapa, os museus são de vital importância para resguardar dados de distribuição dos organismos (Holmes et al., 2016). Contudo, informações mais acuradas e precisas sobre os espécimes depositados em coleções nem sempre estão disponíveis. A falta de padronização e, principalmente, as informações imprecisas, dificultam uma busca mais clara sobre as localidades de coleta dos espécimes depositados. Um exemplo é que as principais coleções de anfíbios do Brasil apresentam em seus acervos espécimes coletados no século XVIII e início do século XIX, onde, entre os curadores e coletores, a prática de se manter informações mais precisas sobre a distribuição de organismos não era comum (Chapman, 2005a).

Até recentemente, ferramentas que permitissem a análise conjunta de bancos de dados, principalmente em biogeografia, eram escassos. No entanto, a capacidade de processamento dos computadores e ausência de programas específicos, que eram fatores limitantes para esse tipo de tarefa, não são mais problemas (Kosak et al., 2008). Com o avanço em capacidade de processamento e de precisão na geração de dados, o Sistema de Informação Geográfico (SIG) surgiu como uma alternativa muito difundida pra solucionar esse problema. Assim, análises biogeográficas podem incluir a quantificação precisa de dados secundários, como as coordenadas das localidades de ocorrências e cálculos da área de distribuição das espécies (Hortal et al., 2008), erros de georreferenciamento podem ser mais facilmente identificados e corrigidos (Hijmans et al., 1999; Chapman, 2005a; Chapman, 2005b) e lacunas de conhecimento podem ser descritas (Funk et al., 2005; Oatham & Boodram, 2006; Langhammer et al., 2007). Contudo, dados originais utilizados em um SIG devem ser precisos, pois conjuntos de dados originais contendo erros comprometerão os resultados, gerando o que Silva (1999) denomina de o lixo organizado. Vale ressaltar que muitas das informações disponíveis na literatura são incompletas. É comum, por exemplo, a não especificação do *datum* utilizado em coordenadas disponibilizadas ou até mesmo a liberação de dados incompletos, com tipos de coordenadas geográficas não inteiramente especificados (e.g.: 45° 22’ / 20° 14’).

Um passo posterior à coleta, organização e plotagem das informações é a interpretação dos padrões de distribuição do organismo em estudo. A identificação do padrão de distribuição é a chave para a interpretação dos processos que modulam a distribuição da biota (Nihei, 2008). Como mencionado, embora os padrões observados possam ser complexos, as espécies não estão distribuídas aleatoriamente. Alguns processos, como extinção, dispersão e vicariância, modulam a distribuição dos organismos (Crisci et al., 2003). O estudo biogeográfico busca analisar esses padrões e levantar hipóteses sobre os processos que modularam e modulam a distribuição dos organismos (Nihei, 2008).

O modelo baseado em vicariância (Croizat et al., 1974; Rosen, 1978; Platnick & Nelson, 1978; Nelson & Platnick, 1981; Wiley, 1988; Humphries & Parenti, 1999), postula que uma biota ancestral se fragmenta com o aparecimento de uma barreira. A barreira interrompe o fluxo gênico entre as populações delimitadas por ela e, consequentemente, esse evento de vicariância resulta em especiação alopátrica, originando novas biotas a partir da biota ancestral (Hausdorf, 2002). A análise de elementos bióticos foi proposta como uma maneira de inferir área de endemismo, levando em consideração o processo de vicariância (Hausdorf & Hennig, 2003). O teste do modelo de vicariância sobre uma biota parte do teste de duas predições: (1) a divisão de uma biota ancestral pelo processo de vicariância apresenta como resultado grupos de táxons regionalizados (elementos bióticos) nos quais a distribuição é mais semelhante com os outros táxons presentes no mesmo elemento biótico do que dos táxons presentes em outros elementos bióticos (Hausdorf, 2002; Hausdorf & Hennig, 2003); (2) a segunda predição é que espécies relacionadas filogeneticamente (resultado de especiação alopátrica em diferentes áreas de endemismos) seriam encontradas em elementos bióticos distintos (Hausdorf & Hennig, 2003), ou seja, espécies co-genericas seriam encontradas em diferentes agrupamentos de espécies com distribuição similar.

A definição de área de endemismo é considerada complexa (Nihei, 2008). Entretanto, uma definição bastante aceita indica que uma área de endemismos corresponde a uma região geográfica que compreende a distribuição de dois ou mais táxons monofiléticos (Harold & Moi, 1994). Embora a definição de área de endemismo seja baseada em distribuição das espécies, algumas unidades geomorfológicas ou paleogeográficas (e.g. complexos serranos, ilhas e continentes) são propostas como áreas endêmicas em muitos estudos, sem mesmo analisar o padrão de distribuição das espécies (Hausdorf, 2002). Como um exemplo, a Serra da Mantiqueira é indicada como uma grande área de endemismos de anuros (Cruz & Feio, 2007), porém não há nenhuma análise biogeográfica por trás dessa afirmação.

1.2 Área de estudo

O Complexo Serrano da Mantiqueira (CSM) estende-se desde o estado do Espírito Santo até o estado de São Paulo e atinge cotas altimétricas de 2892 metros no maciço do Caparaó (Gatto et al., 1983). No CSM, predominam os granitos e gnaisses, além de outras rochas metamórficas de grau médio de xistosidade (Benites et al., 2003). Além dos altos índices de endemismos, o CSM também é conhecido como uma importante divisor de águas para rios que abastecem grandes cidades no sudeste do Brasil, como o Rio Piracicaba, Rio Doce, Rio Paraiba do Sul e o Rio Pomba, cujo vale separa o CSM em duas regiões, Mantiqueira setentrional e Mantiqueira meridional (Gatto et al., 1989).

Atualmente a Mata Atlântica é um dos biomas de maior representatividade em número de espécies de anuros e, principalmente, em número de espécies endêmicas (Haddad et al., 2013; Toledo et al., 2014). Com cerca de 530 espécies descritas, abriga mais de 50% das espécies de anuros conhecidas no Brasil (Toledo et al., 2014). Atualmente, essa grande diversidade é explicada por áreas estáveis (refúgios) que se formaram durante os ciclos de glaciação e interglaciação do Pleistoceno (ca. de 21 milhões de anos; Carnaval & Moritz, 2008). Dois grandes refúgios são identificados: um para o estado de Pernambuco e um para o sul da Bahia. Além disso, os autores indicam a existência de um terceiro refúgio, de menor porte, localizado ao sul do Rio Doce, nos limites entre os Estados do Espírito Santo e Rio de Janeiro (Carnaval & Moritz, 2008; Carnaval et al., 2009). Além disso, microrefúgios foram registrados em áreas menores, como regiões montanhosas e também vales, no Sul e no Sudeste do Brasil, durante os ciclos de glaciação (Rull, 2009; Carnaval et al., 2014).

Mesmo como uma alta representatividade de espécies, os números mais expressivos são os que se referem à conservação das espécies animais e vegetais. Com uma cobertura atual de pouco mais de 7% da original (Morelato & Haddad, 2000), a Mata Atlântica ainda carece de estudos básicos de taxonomia, padrões de distribuição de espécies e trabalhos integrativos, que visem à conservação das espécies de uma maneira mais efetiva (Graham et al., 2006).

1.3 Objetivos

Objetivo Geral

Identificar áreas de endemismos no Complexo Serrano da Mantiqueira baseado na distribuição de anuros.

Objetivos específicos

(1) Mapear os padrões de riqueza de anuros no Complexo Serrano da Mantiqueira;

(2) Identificar unidades biogeográficas naturais no CSM baseado na distribuição de anuros;

(3) Testar as predições do modelo de especiação vicariante para os anuros do CSM;

(4) Acessar a conservação dos padrões biogeográficos encontrados e a eficiência do atual sistemas de áreas protegidas.

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Biogeography of the anurans from the Mantiqueira Mountain Range, southeastern Brazil: The importance of highlands maintenance for species conservation

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Introduction

The search for distribution patterns, diversity, and species richness are the main goals of biogeography studies (Morrone, 2009; Lomolino et al., 2009). At global and continental scales, patterns of distribution and species richness were determined by recent studies on species diversity (Olson et al., 2001; Holt et al., 2013; Jenkins et al., 2015; Vilhena & Antonelli, 2015). Similarly, methods have been developed and improved to detect patterns of distribution (e.g.: Morrone, 1994; Szumik et al., 2002; Laffan et al., 2010; Oliveira et al., 2015; Vilhena & Antonelli, 2015). Both sorts of patterns - geographical distribution and species richness - are crucial to detect natural biogeographical unit (Whittaker et al., 2005; Carvalho et al., 2011; Saiz et al., 2013; Guedes et al., 2014). A natural biogeographical units are those that originated by natural processes, such tectonic change, representing the product of these processes, rather than being chosen for other reasons such as utility (Crisci, 2000; Michaux, 2008).

On the other hand, biogeographical studies conducted in smaller levels, like mountain ranges, watersheds or biomes, are not frequent and patterns of distribution are not well-known (Nogueira et al., 2011). Some methods are more frequently adopted for the identification of natural biogeographical units, as the parsimony analysis of endemism (PAE; Rosen, 1988) and endemism analysis (NDM; Szumik et al., 2002) (e.g.: Carmadelli et al., 2012; Carvalho et al., 2013; Prado et al., 2014; Sandoval et al., 2014; DaSilva et al., 2015). Such methods are used to identify endemicity areas with a unique biota and process at least two species in sympatry (Morrone, 1994; Szumik et al., 2002). Thus, the determination of natural biogeographical units using PAE or NDM based on endemism is effective only in cases of strict sympatry (Casagranda et al., 2012;

Szumik et al., 2012). Since the absolute congruence in the distribution of an endemic biota is rare, these methods are criticized to be used to identify natural biogeographical units (Hausdorf, 2002). Furthermore, due to other natural processes as dispersion and extinction, it is difficult to identify a natural biogeographical units (Hausdorf, 2002; Hausdorf & Hennig, 2006) because such processes might hide general patterns, requiring more effective methods.

Similarity of species distribution should be a strong evidence of biogeographical patterns and one mechanism that might cause this is vicariance (Hausdorf & Hennig, 2006; Guedes et al., 2014). The use of vicariant model (Croizat et al., 1974; Rosen, 1976; Platnick & Nelson 1978; Nelson & Platnick, 1981; Wiley, 1988; Humphries & Parenti, 1991) postulates that biogeographical barriers might split an ancestral biota, resulting in two new biotas that share this common ancestor but are different. In other words, barrier appearance tends to determinate allopatric speciation. Thus, the model based on vicariance tries to identify barriers that might explain species pattern of distribution. Such model has the advantage that a single biogeographical barrier might explain several speciation events, on the contrary of dispersion and extinction, which are specifics (Humphries & Parenti, 1991). The vicariant model can be traced by searching for congruence distribution among different species that might be explained by a single event (Hausdorf, 2002).

Biogeographical units are usually complex and distribution data alone are often not enough to identify areas of endemism (Hausdorf, 2002). Biotic element analysis therefore, is an alternative method to identify groups of taxa whose ranges are significantly more similar among them than to another one (Hausdorf, 2002; Hausdorf & Hennig, 2003) and then, to define natural biogeographical units. The species originating in an area of endemism form a biotic element (Hausdorf, 2002). If speciation is the result of vicariance events, closely related species originate in different areas of endemism and, hence, belong to different biotic elements (Hausdorf & Hennig, 2006).

The Mantiqueira Mountain Range – MMR, is inserted at the Atlantic Rainforest domain – AF (*sensu* Ab'Saber, 1977). The name Mantiqueira came from Tupi-guarani language and means "weeping mountains" underscoring the historical importance of MMR as water source for southeastern region of Brazil (Becker et al., 2013). A biogeographical study on AF proposed Parque Nacional do Itatiaia as an endemic region based on harvestmen distribution (DaSilva et al., 2015). Furthermore, Amorim & Pires (2008) assign an area of endemism to the MMR in Serra da Boa Vista, with core area in Santa Teresa region, using Neotropical database of plants. Even though biological importance, the MMR lack protected areas for biodiversity conservation (Becker et al., 2013).

Herein, we provide the first comprehensive study about richness and biogeographical distribution patterns of the MMR anuran fauna. Also, we discuss the conservation planning based on endemic areas identified for anurans. The aims of our study are: (1) to map the patterns of richness of the anurans in the MMR; (2) to identify natural biogeographical units in MMR region based on anurans distribution; (3) to test the prediction of the vicariant model of speciation framed the patterns of distribution found; (4) to access the conservation of the richest areas and biogeographical patterns found; (5) to review the efficiency of the actual system of protected areas in the conservation of MMR biota.

Material and Methods

Study area

The Serra da Mantiqueira relief (*sensu* IBGE, 2006), ranging from the Espírito Santo State to São Paulo State. According to Gatto et al. (1989), the MMR extends from the Serra da Boa Vista at the south of Espírito Santo State and the Serranias da Zona da Mata Mineira, in the southeastern of Minas Gerais to Itatiaia and Campos do Jordão plateaus, among the states of Minas Gerais, Rio de Janeiro, and São Paulo. Moreover, Cruz & Feio (2007) set that MMR encloses mountains groups, named: Serra da Boa Vista, Serra do Caparaó, Serra de Ibitipoca, Itatiaia plateau, Campos do Jordão plateau, and Poços de Caldas plateau (Fig. 1).

Data sources

We obtained species distribution data by examining specimens vouchers housed at the most representative Brazilian herpetological collections: Coleção de Anfíbios do Museu de Ciências Naturais (MCNAM; Pontifícia Universidade Católica de Minas Gerais, Belo Horizonte, MG), Coleção Célio F. B. Haddad (CFBH; Universidade Estadual Paulista Júlio de Mesquita Filho, Rio Claro, SP), Coleção Herpetológica/Anfíbios da Universidade Federal de Juiz de Fora (CAUFJF, Juiz de Fora, MG), Coleção Herpetológica/Anfíbios da Universidade Federal de Minas Gerais (UFMG-AMP; Belo Horizonte, MG), Laboratório de Zoologia dos Vertebrados (LZV; Universidade Federal de Ouro Preto, Ouro Preto, MG), Museu de Biologia Prof. Mello Leitão (MBML; Santa Teresa, ES), Museu Nacional (MNRJ; Rio de Janeiro, RJ), Museu de Zoologia (MZUSP; Universidade de São Paulo, São Paulo, SP), Museu de Zoologia João Moojen (MZUFV; Universidade Federal de Viçosa, Viçosa, MG), and Museu de Zoologia

Prof. “Adão José Cardoso” (ZUEC; Universidade Estadual de Campinas, Campinas, SP).

The database was then increased by compiling anuran distribution records from the literature, including unpublished data from "gray literature". Detailed species examined in the scientific collections or from literature data are presented in Appendix S1. Geographical coordinates, required to prepare the dataset, were obtained from collections records or by consulting the collectors. Besides that, whenever possible, published data were included in order to improve the species distribution data of the sampled localities. We also accessed Google Earth to approximate the sample locality. Finally, the centroid of the municipality or conservation units was used to represent these records. In order to standardize the systematic and nomenclature used for the sampled species we are following the Amphibians taxonomy proposed by Frost (2016).

Analysis

Data entry and Species richness

We analyzed the species richness of anuran species from MMR region using SpeciesGeoCodeR (Toppel et al., 2014), a R package (Zizka et al., in prep.; R Core Team, 2016). First, we tested the validity of the geographical coordinates of the database by the argument Geoclean. This command plot the records on the polygons used to represent the MMR threshold and verify if all records match to the polygons. Second, the MMR anuran species richness pattern was explored by combining geographic polygons with pointy-locality occurrence data from multiple species. By doing this, it is possible to examine which species occur in which polygon and then compute a summary about species distribution and diversity (Maldonado et al., 2015). In our analysis we consider as polygon a shape of 0.5 x 0.5 degrees grid cells plotted under the MMR (Fig. 2 and Appendix S5).

Biotic elements Analysis

Based on the anuran distribution at the MMR, the predictions of the vicariance models that could explain the observed distribution regarding distribution of anurans were tested using the biotic element analysis (Hausdorf, 2002; Hausdorf & Hennig, 2003). The Biotic element analysis is implemented in *Prabclus* (Hausdorf & Hennig, 2003), a package available in R language (R Core Team, 2016). It is based on tests of two predictions of the vicariance model. The first prediction is based on the assumption that ancestral biota split would produce regionalized groups of taxa (the biotic elements), whereas the second prediction states that closely related species, resulted from vicariance events, would be found within distinct biotic elements (Hausdorf, 2002, Hausdorf & Hennig, 2003). Thus, both predictions are not mutually exclusive, but represent distinct models that could explain the observed distribution of a given taxon in different hierarchical levels. We run biotic element analysis using two datasets. The first included all grid-mapped species from the MMR (hereafter "complete dataset"). The second was a subset including only endemic species from MMR (hereafter "endemic dataset"). Clusters of species plotted in the NMDS 1 and 2 hold most of the variance about all distribution ranges. These clusters are then identified as the endemic biotic elements (EE). Following the definition used by Silva et al. (1997), Nogueira et al. (2011), and Guedes et al. (2014), we considered as endemic species those with locality record fully or largely coincident with the threshold of the MMR.

In order to test the first prediction, three specifications must be made: set the distance measure between the distribution limits of all examined taxa, assign the null model to generate distribution range groups, and perform a statistical test to verify the validity of the model (Hausdorf & Hennig, 2003). We chose *geco* coefficient instead of the *Kulczynski* distance (default in *prabclus*) because *geco* distance also considers the geographical relationships among the occupied units, the grid cells (Hausdorf & Hennig, 2006). For the required *geco* tuning constant, we used f = 0.2 (Hausdorf & Hennig, 2006).

Statistical analysis were performed using Student t-test (Hausdorf & Hennig, 2003) based on the assumption that, given a significant hierarchical clustering, the distribution ranges distances between different groups are expected to be greater than those between the distribution ranges within the same group. In order to test whether this result is not an effect of the interchange with adjacent regions, we repeat the analysis with the endemic dataset (only endemic anurans species).The null model was estimated using Monte Carlo simulation (MCS). MCS produces artificial distribution ranges that cell number distribution approximates the actual distribution of the number of cells per range (Hausdorf & Hennig, 2003).

The biotic elements (BE) were estimated using the model-based Gaussian clustering (MBGC) as implemented in R package *MClust* (Fraley & Raftery, 1998). MBGC operates on a data set where the cases are defined by metric scale variables. Therefore, we performed non-metric multidimensional scaling (NMDS; Kruskal, 1964) on the *geco* matrix, using Kruskal algorithm. As suggested by Hausdorf & Hennig (2003), we used the constant k equal to the number of species/40, rounded up to the next integer (six for the complete dataset and two for the endemic dataset). We named ‘core area’ the region with the highest percentage of species (greater than 75%) of each biotic element (Hausdorf & Hennig, 2003; 2006; Nogueira et al., 2011). Finally, we calculated the percentage of a species distributed in each cell-grid based on the total species distributed among the biotic elements identified.

The presence of closely related species in different biotic elements (i.e.: the second prediction of the vicariance model), were tested using the Chi-square test on the endemic dataset. We disregarded the noise component and the widespread species cluster because this cluster may not be homogeneous and, if so, it would not be result of vicariance events within the study area (Hausdorf & Hennig, 2004).

Conservation of biogeographical patterns

The biotic elements were used to estimate the conservation status of the sampled areas based on the observed biogeographical patterns. The evaluation consisted on comparing the rates of habitat loss of the EE, and quantifying the total coverage of protected areas intersecting the distributions of the endemic species in each EE. First, the distribution areas for each endemic species were estimated by plotting the minimum convex polygon of all endemic species with three or more records. The distribution area of species with a single record or two disjoint locality records were considered as the 10 km radius buffers around record plot (following IUCN, 2013 standardized radius). *Scinax obtriangulatus* was an exception because, besides it has more than two records, the distribution polygon would provide an occurrence area where the species does not occur. Thus, *S. obtriangulatus* distribution area was built with 10 km of radius to represent its range, around the two localities of occurrence.

The potential habitat loss for each species was calculated based on the overlap of endemic species range polygons and official data on deforestation in Brazil up to 2008 (MMA, 2008). Also, the coverage of protected areas for each species in endemic biotic elements were calculated overlapping the specific range polygons and the strictly protected areas (equivalent to IUCN categories I–III; Dudley, 2008) of the Brazilian protected area currently in operation (WWF, 2013).

We compared the rates of habitat loss for endemic species within each biotic element using Kolmogorov–Smirnov test (Crawley, 2007; Guedes et al., 2014). The expected habitat loss for a given species was calculated as the product of its distribution area and the average percentage of habitat loss of all species within its biotic element (following Guedes et al., 2014).

We used the logit transformation calculated in the R package *car* (R Core Team, 2016) for observed and expected habitat loss values because they correspond to proportions of the distribution area of species (see Warton & Hui, 2011). The logit-transformed proportion of species protection and habitat loss among endemic biotic elements was compared using a Kruskal–Wallis test (Hollander & Wolfe, 1973) and multiple comparison tests (see Siegel & Castellan, 1988), implemented in the R package *pgirmess* (R Core Team, 2016).

Spatial analyses were performed using XTools Pro, extension of ArcMap 10.1 (ESRI, 1999). To standardize the analyses, all were conducted in SAD 69 datum, and spatial analyses in South American Alberts Equal Area Conic projection. For all statistical analyses, we used a significance level of $\alpha = 0.05$.

Results

Species richness

We recorded 15022 records (Fig. 2) of 208 species of 15 anurans families, of which 78 are endemic of MMR (Appendixes S1 and S2). The richness of anuran is not uniformly distributed along the entire MMR (Fig. 3), ranging from one to 88 species in the sampled areas (0.5º square grids). The richest area is located in northern of Serra da Boa Vista, in Santa Teresa region (88 species). Other areas also shown high richness as Itatiaia plateau (70 species), Serra do Brigadeiro (62 species) and Serra do Ibitipoca/Rio Preto (62 species) (Fig. 3).

Biotic elements analysis

The biotic elements analysis of the complete dataset (endemic and non-endemic anurans species) indicates that first prediction of the vicariant model cannot be rejected: ranges were significantly clustered, forming distinguishable localized biotas across the MMR. The t-test was 0.252 and significantly smaller (for p-value < 0.001) than expected by chance (for 1000 artificial populations, T varied between 0.269 and 0.324, mean = 0.292). For the endemic dataset (only endemic anurans), the t-test was 0.225 and also significantly smaller (for p-value < 0.001) than expected under the null model (for 1000 artificial populations, T varied between 0.248 and 0.332, mean = 0.287).

As noticed in both datasets, the MMR's anurans were divided into species groups with regionalized distribution ranges. Thus, an alternative was to define the biotic elements accordingly to the species clusters in the first two dimensions of the NMDS analysis. In this analysis using the complete dataset, 110 species (52%) contributed to the detection of seven biotic elements (Fig. 4 and Fig. 6), whereas 99 species (46%) were included in the noise component. Biotic element one (BE 1) was formed by 26 species widespread in the MMR. BE 2 was formed by 24 species concentrated in north portion of the MMR, with disjoint distribution in central areas of the north potion of Serra da Boa vista (Santa Teresa region) and the Serra do Brigadeiro. BE 3 was formed by 18 species, ranging the Serra da Boa Vista, with core area in Santa Teresa region. BE 4 and BE 6 were formed by 15 and 8 species, respectively, located in Itatiaia plateau. Only one area was indicated as the BE 5, comprising 13 species and located in the region of Santa Teresa. Finally, BE 7 was formed by six species distributed in south region of the MMR, with core areas in the region of Campos do Jordão and Monte Verde plateaus.

The analysis with the endemic dataset also detected seven endemic biotic elements (Table 1), based on the range of 36 anurans species (46%), whereas 54% of the species was associated to the noise component (Fig. 5 and Fig. 7). The endemic biotic element one (EE 1) was formed by ten endemic species and is located in Itatiaia plateau. EE 2 was formed by six species with the core area in Campos do Jordão plateau. EE 3 and EE 4 were formed by five endemic species each, ranging the Santa Teresa Region and Campos do Jordão/Itatiaia plateaus, respectively. EE 5 was formed by four species distributed in Serra da Boa Vista and Serra da Torres region. Finally, EE 6 and EE 7 were both formed by three species and are located in Serra do Caparaó region and Poços de Caldas plateau, respectively.

The second prediction of the vicariance model in the endemic dataset showed a chi-squared = 101.42 (p-value = 0.06), not reject the fact that congeneric species were distributed in a homogeneously way through the endemic biotic elements (Hausdorf & Hennig, 2004).

Conservation of biogeographical patterns

The habitat loss for the endemic biotic elements had an average value of the 59% and ranging from 44% to 82% (Appendix S4 and Fig. 8). No significant differences between observed and expected habitat loss for species within each biotic element were detected (Appendix S3). Moreover, the habitat loss was significantly different among different endemic biotic elements (Kruskal-Wallis test: chi-squared = 31,685, p-value < 0.001).

The seven endemic biotic elements, represented by the species, had an average protection of the 31% (Appendix S4 and Fig. 9). The EE seven is completely out of any protection area and the EE 5 has only a small portion (0,05%) inside a protected area (PA). Eight species from other four endemic biotic elements have a small portion of their range protected (0.0% to 12.82%). The area covered by conservation units within the range of each species was significantly different among endemic biotic elements (Fig. 8; Kruskal-Wallis test: chi-squared = 25.323, p-value < 0.001).

Discussion

The general anuran richness and endemism levels found in this study for MMR are bigger than those detected by Cruz & Feio (2007), the most recent syntheses on the subject. Compared to Haddad et al. (2013) and Toledo et al. (2014) data, the number of species identified here for MMR represents about 40% of the actual species number known for AF. We identified 78 endemic species, increasing in 35.5% (+20 species) the number of endemic since the most recent record (Cruz & Feio, 2007 cataloged 58 species). New species descriptions (Targino et al., 2009; Lacerda et al., 2012; Santana et al., 2012), taxonomic revisions (Mângia et al., 2014), and more recent inventories (Moura et al., 2012) partially explain the omission of too many endemic species in the previous study. Also, the present study is the most representative compilation of species distribution data effort for MMR until now, exemplifying that careful revision of representative and regional collections is a valuable tool for conservation purposes.

MMR was already recognized as a center of endemism for insects, amphibians, birds, and plants (Silva et al., 2004; Amorim & Pires, 2006; Cruz & Feio, 2007; DaSilva et al., 2015; Fiaschi & Pirani, 2009). However, geomorphological and paleogeographical units (e.g., islands, continents, and mountain ranges) are considered areas of endemism in most empirical studies without explicit analyses to reinforce it (Hausdorf, 2002). By using point-locality database and accessing the shape of the actual distribution of anurans, we suggest anurans distribution within MMR as not homogenous. The heterogeneous anuran distribution could be observed in MMR, even with a more representative database, which suggests any process as the modeling this pattern. The vicariance model applied to MMR, predicted a clustering of distribution ranges, explained by vicariance (Hausdorf & Hennig, 2003).

BE 1 species are widely distributed in the MMR, inhabiting lowlands and highlands regions (between 200 - 2750 m. a. s. l.). BE1 species distributions coincide with MMR limit proposed by us. Although we did not test such assumption, this result is probably not just by chance and MMR is more likely to be a natural biogeographical unit. In addition, the species distributions of BE 2/BE 3, BE 6/BE 7, support the division of the MMR in two main groups as proposed by Gatto et al. (1987): Mantiqueira northern and Mantiqueira southern. Amorim & Pires (1996), using Brooks Parsimony Analysis, identified an area of endemism that includes the north region of the MMR, compatible with those identified here as Mantiqueira northern, with core area in a region similar with the BE 5 and the EE 3. Also, DaSilva et al. (2015) pointed out the existence of a so called “Maximum Region of Endemism” in the region of Mantiqueira southern, in the Parque Nacional do Itatiaia, as identified by us as BE 4 and EE 1. As expected, the core area of most biotic elements was coincident with the endemic biotic elements. The core area of EE 3 is similar to BE5 and EE 4 has a huge overlap area with BE4.

Poços de Caldas plateau and Maciço of the Itatiaia, a restrict portion of the Itatiaia plateau (see Silva et al., 2010), are formed by intrusive alkaline magmatic rocks originated from a (geological) hot spot, dating from Lower Cretaceous (Filho et al., 2005). The region of Campos do Jordão plateau is a crystalline metamorphic rock sequence, dating from Upper Cretaceous (Modenesi-Gauttieri et al., 2011). Different types of rocks could generate different soil constitutions, and, as consequence, different microhabitats (Benites et al., 2003). Numerous microhabitats and strong environmental gradients in these high elevation rock outcrops could lead to a highly diversified and endemic biota (Ribeiro et al., 2007). Probably based on this soil heterogeneity, Cruz & Feio (2007) speculate that the influence of the geomorphological of MMR might have affected anurans evolution and endemism. The Endemic biotic elements identified in areas that share singular geomorphological history might confirm such idea.

Pellegrino et al. (2005) proposed, for the AF, that rivers could function as underlying factors behind currently observed patterns of biological distribution. Also, Thomé et al. (2014) assign barriers (i.e.: Doce River and Guapiara fault) that could explain the species distribution in the AF. Carnaval & Moritz (2008), however, suggest that climatic changes dynamics, molding different refuges, rather than rivers, were the main causal factor to the diversity of actual AF fauna. Moreover, these authors proposed that the AF maintained large stable areas (Pernambuco refuge, Bahia refuge, and south Doce River refuge) during the Last Glacial Maximum (LGM) (approximately 21.000 years ago). Also, microrefuges have been proposed to have occurred in mountains and valleys of southeastern and southern region of the AF during the LGM (Rull, 2009; Carnaval et al., 2014). In addition, the complex topography along the extent of MMR, that allowed the range of species in elevation, is indicated to be an important factor determining the presence of these cluster patterns in these regions (Vasconcellos et al., 2014).

All endemic biotic elements identified here with exception of EE 5 were composed by anuran species typically from highlands. The proportion of the EE's in highlands could be explained by an altitudinal gradient, which might have operated microrefuges in the LGM. Furthermore, stable areas in highly changeable environmental could have allowed the rise of different phylogenetic lineages through time, leading to a higher species richness and endemism (Graham et al., 2006). A similar conjecture has been proposed to explain the regional distribution of snakes and squamata in the Caatinga and Cerrado, respectively (Guedes et al., 2014; Nogueira et al., 2011).

Although the massive destruction of the AF, the region of Serra da Boa Vista remain as a relatively large fragment inside the AF (Morelato & Haddad, 2000). This region is not shaped by high lands, with altitudinal quotes varying between 600-800 meters. Even so, a high level of richness and one EE has been identified in there. Carnaval & Moritz (2008) predicted that regions located in the south of the Doce River would have small and medium-size refuges that were stable areas during Pleistocene climatic cycles. Thus, the EE and the high diversity found in

Serra da Boa Vista might be explained by both, to be one of the larger remnants of AF and by the keeping of stable areas even along to LGM.

Habitat loss and fragmentation have been described as a major threat to the maintenance of biological diversity in the tropical forests (Laurence, 1999). On the other hand, the level of habitat loss/fragmentation can be used to predict potential areas of occurrence of threatened species or local extinction (Brooks, 2002). The anuran EE's found in the MMR show high rates of habitat loss (45% - 82%). Given the explicitly recommendations to use EE information in conservation strategy (Brooks et al., 1992; Crandall et al., 2000; Moritz, 2002), all EE's found in this study should be considered as high priority for conservation purposes, since the historical factors that explain the anuran distribution could have worked to other groups of organisms as well. It is important to point out that EE 3 and EE5 have only a small proportion of its areas inside current PA's. On the other hand, the Parque Estadual de Campos do Jordão (EE 2 and EE 4), Parque Nacional do Itatiaia (EE 4 and EE 1), and Parque Nacional do Caparaó (EE 6), represents the PA's effectiveness of conservation.

All Endemic biotic elements were composed by species with small distribution range. More than 70% of the species (n = 25 species) has less than 400 km² of estimated distribution range. Among the EE's that are only small portion included inside any PA (25%; n = 9 species) – EE 3 and EE 5 – it is important to increase the range of PA's in order to superimpose this EE's because, as demonstrated by Brown & Lomolino (1998), species with restrict distribution are more susceptible to extinction. Our findings and those of other authors (e.g.: Urbina-Cardona & Loyola, 2010; Villalobos et al., 2013) on the scarce protection in anuran biodiversity, are not surprising. All of these results highlight the inefficiency of the *ad hoc* manner of establishing protected areas to preserve biodiversity of specific taxa (Pressey et al., 1994; Rodrigues et al., 2004; Villalobos et al., 2013).

According to Rodrigues et al. (2004), the real protection of restricted species (small range species) happens when it is completely inside the PA's. Species with small range tend to be rare not only in range size but also in local abundance (Gaston et al., 1997). For instance, the EE7 encompasses three species restricted to Poços de Caldas plateau and there are no integral protection areas in that region. Furthermore, the Poços de Caldas plateau suffers high impact from bauxite mining, activity which could explain the high level of habitat loss in that area (Barros et al., 2012). EE 5 has only one small PA (Monumento Natural Estadual Serra das Torres) and also suffers with high rates of habitat loss, and is represented by species with small range, as well as, the EE 3 that encompasses two PA's (Reserva Biológica Augusto Ruschii and Estação Biológica Santa Lúcia), but is not enough to protected those species.

The MMR are formed by a rich and unique biota of anurans resulted from vicariant events. We identified seven natural biogeographical units (EE 1- EE 7) along the MMR that are compatible to be resulted from vicariance. However, other process could also explain the formation of EE's. The EE 3 is located in a range from 600-800 meters, however the existence of a refuge in the LGM and the high quantity of AF remnants areas could explain this natural biogeographical units. The others EE's (EE 1-EE 4, EE 6 and EE 7) are located in highlands which are likely climatic stable regions (microrefuges) in the LGM. The EE 3, EE 5, and EE 7 achieved high rates of habitat loss and miss effective protection. Then, we emphasize the importance of (1) creating a PA's in Poços de Caldas plateau, (2) increase the protected area of Monumento Natural Estadual Serra das Torres, Reserva Biológica Augusto Ruschii, and Estação Biológica Santa Lúcia and (3) create a PA's in south region of Serra da Boa Vista, covering the region of Pico dos Três Pontões, where the species of EE 5 are distributed. Then, our results highlight the importance of quantitative biogeographic methodologies to identify natural biogeographic units, as provide empirical data that support the importance of highlands conservation in the maintenance of biodiversity.

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3.1 Table

Table 1 - Number of species of endemic biotic elements (EE 1–7), based on 78 endemic anurans, shared with biotic elements (BE 1–7) recovered based on all 208 grid-mapped anurans species from Mantiqueira Mountain Range.

	Biotic element							Noise
Endemic biotic element	BE 1	BE 2	BE 3	BE 4	BE 5	BE 6	BE 7	n
EE 1 - Itatiaia	-	-	-	-	10	-	-	-
EE 2 - Campos do Jordão	-	-	-	-	-	-	2	4
EE 3 - Santa Teresa	-	-	-	4	-	-	-	1
EE 4 - Campos do Jordão/Itatiaia	-	-	-	-	2	-	-	3
EE 5 - Serra das Torres/ Serra da Boa Vista	-	-	-	-	-	-	-	4
EE 6 - Serra da Caparaó	-	-	-	-	-	-	-	3
EE 7 - Poços de Caldas	-	-	-	-	-	-	-	3

3.2 Figures

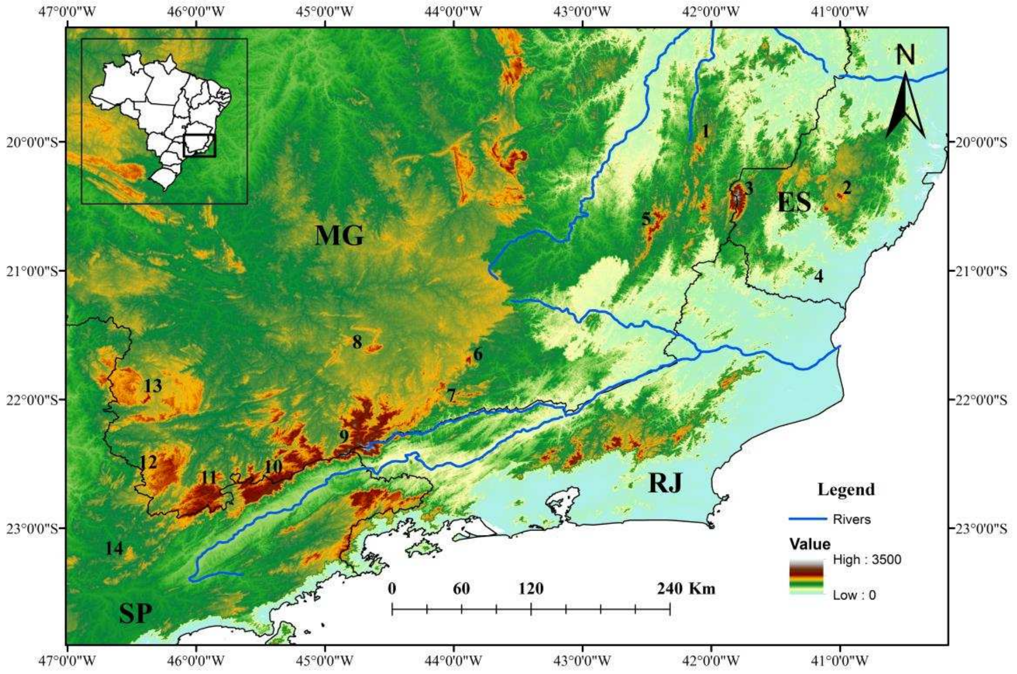


Figure 1 - Map showing the mainly sub regions forming the Mantiqueira Mountain Range (MMR) threshold. (1): Serranias da Zona da Mata Mineira; (2): Serra de Boa Vista; (3): Serra do Caparaó; (4): Serra das Torres; (5): Serra do Brigadeiro; (6): Serra do Ibitipoca; (7): Serra de Rio Preto; (8): Serra de São José; (9): Itatiaia Plateau; (10): Campos do Jordão Plateau; (11): Monte Verde Plateau; (12): Lidóia Plateau; (13): Poços de Caldas Plateau; (14): Serra da Japi.

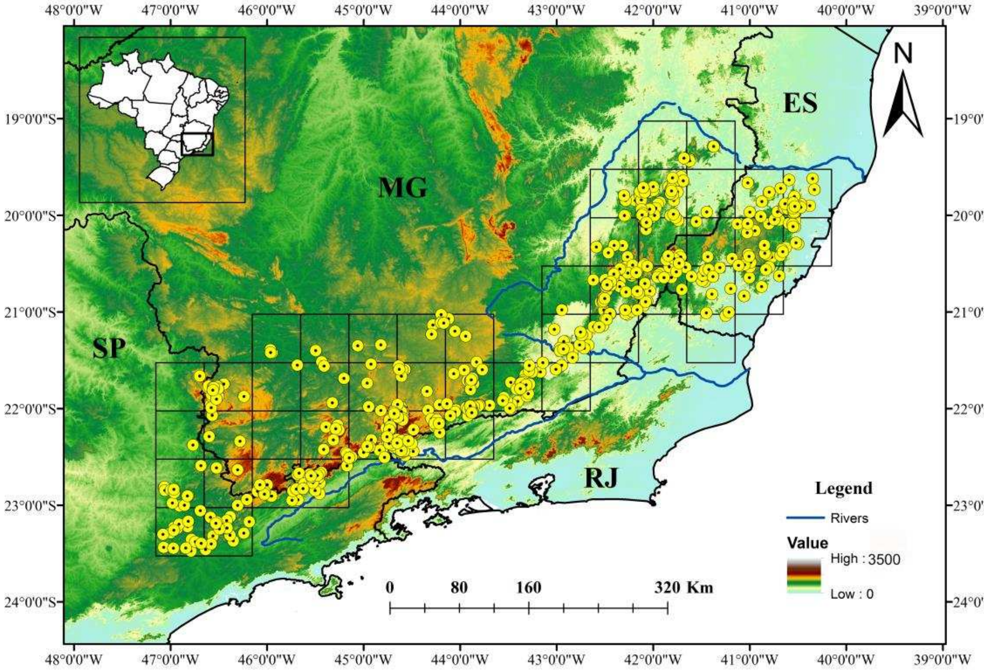


Figure 02 – Plot of species occurrences of anurans records used in the analyses and 0.5° x 0.5° degrees grid cells plotted under MMR.

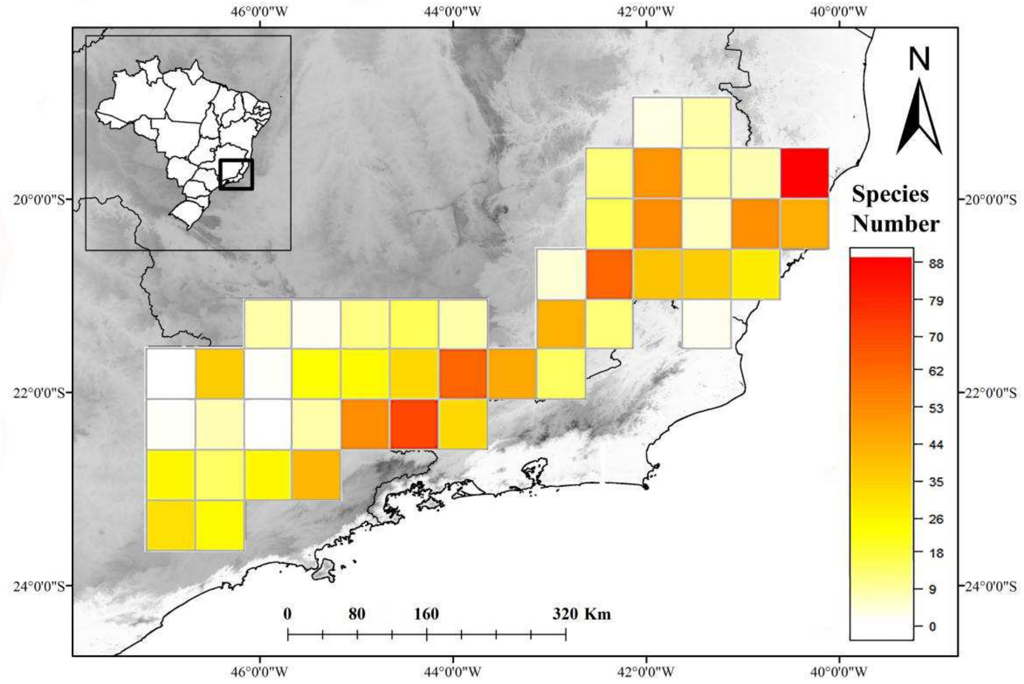


Figure 03 – Species richness through the MMR using species distribution data in SpeciesGeoCodeR.

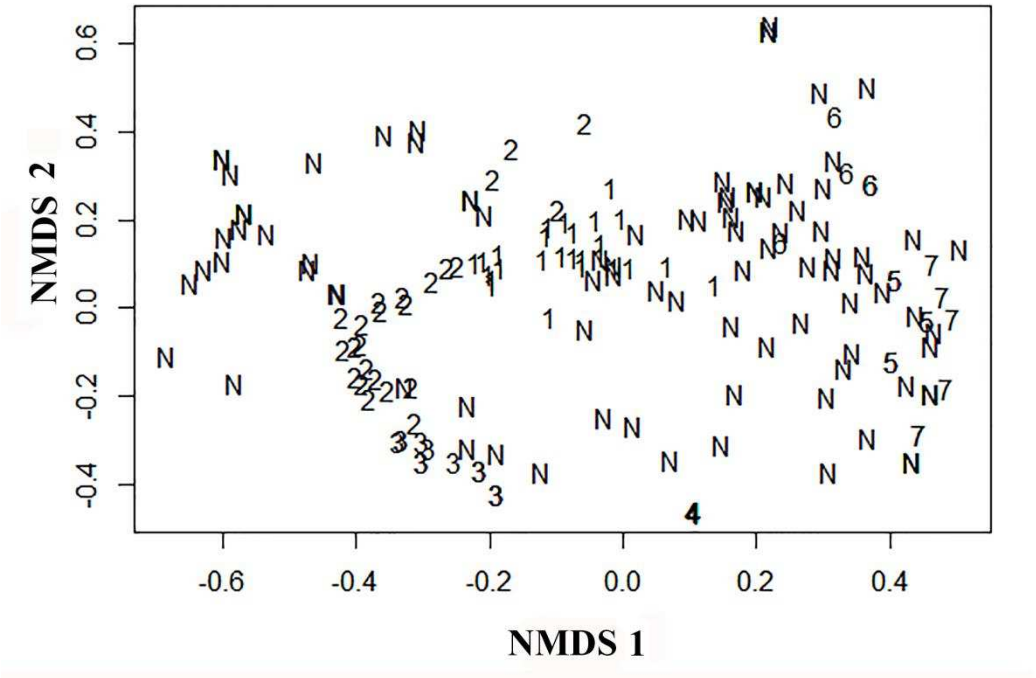


Figure 04 – Species clusters in the first two dimensions of a nonmetric multidimensional scaling analysis, obtained according to the ranges of 208 Mantiqueira anuran species (endemics and nonendemics), mapped on a 0.5° x 0.5° cell grid, analyzed in *MClust*. Characters indicate model-based clustering with noise (N).

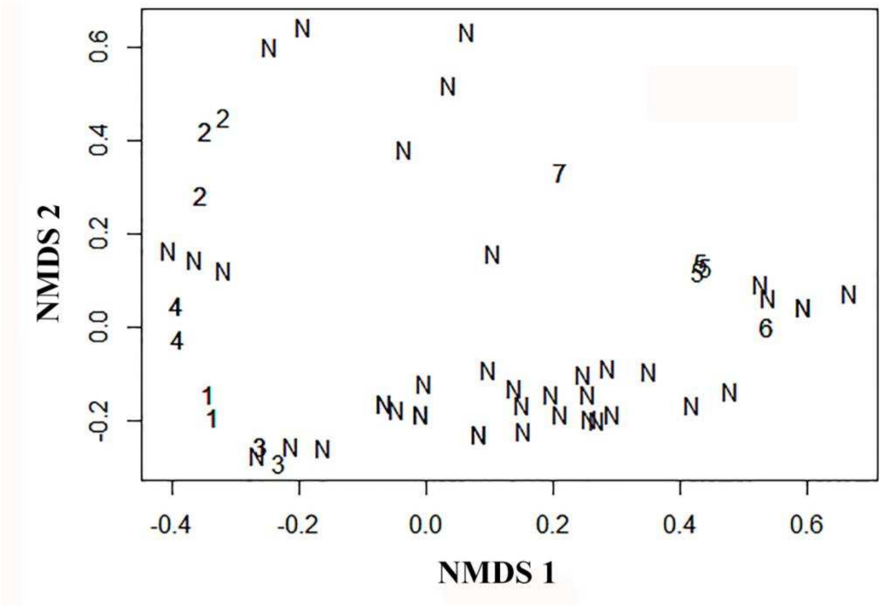


Figure 05 – Species clusters in the first two dimensions of a nonmetric multidimensional scaling analysis, obtained according to the ranges of 78 endemic Mantiqueira anuran species,

mapped on a 0.5° x 0.5° cell grid, analyzed in *MClust*. Characters indicate model-based clustering with noise (N).

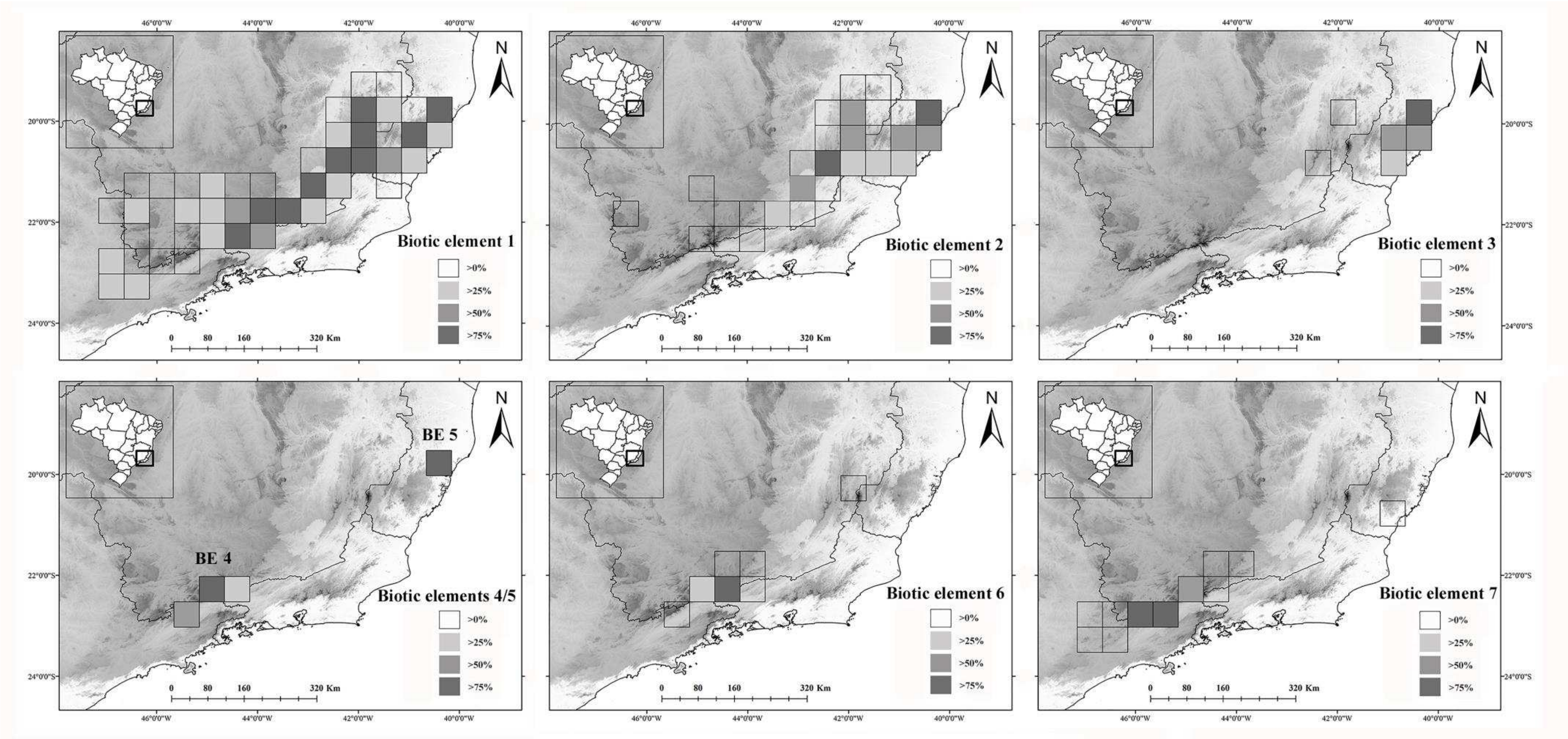


Figure 06 – Distribution of biotic elements (BE 1–7) recovered according to the range of 208 Mantiqueira anuran species (endemics and nonendemics). Shadings indicate the areas where > 75%, > 50%, > 25% and > 0% of the species of an element are present.

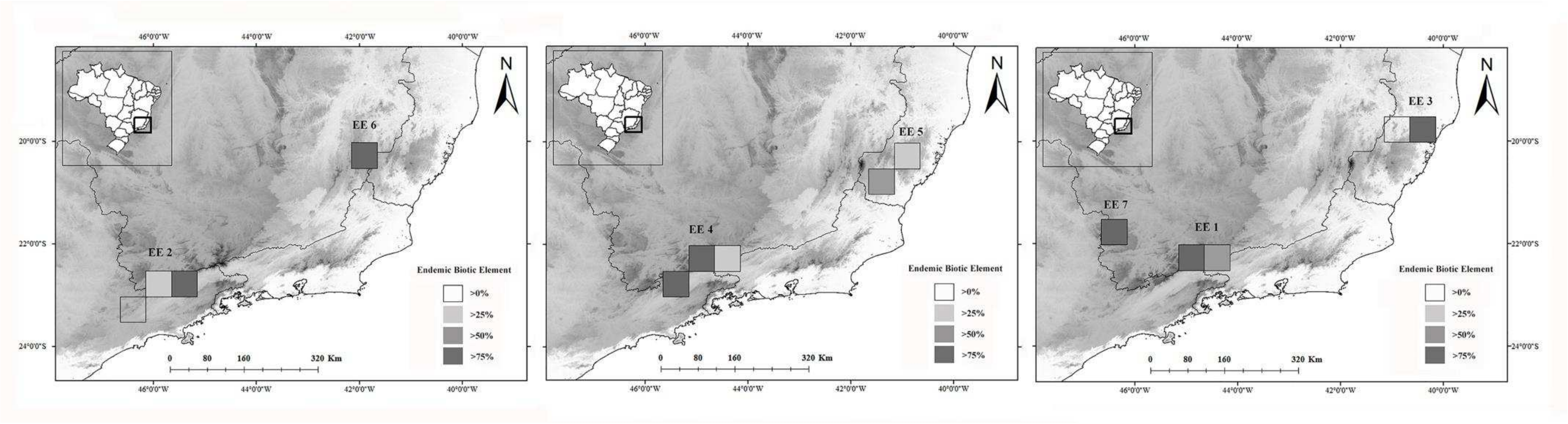


Figure 07 – Distribution of endemic biotic elements (EE 1–7) recovered according to the range of 78 endemic Mantiqueira anuran species. Shadings indicate the areas where > 75%, > 50%, > 25% and > 0% of the species of an element are present.

1

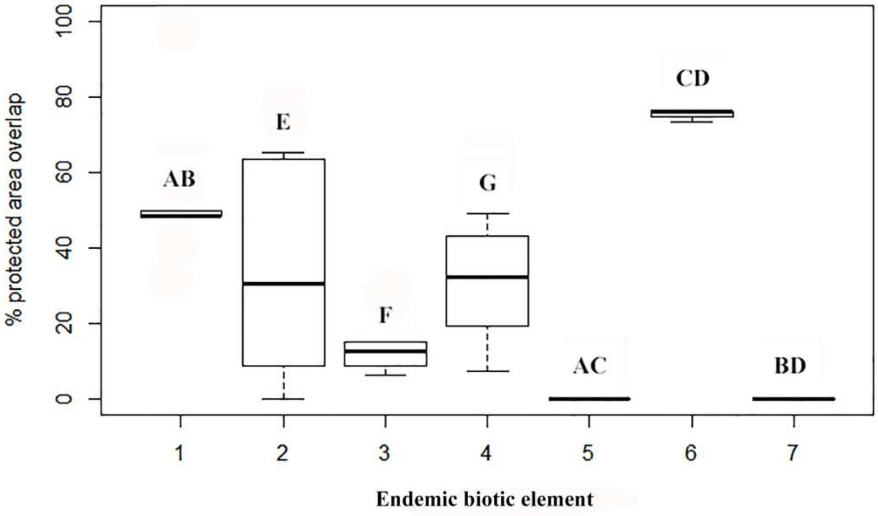


Figure 08 – Percentage of habitat loss of species per endemic biotic elements 1–7. Horizontal bars = median; box = first and third quartiles; whiskers = minimum and maximum values. Common letters indicate significant differences.

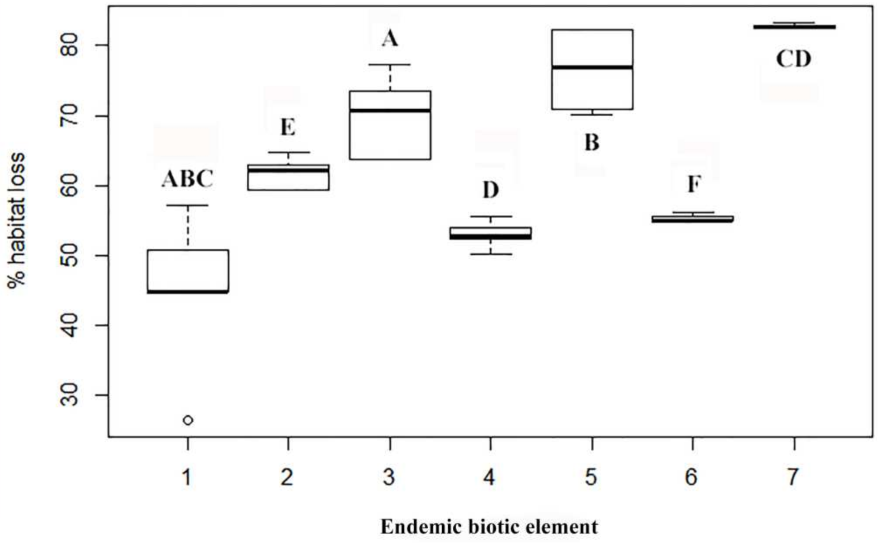


Figure 09 – Percentage of protected areas overlap with species in each endemic biotic element 1–7. Horizontal bars = median; box = first and third quartiles; whiskers = minimum and maximum values. Common letters indicate significant differences.

4. CONCLUSÕES GERAIS

- O modelo vicariante explica a atual distribuição das espécies no Complexo Serrano da Mantiqueira.
- As flutuações do Pleistoceno são indicadas como as principais responsáveis por modelar o processo de vicariância no CSM.
- Alguns processos geomorfológicos também são apresentados como possíveis causas do modelo vicariante.
- Os elementos bióticos endêmicos encontrados estão com altas taxas de perda de habitat e baixas taxas de proteção por unidades de conservação.
- Nós propomos a criação de pelo menos duas unidades de proteção integral, uma no Planalto de Poços de Caldas e uma segunda na Região três Picos, sul de Serra da Boa Vista. Além disso, nós encorajamos a ampliação e/ou criação de outra UC na região de Serra das Torres (ES).

5. Supplementary data

Appendix S1 – All species recorded in the Mantiqueira Mountain Range and used in the analyses.

Adelophryne glandulata, *Adelophryne meridionalis*, *Adenomera marmorata*, *Adenomera thomei*, *Allobates olfersioides*, *Aparasphenodon brunoi*, *Aparasphenodon pomba*, *Aplastodiscus arildae*, *Aplastodiscus callipygius*, *Aplastodiscus cavicola*, *Aplastodiscus leucopygius*, *Aplastodiscus perviridis*, *Aplastodiscus weygoldti*, *Bokermannohyla caramaschii*, *Bokermannohyla circumdata*, *Bokermannohyla gouveai*, *Bokermannohyla hylax*, *Bokermannohyla ibitipoca*, *Bokermannohyla luctuosa*, *Bokermannohyla nanuzae*, *Bokermannohyla vulcaniae*, *Brachycephalus alipioi*, *Brachycephalus atelopoide*, *Brachycephalus* aff. *ephippium*, *Brachycephalus didactylus*, *Brachycephalus ephippium*, *Brachycephalus nodoterga*, *Ceratophrys aurita*, *Chiasmocleis capixaba*, *Chiasmocleis mantiqueira*, *Crossodactylodes bokermanni*, *Crossodactylodes izecksohni*, *Crossodactylus caramaschii*, *Crossodactylus grandis*, *Crossodactylus timbuhy*, *Crossodactylus werneri*, *Cycloramphus bandeirensis*, *Cycloramphus brasiliensis*, *Cycloramphus carvalhoi*, *Cycloramphus eleutherodactylus*, *Cycloramphus fuliginosus*, *Cycloramphus granulosus*, *Dendrophryniscus brevipollicatus*, *Dendrophryniscus carvalhoi*, *Dendropsophus anceps*, *Dendropsophus berthalutzae*, *Dendropsophus bipunctatus*, *Dendropsophus branneri*, *Dendropsophus decipiens*, *Dendropsophus elegans*, *Dendropsophus giesleri*, *Dendropsophus haddadi*, *Dendropsophus microps*, *Dendropsophus minutus*, *Dendropsophus nanus*, *Dendropsophus rubicundulus*, *Dendropsophus ruschii*, *Dendropsophus sanbornii*, *Dendropsophus seniculus*, *Elachistocleis* *cesarii*, *Euparkerella robusta*, *Euparkerella tridactyla*, *Fritziana fissilis*, *Fritziana goeldii*, *Fritziana ohausi*, *Fritziana ulei*, *Gastrotheca albolineata*, *Gastrotheca ernestoi*, *Gastrotheca megacephala*, *Haddadus binotatus*, *Holoaden bradei*, *Holoaden luederwaldti*, *Hylodes amnicola*, *Hylodes babax*, *Hylodes glaber*, *Hylodes japi*, *Hylodes lateristrigatus*, *Hylodes magalhaesi*, *Hylodes sp.*, *Hylodes ornatus*, *Hylodes perere*, *Hylodes regius*, *Hylodes sazimai*, *Hylodes vanzolinii*, *Hypsiboas albomarginatus*, *Hypsiboas albopunctatus*, *Hypsiboas beckeri*, *Hypsiboas bischoffi*, *Hypsiboas crepitans*, *Hypsiboas faber*, *Hypsiboas latistriatus*, *Hypsiboas lundii*, *Hypsiboas pardalis*, *Hypsiboas polytaenius*, *Hypsiboas prasinus*, *Hypsiboas semilineatus*, *Hypsiboas* aff. *freicanecae*, *Hypsiboas stenocephalus*, *Ischnocnema abdita*, *Ischnocnema* aff. *holti*, *Ischnocnema concolor*, *Ischnocnema epipeda*, *Ischnocnema holti*, *Ischnocnema izecksohni*, *Ischnocnema juipoca*, *Ischnocnema melanopygia*, *Ischnocnema oea*, *Ischnocnema verrucosa*, *Ischnocnema vizottoi*, *Itapotihyla langsdorffii*, *Leptodactylus cunicularius*, *Leptodactylus cupreus*, *Leptodactylus furnarius*, *Leptodactylus fuscus*, *Leptodactylus labyrinthicus*, *Leptodactylus latrans*, *Leptodactylus mystacinus*, *Leptodactylus natalensis*, *Leptodactylus spixii*, *Macrogenioglottus alipioi*, *Megaelosia apuana*, *Megaelosia boticariana*, *Megaelosia jordanensis*, *Megaelosia lutzae*, *Melanophryniscus moreirae*, *Melanophryniscus peritus*, *Myersiella microps*, *Odontophrynus americanus*, *Odontophrynus cultripes*, *Paratelmatobius lutzii*, *Paratelmatobius mantiqueira*, *Phasmahyla cochranae*, *Phasmahyla exilis*, *Phasmahyla guttata*, *Phrynomedusa marginata*, *Phyllodytes kautskyi*, *Phyllodytes luteolus*, *Phyllomedusa ayeaye*, *Phyllomedusa burmeisteri*, *Physalaemus* aff. *rupestris*, *Physalaemus centralis*, *Physalaemus crombiei*, *Physalaemus cuvieri*, *Physalaemus feioi*, *Physalaemus* *jordanensis*, *Physalaemus maculiventris*, *Physalaemus maximus*, *Physalaemus obtectus*, *Physalaemus olfersii*, *Physalaemus rupestris*, *Physalaemus signifer*, *Pipa carvalhoi*, *Proceratophrys boiei*, *Proceratophrys itamari*, *Proceratophrys laticeps*, *Proceratophrys mantiqueira*, *Proceratophrys moehringi*, *Proceratophrys palustris*, *Proceratophrys paviotii*, *Proceratophrys phyllostomus*, *Proceratophrys schirchi*, *Pseudopaludicola murundu*, *Pseudopaludicola mystacalis*, *Rhinella crucifer*, *Rhinella granulosa*, *Rhinella icterica*, *Rhinella ornata*, *Rhinella rubescens*, *Rhinella schneideri*, *Scinax alter*, *Scinax arduous*, *Scinax argyreornatus*, *Scinax belloni*, *Scinax* aff. *rizibilis*, *Scinax caldarum*, *Scinax cardosoi*, *Scinax carnevallii*, *Scinax cosenzai*, *Scinax crospedospilus*, *Scinax cuspidatus*, *Scinax duartei*, *Scinax eurydice*, *Scinax flavoguttatus*, *Scinax fuscomarginatus*, *Scinax fuscovarius*, *Scinax hayii*, *Scinax heyeri*, *Scinax hiemalis*, *Scinax kautskyi*, *Scinax longilineus*, *Scinax luizotavioi*, *Scinax obtriangulatus*, *Scinax ranki*, *Scinax squalirostris*, *Scinax* aff *belloni*, *Scinax tripui*, *Scinax x-signatus*, *Scinax* aff. *arduous*. *Scinax* aff. *cozenzai*, *Sphaenorynchus orophilus*, *Thoropa miliaris*, *Thoropa petropolitana*, *Thoropa* aff. *lutzi*, *Trachycephalus imitatrix*, *Trachycephalus mesophaeus*, *Vitreorana eurygnatha*, *Vitreorana uranoscopa*, *Zachaenus carvalhoi*, and *Zachaenus parvulus*.

Appendix S2 – Endemic species recorded at the Mantiqueira Mountain Range and used in the analyses.

Adelophryne glandulata, *Aparasphenodon pomba*, *Bokermannohyla caramaschii*, *Bokermannohyla gouveai*, *Bokermannohyla ibitipoca*, *Bokermannohyla vulcaniae*, *Brachycephalus alipioi*, *Brachycephalus atelopoide* *Brachycephalus* aff. *ephippium*, *Chiasmocleis mantiqueira*, *Crossodactylodes* *bokermanni*, *Crossodactylodes izecksohni*, *Crossodactylus grandis*, *Crossodactylus timbuhy*, *Cycloramphus bandeirensis*, *Cycloramphus carvalhoi*, *Dendrophryniscus carvalhoi*, *Dendropsophus ruschii*, *Euparkerella robusta*, *Euparkerella tridactyla*, *Holoaden bradei*, *Holoaden luederwaldti*, *Hylodes amnicola*, *Hylodes glaber*, *Hylodes japi*, *Hylodes magalhaesi*, *Hylodes sp.*, *Hylodes ornatus*, *Hylodes perere*, *Hylodes regius*, *Hylodes sazimai*, *Hylodes vanzolinii*, *Hypsiboas beckeri*, *Hypsiboas latistriatus*, *Hypsiboas* aff. *freicanecae*, *Ischnocnema abdita*, *Ischnocnema* aff. *holti*, *Ischnocnema concolor*, *Ischnocnema epipeda*, *Ischnocnema holti*, *Ischnocnema melanopygia*, *Ischnocnema oea*, *Ischnocnema vizottoi*, *Megaelosia apuana*, *Megaelosia boticariana*, *Megaelosia jordanensis*, *Megaelosia lutzae*, *Melanoprhyniscus moreirae*, *Melanoprhyniscus peritus*, *Paratelmatobius lutzii*, *Paratelmatobius mantiqueira*, *Phasmahyla exilis*, *Physalaemus* aff. *rupestris*, *Physalaemus feioi*, *Physalaemus jordanensis*, *Physalaemus rupestris*, *Proceratophrys itamari*, *Proceratophrys mantiqueira*, *Proceratophrys moehringi*, *Proceratophrys palustris*, *Proceratophrys paviotii*, *Proceratophrys phyllostomus*, *Scinax* aff. *arduous*, *Scinax* aff. *belloni*, *Scinax* aff. *cosenzai*, *Scinax* aff. *rizibilis*, *Scinax arduous*, *Scinax belloni*, *Scinax caldarum*, *Scinax cosenzai*, *Scinax duartei*, *Scinax heyeri*, *Scinax kautskyi*, *Scinax obtriangulatus*, *Scinax ranki*, *Thoropa* aff. *lutzi*, and *Zachaenus carvalhoi*.

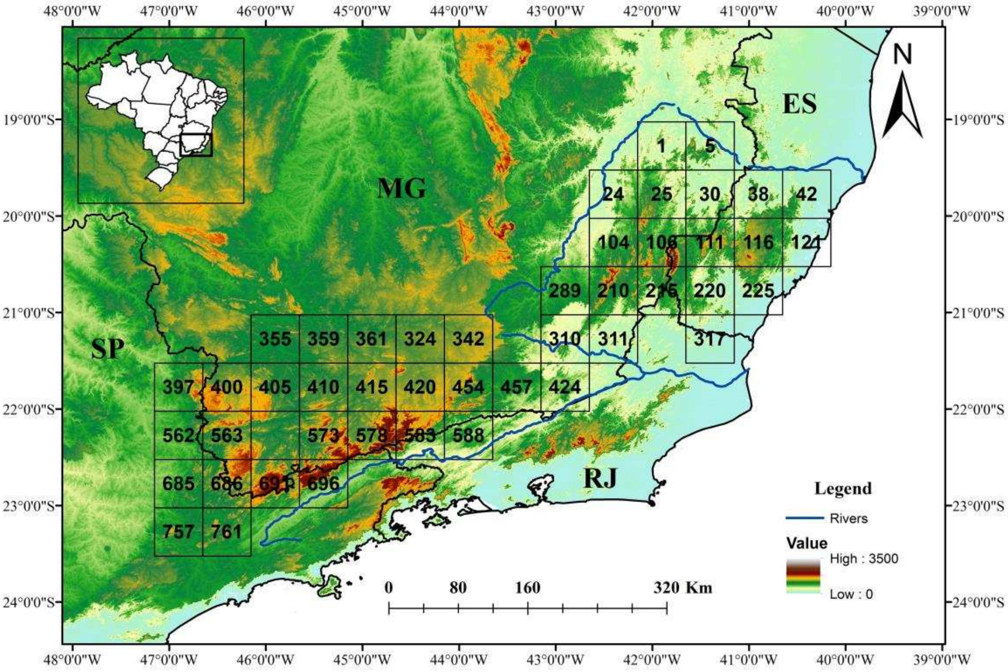
Appendix S3 – Kolmogorov-Smirnov tests of rates of expected and observed habitat loss for the species within each endemic biotic elemento.

Biotic Element	D (Kolmogorov-Smirnov test statistic)	p-value
EE 1	0.40	0.40
EE 2	0.34	0.89
EE 3	0.40	0.81
EE 4	0.40	0.81
EE 5	0.25	1.00
EE 6	0.66	0.51
EE 7	1.00	0.09

Appendix S4 - List of species of anurans recorded from the MMR region, with data on range size, habitat loss, and protected area coverage provided for species that formed endemic biotic elements. sum_nat, remaining natural vegetation; % rem., percentage remaining; % loss, percentage of habitat loss; loss_obs., habitat loss observed; loss_exp, percentage of habitat loss expected, area_real (km^2), real distribution of the taxa; %_protec, percentage in protected areas.

BE	species	count	area(km2)	sum_nat	%_rem	%_loss	loss_obs	loss_exp	area_real(km^2)	Protected area(km^2)	%_protec
1	*Bokermannohyla gouveai*	6	864	476,929858	55,20021505	44,799785	387,070142	400,896	314,28	152,593	48,55320097
1	*Holoaden bradei*	6	864	476,929858	55,20021505	44,799785	387,070142	400,896	314,28	152,592	48,55288278
1	*Hylodes glaber*	7	1008	510,269233	50,62194772	49,3780523	497,730767	467,712	314,28	171,216	54,47880871
1	*Hylodes sp.*	3	432	227,127928	52,57590926	47,4240907	204,872072	200,448	628,56	204,266	32,4974545
1	*Hylodes ornatus*	2	288	211,974663	73,60231354	26,3976865	76,025337	133,632	293,747	293,747	100
1	*Hylodes regius*	11	1584	728,021485	45,96095234	54,0390477	855,978515	734,976	531,439	239,36	45,03997637
1	*Ischnocnema concolor*	6	864	476,929858	55,20021505	44,799785	387,070142	400,896	314,28	152,592	48,55288278
1	*Ischnocnema melanopygia*	6	864	476,929858	55,20021505	44,799785	387,070142	400,896	314,28	153	48,55288278
1	*Melanoprhyniscus moreirae*	12	1728	739,634822	42,80294109	57,1970589	988,365178	801,792	590,477	294	49,80278656
1	*Paratelmatobius lutzii*	10	1440	709,328856	49,25894833	50,7410517	730,671144	668,16	314,28	153	48,55288278
2	*Brachycephalus atelopode*	8	1152	405,587597	35,20725668	64,7927433	746,412403	710,784	314,28	0	0
2	*Hylodes magalhaesi*	13	1872	761,6194519	40,68479978	59,3152002	1110,380548	1155,024	554,28	144,525	26,07436675
2	*Ischnocnema* aff. *holti*	9	1296	491,722902	37,94158194	62,0584181	804,277098	799,632	314,28	204,948	65,21191294
2	*Ischnocnema vizottoi*	13	1872	761,6194519	40,68479978	59,3152002	1110,380548	1155,024	497,126	174,609	35,12369098
2	*Megaelosia boticariana*	14	2016	745,4514986	36,97676084	63,0232392	1270,548501	1243,872	628,56	55,023	8,753818251
2	*Megaelosia jordanensis*	9	1296	491,722902	37,94158194	62,0584181	804,277098	799,632	314,28	199,262	63,40269823
3	*Crossodactylodes bokermanni*	7	1008	345,141517	34,24022986	65,7597701	274,958778	706,608	314,28	28,212	8,976708667
3	*Crossodactylodes izecksohni*	3	432	157,041222	36,35213472	63,6478653	274,958778	302,832	89,262	24,998	28,00519818
3	*Adelophryne glandulata*	9	1296	343,79383	26,5273017	73,4726983	952,20617	908,496	314,28	40,301	12,82327861
3	*Ischnocnema epipeda*	8	1152	261,14812	22,66910764	77,3308924	890,85188	807,552	314,28	195,580	62,23113148
3	*Scinax arduous*	7	1008	295,176818	29,28341448	70,7165855	712,823182	706,608	150,959	22,615	14,98088885
4	*Crossodactylus grandis*	25	3600	1601,994991	44,49986085	55,5001391	1998,005009	1890	917,284	178,608	19,47139599
4	*Cycloramphus carvalhoi*	14	2016	926,5068486	45,95768098	54,042319	1089,493151	1058,4	628,56	203,838	32,4293816
4	*Holoaden luederwaldti*	13	1872	932,6996303	49,8236982	50,1763018	939,3003697	982,8	183,465	13,853	7,550759
4	*Proceratophrys itamari*	13	1872	892,2705858	47,66402702	52,335973	979,7294142	982,8	309,566	133,971	43,27703947
4	*Scinax obtriangulatus*	14	2016	989,719906	49,09324931	50,9067507	1442,725808	1058,4	628,56	308,921	49,14741632
5	*Euparkerella robusta*	15	2160	386,266959	17,88272958	82,1172704	1773,733041	1652,4	628,56	0,104580	0,01663803
5	*Scinax belloni*	7	1008	300,3539009	29,79701398	70,202986	707,6460991	771,12	73,747	0,115	0,155938547
5	*Scinax* aff. *arduous*	8	1152	326,8533351	28,37268534	71,6273147	825,1466649	881,28	314,28	0,00	0
5	*Scinax* aff. *belloni*	9	1296	228,707866	17,64721188	82,3527881	1067,292134	991,44	314,28	0,104580	0,03327606
6	*Cycloramphus bandeirensis*	6	864	389,382712	45,06744352	54,9325565	474,617288	477,792	314,28	239	76,1935217
6	*Hylodes vanzolinii*	6	864	389,382712	45,06744352	54,9325565	474,617288	477,792	314,28	239	76,1935217
6	*Physalaemus* aff. *rupestris*	8	1152	505,499004	43,88012188	56,1198781	646,500996	637,056	314,28	231	73,36419753
7	*Bokermannohyla vulcaniae*	9	1296	215,8142094	16,65233097	83,347669	1080,185791	1062,72	741,5	0	0
7	*Proceratophrys palustris*	9	1296	226,2968052	17,46117324	82,5388268	1069,703195	1062,72	314,28	0	0
7	*Scinax ranki*	2	288	50,0974076	17,39493319	82,6050668	237,9025924	236,16	56,4479	0	0

Appendix S5 – Grids mapped used in all analyses of the study and the matrix os distribution.



areas	1	104	106	111	116	121	210	215	220	225	
	24	25	289	30	310	311	317	324	342	355	
	359	361	38	397	400	405	410	415	42	420	
	424	454	457	5	562	563	573	578	583	588	
	685	686	691	696	757	761					
A_arildae	0	0	1	0	1	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	1	1	0	0	1	0
	0	0	0	0	1	1	1	0	0	0	0
	1	0									
A_brunoi	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0									
A_callipygius		0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	1	0	0	0	0	1
	1	0	0								
A_cavicola		0	0	0	0	1	1	0	1	1	1
	0	1	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0								
A_glandulata		0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0

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          0       0       0       0       0       0       0       0       0       0       0
          0       0       0

A_leucopygius     0       0       1       0       1       0       1       0       0       1
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       1       0       1
          0       0       0       0       0       0       1       1       0       0       1
          0       1       1

A_marmorata       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       1       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          1       0       0       0       0       1       1       0       0       0       0
          0       0       0

A_meridionalis    0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       1
          1       0       0       0       0       0       0       1       0       0       0
          0       0       0

A_olfersioides    0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       1       0       0       0
          1       0       0       0       0       0       0       0       0       0       0
          0       0       0

A_perviridis      0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       1       0       0       0       0       1       0       0
          0       0       0       0       1       1       0       0       0       1       1
          1       0       1

A_pomba   0       0       0       0       0       0       0       0       0       0       0
          0       0       0       1       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0

A_thomei  0       0       0       0       0       0       1       0       0       0       0
          1       0       0       1       0       0       0       0       0       1       0
          0       0       1       1       0       1       1       0       0       0       1
          0       0       0       0       0       1       0       1       1       1       1
          0       0

A_weygoldti       0       0       0       0       1       1       0       0       0       0
          0       1       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       1       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0

B_alipioi 0       0       0       0       1       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       1       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0

B_atelopode       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          1       0       0

B_aff_ephippium.  0       0       0       0       0       0       1       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0

B_caramaschii     0       0       1       1       1       1       1       1       1       1
          0       0       0       0       1       0       0       0       0       0       0
          0       0       0       0       0       0       0       1       0       0       0
          0       0       0       0       0       0       0       0       0       0       0
          0       0       0
```

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B_circumdata    0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   1   0   0   0   1
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0

B_didactylus    0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   1   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0

B_ephippium     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   1   1   0   1   0   1
          1     1   1

B_gouveai 0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   1   0   0   0   0   0   0
          0     0

B_hylax   0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   1   0   0   0   0   0
          0     0

B_ibitipoca     0   0   1   0   1   0   1   1   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   1
          0     0   0   0   0   0   0   1   0   0   0
          0     0   0

B_luctuosa      0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   1   0   0   1   0   1
          1     0   0   0   0   1   1   1   1   0   1
          1     1   1

B_nanuzae       0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   1
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0

B_nodoterga     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     1   1

B_vulcaniae     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   1   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0

C_aurita  0     0   0   0   0   0   1   0   0   0   0
          1     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   1   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   1
          0     1

C_bandeirensis  0   0   1   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0

C_bokermanni    0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   0   0   0   0
          0     0   0   0   0   0   0   1   0   0   0
```

```
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0

C_brasiliensis      0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       1       0       0       0       0
            0       0       0

C_capixaba          0       0       0       0       0       1       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       1       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0

C_caramaschii       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       1

C_carvalhoi         0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       1       0       0       0       0       0
            1       0       0

C_eleutherodactylus 0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            1       0       0

C_fuliginosus       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       1       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0

C_grandis 0         0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       1       1       0       0       0       0       1
            0       0

C_granulosus        0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       1       1       0       0       0       0
            0       0       0

C_izecksohni        0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       1       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0

C_mantiqueira       0       0       0       0       0       0       1       0       0       0
            0       1       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       1
            1       0       0       0       0       1       0       0       0       0       0
            0       0       0

C_timbuhy           0       0       0       0       0       0       0       0       1       0
            0       1       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       1       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0

C_werneri 0         0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       1       0       0       0       0       0
            0       0       0       1       1       1       0       0       1       1       1
            0       0
```

```
D_anceps 0	0	0	0	0	0	0	0	1	1	1
	1	0	0	1	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0

D_berthalutzae	0	0	0	0	0	1	1	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	1
	0	0	0	0	0	0	0	0	0	0	0
	0	1	0

D_bipunctatus	0	1	0	0	0	0	0	0	0	0
	0	0	0	0	1	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0

D_branneri	0	0	1	0	1	1	1	1	1	1
	1	1	0	1	1	1	0	0	0	0	0
	0	1	0	0	0	0	0	1	0	0	0
	1	0	0	0	0	0	0	0	0	0	0
	0	0	0

D_brevipolicatus	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	1
	0	0	0	0	0	0	1	0	0	0	0
	0	0	0

D_carvalhoi	0	0	1	0	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0

D_decipiens	0	0	0	0	1	1	1	1	0	0
	0	1	0	0	1	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	1
	1	0	0	0	0	0	1	0	0	0	0
	0	0	0

D_elegans 0	1	1	1	1	1	1	1	1	1	1
	1	0	0	1	1	0	0	0	0	0	0
	1	0	0	0	0	0	1	0	1	1	1
	0	0	0	0	0	1	1	0	0	0	1
	0	0

D_giesleri 0	0	0	0	1	1	0	0	0	1	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0

D_haddadi0	0	0	0	1	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0

D_microps	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	1
	0	0	0	0	0	1	1	0	0	0	1
	1	1	1

D_minutus	0	0	1	0	1	1	1	1	0	1
	0	1	0	1	1	0	0	1	1	1	0
	0	0	0	1	0	0	1	1	1	0	1
	1	1	0	1	0	1	1	1	1	0	0
	0	1	1

D_nanus 0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	1	0	1	0	0	0	1	0	0
```

```
                0   0   0   0   0   0   0   0   0   0   0
                0   0

D_rubicundulus      0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   1   0
                0   0   0   0   0   1   1   0   0   0   1
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

D_ruschii       0   0   1   0   1   0   1   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   1   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0

D_sanborni          0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   1   0

D_sanbornii         0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   1   0   0   0   0   0   0   0
                0   0   0   0   0   1   0   0   1   0   0
                0   0   1

D_seniculus         0   0   0   0   1   1   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

E_cesarii       0   0   0   0   0   0   1   1   1   0   0
                1   0   0   1   0   0   0   0   0   1   0
                0   0   0   0   0   0   0   0   0   1   1
                0   0   0   0   0   1   1   1   1   0   1
                1   0

E_robusta       0   0   0   0   0   0   0   0   1   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0

E_tridactyla        0   0   0   0   1   1   0   0   0   1
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

F_fissilis      0   0   1   0   1   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   1   1   0   0   0   0   0
                0   0

F_goeldii       0   0   0   1   1   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   1   0   0   0   0
                0   0   0   0   1   0   0   0   0   0   1
                0   0

F_ohausi        0   0   1   0   1   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   1   0   0   0   0   0
                0   0

F_ulei          0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   1   0   0   0   0   0
                0   0
```

```
G_albolineata   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

G_ernestoi0     0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   1   0   0   0   0   0
            0   0

G_megacephala   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

H_albomarginatus    0   1   1   0   1   1   1   1   1   1
            1   1   0   0   1   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   1   1
            1   0   0   0   0   0   0   0   0   0   0
            0   0   0

H_albopunctatus 0   1   1   0   1   1   1   1   1   0
            1   1   0   0   1   1   0   1   0   0   0
            1   0   0   1   0   1   1   1   1   1   1
            1   0   0   0   0   1   1   1   1   0   0
            0   1   1

H_amnicola      0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   1   0   1
            0   0   0   0   0   0   1   1   0   0   0
            0   0   0

H_babax     1   0   1   0   0   0   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0

H_beckeri   0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   1   0   0   0   0
            0   0   1   0   1   1   0   0   0   0   0
            0   0   0   1   0   0   0   0   0   1   0
            0   0

H_binotatus     0   1   1   1   1   1   1   1   1   1
            0   1   0   0   1   1   1   0   0   0   0
            0   0   0   0   0   1   0   1   0   0   1
            1   1   0   0   0   0   1   1   1   0   0
            0   1   0

H_bischoffi     0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   1   0

H_bradei    0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   1   0   0   0   0   0   0
            0   0

H_crepitans     0   1   1   0   1   0   1   1   1   0
            0   1   1   1   1   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

H_faber     1   1   1   0   1   1   1   1   1   1   0
            1   0   1   1   0   0   0   1   0   0   1
            0   0   1   0   1   0   1   1   1   1   1
```

```
            1       0       0       0       1       1       1       1       0       0       0
            1       1

H_glaber    0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       1       1       0       0       0       0       0
            0       0

H_japi      0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            1       0

H_lateristrigatus   0       1       0       0       1       1       0       0       0
            0       1       0       0       1       0       0       0       0       0       0
            0       0       0       0       0       0       0       1       0       0       0
            1       1       0       0       0       0       0       0       0       0       0
            0       0       0

H_latistriatus      0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       1       1       1       0       1       0       1
            1       0       0

H_luederwaldti      0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       1       0       0       0       0       0
            1       0       0

H_lundii    0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       1       0       0       0       1
            0       0       0       0       1       1       0       1       0       1       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0

H_magalhaesi        0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       1
            1       0       0

H_sp.       0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       1       1       0       0       0       0       0
            0       0

H_ornatus   0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       1       1       0       0       0       0       0
            0       0

H_pardalis0         1       1       0       1       1       1       1       1       1       0
            1       1       1       1       1       0       0       0       0       0       0
            0       0       0       0       1       1       1       0       0       1       1
            0       0       0       0       0       1       1       0       0       0       0
            0       0

H_perere    0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       0       0       0       0
            0       0       0       0       0       0       0       1       0       1       0
            0       0       0       0       0       0       1       0       0       0       0
            0       0

H_polytaenius       0       1       1       0       1       0       1       1       1       1
            0       1       0       1       1       1       0       0       0       0       0
            0       0       0       0       0       0       1       0       1       1       1
            1       0       0       0       0       1       1       1       0       0       1
            0       1       0
```

```
H_prasinus      0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   1   0   0   0   0   0   0   0
            0   0   0   1   0   0   0   0   1   1   1
            1   1   1

H_regius    0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   1   1   0   0   0   0   0
            0   0

H_sazimai   0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   1   0
            0   0

H_semilineatus  0   0   0   0   1   1   1   1   1   1
            0   1   0   0   1   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   1   1
            1   0   0   0   0   0   0   1   0   0   0
            0   0   0

H_serranegra_sp.nov.0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   1
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

H_stenocephalus 0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   1   0   0   0   0   0   0   1
            0   0   0   1   0   1   0   0   0   0   0
            0   0   0

H_vanzolini     0   0   1   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

I_abdita    0   0   0   0   1   1   0   1   1   1   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0

I_aff_holti 0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   1
            0   0

I_concolor  0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   1   0   0   0   0   0   0
            0   0

I_epipeda   0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0

I_holti     0   0   0   0   0   0   0   0   0   0   0
            0   0   0   1   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   1   0
            0   0   0   0   1   1   0   0   0   0   0
            0   0

I_izecksohni    0   1   1   0   1   0   1   1   0   0
            0   1   0   0   1   1   0   0   0   0   0
            0   0   0   0   0   0   0   1   1   0   1
```

```
                1       0       0       0       0       0       1       1       0       0       0
                1       0       0

I_juipoca       0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       1       1       0       0       1
                0       0       1       0       1       1       0       1       0       1       1
                0       0       0       0       1       1       1       1       1       1       1
                1       1

I_langsdorffii          0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       1       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                1       0       1

I_melanopygia           0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       1       0       0       0       0       0
                0       0       0

I_oea           0       0       0       0       0       1       0       0       0       1       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       1       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0

I_verrucosa             0       0       1       0       1       1       1       1       1       1
                1       1       0       0       1       0       0       0       0       0       0
                0       0       0       0       0       0       0       1       0       0       0
                1       0       0       0       0       0       0       0       0       0       0
                0       0       0

I_vizottoi      0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       0       0       1       1
                0       0

L_cunicularius          0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       0       1       0       0       0
                0       0       0       1       0       0       1       0       1       0       1
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0

L_cupreus       0       0       0       0       0       1       1       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0       0       0       0       0       1       0       0       0       0
                0       0       0       0       0       0       0       0       0       0       0
                0       0

L_furnarius             0       0       0       0       0       0       0       0       0       0
                0       0       0       0       1       1       0       0       0       1       0
                0       0       0       1       0       0       1       0       1       1       1
                1       0       0       0       0       1       0       1       1       1       0
                1       0       0

L_fuscus        0       0       1       0       1       0       1       1       1       0       0
                1       0       1       1       0       0       0       0       0       0       1
                0       0       0       0       0       1       1       1       1       1       1
                1       0       0       0       0       1       0       1       0       0       0
                0       0

L_labyrinthicus         0       1       0       0       0       0       1       1       0       0
                0       1       0       0       0       0       0       0       0       0       0
                1       0       0       1       0       0       0       0       1       0       0
                1       0       0       0       0       0       0       1       0       0       0
                0       0       0

L_latrans       0       0       1       0       1       1       1       0       1       1       0
                1       0       0       0       0       0       0       0       0       0       0
                0       0       1       0       1       0       1       0       1       1       1
                0       0       0       0       0       1       0       0       0       0       0
                0       0
```

```
L_mystacinus    0    0    0    0    0    0    1    1    1    0
          0     1    0    0    0    0    0    0    0    0    0
          0     0    1    0    0    0    0    0    0    0    0
          1     1    0    0    1    1    1    1    1    0    0
          0     0    0

L_natalensis    0    0    0    0    0    1    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0

L_spixii  0     0    1    1    1    0    1    1    1    0    0
          1     0    0    1    1    0    0    0    0    0    0
          0     0    0    0    0    0    1    0    0    0    1
          0     0    0    0    0    1    0    0    0    0    0
          0     0

M_alipioi 0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    1    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0

M_apuana  0     0    1    0    1    0    1    0    0    0    0
          1     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0

M_boticariana   0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          1     0    1

M_jordanensis   0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          1     0    0

M_lutzae  0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    1    0    0    0    0    0
          0     0

M_microps       0    0    1    0    1    1    0    0    0    1
          0     1    0    0    1    0    0    0    0    0    0
          0     0    0    0    0    1    0    1    1    0    0
          1     0    0    0    1    1    1    0    0    0    0
          0     0    0

M_moreirae      0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    1    1    0    0    0    0
          0     0    0

M_peritus 0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    0    0    1    0
          0     0

O_americanus    0    0    0    0    0    0    0    0    0    0
          0     0    0    0    0    0    0    1    1    0    0
          0     0    0    1    0    1    1    0    1    0    1
          1     0    0    0    1    1    1    1    1    1    1
          1     1    0

O_cultripes     0    0    0    0    0    0    1    0    0    0
          0     0    0    0    0    0    0    1    0    1    0
          1     0    0    1    0    1    1    0    0    0    1
```

```
            0    0    0    0    0    0    1    0    0    0    0
            0    0    0

P_ayeaye    0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    1    0    0    0    0    1    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0

P_boiei     0    0    1    0    1    0    1    1    1    0    0
            1    0    0    1    0    0    0    0    1    0    0
            0    0    0    0    1    0    1    1    0    1    1
            0    0    0    0    1    1    1    1    1    0    0
            1    1

P_burmeisteri    0    1    0    1    0    1    1    1    0
            0    1    1    0    1    0    0    0    0    0    0
            1    0    0    1    0    1    0    1    0    0    1
            1    0    0    0    0    1    1    0    1    0    0
            0    1    1

P_aff._rupestris. 0   0    1    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_carvalhoi      0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    1    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_centralis      0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            1    0    0    0    0    1    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_cochranae      0    0    0    0    0    0    1    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    1    0    1    0    0    1    0    1
            1    0    0    0    0    0    1    0    0    0    0
            1    1    0

P_crombiei       0    0    0    0    0    1    0    0    1    1
            0    1    0    0    1    0    0    0    0    0    0
            0    0    0    0    0    0    0    1    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_cuvieri   0    1    1    0    1    0    1    1    1    1    1
            1    0    0    1    0    0    1    1    1    0    1
            0    0    1    0    1    0    1    0    1    1    1
            0    0    1    0    1    1    1    1    1    1    1
            1    1

P_exilis    0    0    0    0    0    1    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    1    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0

P_feioi     0    0    1    0    0    0    1    1    0    0    0
            1    0    0    1    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    1    0    0    0
            0    0    0    0    0    1    0    0    1    1    1
            0    0

P_guttata   0    0    0    0    0    0    0    0    1    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0
```

```
P_itamari       0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   1   0   0   0   0   0   1
                0   0

P_jordanensis       0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   1   0   0   0   0   0   0   0
                0   0   0   0   0   1   1   0   0   0   0
                1   0   0

P_kautskyi          0   0   0   0   1   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

P_laticeps      0   0   0   0   0   1   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   1   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0

P_luteolus      0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   1   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0

P_lutzii        0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   1   1   0   0   0   0   0
                0   0

P_maculiventris     0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

P_mantiqueira       0   0   1   0   0   0   1   1   0   0
                0   1   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   1
                0   0   0   0   0   1   1   0   0   0   0
                0   0   0

P_marginata         0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

P_maximus           0   0   0   0   1   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

P_moehringi         0   0   0   0   1   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

P_murundu           0   0   0   0   0   0   0   0   0   0
                0   0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   0   1   0   1   0   0
                0   0   0   0   0   0   0   0   0   0   0
                0   0   0

P_mystacalis        0   0   0   0   0   0   1   0   0   0
                0   0   0   0   0   1   0   0   0   0   0
                0   0   0   0   0   0   0   0   0   0   0
```

```
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_obtetus   0    0    0    0    0    1    0    1    0    1    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0

P_olfersii  0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    1    0
            0    0    0    0    0    0    0    0    0    0    0
            0    1

P_palustris      0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    1    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_paviotii  0    0    1    0    1    1    0    0    0    0    0
            1    0    0    0    0    0    0    0    0    0    0
            1    0    0    0    0    0    1    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0

P_phyllostomus   0    0    0    0    0    0    0    0    0    1
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    1    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_rupestris      0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    1
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0

P_schirchi  0    0    0    0    1    1    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    1    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0

P_signifer  0    0    0    0    0    0    1    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    1    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0

Pt_mantiqueira   0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    1    0    0    0    1
            0    0    0

R_crucifer  0    0    1    0    1    1    1    1    1    1    1
            1    0    0    1    1    0    1    1    1    0    0
            0    0    0    0    0    0    1    1    0    1    1
            0    0    1    0    0    0    1    0    0    0    0
            0    0

R_granulosa      0    1    1    0    0    1    1    0    1    0
            1    1    0    0    0    0    0    0    0    0    0
            0    0    0    0    0    0    0    1    0    0    0
            0    1    0    0    0    0    0    0    0    0    0
            0    0    0

R_icterica  0    0    0    0    0    0    0    0    0    0    0
            1    0    0    0    0    0    0    0    0    0    0
            0    0    1    0    0    0    0    1    0    1    0
            0    0    0    0    1    1    1    1    0    0    1
            1    1
```

```
R_ornata 0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   1   0   0
         0   0   1   0   1   0   0   0   0   0   1
         0   1   1   0   0   1   1   1   0   0   0
         1   1

R_rubescens  0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   1   1   0   0
         0   0   0   1   0   0   1   0   1   0   1
         0   0   0   0   0   0   1   1   0   0   0
         0   0   0

R_schneideri 0   0   1   0   0   0   0   0   0   0
         0   1   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   1   1   1   1   0   1
         0   0   0   0   0   0   1   0   1   0   0
         0   0   0

S_alter  0   0   1   0   1   1   1   1   1   1   0
         0   0   0   0   0   0   0   0   0   0   0
         1   0   0   0   0   0   1   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0

S_arduous 0  0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         1   0   0   0   0   0   1   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0

S_argyreornatus  0   0   0   0   1   1   1   1   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   1   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0

S_belloni 0  0   0   0   1   0   0   0   1   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0

S_aff._rizibilis 0   0   0   0   0   0   1   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0

S_caldarum   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   1   0   0   0   0   0   0   0
         0   0   0   1   0   0   0   0   0   0   0
         0   0   0

S_cardosoi   0   0   0   0   0   0   1   0   0   0
         0   0   0   0   1   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   1
         0   0   0   0   0   0   1   1   0   0   0
         0   0   0

S_carnevallii    0   0   1   0   0   0   0   0   0   0
         0   1   0   0   1   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0

S_cosenzai   0   0   1   0   0   0   1   1   0   0
         0   1   0   0   1   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   0   1
         0   0   0   0   0   0   0   0   0   0   0
         0   0   0

S_crospedospilus 0   0   1   0   0   0   1   0   0   0
         0   1   1   0   1   0   0   0   0   0   0
         0   0   0   0   0   0   0   0   0   1   1
```

```
            1   0   0   0   0   0   1   0   0   0   0
            0   0   0

S_cuspidatus    0   0   0   0   0   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

S_duartei   0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   1   1   0   0   1   1   1
            0   0

S_eurydice      0   0   1   0   0   0   1   0   0   1
            1   1   0   0   1   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   1   1
            1   0   0   0   0   0   1   1   0   0   0
            0   1   0

S_flavoguttatus 0   0   0   0   0   0   0   0   0   0
            0   0   0   0   1   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   1   0   1
            1   0   0   0   0   1   1   1   0   0   0
            0   0   0

S_fuscomarginatus   0   0   0   0   0   0   1   0   0   0
            1   1   0   0   0   0   0   1   0   0   0
            0   0   0   0   0   0   1   0   0   0   1
            0   0   0   0   0   0   1   0   0   0   0
            0   0   0

S_fuscovarius   0   1   1   0   1   0   1   1   1   0
            0   1   0   1   1   0   0   0   1   0   0
            1   0   0   1   0   0   1   1   1   1   1
            1   0   0   0   0   1   1   1   1   0   0
            1   1   0

S_hayii     0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   1   0   0   0   1   0   0   0   1
            0   0   0   0   0   0   0   0   0   1   1
            1   1

S_heyeri    0   0   0   0   0   1   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0

S_hiemalis      0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   1   0   1   0   1   1   1
            1   1   1

S_kautskyi      0   0   0   0   1   1   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   1   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

S_longilineus   0   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0   1   0   1   1   0   1   0   0
            0   0   0   0   0   0   0   0   0   0   0
            0   0   0

S_luizotavioi   0   0   1   0   0   0   1   1   0   0
            0   1   0   0   0   0   0   0   0   0   0
            0   0   0   0   0   0   0   0   0   0   1
            1   0   0   0   0   0   0   0   0   0   0
            0   0   0
```

```
S_obtriangulatus	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	1	1	0	0	0	0
	1	0	0

S_orophilus	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	1
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0

S_ranki	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	1	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0

S_squalirostris	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	1	0	0	0	0	0	0	1
	0	0	0	0	0	1	0	0	0	0	0
	0	0	0

S_aff_belloni	0	0	0	0	0	0	0	0	1	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0

S_tripui	0	0	1	0	0	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0

S_x-signatus	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0

Scinax_aff_cozenzai		0	0	0	0	0	0	0	0	0
	0	0	1	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0

Scinax_aff_arduous		0	0	0	0	1	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0

T_imitatrix	0	0	0	0	0	0	0	1	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	1
	0	0	0	0	0	1	1	0	0	0	0
	1	0	0

T_mesophaeus	0	0	0	0	0	1	0	0	0	0
	1	0	0	0	0	0	0	0	0	0	0
	0	1	0	0	0	0	0	1	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0

T_miliaris	1	1	1	1	1	1	1	1	1	1	0
	1	0	1	1	1	0	0	0	0	0	0
	1	0	1	0	0	0	1	1	0	1	1
	1	0	0	0	0	1	1	0	0	0	0
	0	0

T_petropolitana	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0
```

0	0	0	0	0	0	0	0	0	0	0
0	0	0								
T_aff._lutzi	0	0	1	0	0	0	1	0	1	0
0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0
0	0	0								
V_eurygnatha	0	0	1	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	1	1	0	1
0	0	0	0	0	1	1	0	0	1	1
1	1	0								
V_uranoscopa	0	0	1	0	0	1	1	1	0	0
0	0	0	0	0	0	0	1	0	0	0
0	0	0	1	0	0	1	1	1	0	1
1	0	0	0	0	0	1	0	0	0	0
0	1	0								
Z_carvalhoi	0	0	1	0	0	1	1	0	0	0
0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0
1	0	0	0	0	0	0	0	0	0	0
0	0	0								
Z_parvulus	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0
0	0	0								