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DESVENDANDO O PAPEL DO CLIMA NOS PADRÕES DE DIVERSIDADE E ENDEMISMO DE ANFÍBIOS

Ilhéus, Bahia

Agosto de 2025

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DESVENDANDO O PAPEL DO CLIMA NOS PADRÕES DE DIVERSIDADE E ENDEMISMO DE ANFÍBIOS

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"O real não está no início nem no fim, ele se mostra pra gente é no meio da travessia..."

— João Guimarães Rosa

“When you look, you usually find something, but not always what you were looking for.”

— The Hobbit, J.R.R. Tolkien



Dedicado à minha família.

Sumário

Resumo

As mudanças climáticas sempre fizeram parte da história da Terra. No entanto, desde a Revolução Industrial, sua intensidade aumentou em um ritmo sem precedentes, e os padrões de temperatura têm se alterado mais rapidamente do que em qualquer outro intervalo de 50 anos nos últimos dois milênios. Essas transformações afetam diretamente a biodiversidade e o funcionamento dos ecossistemas, embora de forma desigual entre os diferentes grupos. Entre eles, os anfíbios destacam-se pela elevada vulnerabilidade, com cerca de 41% das espécies globalmente ameaçadas. Características como pele permeável, dependência de ambientes úmidos, baixa capacidade de dispersão e ciclos de vida complexos acentuam sua sensibilidade às mudanças ambientais. Nesta tese, tivemos como objetivos: (i) sintetizar, por meio de revisão sistemática, os padrões globais dos efeitos das mudanças climáticas na distribuição de anfíbios e avaliar se as respostas são mais relacionadas aos traços de história de vida ou a fatores biogeográficos; (ii) desenvolver um pacote em R para o cálculo de métricas de endemismo e diversidade; (iii) projetar os impactos de cenários futuros de clima sobre a diversidade taxonômica e filogenética e o endemismo filogenético de sapos neotropicais; (iv) avaliar como as mudanças climáticas alteram a beta diversidade taxonômica, filogenética e funcional desses sapos; e (v) examinar a sobreposição espacial entre hotspots de endemismo, regiões com cobertura de vegetação nativa e unidades de conservação no presente e sob cenários futuros para sapos neotropicais. Como complemento, inclui-se seção anexa de divulgação científica (livro infantil, artigo no Oeco, matéria no UTexas News e postagens em redes sociais) derivadas principalmente do terceiro capítulo. Os resultados do primeiro capítulo demonstram que as características biogeográficas da área de distribuição afetam fortemente a resposta dos anfíbios às mudanças climáticas. Espécies que ocorrem em elevadas altitudes e em habitats florestais são projetadas para uma grande porção de suas áreas climaticamente adequadas, enquanto espécies de habitats secos apresentam expansão projetada. Além disso, identificamos diferenças regionais, com expansões de range projetadas para espécies nas regiões Afrotropical e Neártica. Nossos resultados do segundo capítulo demonstram que o pacote R *phyloraster* requer substancialmente menos RAM em comparação com outros pacotes para calcular métricas espaciais de endemismo. Essa demanda reduzida de memória permite a análise de conjuntos de dados de alta resolução em múltiplas escalas, minimizando as limitações de hardware e aumentando a acessibilidade a medidas espacializadas de diversidade evolutiva. Os resultados do terceiro capítulo indicam que quase metade (42,20%) das espécies de sapos neotropicais estudadas deverá sofrer uma redução em suas áreas de distribuição, com nove espécies (1,71%) previstas para perder toda a sua distribuição até 2050. Prevê-se também que as mudanças climáticas futuras reduzam em grande parte dos Neotrópicos a diversidade taxonômica (TD), filogenética (PD) e o endemismo filogenético (PE) desses sapos. No entanto, a perda de PD e, principalmente, de PE em algumas regiões pode ser muito mais severa do que a perda de TD. Os resultados do quarto capítulo sugerem que as mudanças climáticas futuras irão reorganizar as comunidades de sapos neotropicais, considerando as três dimensões de diversidade avaliadas (taxonômica, filogenética e funcional). Essas mudanças são projetadas para serem impulsionadas principalmente por diferenças de riqueza (ganho e perda de espécies) em grande parte dos Neotrópicos. Espera-se que comunidades futuras experimentem uma homogeneização

filogenética e funcional substancial, tornando-se dominadas por espécies com traits e histórias evolutivas semelhantes. Por fim, o quinto e último capítulo projeta que os centros de paleo-, neo- e endemismo misto devem sofrer uma brusca redução até 2050, especialmente na Mesoamérica e nos Andes. Em contraste, os centros de super-endemismo devem se expandir. A cobertura por unidades de conservação e por cobertura florestal variou entre os tipos de endemismo: centros de neo- e super-endemismo foram melhor representados em áreas protegidas, enquanto paleo- e endemismo misto estiveram mais associados à áreas com maior cobertura florestal. Em conjunto, os resultados desta tese evidenciam que as mudanças climáticas têm o potencial de afetar a distribuição, a diversidade e os padrões de endemismo de anfíbios, tanto globalmente quanto nos Neotrópicos, provocando perdas significativas de diversidade taxonômica e filogenética, além de endemismo, e promovendo a homogeneização das comunidades. Esses achados reforçam a necessidade de estratégias de conservação que considerem múltiplas dimensões da biodiversidade, integrando áreas protegidas e a preservação da cobertura florestal, como forma de mitigar os impactos das mudanças climáticas sobre esses organismos.

Palavras-chave

Macroecologia, Conservação, Aquecimento global, Anurofauna, Neotrópicos

Abstract

Climate change has been part of Earth's history. However, since the Industrial Revolution, its intensity has increased at an unprecedented rate, and temperature patterns have changed more rapidly than in any other 50-year period over the last two millennia. These transformations directly affect biodiversity and ecosystem functioning, although unevenly across different groups. Amphibians stand out for their high vulnerability, with approximately 41% of species globally threatened. Traits such as permeable skin, dependence on humid environments, low dispersal capacity, and complex life cycles amplify their sensitivity to environmental changes. This thesis aimed to: (i) synthesize, through a systematic review, global patterns of climate change effects on amphibian distributions and evaluate whether responses are more strongly related to life-history traits or biogeographical factors; (ii) develop an R package to calculate endemism and diversity metrics; (iii) project the impacts of future climate scenarios on the taxonomic diversity, phylogenetic diversity and phylogenetic endemism of Neotropical frogs; (iv) assess how climate change alters taxonomic, phylogenetic, and functional beta diversity of these frogs; and (v) examine the spatial overlap between endemism hotspots for Neotropical frogs, native vegetation cover, and protected areas in the present and under future scenarios. An additional section on science outreach includes a children's book, an article in *Oeco*, a feature in *UTexas News*, and social media posts, primarily derived from Chapter 3. The results of Chapter 1 demonstrate that the biogeographical characteristics of species' ranges strongly influence amphibian responses to climate change. High-altitude and forest-dependent species are projected to lose substantial portions of their climatically suitable areas, whereas species from dry habitats are projected to expand. Regional differences were also observed, with range expansions projected for species in the Afrotropical and Nearctic regions. Chapter 2 shows that the R package *phyloraster* requires substantially less RAM than other packages to compute spatial endemism metrics, facilitating analyses of high-resolution datasets across scales. Chapter 3 indicates that nearly half (42.2%) of the studied Neotropical frog species are expected to experience reductions in their distribution areas, with nine species (1.71%) projected to lose their entire range by 2050. Future climate change is also predicted to reduce taxonomic diversity (TD), phylogenetic diversity (PD), and phylogenetic endemism (PE) diversity, with losses of PD and especially PE potentially exceeding TD losses in some regions. Chapter 4 suggests that future climate change will reorganize Neotropical frog communities across taxonomic, phylogenetic, and functional dimensions, primarily driven by richness differences, leading to substantial phylogenetic and functional homogenization. Finally, Chapter 5 projects marked reductions in paleo-, neo-, and mixed-endemism centers by 2050, particularly in Mesoamerica and the Andes, while super-endemism centers are expected to expand. Coverage by protected areas and forest varied among endemism types: neo- and super-endemism centers were better represented in protected areas, whereas paleo- and mixed-endemism centers were more strongly associated with forest cover. Overall, the results of this thesis highlight that climate change has the potential to affect amphibian distributions, diversity, and endemism patterns globally and in the Neotropics, causing significant losses in taxonomic and phylogenetic diversity and endemism, while promoting community homogenization. These findings underscore the importance of conservation strategies that consider multiple dimensions of

biodiversity, integrating protected areas and forest conservation to mitigate the impacts of climate change on amphibians.

Keywords

Macroecology, Conservation, Global warming, Anuran fauna, Neotropics

Introdução geral

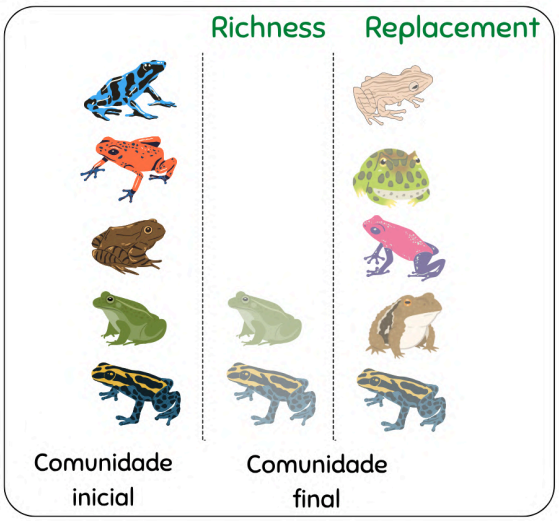
As mudanças climáticas fazem parte da história da vida na Terra (Zachos *et al.*, 2001) e têm sido um dos principais motores dos padrões de extinção, diversificação e distribuição das espécies. Ao longo da história geológica do planeta, períodos de aquecimento e resfriamento ocorreram em escalas temporais extensas (Zachos *et al.*, 2001), moldando a biodiversidade global. No entanto, desde o início da Revolução Industrial, a temperatura média da superfície global tem aumentado mais rapidamente do que em qualquer outro período de 50 anos nos últimos 2000 anos (Intergovernmental Panel On Climate Change, 2023). O sexto relatório do Painel Intergovernamental sobre Mudanças Climáticas demonstrou que a temperatura média global já teve um incremento de aproximadamente 1.1°C, e as projeções indicam que continuará subindo nas próximas décadas, principalmente devido ao uso de fontes de energia não sustentáveis, mudanças no uso do solo, estilo de vida, e padrões globais de consumo (Intergovernmental Panel On Climate Change, 2023).

Essas mudanças no clima têm gerado impactos diretos e indiretos sobre a biodiversidade e o funcionamento dos ecossistemas (Intergovernmental Panel On Climate Change, 2023). De forma geral, essas alterações podem afetar as espécies de três maneiras principais: promovendo a dispersão para novas áreas com condições climáticas mais adequadas; exigindo adaptações às novas condições; ou resultando em extinções locais (Parmesan, 2006; O'Connor *et al.*, 2012). A depender da resposta individual de cada espécie, esses efeitos podem desencadear uma série de consequências ecológicas em cascata, como alterações nas dinâmicas de interações interespecíficas, mudanças nas dinâmicas populacionais, na fenologia e nos padrões migratórios (Jetz *et al.*, 2007; Hof *et al.*, 2011; Powers & Jetz, 2019; Sales *et al.*, 2021). Além disso, podem comprometer processos que ocorrem em outros níveis organizacionais, como comunidades e ecossistemas, moldando os padrões de diversidade (Jetz *et al.*, 2007; Lemes *et al.*, 2014; Alves-Ferreira *et al.*, 2025)) e comprometendo os serviços ecossistêmicos (Mooney *et al.*, 2009).

Esses impactos não ocorrem de forma homogênea entre os grupos taxonômicos. Embora todas as espécies estejam, direta ou indiretamente, sujeitas aos efeitos das mudanças climáticas, nem todas respondem da mesma maneira (Pacifici *et al.*, 2017; Alves-Ferreira *et al.*, 2022a,b). Entre os vertebrados, alguns grupos são particularmente mais vulneráveis, como os anfíbios, considerado um dos vertebrados mais ameaçados globalmente, com cerca de 41% das espécies listadas em alguma categoria de ameaça pela IUCN (IUCN, 2023). Essa alta vulnerabilidade está relacionada a um conjunto de características fisiológicas, ecológicas e de história de vida que os torna particularmente sensíveis a alterações ambientais (Wells, 2007). Por serem ectotérmicos, dependem da temperatura externa para regular seus processos fisiológicos. Além disso, possuem pele permeável, o que facilita a perda de água e a dessecação, ao mesmo tempo em que aumenta a exposição a doenças e à poluição (Wells, 2007). Seu ciclo de vida também contribui para essa fragilidade, pois envolve uma fase larval aquática e uma fase adulta terrestre, tornando-os dependentes de ambos os ambientes (Wells, 2007).

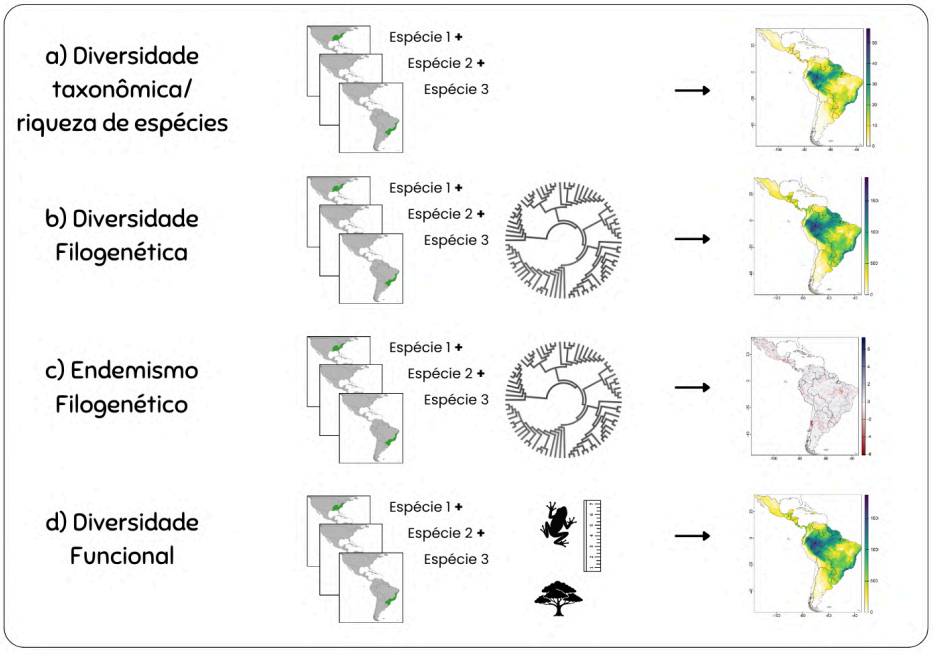
Mesmo dentro do grupo dos anfíbios, as respostas das espécies ainda podem diferir bastante (Alves-Ferreira *et al.*, 2022b,a). Traços de história de vida e aspectos biogeográficos relacionados à área de ocorrência das espécies são fortes candidatos para explicar esses padrões de resposta assimétricos (Alves-Ferreira *et al.*, 2022a,b). Por exemplo, anfíbios com maior tamanho corporal tendem a ser menos afetados pelas mudanças climáticas do que espécies menores, uma vez que a perda de calor por convecção é proporcionalmente menor em organismos de maior porte (Rubalcaba & Olalla‐Tárraga, 2020). O tamanho da área de distribuição também influencia a vulnerabilidade: espécies com distribuições geográficas restritas tendem a ocupar um número menor de micro-habitats e podem ser mais negativamente afetadas caso precisem migrar para novas áreas (Foden *et al.*, 2013). Além disso, espécies restritas a áreas de montanha também podem ser particularmente vulneráveis, pois possuem alto endemismo local (Brooks *et al.*, 2006; La Sorte & Jetz, 2010; Crimmins *et al.*, 2011) e tendem a ocupar faixas de elevação estreitas (Sekercioglu *et al.*, 2008; McCain & Colwell, 2011). Portanto, diversas características podem afetar as respostas individuais que as espécies apresentam diante das mudanças no clima (Pacifici *et al.*, 2017).

As perdas ou ganhos de área de distribuição de cada espécie em nível individual também podem moldar os padrões de diversidade alfa e beta (composição) das comunidades, e esse tem sido um tópico amplamente estudado nos últimos anos (Ochoa-Ochoa *et al.*, 2012; Menéndez‐Guerrero *et al.*, 2020; Mota *et al.*, 2022; Alves-Ferreira *et al.*, 2025). A diversidade beta representa a variação na composição de espécies entre diferentes regiões (beta espacial) ou entre diferentes tempos (beta temporal, e.g. presente e futuro) e pode ser dividida em dois componentes principais (Esquema gráfico 1): *replacement* e *richness* (Cardoso et al., 2014). Esses componentes indicam se as diferenças na composição são decorrentes da perda ou ganhos de espécies (componente *richness*), ou da substituição de determinadas espécies por outras (componente *replacement*). A redução na diversidade beta pode resultar em homogeneização biótica, processo no qual as comunidades tornam-se mais semelhantes ao longo do tempo (Clavel et al., 2011), geralmente devido à perda de espécies especialistas e expansão de espécies generalistas (McKinney & Lockwood, 1999).



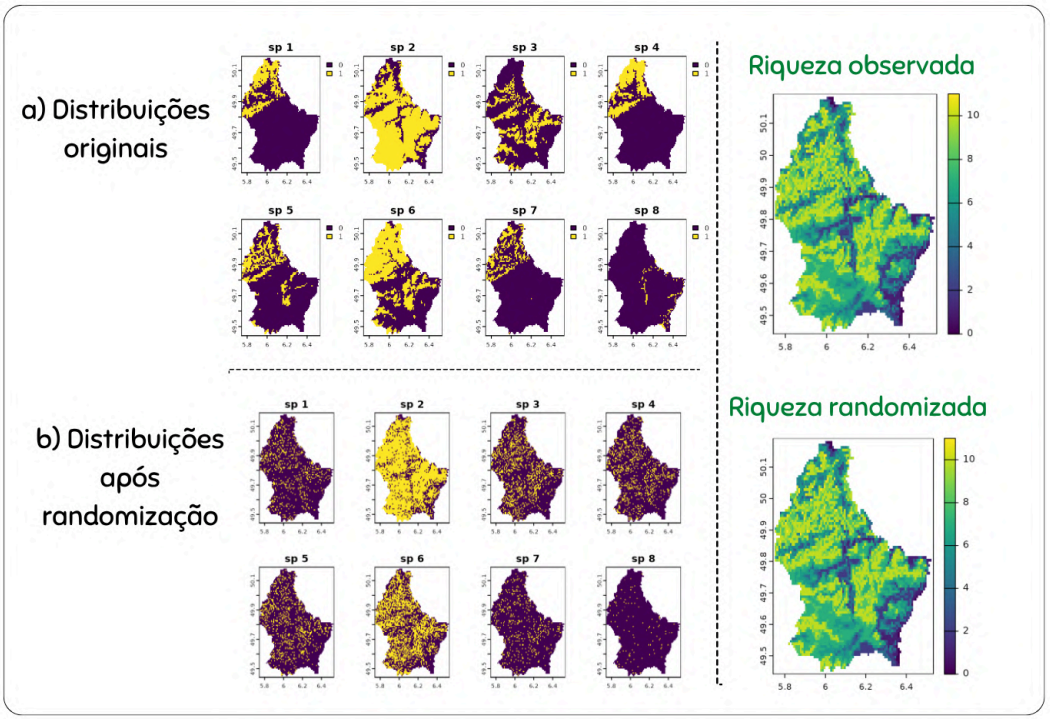
Esquema gráfico 1. Representação dos componentes da diversidade beta — *richness* e *replacement* — e de como esses componentes contribuem para as mudanças na composição das comunidades.

Uma das métricas mais utilizadas para avaliar os padrões de diversidade é a riqueza de espécies ou diversidade taxonômica (SR ou TD), que corresponde à contagem do número de espécies em determinada região (Esquema gráfico 2). Apesar dessa métrica ser bastante informativa, a biodiversidade não se resume apenas ao número de espécies, mas também às informações contidas na topologia e nos ramos das árvores filogenéticas (Mishler *et al.*, 2014), bem como às diferentes funções desempenhadas por cada espécie. Entre as métricas que permitem avaliar outras dimensões da diversidade, destacam-se a diversidade filogenética (PD, (Faith, 1992), (Esquema gráfico 2)), o endemismo filogenético (PE, (Rosauer *et al.*, 2009), (Esquema gráfico 2)) e a diversidade funcional (FD, (Tilman, 2001), (Esquema gráfico 2)). O PD é uma métrica amplamente utilizada que quantifica o acúmulo de história evolutiva em determinada região, por meio da soma do comprimento dos ramos das espécies presentes em uma árvore filogenética (Faith, 1992). Em geral, o PD tende a ser correlacionado com a riqueza de espécies; no entanto, há exceções. Por exemplo, uma região com poucas espécies (baixa riqueza), mas cujas espécies possuem longos ramos na árvore filogenética, pode apresentar alto PD mesmo com baixa riqueza de espécies (Faith, 1992). O PE, por sua vez, utiliza tanto o comprimento do ramo de cada espécie, quanto o tamanho da sua distribuição geográfica para identificar áreas com restrição espacial da história evolutiva. O valor do PE vai depender de fatores como a quantidade de história evolutiva compartilhada entre espécies, o tamanho da distribuição geográfica de cada espécie e a distribuição total do conjunto de espécies presentes em cada local (Rosauer *et al.*, 2009). A FD, por outro lado, se refere aos papeis e funções ecológicas desempenhadas pelas espécies em um ecossistema, e se relaciona com os traits de cada espécie e como elas interagem com o ambiente (Petchey & Gaston, 2006).



Esquema gráfico 2. Representação dos dados necessários para o cálculo das métricas de diversidade usadas nesta tese: a) diversidade taxonômica; b) diversidade filogenética; c) endemismo filogenético; e d) diversidade funcional. O cálculo de TD/SR baseia-se exclusivamente nos rasters de presença-ausência. Para PD e PE, são empregados os rasters de presença-ausência em conjunto com uma árvore filogenética. Já para FD, utilizam-se os rasters de presença-ausência associados aos *traits* de cada espécie, como tamanho corporal e tipo de habitat ocupado.

Muitas métricas de diversidade, como a diversidade filogenética (PD), o endemismo filogenético (PE) e a diversidade funcional (FD), podem apresentar alta correlação com a riqueza de espécies. Isso significa que, à medida que a riqueza aumenta, é comum observar também um aumento na diversidade filogenética, funcional e no endemismo filogenético. Os modelos nulos são muito úteis para comparar padrões com processos aleatórios, permitindo avaliar efeitos da riqueza de espécies em medidas de diversidade (Gotelli e Groves 1996, Gotelli e Ulrich 2012) e testar hipóteses sobre a estrutura da comunidade. O tamanho do efeito padronizado (SES) é amplamente utilizado na literatura sobre estrutura de comunidade e pode ser calculado a partir de modelos nulos (Gotelli e McCabe 2002). Nesta tese, calculamos o SES para as métricas de diversidade usando uma adaptação do modelo nulo SIM5 de Gotelli (2000), o qual randomiza a posição das presenças das espécies no espaço, mantendo constante a riqueza local e preservando o número de pixels ocupados muito próximo ao observado nos dados reais, conforme ilustrado no Esquema Gráfico 3 abaixo.



Modificado do vignette do pacote SESraster (Heming et al., 2023)

Esquema gráfico 3. Representação esquemática do modelo nulo utilizado neste estudo (adaptação do modelo SIM5 de Gotelli, 2000). O esquema mostra: (a) a distribuição real das espécies e a riqueza de espécies calculada a partir dos dados originais; e (b), a distribuição randomizada gerada após aplicação do modelo nulo e a riqueza de espécies calculada com as distribuições randomizadas.

A importância dessas métricas para a conservação é amplamente reconhecida, o que tem levado a inúmeros estudos que investigam padrões macroecológicos e biogeográficos associados a dados filogenéticos e funcionais (Hernández *et al.*, 2013; Burley *et al.*, 2016). Para lidar com a crescente disponibilidade de informações, é fundamental dispor de ferramentas capazes de processar grandes volumes de dados com eficiência. Pacotes como *phyloregion* (Daru *et al.*, 2020), *picante* (Kembel *et al.*, 2010) e *pez* (Pearse *et al.*, 2015) calculam métricas de diversidade a partir de dados matriciais, mas essa abordagem tende a exigir maior poder e tempo de processamento, uma vez que os dados rasterizados precisam ser convertidos para matrizes. Mais recentemente, ferramentas como *divraster* (Mota *et al.*, 2023), *phyloraster* (Alves‐Ferreira *et al.*, 2024) e *net.raster* (Oliveira et al., 2025) passaram a permitir cálculos diretos a partir de rasters ou shapefiles, oferecendo ganhos significativos em desempenho (Alves‐Ferreira *et al.*, 2024) e tornando-se especialmente adequadas para análises em regiões com alto número de espécies e amplas extensões espaciais.

Tais avanços são particularmente relevantes para o estudo da região Neotropical, reconhecida como uma das áreas mais biodiversas do planeta, abrigando diversos ecossistemas e um número excepcionalmente alto de espécies de anfíbios, com aproximadamente 3,000 espécies, sendo 96% destas endêmicas (Bolanos *et al.*, 2008). No entanto, essa riqueza vem acompanhada de uma elevada vulnerabilidade: a região concentra uma proporção desproporcionalmente alta de espécies ameaçadas (Luedtke *et al.*, 2023). Diversos pontos quentes de biodiversidade Neotropicais — como a região Andina, a Floresta Atlântica, a Amazônia, a Mesoamérica, o Cerrado e o Escudo das Guianas — sustentam comunidades únicas, com altos níveis de endemismo, mas que estão sob intensa pressão antrópica (Luedtke *et al.*, 2023). Essa combinação de alta diversidade, elevado endemismo e múltiplas ameaças torna o Neotrópico um cenário prioritário para investigar os impactos de estressores antropogênicos sobre os anfíbios.

Diante disso, esta tese foi estruturada em cinco capítulos em formato de artigos científicos, os quais abordam diferentes aspectos dos efeitos das mudanças climáticas sobre os anfíbios. No primeiro capítulo, realizamos uma revisão sistemática de literatura para avaliar os padrões globais dos efeitos das mudanças climáticas na distribuição de anfíbios (Anura e Caudata) e investigamos se a resposta desses organismos é mais fortemente influenciada por características de história de vida ou por fatores biogeográficos da área de distribuição. No segundo capítulo, apresentamos um pacote em R desenvolvido para calcular métricas de endemismo e diversidade evolutiva a partir de dados em formato raster. No terceiro capítulo, avaliamos como as mudanças climáticas futuras afetam a diversidade taxonômica, a diversidade filogenética e o endemismo filogenético de anuros Neotropicais. No quarto capítulo, analisamos como os padrões de beta diversidade taxonômica, filogenética

e funcional de anuros Neotropicais serão impactados pelas mudanças climáticas futuras. No quinto e último capítulo, investigamos se os hotspots de endemismo de anuros Neotropicais estarão inseridos em áreas com cobertura de vegetação nativa e em unidades de conservação, tanto no presente quanto sob cenários futuros de mudanças climáticas. Também incluímos uma seção anexa dedicada à divulgação científica, composta por um livro infantil sobre os efeitos das mudanças climáticas na biodiversidade, além de materiais derivados do terceiro capítulo, como um artigo no jornal Oeco, uma matéria no UTexas News, e duas postagens publicadas em perfis de divulgação científica no Instagram.

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Capítulo 1

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Unraveling global impacts of climate change on amphibians distributions: A life-history and biogeographic-based approach

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Abstract

Climate change can affect species distribution patterns in three different ways: pushing them to disperse to new suitable areas, forcing them to adapt to novel climatic conditions, or driving them to extinction. However, the biological and geographical traits that lead to these different responses remain poorly explored. Here, we evaluated how ecological and biogeographic traits influence amphibians' response to climate change. We performed a systematic review searching for studies that evaluated the effects of future climate change on amphibian's distribution. Our research returned 31 articles that projected the distribution of 331 amphibians. Our results demonstrate that species inhabiting an elevation above 515 m will lose a significant portion of their climatically suitable area. We also found that as isothermality increases, the amount of area suitable in response to climate change also increases. Another important discovery was that as the size of the baseline area increases, the greater must be the loss of climatically suitable areas. On the other hand, species with very small areas tend to keep their current climatically suitable area in the future. Furthermore, our results indicate that species that inhabit dry habitats tend to expand their suitable area in response to climate change. This result can be explained by the environmental characteristics of these habitats, which tend to present extreme seasonal climates with well-defined periods of drought and rain. We also found that anurans that inhabit exclusively forests are projected to lose a greater portion of their suitable areas, when compared to species that inhabit both forest and open areas, wetlands, and dry and rupestrian environments. The biogeographical realm also influenced anuran's range shifts, with Afrotropic and Nearctic species projected to expand their geographical ranges. The assessment of climate change effects on amphibian

distribution has been the focus of a growing number of studies. Despite this, some regions and species remain underrepresented. Current literature evaluates about 4% of the 7,477 species of Anura and 8% of the 773 species of Caudata and some regions rich in amphibian species remain severely underrepresented, such as Madagascar. Thus, future studies should focus on regions and taxa that remain underrepresented.

Keywords: systematic review, Anura, Caudata, global warming, suitable area, Ecological Niche Model (ENM), species distribution

Introduction

Climate change determines large scale patterns of species distribution in three principal ways: pushing them to disperse to new suitable areas, forcing them to adapt to novel climatic conditions, or driving them to extinction (Holt, 1990; Parmesan, 2006; Diniz-Filho and Bini, 2007; Araújo et al., 2008). While some species are losing part of their current geographic range due to climate change (Zank et al., 2014; Struecker and Milanovich, 2017; Zhang et al., 2020), other species can even expand their suitable areas (Mokhatla et al., 2015; Toranza et al., 2016). Therefore, although we expect that most species are likely to be equally affected by global warming, the response patterns can be quite contrasting (Winter et al., 2016; Vasconcelos et al., 2018; Menéndez-Guerrero et al., 2020).

Among vertebrates, amphibians represent one of the most vulnerable groups to global warming (Pounds, 2001; Blaustein et al., 2010), because almost all species are highly dependent of specific climatic conditions (Zeisset and Beebee, 2008) and have narrow ecological niches (Blaustein et al., 2010). Climate change may increase the vulnerability of amphibians by acting synergistically with other impacts like habitat loss, emerging diseases, and chemical contaminants (Stuart et al., 2004; Collins, 2010). According to the Global Amphibian Assessment (GAA), these threats have already placed 32% of amphibian species under some of IUCN Red List threat categories (i.e., Vulnerable, Endangered, or Critically Endangered) (Stuart et al., 2004). Thus, anticipating the effects of climate change on the amphibians' distribution and identifying the traits that make the species more vulnerable to climate change has become a priority for conservation. In this sense, the use of Ecological Niche Models (ENM, Araújo and Peterson, 2012) has been an essential tool to generate conservation strategies based on the climate effect on distribution (Sillero et al., 2021). The ENMs use occurrence records and bioclimatic variables to make mathematical approximations on species climatic niche and allow the prediction of climatically suitable areas under various climate scenarios (Taylor et al., 2020), allowing the anticipation of species responses to climate change (Urbina-Cardona and Loyola, 2008).

Life history traits can be important candidates to explain the variation in species vulnerability to global warming (Foden et al., 2013; Beissinger and Riddell, 2021). For example, anurans with specialized reproductive modes are expected to be more strongly dependent on the integrity of very specific habitats (Loyola et al., 2008), and therefore should be more negatively affected by climate change than anurans with generalist reproductive modes. Likewise, species that rely on environmental triggers to initiate activities such as

migration or reproduction must also experience heightened sensitivity to climate change (Foden et al., 2013). On the other hand, large ectotherms are expected to be less affected by climate change because the convection limit increases with body size. In this way, heat loss by convection will be lower and make them more resistant to higher temperatures than smaller ectotherms (Seebacher et al., 1999, 2003; Rubalcaba and Olalla-Tárraga, 2020).

The amphibians vulnerability to climate change is also expected to be limited by the amplitude of their thermal tolerance range (Freitas et al., 2010), result of the process of natural selection and adaptation to the extreme temperatures that lineages have experienced throughout their evolution (Denny et al., 2009; Bozinovic et al., 2011; Buckley and Huey, 2016). Therefore, the lineages that tend to experience relatively higher average temperatures and less seasonal variation should have less potential for adaptive rescue (Ghalambor, 2006; Huey et al., 2009), as they already have their maximum thermal tolerance close to or above optimal. In this way, small increases in temperature can have disproportionately large effects on their thermal performance (Pörtner and Knust, 2007; Tewksbury et al., 2008).

Current range size, range of elevation, and biogeographic domain can also be predictors of a "shared destination" in response to climate change, as species found in the same region share certain niche attributes and tend to respond similarly to global warming. For example, species with very narrow distributions tend to occupy a more restricted number of microhabitats and can be more negatively affected by climate change (Foden et al., 2013; Büchi and Vuilleumier, 2014). The same may be true for species coupled with specific environmental conditions (e.g., forest habitats or mountain tops), as suitable climatic conditions can be displaced to regions beyond the species' ability to disperse, which can lead to local extinction. On the other hand, species that are widely distributed and adapted to a variety of habitats may have more available areas with climatic conditions filling the requirements of their niche, even if the suitable conditions have been locally lost (Clavel et al., 2011).

Although it is already known that biological and biogeographic characteristics can influence the intensity and direction of species response to climate change (Foden et al., 2013; Borges et al., 2019; Alves-Ferreira et al., 2022), a few studies have assessed the existence of global patterns on climate change response using these traits. In this study, we assessed the global patterns of climate change effects on amphibian (Anura and Caudata) distributions through a trait- and biogeographical-based analysis of published data. Specifically, we assessed whether the response of amphibians to climate change is more strongly influenced by life history traits (body size, habit, reproductive mode, and habitat specialty) or by biogeographic characteristics (elevation, biogeographical realm, baseline area, isothermality, precipitation, and temperature seasonality).

Material and methods

Data compilation

We performed a systematic review of published studies in two databases (Scopus and ISI Web of Science) for manuscripts that evaluated the effects of climate change on the potential distribution of amphibians. We gathered studies published until February, 2022 (Figure 1) using the following keywords: [("climatic chang*" OR "climate chang*" OR "global warm*" OR "climate warm*" OR "changing climate") AND ("Amphibian*" OR "Anura*" OR "Caudata" OR "Salamander" OR "Frog" OR "Toad") AND ("Geographic range" OR "distribut*" OR "suitab*" OR "niche model*" OR "scenario*" OR "range shift*")]. We used the following eligibility criteria to include studies in our database: they must have (1) assessed the effect of future climate changes on the distribution of Anura or Caudata; (2) presented the size of the potential future distribution; (3) used correlative models. After the first filtering by title and abstract, we excluded studies that evaluated another taxonomic group, worked with invasive species, did not evaluate the effect of climate change on distribution, assessed species at population level only and experimental studies with Critical thermal maximum (CTmax). Our initial search resulted in 1,161 possibly eligible studies. After filtering by eligibility criteria, we obtained 41 studies that modeled the potential distribution of 520 species (Figure 1). For articles that presented the data in graphs, we used the software GetData GraphDigitizer version 2.26 (Fedorov, 2013) to access the information.

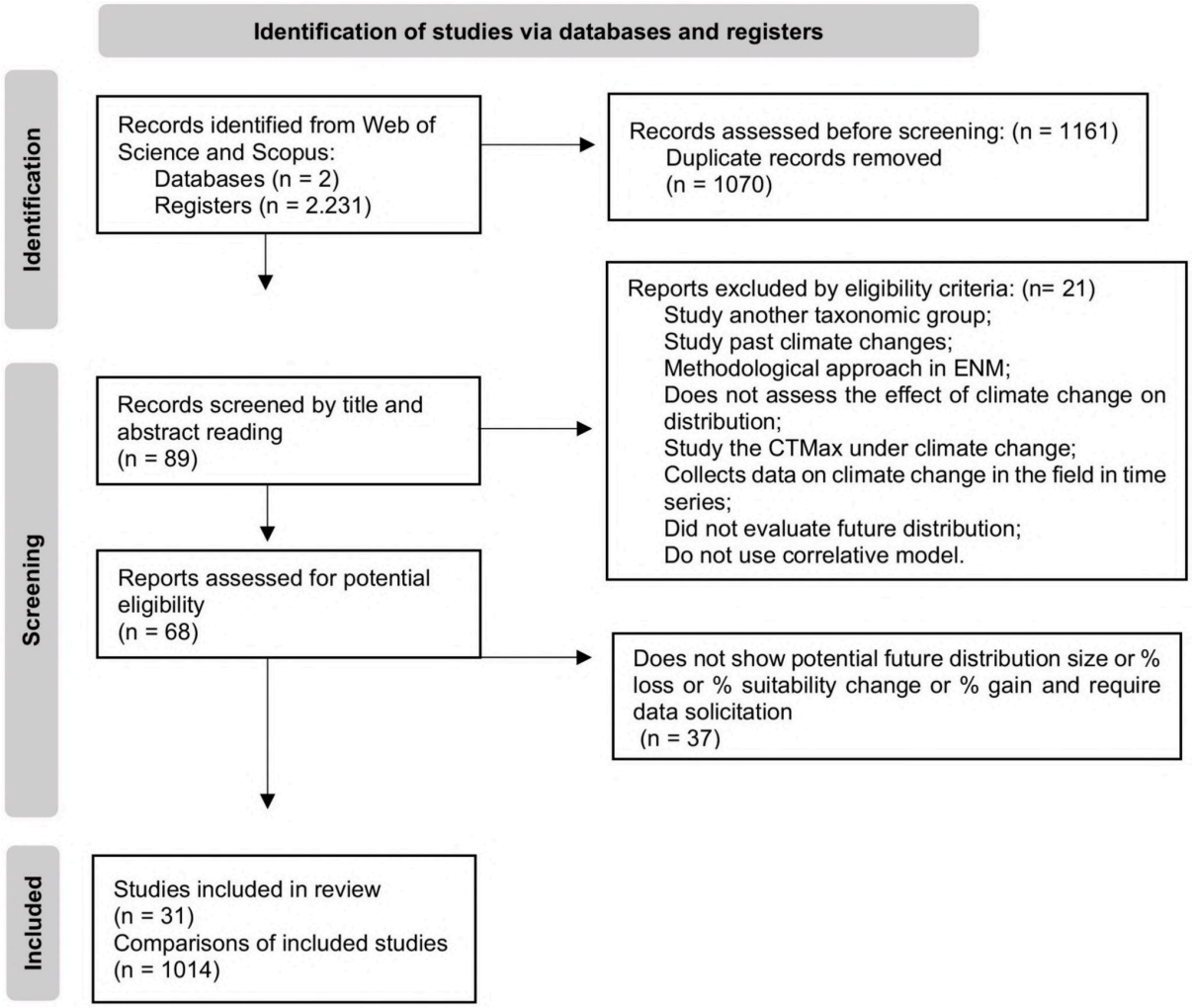

Figure 1. PRISMA diagram representing the selection process of the studies included in our analysis.

Data extraction: Life-history and biogeographic data

We extracted the following information for each study: species, family, order, climatically suitable area size in present and future, and change percentage in climatically suitable areas. Studies that presented data for more than one species had such information recorded as independent data. To associate the climatic suitability with biological and biogeographical attributes, we obtained the biogeographical realm sensu Olson et al. (2001). We achieved the habitat type from the IUCN database (IUCN, 2022) and habit, reproductive mode, and body size (mm) from the AmphiBIO database (Oliveira et al., 2017).

The elevation and bioclimatic variables: Isothermality (BIO3), Temperature Seasonality (BIO4), and Precipitation Seasonality (BIO15) were achieved for baseline scenarios (1970–2000) using resolution of 2.5 arc min from the WorldClim database (Fick and Hijmans, 2017). These variables could be expected to influence amphibian distribution (Whitton et al., 2012; Gouveia et al., 2013; Zank et al., 2014). For example, Sodhi et al. (2008) found that the risk of extinction increases for amphibians that live in regions with very pronounced seasonality of precipitation and temperature.

We used the Global Biodiversity Information Facility (GBIF.org, 2022) database to obtain occurrence records for the species. We considered species with more than three independent occurrence records. Using these records, we extracted the elevation and bioclimatic variables for each occurrence and averaged these values per species. To test whether there is a correlation between continuous variables (Supplementary Figure 1), we conducted a Pearson Correlation test with a threshold of 75%. To measure the association between pairs of categorical variables (Supplementary Figure 2) we used the Goodman Kruskal measure (Goodman and Kruskal, 1972). We used Frost (2022) to update the taxonomic nomenclature.

Statistical analysis

To assess whether the amphibian's response to climate change is influenced by life history traits and by biogeographic features, we built linear mixed models using the "lme4" R package (Bates et al., 2015). Species and studies were treated as random factors to control for species that appear in multiple studies and to control for repetitions within the same study. As isothermality (BIO3) was highly correlated with seasonality of temperature (BIO4) and seasonality of precipitation (BIO15), we kept only isothermality (BIO3) in further analyses. The predictor variables were: body size, habit, reproductive mode, habitat specialty, elevation, biogeographical realm, baseline area, and isothermality (See Supplementary Table 1 for a more detailed description of each variable). Both types of variables are mixed in the models. The response variable was the square root of the relative area, calculated by dividing the area (km2) in the future by the area (km2) in the reference scenario. We generated 130 eligible models from combinations between predictor variables with a minimum limit of zero

(null model) until the maximum of three terms in a single model (excluding the intercept). Finally, we built an average model based on the Akaike Information Criterion corrected for small samples (AICc; Burnham and Anderson, 2002). We calculated the relative importance of each predictor variable using the sum of model weights over all models. All analyses and figures were performed in R (R Core Team, 2022).

Spatial patterns of species area change

We produced a species richness map to identify the regions in the world with the highest number of evaluated species. This map was constructed based on the sum of the binary distributions (absence = 0 or presence = 1) of the species evaluated in the studies included in our review. To demonstrate the spatial pattern of species area changes we cross-referenced the relative proportion of change with the map of binary distributions. Therefore, this map represents the local variability of the climate change effects on species distributions. As species can overlap spatially and this can make it difficult to visualize the spatial trend of loss and gain, we calculated the area change for 5 quantiles (zero, 25, 50, 75, and 100). At one extreme, the lower quantile (0%) represents the lowest values of change (i.e., higher losses to smaller gains) among locally occurring species. The third quantile (50%) represents the central tendency among species. At the other extreme, the upper quantile (100%) represents the highest values of change (i.e., smaller losses to higher gains of area) among species. Since we do not have distribution rasters available for the species of each study, we used the geographic distributions provided by the IUCN (2022) to produce the maps of species richness and area change. All spatial calculations were performed with the "terra" package (Hijmans, 2022) in program R (R Core Team, 2022).

Results

General characteristics of selected papers

Our initial database resulted in 41 manuscripts with data for 520 species. However, not all studies reported suitable baseline and future areas for the species, and not all species have characteristics and occurrence data available to perform our analysis. Therefore, the final dataset included 31 papers that projected the distribution of 331 amphibian species belonging to 35 families from around the globe (Figure 2). Among these species, 268 belong to the order Anura and 64 belong to the order Caudata (see Supplementary Table 2). Among the 331 species evaluated, 112 should gain climatically suitable areas in the future, 214 species are predicted to have adequate climatic conditions reduced and four species should maintain the same area in the present and in the future.

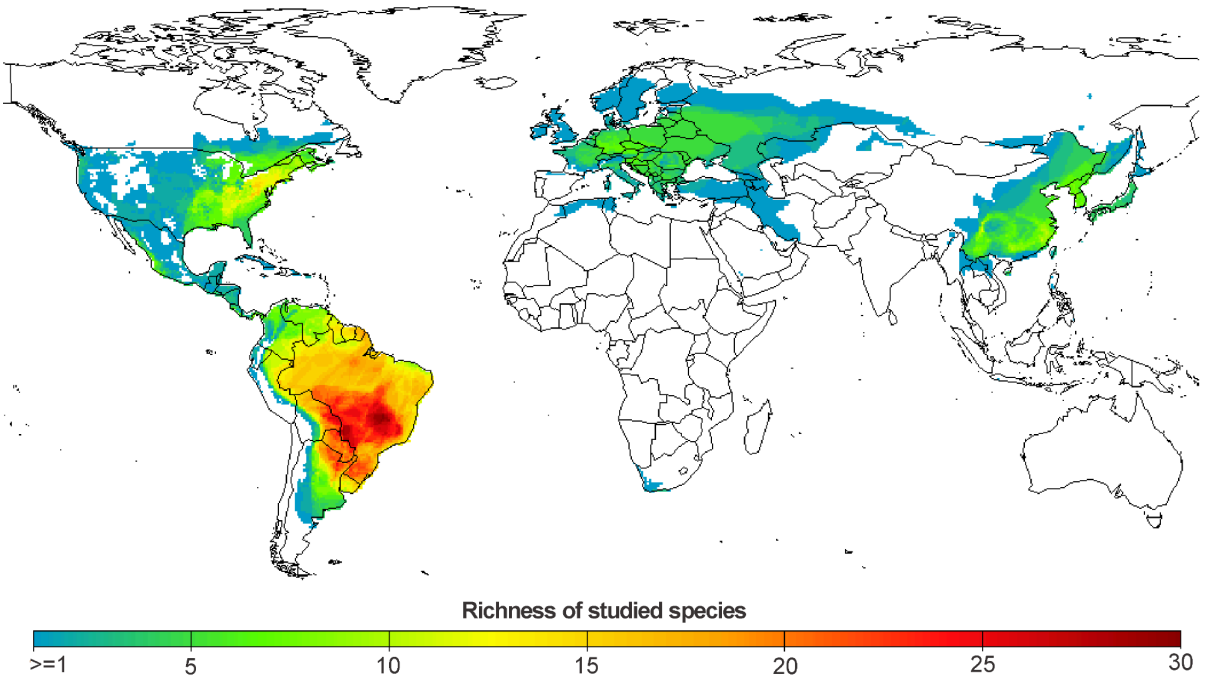

Figure 2. Richness of amphibian species (331 species) studied in the articles included in our review (31 studies). The blue and green colors represent places where a smaller number of species were studied, while the yellow and red colors represent the places with the largest number of species studied.

Biological and biogeographical traits

The most important variables related to amphibian's range shifts (Table 1) were baseline area (W = 0.99), realm (W = 0.54), isothermality (W = 0.47), elevation (W = 0.41), and habitat type (W = 0.30). The average model coefficient shows that all these variables can significantly affect the amount of amphibian's suitable areas in response to climate change (Table 2). On the other hand, habit, population trend, body size, and reproductive mode were of minor importance (W = 0.06) and their effect was not significant (Table 2).

Table 1. The six models relating amphibians range shift and biological and biogeographical traits with the highest rankings among the 130 candidate models and their second-order Akaike information criterion values (AICc), AICc weights (weight), AICc differences (delta), Log-likelihood (loglik), and degrees of freedom (df).

Model	df	logLik	AICc	delta	weight
Isothermality + Elevation + Area	7.000	-515.210	1044.500	0.000	0.333
Habitat + Realm + Area	16.000	-506.298	1045.100	0.590	0.249
Isothermality + Realm + Area	12.000	-510.839	1046.000	1.450	0.162

Elevation + Realm + Area	12.000	-511.167	1046.600	2.100	0.116
Realm + Area	11.000	-512.559	1047.400	2.840	0.080
Habitat + Isothermality + Area	11.000	-512.856	1048.000	3.440	0.060

Table 2. Model-averaged coefficients based on conditional average including estimates, p-value, z value, standard error.

Variables	Estimates	Std. Error	z value	p value
(Intercept)	1.28E+00	4.80E-01	2.661	0.0078
Isothermality	8.65E-03	3.65E-03	2.366	0.018
Elevation	-1.21E-04	5.59E-05	2.157	0.03104
Baseline area	-2.15E-04	5.38E-05	3.982	6.83E-05
Habitat: Forest	-3.64E-01	1.17E-01	3.119	0.00181
Habitat: Forest and open	-3.15E-01	1.01E-01	3.133	0.00173
Habitat: Open areas	-2.37E-01	1.21E-01	1.951	0.05111
Habitat: Rupestrial	-3.94E-01	1.47E-01	2.674	0.00749
Habitat: Wetlands	-3.08E-01	1.90E-01	1.615	0.10621
Realm: IndoMalayan and Palearctic	-7.69E-01	2.43E-01	3.158	0.00159
Realm: IndoMalayan	-8.05E-01	2.85E-01	2.824	0.00475
Realm: Nearctic	-3.67E-01	2.42E-01	1.518	0.12899
Realm: Neartic and Neotropic	-5.32E-01	2.52E-01	2.107	0.03509
Realm: Neotropic	-6.13E-01	2.21E-01	2.774	0.00554
Realm: Palearctic	-7.63E-01	2.29E-01	3.332	0.00086
Habit: Fossorial, terrestrial and aquatic	8.89E-02	2.17E-01	0.41	0.68214
Habit: Fossorial	4.77E-01	4.20E-01	1.136	0.25589
Habit: Terrestrial	-1.32E-01	2.19E-01	0.602	0.54741
Habit: Terrestrial, aquatic and arboreal	8.98E-02	2.05E-01	0.438	0.66152
Body size (mm)	7.03E-03	1.08E-02	0.651	0.51479
Reproductive mode: Direct	-5.24E-01	5.36E-01	0.976	0.32925
Reproductive mode: Larvae	-4.83E-01	5.14E-01	0.939	0.34788
Reproductive mode: Viviparous	-4.90E-01	6.38E-01	0.768	0.44272

The elevation where the species inhabit may explain part of the effect of climate change on suitable areas for amphibians (Beta = −0.002, SE = 0.001, z value = 2.148, p value = 0.031). We found that species inhabiting average elevation above 515 m will lose a significant portion of their climatically suitable area (Figure 3A). Isothermality was another important variable (Beta = 0.008, SE = 0.004, z value = 2.285, p value = 0.022). As

isothermality increases, the amount of suitable area gain in response to climate change also increases (Figure 3B). More specifically, species that occur in regions with higher "temperature uniformity" over a year (i.e., isothermality below ~30%) tend to gain climatically suitable areas, while species that occur in less isothermic regions tend to lose suitable areas with the advancing climate change. Finally, the size of baseline area explained most amphibian distribution changes (Beta = −0.002, SE = 0.001, z value = 3.976, p value = 0.001). We found that as the size of the distribution increases, the greater are projected to be the relative losses in climatically suitable areas. On the other hand, species with very small areas tend to retain most of their current distribution areas in the future (Figure 3C).

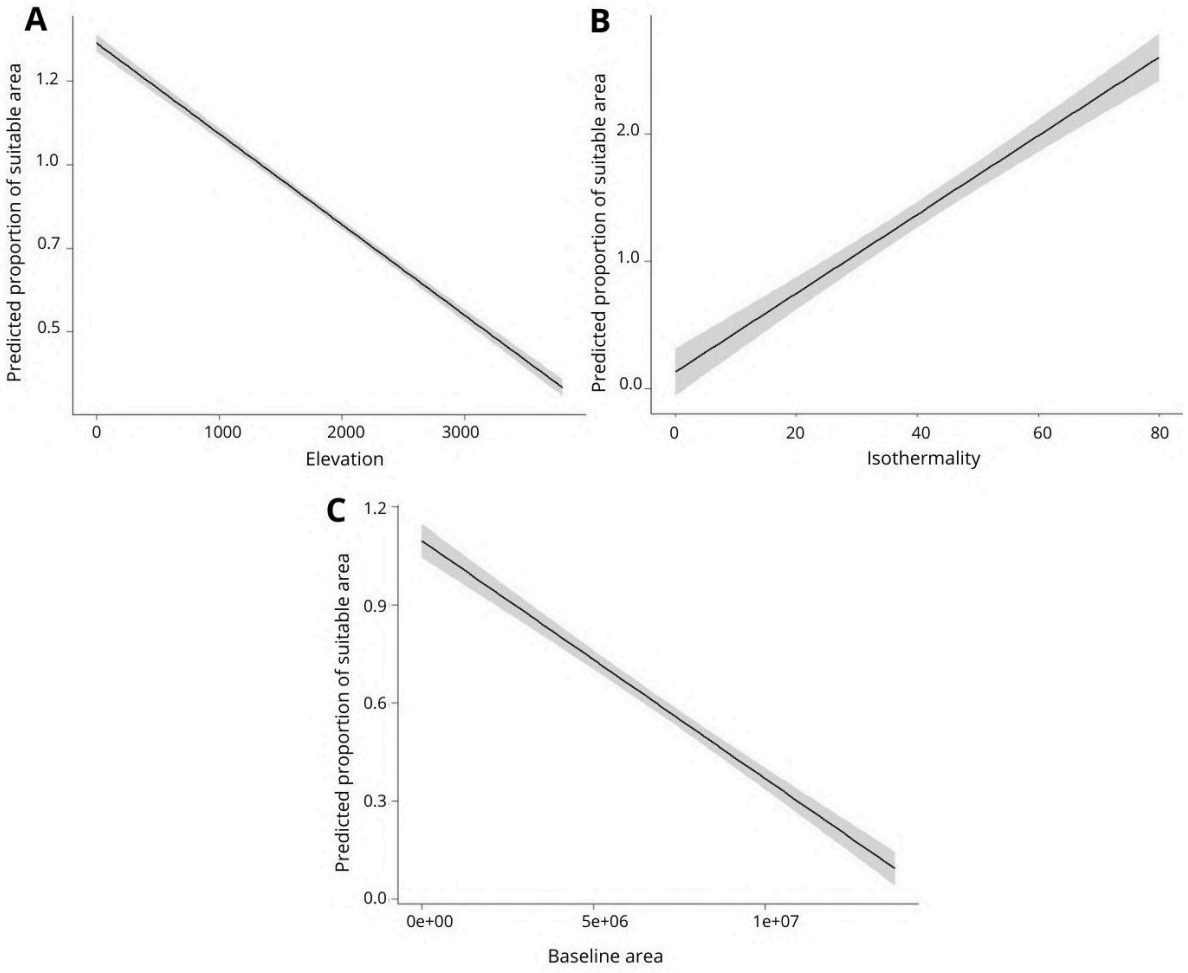

Figure 3. Relationship between the proportion of climatically suitable areas and elevation (A), isothermality (B), and baseline area (C). Values above one indicate gain of suitable area. The gray area represents confidence intervals (95%).

We found that habitat type and biogeographical realm are also good predictors of amphibian's range shifts. Particularly, the results indicate that species that inhabit dry habitats (such as savannas, arid, and semi-arid habitats) tend to expand their suitable area in response

to climate change. We also found that anurans that inhabit exclusively forests (Beta = −0.366, SE = 0.116, z value = 3.149, p value = 0.002) or rupestrial habitats (Beta = −3.957, SE = 1.464, z value = 2.700, p value = 0.007) are projected to lose a greater portion of their suitable area, when compared to species that inhabit both forest and open areas, wetlands, and dry habitats (Figure 4A). The biogeographical realm also influenced anuran's range shifts, with Afrotropic and Nearctic amphibians amphibians projected to expand their suitable areas in response to global warming when compared to species from the other realms (Figure 4B).

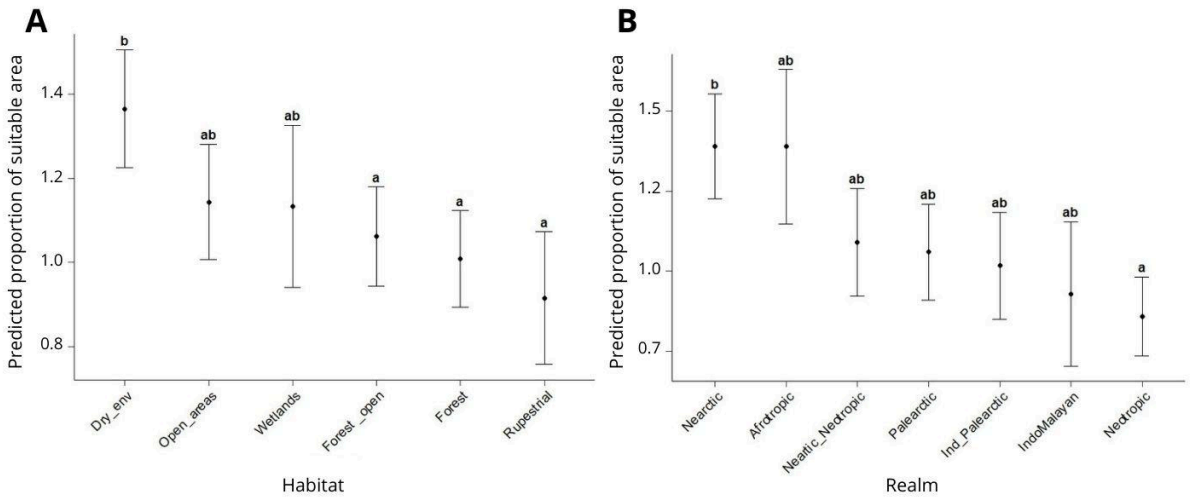

Figure 4. Estimated marginal means of change in climatically suitable area per habitat type (A) and biogeographical realm (B). The standard error of the mean is represented by vertical bars. Letters indicate categories with statistically significant differences.

Spatial patterns of amphibian's area change

The quartile maps show the local variation in species responses to climate change. The 0% quartile map (i.e., minimum area change values across species for species on each pixel) reveals that at least one species will lose part of its current range in most of the studied regions. Only in a few places (e.g., part of the Andean region of Colombia, extreme North Italy, central south part of Bolivia-Austral Yungas region, north-eastern part of Argentina-La Plata Basin region, Midwestern and South region of United States) the species are projected to gain new climatically suitable areas. The 50% quartile map (central tendency) shows that most species are projected to lose suitable areas across most of the studied regions. The 100% quartile map (i.e., maximum values across species on each pixel) shows that at least one species gains suitable area in most regions, but in several regions there will be only loss of suitable area across all species. Another important information to highlight when comparing the 0 and 100% quartiles maps (minimum and maximum values, respectively) is that while a combination of area loss and gain is projected for the species in most regions, in some areas all the species are projected only to lose (i.e., southwestern Russia, north-central Mexico, the northern United States, and the north-central Andean mountain range) or gain (i.e., southern Canada, the southeastern and northeastern United States, the Brazilian Cerrado and the far south of the Atlantic Forest in Brazil) suitable areas in the future (Figure 5).

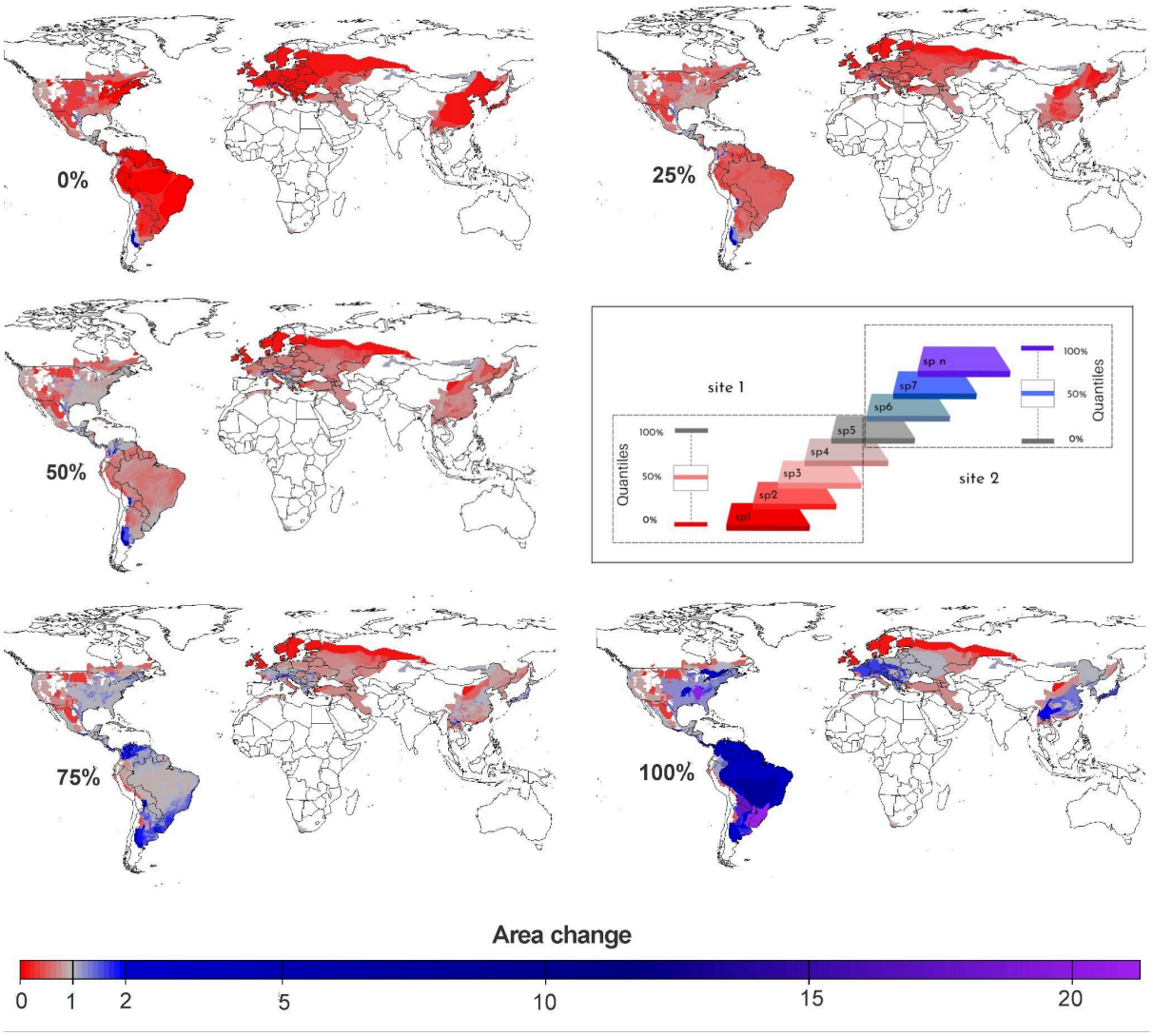

Figure 5. Quartile maps showing the local variation in species responses to climate change. Red indicates losses in suitable areas, gray indicates no change, and blue to purple indicate gains in suitable areas. Quantiles were calculated for the responses of species occurring at each pixel (see graphical scheme of calculations in the center). At one extreme, the lower quantile (0%, minimum values) represents the lowest values of change (i.e., higher losses to smaller gains) among species occurring at each map pixel. The third quantile (50%, median) represents the central tendency among species. At the other extreme, the upper quantile (100%, maximum values) represents the highest values of change (i.e., smaller losses to higher gains of area) among species.

Discussion

In this review, we accessed the global patterns of climate change effects on amphibian distributions through a biological and biogeographical analysis of published data. Our analysis provides evidence that baseline area, isothermality, habitat type, elevation, and realm are consistently important drivers to predict amphibian's range shifts. This finding reinforces the idea that biogeographic variables may be more important than life history traits in

predicting the climate change effects on amphibians' distribution (Alves-Ferreira et al., 2022). To our knowledge, this is the first systematic review of published data that assesses the global effects of climate change on amphibian distribution using biological and biogeographic traits as predictors.

We found that species inhabiting an elevation above 515 m are projected to lose climatically suitable areas. This is because as elevation increases, the available area for the species decreases, and consequently leads to the loss of suitable area. Therefore, it is expected that species that inhabit higher altitudes will be more negatively affected by climate change, since the available climatic area tends to reduce toward the top of the mountains (Nori et al., 2016). Our results also provide evidence that as isothermality increases, the amount of suitable area gain in response to climate change also increases. Therefore, species from less isothermal regions (i.e., regions with lower "temperature uniformity" and more variation over a year, below 30%) tend to lose climatically suitable areas, while species that occur in more isothermal regions (above 30%) tend to gain suitable areas with advancing climate change. The vast majority of the more isothermal areas in our study are located in tropical and subtropical regions (Neotropic, Afrotropic, and IndoMalayan realms). However, the data are mostly from Neotropical regions, with low representation of studied species from the Afrotropic and Australian realms.

We also found that the size of the baseline area is positively correlated with the projected loss of climatically suitable areas. The result indicates that species with a very restricted distribution should suffer a low proportion of losses in their current distribution areas, while widespread species should suffer the highest proportion of losses. This seems contradictory at first glance, as species with restricted ranges are expected to lose more area than widely distributed ones, due to the expectation that restricted ranges result from narrower niches (Slatyer et al., 2013; Saupe et al., 2015; Evans and Jacquemyn, 2022). A possible explanation for the lower proportion of loss for species with very restricted ranges may be related to the extreme specialization that can lead some species to "escape" the full impacts of climate change (Foden et al., 2013). However, this hypothesis requires that these small ranged species are adapted to unique climatic conditions that will remain stable in the future. Thus, it is more likely that range retention is mostly due to climatic stability than specialization to unique climatic conditions (Fjeldså, 1994; Cardoso da Silva et al., 2004; Harrison and Noss, 2017; Wilson et al., 2019).

Furthermore, our results indicate that species that inhabit dry habitats (such as savannas, arid and semi-arid habits) tend to expand their suitable areas in response to climate change. This result can be explained by the environmental characteristics of these habitats, which tend to present extreme seasonal climates with well-defined periods of drought and rain (Murphy and Lugo, 1986; Gentry, 1995). The Intergovernmental Panel of Climate Change projects future warming scenarios that exacerbate the frequency and intensity of drought and water stress (IPCC, 2022). Therefore, global warming is likely to favor drought-resistant anuran species. We also found that anurans that exclusively inhabit forests and rupestrial environments are projected to lose a greater portion of their suitable areas, when compared to species that inhabit both forest and open areas, and dry environments. This

may happen because species strongly associated with specific conditions and requirements (i.e., warm and moist climate found in forests) tend to have a narrow range of available habitats and microhabitats (Foden et al., 2013). In addition, the expansion of dry conditions will unfavour forest habitats. Therefore, it is likely that these species will not have suitable climatic conditions available in the future, which can increase the risk of local extinction.

The biogeographical realm also influenced amphibian's range shifts, with the most Nearctic and Afrotropic species projected to expand their geographical ranges in response to global warming. It is possible that the environmental conditions that the Afrotropic species are adapted to will expand in future climate scenarios. However, this is one of the realms with the lowest number of evaluated species. In total, 21 species were studied, representing only 2.1% of the region's amphibian richness (Vallan et al., 2004). On the other hand, species from the Neotropics are projected to have the highest proportion of area loss among all realms. Neotropics is the realm with the largest number of species studied (170). However, harboring nearly 2,916 species (Bolaños et al., 2008), only a small fraction of the richness of the region (5.6%) was represented by the studies. Therefore, there is a huge amount of species that need to be assessed to allow one to indicate the realm with most species vulnerable to climate change.

Besides identifying spatial patterns of range shift at the realm level, we also detected them at the "regional" level. For example, in some regions such as southwestern Russia, north-central Mexico, the northern United States, and the north-central Andean Mountain range, all of the species studied are only decreasing in area. On the other hand, in southern Canada, the southeastern and northeastern United States, the Brazilian Cerrado, and the far south of the Atlantic Forest in Brazil we observed a great increase in the geographic range size of some amphibian species. The projected expansion of the distribution of these species could lead to biotic homogenization at the community level, as specialists can be extirpated from the environment due to competition with the "winning" species (McKinney and Lockwood, 1999; Clavel et al., 2011).

Our study identifies regions with greatest potential for large-scale conservation due to the presence of several vulnerable species, such as those that inhabit mountain and forest regions. An effective conservation strategy for these species can be the creation of ecological corridors or small reserves. This strategy can reduce the risk of local extinction, as it allows species affected by climate change to move through the landscape and colonize new suitable areas (Ovaskainen, 2002). For species projected to maintain their suitable ranges in the future, a more effective strategy may be to create larger and more widely spaced conservation areas that allow large populations to persist under climate change. Therefore, climate change requires different conservation strategies aimed at the different responses that it can generate (Hannah, 2010).

We conclude that biogeographic variables may be good predictors of the climate change effects on amphibians' distribution. Our results suggest that the baseline area isothermality, habitat type, elevation, and realm explains much of the variation in the intensity and direction of the climate change effect. However, our study shows that, globally, only a small fraction of Anura (3.9% of the 7,477) and Caudata (8% of the 773 species; Frost,

2022) species' response to climate change have been assessed so far. Yet, we were not able to find a single study considering any of the 214 Gymnophiona species. Regions with high amphibian richness also remain underexplored, such as Madagascar, various parts of the African continent, Australia, Chile, Indonesia, and India. Therefore, we recommend that future studies focus on species and regions that are still underrepresented. Given that over 40% of amphibian species are already experiencing population declines due to other threats (IUCN, 2022), it is important to assess the impact of future climate scenarios on species distribution to optimize resources for conservation.

Data availability statement

The datasets and scripts generated for this study are deposited at Harvard Dataverse https://dataverse.harvard.edu/dataverse/climate_change_amphibians.

Author contributions

GA-F: conceptualization, data curation, formal analysis, investigation, methodology, software, validation, visualization, and writing—review and editing. DT and NH: conceptualization, formal analysis, investigation, methodology, project administration, supervision, validation, visualization, and writing—review and editing. MS: conceptualization, project administration, supervision, validation, visualization, writing—review and editing. MC-L: conceptualization, validation, visualization, and writing—review and editing. All authors contributed to the article and approved the submitted version.

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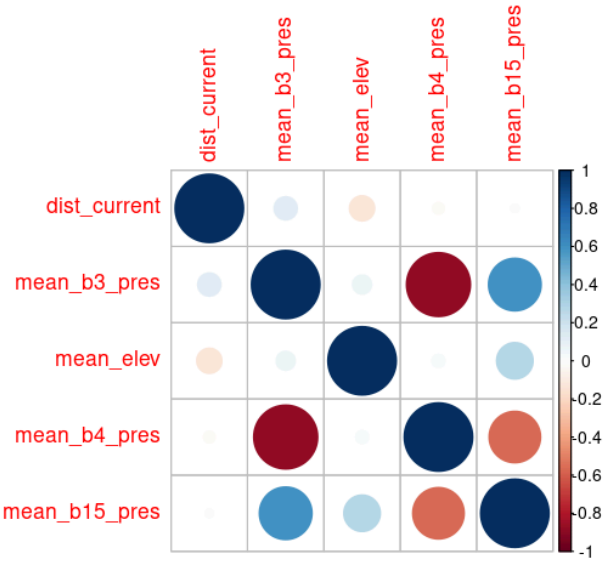
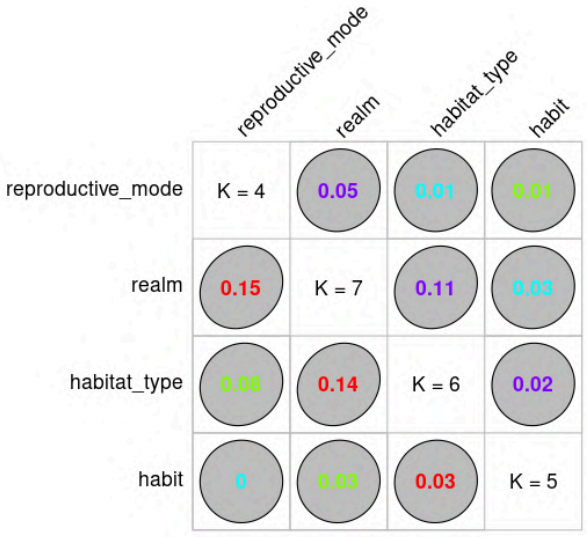
Supplementary material



Supplementary Figure S1. Correlation among continuous variables calculated using the Pearson Coefficient.



Supplementary Figure 2. Correlation among categorical variables calculated using the Goodman Kruskal measure.

Supplementary Table 1. Traits used in the study and a brief description for each one.

Species traits	**Description**
a. Body size	Maximum adult body size (millimeters), reported as snout vent length (SVL) for Anurans and total length (TL) for Caudata.
b. Habit	Vertical foraging stratum to which species is most strongly associated. It can be classified as fossorial, terrestrial, aquatic, or both fossorial - terrestrial - aquatic, or both terrestrial - aquatic - arboreal.
c. Reproductive mode	Type of reproductive mode. It can be classified as larval, viviparous and direct.
d. Habitat	Main habitat types in which the species occur. It can be classified as forest, dry environments, open areas, rocky environments, wetlands and both forest and open areas.
d. Elevation	Mean elevation (meters) extracted for the species occurrence points.
e. Precipitation	Mean annual precipitation (millimeters) extracted for the species occurrence points.
f. Temperature seasonality	Mean temperature seasonality (Degrees Celsius) extracted for the species occurrence points.
g. Biogeographical realm	Biogeographical realm in which the species occur. It can be classified as Indo-Malayan, Neotropic, Afrotropic, Nearctic, Palearctic or both Nearctic-Neotropic or both Indo Malayan-Palearctic.
h. Baseline area	Current distribution (Kilometers) provided by each study for each species.
i. Latitude	Mean latitude extracted for the species occurrence points.
j. Isothermality	Mean isothermality (Percent) extracted for the species occurrence points.

Supplementary Table 2. Database with the studies included in the systematic review. The table includes species name, potential distribution in the present and in the future and the country where the study was conducted.

Author	Distribution Current	Distribution Future	Species name	Country
Andrade-Diaz et al 2021	1371483	2290974	*Leptodactylus bufonius*	Bolivia and Argentina
Andrade-Diaz et al 2021	2702641	3537475	*Leptodactylus elenae*	Bolivia and Argentina
Andrade-Diaz et al 2021	5184600	5060836	*Leptodactylus mystacinus*	Bolivia and Argentina
Andrade-Diaz et al 2021	2928649	2911386	*Odontophrynus americanus*	Bolivia and Argentina
Andrade-Diaz et al 2021	1549931	2286012	*Odontophrynus lavillai*	Bolivia and Argentina
Andrade-Diaz et al 2021	586708	945841	*Pleurodema tucumanum*	Bolivia and Argentina
Andrade-Diaz et al 2021	4909236	5917030	*Rhinella diptycha*	Bolivia and Argentina
Andrade-Diaz et al 2021	60367	17466	*Rhinella rumbolli*	Bolivia and Argentina
Andrade-Diaz et al 2021	8540982	11945261	*Boana raniceps*	Bolivia and Argentina
Andrade-Diaz et al 2021	196416	263176	*Boana riojana*	Bolivia and Argentina
Andrade-Diaz et al 2021	12366502	9490827	*Dendropsophus minutus*	Bolivia and Argentina
Andrade-Diaz et al 2021	5419013	6022262	*Dendropsophus nanus*	Bolivia and Argentina
Andrade-Diaz et al 2021	221081	452080	*Gastrotheca christiani*	Bolivia and Argentina
Andrade-Diaz et al 2021	5920474	7457537	*Leptodactylus chaquensis*	Bolivia and Argentina

Andrade-Diaz et al 2021	13463283	13330390	*Leptodactylus fuscus*	Bolivia and Argentina
Andrade-Diaz et al 2021	2784542	2467649	*Leptodactylus gracilis*	Bolivia and Argentina
Andrade-Diaz et al 2021	2502013	2646514	*Leptodactylus latinasus*	Bolivia and Argentina
Andrade-Diaz et al 2021	241759	220653	*Melanophryniscus rubriventris*	Bolivia and Argentina
Andrade-Diaz et al 2021	1097423	1275311	*Phyllomedusa boliviana*	Bolivia and Argentina
Andrade-Diaz et al 2021	2768005	3906442	*Phyllomedusa sauvagii*	Bolivia and Argentina
Andrade-Diaz et al 2021	3706363	4237679	*Physalaemus biligonigerus*	Bolivia and Argentina
Andrade-Diaz et al 2021	290618	91719	*Physalaemus cuqui*	Bolivia and Argentina
Andrade-Diaz et al 2021	105952	161096	*Pleurodema borellii*	Bolivia and Argentina
Andrade-Diaz et al 2021	2594606	2664312	*Rhinella arenarum*	Bolivia and Argentina
Andrade-Diaz et al 2021	4609832	3706876	*Scinax fuscovarius*	Bolivia and Argentina
Andrade-Diaz et al 2021	2886522	3882199	*Scinax nasicus*	Bolivia and Argentina
Andrade-Diaz et al 2021	116415	104421	*Telmatobius oxycephalus*	Bolivia and Argentina
Andrade-Diaz et al 2021	13784210	15859964	*Trachycephalus typhonius*	Bolivia and Argentina
Alves-Ferreira et al 2021	1152254	1325070	*Pseudis platensis*	Brazil
Alves-Ferreira et al 2021	1152254	1182731	*Pseudis platensis*	Brazil
Alves-Ferreira et al 2021	2796681	2702654	*Pseudis bolbodactyla*	Brazil

Alves-Ferreira et al 2021	2796681	2551385	*Pseudis bolbodactyla*	Brazil
Alves-Ferreira et al 2021	2129168	2179920	*Elachistocleis bicolor*	Brazil
Alves-Ferreira et al 2021	2129168	2093544	*Elachistocleis bicolor*	Brazil
Alves-Ferreira et al 2021	1798667	976048	*Elachistocleis cesarii*	Brazil
Alves-Ferreira et al 2021	1798667	905965	*Elachistocleis cesarii*	Brazil
Alves-Ferreira et al 2021	2596935	1550564	*Leptodactylus elenae*	Brazil
Alves-Ferreira et al 2021	2596935	1446924	*Leptodactylus elenae*	Brazil
Alves-Ferreira et al 2021	1558271	1016836	*Leptodactylus furnarius*	Brazil
Alves-Ferreira et al 2021	1558271	1154016	*Leptodactylus furnarius*	Brazil
Alves-Ferreira et al 2021	1962514	1535216	*Leptodactylus mystaceus*	Brazil
Alves-Ferreira et al 2021	1962514	1409604	*Leptodactylus mystaceus*	Brazil
Alves-Ferreira et al 2021	1866075	1613407	*Leptodactylus mystacinus*	Brazil
Alves-Ferreira et al 2021	1866075	1428677	*Leptodactylus mystacinus*	Brazil
Alves-Ferreira et al 2021	2488970	1444645	*Leptodactylus syphax*	Brazil
Alves-Ferreira et al 2021	2488970	1595670	*Leptodactylus syphax*	Brazil
Alves-Ferreira et al 2021	1537966	1256163	*Leptodactylus troglodytes*	Brazil
Alves-Ferreira et al 2021	1537966	1125995	*Leptodactylus troglodytes*	Brazil

Alves-Ferreira et al 2021	902475	780889	*Odontophrynus americanus*	Brazil
Alves-Ferreira et al 2021	902475	887346	*Odontophrynus americanus*	Brazil
Alves-Ferreira et al 2021	924595	419813	*Odontophrynus cultripes*	Brazil
Alves-Ferreira et al 2021	924595	288125	*Odontophrynus cultripes*	Brazil
Alves-Ferreira et al 2021	2774713	1954632	*Adenomera hylaedactyla*	Brazil
Alves-Ferreira et al 2021	2774713	1782700	*Adenomera hylaedactyla*	Brazil
Alves-Ferreira et al 2021	1381027	398803	*Ameerega flavopicta*	Brazil
Alves-Ferreira et al 2021	1381027	190560	*Ameerega flavopicta*	Brazil
Alves-Ferreira et al 2021	637927	2241903	*Ololygon catharinae*	Brazil
Alves-Ferreira et al 2021	637927	2021152	*Ololygon catharinae*	Brazil
Alves-Ferreira et al 2021	1639811	452284	*Rhinella diptycha*	Brazil
Alves-Ferreira et al 2021	1639811	631405	*Rhinella diptycha*	Brazil
Alves-Ferreira et al 2021	1542018	911073	*Rhinella margaritifera*	Brazil
Alves-Ferreira et al 2021	1542018	739604	*Rhinella margaritifera*	Brazil
Alves-Ferreira et al 2021	1281292	531838	*Rhinella ornata*	Brazil
Alves-Ferreira et al 2021	1281292	437813	*Rhinella ornata*	Brazil
Alves-Ferreira et al 2021	633938	353033	*Rhinella scitula*	Brazil

Alves-Ferreira et al 2021	633938	233918	*Rhinella scitula*	Brazil
Alves-Ferreira et al 2021	638708	1001914	*Trachycephalus nigromaculatus*	Brazil
Alves-Ferreira et al 2021	638708	1046954	*Trachycephalus nigromaculatus*	Brazil
Alves-Ferreira et al 2021	2012698	810548	*Boana albopunctata*	Brazil
Alves-Ferreira et al 2021	2012698	875014	*Boana albopunctata*	Brazil
Alves-Ferreira et al 2021	1814440	2431746	*Boana crepitans*	Brazil
Alves-Ferreira et al 2021	1814440	2655664	*Boana crepitans*	Brazil
Alves-Ferreira et al 2021	624042	183924	*Boana faber*	Brazil
Alves-Ferreira et al 2021	624042	242767	*Boana faber*	Brazil
Alves-Ferreira et al 2021	775007	222961	*Boana lundii*	Brazil
Alves-Ferreira et al 2021	775007	287308	*Boana lundii*	Brazil
Alves-Ferreira et al 2021	1006112	1278096	*Boana multifasciata*	Brazil
Alves-Ferreira et al 2021	1006112	1249348	*Boana multifasciata*	Brazil
Alves-Ferreira et al 2021	2199447	1650358	*Boana punctata*	Brazil
Alves-Ferreira et al 2021	2199447	1789678	*Boana punctata*	Brazil
Alves-Ferreira et al 2021	2203818	1627149	*Boana raniceps*	Brazil

Alves-Ferreira et al 2021	2203818	1771961	*Boana raniceps*	Brazil
Alves-Ferreira et al 2021	100514	108150	*Bokermannohyla saxicola*	Brazil
Alves-Ferreira et al 2021	100514	136551	*Bokermannohyla saxicola*	Brazil
Alves-Ferreira et al 2021	1795650	883994	*Chiasmocleis albopunctata*	Brazil
Alves-Ferreira et al 2021	1795650	641941	*Chiasmocleis albopunctata*	Brazil
Alves-Ferreira et al 2021	2278000	1591790	*Dendropsophus cruzi*	Brazil
Alves-Ferreira et al 2021	2278000	1664794	*Dendropsophus cruzi*	Brazil
Alves-Ferreira et al 2021	1815286	1393837	*Dendropsophus elianeae*	Brazil
Alves-Ferreira et al 2021	1815286	1253972	*Dendropsophus elianeae*	Brazil
Alves-Ferreira et al 2021	1642002	584134	*Dendropsophus jimi*	Brazil
Alves-Ferreira et al 2021	1642002	499479	*Dendropsophus jimi*	Brazil
Alves-Ferreira et al 2021	3140538	2558688	*Dendropsophus melanargyreus*	Brazil
Alves-Ferreira et al 2021	3140538	2645155	*Dendropsophus melanargyreus*	Brazil
Alves-Ferreira et al 2021	2495312	1460311	*Dendropsophus minutus*	Brazil
Alves-Ferreira et al 2021	2495312	1797062	*Dendropsophus minutus*	Brazil
Alves-Ferreira et al 2021	2596934	2149027	*Dendropsophus nanus*	Brazil

Alves-Ferreira et al 2021	2596934	2125870	*Dendropsophus nanus*	Brazil
Alves-Ferreira et al 2021	1907434	1802307	*Dendropsophus rubicundulus*	Brazil
Alves-Ferreira et al 2021	1907434	2014850	*Dendropsophus rubicundulus*	Brazil
Alves-Ferreira et al 2021	1154204	763528	*Dendropsophus sanborni*	Brazil
Alves-Ferreira et al 2021	1154204	782090	*Dendropsophus sanborni*	Brazil
Alves-Ferreira et al 2021	1628540	3210002	*Leptodactylus bolivianus*	Brazil
Alves-Ferreira et al 2021	1628540	2971143	*Leptodactylus bolivianus*	Brazil
Alves-Ferreira et al 2021	2548658	2656391	*Leptodactylus chaquensis*	Brazil
Alves-Ferreira et al 2021	2548658	2672618	*Leptodactylus chaquensis*	Brazil
Alves-Ferreira et al 2021	178385	3001391	*Leptodactylus cunicularius*	Brazil
Alves-Ferreira et al 2021	178385	3008923	*Leptodactylus cunicularius*	Brazil
Alves-Ferreira et al 2021	2756358	2647176	*Leptodactylus fuscus*	Brazil
Alves-Ferreira et al 2021	2756358	2632630	*Leptodactylus fuscus*	Brazil
Alves-Ferreira et al 2021	2052460	1198631	*Leptodactylus labyrinthicus*	Brazil
Alves-Ferreira et al 2021	2052460	1046731	*Leptodactylus labyrinthicus*	Brazil
Alves-Ferreira et al 2021	2231594	2195994	*Leptodactylus latrans*	Brazil
Alves-Ferreira et al 2021	2231594	2442077	*Leptodactylus latrans*	Brazil

Alves-Ferreira et al 2021	2761455	1757239	*Leptodactylus petersii*	Brazil
Alves-Ferreira et al 2021	2761455	1607616	*Leptodactylus petersii*	Brazil
Alves-Ferreira et al 2021	2016760	2032679	*Leptodactylus podicipinus*	Brazil
Alves-Ferreira et al 2021	2016760	2110548	*Leptodactylus podicipinus*	Brazil
Alves-Ferreira et al 2021	1098424	2158748	*Leptodactylus pustulatus*	Brazil
Alves-Ferreira et al 2021	1098424	2044486	*Leptodactylus pustulatus*	Brazil
Alves-Ferreira et al 2021	1063957	1065531	*Physalaemus albifrons*	Brazil
Alves-Ferreira et al 2021	1063957	1064569	*Physalaemus albifrons*	Brazil
Alves-Ferreira et al 2021	2220053	1260149	*Physalaemus albonotatus*	Brazil
Alves-Ferreira et al 2021	2220053	1456066	*Physalaemus albonotatus*	Brazil
Alves-Ferreira et al 2021	2759552	2126026	*Physalaemus centralis*	Brazil
Alves-Ferreira et al 2021	2759552	1911204	*Physalaemus centralis*	Brazil
Alves-Ferreira et al 2021	884407	1801069	*Physalaemus cicada*	Brazil
Alves-Ferreira et al 2021	884407	1936604	*Physalaemus cicada*	Brazil
Alves-Ferreira et al 2021	2691951	1228987	*Physalaemus cuvieri*	Brazil
Alves-Ferreira et al 2021	2691951	1064633	*Physalaemus cuvieri*	Brazil
Alves-Ferreira et al 2021	2313880	1503552	*Physalaemus nattereri*	Brazil

Alves-Ferreira et al 2021	2313880	1305747	*Physalaemus nattereri*	Brazil
Alves-Ferreira et al 2021	1394075	3005683	*Proceratophrys goyana*	Brazil
Alves-Ferreira et al 2021	1394075	2926622	*Proceratophrys goyana*	Brazil
Alves-Ferreira et al 2021	2705029	3592086	*Pseudopaludicola falcipes*	Brazil
Alves-Ferreira et al 2021	2705029	3257074	*Pseudopaludicola falcipes*	Brazil
Alves-Ferreira et al 2021	220380	926533	*Pseudopaludicola mineira*	Brazil
Alves-Ferreira et al 2021	220380	830318	*Pseudopaludicola mineira*	Brazil
Alves-Ferreira et al 2021	2203559	2811184	*Pseudopaludicola mystacalis*	Brazil
Alves-Ferreira et al 2021	2203559	2623574	*Pseudopaludicola mystacalis*	Brazil
Alves-Ferreira et al 2021	1675466	2072925	*Pseudopaludicola saltica*	Brazil
Alves-Ferreira et al 2021	1675466	1780622	*Pseudopaludicola saltica*	Brazil
Alves-Ferreira et al 2021	842368	181504	*Rhinella rubescens*	Brazil
Alves-Ferreira et al 2021	842368	241663	*Rhinella rubescens*	Brazil
Alves-Ferreira et al 2021	2385586	1534336	*Scinax fuscomarginatus*	Brazil
Alves-Ferreira et al 2021	2385586	1213671	*Scinax fuscomarginatus*	Brazil
Alves-Ferreira et al 2021	1865884	741112	*Scinax fuscovarius*	Brazil
Alves-Ferreira et al 2021	1865884	933843	*Scinax fuscovarius*	Brazil

Alves-Ferreira et al 2021	2242403	1484731	*Scinax nasicus*	Brazil
Alves-Ferreira et al 2021	2242403	1547550	*Scinax nasicus*	Brazil
Alves-Ferreira et al 2021	496630	207493	*Scinax squalirostris*	Brazil
Alves-Ferreira et al 2021	496630	197882	*Scinax squalirostris*	Brazil
Alves-Ferreira et al 2021	104367	120948	*Thoropa megatympanum*	Brazil
Alves-Ferreira et al 2021	104367	99311	*Thoropa megatympanum*	Brazil
Borzee et al 2019	10261	6219	*Karsenia koreana*	Korea
Borzee et al 2019	10261	23947	*Karsenia koreana*	Korea
Borzee et al 2019	10261	35172	*Karsenia koreana*	Korea
Borzee et al 2019	10261	33744	*Karsenia koreana*	Korea
Borzee et al 2019	10261	38506	*Karsenia koreana*	Korea
Borzee et al 2019	10261	19417	*Karsenia koreana*	Korea
Borzee et al 2019	10261	36033	*Karsenia koreana*	Korea
Borzee et al 2019	10261	6156	*Karsenia koreana*	Korea
Boyer et al 2020	573	75.636	*Bombina variegata*	Europe
Boyer et al 2020	573	215.448	*Bombina variegata*	Europe
Boyer et al 2020	573	38.391	*Bombina variegata*	Europe

Boyer et al 2020	573	94.545	*Bombina variegata*	Europe
Boyer et al 2020	573	29.796	*Bombina variegata*	Europe
Boyer et al 2020	573	486.477	*Bombina variegata*	Europe
Boyer et al 2020	573	308.274	*Bombina variegata*	Europe
Boyer et al 2020	573	60.165	*Bombina variegata*	Europe
Boyer et al 2020	573	2.292	*Bombina variegata*	Europe
Boyer et al 2020	573	18.336	*Bombina variegata*	Europe
Boyer et al 2020	573	567.843	*Bombina variegata*	Europe
Boyer et al 2020	573	398.235	*Bombina variegata*	Europe
Boyer et al 2020	573	279.624	*Bombina variegata*	Europe
Boyer et al 2020	573	582.741	*Bombina variegata*	Europe
Boyer et al 2020	573	263.007	*Bombina variegata*	Europe
Boyer et al 2020	573	604.515	*Bombina variegata*	Europe
COBOS e BOSCH 2018	3298	1490	*Peltophryne longinasus*	Cuba
COBOS e BOSCH 2018	3298	1821	*Peltophryne longinasus*	Cuba
COBOS e BOSCH 2018	3298	932	*Peltophryne longinasus*	Cuba
COBOS e BOSCH 2018	3298	1788	*Peltophryne longinasus*	Cuba

Cordier et al 2020	3187	0	*Rhinella achalensis*	Argentina
Cordier et al 2020	3187	887	*Rhinella achalensis*	Argentina
Cordier et al 2020	25513	5198	*Boana cordobae*	Argentina
Cordier et al 2020	25513	9938	*Boana cordobae*	Argentina
Cordier et al 2020	27393	5212	*Melanophryniscus stelzneri*	Argentina
Cordier et al 2020	27393	11962	*Melanophryniscus stelzneri*	Argentina
Cordier et al 2020	83654	110303	*Odontophrynus cordobae*	Argentina
Cordier et al 2020	83654	46772	*Odontophrynus cordobae*	Argentina
Cordier et al 2020	3071	0	*Odontophrynus occidentalis*	Argentina
Cordier et al 2020	3071	0	*Odontophrynus occidentalis*	Argentina
Cordier et al 2020	2031	0	*Pleurodema kriegi*	Argentina
Cordier et al 2020	2031	0	*Pleurodema kriegi*	Argentina
Damen et al 2011	547	294.5595	*Ichthyosaura alpestris*	Italy
Damen et al 2011	547	523.6431	*Ichthyosaura alpestris*	Italy
Damen et al 2011	547	536.1147	*Ichthyosaura alpestris*	Italy
Damen et al 2011	547	291.4416	*Ichthyosaura alpestris*	Italy
Damen et al 2011	663	1026.987	*Lissotriton italicus*	Italy

Damen et al 2011	663	595.374	*Lissotriton italicus*	Italy
Damen et al 2011	663	975.0078	*Lissotriton italicus*	Italy
Damen et al 2011	663	569.3844	*Lissotriton italicus*	Italy
Damen et al 2011	1149	571.3977	*Lissotriton vulgaris*	Italy
Damen et al 2011	1149	798.6699	*Lissotriton vulgaris*	Italy
Damen et al 2011	1149	917.0169	*Lissotriton vulgaris*	Italy
Damen et al 2011	1149	498.2064	*Lissotriton vulgaris*	Italy
Duan et al 2016	1431400	1372841.703	*Andrias davidianus*	China
Duan et al 2016	303835	458138.0605	*Scutiger mammatus*	China
Duan et al 2016	143327	150424.5519	*Tylototriton asperrimus*	China
Duan et al 2016	1431400	1309433.583	*Andrias davidianus*	China
Duan et al 2016	27200	34958.53235	*Tylototriton kweichowensis*	China
Duan et al 2016	711743	492528.1809	*Hyla sanchiangensis*	China
Duan et al 2016	711743	497490.6737	*Hyla sanchiangensis*	China
Duan et al 2016	35225	38385.56228	*Paramesotriton caudopunctatus*	China
Duan et al 2016	35225	36621.87496	*Paramesotriton caudopunctatus*	China

Duan et al 2016	10	4.3728102	*Paramesotriton labiatus*	China
Duan et al 2016	10	5.00104285	*Paramesotriton labiatus*	China
Duan et al 2016	411723	497722.2592	*Pelophylax hubeiensis*	China
Duan et al 2016	411723	556110.145	*Pelophylax hubeiensis*	China
Duan et al 2016	2452	2404.387698	*Batrachuperus londongensis*	China
Duan et al 2016	2452	2346.789122	*Batrachuperus londongensis*	China
Duan et al 2016	232900	284418.28	*Batrachuperus tibetanus*	China
Duan et al 2016	232900	302940.6959	*Batrachuperus tibetanus*	China
Duan et al 2016	13581	16736.81697	*Amolops hainanensis*	China
Duan et al 2016	15867	14878.4886	*Batrachuperus yenyuanensis*	China
Duan et al 2016	15867	16472.72384	*Batrachuperus yenyuanensis*	China
Duan et al 2016	256700	226228.8282	*Batrachuperus pinchonii*	China
Duan et al 2016	1345426	857483.5816	*Hylarana latouchii*	China
Duan et al 2016	256700	223393.0941	*Batrachuperus pinchonii*	China
Duan et al 2016	256700	227380.6049	*Batrachuperus pinchonii*	China
Duan et al 2016	256700	228345.1483	*Batrachuperus pinchonii*	China
Duan et al 2016	62900	29417.47991	*Oreolalax rhodostigmatus*	China

Duan et al 2016	15837	23275.3087	*Amolops torrentis*	China
Duan et al 2016	15426	18656.16206	*Buergeria oxycephala*	China
Duan et al 2016	15426	19735.16	*Buergeria oxycephala*	China
Duan et al 2016	69191	72131.58432	*Dryophytes japonicus*	China
Duan et al 2016	69191	70407.40698	*Dryophytes japonicus*	China
Duan et al 2016	764568	885094.9021	*Glyphoglossus yunnanensis*	China
Duan et al 2016	764568	819633.9841	*Glyphoglossus yunnanensis*	China
Duan et al 2016	1345425	811400.9191	*Hylarana latouchii*	China
Duan et al 2016	15713	17975.72995	*Sylvirana spinulosa*	China
Duan et al 2016	90789	104656.6457	*Kaloula rugifera*	China
Duan et al 2016	90790	101279.1389	*Kaloula rugifera*	China
Duan et al 2016	540494	557575.9937	*Leptobrachium liui*	China
Duan et al 2016	540494	537949.2137	*Leptobrachium liui*	China
Duan et al 2016	53409	30780.41051	*Megophrys boettgeri*	China
Duan et al 2016	53408	28225.81823	*Megophrys boettgeri*	China
Duan et al 2016	82991	46156.39905	*Megophrys jingdongensis*	China
Duan et al 2016	82991	40770.64416	*Megophrys jingdongensis*	China

Duan et al 2016	82991	46006.49655	*Megophrys jingdongensis*	China
Duan et al 2016	82991	40887.02659	*Megophrys jingdongensis*	China
Duan et al 2016	53408	28657.67799	*Megophrys minor*	China
Duan et al 2016	53408	31259.75848	*Megophrys minor*	China
Duan et al 2016	16429	22397.32712	*Amolops lifanensis*	China
Duan et al 2016	15713	17649.58357	*Sylvirana spinulosa*	China
Duan et al 2016	601050	283482.5278	*Zhangixalus chenfui*	China
Duan et al 2016	601050	254834.892	*Zhangixalus chenfui*	China
Duan et al 2016	507570	277393.0451	*Zhangixalus omeimontis*	China
Duan et al 2016	507570	241266.928	*Zhangixalus omeimontis*	China
Duan et al 2016	1208146	600412.3176	*Amolops chunganensis*	China
Duan et al 2016	1208146	689416.4334	*Amolops chunganensis*	China
Duan et al 2016	274437	280943.9013	*Amolops granulosus*	China
Duan et al 2016	274437	276333.3597	*Amolops granulosus*	China
Duan et al 2016	292558	146052.7503	*Odorrana versabilis*	China
Duan et al 2016	13581	15973.83639	*Amolops hainanensis*	China
Duan et al 2016	16429	20230.6706	*Amolops lifanensis*	China

Duan et al 2016	65144	88066.32351	*Bufo gargarizans*	China
Duan et al 2016	85957	119555.1983	*Cynops cyanurus*	China
Duan et al 2016	89477	74965.62014	*Amolops loloensis*	China
Duan et al 2016	89477	81735.44996	*Amolops loloensis*	China
Duan et al 2016	291990	296130.4182	*Amolops mantzorum*	China
Duan et al 2016	291990	302860.7877	*Amolops mantzorum*	China
Duan et al 2016	74265	73562.55039	*Oreolalax rugosus*	China
Duan et al 2016	15837	21090.94478	*Amolops torrentis*	China
Duan et al 2016	123474	90404.70313	*Amolops wuyiensis*	China
Duan et al 2016	123474	92319.7077	*Amolops wuyiensis*	China
Duan et al 2016	65144	51507.27033	*Bufo gargarizans*	China
Duan et al 2016	65144	48595.74426	*Bufo gargarizans*	China
Duan et al 2016	65144	95570.5703	*Bufo gargarizans*	China
Duan et al 2016	15632	19306.88671	*Limnonectes fragilis*	China
Duan et al 2016	459000	472622.3468	*Nanorana yunnanensis*	China
Duan et al 2016	85957	110997.8574	*Cynops cyanurus*	China
Duan et al 2016	568622	598653.7215	*Cynops orientalis*	China

Duan et al 2016	568621	600220.5043	*Cynops orientalis*	China
Duan et al 2016	68673	291500.9048	*Hynobius leechii*	China
Duan et al 2016	68673	355791.424	*Hynobius leechii*	China
Duan et al 2016	345833	372702.1059	*Kaloula verrucosa*	China
Duan et al 2016	345832	342485.1062	*Kaloula verrucosa*	China
Duan et al 2016	10609	12629.63963	*Odorrana hainanensis*	China
Duan et al 2016	78200	87844.21492	*Leptobrachium boringii*	China
Duan et al 2016	78200	91176.51308	*Leptobrachium boringii*	China
Duan et al 2016	15633	19880.16187	*Limnonectes fragilis*	China
Duan et al 2016	71772	54578.61871	*Oreolalax major*	China
Duan et al 2016	71772	59511.39164	*Oreolalax major*	China
Duan et al 2016	459000	446904.1428	*Nanorana yunnanensis*	China
Duan et al 2016	150889	144846.7665	*Tylototriton shanjing*	China
Duan et al 2016	1401387	986103.9984	*Nidirana adenopleura*	China
Duan et al 2016	1401388	1035627.463	*Nidirana adenopleura*	China
Duan et al 2016	166600	162877.7799	*Odorrana andersonii*	China
Duan et al 2016	166600	157289.6419	*Odorrana andersonii*	China

Duan et al 2016	260172	273122.1799	*Tylototriton wenxianensis*	China
Duan et al 2016	26726	29591.79931	*Oreolalax schmidti*	China
Duan et al 2016	10609	11881.17081	*Odorrana hainanensis*	China
Duan et al 2016	65551	78726.41669	*Pelophylax nigromaculatus*	China
Duan et al 2016	292559	145247.8053	*Odorrana versabilis*	China
Duan et al 2016	1159330	1577378.822	*Pelophylax plancyi*	China
Duan et al 2016	391809	374354.4782	*Quasipaa exilispinosa*	China
Duan et al 2016	391809	376315.8249	*Quasipaa exilispinosa*	China
Duan et al 2016	2329	2204.823885	*Oreolalax pingii*	China
Duan et al 2016	2329	2241.59079	*Oreolalax pingii*	China
Duan et al 2016	62900	33217.93816	*Oreolalax rhodostigmatus*	China
Duan et al 2016	74265	67562.84182	*Oreolalax rugosus*	China
Duan et al 2016	172147	223449.6722	*Scutiger glandulatus*	China
Duan et al 2016	26726	28001.00737	*Oreolalax schmidti*	China
Duan et al 2016	303835	410223.7671	*Scutiger mammatus*	China
Duan et al 2016	65551	80193.72109	*Pelophylax nigromaculatus*	China
Duan et al 2016	476946	537727.9696	*Rana omeimontis*	China

Duan et al 2016	1159330	1864496.084	*Pelophylax plancyi*	China
Duan et al 2016	469195	501876.9732	*Rana chaochiaoensis*	China
Duan et al 2016	27200	32670.82943	*Tylototriton kweichowensis*	China
Duan et al 2016	260172	279881.8008	*Tylototriton wenxianensis*	China
Duan et al 2016	469195	476081.3804	*Rana chaochiaoensis*	China
Duan et al 2016	172147	232413.2176	*Scutiger glandulatus*	China
Duan et al 2016	476946	559257.3073	*Rana omeimontis*	China
Duan et al 2016	30831	31610.08692	*Tylototriton taliangensis*	China
Duan et al 2016	20995	20271.79133	*Tylototriton verrucosus*	China
Duan et al 2016	143327	158354.972	*Tylototriton asperrimus*	China
Duan et al 2016	20995	21480.97428	*Tylototriton verrucosus*	China
Duan et al 2016	30831	32785.26708	*Tylototriton taliangensis*	China
Duan et al 2016	150889	152956.0244	*Tylototriton shanjing*	China
Enriquez?Urzelai et al 2019	84911	49723	*Rana temporaria*	Europe
Garcia et al 2013	322537	113265.6408	*Lithobates magnaocularis*	Mexico
Garcia et al 2013	322538	208409.2189	*Lithobates magnaocularis*	Mexico

Garcia et al 2013	172311	144418.5015	*Anaxyrus kelloggi*	Mexico
Garcia et al 2013	172311	76646.68978	*Anaxyrus kelloggi*	Mexico
Garcia et al 2013	43752	28065.68294	*Incilius perplexus*	Mexico
Garcia et al 2013	43751	6555.343583	*Incilius perplexus*	Mexico
Garcia et al 2013	418740	272531.0666	*Tlalocohyla smithii*	Mexico
Garcia et al 2013	418740	113718.0593	*Tlalocohyla smithii*	Mexico
Garcia et al 2013	333856	367353.1079	*Triprion spatulatus*	Mexico
Garcia et al 2013	333856	361100.4524	*Triprion spatulatus*	Mexico
Garcia et al 2013	526564	189844.7517	*Agalychnis dacnicolor*	Mexico
Garcia et al 2013	526564	443792.8783	*Agalychnis dacnicolor*	Mexico
Garcia et al 2013	4755	4853.598729	*Bolitoglossa macrinii*	Mexico
Garcia et al 2013	4755	3562.27482	*Bolitoglossa macrinii*	Mexico
Garcia et al 2013	22103	7761.932613	*Charadrahyla juanitae*	Mexico
Garcia et al 2013	22103	1138.415015	*Charadrahyla juanitae*	Mexico
Garcia et al 2013	192298	43218.7832	*Craugastor hobartsmithi*	Mexico
Garcia et al 2013	192298	143162.3996	*Craugastor hobartsmithi*	Mexico
Garcia et al 2013	183051	223701.8678	*Craugastor occidentalis*	Mexico

Garcia et al 2013	183051	191989.2705	*Craugastor occidentalis*	Mexico
Garcia et al 2013	38069	36719.39685	*Craugastor rupinius*	Mexico
Garcia et al 2013	38069	23885.44233	*Craugastor rupinius*	Mexico
Garcia et al 2013	314009	185254.9477	*Craugastor vocalis*	Mexico
Garcia et al 2013	314009	147027.492	*Craugastor vocalis*	Mexico
Garcia et al 2013	24687	27626.33297	*Eleutherodactylus modestus*	Mexico
Garcia et al 2013	24687	26239.22722	*Eleutherodactylus modestus*	Mexico
Garcia et al 2013	71975	9436.2104	*Eleutherodactylus pallidus*	Mexico
Garcia et al 2013	71976	62684.11433	*Eleutherodactylus pallidus*	Mexico
Garcia et al 2013	258560	180386.711	*Exerodonta smaragdina*	Mexico
Garcia et al 2013	258559	237286.2651	*Exerodonta smaragdina*	Mexico
Garcia et al 2013	258559	295397.1935	*Exerodonta sumichrasti*	Mexico
Garcia et al 2013	258560	322032.6016	*Exerodonta sumichrasti*	Mexico
Garcia et al 2013	414	127.93842	*Quilticohyla erythromma*	Mexico
Garcia et al 2013	414	0	*Quilticohyla erythromma*	Mexico
Girardello et al 2009	573	102	*Bombina variegata*	Italy
Girardello et al 2009	573	204	*Bombina variegata*	Italy

Girardello et al 2009	216	282	*Discoglossus pictus*	Italy
Girardello et al 2009	32	0	*Pelobates fuscus*	Italy
Girardello et al 2009	32	0	*Pelobates fuscus*	Italy
Girardello et al 2009	890	606	*Salamandra salamandra*	Italy
Girardello et al 2009	890	497	*Salamandra salamandra*	Italy
Girardello et al 2009	1374	2420	*Hyla intermedia*	Italy
Girardello et al 2009	1374	1252	*Hyla intermedia*	Italy
Girardello et al 2009	547	480	*Ichthyosaura alpestris*	Italy
Girardello et al 2009	547	347	*Ichthyosaura alpestris*	Italy
Girardello et al 2009	1448	1302	*Bufotes viridis*	Italy
Girardello et al 2009	1448	2301	*Bufotes viridis*	Italy
Girardello et al 2009	216	212	*Discoglossus pictus*	Italy
Girardello et al 2009	162	25	*Hyla sarda*	Italy
Girardello et al 2009	162	32	*Hyla sarda*	Italy
Girardello et al 2009	663	439	*Lissotriton italicus*	Italy
Girardello et al 2009	663	529	*Lissotriton italicus*	Italy
Girardello et al 2009	1149	1032	*Lissotriton vulgaris*	Italy

Girardello et al 2009	1149	1625	*Lissotriton vulgaris*	Italy
Girardello et al 2009	2481	845	*Pelophylax lessonae*	Italy
Girardello et al 2009	2481	2893	*Pelophylax lessonae*	Italy
Girardello et al 2009	1169	1181	*Rana dalmatina*	Italy
Girardello et al 2009	1169	650	*Rana dalmatina*	Italy
Girardello et al 2009	904	399	*Rana italica*	Italy
Girardello et al 2009	904	507	*Rana italica*	Italy
Girardello et al 2009	252	104	*Rana latastei*	Italy
Girardello et al 2009	252	238	*Rana latastei*	Italy
Girardello et al 2009	630	453	*Rana temporaria*	Italy
Girardello et al 2009	630	440	*Rana temporaria*	Italy
Girardello et al 2009	184	151	*Salamandra atra*	Italy
Girardello et al 2009	184	123	*Salamandra atra*	Italy
Girardello et al 2009	360	65	*Salamandrina terdigitata*	Italy
Girardello et al 2009	360	27	*Salamandrina terdigitata*	Italy
Kaky 2020	115464	123188	*Pelophylax ridibundus*	Iraq
Kaky 2020	115464	119335	*Pelophylax ridibundus*	Iraq

Kaky 2020	124774	132359	*Bufotes viridis*	Iraq
Kaky 2020	124774	115146	*Bufotes viridis*	Iraq
Kaky 2020	20029	19873	*Neurergus crocatus*	Iraq
Kaky 2020	20029	20130	*Neurergus crocatus*	Iraq
Kim et al 2021	56561	47634	*Bombina orientalis*	Korea
Kim et al 2021	56561	3354	*Bombina orientalis*	Korea
Kim et al 2021	56561	25427	*Bombina orientalis*	Korea
Kim et al 2021	56561	30774	*Bombina orientalis*	Korea
Kim et al 2021	56561	2529	*Bombina orientalis*	Korea
Kim et al 2021	56561	30044	*Bombina orientalis*	Korea
Kim et al 2021	69191	74273	*Dryophytes japonicus*	Korea
Kim et al 2021	69191	41463	*Dryophytes japonicus*	Korea
Kim et al 2021	69191	22798	*Dryophytes japonicus*	Korea
Kim et al 2021	69191	50748	*Dryophytes japonicus*	Korea
Kim et al 2021	69191	23119	*Dryophytes japonicus*	Korea
Kim et al 2021	69191	52626	*Dryophytes japonicus*	Korea
Kim et al 2021	24392	33656	*Kaloula borealis*	Korea

Kim et al 2021	24392	39835	*Kaloula borealis*	Korea
Kim et al 2021	24392	48429	*Kaloula borealis*	Korea
Kim et al 2021	24392	61206	*Kaloula borealis*	Korea
Kim et al 2021	24392	30814	*Kaloula borealis*	Korea
Kim et al 2021	24392	41009	*Kaloula borealis*	Korea
Kim et al 2021	65144	46998	*Bufo gargarizans*	Korea
Kim et al 2021	65144	41381	*Bufo gargarizans*	Korea
Kim et al 2021	65144	62370	*Bufo gargarizans*	Korea
Kim et al 2021	65144	24268	*Bufo gargarizans*	Korea
Kim et al 2021	65144	21368	*Bufo gargarizans*	Korea
Kim et al 2021	65144	48268	*Bufo gargarizans*	Korea
Kim et al 2021	17160	1448	*Bufo stejnegeri*	Korea
Kim et al 2021	17160	4288	*Bufo stejnegeri*	Korea
Kim et al 2021	17160	3916	*Bufo stejnegeri*	Korea
Kim et al 2021	17160	265	*Bufo stejnegeri*	Korea
Kim et al 2021	17160	16158	*Bufo stejnegeri*	Korea
Kim et al 2021	17160	59	*Bufo stejnegeri*	Korea

Kim et al 2021	60730	35123	*Glandirana rugosa*	Korea
Kim et al 2021	60730	19256	*Glandirana rugosa*	Korea
Kim et al 2021	60730	52518	*Glandirana rugosa*	Korea
Kim et al 2021	60730	41887	*Glandirana rugosa*	Korea
Kim et al 2021	60730	34411	*Glandirana rugosa*	Korea
Kim et al 2021	60730	31959	*Glandirana rugosa*	Korea
Kim et al 2021	68673	38858	*Hynobius leechii*	Korea
Kim et al 2021	68673	22711	*Hynobius leechii*	Korea
Kim et al 2021	68673	31160	*Hynobius leechii*	Korea
Kim et al 2021	68673	24299	*Hynobius leechii*	Korea
Kim et al 2021	68673	11747	*Hynobius leechii*	Korea
Kim et al 2021	68673	15452	*Hynobius leechii*	Korea
Kim et al 2021	1585	888	*Hynobius quelpaertensis*	Korea
Kim et al 2021	1585	1220	*Hynobius quelpaertensis*	Korea
Kim et al 2021	1585	1510	*Hynobius quelpaertensis*	Korea
Kim et al 2021	1585	1343	*Hynobius quelpaertensis*	Korea
Kim et al 2021	1585	1427	*Hynobius quelpaertensis*	Korea

Kim et al 2021	1585	253	*Hynobius quelpaertensis*	Korea
Kim et al 2021	45627	76576	*Karsenia koreana*	Korea
Kim et al 2021	45627	79896	*Karsenia koreana*	Korea
Kim et al 2021	45627	84130	*Karsenia koreana*	Korea
Kim et al 2021	45627	87252	*Karsenia koreana*	Korea
Kim et al 2021	45627	87674	*Karsenia koreana*	Korea
Kim et al 2021	45627	78035	*Karsenia koreana*	Korea
Kim et al 2021	28523	55541	*Lithobates catesbeianus*	Korea
Kim et al 2021	28523	42311	*Lithobates catesbeianus*	Korea
Kim et al 2021	28523	40263	*Lithobates catesbeianus*	Korea
Kim et al 2021	28523	27067	*Lithobates catesbeianus*	Korea
Kim et al 2021	28523	37986	*Lithobates catesbeianus*	Korea
Kim et al 2021	28523	62436	*Lithobates catesbeianus*	Korea
Kim et al 2021	10901	2000	*Pelophylax chosenicus*	Korea
Kim et al 2021	10901	168	*Pelophylax chosenicus*	Korea
Kim et al 2021	10901	298	*Pelophylax chosenicus*	Korea
Kim et al 2021	10901	412	*Pelophylax chosenicus*	Korea

Kim et al 2021	10901	3255	*Pelophylax chosenicus*	Korea
Kim et al 2021	10901	4298	*Pelophylax chosenicus*	Korea
Kim et al 2021	65551	71358	*Pelophylax nigromaculatus*	Korea
Kim et al 2021	65551	57881	*Pelophylax nigromaculatus*	Korea
Kim et al 2021	65551	49658	*Pelophylax nigromaculatus*	Korea
Kim et al 2021	65551	44831	*Pelophylax nigromaculatus*	Korea
Kim et al 2021	65551	19902	*Pelophylax nigromaculatus*	Korea
Kim et al 2021	65551	28648	*Pelophylax nigromaculatus*	Korea
Kim et al 2021	47791	33675	*Rana coreana*	Korea
Kim et al 2021	47791	15420	*Rana coreana*	Korea
Kim et al 2021	47791	28215	*Rana coreana*	Korea
Kim et al 2021	47791	25815	*Rana coreana*	Korea
Kim et al 2021	47791	17128	*Rana coreana*	Korea
Kim et al 2021	47791	16617	*Rana coreana*	Korea
Li et al 2013	232900	476000	*Batrachuperus tibetanus*	China
Li et al 2013	17000	0	*Oreolalax multipunctatus*	China
Li et al 2013	1431400	1242700	*Andrias davidianus*	China

Li et al 2013	256700	331500	*Batrachuperus pinchonii*	China
Li et al 2013	42500	15300	*Amolops loloensis*	China
Li et al 2013	27200	0	*Tylototriton kweichowensis*	China
Li et al 2013	62900	17000	*Oreolalax rhodostigmatus*	China
Li et al 2013	459000	176800	*Nanorana yunnanensis*	China
Li et al 2013	166600	209100	*Odorrana andersonii*	China
Li et al 2013	78200	13600	*Leptobrachium boringii*	China
Lyons e Kozak 2019	1943	3569.291	*Plethodon jordani*	EUA
Lyons e Kozak 2019	1943	3730.9486	*Plethodon jordani*	EUA
Lyons e Kozak 2019	7931	14232.1795	*Plethodon metcalfi*	EUA
Lyons e Kozak 2019	7931	14734.2118	*Plethodon metcalfi*	EUA
Lyons e Kozak 2019	7080	13876.092	*Plethodon montanus*	EUA
Lyons e Kozak 2019	7080	14033.976	*Plethodon montanus*	EUA
Medina et al 2020	25859	23065	*Leptodactylus bufonius*	Neotropic
Medina et al 2020	25859	22721	*Leptodactylus bufonius*	Neotropic
Medina et al 2020	15957	13709	*Leptodactylus caatingae*	Neotropic
Medina et al 2020	15957	11968	*Leptodactylus caatingae*	Neotropic

Medina et al 2020	58401	57368	*Leptodactylus elenae*	Neotropic
Medina et al 2020	58401	40075	*Leptodactylus elenae*	Neotropic
Medina et al 2020	50504	38819	*Leptodactylus furnarius*	Neotropic
Medina et al 2020	50504	34526	*Leptodactylus furnarius*	Neotropic
Medina et al 2020	3564	1276	*Leptodactylus jolyi*	Neotropic
Medina et al 2020	3564	1519	*Leptodactylus jolyi*	Neotropic
Medina et al 2020	6986	4435	*Leptodactylus laticeps*	Neotropic
Medina et al 2020	6986	5690	*Leptodactylus laticeps*	Neotropic
Medina et al 2020	38354	22073	*Leptodactylus longirostris*	Neotropic
Medina et al 2020	38354	16018	*Leptodactylus longirostris*	Neotropic
Medina et al 2020	179213	138227	*Leptodactylus mystaceus*	Neotropic
Medina et al 2020	179213	117146	*Leptodactylus mystaceus*	Neotropic
Medina et al 2020	105543	73892	*Leptodactylus mystacinus*	Neotropic
Medina et al 2020	105543	94142	*Leptodactylus mystacinus*	Neotropic
Medina et al 2020	10064	5468	*Leptodactylus natalensis*	Neotropic
Medina et al 2020	10064	4779	*Leptodactylus natalensis*	Neotropic
Medina et al 2020	11502	4435	*Leptodactylus plaumanni*	Neotropic

Medina et al 2020	11502	9457	*Leptodactylus plaumanni*	Neotropic
Medina et al 2020	33635	21708	*Leptodactylus sertanejo*	Neotropic
Medina et al 2020	33635	20777	*Leptodactylus sertanejo*	Neotropic
Medina et al 2020	8100	6278	*Leptodactylus spixi*	Neotropic
Medina et al 2020	8100	7047	*Leptodactylus spixi*	Neotropic
Medina et al 2020	89991	60953	*Leptodactylus syphax*	Neotropic
Medina et al 2020	89991	56498	*Leptodactylus syphax*	Neotropic
Medina et al 2020	41067	34243	*Leptodactylus troglodytes*	Neotropic
Medina et al 2020	41067	41513	*Leptodactylus troglodytes*	Neotropic
Medina et al 2020	22194	12859	*Leptodactylus validus*	Neotropic
Medina et al 2020	22194	14965	*Leptodactylus validus*	Neotropic
Medina et al 2020	48155	28593	*Leptodactylus paraensis*	Neotropic
Medina et al 2020	48155	29099	*Leptodactylus paraensis*	Neotropic
Medina et al 2020	9518	8586	*Leptodactylus savagei*	Neotropic
Medina et al 2020	9518	7371	*Leptodactylus savagei*	Neotropic
Medina et al 2020	365	263	*Leptodactylus albilabris*	Neotropic
Medina et al 2020	365	284	*Leptodactylus albilabris*	Neotropic

Medina et al 2020	61520	48904	*Leptodactylus bolivianus*	Neotropic
Medina et al 2020	61520	47183	*Leptodactylus bolivianus*	Neotropic
Medina et al 2020	1499	972	*Leptodactylus camaquara*	Neotropic
Medina et al 2020	1499	344	*Leptodactylus camaquara*	Neotropic
Medina et al 2020	83734	54513	*Leptodactylus chaquensis*	Neotropic
Medina et al 2020	83734	58482	*Leptodactylus chaquensis*	Neotropic
Medina et al 2020	15309	10712	*Leptodactylus colombiensis*	Neotropic
Medina et al 2020	15309	9680	*Leptodactylus colombiensis*	Neotropic
Medina et al 2020	4860	5326	*Leptodactylus cunicularius*	Neotropic
Medina et al 2020	4860	2511	*Leptodactylus cunicularius*	Neotropic
Medina et al 2020	1377	1438	*Leptodactylus cupreus*	Neotropic
Medina et al 2020	1377	2025	*Leptodactylus cupreus*	Neotropic
Medina et al 2020	8282	4354	*Leptodactylus didymus*	Neotropic
Medina et al 2020	8282	9214	*Leptodactylus didymus*	Neotropic
Medina et al 2020	8829	3341	*Leptodactylus discodactylus*	Neotropic
Medina et al 2020	8829	2936	*Leptodactylus discodactylus*	Neotropic
Medina et al 2020	3564	4212	*Leptodactylus flavopictus*	Neotropic

Medina et al 2020	3564	2349	*Leptodactylus flavopictus*	Neotropic
Medina et al 2020	31509	28877	*Leptodactylus fragilis*	Neotropic
Medina et al 2020	31509	31226	*Leptodactylus fragilis*	Neotropic
Medina et al 2020	203290	159023	*Leptodactylus fuscus*	Neotropic
Medina et al 2020	203290	171396	*Leptodactylus fuscus*	Neotropic
Medina et al 2020	39467	30942	*Leptodactylus gracilis*	Neotropic
Medina et al 2020	39467	34931	*Leptodactylus gracilis*	Neotropic
Medina et al 2020	2106	1701	*Leptodactylus griseigularis*	Neotropic
Medina et al 2020	2106	1863	*Leptodactylus griseigularis*	Neotropic
Medina et al 2020	19926	18245	*Leptodactylus insularum*	Neotropic
Medina et al 2020	19926	17091	*Leptodactylus insularum*	Neotropic
Medina et al 2020	83511	50828	*Leptodactylus knudseni*	Neotropic
Medina et al 2020	83511	61540	*Leptodactylus knudseni*	Neotropic
Medina et al 2020	3503	2977	*Leptodactylus labrosus*	Neotropic
Medina et al 2020	3503	2754	*Leptodactylus labrosus*	Neotropic
Medina et al 2020	96005	85435	*Leptodactylus labyrinthicus*	Neotropic
Medina et al 2020	96005	79238	*Leptodactylus labyrinthicus*	Neotropic

Medina et al 2020	38961	34101	*Leptodactylus latinasus*	Neotropic
Medina et al 2020	38961	33635	*Leptodactylus latinasus*	Neotropic
Medina et al 2020	145739	122756	*Leptodactylus latrans*	Neotropic
Medina et al 2020	145739	108034	*Leptodactylus latrans*	Neotropic
Medina et al 2020	99610	68283	*Leptodactylus leptodactyloides*	Neotropic
Medina et al 2020	99610	64274	*Leptodactylus leptodactyloides*	Neotropic
Medina et al 2020	5083	9842	*Leptodactylus lithonaetes*	Neotropic
Medina et al 2020	5083	4374	*Leptodactylus lithonaetes*	Neotropic
Medina et al 2020	30841	28370	*Leptodactylus melanonotus*	Neotropic
Medina et al 2020	30841	29039	*Leptodactylus melanonotus*	Neotropic
Medina et al 2020	20473	15309	*Leptodactylus myersi*	Neotropic
Medina et al 2020	20473	27884	*Leptodactylus myersi*	Neotropic
Medina et al 2020	3240	2916	*Leptodactylus notoaktites*	Neotropic
Medina et al 2020	3240	2045	*Leptodactylus notoaktites*	Neotropic
Medina et al 2020	143998	97322	*Leptodactylus pentadactylus*	Neotropic
Medina et al 2020	143998	112286	*Leptodactylus pentadactylus*	Neotropic

Medina et al 2020	344	304	*Leptodactylus peritoaktites*	Neotropic
Medina et al 2020	344	648	*Leptodactylus peritoaktites*	Neotropic
Medina et al 2020	135554	101129	*Leptodactylus petersii*	Neotropic
Medina et al 2020	135554	108054	*Leptodactylus petersii*	Neotropic
Medina et al 2020	56457	45887	*Leptodactylus podicipinus*	Neotropic
Medina et al 2020	56457	47628	*Leptodactylus podicipinus*	Neotropic
Medina et al 2020	12515	10145	*Leptodactylus poecilochilus*	Neotropic
Medina et al 2020	12515	9680	*Leptodactylus poecilochilus*	Neotropic
Medina et al 2020	30659	27925	*Leptodactylus pustulatus*	Neotropic
Medina et al 2020	30659	24908	*Leptodactylus pustulatus*	Neotropic
Medina et al 2020	1438	932	*Leptodactylus rhodomerus*	Neotropic
Medina et al 2020	1438	1094	*Leptodactylus rhodomerus*	Neotropic
Medina et al 2020	118058	72576	*Leptodactylus rhodomystax*	Neotropic
Medina et al 2020	118058	74682	*Leptodactylus rhodomystax*	Neotropic
Medina et al 2020	15329	12413	*Leptodactylus rhodonotus*	Neotropic
Medina et al 2020	15329	11219	*Leptodactylus rhodonotus*	Neotropic
Medina et al 2020	12272	7371	*Leptodactylus riveroi*	Neotropic

Medina et al 2020	12272	7027	*Leptodactylus riveroi*	Neotropic
Medina et al 2020	5002	3058	*Leptodactylus rugosus*	Neotropic
Medina et al 2020	5002	2653	*Leptodactylus rugosus*	Neotropic
Medina et al 2020	1681	446	*Leptodactylus sabanensis*	Neotropic
Medina et al 2020	1681	1377	*Leptodactylus sabanensis*	Neotropic
Medina et al 2020	34607	28998	*Leptodactylus vastus*	Neotropic
Medina et al 2020	34607	26406	*Leptodactylus vastus*	Neotropic
Medina et al 2020	3058	2754	*Leptodactylus ventrimaculatus*	Neotropic
Medina et al 2020	3058	3564	*Leptodactylus ventrimaculatus*	Neotropic
Medina et al 2020	6278	4313	*Leptodactylus wagneri*	Neotropic
Medina et al 2020	6278	5042	*Leptodactylus wagneri*	Neotropic
Mokhatla et al 2015	2062.87	926.03	*Breviceps acutirostris*	Africa
Mokhatla et al 2015	4932.29	393.12	*Breviceps fuscus*	Africa
Mokhatla et al 2015	4932.29	124.89	*Breviceps fuscus*	Africa
Mokhatla et al 2015	616.26	1186.73	*Breviceps macrops*	Africa
Mokhatla et al 2015	616.26	3844.29	*Breviceps macrops*	Africa

Mokhatla et al 2015	9332.8	14964.58	*Breviceps namaquensis*	Africa
Mokhatla et al 2015	9332.8	8976.7	*Breviceps namaquensis*	Africa
Mokhatla et al 2015	178	2793.48	*Heleophryne rosei*	Africa
Mokhatla et al 2015	178	4782.9	*Heleophryne rosei*	Africa
Mokhatla et al 2015	88.96	107.31	*Afrixalus knysnae*	Africa
Mokhatla et al 2015	767.61	674.99	*Amietia vandijki*	Africa
Mokhatla et al 2015	767.61	1385.55	*Amietia vandijki*	Africa
Mokhatla et al 2015	12343.73	17.74	*Hyperolius horstockii*	Africa
Mokhatla et al 2015	96487.04	38640.03	*Vandijkophrynus angusticeps*	Africa
Mokhatla et al 2015	96487.04	25278.09	*Vandijkophrynus angusticeps*	Africa
Mokhatla et al 2015	8052.54	2900.09	*Cacosternum capense*	Africa
Mokhatla et al 2015	8052.54	2414.95	*Cacosternum capense*	Africa
Mokhatla et al 2015	22562.89	4215.93	*Cacosternum karooicum*	Africa
Mokhatla et al 2015	22562.89	12337.11	*Cacosternum karooicum*	Africa
Mokhatla et al 2015	35.58	462.97	*Cacosternum platys*	Africa
Mokhatla et al 2015	35.58	178.1	*Cacosternum platys*	Africa
Mokhatla et al 2015	692.98	159.96	*Arthroleptella landdrosia*	Africa

Mokhatla et al 2015	692.98	106.63	*Arthroleptella landdrosia*	Africa
Mokhatla et al 2015	35.95	639.52	*Arthroleptella subvoce*	Africa
Mokhatla et al 2015	35.95	799.08	*Arthroleptella subvoce*	Africa
Mokhatla et al 2015	2219.31	195.73	*Arthroleptella villiersi*	Africa
Mokhatla et al 2015	1333.43	827.96	*Capensibufo rosei*	Africa
Mokhatla et al 2015	1333.43	395.75	*Capensibufo rosei*	Africa
Mokhatla et al 2015	924.94	8837.72	*Heleophryne orientalis*	Africa
Mokhatla et al 2015	924.94	5623.38	*Heleophryne orientalis*	Africa
Mokhatla et al 2015	603.48	12157.59	*Poyntonia paludicola*	Africa
Mokhatla et al 2015	603.48	9611.75	*Poyntonia paludicola*	Africa
Mokhatla et al 2015	30813.79	111.43	*Strongylopus bonaespei*	Africa
Mokhatla et al 2015	30813.79	651.51	*Strongylopus bonaespei*	Africa
Mokhatla et al 2015	9508.06	163458.44	*Strongylopus springbokensis*	Africa
Mokhatla et al 2015	9508.06	231318.72	*Strongylopus springbokensis*	Africa
Mokhatla et al 2015	387878.8	47970.73	*Tomopterna delalandii*	Africa
Mokhatla et al 2015	387878.8	31849.9	*Tomopterna delalandii*	Africa
Nottingham and Pelletier 2021	773333	810342	*Plethodon asupak*	EUA

Nottingham and Pelletier 2021	773333	800058	*Plethodon asupak*	EUA
Nottingham and Pelletier 2021	21315	59076	*Plethodon dunni*	EUA
Nottingham and Pelletier 2021	21315	49557	*Plethodon dunni*	EUA
Nottingham and Pelletier 2021	4966	10291	*Plethodon elongatus*	EUA
Nottingham and Pelletier 2021	4966	9872	*Plethodon elongatus*	EUA
Nottingham and Pelletier 2021	40803	3043	*Plethodon idahoensis*	EUA
Nottingham and Pelletier 2021	40803	5818	*Plethodon idahoensis*	EUA
Nottingham and Pelletier 2021	4668	94862	*Plethodon larselli*	EUA
Nottingham and Pelletier 2021	4668	63888	*Plethodon larselli*	EUA
Nottingham and Pelletier 2021	4530	838	*Plethodon stormi*	EUA
Nottingham and Pelletier 2021	4530	2518	*Plethodon stormi*	EUA
Nottingham and Pelletier 2021	15268	4623	*Plethodon vandykei*	EUA
Nottingham and Pelletier 2021	15268	1045	*Plethodon vandykei*	EUA
Nottingham and Pelletier 2021	42796	97222	*Plethodon vehiculum*	EUA
Nottingham and Pelletier 2021	42796	97970	*Plethodon vehiculum*	EUA
Parra-Olea et al 2005	27025	7204	*Pseudoeurycea leprosa*	Mexico
Parra-Olea et al 2005	44551	39356	*Aquiloeurycea cephalica*	Mexico

Rosenstock et al 2015	80	122	*Melanophryniscus sanmartini*	Uruguai e Brazil
Rosenstock et al 2015	80	219	*Melanophryniscus sanmartini*	Uruguai e Brazil
Schivo et al 2019	104000	306000	*Lepidobatrachus asper*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	104000	440000	*Lepidobatrachus asper*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	138000	178000	*Lysapsus limellum*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	138000	342000	*Lysapsus limellum*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	16000	10000	*Pseudis minuta*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	16000	9000	*Pseudis minuta*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	134000	150000	*Dermatonotus muelleri*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	134000	162000	*Dermatonotus muelleri*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	205000	266000	*Elachistocleis bicolor*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	205000	204000	*Elachistocleis bicolor*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	132000	6000	*Leptodactylus bufonius*	Argentina, Brazil, Paraguai and Uruguai

Schivo et al 2019	132000	3000	*Leptodactylus bufonius*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	81000	211000	*Leptodactylus elenae*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	81000	377000	*Leptodactylus elenae*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	26000	37000	*Leptodactylus mystacinus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	26000	164000	*Leptodactylus mystacinus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	89000	24000	*Odontophrynus americanus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	89000	17000	*Odontophrynus americanus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	112000	460000	*Pithecopus azureus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	112000	323000	*Pithecopus azureus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	767000	986000	*Rhinella bergi*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	767000	835000	*Rhinella bergi*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	87000	95000	*Rhinella diptycha*	Argentina, Brazil, Paraguai and Uruguai

Schivo et al 2019	87000	87000	*Rhinella diptycha*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	37000	13000	*Rhinella dorbignyi*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	37000	45000	*Rhinella dorbignyi*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	50000	26000	*Rhinella icterica*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	50000	37000	*Rhinella icterica*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	128000	47000	*Boana albopunctata*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	128000	37000	*Boana albopunctata*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	44000	13000	*Boana pulchella*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	44000	11000	*Boana pulchella*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	67000	133000	*Boana raniceps*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	67000	219000	*Boana raniceps*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	13000	8000	*Dendropsophus nanus*	Argentina, Brazil, Paraguai and Uruguai

Schivo et al 2019	13000	49000	*Dendropsophus nanus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	63000	8000	*Dendropsophus sanborni*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	63000	64000	*Dendropsophus sanborni*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	21000	59000	*Leptodactylus chaquensis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	21000	97000	*Leptodactylus chaquensis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	153000	5000	*Leptodactylus gracilis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	153000	8000	*Leptodactylus gracilis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	359000	243000	*Leptodactylus labyrinthicus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	359000	127000	*Leptodactylus labyrinthicus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	63000	38000	*Leptodactylus latinasus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	63000	78000	*Leptodactylus latinasus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	104000	39000	*Leptodactylus latrans*	Argentina, Brazil, Paraguai and Uruguai

Schivo et al 2019	104000	33000	*Leptodactylus latrans*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	75000	161000	*Leptodactylus podicipinus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	75000	225000	*Leptodactylus podicipinus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	27000	20000	*Ololygon berthae*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	27000	18000	*Ololygon berthae*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	136000	58000	*Phyllomedusa sauvagii*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	136000	43000	*Phyllomedusa sauvagii*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	149000	71000	*Physalaemus biligonigerus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	149000	49000	*Physalaemus biligonigerus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	276000	120000	*Physalaemus riograndensis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	276000	148000	*Physalaemus riograndensis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	110000	16000	*Pseudopaludicola falcipes*	Argentina, Brazil, Paraguai and Uruguai

Schivo et al 2019	110000	7000	*Pseudopaludicola falcipes*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	185000	214000	*Pseudopaludicola mystacalis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	185000	155000	*Pseudopaludicola mystacalis*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	46000	53000	*Rhinella granulosa*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	46000	46000	*Rhinella granulosa*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	102000	320000	*Scinax acuminatus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	102000	238000	*Scinax acuminatus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	182000	154000	*Scinax fuscomarginatus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	182000	129000	*Scinax fuscomarginatus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	90000	46000	*Scinax fuscovarius*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	90000	51000	*Scinax fuscovarius*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	73000	155000	*Scinax nasicus*	Argentina, Brazil, Paraguai and Uruguai

Schivo et al 2019	73000	85000	*Scinax nasicus*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	37000	21000	*Scinax squalirostris*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	37000	19000	*Scinax squalirostris*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	77000	33000	*Trachycephalus typhonius*	Argentina, Brazil, Paraguai and Uruguai
Schivo et al 2019	77000	46000	*Trachycephalus typhonius*	Argentina, Brazil, Paraguai and Uruguai
Struecker e Milanovich 2017	1762000	1306699.2	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	1762000	1264058.8	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	1762000	348552	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	1762000	1244148.2	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	1762000	175319	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	1762000	568949.8	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	1762000	1306699.2	*Ambystoma laterale*	EUA

Struecker e Milanovich 2017	1762000	1011211.8	*Ambystoma laterale*	EUA
Struecker e Milanovich 2017	2989000	3240374.9	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	3190159.7	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	1634086.3	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	3190159.7	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	3196137.7	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	3001553.8	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	1054220.3	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	2989000	2702653.8	*Ambystoma maculatum*	EUA
Struecker e Milanovich 2017	1389000	1678884.3	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	1389000	1678745.4	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	1389000	1740000.3	*Ambystoma texanum*	EUA

Struecker e Milanovich 2017	1389000	1682495.7	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	1389000	1678884.3	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	1389000	1739028	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	1389000	1682079	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	1389000	1740139.2	*Ambystoma texanum*	EUA
Struecker e Milanovich 2017	848917	189138.7076	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	848917	492966.1019	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	848917	0	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	848917	205947.2642	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	848917	402386.658	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	848917	325814.3446	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	848917	528365.9408	*Eurycea longicauda*	EUA

Struecker e Milanovich 2017	848917	528365.9408	*Eurycea longicauda*	EUA
Struecker e Milanovich 2017	76312	47092.1352	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	228.936	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	87133.0416	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	87133.0416	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	50800.8984	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	46069.5544	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	0	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	76312	83180.08	*Eurycea lucifuga*	EUA
Struecker e Milanovich 2017	140900	398577.92	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	140900	401410.01	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	140900	277967.52	*Ambystoma annulatum*	EUA

Struecker e Milanovich 2017	140900	375878.93	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	140900	172264.34	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	140900	341273.89	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	140900	375878.93	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	140900	371806.92	*Ambystoma annulatum*	EUA
Struecker e Milanovich 2017	470000	97572	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	470000	34498	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	470000	258688	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	470000	46154	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	470000	0	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	470000	53627	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	470000	258688	*Ambystoma jeffersonianum*	EUA

Struecker e Milanovich 2017	470000	96350	*Ambystoma jeffersonianum*	EUA
Struecker e Milanovich 2017	1524847	1405756.449	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	917195.4705	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	1247477.331	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	0	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	1405756.449	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	231471.7746	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	1073949.742	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1524847	952724.4056	*Desmognathus fuscus*	EUA
Struecker e Milanovich 2017	1198566	2157.4188	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	1198566	207232.0614	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	1198566	1027770.345	*Eurycea bislineata*	EUA

Struecker e Milanovich 2017	1198566	956335.8114	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	1198566	506993.418	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	1198566	661968.0018	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	1198566	1027770.345	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	1198566	1200004.279	*Eurycea bislineata*	EUA
Struecker e Milanovich 2017	764568	336180.5496	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	764568	336180.5496	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	764568	0	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	764568	290153.556	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	764568	256512.564	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	764568	254830.5144	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	764568	261099.972	*Gyrinophilus porphyriticus*	EUA

Struecker e Milanovich 2017	764568	109562.5944	*Gyrinophilus porphyriticus*	EUA
Struecker e Milanovich 2017	1454021	1219196.609	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	785752.9484	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	920104.4888	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	1385245.807	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	1385245.807	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	660852.5445	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	307670.8436	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	1454021	103671.6973	*Hemidactylium scutatum*	EUA
Struecker e Milanovich 2017	28523	33674.2538	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	28523	35687.9776	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	28523	33674.2538	*Lithobates catesbeianus*	EUA

Struecker e Milanovich 2017	28523	34087.8373	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	28523	37852.8733	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	28523	32775.7793	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	28523	33865.3579	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	28523	35859.1156	*Lithobates catesbeianus*	EUA
Struecker e Milanovich 2017	3061207	7891179.405	*Lithobates sphenocephalus*	EUA
Struecker e Milanovich 2017	3061205	8121989.106	*Lithobates sphenocephalus*	EUA
Struecker e Milanovich 2017	3061206	7489546.6	*Lithobates sphenocephalus*	EUA
Struecker e Milanovich 2017	3061209	8773731.115	*Lithobates sphenocephalus*	EUA
Struecker e Milanovich 2017	3061210	6594764.703	*Lithobates sphenocephalus*	EUA
Struecker e Milanovich 2017	3061208	9427296.157	*Lithobates sphenocephalus*	EUA
Struecker e Milanovich 2017	3061211	12283109.14	*Lithobates sphenocephalus*	EUA

Struecker e Milanovich 2017	3440000	3191632	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	3117672	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	3674952	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	2973536	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	3674952	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	3431744	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	1250784	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	3440000	1800496	*Notophthalmus viridescens*	EUA
Struecker e Milanovich 2017	1812454	1759530.343	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	1812454	933051.3192	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	1812454	557510.8504	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	1812454	1759530.343	*Plethodon cinereus*	EUA

Struecker e Milanovich 2017	1812454	1584266.041	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	1812454	1715125.22	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	1812454	1447063.274	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	1812454	1318379.04	*Plethodon cinereus*	EUA
Struecker e Milanovich 2017	278593	348909.8732	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	41426.7791	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	344034.4957	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	309656.1195	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	347823.3605	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	316983.1154	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	340997.832	*Plethodon dorsalis*	EUA
Struecker e Milanovich 2017	278593	316983.1154	*Plethodon dorsalis*	EUA

Struecker e Milanovich 2017	113396	0	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	0	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	3492.5968	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	11657.1088	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	62469.8564	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	97010.278	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	97010.278	*Plethodon electromorphus*	EUA
Struecker e Milanovich 2017	113396	27283.0776	*Plethodon electromorphus*	EUA
Sutton et al 2014	848917	844035.7273	*Eurycea longicauda*	EUA
Sutton et al 2014	848917	845860.8988	*Eurycea longicauda*	EUA
Sutton et al 2014	114482	113818.0044	*Plethodon wehrlei*	EUA
Sutton et al 2014	114482	113669.1778	*Plethodon wehrlei*	EUA
Sutton et al 2014	3540	3519.822	*Plethodon welleri*	EUA
Sutton et al 2014	3540	3510.264	*Plethodon welleri*	EUA

Sutton et al 2014	1524847	1518595.127	*Desmognathus fuscus*	EUA
Sutton et al 2014	1524847	1520806.155	*Desmognathus fuscus*	EUA
Sutton et al 2014	303109	301396.4342	*Desmognathus monticola*	EUA
Sutton et al 2014	303109	301093.3252	*Desmognathus monticola*	EUA
Sutton et al 2014	292260	290141.115	*Desmognathus ochrophaeus*	EUA
Sutton et al 2014	292260	289600.434	*Desmognathus ochrophaeus*	EUA
Sutton et al 2014	1198566	1198086.574	*Eurycea bislineata*	EUA
Sutton et al 2014	1198566	1198326.287	*Eurycea bislineata*	EUA
Sutton et al 2014	764568	760898.0736	*Gyrinophilus porphyriticus*	EUA
Sutton et al 2014	764568	759789.45	*Gyrinophilus porphyriticus*	EUA
Sutton et al 2014	59988	59430.1116	*Plethodon hoffmani*	EUA
Sutton et al 2014	59988	59430.1116	*Plethodon hoffmani*	EUA
Sutton et al 2014	11143	11031.57	*Plethodon punctatus*	EUA
Sutton et al 2014	11143	11031.57	*Plethodon punctatus*	EUA
Sutton et al 2014	758984	757541.9304	*Pseudotriton montanus*	EUA
Sutton et al 2014	758984	756023.9624	*Pseudotriton montanus*	EUA
Sutton et al 2014	1065948	1063176.535	*Pseudotriton ruber*	EUA

Sutton et al 2014	1065948	1061844.1	*Pseudotriton ruber*	EUA
Toranza and Maneyro 2013	9270	0	*Melanophryniscus montevidensis*	Uruguay
Toranza and Maneyro 2013	9270	0	*Melanophryniscus montevidensis*	Uruguay
Toranza and Maneyro 2013	9270	0	*Melanophryniscus montevidensis*	Uruguay
Toranza and Maneyro 2013	9270	0	*Melanophryniscus montevidensis*	Uruguay
Toranza et al 2016	19140	66000	*Lysapsus limellum*	Uruguay
Toranza et al 2016	199320	199320	*Pseudis minuta*	Uruguay
Toranza et al 2016	102300	184140	*Leptodactylus furnarius*	Uruguay
Toranza et al 2016	199320	199320	*Leptodactylus mystacinus*	Uruguay
Toranza et al 2016	149160	187440	*Melanophryniscus atroluteus*	Uruguay
Toranza et al 2016	199320	199320	*Odontophrynus americanus*	Uruguay
Toranza et al 2016	101640	102960	*Phyllomedusa iheringii*	Uruguay
Toranza et al 2016	56100	187440	*Rhinella diptycha*	Uruguay
Toranza et al 2016	141240	194040	*Rhinella dorbignyi*	Uruguay
Toranza et al 2016	185460	135300	*Rhinella dorbignyi*	Uruguay
Toranza et al 2016	199320	199320	*Scinax granulatus*	Uruguay

Toranza et al 2016	199320	199320	*Boana pulchella*	Uruguay
Toranza et al 2016	190740	186120	*Dendropsophus minutus*	Uruguay
Toranza et al 2016	181500	194040	*Dendropsophus nanus*	Uruguay
Toranza et al 2016	199320	199320	*Dendropsophus sanborni*	Uruguay
Toranza et al 2016	199320	199320	*Elachistocleis ovalis*	Uruguay
Toranza et al 2016	199320	199320	*Leptodactylus bolivianus*	Uruguay
Toranza et al 2016	113520	192720	*Leptodactylus chaquensis*	Uruguay
Toranza et al 2016	199320	199320	*Leptodactylus gracilis*	Uruguay
Toranza et al 2016	199320	199320	*Leptodactylus latinasus*	Uruguay
Toranza et al 2016	106260	190080	*Leptodactylus podicipinus*	Uruguay
Toranza et al 2016	199320	199320	*Limnomedusa macroglossa*	Uruguay
Toranza et al 2016	199320	199320	*Pseudopaludicola falcipes*	Uruguay
Toranza et al 2016	140580	185460	*Rhinella achavali*	Uruguay
Toranza et al 2016	141240	55440	*Rhinella arenarum*	Uruguay
Toranza et al 2016	17820	0	*Melanophryniscus montevidensis*	Uruguay
Toranza et al 2016	52140	180840	*Scinax nasicus*	Uruguay
Toranza et al 2016	47520	86460	*Melanophryniscus sanmartini*	Uruguay

Toranza et al 2016	199320	199320	*Ololygon berthae*	Uruguay
Toranza et al 2016	196680	199320	*Physalaemus biligonigerus*	Uruguay
Toranza et al 2016	180840	199320	*Physalaemus cuvieri*	Uruguay
Toranza et al 2016	199320	197340	*Physalaemus gracilis*	Uruguay
Toranza et al 2016	143220	143220	*Physalaemus henselii*	Uruguay
Toranza et al 2016	189420	195360	*Physalaemus riograndensis*	Uruguay
Toranza et al 2016	86460	75240	*Pleurodema bibroni*	Uruguay
Toranza et al 2016	199320	199320	*Scinax squalirostris*	Uruguay
Toranza et al 2016	29040	153120	*Scinax fuscovarius*	Uruguay
Ureta et al 2018	5165916	5414138.264	*Anaxyrus cognatus*	Mexico
Ureta et al 2018	5165915	2925974.256	*Anaxyrus cognatus*	Mexico
Ureta et al 2018	5165915	5585852.23	*Anaxyrus cognatus*	Mexico
Ureta et al 2018	5165915	3839824.62	*Anaxyrus cognatus*	Mexico
Ureta et al 2018	28523	52869.66234	*Lithobates catesbeianus*	Mexico
Ureta et al 2018	28523	24201.7655	*Lithobates catesbeianus*	Mexico
Ureta et al 2018	28523	72101.00986	*Lithobates catesbeianus*	Mexico
Ureta et al 2018	28523	24026.34905	*Lithobates catesbeianus*	Mexico

Ureta et al 2018	298501	240200.7697	*Lithobates forreri*	Mexico
Ureta et al 2018	298503	228647.3279	*Lithobates forreri*	Mexico
Ureta et al 2018	298502	712882.4764	*Lithobates forreri*	Mexico
Ureta et al 2018	298500	865363.44	*Lithobates forreri*	Mexico
Vargas-Jaime et al 2021	49	41	*Pseudoeurycea leprosa*	Mexico
Vargas-Jaime et al 2021	49	40	*Pseudoeurycea leprosa*	Mexico
Vargas-Jaime et al 2021	6011	5371	*Pseudoeurycea robertsi*	Mexico
Vargas-Jaime et al 2021	6011	4770	*Pseudoeurycea robertsi*	Mexico
Vargas-Jaime et al 2021	96	83	*Aquiloeurycea cephalica*	Mexico
Vargas-Jaime et al 2021	96	90	*Aquiloeurycea cephalica*	Mexico
Vargas-Jaime et al 2021	366	354	*Isthmura bellii*	Mexico
Vargas-Jaime et al 2021	366	248	*Isthmura bellii*	Mexico
Vasconcelos e Prado 2016	4687700	2440555	*Dendropsophus minutus*	Neotropic
Vasconcelos e Prado 2016	3020782	2600972	*Dendropsophus nanus*	Neotropic
Vasconcelos e Prado 2016	4079507	2308102	*Scinax fuscomarginatus*	Neotropic
Vasconcelos e Prado 2016	4129764	2843504	*Scinax fuscovarius*	Neotropic

Zank et al 2014	469971	296423	*Melanophryniscus atroluteus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	469971	140370	*Melanophryniscus atroluteus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	658511	431161	*Melanophryniscus fulvoguttatus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	658511	485584	*Melanophryniscus fulvoguttatus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	7431	2175	*Melanophryniscus cambaraensis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	7431	2766	*Melanophryniscus cambaraensis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	289317	276871	*Melanophryniscus devincenzii*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	289317	282512	*Melanophryniscus devincenzii*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia

Zank et al 2014	221801	172063	*Melanophryniscus dorsalis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	221801	184368	*Melanophryniscus dorsalis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	452948	427	*Melanophryniscus estebani*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	452948	440	*Melanophryniscus estebani*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	720505	714312	*Melanophryniscus klappenbachi*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	720505	714987	*Melanophryniscus klappenbachi*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	4461	1591	*Melanophryniscus macrogranulosus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	4461	2046	*Melanophryniscus macrogranulosus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia

Zank et al 2014	14148	0	*Melanophryniscus montevidensis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	14148	6	*Melanophryniscus montevidensis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	35326	15896	*Melanophryniscus moreirae*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	35326	35218	*Melanophryniscus moreirae*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	184733	134105	*Melanophryniscus pachyrhynus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	184733	112981	*Melanophryniscus pachyrhynus*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	72980	54111	*Melanophryniscus rubriventris*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	72980	20184	*Melanophryniscus rubriventris*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia

Zank et al 2014	393367	202733	*Melanophryniscus sanmartini*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	393367	184850	*Melanophryniscus sanmartini*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	75275	58971	*Melanophryniscus simplex*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	75275	33831	*Melanophryniscus simplex*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	74439	11727	*Melanophryniscus spectabilis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	74439	3067	*Melanophryniscus spectabilis*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	58018	34	*Melanophryniscus stelzneri*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	58018	16628	*Melanophryniscus stelzneri*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia

Zank et al 2014	225923	79959	*Melanophryniscus tumifrons*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zank et al 2014	225923	72230	*Melanophryniscus tumifrons*	northern Argentina, central and southern Brazil, Uruguay, Paraguay, and Bolivia
Zhang et al 2019	1431400	201827.4	*Andrias davidianus*	China
Zhang et al 2019	1431400	450891	*Andrias davidianus*	China
Zhang et al 2019	1431400	450891	*Andrias davidianus*	China
Zhang et al 2019	1431400	372164	*Andrias davidianus*	China
Zhang et al 2020	1431400	1169453.8	*Andrias davidianus*	China
Zhang et al 2020	1431400	1175179.4	*Andrias davidianus*	China

Supplementary Material. List of references of the eligible studies used in our literature review.

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Capítulo 2

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phyloraster: an R package to calculate measures of endemism and evolutionary diversity for rasters

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Abstract

The spatial exploration of richness, endemism, and evolutionary diversity patterns has become an important part of biogeographic research and conservation planning. As the volume and complexity of biogeographical and phylogenetic data increase, the need for efficient tools to manipulate and analyze these datasets becomes essential. The 'phyloraster' package addresses this need by facilitating the analysis of evolutionary diversity and endemism for rasters. Our package offers a set of functions to support the linkage of species distribution models (SDMs) with phylogenies, providing then an understanding of the spatial distribution of biodiversity. It covers three main stages: pre-processing, processing, and post-processing of macroecological and phylogenetic data. During the pre-processing step, basic functions are provided to prepare the data. The processing step combines functions to calculate indices including species richness, Faith's phylogenetic diversity, phylogenetic endemism, weighted endemism, and evolutionary distinctiveness. Additionally, this step includes functions to compute the standardized effect size for each metric using spatial and phylogenetic randomization methods, ensuring proper control for richness effects. The post-processing stage includes functions to calculate the change of metrics between different times (e.g. present and future). In relation to processing in our functions, we show that 'phyloraster' takes up considerably less RAM than the other packages when computing the same metrics (weighted endemism). Lower RAM usage minimizes the hardware requirements to work with high-resolution datasets from local to global scales. This broadens user accessibility of the spatialized measures of endemism and evolutionary diversity.

Background

Species diversity is not constant over time and space (Weber et al. 2014), which has intrigued scientists since the time of Darwin and Wallace. Mapping endemism patterns is a crucial approach for characterizing the distribution of biodiversity (Rosauer et al. 2009). It serves as an important part of biogeographic research to identify regions with taxa that should be prioritized for global conservation efforts (Rosauer et al. 2009). The absolute concept of endemism states that a taxon is classified as endemic when it is restricted to a particular region and does not occur anywhere else (Anderson 1994). Weighted endemism (WE; Williams et al. 1994) is a widely employed measure for evaluating centers of endemism, which weight the species range by the proportion of the range of each species present in a given region (Laffan et al. 2016). This metric can be used to identify regions with a significant concentration of species with restricted distribution (Williams et al. 1994, Crisp et al. 2001, Slatyer et al. 2007, Rosauer et al. 2009). In this way, its maximization can be used as an optimization criterion for the allocation of conservation resources.

Taxon-based measures can exclude an important biodiversity facet: the spatial restriction of evolutionary diversity. The accumulation of evolutionary heritage and its variation can be incorporated into the endemism patterns through the phylogenetic relationships between species (Rosauer et al. 2009). Phylogenetic diversity (PD; Faith 1992) is a simple and broadly used measure that assesses the cumulative evolutionary history of a set of taxa distributed in a region (Faith 1992, Moritz and Faith 1998). This metric sums the branch lengths from a set of species that often share a geographic location and may reflect the contribution of each taxon to the group diversity. PD is considered a robust metric in the presence of taxonomic uncertainties because it uses branch lengths of a phylogeny as a measure of diversity, which tends to be less susceptible to change than species or nodes (Mace et al. 2003).

To evaluate the relative contribution of species to PD (i.e. the species ‘originality'), researchers often use evolutionary distinctiveness (ED; Pavoine et al. 2005, Isaac et al. 2007). This metric allows the evaluation of species that are evolutionarily distinct in the community (Isaac et al. 2007) and can be applied to the conservation of unique species or entire regions (Cadotte and Davies 2010). Information about the 'originality' of each species can be combined with the risk of extinction to identify species that are evolutionarily distinct and that are globally threatened (EDGE approach; Isaac et al. 2007).

An additional metric widely used is phylogenetic endemism (PE), which uses the sum of the branch length weighted by the clade range to identify regions with a spatial concentration of evolutionary isolation (Rosauer et al. 2009, Rosauer and Jetz 2014). A region with high PE may be formed in areas that harbor taxa with long branch lengths restricted to that area (Rosauer and Jetz 2014). As PE enables the identification of areas with restricted and evolutionarily unique biota, this metric also can be used as an index of ecological vulnerability, allowing the identification of priority regions for conservation.

The importance of these metrics (WE, PD, ED and PE) for conservation is extensively recognized, leading to many studies that investigate macroecological and biogeographical patterns linked with phylogenetic data (Faith et al. 2004, Barratt et al. 2017, Faith 2018). To explore these research questions, a wide array of existing R packages (www.r-project.org), such as ‘phyloregion' (Daru et al. 2020), ‘picante' (Kembel et al. 2010), and ‘pez' (Pearse et al. 2015), offer calculations of evolutionary diversity using a diversity of data structures like vectors, large matrices, sparse matrices, and even presence-absence rasters – as demonstrated by ‘EcoPhyloMapper' (Title et al. 2022). Additionally, there are packages outside the R ecosystem that address these metrics, including ‘Biodiverse' (Laffan et al. 2010), ‘SDMToolbox' (www.sdmtoolbox.org), and ‘lifemapper' (https://lifemapper.github.io/). However, some of these packages do not efficiently handle large data sets or they take a long time to perform calculations.

Here, we introduce ‘phyloraster', an R package (www.r-project.org) designed to compute measures of endemism and evolutionary diversity using presence-absence rasters and phylogenetic information as input. Our package offers a range of functions, including calculations for species richness, Faith's phylogenetic diversity (Faith 1992), phylogenetic endemism (Rosauer et al. 2009), evolutionary distinctiveness (Isaac et al. 2007), and weighted endemism (Williams et al. 1994). Moreover, ‘phyloraster' includes functions to generate null models through various spatial randomization methods, allowing researchers to control for richness effects (Gotelli and Groves 1996, Gotelli and Ulrich 2012). With these comprehensive tools, our package aims to enhance the analysis of spatial patterns of endemism and evolutionary diversity providing valuable insights for conservation and ecological research.

Novelty

The increasing size and complexity of biogeographical and phylogenetic data highlight the need to provide functions that allow efficient and fast manipulation of these datasets (Daru et al. 2020). The package ‘phyloraster' provides a set of functions to support the results derived from species distribution models (SDMs) or distribution polygons with phylogenetic data. Currently, many researchers are using SDMs to predict the potential distribution of species. Despite the usefulness of these models for biogeographical studies, the results generated by SDMs are provided in raster format, usually for large regions and at high resolution. Therefore, analyzing the rasters generated by the SDMs can generate scaling issues and easily exhaust the available RAM, even using sparse matrices to store the site-by-species data. Our package efficiently handles large datasets as we provide functions to calculate diversity measures directly from geospatial data such as raster objects (details in ‘Raster implementations' section). One of the main advantages of using rasters as input is that only the information about the data structure (e.g. row numbers, extent, resolution, cell numbers) is loaded in the RAM, without necessarily loading all raster cells at the same time (Hijmans 2022).

Our package also differs from others in the calculation of phylogenetic endemism and weighted endemism because the code corrects non-equal areas for a geographic coordinate

system. Most existing packages calculate the range size of each species assuming that all cells have equal sizes. In this case, if the user has projected the data onto a coordinate system that does not assume that the area size is equal, there may be bias in the range size estimation and all related metrics (e.g. WE, PE) to large extents. For example, two species occupying the same number of cells in a geographic coordinate system, one at the equator and another at a subtropical latitude, will differ in the area occupied, with the tropical species having a larger range size than the subtropical one. Yet, naive calculations will erroneously consider both as having the same range size. Our function addresses this problem by calculating the range size of each species considering the actual size of raster cells (examples of cellSize() function of ‘terra' package; for more information about projections see https://proj.org/operations/projections/index.html).

Finally, ‘phyloraster' performs spatial randomization procedures implemented in the ‘SESraster' R package (Heming et al. 2023). ‘SESraster' currently has six algorithms for randomizing binary species distribution rasters (details in ‘Spatial and phylogenetic randomizations' section) and allows the use of custom randomization algorithms. This implementation represents a novelty, as this breadth of randomization methods is not available in similar packages that calculate evolutionary diversity and endemism metrics. The available randomization functions allow the creation of communities that vary in distribution patterns for comparison with the observed patterns of evolutionary diversity (Kembel et al. 2010). In cases where patterns of evolutionary diversity and species richness are closely related, it can be very interesting to apply these randomization methods to test hypotheses about the phylogenetic community structure (Kembel et al. 2010), such as Li et al. (2015) and Mazel et al., (2016). More details about each randomization method can be obtained in the ‘SESraster' vignettes.

Raster implementations

One of the main advantages of using rasters as input is that if there is enough RAM available to store and process the raster data, it can be entirely loaded in RAM, otherwise the rasters are saved on the disk and only the information about the data structure (e.g. row numbers, extent, resolution, number of cells) is loaded in the RAM (Hijmans 2022). Furthermore, the calculations are applied to one cell at a time preventing filling up the RAM during raster processing. Function implementation in ‘phyloraster' also ensures that a minimal number of temporary raster files are created during processing and that these temporary files are automatically cleaned up after use. Finally, randomization procedures implemented in ‘phyloraster' derive from the ‘SESraster' R package (Heming et al. 2023), which are specifically designed for raster data (details in ‘Spatial and phylogenetic randomizations' section available in the ‘SESraster' vignette).

Methods and features

‘phyloraster' is written in R (ver. >= 2.10, www.r-project.org) language and environment. The R packages used as dependencies are: ‘terra' (ver. >= 1.6) (Hijmans 2022), ‘ape' (ver. >= 5.6) (Paradis and Schliep 2019), ‘SESraster' (ver. >= 0.7) (Heming et al. 2023),

and ‘phylobase'(ver. >= 0.810) (Hackathon 2020). Users are free to suggest improvements and report issues through the topic ‘Issues' on the GitHub repository. The package can be installed from CRAN and loaded running the following code:

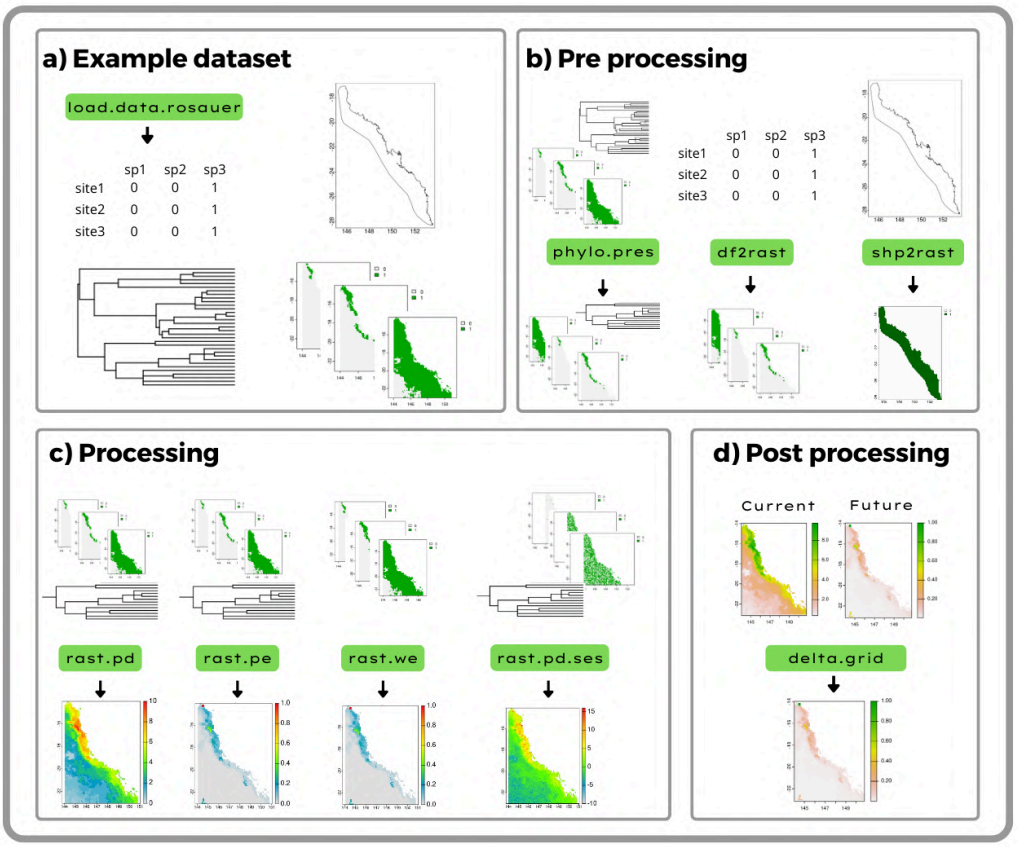
```
install.packages(“phyloraster”)

library(phyloraster)
```

Data preparation

The functions of the ‘phyloraster' package encompass pre-processing, processing and post-processing of macroecological and phylogenetic data (Box 1). In the first step, we offer support to manipulate matrices, shapefiles, rasters, and phylogenetic trees, including functions to generate the required data structures for performing subsequent analyses.

The function df2rast() converts traditional community matrices (i.e. species in columns and sites in rows, with coordinates in the two first columns) into binary distribution rasters. The package contains one dataset that allows visualizing the structure expected to matrices, with species in the columns and sites in the rows. This dataset contains presence records for 33 Australian tree frogs with coordinates for each site (Rosauer 2017). Another dataset widely used in macroecological analyses are the shapes of species distribution provided by the International Union for the Conservation of Nature's Spatial Database (www.iucnredlist.org/resources/spatial-data-download). The shp2rast() function allows working with vectorized distribution data by converting shapefiles to raster stack.

An important step in macroecological and biogeographic analyses paired with evolutionary hypotheses is to ensure that phylogenetic and distribution data match. In this sense, ‘phyloraster' implements the function phylo.pres(). This function reorders the raster stack to match the order of the tips of the tree, extracts a sub-tree containing only species present in the raster stack, and gets the branch length and descendant number for each species. The user also has the option to compute branch length and descendant number using the full supplied tree or the tree subsetted by the species present in the raster. Notice the implications of using the full or the subsetted tree. Consider, for instance, a scenario where a clade comprises three species (A–C), and the particular area of study involves two of these species (A, B). Furthermore, let's assume that species A and B share a branch, denoted as D (the ‘phyloraster' vignette). Using the full phylogenetic tree will estimate the whole length of branches for these two species, including the branch shared between them (D), that connects them with the ancestor shared with the species absent from that specific region. On the other hand, when using the subsetted tree, branch D will be disregarded and only the terminal branches will be used to calculate branch length, so that the calculated branch lengths of the species A and B will be shorter.



Box 1. Schematic examples of the functions available in the package. The functions of 'phyloraster ' are focused on pre-processing, processing, and post-processing of macroecological and phylogenetic data. The example dataset includes shapefiles from IUCN, matrices of presence-absence, phylogeny, and raster of presence-absence for 33 tree frog species from Australia.

Endemism measures

The 'phyloraster' R package implements functions for calculating spatial patterns of endemism based on the weighted endemism method (WE; Williams et al. 1994, Crisp et al. 2001) through the function rast.we(). WE weight the species range by the proportion of the range of each species present in a given region Eq. 1 (Laffan et al. 2016),

$$WE = \sum_{\{c \in C\}} \frac{r_c}{R_c} \quad (1)$$

where r is the local range (in our case, the cell area) of taxon c, R_c is the total range size of the taxon c and C is the subset of taxa that occur in a given region (Eq. 1). Most implementations usually account for the size of the distribution area of the species based on the number of cells that the species occupies and consider all cells to be the same size (Laffan et al. 2016). However, our function calculates the range size of each species treating all cells

as the actual cell size. The rast.we() function inputs a presence/absence raster for a given community and returns a raster with the values of weighted endemism by each pixel for the extent of the input rasters.

Evolutionary measures

The ‘phyloraster' package implements three types of measures to calculate evolutionary diversity through the functions rast.pd(), rast.pe() and rast.ed(). The first is Faith's phylogenetic diversity (PD), calculated as the sum of the branch lengths for all species occurring in a given region (Eq. 2) (Faith 1992),

$$PD = \sum_{\{c \in C\}} L_c \qquad (2)$$

where L_c is the branch lengths of species *c* and *C* is the set of branches in a given region (Eq. 2).

The second metric is evolutionary distinctiveness (ED; Isaac et al. 2007) or ‘fair proportion' (Redding et al. 2014), which is calculated dividing the total phylogenetic diversity of a clade among its members (Isaac et al. 2007). The calculation is done using both branch lengths and the number of descendants (Eq. 3),

$$ED_j = \sum_{b \in C(j,root)} \frac{L_b}{N_b} \qquad (3)$$

where L_b is the edge length of branch *b*, N_b stands for the number of species that descend from branch *b* and $C_{(j,\ root)}$ for the set of branches between species j, the tip of the tree and the root of the tree.

The third measure of diversity is phylogenetic endemism (PE), which calculates the degree to which PD is restricted to a specific region (Rosauer et al. 2009, Laffan et al. 2016). Therefore, to calculate PE for a given region we consider both ranges size and branch lengths for each species (Eq. 4),

$$PE = \sum_{\{c \in C\}} L_c \frac{r_c}{R_c} \qquad \text{(equation 4)}$$

where L_c is the branch length of taxon *c,* r_c is the local range (in our case, the cell area) of branch *c*, and R_c is the range sizes of the clade. C is the set of branches in a given region.

Standardized effect size

Null models are a widely used method to compare patterns against random processes, allowing for example, to evaluate richness effects in diversity measures (Gotelli and Groves 1996, Gotelli and Ulrich 2012), and to test hypotheses about the community structure. The standardized effect size (SES) is widely used in the community structure literature and can be calculated from null models (Gotelli and McCabe 2002). The SES is commonly used to measure the deviation from the null expectation in standard deviation units (Eq. 5), and enables an estimation of the relative position of the observed value with respect to the null distribution generated by the randomization (Mazel et al. 2016).

$$SES = \frac{Metric_{obs} - Mean\left(Metric_{null}\right)}{SD\left(Metric_{null}\right)} \quad (5)$$

where $Metric_{obs}$ represents the observed value for the metric, mean($Metric_{null}$) represents the mean of randomizations calculated for n times and SD($Metric_{null}$) represents the standard deviation of the randomizations.

Spatial and phylogenetic randomization

The randomization procedure for the calculation of SES is done internally in the functions rast.we.ses(), rast.pd.ses(), rast.ed.ses(), rast.pe.ses() and geo.phylo.ses() through the package ‘SESraster' (Heming et al. 2023). ‘SESraster' currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in ‘SESraster' are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). The randomization algorithms currently available in ‘SESraster' are: SIM1 (species occurrence equiprobable and site richness equiprobable), SIM2 (species occurrence fixed and site richness equiprobable), SIM3 (species occurrence equiprobable and site richness fixed), SIM5 (species occurrence proportional and site richness fixed), SIM6 (species occurrence proportional and site richness fixed) and SIM9 (species occurrence fixed and site richness fixed, similar to the preserved model of Laffan and Crisp 2003). In addition, ‘SESraster' (consequently ‘phyloraster') supports user's custom randomization algorithms for SES calculation, as long as the function returns objects of class SpatRaster. This allows complete flexibility for using any algorithm not yet implemented by the package. To see more details about the randomization methods cited above, review the documentation of the ‘SESRaster' package.

By default, the ‘phyloraster' uses the function bootspat_str() from the ‘SESraster' package to conduct the randomizations, but the user is free to choose any of the other

methods mentioned above through the spat_alg argument in the *.ses() functions of the ‘phyloraster' package. The function bootspat_str() is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells. This method differs from Laffan and Crisp (2003) because their implementation shuffles the species presences across the raster, while bootspat_str() samples presences based on probabilities computed from their frequencies (Heming et al. 2023). Although species frequencies are not exact, the variation is relatively small, not compromising species range size patterns. The randomization will not assign values to cells with no data. The preserved model of Laffan and Crisp (2003), for retaining the richness pattern and the range size of the species (SIM9, fixed-fixed, Gotelli 2000), is available in the bootspat_ff() function of ‘SESraster'.

Note that although species range sizes are estimated using the size of the raster cell, the currently available randomization methods do not take this information into account, as shuffling is made based on the number of occupied pixels. In a geographic coordinate system, the area of the smaller polar pixels (above 60° N and 60° S – higher latitude) is nearly five times smaller than the larger equatorial pixels (close to 0° – lower latitudes). So, if a strictly equatorial species that occupies ten pixels is assigned to ten polar pixels, its range area will be nearly five times smaller than it actually is. This affects the randomized metrics especially on large latitudinal extents. We are not aware of any randomization algorithm implemented in R that explicitly overcomes this limitation and we are sure that further attention is needed to solve this shortcoming. Phylogenetic randomization can also be done using the package ‘SESraster'. The randomization can shuffle taxon branch lengths prior to PD and ED calculations.

Post-processing analysis

The ‘phyloraster' package offers a function to evaluate the change in the community over time. This function can be applied to the results obtained from the functions geo.phylo() or rast.sr(), rast.we(), rast.pd(), rast.ed() and rast.pe(), which can represent different time points such as baseline, past and future scenarios. The delta.grid() function allows to evaluate the change in the community diversity metrics through time. By comparing present and future diversity patterns, delta.grid() reveals any variations across regions, highlighting diversity shifts resulting from environmental changes.

Implementation examples

To demonstrate how ‘phyloraster' can be used, we developed a study case where we calculated endemism and evolutionary diversity patterns for 33 tree frog species of the subfamily Pelodryadinae from Australia (Rosauer 2017). This dataset can be accessed through the function load.data.rosauer(). To perform the calculations, first, we transform the presence and absence matrix into a raster using the df2rast() function. The function maintains the original resolution of the data. In this case, the grid cells have a resolution of 0.1°. Then, we use the phylo.pres() function to sort the raster according to the tree order, extract the

branch length for each species, and subset the phylogenetic tree maintaining only the species that are present in the raster. With the raster sorted and the branch lengths in hand, we can calculate Faith's phylogenetic diversity using the rast.pd() function. Because richness is positively correlated with Faith's phylogenetic diversity (Tucker and Cadotte 2013), we calculated the SES through the function rast.pd.ses(), using the argument random = ‘spat' and the argument spat_alg = ‘bootspat_str' (Supporting information, Fig. S1). We used 999 simulations, defined through the argument *aleats* of the rast.pd.ses() function.

To calculate the WE, we weight the species range by the proportion of the range of each species present in a given region. This calculation is done internally in the rast.we() function (Supporting information, Fig. S1). The spatial patterns of weighted endemism can also be calculated using the geo.phylo() function. After that, we calculate PE through the rast.pe() function using the raster stack with presence-absences and a phylogenetic tree for a set of species. The clade range is calculated internally in the function rast.pe().

The results can be seen in the Supporting information. PD was highest in the northeast and shows a decrease towards the region south (Supporting information, Fig. S1). Meanwhile, PE has the highest values concentrated in the extreme north of the region above latitude −16, and moderate PE values between latitude −16 and −18 (Supporting information, Fig. S1). A small fraction of PE can also be found in the south of the region, between longitudes 144 and 146 (Supporting information, Fig. S1). WE patterns are congruent with PE (Supporting information, Fig. S1).

In addition, we calculated the temporal difference in the PD and the PE through the function delta.grid (Supporting information). To assess temporal changes, let's assume that by 2050, four species *Litoria lorica, Litoria rheocola, Litoria nyakalensis* and *Litoria infrafrenata* will be completely extinct due to climate change and calculated the PD and PE for baseline and future scenarios. The results generated by the function shows that the potential loss of four species in the future will decrease the PD by up to 2.365. With the loss of these species, PE should also change, with some regions gaining up to 0.014 and others losing up to 0.082. The script and dataset used to run the example implementation and generate the figures can be accessed at: Alves-Ferreira et al. 2022.

Performance comparisons

We compared the performance of ‘phyloraster' with two packages that have similar functionalities: ‘epm'(Title et al. 2022) and ‘phyloregion'(Daru et al. 2020). For the performance comparison, we evaluated the patterns of weighted endemism (WE) and phylogenetic diversity (PD) using a dataset of geographical distribution (presence and absence) of 82 tree frog species of the subfamily Pelodryadinae. We tested the performance using two different resolutions (0.1° and 0.05°) and considered both the functions for data preparation from each package and the specific function for calculating the metrics WE and PD. The script and dataset used to compare packages can be accessed from: https://doi.org/10.7910/DVN/QSNTSG. To run the tests we used a machine with the following specifications: ‘AMD® Ryzen 7 4800h with radeon graphics × 16 cores' with

46.4GB RAM, 16GB SWAP, and 256GB SSD. The software used was Linux Ubuntu 20.04.6 LTS, and the R ver. is 4.3.1 (2023-06-16, www.r-project.org). For simplicity we show only the results for the high resolution dataset. The results for the low resolution dataset can be found in the Supporting information, Table S1.

According to the benchmarking, loading and preparing data at high resolution (0.05°) before WE calculation requires considerably more RAM in the ‘epm' (562.07 MB) and in the ‘phyloregion' (210.01 MB) than in the ‘phyloraster' (83.22 KB) (Table 1). The WE calculation also consumes more RAM in ‘epm'(338.88 MB) and ‘phyloregion' (574.95 KB) packages than in ‘phyloraster' (8.38 KB). We also found that loading data to calculate the PD in ‘phyloraster' (18.29 MB) consumes relatively less RAM than in the ‘epm' (113.22 MB) and in the ‘phyloregion' (210.01 MB) (Table 1). For the PD calculation, the results show that ‘phyloraster' (44.27 MB) and ‘epm' (59.06 MB) uses slightly more RAM than the ‘phyloregion' (2.99 MB) (Table 1).

Table 1. Comparison of ‘phyloraster' against ‘epm'and ‘phyloregion'for analysis of endemism and phylogenetic diversity for tree frog species of Australia.

Metric	Package	Step	Specific functions of each package	Memory allocation	Time	Spatial resolution
Weighted endemism	*epm*	Data import	(createEPMgrid)	562.07MB	00m 00.89s	0.05°
	phyloraster	Data import	(shp2rast)	82.34KB	00m 01.11s	0.05°
	phyloregion	Data import	(raster2comm)	4.18GB	02m 49.79s	0.05°
	epm	Metric calculation	(gridMetrics)	338.88MB	00m 00.18s	0.05°
	phyloraster	Metric calculation	(rast.we)	8.38KB	00m 00.12s	0.05°
	phyloregion	Metric calculation	(weighted_endemism)	2.12MB	00m 00.00s	0.05°
Phylogenetic diversity	*epm*	Data import	(createEPMgrid), (addPhylo)	113.22MB	00m 00.14s	0.05°
	phyloraster	Data import	(shp2rast), (phylo.pres)	5.9GB	00m 03.45s	0.05°

	phyloregion	Data import	(raster2comm)	4.08GB	02m 49.44s	0.05°
	epm	Metric calculation	(gridMetrics)	59.06MB	00m 00.07s	0.05°
	phyloraster	Metric calculation	(rast.pd)	176.79MB	00m 03.54s	0.05°
	phyloregion	Metric calculation	(PD)	12.2MB	00m 00.00s	0.05°

The lower RAM usage in ‘phyloraster' functions is due to the main dependency on the ‘terra' package, as explained in the ‘Raster implementations' section. Faster calculations and substantial low RAM usage minimizes the hardware requirements to work with high-resolution datasets from local to global scales. The functions of ‘phyloraster' broadens user accessibility of the spatialized measures of endemism and evolutionary diversity. By allowing users without access to machines with high processing power and large amounts of RAM to perform analyses of spatial evolutionary patterns, we also hope to promote research equity for low income researchers (as discussed for other scientific topics by Williams et al. 2023).

Conclusions and future directions

The ‘phyloraster' package aims to unite species range data with phylogenetic information and facilitate the spatial analysis of taxon richness, phylogenetic diversity and phylogenetic endemism. The main novelty of this package is the capacity to calculate measures of diversity and endemism directly for rasters with very efficient memory usage and fast processing time. We have shown that the ‘phyloraster' is lighter and faster than its counterparts, which may allow users to work with high-resolution datasets from local to global scales. By reducing the dependency on machines with high processing power and large amounts of RAM, we hope that research equity for low income researchers is being promoted. In addition, our package differs from others in the calculation of phylogenetic endemism and weighted endemism because it takes into account the latitudinal variation of the pixel area, which affects the estimated range size (and all subsequent analyses) of species occurring along a latitudinal gradient. In upcoming versions, we plan to expand the package functionalities, adding functions for calculating neo and paleo endemism (Mishler et al. 2014), mean pairwise distance between all species in an assemblage (MPD), and pairwise distance between the closest relatives in an assemblage (MNTD) (Webb et al. 2002).

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Author contributions

Gabriela Alves-Ferreira: Conceptualization (lead); Data curation (lead); Methodology (equal); Software (equal); Validation (lead); Visualization (lead); Writing – original draft (lead); Writing – review and editing (lead). Flávio Mariano Machado Mota: Methodology (supporting); Software (supporting); Validation (supporting); Visualization (supporting); Writing – review and editing (supporting). Daniela Custódio Talora: Conceptualization (supporting); Supervision (supporting); Validation (supporting); Visualization (supporting); Writing – review and editing (supporting). Cynthia Valéria Oliveria: Conceptualization (supporting); Validation (supporting); Visualization (supporting); Writing – review and editing (supporting). Mirco Solé: Conceptualization (supporting); Supervision (supporting); Validation (supporting); Visualization (supporting); Writing – review and editing (supporting). Neander Marcel Heming: Conceptualization (supporting); Data curation (supporting); Methodology (equal); Software (equal); Supervision (lead); Validation (supporting); Writing – review and editing (supporting).

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Data availability statement

The data and scripts used in this article are available on Harvad Dataverse Repository: https://doi.org/10.7910/DVN/QSNTSG.

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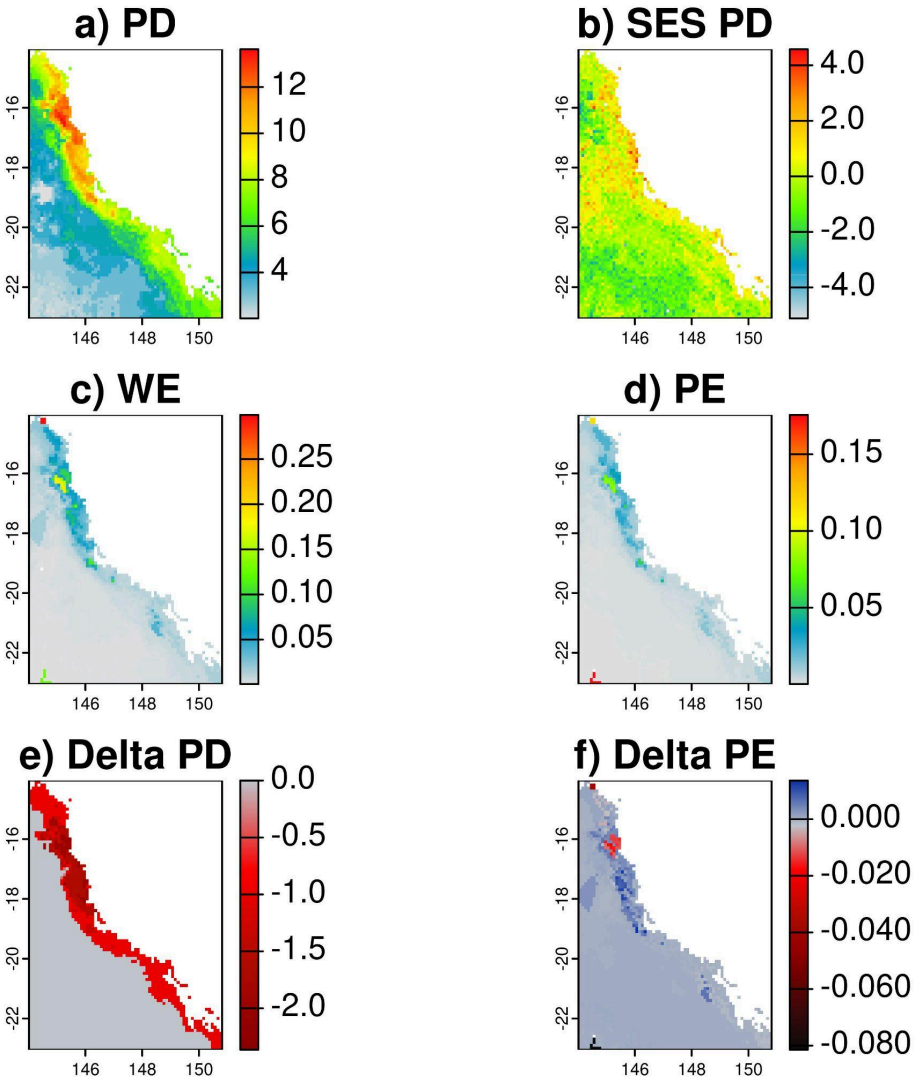
Supplementary material



Supplementary Figure 1. a) Phylogenetic diversity for 33 tree frog species from Australia. b) Standardized effect size (SES) of phylogenetic diversity calculated using spatial randomization based on 999 iterations. c) Weighted endemism for 33 tree frog species from Australia. d) Standardized effect size (SES) of weighted endemism calculated using spatial randomization based on 999 iterations. e) Phylogenetic endemism for 33 tree frog species from Australia. f) Standardized effect size (SES) of phylogenetic endemism calculated using spatial randomization based on 999 iterations.

Table Supplementary 1. Comparison of phyloraster against epm and phyloregion for analysis of endemism and phylogenetic diversity for tree frog species of Australia.

Metric	**Package**	**Step**	**Specific functions of each package**	**Memory allocation**	**Time**	**Spatial resolution**
Weighted endemism	*epm*	Data importation	(createEPMgrid)	140.96MB	00m 00.18s	0.1°
	phyloraster	Data importation	(shp2rast)	82.12KB	00m 00.54s	0.1°
	phyloregion	Data importation	(rast2comm)	210.01MB	00m 01.30s	0.1°
	epm	Metric calculation	(gridMetrics)	82.07MB	00m 00.40s	0.1°
	phyloraster	Metric calculation	(rast.we)	60.24KB	00m 00.50s	0.1°
	phyloregion	Metric calculation	(weighted_endemism)	692.22KB	00m 00.46s	0.1°
Phylogenetic diversity	*epm*	Data importation	(createEPMgrid), (addPhylo)	113.22MB	00m 00.54s	0.1°
	phyloraster	Data importation	(shp2rast), (phylo.pres)	17.97MB	00m 00.53s	0.1°
	phyloregion	Data importation	(rast2comm)	210.01MB	00m 01.42s	0.1°
	epm	Metric calculation	(gridMetrics)	59.13MB	00m 00.52s	0.1°

	phyloraster	Metric calculation	(rast.pd)	44.27MB	00m 01.09s	0.1°
	phyloregion	Metric calculation	(PD)	3.33MB	00m 00.51s	0.1°

Capítulo 3

Manuscrito publicado na Nature Communications

Climate change is projected to shrink phylogenetic endemism of Neotropical frogs

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Abstract

Climate change is widely recognized as one of the main threats to biodiversity [1] and predicting its consequences is critical to conservation efforts. A wide range of studies have evaluated the effects of future climate using taxon-based metrics [2], but few studies to date have applied a phylogenetic approach to forecast these impacts. To date, an analysis of the effect of climate change on phylogenetic endemism patterns of Neotropical frogs has not been done. Here, we show that future climate change is expected to significantly modify not only species richness (SR), but also phylogenetic diversity (PD) and phylogenetic endemism (PE) of Neotropical frogs. Our results show that by 2050, the ranges of 42.20% (n = 213) of species are projected to shrink and 1.71% of species (n = 9) are projected to disappear. Furthermore, we find that areas of high SR and PD are not always congruent with areas of high PE. Our study highlights the projected impacts of climate change on Neotropical frog diversity and identifies target areas for conservation efforts that consider not just species numbers, but also distinct evolutionary histories.

Main

Climate change is one of the main threats to biodiversity [1]. Over the past century, human activities have led to rises in the emission of greenhouse gasses, resulting in an increase of Earth's surface temperature [1]. As a consequence, there has been renewed interest in understanding effects of climate change by forecasting the persistence of species in future environments [3]. These forecasting attempts have focused on many different species traits and roles. For example, studies have evaluated the effects of climate change on geographic

ranges, biotic interactions, population dynamics, and ecosystem functions [4–8]. However, biodiversity is not just about species, but also about the information contained in the topology and branches of phylogenetic trees, which carry important information about the evolutionary history of species [9]. Given the magnitude of projected climate change, it is a priority to conserve the evolutionary heritage of biodiversity [10]. The conservation of species with distinct genetic heritage may be key for adaptation to future non-analogous climatic conditions caused by global warming [10].

Prior studies have concentrated on documenting and forecasting changes in diversity based on species richness (SR) [3,4]. However, this approach undervalues the important contribution of evolutionary history and thus may miss key aspects of diversity related to innovations arising in the diversification of clades. Phylogenetic diversity (PD) is a widely used metric that assesses the shared evolutionary history of species by using the sum of the branch lengths of all species that inhabit a given region [11]. These branch lengths represent the amount of evolutionary change that occurred since lineages diverged from a common ancestor, reflecting both the time and the evolutionary processes that led to species' current adaptations. Regions with high PD may consist of areas containing many species from a species-rich clade, or alternatively, a few species with long branches. Conversely, if a region has many species but several are closely related, the PD score will be lower [11].

PD does not take into account rarity in species' distributions [12]. A second metric, developed to address this shortcoming, is phylogenetic endemism (PE), which integrates evolutionary heritage with information on species distributions [12,13]. PE identifies areas with potential loss of evolutionary history through the sum of the branch lengths of a set of species that occur in a given region, weighted by species range sizes [12,13]. Thus, PE measures the spatial restriction of the evolutionary history of species, which can depend on the total distribution of the set of species that occur in a region, the range size of each species, and the amount of evolutionary history shared among them [12].

PD is expected to decrease with climate change, while PE should increase and be spatially displaced to new areas that are predicted to remain climatically suitable [10]. The increase in PE is a consequence of species becoming more restricted spatially in the future [10]. Therefore, as species distribution decreases, endemism patterns are expected to increase, increasing PE values. While some species are expected to experience range contractions, others may benefit from the new climatic conditions and expand their distributions, possibly decreasing endemism patterns and PE values. One way to forecast the effect of projected future climate change on the tree of life is through the combination of species distribution models (SDMs [14]) and diversity metrics [15]. SDMs associate occurrence data with environmental variables to predict the potential distribution of species in time and space [14]. Combining SDMs and metrics of evolutionary heritage can identify areas that need to be conserved now to increase the retention of those unique aspects of the tree of life. Including evolutionary proxies can provide a way to identify regions with a rich and spatially restricted evolutionary legacy that need to be prioritized for conservation [16].

Amphibians are the most threatened vertebrate class (40.3% of species are endangered [17]), and they are highly impacted by climate change, as most species depend on very specific climatic conditions and have limited dispersal capacity [18]. Currently, approximately 3,000 species of amphibians are known from the Neotropics, and 94% of those are endemic to the region [19]. The Neotropics face other severe anthropogenic pressures including deforestation and overexploitation of natural resources, which combined with climate change, are rapidly leading to high rates of species loss and potentially phylogenetic losses as well. Here, we ask how future scenarios of climate change will affect patterns of SR, PD, and PE of Neotropical frogs (toads -Bufonidae and treefrogs -Hylidae). Projected increases in temperature and reductions in precipitation are expected to shrink the potential distributions of species, resulting in lower SR and PD in the future. We also expect that regions predicted to lose SR will be congruent with the regions predicted to lose PD in the future, given the spatial correlation between the two metrics. In contrast, we expect PE to increase, due to reductions in potential distributions. However, the exact degree to which PE increases will depend on the relative reduction in species' distributions and the identity of species that are lost.

We show that by 2050, the ranges of 42% of species are expected to shrink and 1.71% to disappear. Decreasing range areas in response to climate change could lead to a meltdown in ecosystems, and potential loss of functional and genetic diversity in the future. Our models also reveal projected shifts in geographic patterns of SR, PD, and PE in the future and show that some centers of high PE are not areas of particularly high SR or high PD. Identifying regions predicted to have high PE in the future have particular importance from a conservation perspective, as these areas are likely to harbor species with distinct genetic heritage crucial for adaptation to non-analogous climatic conditions.

Results

General patterns of loss and gain of range areas. The model metrics obtained through block cross-validation showed a good fit, with mean values of Area Under Curve of 0.78 and Omission Rate of 0.08 (Table S2). Our projections indicate that 42.20% (n = 213) of species are expected to suffer a reduction in range by 2050 under the pessimistic climate scenario. Furthermore, 1.71% (n = 9) of frog species are projected to completely lose their ranges by 2050 (Table 1), including *Aplastodiscus leucopygius, Boana microderma, Boana platanera, Boana ventrimaculata, Dendropsophus bokermanni, Dendropsophus stingi Exerodonta xera, Hyloscirtus armatus,* and *Rhinella ornata* (Table 1). Some of these species have long branch lengths, such as *Dendropsophus stingi* (16.579 Myr) and *Boana microderma* (14.337 Myr) (Table 1). In contrast, many species (n = 304, 57.79%) are projected to gain range areas, among them *Megastomatohyla mixe, Incilius spiculatus, Megastomatohyla nubicola, Dryophytes cinereus,* and *Charadrahyla altipotens* (Table S3).

Table 1. Species projected to lose all of their range area by 2050 with the percentage of loss under both pessimistic and optimistic emission scenarios, their threat category according to the IUCN (2024), and branch length (Myr). LC = Least Concern, NT = Near Threatened, VU = Vulnerable

Species	Family	Country	IUCN category	Branch length	% loss-Optimistic	% loss-Pessimistic
Aplastodiscus leucopygius	Hylidae	Brazil	LC	5.302	-99.944	-100
Boana microderma	Hylidae	Colombia, Peru and Brazil	LC	14.337	-100	-100
Boana platanera	Hylidae	Panama, Colombia, Venezuela, and Trinidad and Tobago	LC	3.572	-99.955	-100
Boana ventrimaculata	Hylidae	Ecuador and Brazil	LC	0.371	-99.862	-100
Dendropsophus bokermanni	Hylidae	Colombia, Ecuador, Peru, and Brazil	LC	3.342	-99.895	-100
Dendropsophus stingi	Hylidae	Colombia	LC	16.579	-54.775	-100
Exerodonta xera	Hylidae	Mexico	VU	3.031	-100	-100
Hyloscirtus armatus	Hylidae	Peru and Bolivia	NT	8.494	-89.318	-100
Rhinella ornata	Bufonidae	Brazil and Argentina	LC	0.795	-99.416	-100

Most of the species that are projected to lose range areas in the future are classified as Least Concern (LC) by the IUCN (Fig. 1a and Table S4). We also identified seven species (four toads and three treefrogs) currently categorized as threatened (Vulnerable -VU, Endangered -EN, or Critically Endangered -CR) projected to lose range area (Fig. 1a and Table S4). Our models indicate that while fewer species (213) are expected to lose their range in the future, these species belong to lineages sharing a similar average amount of evolutionary history when compared to those projected to expand their range (304 species) (Fig. 1b). Furthermore, the mean projected decrease in range area (mean = -8.366 + 11 km2 and SD = 1.430 +11 km2) is significantly larger than the mean projected increase (mean = 7.109 +11 km^2 and SD = 1.424 +11 km^2) in range area (W = 1401, p-value < 0.001, Fig. 1c). The estimated direction of change in future range size is influenced by current range sizes, and species with large current ranges are projected to have a higher decrease in their ranges in the future than species with small current ranges (Spearman's rank correlation = -0.571, $p < 0.001$; Fig. S3).

The most important variables in predicting range areas for toads were the Precipitation of Driest Quarter (BIO 17), Annual Precipitation (BIO 12), and Annual Mean Temperature (BIO 1) (Table S5). For treefrogs, the most important variables were the Annual Mean Temperature (BIO 1), Mean Temperature of Warmest Quarter (BIO 10), and Minimum Temperature of Coldest Month (BIO 6) (Table S5).

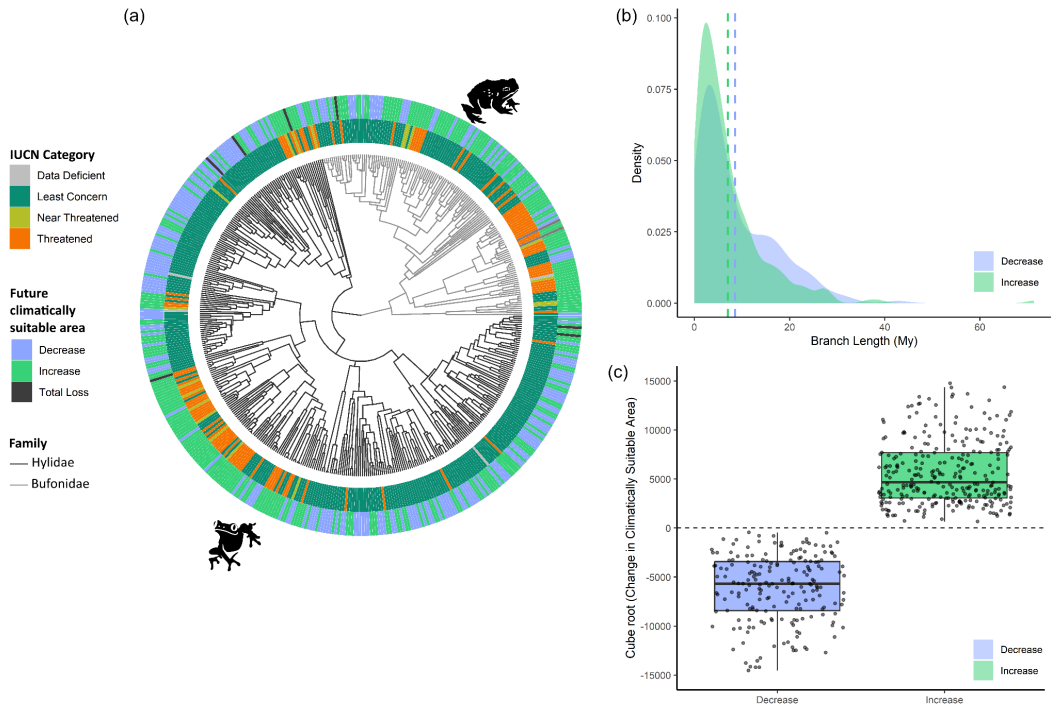

Fig. 1 Phylogenetic tree of 497 Neotropical frogs in the families Hylidae (treefrogs) (black branches) and Bufonidae (toads) (gray branches) and the values of branch length and change climatic suitable area for species. Panel (a) shows the phylogenetic tree for the studied frogs, the future range area and IUCN category. In the legend, the orange color represents threatened species, which includes Critically Endangered, Endangered, and Vulnerable, the yellow color represents Near Threatened species, green color represents Least Concern species, and gray color represents Data Deficient species. Light green colors represent species that will increase range area in the future, purple color represent species that will lose a part of their area, and black color represent species that will lose their entire range area in the future. Panel (b) presents the density of branch length for species that will lose and gain range area in 2050. The dotted lines in panel (b) represent the means of branch lengths for species expected to increase and decrease range area. The panel (c) shows a boxplot with the projected change in climatic suitable area for species. The horizontal black line in the boxplot represents the median and the black dots represent the change in range area for each species. The vertical lines represent the minimum and maximum values.

Species richness patterns. Our models reveal that Neotropical frogs are predicted to have two large regions with high SR; the first in southeastern Brazil, and the second in

northwestern South America, including northwest Brazil, eastern Ecuador, northeastern Peru, and southern Colombia (Fig. 2a and Fig. S4a). However, according to our forecasts, SR is expected to change in several regions, in both optimistic and pessimistic emission scenarios (Fig. 2b and Fig. S4b). The regions projected to have the highest reduction in SR, under both optimistic and pessimistic scenarios, are the Guiana Shield, eastern Venezuela, eastern and northeastern Peru, southeast, northwest, northern and central Brazil, and northeastern and southeastern Bolivia (Fig. 2c and Fig. S4c). The models also predict regions where the SR will increase in the future, including southern Mexico, Costa Rica, central Ecuador, central Colombia, southern Peru, and Central Bolivia (Fig. 2c and Fig. S4c).

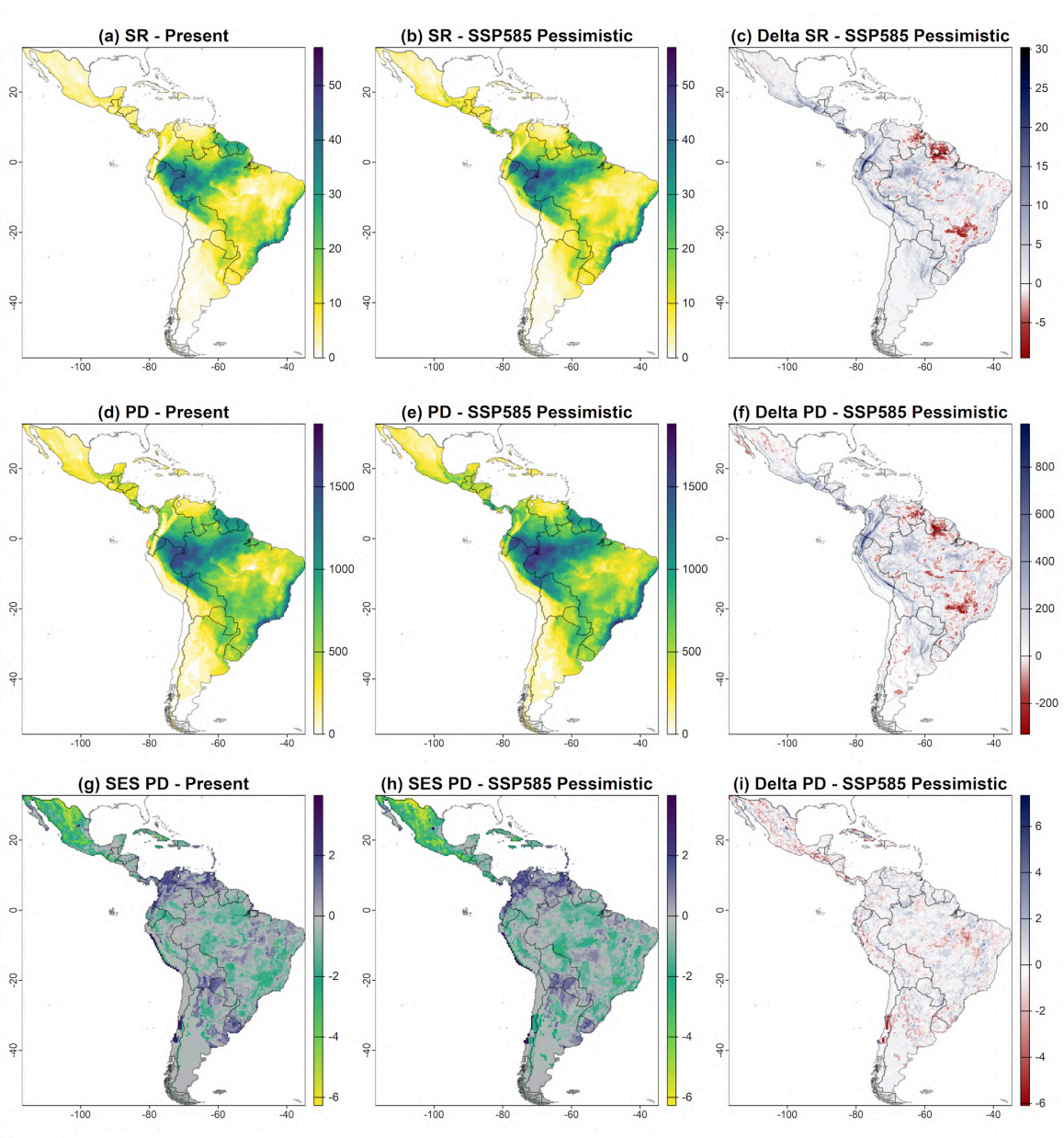

Fig. 2 Species richness (SR), Phylogenetic diversity (PD), and Standardized effect size for Phylogenetic diversity (SES PD) of 497 Neotropical toads and treefrogs. (a) SR for the present scenario, (b) SR for the pessimistic 2050 scenario, (c), differences in SR between present and the pessimistic 2050 scenario, (d) PD for the present scenario, (e) PD for the

pessimistic 2050 scenario, (f) differences in PD between present and the pessimistic 2050 scenario, (g) SES PD for the present, (h) SES PD for the pessimistic 2050 scenario, and (i) differences in SES PD between present and the pessimistic 2050 scenario. Purple and dark green colors represent regions with high SR and PD, while light green and yellow colors represent regions with low SR and PD. Red colors represent species losses in SR, PD, and SES PD, gray/white color represents areas where SR, PD, and SES PD are not predicted to change, and blue color represents SR, PD, and SES PD gains in the future. In the panels (g) and (h) yellow and green colors represent regions where PD is lower than expected randomly and blue and purple colors represent regions where PD is higher than expected randomly.

Phylogenetic diversity patterns. As expected, regions that harbor high PD in the present are the same areas predicted to harbor high SR (Fig. 2d and Fig. S4d). Likewise, PD projected in the future is spatially congruent with areas forecast to have high SR in 2050 (Fig. 2e and Fig. S4e). Our models project a marked decrease in PD in the Guiana Shield, northern Mexico, central and northern Argentina, Cuba, central and northern Brazil, eastern Amazon, and the northern Andes (Fig. 2f and Fig. S4f). The models also predict an increase in PD in the future in the same regions predicted to have an increase in SR (Fig. 2f and Fig. S4f).

PD is predicted to be higher than SR in the present across northern Colombia, Venezuela, western Peru, western Chile, central Brazil, southern Bolivia, Uruguay, and northern Paraguay (positive values of SES PD, Fig. 2g and Fig. S4g). Conversely, SR is expected to be higher than PD in the present (negative values of SES PD, Fig. 2g and Fig. S4g) in Mexico, Jamaica, Cuba, northern Peru, as well as in southeastern, northern, and central Brazil. In the future, SR is predicted to be higher than PD in Cuba, Jamaica, western Chile, western Peru, southern Mexico, and northern Brazil (Fig. 2h, 2i and Fig. S4h, S4i).

Phylogenetic endemism patterns. We also predicted current centers of PE and projected their change into the future. PE is currently concentrated in the Guiana Shield, southeastern Brazil, the northern Andes, southern Mexico, nuclear and Isthmian Central America (Guatemala, Honduras, and Costa Rica), Jamaica and northern Cuba (Fig. 3a and Fig. S5a). Climate change is projected to shift the spatial patterns of PE across the Neotropics, in both optimistic and pessimistic emission scenarios (Fig. 3b, 3c and Fig. S5b, S5c), resulting in centers of PE more spatially restricted. The value of PE in most regions is expected to decrease substantially in the future, mainly for Guiana Shield, southern Mexico, Panama, Ecuador, and southeastern Brazil (Fig. 3b, 3c and Fig. S5b, S5c). The exceptions projected to increase PE in the future are northwestern and southeastern Colombia, southeastern Costa Rica, and a small center in southern Brazil (Fig. 3b, 3c and Fig. S5b, S5c).

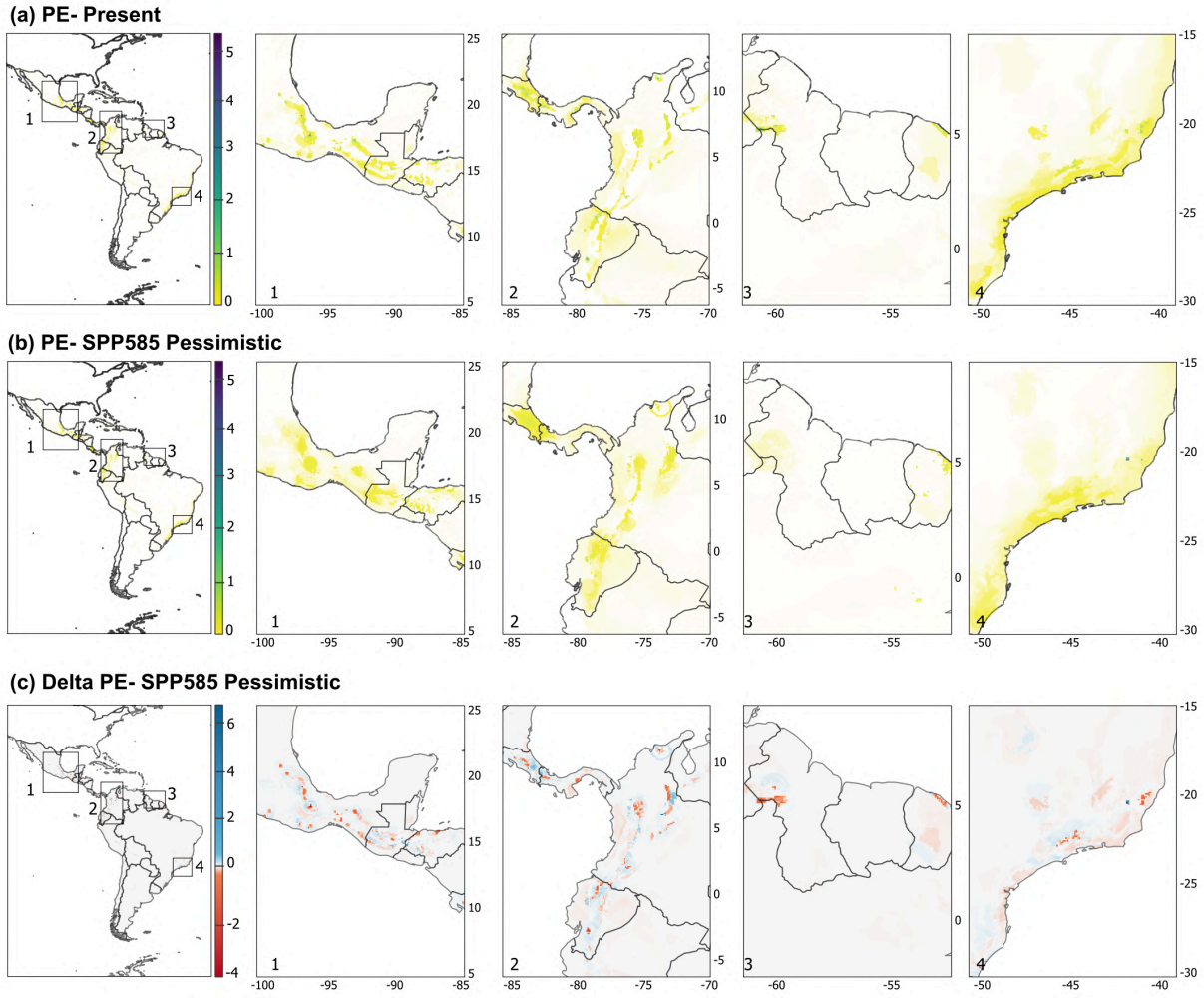

Fig. 3 Phylogenetic endemism (PE) of 497 Neotropical toads and treefrogs. (a) PE for the present scenario, (b) PE for the pessimistic 2050 scenario, (c) differences in PE between present and the pessimistic 2050 scenario. In panels (a) and (b), purple and green colors represent regions with high PE, while yellow colors represent regions with low PE. In panel (c), red colors represent losses in PE, gray/white color represents areas where PE is not predicted to change, and blue color represents PE gains in the future.

Relationship between diversity metrics. As predicted, PD and SR showed a very strong relationship in the present (Pseudo $R^2 = 0.993$) and in the future (Pseudo $R^2 = 0.994$, Fig. S6a, S6b, S6c), but the magnitude of the relationship varies across space. SR and PD are both high in Guiana Shield, southeastern and northern Brazil, eastern Peru, Colombia, Ecuador, and Bolivia (Fig. 4a, 4b, 4c). PE showed a weak relationship with SR in the present (Pseudo $R^2 = 0.017$) and future (Pseudo $R^2 = 0.047$, Fig. S6d, S6e, S6f). Regions where both PE and SR are high are located in southeastern Brazil, Amazon (Brazil, Peru, Ecuador, and Colombia), Costa Rica, and French Guiana (Fig. 4d, 4e, 4f). PE is higher than SR in southern and northern Mexico, nuclear and Isthmian Central America (except by Costa Rica), Caribbean Islands (Cuba, Haiti, Jamaica, Dominican Republic, and The Bahamas), southern Brazil, western Colombia, Ecuador, and Central Chile (Fig. 4d, 4e, 4f). Our models suggest

important areas for the conservation of the phylogenetic component (higher PD and SES PD, Fig. 4g, 4h, 4i) in southeastern and northern Brazil, southern Paraguay, northern Bolivia, northeastern Peru, eastern Colombia, southern Venezuela, and northern Guyana (Fig. 4g, 4h, 4i).

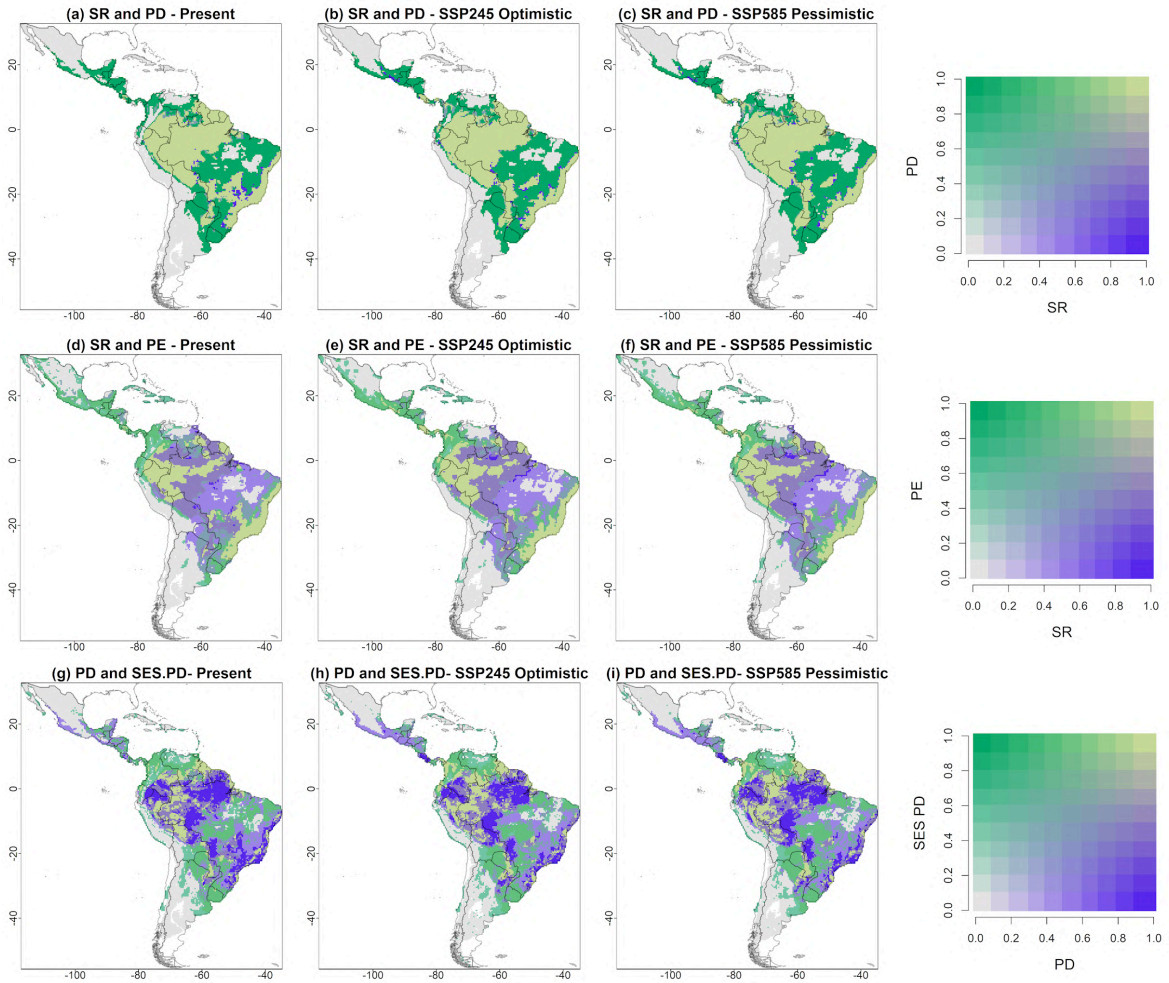

Fig. 4 Bivariate maps illustrating the relationship between species richness (SR), phylogenetic diversity (PD), phylogenetic endemism (PE), and standardized effect size of PD (SES PD) of 497 Neotropical toads and treefrogs. (a) SR and PD for the present scenario, (b) SR and PD for the optimistic 2050 scenario, (c) SR and PD for the pessimistic 2050 scenario, (d) SR and PE for the present scenario, (e) SR and PE for the optimistic 2050 scenario, (f) SR and PE for the pessimistic 2050 scenario, (g) PD and SES PD for the present, (h) PD and SES PD for the optimistic 2050 scenario, and (i) PD and SES PD for the pessimistic 2050 scenario. In panels (a) to (i), light green indicates regions where both PD, PE, SR and SES PD are high, gray shows areas where both are low, dark green highlights regions where only PD, PE or SES PD is high, and purple colors areas where only SR or PD is high.

Discussion

Our models indicate that almost half (42.20%) of the studied frog species are expected to experience a reduction in their range areas, with nine species (1.71%) predicted to lose their entire range by 2050. The future climate change is also predicted to shift the SR, PD, and PE of Neotropical frogs and make communities more clustered spatially. However, the loss of PD and, mainly, PE in some regions can be much more severe than the loss of SR. The reduction in PD and PE can be driven by the loss of species with long branch lengths, which represent deep evolutionary histories. These branch lengths reflect the amount of evolutionary divergence accumulated over time, and the loss of such species can lead to a significant reduction in the unique evolutionary history of Neotropical frogs.

Some species projected to lose range are threatened according to the IUCN red list (VU, EN, CR) [20], which underscores an urgent need for targeted conservation action. To be categorized as threatened, a species must be suffering substantial extinction risk due to threats such as disease (chytridiomycosis for anurans), habitat loss, fragmentation, or invasive species [20]. Adding climate change to this mix of stressors [21] will make the persistence of the species in changing habitats much more challenging. Some examples of threatened toad species are the Harlequin frogs (genus *Atelopus*), which have been suffering reductions in their populations due to pathogen spread (chytridiomycosis), habitat loss, and the indirect interaction of climate change with disease agents [22]. These species should be a priority for global conservation and their populations must be monitored to avoid potential declines or extinctions in the next 30 years. Moreover, species classified as "Least Concern" (LC) that are projected to lose range area underscores that the conservation status of non-threatened species may change rapidly in the next few years. The rapid onset of these threats requires a more inclusive approach, incorporating predictive models or more ideally observational studies with climate change effects in the last years into the risk assessments to ensure that climate change impacts are adequately represented.

Our results also show that SR and PD of Neotropical frogs are projected to be currently concentrated in two large regions; the first in southeastern Brazil, and the second in northwestern South America. These regions are known to have high SR not just for frogs, but also for other vertebrates such as birds [23], mammals [24], and reptiles [25]. The high diversity of plants and animals may be related to the highly complex biogeographic history of the Neotropics[26]. Events such as the rise of the Andes, the closure of the Isthmus of Panama, and river formation in Amazon may have shaped the diversity that we see today [23].

Our models suggest that climate change is projected to shift the diversity patterns of Neotropical frogs. Tropical species are expected to show particular sensitivity to climate change, as they typically live near their critical thermal maximum and show fitness declines under shifting climates [27]. However, temperature is not the only factor determining species distribution [28] and other climate variables, such as precipitation regimes or water balance, may also be closely related to species range shifts [28]. Our results support this, as the models showed that precipitation of driest quarter (BIO 17) and annual precipitation (BIO 12) are the main drivers of range shifts for toads. These organisms can be strongly affected by drought

because they are dependent on water availability for reproduction [29]. Even for species with direct development, which do not deposit their eggs directly in water, the risk of water loss through evaporation is among the greatest threats to embryo development [30].

If species are able to change their distributions in the future, novel communities may arise, possibly holding low species richness, low functional and genetic diversity. Our models projected a marked decrease in SR and PD in the Guiana Shield, southeastern Brazil, east Amazonia, and the northern Andes. The projected impact of climate change on evolutionarily distinct taxa [11] leads to phylogenetic homogenization of future communities [31,32] and reduction in the ecosystem services provided by those species [31]. Frogs can provide different services for human society, including provisioning , regulating (e.g. predation of insects and prey population regulations), cultural (e.g. mythology, literature, and art), and supporting services (e.g. ecosystem functions) [33].

By 2050, the western Amazon and some parts of the Atlantic Rainforest are predicted to hold or even experience an increase in SR and PD of Neotropical frogs. These regions represent areas of higher importance for conservation as they are inhabited by a high number of species, including birds, reptiles, mammals [23–25,34], and our projections indicate that the Neotropical frog diversity will be maintained there in the future. Despite their high priority for conservation, the Amazon and the Atlantic Rainforest are also the world's most threatened regions in the world and are losing natural habitats due to urbanization and extensive deforestation [36,37].

The spatial patterns of PE for Neotropical frogs are also predicted to shift under climate change. Regions with geographically rare and evolutionary distinct lineages (PE hotspots) in the Amazon, southeastern Brazil, Guiana Shield, and Southern Mexico are projected to suffer substantial decreases in the future. These PE hotspots may host species with distinct trait diversity and possibly represent regions predicted to maximize ecosystem functions [12,38]. PE is predicted to increase in northwestern and southeastern Colombia and in the northern Guiana Shield in the future, due to the reductions in the distributions of phylogenetically distinct lineages. As PE is considered a measure of rarity, it should increase in regions where the remaining distribution of the species are concentrated [10].

Our models show that some centers of high PE are not areas of particularly high SR or high PD, such as the Caribbean Islands (Cuba, Haiti, Jamaica, Dominican Republic, and The Bahamas). These areas have one characteristic in common: geographic isolation. The spatial isolation is considered an important predictor of centers of endemism and can provide the conditions for diversification and maintenance of range-restricted clades [39]. Geographic barriers can favor the maintenance of these clades through vicariance forces, and speciation processes, mainly through allopatric speciation and reduction in gene flow. These islands are known for also harboring high endemism for other groups, such as mammals [39], birds [40], and reptiles [40].

Our analyses predict regions where frog diversity may be overlooked when solely considering SR. There are important areas for the conservation of the phylogenetic

component (higher PD and SES PD) in southeastern and northern Brazil, southern Paraguay, northern Bolivia, northeastern Peru, eastern Colombia, southern Venezuela, and northern Guyana. Similarly, Caribbean Islands, Mexico, and northern Colombia demonstrate elevated PE despite their relatively low SR. In fact, biodiversity metrics can vary across space and show high spatial incongruence due to different mechanisms that affect the relationship between diversity metrics [38]. For instance, the phylogenetic tree topology and the number of highly distinct species shape the relationship between SR and PD, and tend to decrease the correlation between these metrics [38]. Therefore, considering the spatial inconsistencies between diversity metrics, approaches that weight species by their phylogenetic contributions or endemism can offer best case scenarios for decision makers [31,38].

With the advance of climate change, species are predicted to experience novel climatic conditions and will have to adapt or shift their distribution to newly inhabited environments [41]. Range shift in response to climate change is a dynamic process affected by different mechanisms, such as migration, gene flow, novel communities, and new biotic interactions. Limits in dispersal and migration may reduce the capacity of species to track climatically suitable conditions [41]. Biotic interactions such as competition and consumption/predation can also prevent the establishment of new populations at novel range limits [42]. For example, if a required prey is not present in the novel area, a species may not be able to expand their range boundaries; likewise species can be excluded from some regions due to competitive interactions with new community members [42]. Therefore, there are ecological and evolutionary processes arising in non-equilibrium situations that may limit, or in some cases possibly accelerate, range expansions. As limited data exist to evaluate the potential importance of these mechanisms in our predictions, this is an added component of model uncertainty.

Our forecasts, like any empirical model, contain a certain amount of uncertainty. This uncertainty arises from the data observation process and our modeling assumptions. For example, we assume that climate variation within current ranges is a reasonable approximation of the species future requirements and that species will respond to climate change by occupying emerging areas compatible with identified niche constraints and that are accessible according to identified migration rates. Substitution of space for time can break down, especially in highly under-parameterized models [43]. The assumption of niche conservatism disregards the ability of species to persist through adaptation and plasticity when confronted with novel conditions [44]. If non-analog climatic conditions appear in the future and replace the present climate combinations, species will decline their range area due to a purely statistical phenomenon, because our models do not account for acclimatization, plasticity, or adaptation. Nonetheless, we believe that our models are sufficiently flexible to capture the species-climate relationships needed for forecasting, as has been demonstrated in previous studies [45,46].

We predicted that at least 42.20% of toads and treefrogs will lose range in the future due to climate change. At first glance, this result does not seem so alarming because the percentage of species gaining range area is higher than the percentage of species losing range

area [20]. However, our database covers only 19% of all Neotropical frogs due to lack of occurrence data for many species. The low number of species we were able to include in our study certainly underestimates the effect of climate change on Neotropical frogs, because many of the species excluded from our study have highly restricted distributions and are already classified as threatened by IUCN [20]. For example, many species from the genus *Atelopus* and *Melanophryniscus* are already threatened, but are data deficient in terms of their distribution. The continued documentation of species occurrences through field work is a key step to guarantee a representative assessment of climate change effects on a higher number of frog species, especially for endemic and threatened species.

Few studies this far have addressed how future climate change may affect the PE of Neotropical frogs. Our models predict that northwestern and southeastern Colombia and northern Guiana Shield are predicted to hold a high PE in the future, becoming an important refugium for species with deep evolutionary histories and restricted distribution. In contrast, other important hotspots of biodiversity are predicted to lose PE. This result highlights the need of an integrative approach to conservation forecasting, that considers both SR and phylogenetic information to assure the conservation of frog evolutionary history and provides best-case scenarios for managers in the future [31,38]. The conservation of species with distinct genetic heritage provides high potential for future adaptation to non-analogous climatic conditions caused by global warming.

Methods

Data gathering. Using SDMs we constructed potential distribution maps for 526 Neotropical frogs in the families Bufonidae (toads) and Hylidae (treefrogs). Species with a minimum of seven occurrence records were selected. The number of evaluated species represents 22% of all Bufonidae species and 33% of Neotropical Bufonidae species. For Hylidae, the number of evaluated species represents 35% of all Hylidae species and 39% of Neotropical Hylidae species. These two families were selected because they are highly speciose in the Neotropics and because they include a large number of species currently classified as threatened (~32%, 440 species) according to the IUCN [20]. Anuran occurrence records were obtained using the Global Biodiversity Information Facility (GBIF [47]). See details on occurrence filtering in the supplementary material.

Bioclimatic variables were obtained from the WorldClim database v2.1 [48] with a spatial resolution of 2.5 minutes (~5 km²) for the baseline (1970-2000, hereafter called present) and for the future (2050). To reduce problems with collinearity between environmental variables, we calculated a correlation matrix using Pearson's coefficient and selected variables with $r < 0.75$ for use in model calibration. For future projections, we selected three global circulation models (GCM): CCSM4, MPI-ESM-LR, and MIROC6, and calculated a weighted mean of the three GCMs. We projected future climate models using two Shared Socioeconomic Pathways (SSPs): SSP245, considered an optimistic scenario for the emission of greenhouse gasses, in which emission should start decreasing from 2040 and

SSP585, considered a pessimistic scenario, with CO^2 emission levels decreasing only after 2080.

Species distribution models. We followed the ODMAP (Overview, Data, Model, Assessment, and Prediction) standardized protocol [49] to describe the methodology for the SDMs. In this section, we provide a summary of the 'overview' component, while detailed information on each modeling step is available in the supplementary material**.** The calibration area was based on the minimum convex polygon (MCP), constructed using 100% of the filtered occurrence points, surrounded by a 1.5° (~150 km² at the equator) buffer. This area is typically defined based on the species' accessible region, known as M in the Biotic, abiotic, and movement (BAM) framework, which considers the region where the species could have dispersed to and colonized over a relevant time period [50]. The MCP and buffer were first made using the *ENMwizard* package [51] and then models were calibrated with the present climate scenario (1970-2000). To assess the impact of future climate change on the potential distribution of frogs, SDMs were built combining the occurrence records and bioclimatic variables, using the MaxEnt algorithm (version 3.4.1) [52,53] through the *ENMwizard* [51]. To avoid over-fitting, we conducted a grid-search for the optimal hyper-parameters based on cross-validated performance measures. See details on model calibration and model selection in the supplementary material.

We projected the best models for each species for three climatic scenarios (present, 2050 optimistic and 2050 pessimistic) to the extension limits of the Neotropics. We converted potential continuous distributions of each species into a presence/absence distribution (1 = presence and 0 = absence) applying the cut-off threshold of 10%. This is a relatively conservative threshold, which typically results in a larger estimated area of occupancy than the actual one. However, it has a low likelihood of omitting true presence points, thereby helping to reduce the overestimation of species range. SDMs often identify large range areas that have not yet been and possibly will never be colonized by the species due to dispersal limitations. To address this overprediction, we used a distance constraint layer based on species dispersal abilities to crop the presence/absence models. See details on overprediction removal and how we defined species dispersal abilities in the supplementary material.

Species richness, Phylogenetic diversity, and Phylogenetic endemism. Species richness (SR) was calculated using the sum of presence/absence maps (equation 1) in the package *phyloraster* [54],

$$SR = \sum_{c \in C} S_c$$

(equation 1)

where S_c is the presence of species c and C is the set of species in a specific region (equation 1). We calculated the percentage change (PC) in the range area of each species by subtracting the area in the future from the area in the present and multiplying this value by 100 (equation 2),

$$PC = \frac{\left(F_i - P_i\right)}{P_i} * 100$$

(equation 2)

where F_i represents the area in the future for the species i and P_i represents the area in the present for the species i. We assessed the correlation between the percentage change in range area and the current range size. Additionally, we tested whether the mean increase and decrease in range area differ significantly. See details on range area analysis in the supplementary material.

We used the phylogenetic tree of Portik et al. [55] to assess phylogenetic relationships among species. This time-calibrated phylogeny includes 5,242 anuran species, with data from 307 genetic markers, and was constructed using maximum-likelihood analysis [55]. See details on branch length calculations in the supplementary material. Based on the distribution models converted to a presence/absence distribution and the anuran phylogenetic tree [55], we calculated phylogenetic diversity (PD [11]) and phylogenetic endemism (PE [12,13]) for the present and the future using the function geo.phylo in the package *phyloraster* [54]. PD uses the sum of the branch lengths of a set of species in a given region to assess their accumulated evolutionary history (equation 3) [11],

$$PD = \sum_{c \in C} L_c$$

(equation 3)

where L_c is the branch lengths of species c and C are the branches in a specific region (equation 3). To assess the relationship between species richness and phylogenetic diversity, we fitted a spatial autoregressive (SAR) model. We used null-models to assess whether phylogenetic diversity is lower or higher than expected on the basis of species richness. See details on spatial autoregressive models and null models in the supplementary material.

PE weights the sum of the length of the branches by the inverse of range size of the species to identify regions with high spatially restricted phylogenetic diversity,

$$PE = \sum_{c \in C} L_c \frac{r_c}{R_c}$$

(equation 4)

where L_c is the branch length of taxon c, r_c is the local range of branch c, and R_c is the range area of the clade (equation 4). C are the branches in a specific region. To assess the magnitude and direction of the impacts of climate change on SR, PD, and PE we calculated the spatial difference (delta) between these metrics for present and future scenarios in *phyloraster* [54]. We also made bivariate maps illustrating the relationship between species

richness, phylogenetic diversity, and phylogenetic endemism using the *bivariatemaps* R package [56].

Data Availability The datasets generated and analyzed during the current study are available in the Harvard Dataverse Digital Repository: DOI https://doi.org/10.7910/DVN/HZJMRM.

Code Availability Datasets and codes necessary to the analyses described here are available in the GitHub: https://github.com/gabferreira/phylo_endemism_frogs.

Competing interests The authors declare no competing interests.

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Supplementary material

Occurrence filtering. We performed quality control on occurrence data using the *scrubr* package [1] to eliminate duplicates and unlikely or impossible coordinates. We also excluded records with latitude and longitude coordinates of zero, occurrences located within 2 km of country or capital centroids, occurrences within 2 km of zoos or herbaria, and those located over the ocean using the R package *CoordinateCleaner* [2]. We thinned occurrences to reduce spatial bias and redundancy in climatic values using the envThin optimization algorithm 2 in the *ENMwizard* R package [3]. Environmental filters are effective in reducing sampling bias and improves model performance, while still preserving the signal of the species' ecological niche [4,5]. To filter the occurrences, we selected five least correlated bioclimatic variables (Bio 1, bio 2, bio 4, bio 12 and bio 15) for the current scenario (1970-2000, within 2.5 arc minutes, Fick and Hijmans 2017) and performed a Principal Component Analysis (PCA). We selected the first three axes of the PCA, which explained

80% of the climatic variance, and removed the environmentally/climatically clustered or oversampled occurrences. At the end of filtering, 148 species of toads and 379 species of tree frogs were retained (Table S1). The sample size per taxon ranges from 7 to 11,534 occurrences per species (Table S2).

We calculated the representation of GBIF [6] data by the species range provided by IUCN [7]. First, we built a Minimum Convex Polygon (MCP) with the filtered GBIF points using the *terra* R package [8]. Then, we intersected this MCP with the IUCN range for each species. After that, we calculated the area of the IUCN range (km^2) and the area of the intersected MCP built with the GBIF points (km^2). Finally, we calculated the proportion by dividing the intersected MCP area (km^2) by the total IUCN range area (km^2), resulting in values between 0 and 1, where 1 indicates that the IUCN range area is fully covered by GBIF points. The distribution of these values is shown in Fig. S1. The representation of GBIF data inside the IUCN species range is good (mean = 0.84, Standard deviation = 0.29).

Table S1. Number of species at each step of the occurrence filtering. Number of species of toads and treefrogs with data available in GBIF (first row), number of species remaining after filtering the occurrence records (second row), and number of species after applying the environmental filter (third row).

	Toads	**Treefrogs**	**All species**
Species with data from GBIF	444	949	1393
Coordinates filtering	218	465	683
Environmental filtering	148	379	526

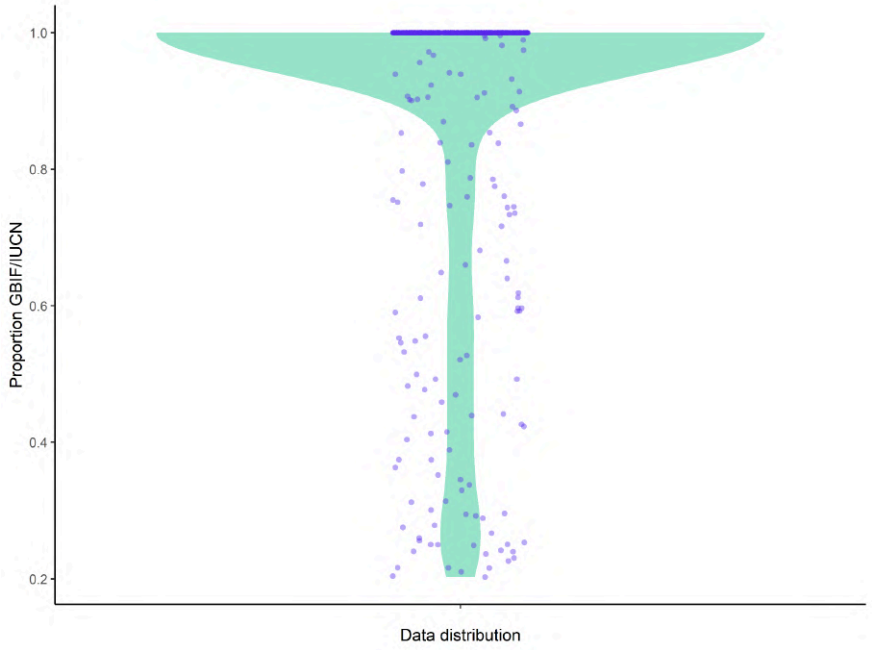

Fig. S1 Violin plot showing the proportion of species ranges occupied by the GBIF data used in the models. The purple dots represent the proportion for each species.

Species distribution models. The preliminary species distribution models were adjusted by calibrating options of Feature Classes (FC) and Regularization Multipliers (RMs), giving variable complexity to the models. These parameters concern transformations of environmental variables and penalize model complexity, respectively [9,10]. The models were built using all combinations of four FCs: "L" is linear, "P" product, "Q" quadratic and "H" hinge. The RM values varied from 0.5 to 4.5 with intervals of 0.5. We evaluated and calibrated the models using spatial "block" cross validation with four partitions. The "block" method strategically partitions the occurrence points into four spatially independent blocks and runs four iterations using one of the blocks to evaluate the model and the others for calibration [11].

To identify the optimal and co-optimal combinations of model settings (FC and RM) before transferring to novel conditions, we evaluated model performance using sequential criteria [12]. We applied a threshold-dependent measure, specifically an omission rate, to avoid models that overfit to the calibration data. The omission rate applied in this study was based on the lowest presence threshold (LPT = 0% calibration omission rate [13]). The LPT method sets the threshold to the lowest value of the prediction for any pixel that contains a calibration occurrence [13] and an omission rate of zero for evaluation occurrences. Models with omission rates higher than this expected value are considered more overfitted. Since multiple combinations of settings can yield the lowest omission rate, we employed an additional evaluation metric to enhance discriminatory power: the Area Under Curve (AUC). Therefore, we determined the optimal combination for each species as the top performing 10% of the models with the lowest average omission rate and the highest average AUC [12].

Uncertainty in forecasts of SDMs. SDMs can present uncertainties related to the algorithm, model parameterization, climate scenarios, thresholding, and dispersal scenario [14–16]. We addressed algorithmic uncertainty by using Maxent, since the tuned algorithm performs better or similarly to other algorithms [17,18]. Uncertainty in the parameterization of each model was reduced with cross validation. After cross-validation, we calculated the average suitability across the 10% models with the best performance (lowest omission rate and highest AUC [12]).

Different Global Climate Models (GCMs) rely on varying parameters and incorporate different functions to represent atmospheric circulation dynamics, oceanic effects, and feedbacks between the land surface and the atmosphere; they can project different outcomes for the same level of greenhouse gas emissions. Therefore, to minimize the uncertainty about the choice of just one GCM [19], we selected three GCMs: CCSM4, MPI-ESM-LR, and MIROC6. Then, we built a consensus model for each species with the projection resultant from each GCMs. Regarding the uncertainty in greenhouse gas emission scenarios, two Shared Socioeconomic Pathways (SSPs) were selected: SSP245 and SSP585. The uncertainty in dispersal scenarios was addressed by applying a method to remove the overprediction described in details above.

Removing overprediction. SDMs often identify large climatically suitable areas that have not yet been and possibly will never be colonized by the species due to dispersal limitations. To address this overprediction, we used a distance constraint layer based on species dispersal abilities to crop the presence/absence models for the present and the future. The restriction layer was created based on the range maps of each species obtained from IUCN [7], surrounded by a buffer with the dispersal capacity for each group (toads and treefrogs). For toads, we considered a dispersal capacity of 3,300 meters per generation [20] and used this value to create a buffer that surrounds the IUCN range maps. With this IUCN range map for each species surrounded by a buffer of 3,300 meters, we cropped the models for the present baseline for toads. Considering that each anuran generation lives on average 2.5 years [21] and we have 20 generations between 2000-2050, these species could disperse up to 66,000 meters (3,300 meters multiplied by 20) by 2050. For treefrogs, we used a buffer of 2,300 meters [20] surrounding the IUCN range maps for the present and a buffer of 46,000 meters (2,300 meters multiplied by 20) for the future. Then, we cropped the present and future presence absence maps for treefrogs.

Branch length calculations. To assess whether missing species in the tree affect branch length calculations, we computed branch lengths using both the full tree (5,242 species) and a pruned version containing only the species present in the raster (497 species). We then performed a paired t-test to compare the differences. The test revealed no significant differences in branch lengths before and after pruning ($t = -1.002$, $df = 995.01$, p-value = 0.316). Additionally, we calculated phylogenetic diversity using branch lengths derived from

both the full and pruned trees to examine potential spatial differences in the present (Fig. S2). The results were highly similar, therefore we choose to use the branch lengths from the pruned phylogenetic tree in our analysis.

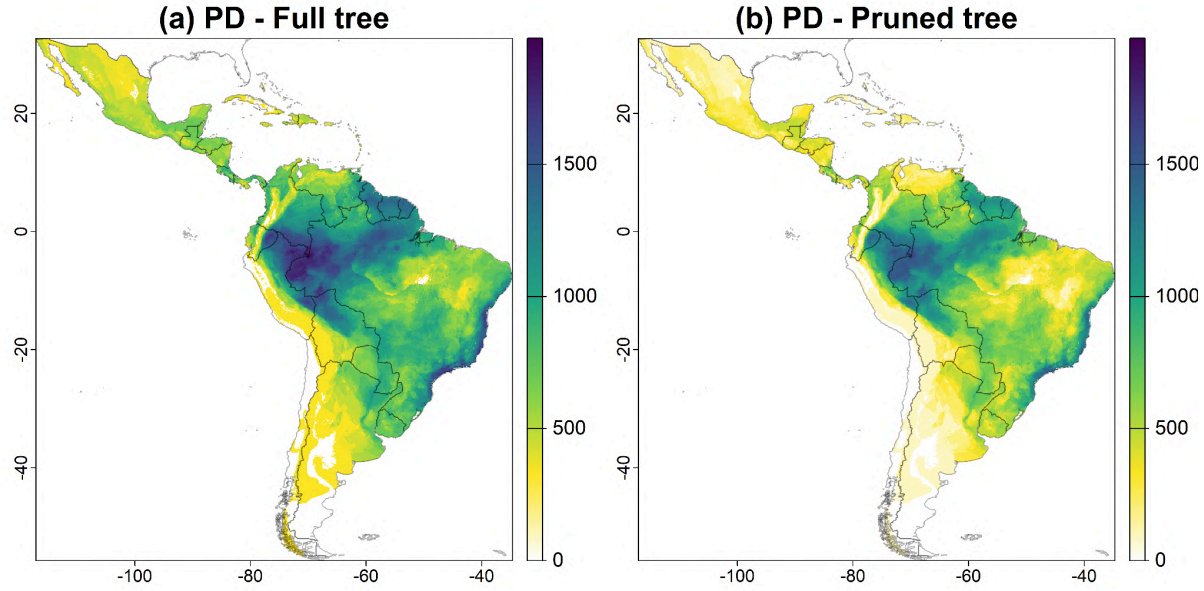

Fig. S2 Phylogenetic diversity (PD) of 497 Neotropical toads and treefrogs. PD was calculated using branch lengths derived from both the (**a**) full and (**b**) pruned tree. Purple and dark green colors represent regions with high PD, while light green and yellow colors represent regions with low PD.

Range area analysis. After calculating the percentage change in range area for each species, we assessed whether there is a significant difference between the mean increase and decrease in range area using a Mann-Whitney-Wilcoxon test, as the data were not normally distributed. Additionally, we conducted a Spearman correlation test between the percentage change in area and the current range area to determine whether species with smaller ranges are experiencing greater range reductions than those with wider distributions.

Spatial autoregressive models. To assess the relationship between species richness, phylogenetic diversity and phylogenetic endemism, we fitted a linear model. Residuals were tested for normality using the Anderson-Darling test. We then evaluated spatial autocorrelation by constructing a spatial weights matrix based on k-nearest neighbors. Spatial autocorrelation of the residuals was assessed using Moran's I test. To account for spatial dependencies, we fitted a spatial autoregressive (SAR) model, optimizing the model using a neighborhood structure generated from the spatial data grid.

Randomization tests. We used null-models to assess whether phylogenetic diversity is lower or higher than expected on the basis of species richness using the R packages *SESraster* [22] and *phyloraster* [23]. The null model used (bootspat_str in SESraster [22] is equivalent to the SIM5 (proportional-fixed) method of Gotelli [24]. This method partially relaxes the spatial structure of species distribution, while keeping the observed richness across cells. We ran this null model 999 times and calculated PD in each trial. Then, we calculated the standardized effect size (SES) using the following formula (equation 1),

$$SES = \frac{Metric_{obs} - Metric_{null}}{SD\left(Metric_{null}\right)}$$

(equation 1)

where $Metric_{obs}$ is the observed value for the metric, mean ($Metric_{rand}$) is the mean of the metric calculated based on 999 randomizations, and SD ($Metric_{rand}$) is the standard deviation of the 999 randomization. Positive values of SES represent regions where the observed phylogenetic diversity is higher than expected at random and negative values of SES represent regions where the observed values are lower than expected randomly.

ODMAP protocol detailing the steps for the Species Distribution Models.

– ODMAP Protocol –

Overview

Model objective

Model objective: Forecast and transfer

Target output: Suitable vs. unsuitable habitat

Focal Taxon

Focal Taxon: Using SDMs we constructed potential distribution maps for Neotropical frogs in the families Bufonidae (toads) and Hylidae (treefrogs).

Location

Location: Our focal study area is the Neotropical region.

Scale of Analysis

Spatial extent: -179.141, -12.155, -59.473, 83.623 (xmin, xmax, ymin, ymax)

Spatial resolution: Community boundaries were defined as grid cell of 2.5 arc minutes (~ 5km²)

Temporal extent: We used occurrence records collected until 2024.

Temporal resolution: We used the present (1970-2000) and a future climate scenario (2050). For 2050, we considered two Shared Socioeconomic Pathways (SSPs) representing optimistic (SSP370) and pessimistic (SSP585) greenhouse gas scenarios.

Boundary: natural

Biodiversity data

Observation type: Anuran occurrence records were obtained using the Global Biodiversity Information Facility (GBIF [6]).

Response data type: presence/background

Predictors

Predictor types: climatic

Hypotheses

Hypotheses: We ask how future scenarios of climate change will affect patterns of species richness, phylogenetic diversity, and phylogenetic endemism of Neotropical frogs (toads and treefrogs). Projected increases in temperature and reductions in precipitation are expected to shrink the potential distributions of species, resulting in lower SR and PD in the future. In contrast, we expect PE to increase, due to reductions in potential distributions. However, the exact degree to which PE increases will depend on the relative reduction in species' distributions and the identity of species that are lost.

Assumptions

Model assumptions: Our assumptions are that occurrence records are accurate and representative, species are at equilibrium with their environment, and the ecological niche is preserved over time. Additionally, our models do not account for the potential adaptation of species to climate change.

Algorithms

Modelling techniques: maxent

Model complexity: We created SDMs with tuned hyperparameters because default hyperparameter values often do not return the best models [25].

Model averaging: Consensual models for each species were developed using the top 10% of MaxEnt models, selected based on the lowest Omission Rate (OR) and the highest average Area Under the Curve (AUC) values, following the criteria outlined by Boria et al. [12].

Workflow

Model workflow: The calibration area was based on the minimum convex polygon (MCP), constructed using 100% of the filtered occurrence points, surrounded by a 1.5° (~150 km² at the equator) buffer. The models were calibrated with the present climate scenario

(1970-2000). SDMs were built combining the occurrence records and bioclimatic variables, using the MaxEnt algorithm (version 3.4.1) through the R package *ENMwizard* [3]. To avoid over-fitting, we conducted a grid-search for the optimal hyper-parameters based on cross-validated performance measures. The preliminary SDMs were adjusted by calibrating options of Feature Classes (FC) and Regularization Multipliers (RMs), giving variable complexity to the models. These parameters concern transformations of environmental variables and penalize model complexity, respectively. The models were built using all combinations of four FCs: "L" is linear, "P" product, "Q" quadratic and "H" hinge. The RM values varied from 0.5 to 4.5 with intervals of 0.5. We used the ENMevaluate_b function from ENMwizard to apply the "block" method of geographic partitioning in the occurrence records for each species. To identify the optimal and co-optimal combinations of model settings (FC and RM) before transferring to novel conditions, we evaluated model performance using sequential criteria [12]. We applied a threshold-dependent measure, specifically an omission rate, to avoid models that overfit to the calibration data. The omission rate applied in this study was based on the lowest presence threshold (LPT = 0% calibration omission rate [13]). The LPT method sets the threshold to the lowest value of the prediction for any pixel that contains a calibration occurrence [13] and an omission rate of zero for evaluation occurrences. Since multiple combinations of settings can yield the lowest omission rate, we employed an additional evaluation metric to enhance discriminatory power: the Area Under Curve (AUC). Therefore, we determined the optimal combination for each species as the top performing 10% of the models with the lowest average omission rate and the highest average AUC.
We projected the best models for each species for three climatic scenarios (present, 2050 optimistic and 2050 pessimistic) to the extension limits of the Neotropics. We converted potential continuous distributions of each species into a presence/absence binary distribution (1 = presence and 0 = absence) applying the cut-off threshold of 10%.

Software

Software: R 4.3.2 and R Packages *ENMwizard* [3] and *CoordinateCleaner* [2].

Code availability: https://github.com/gabferreira/phylo_endemism_frogs/tree/main/codes

Data availability: https://github.com/gabferreira/phylo_endemism_frogs/tree/main/data

Data

Biodiversity data

Taxon names: We focused on species of toads from the Bufonidae family and tree frogs from the Hylidae family (Table S1). The taxonomic names are available in Table S1.

Taxonomic reference system: The taxonomic nomenclature follows Frost [26].

Ecological level: communities, species

Data sources: Anuran occurrence records were obtained using the Global Biodiversity Information Facility (GBIF [6])

Sample size: The sample size per taxon ranges from 7 to 11,534 occurrences per species. The number of occurrences per species can be seen in Table S1.

Clipping: Our main study area is the Neotropical region. However, we calibrated the SDMs considering the entire extent of the New World, since many species we are evaluating occur in other biomes outside the Neotropical region. The models were projected for the Neotropics.

Scaling: We thinned occurrences to reduce spatial bias and redundancy in climatic values using the envThin optimization algorithm [4] in the *ENMwizard* package [3]. Environmental filters are effective in reducing sampling bias and improves model performance, while still preserving the signal of the species' ecological niche [4,5]. To filter the occurrences, we selected five least correlated bioclimatic variables (Bio 1, bio 2, bio 4, bio 12 and bio 15) for the current scenario (1970-2000, within 2.5 arc minutes) and performed a Principal Component Analysis (PCA). We selected the first three axes of the PCA, which explained 80% of the climatic variance, and removed the environmentally/climatically clustered or oversampled occurrences.

Cleaning: We performed quality control on occurrence data using the *scrubr* package [1] to eliminate duplicates and unlikely or impossible coordinates. We also excluded records with latitude and longitude coordinates of zero, occurrences located within 2 km of country or capital centroids, occurrences within 2 km of zoos or herbaria, and those located over the ocean using the R package *CoordinateCleaner* [2]. At the end of filtering, 106 species of toads and 278 species of tree frogs were retained (Table S1). The sample size per taxon ranges from 7 to 11,534 occurrences per species (Table S1).

Background data: We randomly sampled 10.000 background points throughout the calibration area.

Data partitioning

Validation data: We evaluated and calibrated the models using spatial block cross validation with four partitions. The "block" method strategically partitions the occurrence points into four spatially independent blocks and runs four iterations using one of the blocks to evaluate the model and the others for calibration [11].

Test data: There was no truly independent dataset available.

Predictor variables

Predictor variables: We selected bioclimatic variables for each species with Pearson correlation < 0.75 for use in model calibration. The same variables were used to project the potential distribution for future scenarios.

Data sources: URL: https://www.worldclim.org/data/worldclim21.html Version 2.1 Accession date: 01/13/2024

Spatial extent: -179.141, -12.155, -59.473, 83.623 (xmin, xmax, ymin, ymax)

Spatial resolution: 5 km²

Coordinate reference system: The coordinate reference system is WGS84 (EPSG:4326).

Temporal extent: Bioclimatic variables were obtained for the present (1970-2000).

Dimension reduction: We selected bioclimatic variables for each species with Pearson correlation < 0.75 for use in model calibration.

Transfer data

Data sources: URL: https://www.worldclim.org/data/worldclim21.html Version 2.1 Accession date: 01/13/2024

Spatial extent: -179.141, -12.155, -59.473, 83.623 (xmin, xmax, ymin, ymax)

Spatial resolution: 5 km²

Temporal extent: Bioclimatic variables were obtained for the future (2050).

Models and scenarios: For future projections, we selected three global circulation models (GCM): CCSM4, MPI-ESM-LR, and MIROC6, and calculated a weighted mean of the three GCMs. We projected future climate models using two Shared Socioeconomic Pathways (SSPs): SSP245, considered an optimistic scenario for the emission of greenhouse gasses, in which emission should start decreasing from 2040 and SSP585, considered a pessimistic scenario, with CO2 emission levels decreasing only after 2080

Model

Variable pre-selection

Variable pre-selection: We selected bioclimatic variables for each species with Pearson correlation < 0.75 for use in model calibration. The same variables were used to project the potential distribution for future scenarios.

Multicollinearity

Multicollinearity: The method used for identifying and dealing with multicollinearity was the calculation of the Pearson Correlation.

Model settings

maxent: featureSet (Linear, product, quadratic and hinge), regularizationMultiplierSet (Values from 0.5 to 4.5 with intervals of 0.5)

Model settings (extrapolation): Extrapolation was limited because we applied an a posteriori method to the final results, which retains only the climatically suitable pixels that intersect the known ranges for each species, surrounded by a buffer with the dispersal capacity for each family.

Model selection - model averaging - ensembles

Model selection: To identify the optimal and co-optimal combinations of model settings (FC and RM) before transferring to novel conditions, we evaluated model performance using sequential criteria [12]. We applied a threshold-dependent measure, specifically an omission rate, to avoid models that overfit to the calibration data. The omission rate applied in this study was based on the lowest presence threshold (LPT = 0% calibration omission rate [13]). The LPT method sets the threshold to the lowest value of the prediction for any pixel that contains a calibration occurrence [13] and an omission rate of zero for evaluation occurrences. Models with omission rates higher than this expected value are considered more overfitted. Since multiple combinations of settings can yield the lowest omission rate, we employed an additional evaluation metric to enhance discriminatory power: the Area Under Curve (AUC). Therefore, we determined the optimal combination for each species as the top performing 10% of the models with the lowest average omission rate and the highest average AUC. We excluded models that did not meet the minimum AUC value of 0,7.

Model ensembles: Consensual models for each species were developed using the top 10% of MaxEnt models, selected based on the lowest Omission Rate (OR) and the highest average Area Under the Curve (AUC) values, following the criteria outlined by Boria et al. (2017).

Analysis and Correction of non-independence

Spatial autocorrelation: We used spatial block cross validation to address spatial autocorrelation between calibration and validation occurrence records.

Threshold selection

Threshold selection: We converted potential continuous distributions of each species into a presence/absence distribution (1 = presence and 0 = absence) applying the cut-off threshold of 10%.

Assessment

Performance statistics

Performance on training data: AUC, Omission Rate

Performance on validation data: AUC, Omission Rate

Plausibility check

Expert judgment: The presence-absence and the continuous maps were carefully checked by specialists in neotropical anurans.

Prediction

Prediction output

Prediction unit: The models produced continuous suitability maps and presence-absence maps.

Uncertainty quantification

Algorithmic uncertainty: We addressed algorithmic uncertainty by using Maxent, since the tuned algorithm performs better or similarly to other algorithms [17,18]. Parameter uncertainty: Uncertainty in the parameterization of each model was reduced with cross validation. After cross-validation we applied a model selection technique of the 10% of models with the best performance (lowest omission rate and highest AUC [12]) and calculated an average of these models for each species.

Scenario uncertainty: To minimize the uncertainty about the choice of just one GCM [19], we selected three GCMs: CCSM4, MPI-ESM-LR, and MIROC6. Then, we built a consensus model for each species with the projection resultant from each GCMs.

Novel environments: To address the overprediction in the SDMs, we used a distance constraint layer based on species dispersal abilities to crop the presence absence models for the present and the future. The constraint layer was developed using species range maps sourced from the IUCN [7], with a buffer representing the dispersal ability specific to each group (toads and treefrogs). For toads, we assumed a dispersal ability of 3,300 meters per generation. Given that each anuran generation has an average of 2.5 years, and there are 20 generations between 2000 and 2050, the species could potentially spread up to 66,000 meters (3,300 meters multiplied by 20) by the year 2050. The IUCN range map with a buffer of 3,300 meters and 66,000 meters was used to crop the models of the toads for the present and future, respectively. For treefrogs, we applied a 2,300 meter buffer around the IUCN range maps for the present and extended this to a 46,000 meter buffer (2,300 meters multiplied by 20) for future projections.

Results

Table S2 Species modeled, evaluation metrics, and number of occurrences used in the models. AICc = Akaike Information Criteria corrected for small samples, OR = Omission Rate, AUC = Area Under Curve.

Table S2 is available in the Harvard Dataverse Digital Repository: DOI https://doi.org/10.7910/DVN/HZJMRM

Table S3 Species modeled, their IUCN status, branch length (Myr), and their range area in present, future optimistic, and future pessimistic.

Table S3 is available in the Harvard Dataverse Digital Repository: DOI https://doi.org/10.7910/DVN/HZJMRM

Table S4 Percentage of toads (Bufonidae) and treefrogs (Hylidae) projected to gain or lose range area in the future and their conservation status according to IUCN (2024). DD = Data Deficient, LC = Least Concern, NT = Near Threatened, VU = Vulnerable, EN = Endangered, CR = Critically Endangered.

Families	IUCN Category (%)					
	DD	**LC**	**NT**	**VU**	**EN**	**CR**
Toads						
Decrease	0.000	25.000	0.000	0.676	1.351	0.676
Increase	0.676	35.811	4.730	4.054	8.784	14.189
Total Loss	0.000	0.676	0.000	0.000	0.000	0.000
Treefrogs						
Decrease	0.528	43.799	0.000	0.264	0.264	0.264
Increase	0.792	32.982	2.902	6.069	7.388	2.375
Total Loss	0.000	1.583	0.264	0.264	0.000	0.000

Table S5 Relative importance of each bioclimatic variable for toads (Bufonidae) and treefrogs (Hylidae). These values were calculated based on the relative contribution of each variable divided by the number of times the variable was considered the most important.

Group	Variable	Relative importance	Group	Variable	Relative importance
Toads	Bio 17	17.751	**Treefrogs**	Bio 1	6.173
	Bio 12	10.890		Bio 10	5.359
	Bio 1	9.653		Bio 6	3.130
	Bio 16	6.337		Bio 11	2.642
	Bio 11	5.747		Bio 17	2.435
	Bio 6	5.664		Bio 16	1.856
	Bio 9	5.203		Bio 9	1.825
	Bio 8	3.745		Bio 14	1.073
	Bio 14	3.364		Bio 7	0.914
	Bio 18	1.526		Bio 12	0.897
	Bio 19	1.486		Bio 13	0.860
	Bio 13	1.359		Bio 8	0.845
	Bio 7	1.327		Bio 19	0.715
	Bio 5	1.216		Bio 15	0.509

Bio 4	1.161		Bio 5	0.507
Bio 2	1.035		Bio 18	0.423
Bio 15	0.940		Bio 3	0.404
Bio 3	0.845		Bio 2	0.388
Bio 10	0.000		Bio 4	0.366

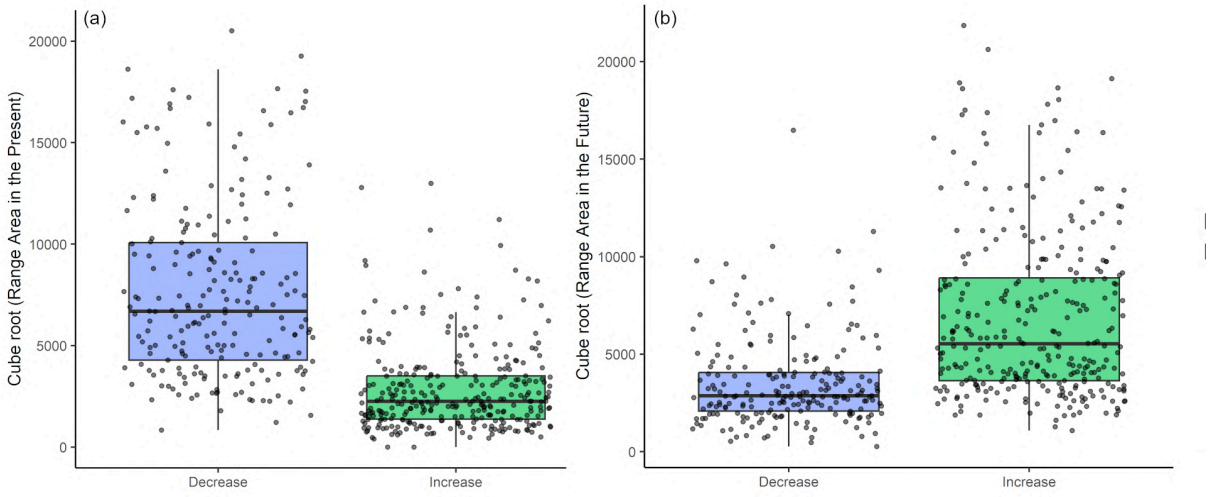

Fig. S3 Boxplots showing the values of decrease and increase in range area for 497 Neotropical frogs. Range area in the (**a**) present and in the (**b**) future pessimistic, and the direction of species response to future climate change (decrease or increase). Decrease is represented by the purple color and increase by the green color. The black horizontal line in the boxplot represents the median and the black dots represent the range area for each species in the present and in the future. The vertical lines represent the minimum and maximum values.

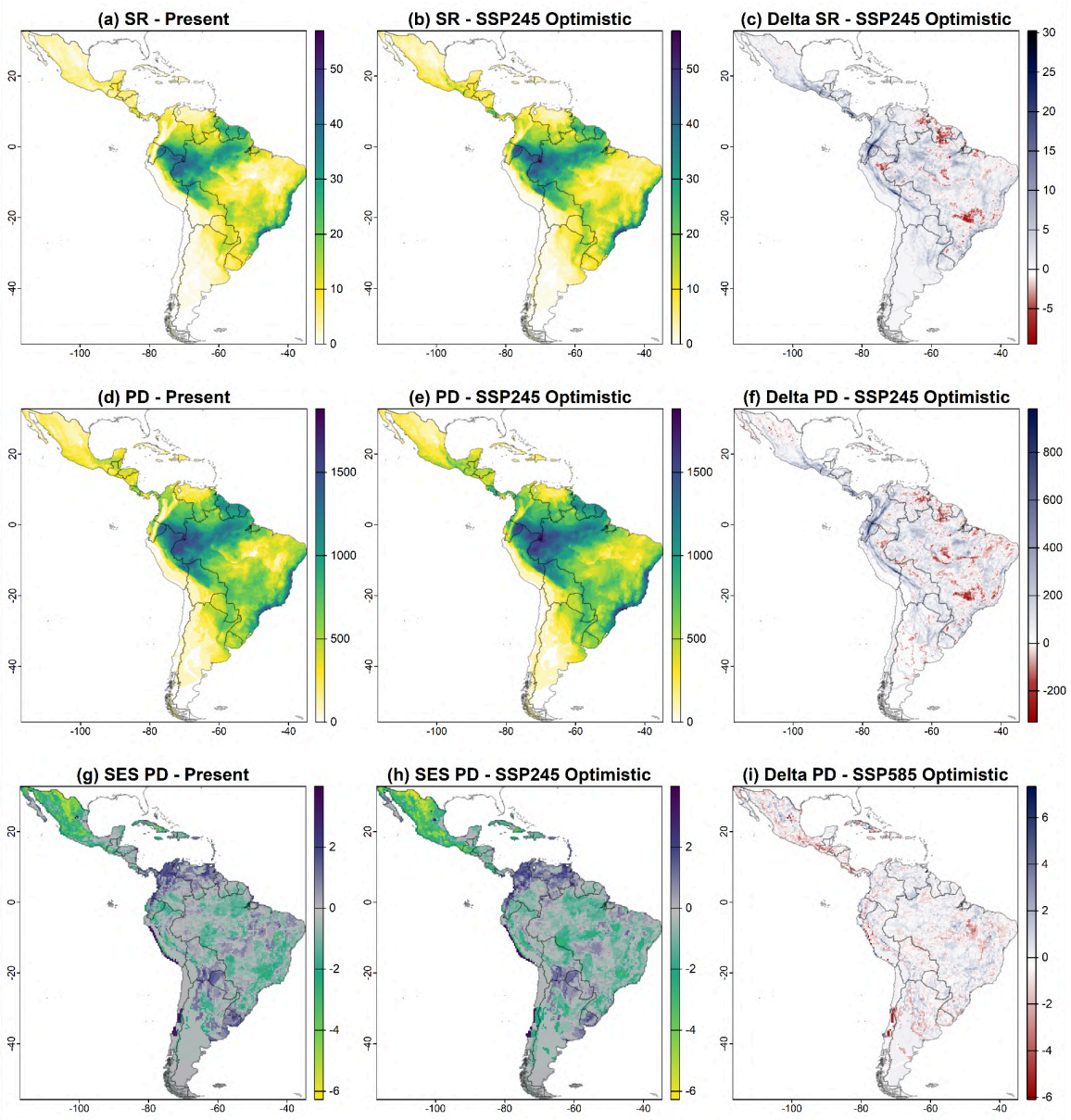

Fig. S4 Species richness (SR), Phylogenetic diversity (PD), and Standardized effect size for Phylogenetic diversity (SES PD) of 497 Neotropical toads and treefrogs. (**a**) SR for the present scenario, (**b**) SR for the optimistic 2050 scenario, (**c**) differences in SR between present and the optimistic 2050 scenario, (**d**) PD for the present scenario, (**e**) PD for the optimistic 2050 scenario, (**f**) differences in PD between present and the optimistic 2050 scenario, (**g**) SES PD for the present, (**h**) SES PD for the optimistic 2050 scenario, and (**i**) differences in SES PD between present and the optimistic 2050 scenario. Purple and dark green colors represent regions with high SR and PD, while light green and yellow colors represent regions with low SR and PD. Red colors represent species losses in SR, PD, and SES PD, gray/white color represents areas where SR, PD, and SES PD are not predicted to change, and blue color represents SR, PD, and SES PD gains in the future. In the panels (**g**)

and (**h**) yellow and green colors represent regions where PD is lower than expected randomly and blue and purple colors represent regions where PD is higher than expected randomly.

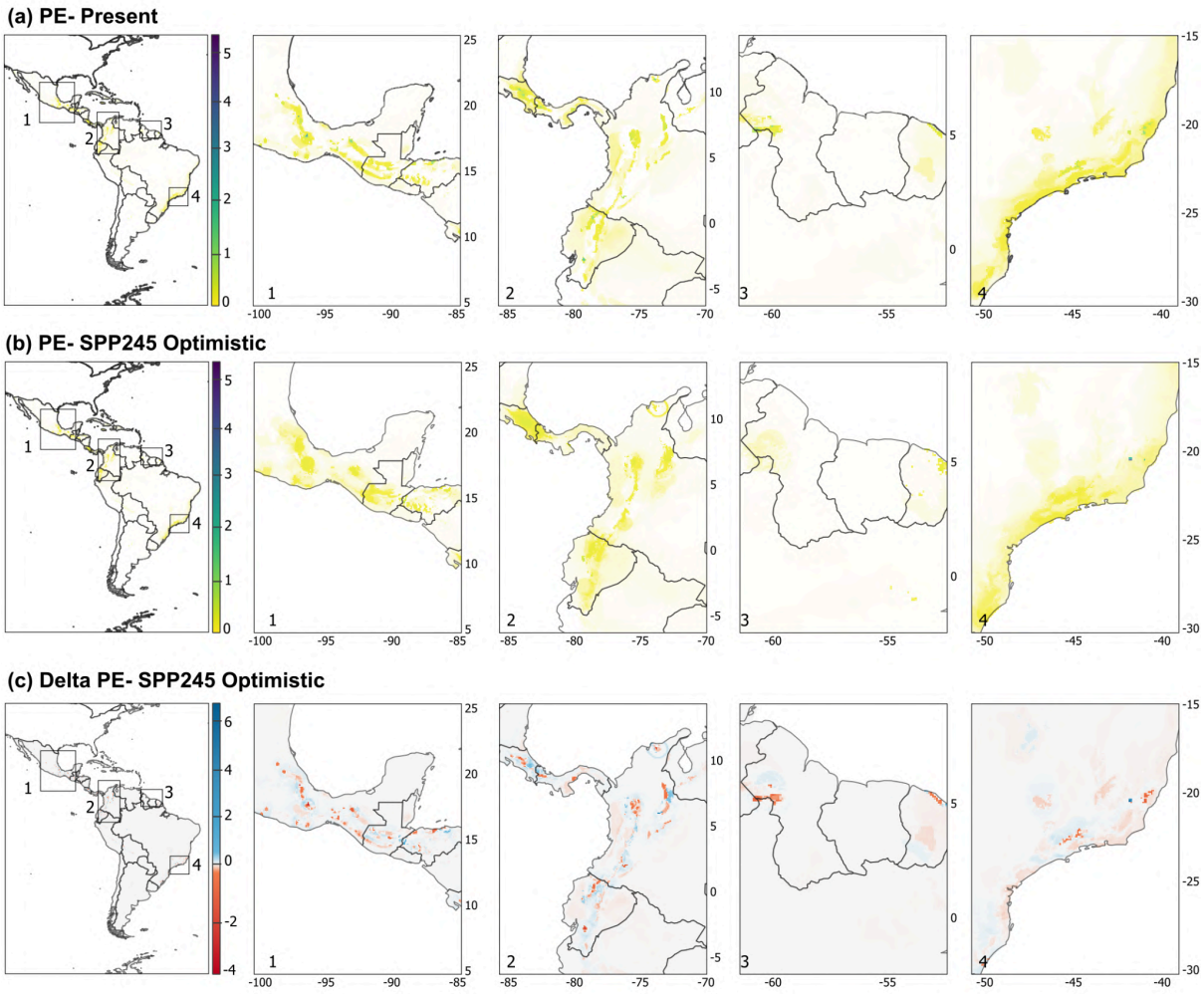

Fig. S5 Phylogenetic endemism (PE) of 497 Neotropical toads and treefrogs. (**a**) PE for the present scenario, (**b**) PE for the optimistic 2050 scenario, (**c**) differences in PE between present and the optimistic 2050 scenario. In panels (**a**) and (**b**), purple and green colors represent regions with high PE, while yellow white colors represent regions with low PE. In panel (**c**) red colors represent losses in PE, gray/white color represents areas where PE is not predicted to change, and blue color represents PE gains in the future.

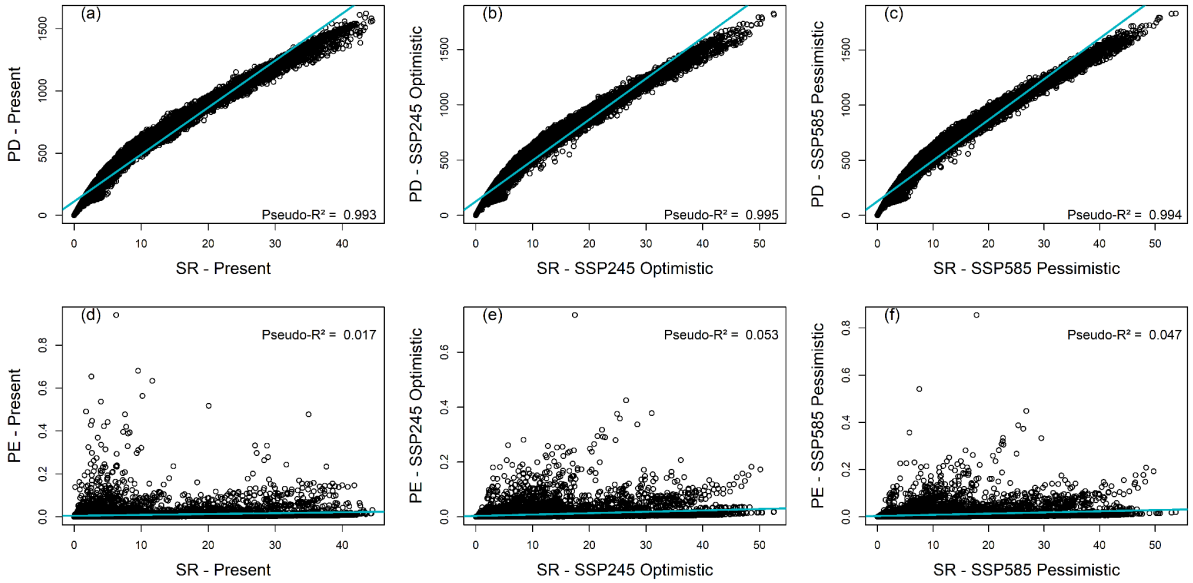

Fig. S6 Relationship between diversity metrics. Species richness plotted against phylogenetic diversity for the (**a**) present scenario, (**b**) optimistic 2050 scenario, and (**c**) pessimistic 2050 scenario. Species richness plotted against phylogenetic endemism for the (**d**) present scenario, (**e**) optimistic 2050 scenario, and (**f**) pessimistic 2050 scenario. The blue line in the panels represents the regression line.

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Capítulo 4

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Climate change is projected to reshape Neotropical frog communities

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Abstract

Climate change is projected to affect the patterns of species distributions and reshape communities. Most studies have focused on evaluating how climate change affects taxonomic beta diversity (changes in species composition), but few have examined how the functional (shifts in functional traits) and phylogenetic (changes in evolutionary lineages) dimensions of beta diversity are projected to be impacted. Here, we investigate how future climatic scenarios may affect taxonomic, phylogenetic, and functional beta diversity in 497 frog species from the families Bufonidae and Hylidae across the Neotropics. Using species distribution models, we projected the potential distributions of Neotropical frogs for the present and for 2050, and calculated beta diversity across three dimensions of diversity, explicitly disentangling its replacement and richness (species gains and losses) components. Our results indicate that over 42% of species could experience range contractions, and almost 2% may lose their entire range. These range contractions are expected to drive changes in species composition and alter patterns of beta diversity in the Neotropics. Across all three dimensions, changes were primarily driven by richness differences rather than species replacement. Our findings indicate that amphibian communities in the Neotropics are projected to undergo substantial phylogenetic and functional homogenization in the future, becoming dominated by species with more similar functional traits and phylogenetic composition. These results underscore the importance of integrating multidimensional perspectives of biodiversity into conservation planning, as each dimension may respond differently to climate change.

Keywords. composition changes, Anura, amphibians, species distribution models, species replacement

Introduction

Understanding the global patterns of species distribution and diversity has long been a central focus in macroecology and biogeography. Among the factors shaping these patterns, climate plays a key role, influencing biodiversity through mechanisms such as niche conservatism, physiological tolerance, and diversification rates (Wang *et al.*, 2021). For example, species with narrow physiological tolerances tend to be restricted to regions with specific climatic conditions. As climate change accelerates, understanding how these large-scale patterns might shift becomes increasingly urgent (Intergovernmental Panel On Climate Change (Ipcc), 2023).

Climate change is expected to drive substantial shifts in species distributions, particularly when species are unable to adapt rapidly to new environmental conditions (Weiskopf *et al.*, 2020; Antão *et al.*, 2022; Bradley *et al.*, 2024). In such cases, species must track suitable climates by dispersing into new areas, a process underscored in recent studies of range shift dynamics (Lawlor *et al.*, 2024). These range shifts can lead to profound impacts on biodiversity at both local and regional scales, especially in terms of species composition (i.e., beta diversity; (Whittaker, 1960; Baselga, 2010). Beta diversity, which describes the variation in species composition among communities, can be partitioned into two components: replacement and richness (Cardoso *et al.*, 2014). These components reflect whether communities become more distinct due to differences in species richness (through gains or losses) or through the replacement of some species by others (e.g., (Hidasi-Neto *et al.*, 2019). Declines in beta diversity can further lead to biotic homogenization, a process by which communities become increasingly similar over time (Clavel *et al.*, 2011), often as a result of specialist species extinctions and the expansion of generalists (McKinney & Lockwood, 1999).

Changes in beta diversity can be assessed across multiple dimensions of biodiversity (e.g., (Xu *et al.*, 2023). Taxonomic beta diversity reflects shifts in species identities, phylogenetic beta diversity captures alterations in the evolutionary history of communities, and functional beta diversity reveals changes in ecological traits (Swenson, 2011; Muvengwi *et al.*, 2022). These dimensions often respond differently to environmental change, providing complementary insights into biodiversity reorganization. For example, diverse communities composed of specialized species are increasingly being replaced by communities dominated by widespread generalists (McKinney & Lockwood, 1999; Clavel *et al.*, 2011). Even when generalist species expand their ranges, they may not fully replace the ecological functions or evolutionary heritage of the species lost, leading to functional homogenization and the erosion of evolutionary history, often without an evident decline in taxonomic diversity (Galetti *et al.*, 2013). Therefore, considering multiple dimensions of biodiversity is crucial to fully understand the consequences of climate change.

Climate-induced shifts in beta diversity have been documented in a variety of taxonomic groups, including birds (Mota *et al.*, 2022a), trees (Xu *et al.*, 2023), mammals (Hidasi-Neto *et al.*, 2019), and amphibians (Menéndez‐Guerrero *et al.*, 2020). Among these, amphibians are particularly vulnerable. Over the past three decades, around 185 amphibian species have gone extinct, and nearly 41% of the 8,009 species evaluated by the IUCN Red List are now considered threatened (IUCN, 2024). While all amphibians are affected, some

are at greater risk, with clear taxonomic and geographic patterns emerging. The Neotropical region, in particular, harbors an exceptionally rich amphibian fauna (Bolanos *et al.*, 2008; Herrera‐Lopera *et al.*, 2025) and a disproportionately high number of threatened species (IUCN, 2024). Areas such as the Caribbean, Mesoamerica, the Andean region, the Coastal Atlantic Forest, the Amazon Basin, and the Guiana Shield are recognized as hotspots for vulnerable and endangered amphibians (Luedtke *et al.*, 2023).

Within amphibians, frogs (order Anura) are especially sensitive due to their physiological dependence on moist environments, high sensitivity to changes in temperature and precipitation, and strong habitat specificity for thermoregulation, reproduction, and survival (Wells, 2007). These traits make them particularly vulnerable to climate change and valuable as bioindicators of environmental disturbance. In this context, we investigate how future climatic scenarios may affect the temporal patterns of taxonomic, phylogenetic, and functional beta diversity of Neotropical frogs, with the goal of understanding whether climate change is likely to restructure frog communities in the region. We hypothesize a reduction in taxonomic, phylogenetic, and functional dimensions of diversity due to the range contraction of most species, with a clear predominance of the loss pattern over replacement. We also expect the different dimensions of diversity to respond unevenly to climate change, with stronger effects on functional and phylogenetic diversity, driven by the loss of functional traits and phylogenetic lineages, even in cases where taxonomic diversity remains unchanged.

Methods

Occurrence records

We focused on Neotropical frog species from the Bufonidae (toads) and Hylidae (treefrogs) families. These two families encompass a broad range of species, from endemic and endangered species, to widely distributed species of least concern. We acquired the occurrence data for all species from the Global Biodiversity Information Facility (GBIF: http://www.gbif.org). Initially, we obtained occurrence records for 1393 species, but these occurrences were filtered to eliminate the duplicates, impossible coordinates (latitude and longitude equal to 0), occurrences located within 2 km of country or capital centroids, and occurrences within 2 km of zoos or herbaria using the R package *CoordinateCleaner* (Zizka *et al.*, 2019). We applied an environmental filter to reduce sampling bias (Varela *et al.*, 2014; Castellanos *et al.*, 2019). To apply the environmental filter, we selected five bioclimatic variables (Bio 1, Bio 2, Bio 4, Bio 12, and Bio 15) from the WorldClim database v2.1 (Fick & Hijmans, 2017) at a 2.5 arc minute resolution, with lower values of Pearson correlation (<0.75) for the current scenario. We performed a Principal Component Analysis (PCA) and kept the first three axes, which together explained 80% of the climatic variation. Based on these axes, we filtered the occurrence data, removing records located within 2.5 arc-minute grid cells that showed redundant climatic conditions. Only species with a minimum of seven records were considered. After this filtering process, we retained 526 species in total, comprising 148 toads and 378 treefrogs.

Bioclimatic variables

We obtained bioclimatic variables from WorldClim v2.1 (Fick & Hijmans, 2017) at 2.5 arc-minute resolution for present (1970–2000) and 2050. To minimize collinearity among predictors, we calculated a Pearson correlation matrix and retained only variables with correlation values below 0.75. Future climate projections were based on three General Circulation Models (GCMs)—CCSM4, MPI-ESM-LR, and MIROC6—and we generated a weighted average across them. These models were selected due to their relatively low error rates and good performance in the Neotropical region (Cannon, 2020). Projections followed a single Shared Socioeconomic Pathway, SSP585, which represents a high-emission trajectory where reductions in CO_2 emissions occur only after 2080. This pessimistic pathway was adopted as it is widely used in biodiversity assessments, allowing comparability with previous studies.

Species traits

We collected ecological traits for each species using the Tetrapoda database (Moura *et al.*, 2024). The traits collected include body mass as a continuous variable, and activity time (diurnal, nocturnal), reproductive strategy (larval, direct), and microhabitat (terrestrial, arboreal, aquatic, fossorial) as a categorical variable (Supplementary Table S2). These traits were selected because they provide valuable information about the ecological role, life history, and interactions with the environment for amphibians (Cervantes-López *et al.*, 2025). We tested the correlation of categorical traits using the Goodman Kruskal measure. None of the variables showed significant correlations; therefore, all were included in the study. See Supplementary Table S2 to visualize the traits for each species.

Phylogenetic tree

We used the phylogenetic tree from (Portik *et al.*, 2023) to represent the phylogenetic relationships among species. This tree includes more than 5,000 anuran species and was pruned to retain only those evaluated in this study. To calculate the branch length for each species and subsequently use this information in the phylogenetic diversity calculations, we applied the 'phylo.pres' function from the *phyloraster* package (Alves‐Ferreira *et al.*, 2024).

Species distribution models

To delimit the calibration area, we generated a minimum convex polygon (MCP) encompassing all filtered occurrences and expanded it with a 1.5° buffer (~150 km² at the equator). Both the MCP and buffer were constructed in R using the *ENMwizard* R package (Heming et al., 2018), and models were calibrated using climate data from 1970-2000. To assess future distributional shifts under climate change, we used species distribution models (SDMs) that combined occurrence records with bioclimatic predictors, relying on the MaxEnt algorithm (version 3.4.1; (Phillips *et al.*, 2006, 2017) in the *ENMwizard* R package (Heming *et al.*, 2018).

To reduce overfitting, we explored a range of model parameterizations and assessed their performance using cross-validation. Initial models were tuned by adjusting Feature Classes (FCs) and Regularization Multipliers (RMs), which control variable transformations and model complexity, respectively. We tested FCs—linear (L), product (P), quadratic (Q), and hinge (H)—in combination with RM values from 0.5 to 4.5 (increments of 0.5). Model

evaluation followed the Block cross-validation approach, which partitions occurrence records into four geographically distinct subsets. Each subset was iteratively used for testing while the others were used for training.

We retained the top 10% of candidate models for each species, prioritizing those with the lowest omission rates (OR) and highest AUC scores, and generated a consensus model by averaging them (Boria *et al.*, 2017). These consensus models were projected across the Neotropical region for both current and future climates. Continuous suitability maps were then transformed into binary presence–absence predictions using a 10% threshold. This threshold was applied to exclude marginal occurrences in low-suitability areas and to minimize spatial biases and uncertainties linked to outlier records (Ahmadi *et al.*, 2020).

To reduce potential overprediction in SDMs, we applied dispersal-based spatial constraints to clip the binary maps for both present and future scenarios. These constraints were derived from IUCN range polygons (IUCN, 2023), with buffers reflecting the estimated dispersal capacity of each group (toads vs. treefrogs). For toads, we assumed a dispersal distance of 3,300 m per generation (Smith & Green, 2005). Considering an average generation time of 2.5 years (Oliveira *et al.*, 2017), this corresponds to ~20 generations between 2000 and 2050, resulting in a maximum potential spread of 66 km by mid-century. Consequently, current toad models were cropped with a 3.3 km buffer, while future projections used a 66 km buffer. For treefrogs, we used a buffer of 2.3 km for present conditions and 46 km (2,300 m × 20 generations) for 2050 (Smith & Green, 2005). The final presence–absence maps were clipped according to these dispersal-adjusted buffers.

Diversity metrics

We calculated beta diversity for three biodiversity facets (taxonomic - TD), phylogenetic - PD, and functional diversity - FD) for the present and for the year 2050 under both optimistic and pessimistic greenhouse gas emission scenarios using the function "temp.beta" from the *divraster* package (Mota *et al.*, 2023). We adopted a unified, tree-based framework in which TD, PD, and FD were computed in a standardized way, ensuring full comparability among facets (Cardoso *et al.*, 2014). For TD, we employed a tree in which all species had branch lengths of 1; for PD, we used a dated phylogenetic tree; and for FD, we constructed a dendrogram derived from a trait-based distance matrix. In all cases, diversity was represented as the sum of the branch lengths connecting the species within a community, reflecting their taxonomic, functional, or phylogenetic relationships (Faith, 1992; Petchey & Gaston, 2006).

To estimate temporal beta diversity (βt), we used the Jaccard dissimilarity index between each cell in the future and baseline scenarios. We partitioned beta diversity into replacement (ßrepl) and richness difference (ßrich) components (see (Cardoso *et al.*, 2014). The relative dominance of these components can be assessed using the ratio 'ßrepl / ßtotal'. Ratio values close to 1 represent the predominance of the replacement component and values close to 0 indicate predominance of the richness component. All temporal beta diversity metrics (i.e., ßtotal and ßratio across the three dimensions) vary between 0 and 1. All analyses were carried out in R v4.4.1 (R core team 2025).

Results

The model performance values obtained using the block cross-validation showed a good fit, with average values of 0.78 (SD = 0.09) for the Area Under the Curve and 0.08 (SD = 0.11) for the Omission Rate (Supplementary Table S3). Our projections suggest that by the year 2050, under a pessimistic climate scenario, over 42.2% of frog species may lose part of their ranges, 56.09% projected to gain range areas, and a small fraction facing complete range loss (1.71%, 9 species).

The projected losses and gains in species' potential distributions are expected to alter beta diversity patterns, with relatively low concordance among the three biodiversity facets (Figure 1). High values of total taxonomic beta diversity are predicted mainly for the Andes, Caribbean Islands, Brazil, northern and central Mexico, western Colombia, central Ecuador, Chile, and central to southern Argentina (Figure 1a). The richness and replacement components of taxonomic diversity show partial divergence across the Neotropics (Figure 1b, c). For example, large areas of Brazil and the Guiana Shield are projected to be dominated by species replacement, whereas a small area in northeast Brazil is dominated by the richness component. In contrast, the Andes are predicted to be primarily driven by the richness component (species gains or losses), a pattern also evident in southern Mexico, western Colombia, central Ecuador, Argentina, Chile, the Caribbean Islands, and Central America (Figure 1b, c; Figure 2a).

Patterns of phylogenetic beta diversity show some similarities with those of taxonomic beta diversity, but also display important deviations. For instance, many areas with total taxonomic beta diversity values close to 1 exhibit intermediate values for phylogenetic diversity, such as the Guiana Shield, northern Brazil, Venezuela, the Dominican Republic, and central Mexico (Figure 1d). The richness and replacement components also vary (Figure 1e, f). In phylogenetic beta diversity, the replacement component contributes slightly less compared to taxonomic beta diversity (Figure 1f; Figure 2b).

For functional beta diversity, the variation in patterns is even greater compared to the phylogenetic and taxonomic dimensions (Figure 1g–i; Figure 2c). Functional total beta diversity reaches its highest values in central and northeastern Brazil, the Andes, northern Mexico, Cuba, and northern Venezuela (Figure 1g). Most of the functional beta diversity is dominated by the richness component, especially in the Andes, central Brazil, southern Mexico, and Cuba (Figure 1h). The replacement component is far less prominent in this diversity dimension but still dominates small regions in central Brazil and northern Mexico (Figure 1i; Figure 2c).

Climate change is projected to drive increased biotic homogenization (i.e., lower values of total beta diversity) for both the phylogenetic and functional dimensions (Figure 1d,g). Regions projected to experience biotic homogenization in the phylogenetic dimension are concentrated in southern Mexico, Central America, northern Brazil, the Caribbean Islands, and the Guiana Shield. For the functional dimension, regions expected to undergo biotic homogenization include all areas mentioned above for the phylogenetic dimension, as well as additional regions such as Peru, Uruguay, southeastern Brazil, Venezuela, and eastern Colombia (Figure 1d,g).

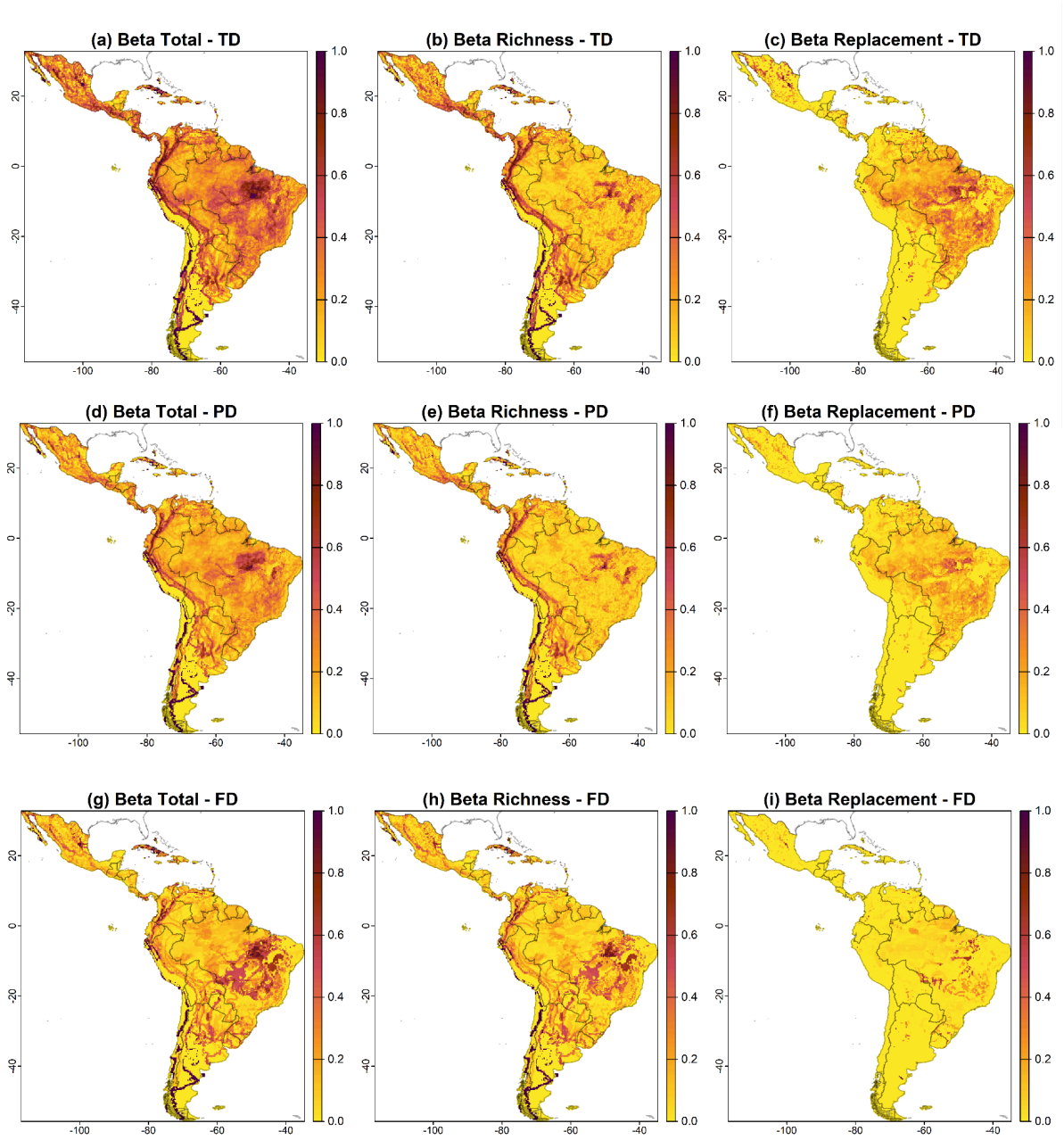

Fig. 1 Taxonomic (TD), Phylogenetic (PD), and Functional (FD) beta diversity of 497 Neotropical toads and treefrogs. (a) Total beta diversity (TD), (b) richness component of TD, (c) replacement component of TD, (d) total beta diversity (PD), (e) richness component of PD, (f) replacement component of PD, (g) total beta diversity (FD), (h) richness component of FD, and (i) replacement component of FD. Red and dark orange colors indicate regions with higher dissimilarity in species composition, evolutionary history, or functional traits, whereas light orange to yellow colors indicate lower levels of dissimilarity.

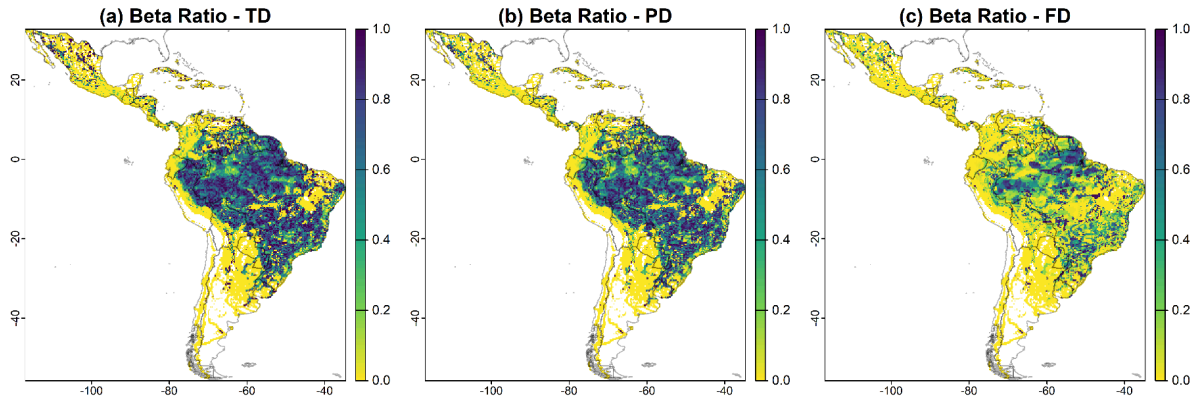

Fig. 2 Beta diversity ratio (βratio) for taxonomic (TD), phylogenetic (PD), and functional (FD) diversity of 497 Neotropical toads and treefrogs. The βratio expresses the relative contribution of species replacement versus richness difference to total beta diversity. Values close to 1 indicate that beta diversity is dominated by species replacement, whereas values close to 0 indicate that it is dominated by richness differences (species gains or losses). Intermediate values represent mixed contributions of both processes. Dark purple represent higher dominance of replacement, while green and yellow colors represent higher dominance of richness.

Discussion

Our study indicates that climate change is projected to cause severe changes in the distribution of Neotropical frogs, with more than 40% of species expected to experience range contractions, almost 2% are projected to lose their entire range, and 56.09% expected to gain range areas in the future. These changes in distribution are expected to alter species composition (e.g., beta diversity), impacting the three dimensions of diversity evaluated in this study (taxonomic, phylogenetic, and functional). However, each dimension is projected to respond in distinct ways, as we hypothesized. We showed that the phylogenetic and functional dimensions should present a higher biotic homogenization than the taxonomic dimension. We also showed that the richness component dominates the patterns of beta diversity across all three dimensions for most of the Neotropical region, indicating that changes in frog composition are more strongly driven by species gains and losses than by species replacement.

Climate change is projected to affect the distribution of frog species in the Neotropics, with more than 40% of the species projected to lose a part of their range area and almost 58% projected to gain range areas. The reduction in the potential distribution of amphibians in response to climate change found here is in agreement with previous studies conducted with amphibians in different regions of the globe (e.g. De Albuquerque et al., 2024; Vaissi & Mohammadi, 2024; Carné et al., 2025). For example, in the drylands of the southwestern United States and Mexico, 80% of amphibian species are expected to lose part of their ranges (De Albuquerque *et al.*, 2024). Similarly, 60% of frog species in Madagascar may suffer range contractions under climate change scenarios (Carné et al., 2025). This result was also observed for other taxonomic groups, such as birds (Mota *et al.*, 2022b; Ahmadi *et al.*, 2024), plants (Cahyaningsih *et al.*, 2021; Leão *et al.*, 2021; Suarez-Contento *et al.*, 2024), and

mammals (Hidasi-Neto *et al.*, 2019). The loss and gain of range area of each species can lead to a reorganization of frog communities in the future.

As climate change advances, species typically face three alternatives: dispersal to new areas, adaptation to changing conditions, or extinction (Souza *et al.*, 2023). Dispersal can modify existing diversity patterns by altering both species composition and local richness (Cadotte 2006). When the species establishes in a new optimal area, novel communities emerge, triggering new interactions and reshaping ecosystem structure. Our results indicate that Neotropical frog communities are projected to undergo substantial restructuring under future scenarios. Taxonomic beta diversity is expected to increase in regions such as the northern Andes, Caribbean Islands, Brazil, northern and central Mexico, western Colombia, central Ecuador, Chile, and central to southern Argentina, suggesting higher dissimilarity among communities.

For the taxonomic, functional and phylogenetic dimensions of diversity, the restructuring of the communities appears to be primarily driven by species losses and gains, rather than by direct replacement. The relative contributions of richness differences and replacement to total beta diversity can be influenced by multiple factors, including climate, biotic interactions, geological history, and anthropogenic disturbances (Melo *et al.*, 2009; Baselga, 2010; Dobrovolski *et al.*, 2012; Cardoso *et al.*, 2014). The relative importance of the beta diversity components may also vary across taxonomic groups. For instance, (Dobrovolski *et al.*, 2012) showed that amphibians tend to be more strongly influenced by the richness difference component compared to mammals and birds, largely due to their limited dispersal capacity, which constrains their ability to recolonize suitable habitats.

As expected, we found that the phylogenetic and functional dimensions are projected to exhibit greater biotic homogenization than the taxonomic dimension. This indicates that future communities may become more similar in terms of functional traits and show reduced phylogenetic variation, even if the species identities differ. The loss of specialist species may compromise key ecosystem services, impacting ecosystem structure and functioning (Rogers & McCarty, 2000). Amphibians, in particular, play critical ecological roles as both predators and prey, contributing to population regulation and nutrient cycling. The reduction in the ecological functions performed by these organisms can generate imbalances in the ecosystem, negatively impacting its overall integrity (Hopkins, 2007).

The higher levels of phylogenetic homogenization projected in our study suggest that, although species replacement is expected to occur in some parts of the Neotropics, such as Brazil and the Guiana Shield, future communities will increasingly share closely related lineages. This pattern may be explained by the broader environmental tolerance and persistence of more generalist species, while more restricted or evolutionarily ancient lineages are likely to be more vulnerable (Saladin *et al.*, 2020). For instance, species with long branch lengths are usually more vulnerable to climate change, such as *Dendropsophus stingi*, which is over 16 million years old and is projected to lose its entire range by 2050 (Alves-Ferreira *et al.*, 2025). The loss of such species can reduce the adaptive potential of communities, limiting their ability to respond to rapid future environmental changes (González-Orozco et al., 2016). Conserving species with unique evolutionary heritage is therefore crucial to safeguard this adaptive capacity under future non-analog climatic conditions (González-Orozco *et al.*, 2016).

Similarly, functional homogenization indicates that frog communities are likely to be dominated by species with overlapping ecological roles. In our study, the functional dimension showed the highest levels of biotic homogenization. The reduction of functionally unique species could impact critical ecosystem processes, such as nutrient cycling in aquatic systems and the regulation of prey populations, because these species often occupy irreplaceable functional roles (Petchey & Gaston, 2002; Clavel *et al.*, 2011). Ecosystems dominated by redundant traits may be less capable of buffering against novel disturbances, thereby increasing their vulnerability under accelerating global change (Mariano-Neto & Santos, 2023). According to our results, more attention should be focused on the Amazon, Atlantic Forest, Andes, and Central America, as these regions are projected to experience the highest levels of functional homogenization. Some of these regions, such as the Amazon and Atlantic Forest, already undergo high levels of land conversion, suggesting that homogenization will be particularly pronounced where anthropogenic activities have already taken place, with potential consequences for both ecosystem functioning and local climate (Hidasi-Neto *et al.*, 2019).

Together, these findings underscore that taxonomic, phylogenetic, and functional dimensions of beta diversity respond in complementary but non-congruent ways to climate change (Hidasi-Neto *et al.*, 2019; Xu *et al.*, 2023). Evaluating only taxonomic patterns would overlook important aspects of evolutionary history and ecosystem functioning (Faith, 1992; Mishler *et al.*, 2014; Alves-Ferreira *et al.*, 2025). From a conservation perspective, regions of high beta diversity, particularly the northern Andes, Caribbean Islands, and central Brazil, emerge as critical areas where the conservation of evolutionary lineages and ecological functions must be prioritized. Ultimately, safeguarding the Neotropical frog communities will require integrative strategies that explicitly consider multiple facets of biodiversity in the face of ongoing global change.

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Supplementary material

Table S1. List of ecological traits used to calculate the functional diversity.

Trait type	Ecological trait	Value	Funcional meaning
Numerical	Body length	Snout vent length, millimeters	Linked to nutrient cycling and the transfer of energy through trophic networks, in which the organism can act as either predator or prey.
Categorical	Activity time	Diurnal; nocturnal	Related to the range of prey and predators interacting with the species. It also reflects the dynamics of matter balance and energy flux across time.
Categorical	Microhabitat	Fossorial; terrestrial; aquatic; arboreal	Related to the diversity of resources accessible to species within their environment, while also playing a role in nutrient cycling and the movement of energy through trophic chains where species act as consumers or prey.
Categorical	Reproductive strategy	Larval or direct development	Refers to the balance of energy allocation for reproduction and its role in sustaining energy transfer within food webs, both as predator and as prey.

Table S2. List of species and their respective traits.

Species	Body Length (mm)	Activity Time	Microhabitat	Reproductive strategy	Source
Amazophrynella minuta	21	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus boreas	130	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus californicus	72	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus cognatus	114	Diurnal	Fossorial	Larvae	Moura et al., 2024

Anaxyrus compactilis	91	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus debilis	45.3	Nocturnal	Fossorial	Larvae	Moura et al., 2024
Anaxyrus kelloggi	48.8	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus mexicanus	70	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus punctatus	76	Nocturnal	Fossorial	Larvae	Moura et al., 2024
Anaxyrus retiformis	60	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Anaxyrus speciosus	92	Diurnal	Fossorial	Larvae	Moura et al., 2024
Anaxyrus woodhousii	127	Nocturnal	Fossorial	Larvae	Moura et al., 2024
Aplastodiscus albofrenatus	80	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus albosignatus	39.9	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus arildae	36.14	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus cavicola	46	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus cochranae	50.3	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus ehrhardti	45	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus leucopygius	45.1	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus perviridis	39.66	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Aplastodiscus weygoldti	41.7	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Atelopus barbotini	34.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus bomolochos	50.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus carrikeri	62.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus chiriquiensis	58	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus coynei	32	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus cruciger	50	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus ebenoides	48	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus elegans	35.7	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus exiguus	35.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus flavescens	40	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus franciscus	26.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus hoogmoedi	41.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus ignescens	48.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus laetissimus	57.43	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus limosus	40.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus longirostris	47.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus mindoensis	29	Diurnal	Terrestrial	Larvae	Moura et al., 2024

Atelopus muisca	42.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus nanay	39.6	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus nepiozomus	32.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus palmatus	31.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus pastuso	50.7	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus peruensis	45.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus podocarpus	52.9	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus pulcher	35.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus senex	43	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus sernai	33.3	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus spumarius	34	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus spurrelli	34	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus subornatus	39	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus varius	60	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus walkeri	49.3	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atelopus zeteki	63	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Atlantihyla spinipollex	46	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Boana albomarginata	53	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana albopunctata	63	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana alfaroi	36.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana almendarizae	44.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana atlantica	43.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana bandeirantes	31.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana bischoffi	52	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana boans	99.54	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Boana caingua	33.44	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana calcarata	58	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana callipleura	51.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana cinerascens	43	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana cordobae	61.8	Diurnal	Aquatic	Larvae	Moura et al., 2024
Boana crepitans	60.33	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana curupi	48.46	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana dentei	54	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana faber	98.9	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Boana fasciata	51.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana geographica	56.41	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana heilprini	54.3	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Boana joaquini	49	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana lanciformis	83.87	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana lemai	40	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana leptolineata	39	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana lundii	71	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana maculateralis	53	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana marginata	48.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana microderma	34	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana multifasciata	48.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana nympha	34.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana ornatissima	42	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana pardalis	61.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana pellucens	61.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana picturata	69.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Boana polytaenia	27	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana prasina	47.6	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana pugnax	75.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana pulchella	44.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana punctata	39.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana raniceps	73.6	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana riojana	62.7	Diurnal	Arboreal	Larvae	Moura et al., 2024
Boana rosenbergi	95	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana rubracyla	59	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana rufitela	55	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana semiguttata	48	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana semilineata	48.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana sibleszi	35.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana steinbachi	36.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Boana wavrini	113	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Boana xerophylla	57	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Bokermannohyla alvarengai	126.63	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Bokermannohyla caramaschii	70	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Bokermannohyla circumdata	61.29	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Bokermannohyla hylax	65.38	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Bokermannohyla ibitiguara	48.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Bokermannohyla luctuosa	61.9	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Bokermannohyla sapiranga	57.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Bromeliohyla bromeliacia	35.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Bromeliohyla dendroscarta	34.6	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Charadrahyla altipotens	80.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Charadrahyla chaneque	79.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Charadrahyla nephila	81	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Charadrahyla taeniopus	70	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Corythomantis greeningi	86.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendrophryniscus berthalutzae	24	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendrophryniscus brevipollicatus	22.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus acreanus	41.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus anceps	42	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Dendropsophus berthalutzae	24	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus bifurcus	35	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus bipunctatus	27.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus bogerti	33.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus bokermanni	28	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus branneri	23.6	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus brevifrons	22	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus carnifex	32.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus columbianus	35.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus cruzi	19.85	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus decipiens	21	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus ebraccatus	37	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus elegans	22	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus elianeae	24	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus gaucheri	19.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus giesleri	35.9	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus gryllatus	30.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Dendropsophus haddadi	27	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus haraldschultzi	25	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus jimi	23	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus joannae	20.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus koechlini	29	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus labialis	61	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus leali	28	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus leucophyllatus	50	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus luddeckei	50	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus luteoocellatus	31	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus manonegra	32.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus marmoratus	56	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus mathiassoni	21.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus melanargyreus	50	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus meridensis	50	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus microcephalus	32	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus microps	27.6	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Dendropsophus minusculus	19.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus minutus	27.64	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus miyatai	25	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus nanus	23.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus norandinus	35.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus oliveirai	34	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus padreluna	34.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus parviceps	27	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus pauiniensis	24	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus phlebodes	28	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus praestans	31.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus pseudomeridianus	22.7	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus rhodopeplus	30	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Dendropsophus riveroi	27	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus robertmertensi	28.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus rossalleni	23	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Dendropsophus rubicundulus	19.25	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Dendropsophus ruschii	29	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus sanborni	17.47	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus sarayacuensis	33.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus sartori	28.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus schubarti	25.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus seniculus	43	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus shiwiarum	18.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus soaresi	33	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dendropsophus stingi	26.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus subocularis	26.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus timbeba	26.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus triangulum	33.35	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus tritaeniatus	22	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus virolinensis	34	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus walfordi	20	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dendropsophus werneri	22.02	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Dryaderces pearsoni	54.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Dryophytes arenicolor	57.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes cinereus	66	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes euphorbiaceus	43.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes eximius	37.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes plicatus	47.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes squirellus	45	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes walkeri	37.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Dryophytes wrightorum	48	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla chamulae	31.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla ignicolor	32.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla rufioculis	40	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla salvavida	37	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla schmidtorum	38.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla soralia	37.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Duellmanohyla uranochroa	40	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Ecnomiohyla miliaria	113	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Exerodonta bivocata	29.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Exerodonta catracha	32.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Exerodonta chimalapa	26.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Exerodonta melanomma	31.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Exerodonta smaragdina	28.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Exerodonta sumichrasti	33.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Exerodonta xera	35	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus alytolylax	44	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus antioquia	63.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Hyloscirtus armatus	72	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus bogotensis	57.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus callipeza	33	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus colymba	43.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus criptico	72	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Hyloscirtus denticulentus	52.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus larinopygion	47.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus palmeri	50	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus phyllognathus	37.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Hyloscirtus platydactylus	42.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus psarolaimus	63.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Hyloscirtus tigrinus	63.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius alvarius	165	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius aucoinae	104.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius bocourti	64.85	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius campbelli	90	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius canaliferus	52	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius cavifrons	88.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius coccifer	99	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius coniferus	95	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius cristatus	75	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius gemmifer	99.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius ibarrai	94	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius leucomyos	96	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius luetkenii	107	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius macrocristatus	75	Diurnal	Terrestrial	Larvae	Moura et al., 2024

Incilius marmoreus	70	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius mazatlanensis	86	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius mccoyi	86.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius melanochlorus	106.7	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius nebulifer	125	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Incilius occidentalis	74	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius perplexus	66	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius porteri	76	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius spiculatus	102.7	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius tacanensis	53	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius tutelarius	103.6	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Incilius valliceps	82.9	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla angustilineata	37	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla debilis	32	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla lancasteri	41.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla picadoi	35.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla pictipes	45.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Isthmohyla pseudopuma	52	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla rivularis	43	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla tica	43	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Isthmohyla zeteki	35.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Itapotihyla langsdorffii	97.52	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Lysapsus bolivianus	21	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Lysapsus laevis	21	Nocturnal	Fossorial	Larvae	Moura et al., 2024
Lysapsus limellum	20.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Megastomatohyla mixe	33.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Megastomatohyla mixomaculata	36.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Megastomatohyla nubicola	37.3	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus atroluteus	22.63	Diurnal	Fossorial	Larvae	Moura et al., 2024
Melanophryniscus klappenbachi	31.9	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus macrogranulosus	37	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus montevidensis	29	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus moreirae	30	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus pachyrhynus	33.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024

Melanophryniscus rubriventris	45	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus simplex	29.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus stelzneri	28.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Melanophryniscus tumifrons	29.9	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Myersiohyla chamaeleo	56.9	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Nannophryne cophotis	55	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Nannophryne variegata	35	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Nesorohyla kanaima	49.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Nyctimantis rugiceps	67.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Oreophrynella macconnelli	22.2	Nocturnal	Terrestrial	Direct	Moura et al., 2024
Osornophryne antisana	21.5	Nocturnal	Terrestrial	Direct	Moura et al., 2024
Osornophryne bufoniformis	30	Nocturnal	Terrestrial	Direct	Moura et al., 2024
Osornophryne guacamayo	25.7	Nocturnal	Terrestrial	Direct	Moura et al., 2024
Osornophryne occidentalis	36	Nocturnal	Terrestrial	Direct	Moura et al., 2024
Osornophryne percrassa	21.3	Nocturnal	Terrestrial	Direct	Moura et al., 2024
Osteocephalus alboguttatus	65	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus buckleyi	68.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Osteocephalus cabrerai	60	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus cannatellai	70.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus carri	64.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus castaneicola	57.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus deridens	76	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus festae	84.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus fuscifacies	53.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus helenae	43.88	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus leprieurii	58.35	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus mimeticus	82.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus mutabor	75.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus oophagus	62.7	Diurnal	Aquatic	Larvae	Moura et al., 2024
Osteocephalus planiceps	79.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus subtilis	51.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus taurinus	90.33	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus verruciger	73	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteocephalus vilarsi	62.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Osteocephalus yasuni	65	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteopilus dominicensis	46.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteopilus marianae	40	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteopilus ocellatus	76	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Osteopilus pulchrilineatus	43	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteopilus septentrionalis	66	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteopilus vastus	142	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Osteopilus wilderi	29	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Peltophryne empusa	76	Nocturnal	Fossorial	Larvae	Moura et al., 2024
Peltophryne fustiger	198	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Peltophryne guentheri	101	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Peltophryne longinasus	35	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Peltophryne peltocephala	170	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Peltophryne taladai	147	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Phyllodytes edelmoi	28.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Phyllodytes luteolus	26	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Plectrohyla acanthodes	63.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024

Plectrohyla avia	90.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla glandulosa	50	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla guatemalensis	76.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla hartwegi	77	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla ixil	47	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla lacertosa	72.3	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla matudai	49	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla pokomchi	55.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla quecchi	47	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Plectrohyla sagorum	52	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Pseudacris cadaverina	51	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Pseudacris clarkii	32	Diurnal	Fossorial	Larvae	Moura et al., 2024
Pseudacris crucifer	37	Diurnal	Fossorial	Larvae	Moura et al., 2024
Pseudacris hypochondriaca	50	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Pseudis bolbodactyla	58	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Pseudis cardosoi	56	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Pseudis minuta	51.1	Nocturnal	Aquatic	Larvae	Moura et al., 2024

Pseudis paradoxa	75	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Pseudis platensis	57.35	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Ptychohyla euthysanota	53.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Ptychohyla hypomykter	44	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Ptychohyla leonhardschultzei	43.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Ptychohyla macrotympanum	44.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Ptychohyla zophodes	43	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Quilticohyla acrochorda	57.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo blombergi	250	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo caeruleostictus	92.3	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo ecuadorensis	156.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo glaberrimus	44.83	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo guttatus	99.12	Diurnal	Fossorial	Larvae	Moura et al., 2024
Rhaebo haematiticus	62	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo hypomelas	72.1	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhaebo nasicus	67	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella achavali	119	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Rhinella acutirostris	35.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella alata	50.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella arenarum	115.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella arunco	135	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella bergi	43	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella castaneotica	49.11	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella centralis	61.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella crucifer	68.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella dapsilis	81	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella diptycha	184.83	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella dorbignyi	68.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella festae	40.5	Diurnal	Terrestrial	Direct	Moura et al., 2024
Rhinella granulosa	64.47	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella henseli	78.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella hoogmoedi	63.94	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella humboldti	63.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella icterica	149.6	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Rhinella limensis	80	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella macrorhina	51	Diurnal	Terrestrial	Direct	Moura et al., 2024
Rhinella major	51.28	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella margaritifera	74.17	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella marina	99.47	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella merianae	77.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella mirandaribeiroi	58	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella nicefori	34	Diurnal	Terrestrial	Direct	Moura et al., 2024
Rhinella ocellata	53	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella ornata	57.23	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella poeppigii	220	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella proboscidea	50.63	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella pygmaea	49.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella roqueana	81	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella rubescens	112.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella ruizi	50.3	Diurnal	Terrestrial	Direct	Moura et al., 2024
Rhinella scitula	50.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Rhinella spinulosa	100	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella stanlaii	59.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella sternosignata	49	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Rhinella veraguensis	63.7	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sarcohyla arborescandens	51.6	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sarcohyla bistincta	67.6	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sarcohyla celata	56.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sarcohyla charadricola	50.9	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sarcohyla cyclada	39.5	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sarcohyla pentheter	56.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Scarthyla goinorum	23	Diurnal	Aquatic	Larvae	Moura et al., 2024
Scarthyla vigilans	21	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Scinax acuminatus	48	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax agilis	19.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax altae	40	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax alter	31.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax arduous	24.5	Diurnal	Arboreal	Larvae	Moura et al., 2024

Scinax argyreornatus	23	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax auratus	18.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax blairi	32.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax boesemani	40	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax boulengeri	53	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Scinax caldarum	35	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax cardosoi	34.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax catharinae	33	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax crospedospilus	37.6	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax cruentomma	27.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax curicica	31.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax cuspidatus	32.5	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax duartei	37	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax elaeochroa	40.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax eurydice	53.95	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax flavoguttatus	45.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax funereus	39.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Scinax fuscomarginatus	21.89	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax fuscovarius	47.6	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax garbei	49.1	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax granulatus	45	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax hayii	39.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax ictericus	36.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax imbegue	38	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax jolyi	43.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax kennedyi	37.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax littoralis	39.9	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax longilineus	48	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax luizotavioi	30	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax nasicus	29.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax nebulosus	23.8	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax obtriangulatus	39	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax oreites	39.3	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax pachycrus	25.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024

Scinax pedromedinae	31.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax perereca	36.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax perpusillus	25	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax proboscideus	46	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax quinquefasciatus	30	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Scinax rizibilis	34	Diurnal	Arboreal	Larvae	Moura et al., 2024
Scinax rostratus	52.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax ruber	42.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax similis	36.4	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax squalirostris	20.89	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax staufferi	32	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Scinax strigilatus	38.3	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax sugillatus	45.4	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Scinax trapicheiroi	27.54	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax tymbamirim	31.2	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax uruguayus	25.8	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Scinax wandae	26.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Smilisca baudinii	60	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Smilisca cyanosticta	70	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Smilisca dentata	65.5	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Smilisca fodiens	70	Diurnal	Fossorial	Larvae	Moura et al., 2024
Smilisca phaeota	81	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Smilisca puma	46	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Smilisca sila	62.2	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Smilisca sordida	36.38	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Sphaenorhynchus caramaschii	23.09	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Sphaenorhynchus carneus	16	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Sphaenorhynchus dorisae	37.82	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Sphaenorhynchus lacteus	48	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Sphaenorhynchus planicola	27.9	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Sphaenorhynchus platycephalus	33	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Sphaenorhynchus prasinus	31	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Sphaenorhynchus surdus	28	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Tepuihyla exophthalma	32.7	Nocturnal	Terrestrial	Larvae	Moura et al., 2024

Tepuihyla tuberculosa	90	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Tlalocohyla godmani	45	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Tlalocohyla loquax	77	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Tlalocohyla picta	31	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Tlalocohyla smithii	30.9	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Trachycephalus coriaceus	169	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Trachycephalus cunauaru	70.78	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Trachycephalus hadroceps	53.9	Nocturnal	Aquatic	Larvae	Moura et al., 2024
Trachycephalus imitatrix	78	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Trachycephalus jordani	75.4	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Trachycephalus mesophaeus	73.11	Diurnal	Arboreal	Larvae	Moura et al., 2024
Trachycephalus nigromaculatus	91.1	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Trachycephalus resinifictrix	88	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Trachycephalus venulosus	86	Nocturnal	Arboreal	Larvae	Moura et al., 2024
Triprion petasatus	75.2	Diurnal	Terrestrial	Larvae	Moura et al., 2024
Triprion spatulatus	113	Nocturnal	Terrestrial	Larvae	Moura et al., 2024
Triprion spinosus	80	Diurnal	Terrestrial	Larvae	Moura et al., 2024

Table S3. Evaluation metrics and occurrences numbers calculated from the 135 models of each species.

Species	Average AICc	Average Delta AICc	Average OR	Average AUC	Occurrences
Amazophrynella minuta	1982.686	21.855	0.08	0.645	91
Amazophrynella siona	1522.59	4.609	0.198	0.679	109
Anaxyrus boreas	7451.978	484.576	0	0.905	8239
Anaxyrus californicus	2016.36	61.721	0.006	0.842	237
Anaxyrus cognatus	15143.709	429.199	0	0.837	1961
Anaxyrus compactilis	4615.642	110.676	0.021	0.833	234
Anaxyrus debilis	9923.204	25.38	0.075	0.608	644
Anaxyrus kelloggi	897.911	6.292	0.096	0.643	60
Anaxyrus mexicanus	515.782	3.8	0.063	0.808	39
Anaxyrus punctatus	50322.543	173.691	0.006	0.706	3564
Anaxyrus retiformis	1347.291	26.654	0.039	0.824	83
Anaxyrus speciosus	24735.915	546.951	0.002	0.736	1377
Anaxyrus woodhousii	13442.998	64.149	0.013	0.712	4707
Aplastodiscus albofrenatus	135.508	8.706	0.083	0.86	16
Aplastodiscus albosignatus	484.389	4.6	0.107	0.777	36
Aplastodiscus arildae	385.321	1.927	0	0.878	37
Aplastodiscus cavicola	146.833	6.308	0.069	0.799	12
Aplastodiscus cochranae	80.192	25.241	0.5	0.865	8
Aplastodiscus ehrhardti	297.841	1.632	0	0.802	27

Aplastodiscus leucopygius	358.464	3.016	0.036	0.882	66
Aplastodiscus lutzorum	52.08	17.662	0.25	0.902	7
Aplastodiscus perviridis	707.387	13.523	0.032	0.73	82
Aplastodiscus weygoldti	118.021	26.916	0.167	0.922	7
Atelopus barbotini	356.737	3.951	0.214	0.718	32
Atelopus bomolochos	401.154	4.896	0.156	0.637	35
Atelopus carrikeri	84.776	1.351	0.125	0.528	13
Atelopus chiriquiensis	227.396	6.267	0.143	0.737	22
Atelopus coynei	688.361	86.6	0.006	0.825	54
Atelopus cruciger	274.836	9.386	0.063	0.886	30
Atelopus ebenoides	111.26	33.759	0.25	0.785	9
Atelopus elegans	370.868	2.652	0.014	0.715	32
Atelopus exiguus	116.401	5.626	0	0.607	26
Atelopus flavescens	507.866	1.736	0.125	0.875	144
Atelopus franciscus	497.502	5.262	0.1	0.594	40
Atelopus hoogmoedi	1754.812	31.39	0.023	0.768	97
Atelopus ignescens	1315.708	3.924	0.012	0.937	138
Atelopus laetissimus	19.224	9.447	0.25	0.834	8
Atelopus limosus	88.456	39.73	0.036	0.931	12
Atelopus longirostris	304.605	50.869	0.014	0.773	74
Atelopus manauensis	255.159	8.641	0.094	0.847	37
Atelopus mindoensis	151.639	4.93	0.152	0.886	16

Atelopus muisca	64.531	18.389	0.188	0.72	11
Atelopus nanay	153.838	4.185	0	0.587	33
Atelopus nepiozomus	96.13	7.99	0.2	0.748	7
Atelopus palmatus	121.878	15.959	0	0.814	15
Atelopus pastuso	128.364	2.997	0	0.575	20
Atelopus peruensis	77.368	5.403	0.475	0.804	11
Atelopus podocarpus	49.697	2.108	0.25	0.76	8
Atelopus pulcher	330.793	2.894	0.113	0.895	25
Atelopus senex	130.221	10.185	0.25	0.814	20
Atelopus sernai	92.261	15.245	0.2	0.949	7
Atelopus spumarius	1180.359	25.918	0.018	0.822	60
Atelopus spurrelli	289.956	3.844	0.104	0.71	29
Atelopus subornatus	55.869	0.189	0	0.754	11
Atelopus varius	616.496	25.817	0.032	0.813	54
Atelopus walkeri	62.488	18.752	0.107	0.941	13
Atelopus zeteki	100.949	7.851	0.167	0.921	18
Atlantihyla spinipollex	346.558	1.893	0.05	0.885	25
Boana albomarginata	1739.911	48.887	0.077	0.802	373
Boana albopunctata	1681.738	29.601	0.099	0.71	227
Boana alfaroi	1449.118	8.314	0	0.733	91
Boana almendarizae	2027.257	47.368	0.05	0.847	126
Boana appendiculata	3079.086	109.179	0.022	0.768	194
Boana atlantica	286.135	7.603	0.063	0.917	17

Boana bandeirantes	83.749	21.584	0.375	0.753	12
Boana bischoffi	879.672	11.211	0.021	0.741	201
Boana boans	18877.563	452.384	0.003	0.77	739
Boana caingua	373.955	4.343	0	0.561	30
Boana calcarata	5841.286	198.525	0.021	0.731	280
Boana callipleura	258.891	0.759	0.089	0.738	19
Boana cinerascens	2080.489	5.78	0.012	0.67	492
Boana cordobae	349.045	3.427	0.042	0.93	113
Boana courtoisae	442.698	6.82	0.063	0.88	37
Boana crepitans	12380.497	208.078	0.015	0.712	503
Boana curupi	194.474	2.602	0.167	0.724	18
Boana dentei	327.239	2.589	0.043	0.901	61
Boana diabolica	121.681	0	0.25	0.841	17
Boana faber	2758.841	7.665	0	0.908	721
Boana fasciata	4555.519	85.529	0.004	0.703	209
Boana geographica	9451.871	182.166	0.024	0.765	397
Boana heilprini	648.92	5.49	0.169	0.704	61
Boana joaquini	158.577	6.985	0.25	0.752	18
Boana lanciformis	2632.093	70.818	0.01	0.605	682
Boana lemai	75.875	5.011	0.75	0.55	10
Boana leptolineata	332.71	5.674	0.093	0.809	39
Boana lundii	744.96	1.998	0	0.762	82
Boana maculateralis	1209.147	20.317	0	0.822	59

Boana marginata	399.885	4.601	0	0.755	25
Boana microderma	176.946	10.727	0.125	0.816	15
Boana multifasciata	2786.102	21.652	0.015	0.833	140
Boana nigra	264.096	5.453	0.012	0.748	27
Boana nympha	377.781	16.111	0.063	0.741	68
Boana ornatissima	453.11	5.478	0.083	0.852	30
Boana pardalis	1698.715	29.536	0	0.844	94
Boana pellucens	742.124	7.276	0.025	0.838	243
Boana picturata	552.221	6.98	0.036	0.839	183
Boana platanera	12869.106	215.787	0.005	0.625	615
Boana polytaenia	1466.86	11.636	0.013	0.954	82
Boana prasina	543.612	7.939	0.016	0.851	86
Boana pugnax	10874.787	283.363	0.002	0.772	557
Boana pulchella	19142.941	261.57	0.001	0.898	916
Boana punctata	13179.523	380.746	0.004	0.764	523
Boana raniceps	2904.795	14.501	0.018	0.708	545
Boana riojana	1032.993	45.272	0.015	0.772	193
Boana rosenbergi	1217.97	17.739	0.033	0.743	583
Boana rubracyla	334.583	4.143	0.143	0.831	32
Boana rufitela	4130.95	52.504	0	0.786	250
Boana semiguttata	222.714	5.536	0.25	0.584	18
Boana semilineata	1170.154	16.838	0	0.883	219
Boana sibleszi	155.882	3.355	0	0.779	15

Boana steinbachi	533.468	52.021	0.031	0.817	35
Boana ventrimaculata	470.314	9.05	0.031	0.637	36
Boana wavrini	657.341	7.453	0.036	0.776	68
Boana xerophylla	7260.508	91.148	0	0.633	334
Bokermannohyla alvarengai	207.478	3.155	0.063	0.706	22
Bokermannohyla caramaschii	315.043	13.965	0	0.878	27
Bokermannohyla circumdata	635.18	7.191	0.031	0.923	81
Bokermannohyla hylax	300.246	7.828	0.063	0.827	79
Bokermannohyla ibitiguara	74.42	9.042	0	0.892	9
Bokermannohyla luctuosa	369.737	9.328	0	0.846	29
Bokermannohyla sapiranga	159.848	0.876	0.25	0.628	14
Bromeliohyla bromeliacia	286.721	12.409	0.063	0.917	43
Bromeliohyla dendroscarta	310.86	2.086	0.063	0.614	30
Charadrahyla altipotens	65.113	4.506	0.071	0.936	9
Charadrahyla chaneque	519.973	19.501	0	0.577	25
Charadrahyla nephila	432.16	26.154	0.042	0.802	46
Charadrahyla taeniopus	548.328	9.603	0.022	0.885	121
Corythomantis greeningi	584.322	10.375	0.031	0.851	36
Dendrophryniscus berthalutzae	90.746	4.206	0	0.889	12

Dendrophryniscus brevipollicatus	559.603	4.626	0.024	0.857	40
Dendrophryniscus haddadi	79.345	0.824	0.25	0.72	10
Dendropsophus acreanus	344.41	6.626	0	0.629	32
Dendropsophus anceps	530.254	6.019	0.188	0.861	33
Dendropsophus arndti	94.272	6.704	0	0.979	24
Dendropsophus berthalutzae	599.728	15.36	0	0.873	42
Dendropsophus bifurcus	924.107	16.772	0.021	0.898	301
Dendropsophus bipunctatus	642.105	11.208	0	0.887	61
Dendropsophus bogerti	1226.321	2.02	0	0.926	232
Dendropsophus bokermanni	505.052	3.534	0.167	0.766	67
Dendropsophus branneri	872.036	19.3	0	0.941	76
Dendropsophus brevifrons	873.447	12.034	0.138	0.708	119
Dendropsophus carnifex	320.839	6.154	0.036	0.955	139
Dendropsophus columbianus	1922.669	81.014	0.009	0.809	283
Dendropsophus counani	45.815	6.406	0.25	0.942	7
Dendropsophus cruzi	201.631	6.072	0.125	0.809	11
Dendropsophus decipiens	611.655	11.624	0.036	0.89	49
Dendropsophus ebraccatus	3989.269	24.886	0	0.792	699
Dendropsophus elegans	2010.731	29.498	0.043	0.769	266

Dendropsophus elianeae	838.343	6.979	0.091	0.803	42
Dendropsophus gaucheri	65.927	0.329	0.464	0.933	7
Dendropsophus giesleri	258.634	7.473	0.125	0.825	18
Dendropsophus gryllatus	NA	NA	0.333	0.992	10
Dendropsophus haddadi	447.311	43.622	0.031	0.837	25
Dendropsophus haraldschultzi	173.001	4.875	0.083	0.939	24
Dendropsophus jimi	376.646	8.445	0.042	0.748	19
Dendropsophus joannae	122.509	3.925	0.25	0.875	12
Dendropsophus kamagarini	491.256	26.728	0	0.798	34
Dendropsophus koechlini	204.065	21.247	0.19	0.906	19
Dendropsophus labialis	1117.246	68.042	0.011	0.92	68
Dendropsophus leali	659.643	1.913	0	0.619	61
Dendropsophus leucophyllatus	2622.686	12.68	0.001	0.715	243
Dendropsophus luddeckei	261.024	12.825	0.068	0.941	23
Dendropsophus luteoocellatus	72.808	10.739	0	0.883	7
Dendropsophus manonegra	163.06	4.265	0.111	0.874	17
Dendropsophus marmoratus	1520.93	10.113	0.031	0.678	221
Dendropsophus mathiassoni	1456.438	4.917	0.028	0.756	225
Dendropsophus melanargyreus	704.406	4.106	0	0.693	74

Dendropsophus meridensis	210.702	85.059	0.125	0.881	10
Dendropsophus microcephalus	26762.418	740.625	0	0.784	1125
Dendropsophus microps	806.694	8.683	0	0.852	101
Dendropsophus minusculus	303.384	2.559	0.071	0.768	35
Dendropsophus minutus	8031.84	92.595	0.003	0.739	861
Dendropsophus miyatai	172.193	2.636	0.25	0.572	27
Dendropsophus molitor	6052.614	146.436	0	0.913	440
Dendropsophus nanus	4394.032	51.484	0.017	0.755	402
Dendropsophus norandinus	126.334	0.83	0.143	0.794	16
Dendropsophus oliveirai	510.014	54.836	0	0.556	24
Dendropsophus padreluna	231.196	6.139	0	0.799	23
Dendropsophus parviceps	1721.91	21.201	0.046	0.762	317
Dendropsophus pauiniensis	320.218	27.536	0	0.838	23
Dendropsophus phlebodes	1093.891	4.341	0.142	0.703	141
Dendropsophus praestans	NA	NA	0.667	0.675	8
Dendropsophus pseudomeridianus	87.976	7.651	0.05	0.801	14
Dendropsophus reticulatus	2320.149	32.039	0.061	0.818	132
Dendropsophus rhodopeplus	1849.65	27.264	0.038	0.651	300
Dendropsophus riveroi	366.976	0.663	0.063	0.581	32

Dendropsophus robertmertensi	1101.111	4.895	0.033	0.812	98
Dendropsophus rossalleni	316.27	7.844	0.25	0.706	16
Dendropsophus rubicundulus	771.628	6.337	0	0.594	54
Dendropsophus ruschii	25.015	4.91	0.25	0.995	7
Dendropsophus sanborni	1968.94	7.691	0.057	0.712	192
Dendropsophus sarayacuensis	1443.451	22.624	0.047	0.719	263
Dendropsophus sartori	350.538	4.422	0.093	0.851	36
Dendropsophus schubarti	234.401	8.462	0.125	0.85	23
Dendropsophus seniculus	452.223	3.893	0	0.815	50
Dendropsophus shiwiarum	348.428	2.55	0	0.693	30
Dendropsophus soaresi	88.001	0.625	0.25	0.867	12
Dendropsophus stingi	108.26	2.946	0.333	0.635	10
Dendropsophus subocularis	445.861	8.304	0.03	0.725	31
Dendropsophus timbeba	124.722	2.8	0.25	0.897	11
Dendropsophus triangulum	1602.773	8.691	0.024	0.71	163
Dendropsophus tritaeniatus	97.027	15.841	0.5	0.795	7
Dendropsophus virolinensis	301.118	7.018	0.071	0.822	28
Dendropsophus walfordi	1301.57	137.487	0.054	0.78	63
Dendropsophus werneri	441.39	1.979	0.125	0.837	68

Dryaderces pearsoni	101.059	0.524	0.125	0.847	11
Dryophytes arenicolor	51245.692	2496.132	0.003	0.706	3122
Dryophytes cinereus	120399.567	2188.711	0.023	0.731	8222
Dryophytes euphorbiaceus	1641.608	14.697	0.01	0.845	111
Dryophytes eximius	29592.949	210.078	0	0.794	1474
Dryophytes plicatus	4055.881	69.591	0.004	0.843	269
Dryophytes squirellus	76199.961	378.739	0	0.795	4982
Dryophytes walkeri	1220.381	88.772	0	0.923	76
Dryophytes wrightorum	1820.161	17.19	0	0.895	167
Duellmanohyla chamulae	343.979	6.487	0.049	0.863	28
Duellmanohyla ignicolor	530.899	6.691	0	0.802	23
Duellmanohyla rufioculis	585.946	32.91	0.095	0.795	132
Duellmanohyla salvavida	NA	NA	0.333	0.684	7
Duellmanohyla schmidtorum	549.156	3.483	0.071	0.751	52
Duellmanohyla soralia	152.59	1.609	0	0.82	21
Duellmanohyla uranochroa	511.99	24.08	0.031	0.813	53
Ecnomiohyla miliaria	154.148	6.017	0.083	0.772	11
Exerodonta bivocata	203.517	9.188	0	0.911	12
Exerodonta catracha	52.246	3.559	0.125	0.728	8
Exerodonta chimalapa	207.682	2.421	0.25	0.777	17

Exerodonta melanomma	488.799	6.067	0.042	0.746	40
Exerodonta smaragdina	1043.461	11.587	0.003	0.767	102
Exerodonta sumichrasti	1034.263	1.312	0.077	0.678	96
Exerodonta xera	192.699	2.483	0	0.771	24
Hyloscirtus alytolylax	485.835	11.715	0	0.863	112
Hyloscirtus antioquia	97.528	29.386	0.125	0.891	10
Hyloscirtus armatus	304.03	0.225	0	0.676	18
Hyloscirtus bogotensis	630.488	6.323	0.031	0.832	50
Hyloscirtus callipeza	339.797	8.708	0.186	0.757	26
Hyloscirtus colymba	322.976	5.952	0.063	0.71	29
Hyloscirtus conscientia	72.459	2.881	0	0.566	16
Hyloscirtus criptico	75.804	8.964	0.188	0.811	9
Hyloscirtus denticulentus	216.574	106.658	0.083	0.827	15
Hyloscirtus larinopygion	650.141	7.304	0.056	0.897	95
Hyloscirtus mashpi	155.73	7.358	0	0.746	25
Hyloscirtus palmeri	841.972	17.617	0.139	0.712	120
Hyloscirtus phyllognathus	893.598	21.382	0.172	0.807	97
Hyloscirtus platydactylus	67.361	4.577	0.25	0.856	7
Hyloscirtus psarolaimus	171.236	1.246	0	0.678	19
Hyloscirtus tigrinus	74.624	1.147	0.25	0.839	11
Incilius alvarius	3971.516	58.061	0	0.724	1306

Incilius aucoinae	534.742	6.539	0.028	0.914	147
Incilius bocourti	1117.571	13.873	0.014	0.897	145
Incilius campbelli	454.683	6.687	0.042	0.87	49
Incilius canaliferus	1665.16	7.555	0	0.903	193
Incilius cavifrons	638.511	32.654	0.05	0.88	86
Incilius coccifer	2756.817	92.424	0	0.708	287
Incilius coniferus	1667.934	45.781	0.037	0.782	238
Incilius cristatus	514.625	44.237	0	0.805	72
Incilius gemmifer	294.883	4.485	0.08	0.873	22
Incilius ibarrai	323.776	3.929	0.05	0.871	36
Incilius leucomyos	263.865	6.672	0.05	0.893	23
Incilius luetkenii	1675.115	19.43	0	0.842	280
Incilius macrocristatus	786.609	7.883	0	0.74	51
Incilius marmoreus	5137.658	30.688	0.008	0.803	616
Incilius mazatlanensis	4633.973	18.404	0.007	0.829	698
Incilius mccoyi	183.758	4.663	0	0.732	19
Incilius melanochlorus	947.554	52.759	0.028	0.862	197
Incilius nebulifer	4143.043	70.531	0	0.799	4363
Incilius occidentalis	8883.076	0	0.005	0.702	931
Incilius perplexus	1408.169	10.18	0.039	0.757	112
Incilius porteri	348.635	11.151	0	0.971	76
Incilius spiculatus	123.91	2.42	0.083	0.914	12
Incilius tacanensis	237.767	4.939	0	0.936	25

Incilius tutelarius	456.108	9.802	0.042	0.829	36
Incilius valliceps	53825.348	328.176	0	0.791	2464
Isthmohyla angustilineata	117.816	16.226	0.125	0.918	12
Isthmohyla debilis	NA	NA	0.25	0.806	8
Isthmohyla lancasteri	269.04	7.546	0.071	0.765	32
Isthmohyla picadoi	208.788	4.623	0.188	0.83	18
Isthmohyla pictipes	233.27	13.121	0.071	0.81	27
Isthmohyla pseudopuma	679.239	20.199	0.042	0.913	100
Isthmohyla rivularis	439.325	14.825	0.036	0.85	47
Isthmohyla tica	327.212	11.18	0.05	0.885	31
Isthmohyla zeteki	189.41	2.649	0.1	0.745	19
Itapotihyla langsdorffii	848.321	5.092	0	0.871	180
Lysapsus bolivianus	269.607	23.29	0	0.81	19
Lysapsus laevis	223.407	23.598	0.193	0.829	18
Lysapsus limellum	1044.109	2.891	0.021	0.846	138
Megastomatohyla mixe	124.6	3.505	0	0.782	13
Megastomatohyla mixomaculata	382.856	34.696	0.054	0.896	26
Megastomatohyla nubicola	87.697	2.039	0.2	0.827	10
Melanophryniscus atroluteus	301.436	4.043	0.161	0.864	22
Melanophryniscus klappenbachi	482.49	4.547	0	0.746	33
Melanophryniscus macrogranulosus	NA	NA	0.333	0.998	7

Melanophryniscus montevidensis	106.884	23.252	0.343	0.802	7
Melanophryniscus moreirae	86.509	2.806	0.2	0.839	12
Melanophryniscus pachyrhynus	NA	NA	0.25	0.753	9
Melanophryniscus rubriventris	301.256	3.231	0.047	0.762	31
Melanophryniscus simplex	133.792	3.472	0.25	0.72	14
Melanophryniscus stelzneri	781.844	52.564	0.222	0.651	32
Melanophryniscus tumifrons	323.161	4.539	0.063	0.722	20
Myersiohyla chamaeleo	21.71	0.515	0.25	0.711	7
Nannophryne cophotis	118.512	17.499	0.375	0.703	9
Nannophryne variegata	645.075	9.706	0.004	0.869	75
Nesorohyla kanaima	160.466	4.34	0.188	0.904	17
Nyctimantis rugiceps	530.537	3.153	0	0.802	38
Oreophrynella macconnelli	73.348	3.212	0.5	0.585	7
Osornophryne antisana	113.016	7.815	0.25	0.873	18
Osornophryne bufoniformis	261.456	4.068	0.25	0.832	27
Osornophryne guacamayo	346.697	17.656	0.063	0.786	35
Osornophryne occidentalis	104.104	51.703	0.25	0.714	13
Osornophryne percrassa	309.817	4.649	0.05	0.965	39
Osteocephalus alboguttatus	450.723	4.578	0	0.749	27

Osteocephalus buckleyi	2671.62	80.318	0	0.779	122
Osteocephalus cabrerai	660.905	8.784	0	0.739	42
Osteocephalus cannatellai	776.517	8.213	0	0.555	47
Osteocephalus carri	218.001	2.481	0	0.889	22
Osteocephalus castaneicola	823.185	15.049	0.071	0.82	42
Osteocephalus deridens	1301.368	18.6	0	0.725	62
Osteocephalus festae	139.825	9.288	0	0.796	23
Osteocephalus fuscifacies	1223.535	19.591	0.063	0.711	70
Osteocephalus helenae	516.338	4.619	0	0.595	27
Osteocephalus leprieurii	2897.246	78.059	0	0.556	135
Osteocephalus mimeticus	425.042	37.887	0.25	0.893	22
Osteocephalus mutabor	1301.88	21.081	0.018	0.872	79
Osteocephalus oophagus	791.858	2.556	0	0.844	123
Osteocephalus planiceps	939.785	4.832	0.023	0.781	227
Osteocephalus subtilis	NA	NA	0.333	0.755	8
Osteocephalus taurinus	15993.811	187.731	0.002	0.704	677
Osteocephalus verruciger	1647.726	125.292	0.009	0.945	116
Osteocephalus vilarsi	196.223	5.286	0.06	0.941	15
Osteocephalus yasuni	348.006	13.414	0	0.738	85
Osteopilus dominicensis	2006.874	11.213	0	0.571	394

Osteopilus marianae	41.265	0.07	0.375	0.582	10
Osteopilus ocellatus	4520.812	89.309	0.004	0.772	182
Osteopilus pulchrilineatus	594.748	4.928	0	0.576	45
Osteopilus septentrionalis	3214.373	12.214	0.013	0.927	3178
Osteopilus vastus	490.699	5.4	0.027	0.711	43
Osteopilus wilderi	96.729	1.165	0.167	0.751	16
Peltophryne empusa	179.712	3.456	0.25	0.867	19
Peltophryne fustiger	138.734	0	0.188	0.653	25
Peltophryne guentheri	638.865	2.24	0.05	0.763	52
Peltophryne longinasus	NA	NA	0.25	0.705	12
Peltophryne peltocephala	860.427	7.02	0.167	0.566	161
Peltophryne taladai	52.596	1.145	0.25	0.861	9
Phyllodytes edelmoi	88.881	6.331	0.292	0.832	29
Phyllodytes luteolus	377.114	3.823	0	0.885	48
Plectrohyla acanthodes	340.513	0.824	0.136	0.781	41
Plectrohyla avia	133.876	4.946	0	0.992	16
Plectrohyla glandulosa	312.016	7.807	0.1	0.947	34
Plectrohyla guatemalensis	932.353	13.903	0.036	0.88	74
Plectrohyla hartwegi	303.176	4.344	0.063	0.778	21
Plectrohyla ixil	281.866	2.989	0.063	0.809	38
Plectrohyla lacertosa	412.545	20.939	0.036	0.927	44

Plectrohyla matudai	1049.678	22.992	0	0.832	145
Plectrohyla pokomchi	NA	NA	0.333	0.887	7
Plectrohyla quecchi	71.074	1.177	0	0.732	11
Plectrohyla sagorum	576.825	3.981	0.028	0.906	62
Pseudacris cadaverina	2422.558	32.149	0.011	0.854	1805
Pseudacris clarkii	3222.82	53.694	0.024	0.738	689
Pseudacris crucifer	14449.256	288.895	0.074	0.702	11534
Pseudacris hypochondriaca	1325.01	54.958	0.102	0.743	88
Pseudis bolbodactyla	364.534	2.292	0.038	0.81	19
Pseudis cardosoi	351.172	1.717	0.208	0.781	26
Pseudis minuta	1850.662	4.867	0.011	0.808	267
Pseudis paradoxa	2156.948	14.205	0.012	0.633	250
Pseudis platensis	604.5	2.204	0.085	0.809	98
Ptychohyla euthysanota	1009.08	26.491	0.018	0.837	130
Ptychohyla hypomykter	815.92	24.669	0.021	0.911	72
Ptychohyla leonhardschultzei	700.063	10.483	0	0.815	56
Ptychohyla macrotympanum	228.346	15.371	0.1	0.822	17
Ptychohyla zophodes	522.292	13.857	0.036	0.719	49
Quilticohyla acrochorda	62.724	0.784	0.375	0.717	10
Rhaebo blombergi	328.098	3.186	0.063	0.823	29
Rhaebo caeruleostictus	273.891	8.415	0.05	0.799	21
Rhaebo ecuadorensis	808.237	3.16	0	0.665	61

Rhaebo glaberrimus	963.97	40.879	0.055	0.723	79
Rhaebo guttatus	3373.205	27.85	0.029	0.72	389
Rhaebo haematiticus	5278.474	199.51	0.008	0.611	826
Rhaebo hypomelas	131.871	5.344	0.125	0.903	11
Rhaebo nasicus	114.73	1.35	0.125	0.923	11
Rheohyla miotympanum	10228.847	193.742	0	0.849	616
Rhinella achavali	176.884	8.909	0.5	0.716	15
Rhinella acutirostris	7783.887	544.55	0.001	0.949	316
Rhinella alata	597.591	5.051	0.229	0.853	542
Rhinella arenarum	4434.693	67.638	0.002	0.819	1143
Rhinella arunco	107.323	5.522	0.375	0.769	15
Rhinella beebei	2831.989	38.445	0.031	0.717	149
Rhinella bergi	407.797	5.031	0.038	0.722	36
Rhinella castaneotica	573.841	1.9	0.042	0.703	133
Rhinella centralis	150.447	26.57	0.25	0.666	13
Rhinella crucifer	3866.428	56.455	0	0.786	192
Rhinella dapsilis	593.814	10.148	0	0.748	129
Rhinella diptycha	35326.546	57.873	0	0.712	1442
Rhinella dorbignyi	1432.03	21.173	0	0.866	580
Rhinella festae	3022.297	406.677	0.014	0.728	146
Rhinella granulosa	6752.037	86.411	0	0.786	286
Rhinella henseli	343.585	3.843	0.043	0.791	24
Rhinella hoogmoedi	1006.965	5.791	0.003	0.962	61

Rhinella horribilis	120542.795	323.249	0	0.711	5178
Rhinella humboldti	3815.465	21.26	0.006	0.672	539
Rhinella icterica	3986.125	41.75	0	0.848	802
Rhinella limensis	382.887	2.032	0.042	0.862	29
Rhinella macrorhina	416.67	12.255	0.036	0.891	44
Rhinella major	3993.656	35.722	0.003	0.808	192
Rhinella margaritifera	7499.273	74.895	0.003	0.762	1102
Rhinella marina	85489.922	1312.673	0	0.53	3883
Rhinella merianae	490.613	8.087	0.05	0.593	62
Rhinella mirandaribeiroi	976.323	0.928	0	0.709	59
Rhinella nicefori	43.218	1.915	0.125	0.702	11
Rhinella ocellata	65.04	5.669	0.333	0.598	7
Rhinella ornata	2373.147	16.419	0	0.828	574
Rhinella poeppigii	725.481	7.971	0.028	0.552	75
Rhinella proboscidea	528.458	7.505	0	0.869	72
Rhinella pygmaea	358.422	21.561	0.083	0.95	25
Rhinella roqueana	570.004	3.976	0	0.655	33
Rhinella rubescens	694.244	5.417	0	0.731	66
Rhinella ruizi	214.191	9.495	0	0.954	20
Rhinella scitula	290.274	2.713	0.125	0.705	12
Rhinella spinulosa	10601.238	283.762	0.002	0.812	442
Rhinella stanlaii	309.643	19.245	0.063	0.801	20

Rhinella sternosignata	960.396	31.504	0.021	0.805	100
Rhinella veraguensis	289.82	4.234	0	0.919	19
Sarcohyla arborescandens	779.242	3.783	0.021	0.844	52
Sarcohyla bistincta	799.728	5.252	0.063	0.778	51
Sarcohyla celata	39.653	5.292	0.667	0.563	7
Sarcohyla charadricola	174.711	3.62	0.034	0.74	23
Sarcohyla cyclada	133.413	7.119	0	0.836	27
Sarcohyla hapsa	373.606	11.875	0.042	0.906	43
Sarcohyla pentheter	109.804	38.562	0.125	0.874	9
Scarthyla goinorum	609.833	4.059	0.083	0.72	47
Scarthyla vigilans	1660.195	8.03	0.005	0.848	214
Scinax acuminatus	2132.989	4.997	0.103	0.732	218
Scinax agilis	128.364	16.642	0.167	0.75	7
Scinax altae	254.911	14.065	0.188	0.728	25
Scinax alter	1280.649	11.286	0	0.877	91
Scinax arduous	38.559	5.058	0.333	0.628	7
Scinax argyreornatus	475.1	66.407	0	0.764	23
Scinax auratus	137.556	6.321	0.125	0.844	12
Scinax blairi	126.882	5.383	0.25	0.796	10
Scinax boesemani	1089.046	14.131	0	0.847	140
Scinax boulengeri	1115.047	23.655	0	0.849	246
Scinax caldarum	24.203	5.921	0	0.884	7

Scinax caprarius	196.562	4.887	0.179	0.72	18
Scinax cardosoi	NA	NA	0.5	0.594	7
Scinax catharinae	510.522	5.851	0	0.869	23
Scinax crospedospilus	310.763	1.056	0.125	0.824	44
Scinax cruentomma	1834.645	56.09	0.025	0.857	84
Scinax curicica	71.031	4.87	0.125	0.736	8
Scinax cuspidatus	406.401	11.226	0.107	0.797	42
Scinax duartei	119.899	2.008	0.125	0.837	12
Scinax elaeochroa	1531.266	40.317	0	0.824	388
Scinax eurydice	507.569	3.449	0.083	0.779	42
Scinax flavoguttatus	128.366	0.053	0.125	0.8	12
Scinax funereus	352.789	3.706	0.125	0.715	55
Scinax fuscomarginatus	3623.727	90.296	0.061	0.777	151
Scinax fuscovarius	17110.286	219.374	0.006	0.865	715
Scinax garbei	2609.719	15.239	0.036	0.648	330
Scinax granulatus	2174.33	21.85	0.029	0.682	326
Scinax hayii	736.945	8.449	0	0.851	121
Scinax ictericus	289.156	6.346	0	0.911	25
Scinax imbegue	481.049	3.648	0	0.612	39
Scinax jolyi	93.883	8.945	0.464	0.787	13
Scinax kennedyi	316.899	3.682	0.05	0.819	46
Scinax littoralis	192.52	3.882	0.091	0.866	11
Scinax longilineus	NA	NA	0.2	0.621	7

Scinax luizotavioi	54.604	0.159	0.25	0.831	7
Scinax nasicus	3924.111	31.43	0.006	0.787	427
Scinax nebulosus	785.379	13.221	0.142	0.583	99
Scinax obtriangulatus	100.134	10.172	0.25	0.854	9
Scinax oreites	132.48	15.141	0.304	0.841	13
Scinax pachycrus	276.173	31.602	0	0.804	20
Scinax pedromedinae	535.606	14.017	0.005	0.912	34
Scinax perereca	599.792	5.299	0	0.766	93
Scinax perpusillus	211.955	7.509	0.06	0.872	14
Scinax proboscideus	369.597	24.898	0.036	0.906	30
Scinax quinquefasciatus	699.839	3.734	0.136	0.801	197
Scinax rizibilis	89.529	6.096	0.25	0.625	9
Scinax rostratus	2968.849	20.835	0.005	0.741	326
Scinax ruber	10326.96	196.507	0.005	0.526	1449
Scinax similis	1180.843	30.454	0	0.752	58
Scinax squalirostris	2336.271	8.651	0.107	0.729	211
Scinax staufferi	7986.417	26.495	0	0.738	912
Scinax strigilatus	402.3	6.558	0	0.819	16
Scinax sugillatus	449.741	8.859	0.087	0.776	72
Scinax trapicheiroi	123.728	23.381	0.167	0.895	7
Scinax tsachila	1229.217	6.105	0.109	0.705	93
Scinax tymbamirim	373.46	3.452	0.063	0.825	67
Scinax uruguayus	NA	NA	0.333	0.678	7

Scinax wandae	1353.85	17.089	0.034	0.706	162
Scinax x-signatus	2959.346	4.518	0.017	0.706	372
Smilisca baudinii	3967.752	5.993	0	0.716	3486
Smilisca cyanosticta	966.956	7.542	0.154	0.712	121
Smilisca dentata	264.702	2.187	0	0.797	24
Smilisca fodiens	1589.738	2.988	0.013	0.724	312
Smilisca manisorum	1170.853	78.637	0.011	0.88	93
Smilisca phaeota	2299.438	18.747	0	0.559	1253
Smilisca puma	316.524	9.937	0.007	0.843	44
Smilisca sila	1195.642	35.746	0	0.786	268
Smilisca sordida	1315.471	9.76	0	0.869	296
Sphaenorhynchus caramaschii	443.648	3.595	0.167	0.609	32
Sphaenorhynchus carneus	409.23	6.085	0.1	0.713	33
Sphaenorhynchus dorisae	480.782	3.255	0	0.785	45
Sphaenorhynchus lacteus	1889.57	24.507	0.032	0.763	223
Sphaenorhynchus planicola	280.963	3.303	0	0.942	33
Sphaenorhynchus platycephalus	139.842	19.053	0	0.849	9
Sphaenorhynchus prasinus	177.341	24.393	0.333	0.891	10
Sphaenorhynchus surdus	224.873	2.779	0.083	0.591	21
Tepuihyla exophthalma	39.153	5.867	0.25	0.867	8

Tepuihyla tuberculosa	151.57	3.153	0	0.764	18
Tepuihyla warreni	74.144	6.57	0.125	0.514	7
Tlalocohyla godmani	463.999	6.414	0.02	0.841	44
Tlalocohyla loquax	1707.822	5.006	0.038	0.64	292
Tlalocohyla picta	1767.775	16.633	0.006	0.752	233
Tlalocohyla smithii	2033.508	16.421	0.01	0.815	368
Trachycephalus coriaceus	463.17	4.787	0	0.782	47
Trachycephalus cunauaru	766.442	15.832	0.056	0.86	36
Trachycephalus hadroceps	396.795	11.267	0.012	0.782	35
Trachycephalus imitatrix	169.956	2.013	0.25	0.65	16
Trachycephalus jordani	650.028	14.714	0.037	0.796	190
Trachycephalus macrotis	416.968	12.361	0.237	0.635	39
Trachycephalus mesophaeus	1021.493	16.344	0.011	0.853	216
Trachycephalus nigromaculatus	416.48	2.288	0.083	0.898	44
Trachycephalus quadrangulum	1134.069	0	0.079	0.7	90
Trachycephalus resinifictrix	698.922	19.464	0.063	0.748	82
Trachycephalus typhonius	27098.97	161.772	0.001	0.649	1028
Trachycephalus venulosus	2712.986	16.268	0	0.673	113
Trachycephalus vermiculatus	27365.295	90.776	0.001	0.81	1351

Triprion petasatus	606.165	4.944	0	0.726	261
Triprion spatulatus	891.524	17.616	0.019	0.944	64
Triprion spinosus	788.219	57.492	0.011	0.748	47

Capítulo 5

Manuscrito a ser submetido na revista Global Change Biology

Spatial overlap of endemism hotspots of Neotropical frogs with protected areas and forest cover under climate change scenarios

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Abstract

Understanding how evolutionary history is distributed and how it may be affected by global change is essential for biodiversity conservation. We investigated present and future patterns of phylogenetic endemism (PE) for 497 Neotropical frogs (Bufonidae and Hylidae) under climate and land-use change. Using species distribution models (SDMs) combined with a time-calibrated phylogeny, we identified hotspots of neo-, paleo-, mixed-, and super-endemism across the Neotropics. We also quantified the extent to which these centers overlap with protected areas (PAs) and forest cover, both currently and under a 2050 climate scenario. Our results revealed that present hotspots of endemism are concentrated in the Atlantic Forest, Andes, Caribbean, Mesoamerica, and Guiana Shield. However, by 2050, we project a marked reduction in paleo-, neo-, and mixed-endemism centers, particularly in Mesoamerica and the Andes. In contrast, super-endemism centers are expected to expand, likely reflecting the contraction of suitable ranges into localized refugia. Coverage by PAs and forest cover varied among endemism types: neo- and super-endemism centers were best represented in PAs, while paleo- and mixed-endemism centers were more strongly associated with forest cover. These results highlight the complementary role of PAs and forest cover in safeguarding evolutionary heritage and highlight the need for integrated conservation strategies to ensure the long-term persistence of Neotropical frogs.

Keywords: endemism centers, land-use change, climatic alterations, amphibians, conservation

Introduction

Phylogenetic measures of diversity and endemism can be useful for understanding the distribution pattern of biodiversity. Geographically restricted and evolutionarily unique species are often used to guide conservation prioritization because they might be at an inherent risk of extinction (Forest et al., 2007). One way to identify the spatial concentration of those species is through the calculation of phylogenetic endemism (PE, (Laffan et al.,

2016; Rosauer et al., 2009), which uses species range sizes and branch lengths to identify areas with geographically restricted and evolutionarily unique species. These areas of highly significant PE can be inhabited by neo-, paleo-, mixed- (neo- and paleo-), or super-endemic lineages (Gillespie & Roderick, 2002; Kraft et al., 2010; Stebbins & Major, 1965), and can be identified using the Categorical Analysis of Neo- and Paleo-endemism (CANAPE, (Mishler et al., 2014).

Areas of Neo-endemism are usually occupied by lineages that diverged recently and likely have had limited time to disperse to regions outside their ancestral area. On the other hand, areas of paleo-endemism are expected to hold ancient lineages that were possibly widely distributed in the deep past and are now restricted to smaller regions (Kraft et al., 2010; Stebbins & Major, 1965). Areas with both neo- and paleo-endemism are classified as areas of mixed-endemism (Gillespie & Roderick, 2002). Meanwhile, areas of super-endemism can be classified as centers of mixed endemism that are statistically highly significant (Nitta et al., 2023). Centers of neo-endemism should present higher potential for adaptation in the future (González-Orozco et al., 2016), while paleo-endemic centers should harbor lineages highly adapted to areas climatically stable over time (Cai et al., 2023). Given these evolutionary and biogeographical processes underlying the formation of centers of neo- and paleo-endemism, we expect an asymmetric effect of climate change on species, with a higher negative effect in ancient lineages, as we expect that these species are more adapted to the past climatic conditions (Cai et al., 2023).

Protecting areas where rapidly diversifying and range-restricted lineages (neo-endemics) inhabit is a priority for conservation, because these species hold the evolutionary potential for the future (González-Orozco et al., 2016). Furthermore, it is also important to protect areas where restricted older lineages (paleo-endemics) are distributed to conserve unique evolutionary history and possibly unique functional attributes. Paleo-endemic centers can hold species or clades with no living close relatives, such as the reptile Tuatara (González-Orozco et al., 2016). Protected Areas (PAs) are one of the most efficient strategies used to protect biodiversity (Chape et al., 2005), because these areas maintain habitats and original landscape for species and protect coexisting organisms (Quan et al., 2018). However, in many cases, locations of PAs are determined based primarily on species richness, treating species as equal entities, without considering their unique evolutionary history and functional traits (Faith, 1992; Hewett-Emmett & Tashian, 1996). Currently, approximately 10% of the global network of protected areas is connected through intact lands (Ward et al., 2020), but it is not clear if these protected areas are conserving regions where endemic centers are concentrated.

Forecasting the outcome of conservation efforts is only as good as our ability to build accurate models. A challenge we have building models of different conservation scenarios is that many different stressors are changing and interacting at the same time. For example, to understand the effects of climatic shifts on biodiversity, it is also important to consider the changes that may occur in the coverage of habitat available within the centers of endemism in climatically suitable areas (Guo et al., 2023). Climatically suitable areas might determine where a species can occur, but the availability of suitable habitat in that area will ultimately determine whether the species can persist there (Newbold et al., 2015). Therefore, in addition

to forecasting areas with suitable climates in the future, it is also important to assess whether these areas have native vegetation or have been converted into pastures or plantations.

Considering both land use patterns and climate change in our forecasts is particularly important for Neotropical amphibians, one of the most threatened vertebrate groups globally (IUCN, 2023). Their declines are mainly driven by habitat loss, disease, climate change, and land-use transformations, largely consequences of the exponential growth in the human population (Luedtke et al., 2023). The high sensitivity of amphibians is a consequence of their life-history traits, such as physiological reliance on moist environments, high sensitivity to changes in temperature and precipitation, and limited dispersal capacity (Wells, 2007). These declines exhibit a strong geographical bias, with biodiversity-rich regions like the Neotropics harboring a disproportionately high number of threatened species (Luedtke et al., 2023). Specific areas within the Neotropics, such as the Caribbean islands, Mesoamerica, the Andean region, the Coastal Atlantic Forest, the Amazon Basin, and the Guiana Shield, stand out as critical hotspots for the most vulnerable and endangered amphibians (Luedtke et al., 2023).

The vulnerability of Neotropical amphibians underscores the need to better understand how proximal stressors will affect their phylogenetic endemism centers. Moreover, it's also important to evaluate if these centers will be located inside protected areas and areas with forest cover in the future. Here we forecast distribution of endemism centers of Neotropical frogs under future climate change to understand how land use will affect the success of conservation scenarios in the future. Our specifics aims were (1) to investigate whether areas with forest cover and protected areas are will ensure the conservation of neo-, paleo-, super-, and mixed- endemism of Neotropical frogs in the future and (2) to evaluate if paleo-endemism centers are more vulnerable to climate change than neo-endemism centers. By addressing these objectives, our study provides an integrated view of how climate and land-use change may reshape evolutionary hotspots for frogs in the Neotropics. The findings will contribute to a better understanding of where conservation efforts should be focused to ensure the long-term persistence of Neotropical frogs and their unique evolutionary heritage.

Methods

Data gathering

We applied Species Distribution Models (SDMs) to generate potential distribution maps for 526 Neotropical frog species from the Bufonidae (toads) and Hylidae (treefrogs) families. This number represents 33% of Neotropical Bufonidae species and 39% of Neotropical Hylidae species. These two families encompass a broad range of species, from endemic and endangered species such as the genus *Atelopus*, to widely distributed species of least concern, such as those in the genus *Rhinella* and *Boana*. Occurrence data for all species were acquired from the Global Biodiversity Information Facility (GBIF: http://www.gbif.org). We obtained occurrence records for 1393 species of toads and treefrogs. We filtered the occurrences and eliminated the duplicates, impossible coordinates (latitude and longitude equal to 0), occurrences located within 2 km of country or capital centroids, and occurrences within 2 km of zoos or herbaria using the package coordinateCleaner (Zizka et al., 2019). After the quality control, we retained 683 species. We also applied an

environmental filter to reduce sampling bias, while still preserving the signal of the species' ecological niche (Castellanos et al., 2019; Varela et al., 2014). To filter the occurrences, we selected five bioclimatic variables (Bio 1, Bio 2, Bio 4, Bio 12, and Bio 15) from the WorldClim database v2.1 (Fick & Hijmans, 2017), that exhibited the least Pearson correlation (<0.75) for the current scenario at a 2.5 arc minute resolution. We then conducted a Principal Component Analysis (PCA), retaining the first three components, which captured 80% of the climatic variation. Using the three first axes of the PCA, we filtered the occurrences and removed the records inside a grid of 2.5 arc minutes with redundant climatic values. We retained species with at least 7 occurrence records. At the end of the filtering, we retrieved 526 species, including 148 toads and 379 treefrog species (Supplementary Table S1).

Bioclimatic data were acquired from the WorldClim v2.1 database (Fick & Hijmans, 2017), with a spatial resolution of 2.5 arc minutes (~5 km²) for both the present (1970-2000) and future climate scenarios (2050). To reduce the collinearity, we computed a Pearson's correlation matrix and selected variables with $r < 0.75$. For future predictions, we utilized three global climate models (GCMs): CCSM4, MPI-ESM-LR, and MIROC6, and generated a weighted average across them. Projections were made using one Shared Socioeconomic Pathway (SSP): SSP585, a more pessimistic scenario where reductions in CO2 emissions occur only after 2080.

Species distribution models

We defined the calibration area using a minimum convex polygon (MCP) that included all filtered occurrence points, with a buffer of 1.5° (~150 km² at the equator) added around it. This MCP and buffer were created using the ENMwizard R package (Heming et al., 2018), and models were calibrated using climate data from 1970-2000. To predict the potential effects of future climate change on frog distributions, species distribution models (SDMs) were applied by integrating occurrence data with bioclimatic variables, using the MaxEnt algorithm (version 3.4.1; (Phillips et al., 2006, 2017) in ENMwizard R package (Heming et al., 2018).

To minimize model overfitting, we generated multiple models with hyper-parameters, evaluated through cross-validated performance metrics. The preliminary models were adjusted by calibrating options of Feature Classes (FC) and Regularization Multipliers (RMs), which are related to transformations of environmental variables and penalization of model complexity, respectively. We used the FCs: “L” is linear, “P” product, “Q” quadratic and “H” hinge and RM values ranging from 0.5 to 4.5 with intervals of 0.5 and the combination of different FCs and RMs, generating 70 models per species. We applied the Block cross-validation method to geographically partition the occurrence records for each species. This approach divides the occurrence data into four spatially distinct blocks, performing four iterations where one block is used for model evaluation, while the remaining three blocks are used for calibration. For each species, we selected the 10% candidate models with the lowest omission rate (OR) and the highest Area Under the Curve (AUC) and created a consensual average model (Boria et al., 2017). We projected the consensual model for each species for the present, and future using the Neotropical limits. The continuous maps were converted into presence-absence maps using the cut-off threshold of 10%.

To address the overprediction in the SDMs, we used a distance constraint layer based on species dispersal abilities to crop the binary models for the present and the future. The constraint layer was developed using species range maps sourced from the IUCN (IUCN, 2023), with a buffer representing the dispersal ability specific to each group (toads and treefrogs). For toads, we assumed a dispersal ability of 3,300 meters per generation (Smith & Green, 2005). Given that each anuran generation has an average of 2.5 years (Oliveira et al., 2017), and there are 20 generations between 2000 and 2050, the species could potentially spread up to 66,000 meters (3,300 meters multiplied by 20) by the year 2050. The IUCN range map with a buffer of 3,300 meters and 66,000 meters was used to crop the models of the toads for the present and future, respectively. For treefrogs, we applied a 2,300 meter (Smith & Green, 2005)buffer around the IUCN range maps for the present and extended this to a 46,000 meter buffer (2,300 meters multiplied by 20) for future projections. Afterward, we cropped the presence-absence maps for both present and future scenarios.

Phylogenetic endemism and development of the null hypothesis

To estimate phylogenetic endemism, we used a time-calibrated phylogeny including 5,242 anuran species, based on maximum likelihood analyses of 307 genetic markers (Portik et al., 2023). We obtained branch lengths for each species by pruning the phylogenetic tree to include only the species modeled in our study. We used 497 species in the analysis because some of them do not present phylogenetic information on the tree (Supplementary Table S1). Using presence absence maps and the branch lengths of the phylogenetic tree, we calculated PE (Laffan et al., 2016; Rosauer et al., 2009) using the R package *phyloraster* (Alves‐Ferreira et al., 2024). Next, we constructed an alternate phylogenetic tree with all branch lengths set to a constant value (we arbitrarily uses 1 as (Mishler et al., 2014; Nitta et al., 2023) and then the tree is rescaled, so the sum of all branch lengths is 1 (Mishler et al., 2014). PE is then calculated using the alternate tree (hereafter called alternate PE). Afterwards, we calculated a derived metric of PE, the Relative Phylogenetic Endemism (RPE, (Mishler et al., 2014)), which is the ratio of PE divided by alternate PE (Mishler et al., 2014). RPE is used to inform how much of the observed values differs from the null expectation (Mishler et al., 2014). This in combination with the spatial randomization test explained above, will tell the extent to which differential branch lengths are important to the patterns of PE (Mishler et al., 2014).

Randomization tests

To determine the statistical significance of the PE, alternate PE, and RPE, the observed values are compared to a distribution of values obtained from a set of random communities (Nitta et al., 2023). The randomization method partially relaxes the spatial structure of species distribution, while keeping the observed richness across cells. This method corresponds to the SIM5 (proportional-fixed) described by (Gotelli, 2000) and was calculated using the function rast.pe.ses from the package *phyloraster* (Alves‐Ferreira et al., 2024) and *SESraster* (Heming et al., 2024). We ran this null model 999 times and calculated PE and RPE in each trial. These values formed a null distribution for each grid cell used to calculate the significance of observed values. Then, a two tailed test was applied to evaluate if the PE and RPE are significantly higher or significantly lower than the null. If the observed

value was within the top 2.5% of the distribution for a given grid cell, it was considered significantly high; if it was within the bottom 2.5%, it was considered significantly low.

Identifying areas of endemism

To identify areas of neo, paleo, and mixed endemism, we used the two-step process called CANAPE (Mishler et al., 2014). This was done by comparing significance values obtained in the previous step (Randomization tests). First, to be considered as significantly endemic (hereafter referred to as a phylogenetic endemism center), a grid cell must show a significantly high PE or alternate PE or both (one-tailed test, $\alpha = 0.05$). If the grid cell passes in this test, it will be classified into three categories of centers of endemism: (1) if a cell has a significantly high or low RPE (two-tailed test, $\alpha = 0.05$), it is classified as a center of paleo-endemism or neo-endemism, respectively; (2) If a cell is not significant for RPE, but is significantly high for PE or alternate PE or both, the cell is classified as a center of mixed-endemism. This category represents areas with a mixture of rare long and short phylogenetic branches, without a clear dominance of either paleo-endemism or neo-endemism (Mishler et al., 2014); (3) Finally, the mixed-endemism areas can be further classified based on the p-value; if a cell has both PE and alternate PE significant at the $\alpha = 0.01$ level, the grid cell can be classified as a center of super-endemism.

Spatial overlap with protected areas and forest cover

We quantified the overlap between global terrestrial protected areas from the World Database on Protected Areas (UNEP-WCMC & IUCN, 2024) and centers of phylogenetic endemism. Additionally, we quantified the overlap between forest cover and phylogenetic endemism centers. To represent the current forest cover, we used the dataset for 2015 (Chen et al., 2022), while for future projections, we used data for 2050 under the SSP585 scenario (Chen et al., 2022). Forest cover includes broadleaf evergreen trees, broadleaf deciduous trees, needleleaf evergreen trees, needleleaf deciduous trees, and shrubs (Chen et al., 2022). After identifying the overlapping areas, we calculated the percentage of cells located within protected areas (PAs) and areas with forest cover for each climatic scenario.

Results

Model evaluation using block cross-validation showed good performance, with average AUC values of 0.78 (SD = 0.09) and omission rate of 0.08 (SD = 0.11) (Supplementary Table S2). Hotspots of high phylogenetic endemism for Neotropical frogs are currently concentrated in five main regions: the Atlantic Coastal Forest, Andes, Amazon, Caribbean Islands, Mesoamerica, and the Guiana Shield (Figure 1a). These hotspots can be classified into centers of neo, paleo, mixed, and super endemism. Neo-endemism centers are highly restricted in the Neotropics (40 cells, 0.13%), occurring only in Mesoamerica, Andes, and the Guiana Shield (Figure 1a). Paleo-endemism centers are also very restricted (231, 0.78%), and are currently distributed in the Atlantic Coastal Forest, Andes, and Mesoamerica. Mixed-endemism centers (2,433 cells, 8.21%) and super-endemism centers (534 cells, 1.80%), on the other hand, are widely distributed across the Neotropics, including centers in

the Atlantic Coastal Forest, Andes, Caribbean Islands, Mesoamerica, and the Guiana Shield (Figure 1a).

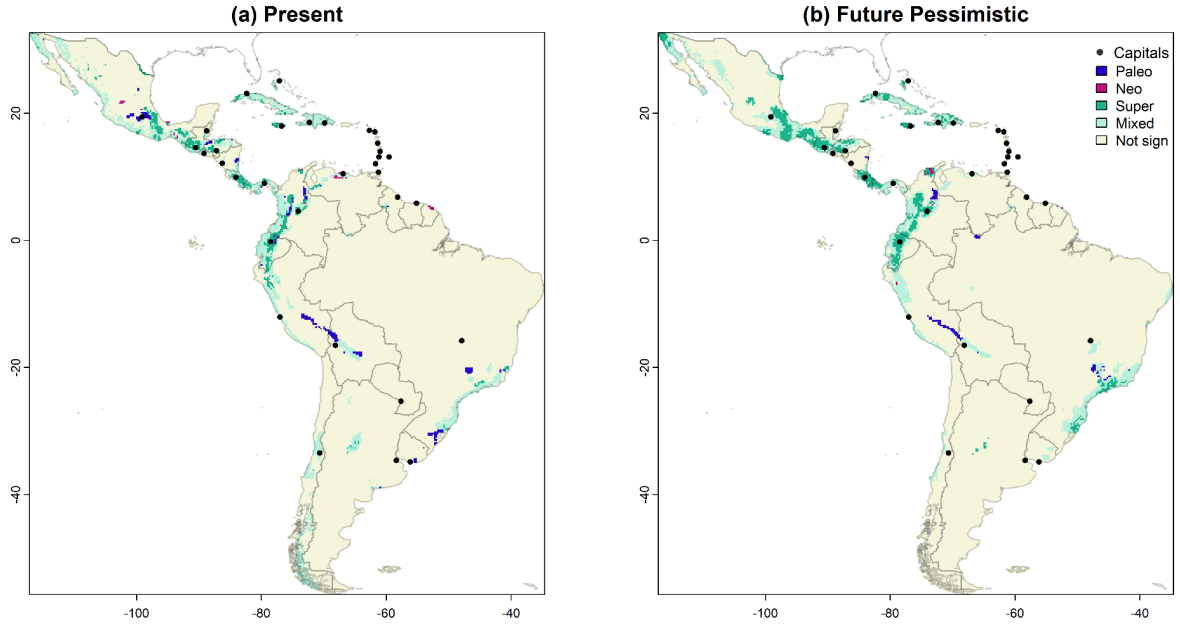

Figure 1. Centers of phylogenetic endemism for 497 Neotropical toads and treefrogs. (a) Centers of phylogenetic endemism for the present scenario, and (b) Centers of phylogenetic endemism for the 2050 climate scenario. Light green represents centers of mixed-endemism, dark green centers of super-endemism, dark blue centers of paleo-endemism, red centers of neo-endemism, and beige areas that are not significant.

Neo-, paleo-, and mixed-endemism centers are projected to decline by 2050 (Figure 1b). In the future, neo-endemism centers (18 cells, 0.06%) are expected to contract significantly in several Neotropical regions, such as Guiana Shield and the Andes, and may disappear entirely from the Atlantic Coastal Forest and Mesoamerica. Paleo-endemism centers (106 cells, 0.35%) are also predicted to shrink, particularly in the Atlantic Coastal Forest, Mesoamerica, and the Andes (Figure 1b). Mixed-endemism centers (2,296 cells, 7.75%) are projected to decline as well, with the greatest contraction occurring in the Andes. In contrast, super-endemism centers are expected to expand (928 cells, 3.13%), especially in the Atlantic Coastal Forest, the Andes, the Caribbean Islands, and Mesoamerica (Figure 1b).

The coverage of protected areas varies among the centers of phylogenetic endemism depends on the type of endemism and climatic scenario (Figures 2a and 2b). Under current conditions, protected area coverage is highest for neo-endemism centers (65%), followed by super-endemism (56.92%) and paleo-endemism centers (53.24%), while mixed-endemism centers show the lowest coverage (44.01%). In future scenarios, protected area coverage is projected to decrease—from 56.92% to 50.10% for super-endemism centers, from 53.24% to 30.18% for paleo-endemism centers, and from 44.01% to 38.58% for mixed-endemism centers. In contrast, the remaining neo-endemism cells in the Guiana Shield and the Andes are expected to experience an increase in protected area coverage, from 65% to 72.22% (Figure 3).

The forest cover in the centers of significant phylogenetic endemism varied according to the type of endemism and the climatic scenario (Figures 2c and 2d). In the present scenario

(Figure 3), centers of super-endemism are the most represented, with 84.3% of their area containing forest cover. This is followed by mixed-endemism centers at 69.7%, paleo-endemism centers at 63%, and, finally, neo-endemism centers, with only 47.5% of their area containing forest cover. Under future climate scenarios (Figure 3), the percentage of coverage by forest is projected to decline in the super-endemism (from 84.3% to 76.8%), mixed-endemism (from 69.7% to 56.6%), and paleo-endemism (from 63% to 58.1%). In contrast, centers of neo-endemism are expected to experience a slight increase of forest coverage, rising from 47.5% to 50%.

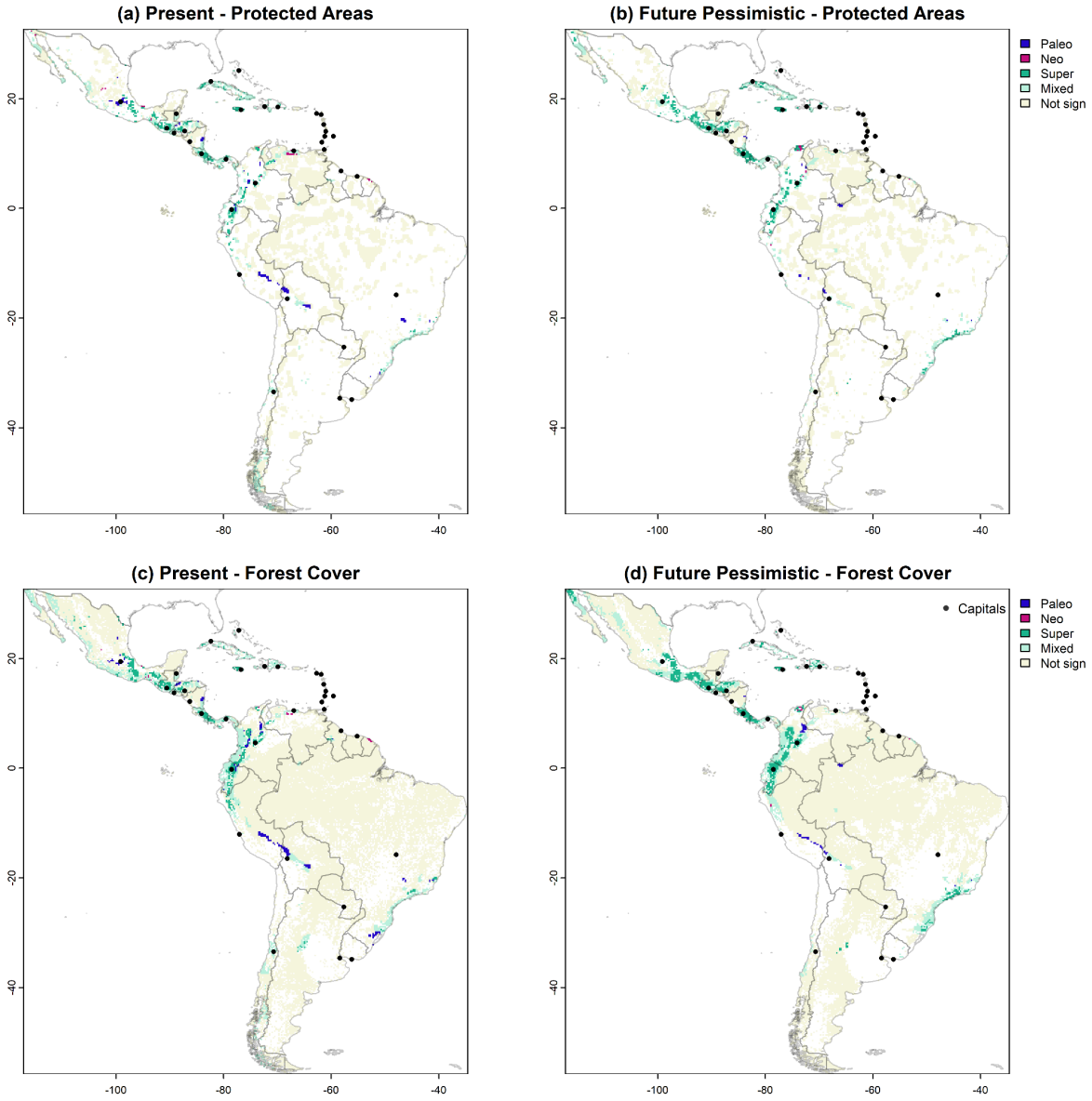

Figure 2. Centers of phylogenetic endemism for 497 Neotropical toads and treefrogs. (a) Centers of phylogenetic endemism cropped by protected areas in present, (b) Centers of phylogenetic endemism cropped by protected areas in the 2050 scenario, (c) Centers of phylogenetic endemism cropped by areas with forest cover in present, and (d) Centers of phylogenetic endemism cropped by areas with forest cover under a future climate scenario. Light green represents centers of mixed-endemism, dark green centers of super-endemism,

dark blue centers of paleo-endemism, red centers of neo-endemism, and beige represents areas that are not significant.

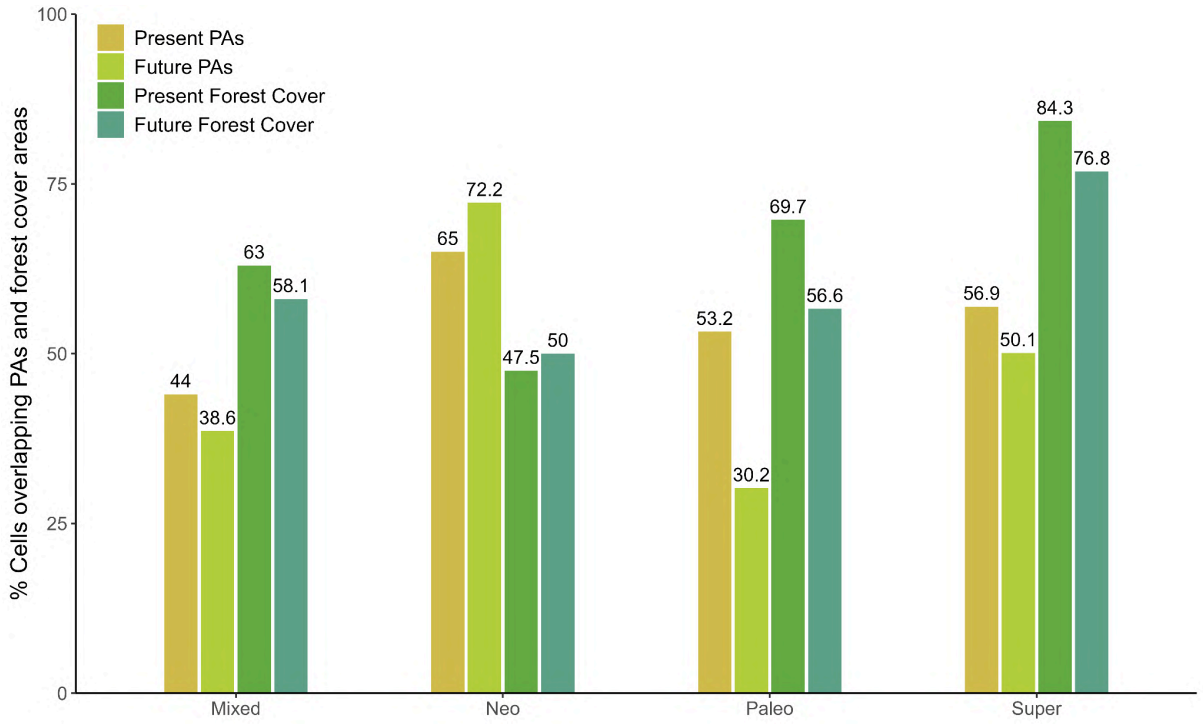

Figure 3. Percentage of overlap between protected areas, areas with forest cover and centers of phylogenetic endemism for 497 Neotropical toads and treefrogs. Green represents the centers of phylogenetic endemism in the present scenario overlapping with areas with forest cover, blue represents the centers of phylogenetic endemism under a future climate scenario overlapping with areas with forest cover. Yellow represents the centers of phylogenetic endemism in the present scenario overlapping with PAs and light green represents the centers of phylogenetic endemism under a future climate scenario overlapping with PAs. The numbers in the bars represent the percentage of cells overlapping PAs and areas with forest cover.

Discussion

Here, we assessed the spatial distribution of the current and future centers of phylogenetic endemism for Neotropical frogs under climate change scenarios and, for the first time, quantified the extent to which they fall within protected areas and forest covered areas both now and in the future. Our results predict hotspots of endemism for Neotropical frogs in five key regions: the Atlantic Coastal Forest, Andes, Caribbean Islands, Mesoamerica, and the Guiana Shield. However, under a future climate scenario, our models project a decline in mixed-, paleo-, and neo-endemism. Protected areas and areas with forest cover are predicted to play a complementary role in conserving phylogenetic endemism hotspots. Nonetheless, the percentage of coverage of the PAs and forest is expected to vary depending on the type of endemism and the climatic scenario considered.

Regions identified in this study as hotspots of super-, mixed-, neo-, and paleo-endemism for Neotropical frogs—such as the Andes, the Coastal Atlantic Forest, the

Caribbean Islands, Mesoamerica, and the Guiana Shield—often emerge as biodiversity hotpoints for other taxonomic groups (e.g. (Azevedo et al., 2020; Böhm et al., 2013; Dalapicolla et al., 2021; Loiseau et al., 2020; Rangel et al., 2018; Shi et al., 2005). The emergence of such hotpoints is often linked to climatic stability, geographic isolation, formation of physical barriers, and emergence of novel environments (Harrison & Noss, 2017). In the Neotropical region, these factors are evident throughout its complex geological and ecological history. For example, the rise of the Andes began approximately 25 million years ago (Gregory-Wodzicki, 2000) and contributed to a highly heterogeneous environment that drove species diversification. The Andes also provided new high-altitude habitats, created dispersal barriers that promoted vicariance (Miller et al., 2008), acted as climatic refugia during periods of environmental change (Fjeldså et al., 2012), and reduced regional climatic velocity, offering long-term shelters for species (Burrows et al., 2014). In addition to the Andes, other non-Andean mountain systems in South America, such as the Serra do Mar Range, the Mantiqueira Mountains, the Northeastern Highlands, the Central Brazilian Highlands, and the Pantepui region, have played pivotal roles to both the diversification of new species and the preservation of ancient lineages (Guedes et al., 2020).

These rich centers of endemism, which took millions of years to emerge, are projected to face significant threats under climate change scenarios. Our projections indicate that at least half of the paleo- and neo-endemism hotspots for Neotropical frogs will experience reductions by 2050. Mesoamerica, a highly biodiverse region, is projected to suffer the most severe impacts, with the complete extinction of neo-endemism centers and a significant reduction of paleo-endemism centers. This result contradicts our expectations, as we anticipated that centers of paleo-endemism would be more affected by climate change than centers of neo-endemism. The loss of neo-endemic centers is especially alarming in the context of climate change, as these areas harbor species that represent recent evolutionary radiations with high adaptive potential (González-Orozco et al., 2016). The disappearance of paleo-endemic centers is also concerning, as these regions often contain species with no close living relatives and can lead to the loss of unique evolutionary history and functional attributes (González-Orozco et al., 2016). As these endemism centers shrink or disappear, the Neotropics risk losing not only species, but also the evolutionary heritage and evolutionary potential that sustain its biodiversity (Alves-Ferreira et al., 2025).

In contrast with the reduction of paleo-, mixed-, and neo- endemism centers, the models projected an increase in size and number of super-endemism centers by 2050. The higher increase in super-endemic centers is projected to occur in Mesoamerica, mainly in Mexico, Guatemala, Honduras, and Costa Rica. This pattern is likely driven by the contraction of climatically suitable areas for many species (González-Orozco et al., 2016; Mishler et al., 2014), which could concentrate them into highly localized refugia. These predicted new centers of super-endemism are important for future conservation, as they harbor lineages with rare long branches and range-restricted short branches (González-Orozco et al., 2016).

Our analyses predict that protected areas will contribute significantly to preservation of hotspots of frog phylogenetic endemism, however, this contribution will vary with the climatic scenario and endemism type. For example, our results for the present indicate that PAs are more effective at maintaining centers of neo- and super-endemism compared to

centers of paleo- and mixed-endemism. In the future, however, the effectiveness of PAs is expected to decline for all types of endemism except for neo-endemism. While these findings emphasize the importance of the current PA network to conserve the phylogenetic endemism, they also raise concerns about its long-term sufficiency. Some studies have shown that the coverage of protected areas has decreased by an average of 1.1 million km² between 2006 and 2018 (Lewis et al., 2019). If the decline continues in the future, many of the areas of phylogenetic endemism that we currently consider protected will be at high vulnerability. In addition to the decrease in coverage of protected areas, many current protected areas remain isolated and poorly connected, compromising their capacity to conserve biodiversity (Maxwell et al., 2020).

Our results reveal a trade-off between the coverage of protected areas and coverage of forest. For example, although neo-endemism centers exhibit low forest vegetation coverage, they are predominantly covered by protected areas both in the present and under future scenarios. On the other hand, for other types of phylogenetic endemism, despite modest coverage by protected areas, these regions present high forest coverage. In terms of forest coverage, neo-endemism centers are the most vulnerable due to their lower forest cover. However, the existing network of protected areas will, fortunately, safeguard a significant portion of these centers. Thus, enhancing the effectiveness of currently established protected areas is crucial for conserving this type of endemism (e.g.(Guo et al., 2023)). Conservation measures outside protected areas, such as habitat conservation and restoration, are essential for conserving the evolutionary history of these species (Fremout et al., 2020). This is especially critical for paleo-endemism centers, which are projected to have two-thirds of their area unprotected under future climate scenarios.

We evaluated whether protected areas and forest cover can contribute to the conservation of phylogenetic endemism in Neotropical anurans. Our findings demonstrate that PAs and forest cover remnants play complementary roles in the conservation of endemism under both current and future scenarios. Conserving phylogenetic endemism is crucial from an evolutionary perspective, as these areas may harbor species with distinctive genetic heritage and high adaptive potential to climate change (González-Orozco et al., 2016; Guo et al., 2023). Additionally, they may contain species with distinctive life-history traits and no close phylogenetic relatives, highlighting their irreplaceable value for biodiversity conservation.

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Supplementary material

Table S1. Species evaluated in this study, along with their families and branch lengths.

Species	Family	Branch Length
Amazophrynella minuta	Bufonidae	32.988
Anaxyrus boreas	Bufonidae	2.744
Anaxyrus californicus	Bufonidae	1.060
Anaxyrus cognatus	Bufonidae	11.342
Anaxyrus compactilis	Bufonidae	13.521
Anaxyrus debilis	Bufonidae	3.586
Anaxyrus kelloggi	Bufonidae	2.687
Anaxyrus mexicanus	Bufonidae	1.060
Anaxyrus punctatus	Bufonidae	19.998
Anaxyrus retiformis	Bufonidae	3.586
Anaxyrus speciosus	Bufonidae	2.687
Anaxyrus woodhousii	Bufonidae	2.395
Aplastodiscus albofrenatus	Hylidae	15.712
Aplastodiscus albosignatus	Hylidae	9.497
Aplastodiscus arildae	Hylidae	5.712
Aplastodiscus cavicola	Hylidae	1.481
Aplastodiscus cochranae	Hylidae	9.879
Aplastodiscus ehrhardti	Hylidae	4.023
Aplastodiscus leucopygius	Hylidae	5.302
Aplastodiscus perviridis	Hylidae	3.222

Aplastodiscus weygoldti	Hylidae	5.712
Atelopus barbotini	Bufonidae	3.044
Atelopus bomolochos	Bufonidae	1.641
Atelopus carrikeri	Bufonidae	7.155
Atelopus chiriquiensis	Bufonidae	6.872
Atelopus coynei	Bufonidae	0.125
Atelopus cruciger	Bufonidae	4.290
Atelopus ebenoides	Bufonidae	1.961
Atelopus elegans	Bufonidae	0.628
Atelopus exiguus	Bufonidae	0.758
Atelopus flavescens	Bufonidae	1.305
Atelopus franciscus	Bufonidae	1.897
Atelopus hoogmoedi	Bufonidae	4.209
Atelopus ignescens	Bufonidae	2.632
Atelopus laetissimus	Bufonidae	3.213
Atelopus limosus	Bufonidae	2.531
Atelopus longirostris	Bufonidae	1.198
Atelopus mindoensis	Bufonidae	4.948
Atelopus muisca	Bufonidae	2.629
Atelopus nanay	Bufonidae	0.758
Atelopus nepiozomus	Bufonidae	0.082
Atelopus palmatus	Bufonidae	3.473
Atelopus pastuso	Bufonidae	1.618

Atelopus peruensis	Bufonidae	0.152
Atelopus podocarpus	Bufonidae	3.532
Atelopus pulcher	Bufonidae	4.970
Atelopus senex	Bufonidae	0.174
Atelopus sernai	Bufonidae	0.880
Atelopus spumarius	Bufonidae	2.891
Atelopus spurrelli	Bufonidae	7.155
Atelopus subornatus	Bufonidae	1.095
Atelopus varius	Bufonidae	0.174
Atelopus walkeri	Bufonidae	5.198
Atelopus zeteki	Bufonidae	0.930
Atlantihyla spinipollex	Hylidae	8.836
Boana albomarginata	Hylidae	28.992
Boana albopunctata	Hylidae	3.158
Boana alfaroi	Hylidae	3.822
Boana almendarizae	Hylidae	9.906
Boana atlantica	Hylidae	6.946
Boana bandeirantes	Hylidae	5.307
Boana bischoffi	Hylidae	5.348
Boana boans	Hylidae	14.021
Boana caingua	Hylidae	4.803
Boana calcarata	Hylidae	9.906
Boana callipleura	Hylidae	6.023

Boana cinerascens	Hylidae	17.061
Boana cordobae	Hylidae	6.509
Boana crepitans	Hylidae	10.294
Boana curupi	Hylidae	4.311
Boana dentei	Hylidae	15.510
Boana faber	Hylidae	15.618
Boana fasciata	Hylidae	1.015
Boana geographica	Hylidae	3.005
Boana heilprini	Hylidae	22.896
Boana joaquini	Hylidae	6.936
Boana lanciformis	Hylidae	13.108
Boana lemai	Hylidae	8.222
Boana leptolineata	Hylidae	5.513
Boana lundii	Hylidae	5.679
Boana maculateralis	Hylidae	6.340
Boana marginata	Hylidae	5.348
Boana microderma	Hylidae	14.337
Boana multifasciata	Hylidae	6.315
Boana nympha	Hylidae	3.296
Boana ornatissima	Hylidae	18.259
Boana pardalis	Hylidae	10.111
Boana pellucens	Hylidae	5.295
Boana picturata	Hylidae	1.432

Boana polytaenia	Hylidae	0.659
Boana prasina	Hylidae	6.656
Boana pugnax	Hylidae	5.450
Boana pulchella	Hylidae	6.509
Boana punctata	Hylidae	17.061
Boana raniceps	Hylidae	25.362
Boana riojana	Hylidae	4.212
Boana rosenbergi	Hylidae	3.572
Boana rubracyla	Hylidae	17.685
Boana rufitela	Hylidae	5.295
Boana semiguttata	Hylidae	4.123
Boana semilineata	Hylidae	0.371
Boana sibleszi	Hylidae	10.392
Boana steinbachi	Hylidae	5.348
Boana wavrini	Hylidae	1.259
Boana xerophylla	Hylidae	3.572
Bokermannohyla alvarengai	Hylidae	16.617
Bokermannohyla caramaschii	Hylidae	6.618
Bokermannohyla circumdata	Hylidae	2.503
Bokermannohyla hylax	Hylidae	2.503
Bokermannohyla ibitiguara	Hylidae	1.934
Bokermannohyla luctuosa	Hylidae	5.235
Bokermannohyla sapiranga	Hylidae	1.882

Bromeliohyla bromeliacia	Hylidae	11.940
Bromeliohyla dendroscarta	Hylidae	11.940
Charadrahyla altipotens	Hylidae	11.185
Charadrahyla chaneque	Hylidae	4.791
Charadrahyla nephila	Hylidae	4.791
Charadrahyla taeniopus	Hylidae	11.237
Corythomantis greeningi	Hylidae	20.486
Dendrophryniscus berthalutzae	Bufonidae	1.268
Dendrophryniscus brevipollicatus	Bufonidae	2.397
Dendropsophus acreanus	Hylidae	22.862
Dendropsophus anceps	Hylidae	5.634
Dendropsophus berthalutzae	Hylidae	1.825
Dendropsophus bifurcus	Hylidae	3.461
Dendropsophus bipunctatus	Hylidae	1.970
Dendropsophus bogerti	Hylidae	3.291
Dendropsophus bokermanni	Hylidae	3.342
Dendropsophus branneri	Hylidae	1.807
Dendropsophus brevifrons	Hylidae	1.142
Dendropsophus carnifex	Hylidae	13.867
Dendropsophus columbianus	Hylidae	16.388
Dendropsophus cruzi	Hylidae	17.067
Dendropsophus decipiens	Hylidae	3.291
Dendropsophus ebraccatus	Hylidae	21.026

Dendropsophus elegans	Hylidae	8.241
Dendropsophus elianeae	Hylidae	11.496
Dendropsophus gaucheri	Hylidae	2.415
Dendropsophus giesleri	Hylidae	16.856
Dendropsophus gryllatus	Hylidae	1.825
Dendropsophus haddadi	Hylidae	6.460
Dendropsophus haraldschultzi	Hylidae	7.038
Dendropsophus jimi	Hylidae	1.628
Dendropsophus joannae	Hylidae	12.230
Dendropsophus koechlini	Hylidae	2.454
Dendropsophus labialis	Hylidae	4.176
Dendropsophus leali	Hylidae	7.038
Dendropsophus leucophyllatus	Hylidae	1.678
Dendropsophus luddeckei	Hylidae	3.760
Dendropsophus luteoocellatus	Hylidae	12.810
Dendropsophus manonegra	Hylidae	1.551
Dendropsophus marmoratus	Hylidae	15.803
Dendropsophus mathiassoni	Hylidae	16.524
Dendropsophus melanargyreus	Hylidae	15.803
Dendropsophus meridensis	Hylidae	3.760
Dendropsophus microcephalus	Hylidae	7.739
Dendropsophus microps	Hylidae	3.042
Dendropsophus minusculus	Hylidae	12.726

Dendropsophus minutus	Hylidae	17.710
Dendropsophus miyatai	Hylidae	5.118
Dendropsophus nanus	Hylidae	1.438
Dendropsophus norandinus	Hylidae	4.703
Dendropsophus oliveirai	Hylidae	1.807
Dendropsophus padreluna	Hylidae	11.905
Dendropsophus parviceps	Hylidae	1.628
Dendropsophus pauiniensis	Hylidae	19.265
Dendropsophus phlebodes	Hylidae	7.739
Dendropsophus praestans	Hylidae	2.284
Dendropsophus pseudomeridianus	Hylidae	1.678
Dendropsophus rhodopeplus	Hylidae	2.492
Dendropsophus riveroi	Hylidae	10.640
Dendropsophus robertmertensi	Hylidae	7.349
Dendropsophus rossalleni	Hylidae	2.415
Dendropsophus rubicundulus	Hylidae	4.703
Dendropsophus ruschii	Hylidae	16.856
Dendropsophus sanborni	Hylidae	7.073
Dendropsophus sarayacuensis	Hylidae	17.327
Dendropsophus sartori	Hylidae	4.725
Dendropsophus schubarti	Hylidae	26.287
Dendropsophus seniculus	Hylidae	21.033
Dendropsophus shiwiarum	Hylidae	5.634

Dendropsophus soaresi	Hylidae	6.235
Dendropsophus stingi	Hylidae	16.579
Dendropsophus subocularis	Hylidae	3.342
Dendropsophus timbeba	Hylidae	1.809
Dendropsophus triangulum	Hylidae	14.122
Dendropsophus tritaeniatus	Hylidae	10.747
Dendropsophus virolinensis	Hylidae	6.235
Dendropsophus walfordi	Hylidae	4.845
Dendropsophus werneri	Hylidae	2.284
Dryaderces pearsoni	Hylidae	29.470
Dryophytes arenicolor	Hylidae	10.451
Dryophytes cinereus	Hylidae	15.432
Dryophytes euphorbiaceus	Hylidae	2.220
Dryophytes eximius	Hylidae	2.701
Dryophytes plicatus	Hylidae	2.220
Dryophytes squirellus	Hylidae	20.462
Dryophytes walkeri	Hylidae	4.269
Dryophytes wrightorum	Hylidae	8.365
Duellmanohyla chamulae	Hylidae	0.359
Duellmanohyla ignicolor	Hylidae	0.162
Duellmanohyla rufioculis	Hylidae	22.579
Duellmanohyla salvavida	Hylidae	3.548
Duellmanohyla schmidtorum	Hylidae	7.939

Duellmanohyla soralia	Hylidae	10.938
Duellmanohyla uranochroa	Hylidae	5.056
Ecnomiohyla miliaria	Hylidae	0.957
Exerodonta bivocata	Hylidae	2.261
Exerodonta catracha	Hylidae	9.940
Exerodonta chimalapa	Hylidae	1.581
Exerodonta melanomma	Hylidae	3.744
Exerodonta smaragdina	Hylidae	1.581
Exerodonta sumichrasti	Hylidae	3.744
Exerodonta xera	Hylidae	3.031
Hyloscirtus alytolylax	Hylidae	7.911
Hyloscirtus antioquia	Hylidae	8.871
Hyloscirtus armatus	Hylidae	8.494
Hyloscirtus bogotensis	Hylidae	0.455
Hyloscirtus callipeza	Hylidae	12.518
Hyloscirtus colymba	Hylidae	27.208
Hyloscirtus criptico	Hylidae	2.990
Hyloscirtus denticulentus	Hylidae	22.872
Hyloscirtus larinopygion	Hylidae	9.129
Hyloscirtus palmeri	Hylidae	22.872
Hyloscirtus phyllognathus	Hylidae	15.159
Hyloscirtus platydactylus	Hylidae	2.261
Hyloscirtus psarolaimus	Hylidae	5.212

Hyloscirtus tigrinus	Hylidae	5.299
Incilius alvarius	Bufonidae	1.444
Incilius aucoinae	Bufonidae	14.634
Incilius bocourti	Bufonidae	4.091
Incilius campbelli	Bufonidae	3.469
Incilius canaliferus	Bufonidae	6.117
Incilius cavifrons	Bufonidae	4.156
Incilius coccifer	Bufonidae	8.182
Incilius coniferus	Bufonidae	2.592
Incilius cristatus	Bufonidae	9.797
Incilius gemmifer	Bufonidae	6.698
Incilius ibarrai	Bufonidae	6.453
Incilius leucomyos	Bufonidae	3.469
Incilius luetkenii	Bufonidae	5.811
Incilius macrocristatus	Bufonidae	4.348
Incilius marmoreus	Bufonidae	9.154
Incilius mazatlanensis	Bufonidae	6.584
Incilius mccoyi	Bufonidae	1.444
Incilius melanochlorus	Bufonidae	8.748
Incilius nebulifer	Bufonidae	3.647
Incilius occidentalis	Bufonidae	11.312
Incilius perplexus	Bufonidae	6.117
Incilius porteri	Bufonidae	4.644

Incilius spiculatus	Bufonidae	4.156
Incilius tacanensis	Bufonidae	18.526
Incilius tutelarius	Bufonidae	3.920
Incilius valliceps	Bufonidae	3.647
Isthmohyla angustilineata	Hylidae	0.170
Isthmohyla debilis	Hylidae	0.537
Isthmohyla lancasteri	Hylidae	1.071
Isthmohyla picadoi	Hylidae	27.707
Isthmohyla pictipes	Hylidae	0.367
Isthmohyla pseudopuma	Hylidae	1.071
Isthmohyla rivularis	Hylidae	2.661
Isthmohyla tica	Hylidae	0.367
Isthmohyla zeteki	Hylidae	23.555
Itapotihyla langsdorffii	Hylidae	42.724
Lysapsus bolivianus	Hylidae	1.657
Lysapsus laevis	Hylidae	18.309
Lysapsus limellum	Hylidae	1.657
Megastomatohyla mixe	Hylidae	13.468
Megastomatohyla mixomaculata	Hylidae	11.616
Megastomatohyla nubicola	Hylidae	4.297
Melanophryniscus atroluteus	Bufonidae	8.647
Melanophryniscus klappenbachi	Bufonidae	1.515
Melanophryniscus macrogranulosus	Bufonidae	8.647

Melanophryniscus montevidensis	Bufonidae	0.160
Melanophryniscus moreirae	Bufonidae	14.463
Melanophryniscus pachyrhynus	Bufonidae	1.314
Melanophryniscus rubriventris	Bufonidae	3.810
Melanophryniscus simplex	Bufonidae	18.635
Melanophryniscus stelzneri	Bufonidae	1.634
Melanophryniscus tumifrons	Bufonidae	1.515
Myersiohyla chamaeleo	Hylidae	5.290
Nannophryne cophotis	Bufonidae	0.810
Nannophryne variegata	Bufonidae	27.786
Nesorohyla kanaima	Hylidae	71.365
Nyctimantis rugiceps	Hylidae	26.020
Oreophrynella macconnelli	Bufonidae	1.062
Osornophryne antisana	Bufonidae	2.729
Osornophryne bufoniformis	Bufonidae	1.573
Osornophryne guacamayo	Bufonidae	12.282
Osornophryne occidentalis	Bufonidae	6.071
Osornophryne percrassa	Bufonidae	0.749
Osteocephalus alboguttatus	Hylidae	9.449
Osteocephalus buckleyi	Hylidae	2.251
Osteocephalus cabrerai	Hylidae	7.440
Osteocephalus cannatellai	Hylidae	1.683
Osteocephalus carri	Hylidae	1.388

Osteocephalus castaneicola	Hylidae	10.905
Osteocephalus deridens	Hylidae	5.513
Osteocephalus festae	Hylidae	11.035
Osteocephalus fuscifacies	Hylidae	5.513
Osteocephalus helenae	Hylidae	1.388
Osteocephalus leprieurii	Hylidae	12.853
Osteocephalus mimeticus	Hylidae	14.508
Osteocephalus mutabor	Hylidae	2.935
Osteocephalus oophagus	Hylidae	6.329
Osteocephalus planiceps	Hylidae	9.717
Osteocephalus subtilis	Hylidae	7.379
Osteocephalus taurinus	Hylidae	6.329
Osteocephalus verruciger	Hylidae	1.683
Osteocephalus vilarsi	Hylidae	7.373
Osteocephalus yasuni	Hylidae	12.853
Osteopilus dominicensis	Hylidae	15.797
Osteopilus marianae	Hylidae	17.866
Osteopilus ocellatus	Hylidae	9.898
Osteopilus pulchrilineatus	Hylidae	15.797
Osteopilus septentrionalis	Hylidae	28.174
Osteopilus vastus	Hylidae	30.919
Osteopilus wilderi	Hylidae	9.898
Peltophryne empusa	Bufonidae	7.172

Peltophryne fustiger	Bufonidae	4.407
Peltophryne guentheri	Bufonidae	16.456
Peltophryne longinasus	Bufonidae	10.397
Peltophryne peltocephala	Bufonidae	2.173
Peltophryne taladai	Bufonidae	11.786
Phyllodytes edelmoi	Hylidae	7.310
Phyllodytes luteolus	Hylidae	3.860
Plectrohyla acanthodes	Hylidae	2.066
Plectrohyla avia	Hylidae	2.482
Plectrohyla glandulosa	Hylidae	8.890
Plectrohyla guatemalensis	Hylidae	2.951
Plectrohyla hartwegi	Hylidae	2.096
Plectrohyla ixil	Hylidae	8.291
Plectrohyla lacertosa	Hylidae	2.482
Plectrohyla matudai	Hylidae	6.534
Plectrohyla pokomchi	Hylidae	3.387
Plectrohyla quecchi	Hylidae	0.666
Plectrohyla sagorum	Hylidae	6.337
Pseudacris cadaverina	Hylidae	13.258
Pseudacris clarkii	Hylidae	0.251
Pseudacris crucifer	Hylidae	18.967
Pseudacris hypochondriaca	Hylidae	13.258
Pseudis bolbodactyla	Hylidae	9.333

Pseudis cardosoi	Hylidae	2.098
Pseudis minuta	Hylidae	2.098
Pseudis paradoxa	Hylidae	9.333
Pseudis platensis	Hylidae	1.424
Ptychohyla euthysanota	Hylidae	5.562
Ptychohyla hypomykter	Hylidae	7.824
Ptychohyla leonhardschultzei	Hylidae	0.162
Ptychohyla macrotympanum	Hylidae	4.944
Ptychohyla zophodes	Hylidae	1.318
Quilticohyla acrochorda	Hylidae	4.944
Rhaebo blombergi	Bufonidae	11.646
Rhaebo caeruleostictus	Bufonidae	36.486
Rhaebo ecuadorensis	Bufonidae	3.746
Rhaebo glaberrimus	Bufonidae	3.746
Rhaebo guttatus	Bufonidae	6.416
Rhaebo haematiticus	Bufonidae	24.195
Rhaebo hypomelas	Bufonidae	1.096
Rhaebo nasicus	Bufonidae	38.907
Rhinella achavali	Bufonidae	2.373
Rhinella acutirostris	Bufonidae	5.121
Rhinella alata	Bufonidae	5.503
Rhinella arenarum	Bufonidae	4.482
Rhinella arunco	Bufonidae	5.675

Rhinella bergi	Bufonidae	0.841
Rhinella castaneotica	Bufonidae	9.815
Rhinella centralis	Bufonidae	1.858
Rhinella crucifer	Bufonidae	2.764
Rhinella dapsilis	Bufonidae	1.178
Rhinella diptycha	Bufonidae	1.178
Rhinella dorbignyi	Bufonidae	5.121
Rhinella festae	Bufonidae	6.240
Rhinella granulosa	Bufonidae	3.466
Rhinella henseli	Bufonidae	14.172
Rhinella hoogmoedi	Bufonidae	2.436
Rhinella humboldti	Bufonidae	0.091
Rhinella icterica	Bufonidae	0.417
Rhinella limensis	Bufonidae	6.244
Rhinella macrorhina	Bufonidae	1.419
Rhinella major	Bufonidae	1.945
Rhinella margaritifera	Bufonidae	1.828
Rhinella merianae	Bufonidae	9.534
Rhinella mirandaribeiroi	Bufonidae	1.945
Rhinella nicefori	Bufonidae	4.021
Rhinella ocellata	Bufonidae	2.681
Rhinella ornata	Bufonidae	0.795
Rhinella poeppigii	Bufonidae	8.490

Rhinella proboscidea	Bufonidae	7.353
Rhinella pygmaea	Bufonidae	12.813
Rhinella roqueana	Bufonidae	2.558
Rhinella rubescens	Bufonidae	2.413
Rhinella ruizi	Bufonidae	1.201
Rhinella scitula	Bufonidae	4.482
Rhinella spinulosa	Bufonidae	2.494
Rhinella stanlaii	Bufonidae	5.641
Rhinella sternosignata	Bufonidae	11.659
Rhinella veraguensis	Bufonidae	2.725
Sarcohyla arborescandens	Hylidae	1.628
Sarcohyla bistincta	Hylidae	5.441
Sarcohyla celata	Hylidae	0.666
Sarcohyla charadricola	Hylidae	0.735
Sarcohyla cyclada	Hylidae	1.628
Sarcohyla pentheter	Hylidae	2.312
Scarthyla goinorum	Hylidae	6.198
Scarthyla vigilans	Hylidae	6.198
Scinax acuminatus	Hylidae	17.400
Scinax agilis	Hylidae	4.144
Scinax altae	Hylidae	17.172
Scinax alter	Hylidae	2.905
Scinax arduous	Hylidae	10.211

Scinax argyreornatus	Hylidae	26.588
Scinax auratus	Hylidae	4.144
Scinax blairi	Hylidae	0.012
Scinax boesemani	Hylidae	4.017
Scinax boulengeri	Hylidae	5.791
Scinax caldarum	Hylidae	0.258
Scinax cardosoi	Hylidae	19.335
Scinax catharinae	Hylidae	14.724
Scinax crospedospilus	Hylidae	3.505
Scinax cruentomma	Hylidae	24.130
Scinax curicica	Hylidae	14.319
Scinax cuspidatus	Hylidae	12.595
Scinax duartei	Hylidae	3.326
Scinax elaeochroa	Hylidae	3.447
Scinax eurydice	Hylidae	21.869
Scinax flavoguttatus	Hylidae	3.326
Scinax funereus	Hylidae	2.293
Scinax fuscomarginatus	Hylidae	0.012
Scinax fuscovarius	Hylidae	1.861
Scinax garbei	Hylidae	6.968
Scinax granulatus	Hylidae	25.004
Scinax hayii	Hylidae	0.731
Scinax ictericus	Hylidae	3.146

Scinax imbegue	Hylidae	1.299
Scinax jolyi	Hylidae	7.349
Scinax kennedyi	Hylidae	2.027
Scinax littoralis	Hylidae	4.399
Scinax longilineus	Hylidae	7.542
Scinax luizotavioi	Hylidae	1.122
Scinax nasicus	Hylidae	21.065
Scinax nebulosus	Hylidae	0.363
Scinax obtriangulatus	Hylidae	14.063
Scinax oreites	Hylidae	3.999
Scinax pachycrus	Hylidae	9.169
Scinax pedromedinae	Hylidae	6.097
Scinax perereca	Hylidae	3.505
Scinax perpusillus	Hylidae	1.983
Scinax proboscideus	Hylidae	6.968
Scinax quinquefasciatus	Hylidae	5.812
Scinax rizibilis	Hylidae	3.999
Scinax rostratus	Hylidae	15.593
Scinax ruber	Hylidae	1.286
Scinax similis	Hylidae	3.499
Scinax squalirostris	Hylidae	5.248
Scinax staufferi	Hylidae	21.439
Scinax strigilatus	Hylidae	17.400

Scinax sugillatus	Hylidae	5.791
Scinax trapicheiroi	Hylidae	0.203
Scinax tymbamirim	Hylidae	22.131
Scinax uruguayus	Hylidae	7.733
Scinax wandae	Hylidae	0.258
Scinax x signatus	Hylidae	1.286
Smilisca baudinii	Hylidae	24.519
Smilisca cyanosticta	Hylidae	15.630
Smilisca dentata	Hylidae	5.622
Smilisca fodiens	Hylidae	21.085
Smilisca phaeota	Hylidae	10.612
Smilisca puma	Hylidae	10.612
Smilisca sila	Hylidae	16.984
Smilisca sordida	Hylidae	5.622
Sphaenorhynchus caramaschii	Hylidae	2.413
Sphaenorhynchus carneus	Hylidae	2.259
Sphaenorhynchus dorisae	Hylidae	0.389
Sphaenorhynchus lacteus	Hylidae	7.149
Sphaenorhynchus planicola	Hylidae	2.413
Sphaenorhynchus platycephalus	Hylidae	0.389
Sphaenorhynchus prasinus	Hylidae	2.259
Sphaenorhynchus surdus	Hylidae	8.258
Tepuihyla exophthalma	Hylidae	12.833

Tepuihyla tuberculosa	Hylidae	3.614
Tlalocohyla godmani	Hylidae	18.433
Tlalocohyla loquax	Hylidae	18.433
Tlalocohyla picta	Hylidae	23.944
Tlalocohyla smithii	Hylidae	23.944
Trachycephalus coriaceus	Hylidae	12.435
Trachycephalus cunauaru	Hylidae	0.839
Trachycephalus hadroceps	Hylidae	2.791
Trachycephalus imitatrix	Hylidae	1.598
Trachycephalus jordani	Hylidae	2.386
Trachycephalus mesophaeus	Hylidae	2.431
Trachycephalus nigromaculatus	Hylidae	13.773
Trachycephalus resinifictrix	Hylidae	8.434
Trachycephalus venulosus	Hylidae	4.296
Triprion petasatus	Hylidae	19.011
Triprion spatulatus	Hylidae	25.453
Triprion spinosus	Hylidae	19.011

Table S2. Evaluation metrics and occurrences numbers calculated from the 135 models of each species.

Species	Average AICc	Average Delta AICc	Average OR	Average AUC	Occurrences
Amazophrynella minuta	1982.686	21.855	0.08	0.645	91
Amazophrynella siona	1522.59	4.609	0.198	0.679	109

Anaxyrus boreas	7451.978	484.576	0	0.905	8239
Anaxyrus californicus	2016.36	61.721	0.006	0.842	237
Anaxyrus cognatus	15143.709	429.199	0	0.837	1961
Anaxyrus compactilis	4615.642	110.676	0.021	0.833	234
Anaxyrus debilis	9923.204	25.38	0.075	0.608	644
Anaxyrus kelloggi	897.911	6.292	0.096	0.643	60
Anaxyrus mexicanus	515.782	3.8	0.063	0.808	39
Anaxyrus punctatus	50322.543	173.691	0.006	0.706	3564
Anaxyrus retiformis	1347.291	26.654	0.039	0.824	83
Anaxyrus speciosus	24735.915	546.951	0.002	0.736	1377
Anaxyrus woodhousii	13442.998	64.149	0.013	0.712	4707
Aplastodiscus albofrenatus	135.508	8.706	0.083	0.86	16
Aplastodiscus albosignatus	484.389	4.6	0.107	0.777	36
Aplastodiscus arildae	385.321	1.927	0	0.878	37
Aplastodiscus cavicola	146.833	6.308	0.069	0.799	12
Aplastodiscus cochranae	80.192	25.241	0.5	0.865	8
Aplastodiscus ehrhardti	297.841	1.632	0	0.802	27
Aplastodiscus leucopygius	358.464	3.016	0.036	0.882	66
Aplastodiscus lutzorum	52.08	17.662	0.25	0.902	7
Aplastodiscus perviridis	707.387	13.523	0.032	0.73	82
Aplastodiscus weygoldti	118.021	26.916	0.167	0.922	7

Atelopus barbotini	356.737	3.951	0.214	0.718	32
Atelopus bomolochos	401.154	4.896	0.156	0.637	35
Atelopus carrikeri	84.776	1.351	0.125	0.528	13
Atelopus chiriquiensis	227.396	6.267	0.143	0.737	22
Atelopus coynei	688.361	86.6	0.006	0.825	54
Atelopus cruciger	274.836	9.386	0.063	0.886	30
Atelopus ebenoides	111.26	33.759	0.25	0.785	9
Atelopus elegans	370.868	2.652	0.014	0.715	32
Atelopus exiguus	116.401	5.626	0	0.607	26
Atelopus flavescens	507.866	1.736	0.125	0.875	144
Atelopus franciscus	497.502	5.262	0.1	0.594	40
Atelopus hoogmoedi	1754.812	31.39	0.023	0.768	97
Atelopus ignescens	1315.708	3.924	0.012	0.937	138
Atelopus laetissimus	19.224	9.447	0.25	0.834	8
Atelopus limosus	88.456	39.73	0.036	0.931	12
Atelopus longirostris	304.605	50.869	0.014	0.773	74
Atelopus manauensis	255.159	8.641	0.094	0.847	37
Atelopus mindoensis	151.639	4.93	0.152	0.886	16
Atelopus muisca	64.531	18.389	0.188	0.72	11
Atelopus nanay	153.838	4.185	0	0.587	33
Atelopus nepiozomus	96.13	7.99	0.2	0.748	7
Atelopus palmatus	121.878	15.959	0	0.814	15
Atelopus pastuso	128.364	2.997	0	0.575	20

Atelopus peruensis	77.368	5.403	0.475	0.804	11
Atelopus podocarpus	49.697	2.108	0.25	0.76	8
Atelopus pulcher	330.793	2.894	0.113	0.895	25
Atelopus senex	130.221	10.185	0.25	0.814	20
Atelopus sernai	92.261	15.245	0.2	0.949	7
Atelopus spumarius	1180.359	25.918	0.018	0.822	60
Atelopus spurrelli	289.956	3.844	0.104	0.71	29
Atelopus subornatus	55.869	0.189	0	0.754	11
Atelopus varius	616.496	25.817	0.032	0.813	54
Atelopus walkeri	62.488	18.752	0.107	0.941	13
Atelopus zeteki	100.949	7.851	0.167	0.921	18
Atlantihyla spinipollex	346.558	1.893	0.05	0.885	25
Boana albomarginata	1739.911	48.887	0.077	0.802	373
Boana albopunctata	1681.738	29.601	0.099	0.71	227
Boana alfaroi	1449.118	8.314	0	0.733	91
Boana almendarizae	2027.257	47.368	0.05	0.847	126
Boana appendiculata	3079.086	109.179	0.022	0.768	194
Boana atlantica	286.135	7.603	0.063	0.917	17
Boana bandeirantes	83.749	21.584	0.375	0.753	12
Boana bischoffi	879.672	11.211	0.021	0.741	201
Boana boans	18877.563	452.384	0.003	0.77	739
Boana caingua	373.955	4.343	0	0.561	30
Boana calcarata	5841.286	198.525	0.021	0.731	280

Boana callipleura	258.891	0.759	0.089	0.738	19
Boana cinerascens	2080.489	5.78	0.012	0.67	492
Boana cordobae	349.045	3.427	0.042	0.93	113
Boana courtoisae	442.698	6.82	0.063	0.88	37
Boana crepitans	12380.497	208.078	0.015	0.712	503
Boana curupi	194.474	2.602	0.167	0.724	18
Boana dentei	327.239	2.589	0.043	0.901	61
Boana diabolica	121.681	0	0.25	0.841	17
Boana faber	2758.841	7.665	0	0.908	721
Boana fasciata	4555.519	85.529	0.004	0.703	209
Boana geographica	9451.871	182.166	0.024	0.765	397
Boana heilprini	648.92	5.49	0.169	0.704	61
Boana joaquini	158.577	6.985	0.25	0.752	18
Boana lanciformis	2632.093	70.818	0.01	0.605	682
Boana lemai	75.875	5.011	0.75	0.55	10
Boana leptolineata	332.71	5.674	0.093	0.809	39
Boana lundii	744.96	1.998	0	0.762	82
Boana maculateralis	1209.147	20.317	0	0.822	59
Boana marginata	399.885	4.601	0	0.755	25
Boana microderma	176.946	10.727	0.125	0.816	15
Boana multifasciata	2786.102	21.652	0.015	0.833	140
Boana nigra	264.096	5.453	0.012	0.748	27
Boana nympha	377.781	16.111	0.063	0.741	68

Boana ornatissima	453.11	5.478	0.083	0.852	30
Boana pardalis	1698.715	29.536	0	0.844	94
Boana pellucens	742.124	7.276	0.025	0.838	243
Boana picturata	552.221	6.98	0.036	0.839	183
Boana platanera	12869.106	215.787	0.005	0.625	615
Boana polytaenia	1466.86	11.636	0.013	0.954	82
Boana prasina	543.612	7.939	0.016	0.851	86
Boana pugnax	10874.787	283.363	0.002	0.772	557
Boana pulchella	19142.941	261.57	0.001	0.898	916
Boana punctata	13179.523	380.746	0.004	0.764	523
Boana raniceps	2904.795	14.501	0.018	0.708	545
Boana riojana	1032.993	45.272	0.015	0.772	193
Boana rosenbergi	1217.97	17.739	0.033	0.743	583
Boana rubracyla	334.583	4.143	0.143	0.831	32
Boana rufitela	4130.95	52.504	0	0.786	250
Boana semiguttata	222.714	5.536	0.25	0.584	18
Boana semilineata	1170.154	16.838	0	0.883	219
Boana sibleszi	155.882	3.355	0	0.779	15
Boana steinbachi	533.468	52.021	0.031	0.817	35
Boana ventrimaculata	470.314	9.05	0.031	0.637	36
Boana wavrini	657.341	7.453	0.036	0.776	68
Boana xerophylla	7260.508	91.148	0	0.633	334

Bokermannohyla alvarengai	207.478	3.155	0.063	0.706	22
Bokermannohyla caramaschii	315.043	13.965	0	0.878	27
Bokermannohyla circumdata	635.18	7.191	0.031	0.923	81
Bokermannohyla hylax	300.246	7.828	0.063	0.827	79
Bokermannohyla ibitiguara	74.42	9.042	0	0.892	9
Bokermannohyla luctuosa	369.737	9.328	0	0.846	29
Bokermannohyla sapiranga	159.848	0.876	0.25	0.628	14
Bromeliohyla bromeliacia	286.721	12.409	0.063	0.917	43
Bromeliohyla dendroscarta	310.86	2.086	0.063	0.614	30
Charadrahyla altipotens	65.113	4.506	0.071	0.936	9
Charadrahyla chaneque	519.973	19.501	0	0.577	25
Charadrahyla nephila	432.16	26.154	0.042	0.802	46
Charadrahyla taeniopus	548.328	9.603	0.022	0.885	121
Corythomantis greeningi	584.322	10.375	0.031	0.851	36
Dendrophryniscus berthalutzae	90.746	4.206	0	0.889	12
Dendrophryniscus brevipollicatus	559.603	4.626	0.024	0.857	40
Dendrophryniscus haddadi	79.345	0.824	0.25	0.72	10
Dendropsophus acreanus	344.41	6.626	0	0.629	32

Dendropsophus anceps	530.254	6.019	0.188	0.861	33
Dendropsophus arndti	94.272	6.704	0	0.979	24
Dendropsophus berthalutzae	599.728	15.36	0	0.873	42
Dendropsophus bifurcus	924.107	16.772	0.021	0.898	301
Dendropsophus bipunctatus	642.105	11.208	0	0.887	61
Dendropsophus bogerti	1226.321	2.02	0	0.926	232
Dendropsophus bokermanni	505.052	3.534	0.167	0.766	67
Dendropsophus branneri	872.036	19.3	0	0.941	76
Dendropsophus brevifrons	873.447	12.034	0.138	0.708	119
Dendropsophus carnifex	320.839	6.154	0.036	0.955	139
Dendropsophus columbianus	1922.669	81.014	0.009	0.809	283
Dendropsophus counani	45.815	6.406	0.25	0.942	7
Dendropsophus cruzi	201.631	6.072	0.125	0.809	11
Dendropsophus decipiens	611.655	11.624	0.036	0.89	49
Dendropsophus ebraccatus	3989.269	24.886	0	0.792	699
Dendropsophus elegans	2010.731	29.498	0.043	0.769	266
Dendropsophus elianeae	838.343	6.979	0.091	0.803	42
Dendropsophus gaucheri	65.927	0.329	0.464	0.933	7
Dendropsophus giesleri	258.634	7.473	0.125	0.825	18

Dendropsophus gryllatus	NA	NA	0.333	0.992	10
Dendropsophus haddadi	447.311	43.622	0.031	0.837	25
Dendropsophus haraldschultzi	173.001	4.875	0.083	0.939	24
Dendropsophus jimi	376.646	8.445	0.042	0.748	19
Dendropsophus joannae	122.509	3.925	0.25	0.875	12
Dendropsophus kamagarini	491.256	26.728	0	0.798	34
Dendropsophus koechlini	204.065	21.247	0.19	0.906	19
Dendropsophus labialis	1117.246	68.042	0.011	0.92	68
Dendropsophus leali	659.643	1.913	0	0.619	61
Dendropsophus leucophyllatus	2622.686	12.68	0.001	0.715	243
Dendropsophus luddeckei	261.024	12.825	0.068	0.941	23
Dendropsophus luteoocellatus	72.808	10.739	0	0.883	7
Dendropsophus manonegra	163.06	4.265	0.111	0.874	17
Dendropsophus marmoratus	1520.93	10.113	0.031	0.678	221
Dendropsophus mathiassoni	1456.438	4.917	0.028	0.756	225
Dendropsophus melanargyreus	704.406	4.106	0	0.693	74
Dendropsophus meridensis	210.702	85.059	0.125	0.881	10
Dendropsophus microcephalus	26762.418	740.625	0	0.784	1125

Dendropsophus microps	806.694	8.683	0	0.852	101
Dendropsophus minusculus	303.384	2.559	0.071	0.768	35
Dendropsophus minutus	8031.84	92.595	0.003	0.739	861
Dendropsophus miyatai	172.193	2.636	0.25	0.572	27
Dendropsophus molitor	6052.614	146.436	0	0.913	440
Dendropsophus nanus	4394.032	51.484	0.017	0.755	402
Dendropsophus norandinus	126.334	0.83	0.143	0.794	16
Dendropsophus oliveirai	510.014	54.836	0	0.556	24
Dendropsophus padreluna	231.196	6.139	0	0.799	23
Dendropsophus parviceps	1721.91	21.201	0.046	0.762	317
Dendropsophus pauiniensis	320.218	27.536	0	0.838	23
Dendropsophus phlebodes	1093.891	4.341	0.142	0.703	141
Dendropsophus praestans	NA	NA	0.667	0.675	8
Dendropsophus pseudomeridianus	87.976	7.651	0.05	0.801	14
Dendropsophus reticulatus	2320.149	32.039	0.061	0.818	132
Dendropsophus rhodopeplus	1849.65	27.264	0.038	0.651	300
Dendropsophus riveroi	366.976	0.663	0.063	0.581	32
Dendropsophus robertmertensi	1101.111	4.895	0.033	0.812	98
Dendropsophus rossalleni	316.27	7.844	0.25	0.706	16

Dendropsophus rubicundulus	771.628	6.337	0	0.594	54
Dendropsophus ruschii	25.015	4.91	0.25	0.995	7
Dendropsophus sanborni	1968.94	7.691	0.057	0.712	192
Dendropsophus sarayacuensis	1443.451	22.624	0.047	0.719	263
Dendropsophus sartori	350.538	4.422	0.093	0.851	36
Dendropsophus schubarti	234.401	8.462	0.125	0.85	23
Dendropsophus seniculus	452.223	3.893	0	0.815	50
Dendropsophus shiwiarum	348.428	2.55	0	0.693	30
Dendropsophus soaresi	88.001	0.625	0.25	0.867	12
Dendropsophus stingi	108.26	2.946	0.333	0.635	10
Dendropsophus subocularis	445.861	8.304	0.03	0.725	31
Dendropsophus timbeba	124.722	2.8	0.25	0.897	11
Dendropsophus triangulum	1602.773	8.691	0.024	0.71	163
Dendropsophus tritaeniatus	97.027	15.841	0.5	0.795	7
Dendropsophus virolinensis	301.118	7.018	0.071	0.822	28
Dendropsophus walfordi	1301.57	137.487	0.054	0.78	63
Dendropsophus werneri	441.39	1.979	0.125	0.837	68
Dryaderces pearsoni	101.059	0.524	0.125	0.847	11
Dryophytes arenicolor	51245.692	2496.132	0.003	0.706	3122

Dryophytes cinereus	120399.567	2188.711	0.023	0.731	8222
Dryophytes euphorbiaceus	1641.608	14.697	0.01	0.845	111
Dryophytes eximius	29592.949	210.078	0	0.794	1474
Dryophytes plicatus	4055.881	69.591	0.004	0.843	269
Dryophytes squirellus	76199.961	378.739	0	0.795	4982
Dryophytes walkeri	1220.381	88.772	0	0.923	76
Dryophytes wrightorum	1820.161	17.19	0	0.895	167
Duellmanohyla chamulae	343.979	6.487	0.049	0.863	28
Duellmanohyla ignicolor	530.899	6.691	0	0.802	23
Duellmanohyla rufioculis	585.946	32.91	0.095	0.795	132
Duellmanohyla salvavida	NA	NA	0.333	0.684	7
Duellmanohyla schmidtorum	549.156	3.483	0.071	0.751	52
Duellmanohyla soralia	152.59	1.609	0	0.82	21
Duellmanohyla uranochroa	511.99	24.08	0.031	0.813	53
Ecnomiohyla miliaria	154.148	6.017	0.083	0.772	11
Exerodonta bivocata	203.517	9.188	0	0.911	12
Exerodonta catracha	52.246	3.559	0.125	0.728	8
Exerodonta chimalapa	207.682	2.421	0.25	0.777	17
Exerodonta melanomma	488.799	6.067	0.042	0.746	40
Exerodonta smaragdina	1043.461	11.587	0.003	0.767	102

Exerodonta sumichrasti	1034.263	1.312	0.077	0.678	96
Exerodonta xera	192.699	2.483	0	0.771	24
Hyloscirtus alytolylax	485.835	11.715	0	0.863	112
Hyloscirtus antioquia	97.528	29.386	0.125	0.891	10
Hyloscirtus armatus	304.03	0.225	0	0.676	18
Hyloscirtus bogotensis	630.488	6.323	0.031	0.832	50
Hyloscirtus callipeza	339.797	8.708	0.186	0.757	26
Hyloscirtus colymba	322.976	5.952	0.063	0.71	29
Hyloscirtus conscientia	72.459	2.881	0	0.566	16
Hyloscirtus criptico	75.804	8.964	0.188	0.811	9
Hyloscirtus denticulentus	216.574	106.658	0.083	0.827	15
Hyloscirtus larinopygion	650.141	7.304	0.056	0.897	95
Hyloscirtus mashpi	155.73	7.358	0	0.746	25
Hyloscirtus palmeri	841.972	17.617	0.139	0.712	120
Hyloscirtus phyllognathus	893.598	21.382	0.172	0.807	97
Hyloscirtus platydactylus	67.361	4.577	0.25	0.856	7
Hyloscirtus psarolaimus	171.236	1.246	0	0.678	19
Hyloscirtus tigrinus	74.624	1.147	0.25	0.839	11
Incilius alvarius	3971.516	58.061	0	0.724	1306
Incilius aucoinae	534.742	6.539	0.028	0.914	147
Incilius bocourti	1117.571	13.873	0.014	0.897	145

Incilius campbelli	454.683	6.687	0.042	0.87	49
Incilius canaliferus	1665.16	7.555	0	0.903	193
Incilius cavifrons	638.511	32.654	0.05	0.88	86
Incilius coccifer	2756.817	92.424	0	0.708	287
Incilius coniferus	1667.934	45.781	0.037	0.782	238
Incilius cristatus	514.625	44.237	0	0.805	72
Incilius gemmifer	294.883	4.485	0.08	0.873	22
Incilius ibarrai	323.776	3.929	0.05	0.871	36
Incilius leucomyos	263.865	6.672	0.05	0.893	23
Incilius luetkenii	1675.115	19.43	0	0.842	280
Incilius macrocristatus	786.609	7.883	0	0.74	51
Incilius marmoreus	5137.658	30.688	0.008	0.803	616
Incilius mazatlanensis	4633.973	18.404	0.007	0.829	698
Incilius mccoyi	183.758	4.663	0	0.732	19
Incilius melanochlorus	947.554	52.759	0.028	0.862	197
Incilius nebulifer	4143.043	70.531	0	0.799	4363
Incilius occidentalis	8883.076	0	0.005	0.702	931
Incilius perplexus	1408.169	10.18	0.039	0.757	112
Incilius porteri	348.635	11.151	0	0.971	76
Incilius spiculatus	123.91	2.42	0.083	0.914	12
Incilius tacanensis	237.767	4.939	0	0.936	25
Incilius tutelarius	456.108	9.802	0.042	0.829	36
Incilius valliceps	53825.348	328.176	0	0.791	2464

Isthmohyla angustilineata	117.816	16.226	0.125	0.918	12
Isthmohyla debilis	NA	NA	0.25	0.806	8
Isthmohyla lancasteri	269.04	7.546	0.071	0.765	32
Isthmohyla picadoi	208.788	4.623	0.188	0.83	18
Isthmohyla pictipes	233.27	13.121	0.071	0.81	27
Isthmohyla pseudopuma	679.239	20.199	0.042	0.913	100
Isthmohyla rivularis	439.325	14.825	0.036	0.85	47
Isthmohyla tica	327.212	11.18	0.05	0.885	31
Isthmohyla zeteki	189.41	2.649	0.1	0.745	19
Itapotihyla langsdorffii	848.321	5.092	0	0.871	180
Lysapsus bolivianus	269.607	23.29	0	0.81	19
Lysapsus laevis	223.407	23.598	0.193	0.829	18
Lysapsus limellum	1044.109	2.891	0.021	0.846	138
Megastomatohyla mixe	124.6	3.505	0	0.782	13
Megastomatohyla mixomaculata	382.856	34.696	0.054	0.896	26
Megastomatohyla nubicola	87.697	2.039	0.2	0.827	10
Melanophryniscus atroluteus	301.436	4.043	0.161	0.864	22
Melanophryniscus klappenbachi	482.49	4.547	0	0.746	33
Melanophryniscus macrogranulosus	NA	NA	0.333	0.998	7
Melanophryniscus montevidensis	106.884	23.252	0.343	0.802	7

Melanophryniscus moreirae	86.509	2.806	0.2	0.839	12
Melanophryniscus pachyrhynus	NA	NA	0.25	0.753	9
Melanophryniscus rubriventris	301.256	3.231	0.047	0.762	31
Melanophryniscus simplex	133.792	3.472	0.25	0.72	14
Melanophryniscus stelzneri	781.844	52.564	0.222	0.651	32
Melanophryniscus tumifrons	323.161	4.539	0.063	0.722	20
Myersiohyla chamaeleo	21.71	0.515	0.25	0.711	7
Nannophryne cophotis	118.512	17.499	0.375	0.703	9
Nannophryne variegata	645.075	9.706	0.004	0.869	75
Nesorohyla kanaima	160.466	4.34	0.188	0.904	17
Nyctimantis rugiceps	530.537	3.153	0	0.802	38
Oreophrynella macconnelli	73.348	3.212	0.5	0.585	7
Osornophryne antisana	113.016	7.815	0.25	0.873	18
Osornophryne bufoniformis	261.456	4.068	0.25	0.832	27
Osornophryne guacamayo	346.697	17.656	0.063	0.786	35
Osornophryne occidentalis	104.104	51.703	0.25	0.714	13
Osornophryne percrassa	309.817	4.649	0.05	0.965	39
Osteocephalus alboguttatus	450.723	4.578	0	0.749	27
Osteocephalus buckleyi	2671.62	80.318	0	0.779	122

Osteocephalus cabrerai	660.905	8.784	0	0.739	42
Osteocephalus cannatellai	776.517	8.213	0	0.555	47
Osteocephalus carri	218.001	2.481	0	0.889	22
Osteocephalus castaneicola	823.185	15.049	0.071	0.82	42
Osteocephalus deridens	1301.368	18.6	0	0.725	62
Osteocephalus festae	139.825	9.288	0	0.796	23
Osteocephalus fuscifacies	1223.535	19.591	0.063	0.711	70
Osteocephalus helenae	516.338	4.619	0	0.595	27
Osteocephalus leprieurii	2897.246	78.059	0	0.556	135
Osteocephalus mimeticus	425.042	37.887	0.25	0.893	22
Osteocephalus mutabor	1301.88	21.081	0.018	0.872	79
Osteocephalus oophagus	791.858	2.556	0	0.844	123
Osteocephalus planiceps	939.785	4.832	0.023	0.781	227
Osteocephalus subtilis	NA	NA	0.333	0.755	8
Osteocephalus taurinus	15993.811	187.731	0.002	0.704	677
Osteocephalus verruciger	1647.726	125.292	0.009	0.945	116
Osteocephalus vilarsi	196.223	5.286	0.06	0.941	15
Osteocephalus yasuni	348.006	13.414	0	0.738	85
Osteopilus dominicensis	2006.874	11.213	0	0.571	394
Osteopilus marianae	41.265	0.07	0.375	0.582	10

Osteopilus ocellatus	4520.812	89.309	0.004	0.772	182
Osteopilus pulchrilineatus	594.748	4.928	0	0.576	45
Osteopilus septentrionalis	3214.373	12.214	0.013	0.927	3178
Osteopilus vastus	490.699	5.4	0.027	0.711	43
Osteopilus wilderi	96.729	1.165	0.167	0.751	16
Peltophryne empusa	179.712	3.456	0.25	0.867	19
Peltophryne fustiger	138.734	0	0.188	0.653	25
Peltophryne guentheri	638.865	2.24	0.05	0.763	52
Peltophryne longinasus	NA	NA	0.25	0.705	12
Peltophryne peltocephala	860.427	7.02	0.167	0.566	161
Peltophryne taladai	52.596	1.145	0.25	0.861	9
Phyllodytes edelmoi	88.881	6.331	0.292	0.832	29
Phyllodytes luteolus	377.114	3.823	0	0.885	48
Plectrohyla acanthodes	340.513	0.824	0.136	0.781	41
Plectrohyla avia	133.876	4.946	0	0.992	16
Plectrohyla glandulosa	312.016	7.807	0.1	0.947	34
Plectrohyla guatemalensis	932.353	13.903	0.036	0.88	74
Plectrohyla hartwegi	303.176	4.344	0.063	0.778	21
Plectrohyla ixil	281.866	2.989	0.063	0.809	38
Plectrohyla lacertosa	412.545	20.939	0.036	0.927	44
Plectrohyla matudai	1049.678	22.992	0	0.832	145

Plectrohyla pokomchi	NA	NA	0.333	0.887	7
Plectrohyla quecchi	71.074	1.177	0	0.732	11
Plectrohyla sagorum	576.825	3.981	0.028	0.906	62
Pseudacris cadaverina	2422.558	32.149	0.011	0.854	1805
Pseudacris clarkii	3222.82	53.694	0.024	0.738	689
Pseudacris crucifer	14449.256	288.895	0.074	0.702	11534
Pseudacris hypochondriaca	1325.01	54.958	0.102	0.743	88
Pseudis bolbodactyla	364.534	2.292	0.038	0.81	19
Pseudis cardosoi	351.172	1.717	0.208	0.781	26
Pseudis minuta	1850.662	4.867	0.011	0.808	267
Pseudis paradoxa	2156.948	14.205	0.012	0.633	250
Pseudis platensis	604.5	2.204	0.085	0.809	98
Ptychohyla euthysanota	1009.08	26.491	0.018	0.837	130
Ptychohyla hypomykter	815.92	24.669	0.021	0.911	72
Ptychohyla leonhardschultzei	700.063	10.483	0	0.815	56
Ptychohyla macrotympanum	228.346	15.371	0.1	0.822	17
Ptychohyla zophodes	522.292	13.857	0.036	0.719	49
Quilticohyla acrochorda	62.724	0.784	0.375	0.717	10
Rhaebo blombergi	328.098	3.186	0.063	0.823	29
Rhaebo caeruleostictus	273.891	8.415	0.05	0.799	21
Rhaebo ecuadorensis	808.237	3.16	0	0.665	61
Rhaebo glaberrimus	963.97	40.879	0.055	0.723	79

Rhaebo guttatus	3373.205	27.85	0.029	0.72	389
Rhaebo haematiticus	5278.474	199.51	0.008	0.611	826
Rhaebo hypomelas	131.871	5.344	0.125	0.903	11
Rhaebo nasicus	114.73	1.35	0.125	0.923	11
Rheohyla miotympanum	10228.847	193.742	0	0.849	616
Rhinella achavali	176.884	8.909	0.5	0.716	15
Rhinella acutirostris	7783.887	544.55	0.001	0.949	316
Rhinella alata	597.591	5.051	0.229	0.853	542
Rhinella arenarum	4434.693	67.638	0.002	0.819	1143
Rhinella arunco	107.323	5.522	0.375	0.769	15
Rhinella beebei	2831.989	38.445	0.031	0.717	149
Rhinella bergi	407.797	5.031	0.038	0.722	36
Rhinella castaneotica	573.841	1.9	0.042	0.703	133
Rhinella centralis	150.447	26.57	0.25	0.666	13
Rhinella crucifer	3866.428	56.455	0	0.786	192
Rhinella dapsilis	593.814	10.148	0	0.748	129
Rhinella diptycha	35326.546	57.873	0	0.712	1442
Rhinella dorbignyi	1432.03	21.173	0	0.866	580
Rhinella festae	3022.297	406.677	0.014	0.728	146
Rhinella granulosa	6752.037	86.411	0	0.786	286
Rhinella henseli	343.585	3.843	0.043	0.791	24
Rhinella hoogmoedi	1006.965	5.791	0.003	0.962	61
Rhinella horribilis	120542.795	323.249	0	0.711	5178

Rhinella humboldti	3815.465	21.26	0.006	0.672	539
Rhinella icterica	3986.125	41.75	0	0.848	802
Rhinella limensis	382.887	2.032	0.042	0.862	29
Rhinella macrorhina	416.67	12.255	0.036	0.891	44
Rhinella major	3993.656	35.722	0.003	0.808	192
Rhinella margaritifera	7499.273	74.895	0.003	0.762	1102
Rhinella marina	85489.922	1312.673	0	0.53	3883
Rhinella merianae	490.613	8.087	0.05	0.593	62
Rhinella mirandaribeiroi	976.323	0.928	0	0.709	59
Rhinella nicefori	43.218	1.915	0.125	0.702	11
Rhinella ocellata	65.04	5.669	0.333	0.598	7
Rhinella ornata	2373.147	16.419	0	0.828	574
Rhinella poeppigii	725.481	7.971	0.028	0.552	75
Rhinella proboscidea	528.458	7.505	0	0.869	72
Rhinella pygmaea	358.422	21.561	0.083	0.95	25
Rhinella roqueana	570.004	3.976	0	0.655	33
Rhinella rubescens	694.244	5.417	0	0.731	66
Rhinella ruizi	214.191	9.495	0	0.954	20
Rhinella scitula	290.274	2.713	0.125	0.705	12
Rhinella spinulosa	10601.238	283.762	0.002	0.812	442
Rhinella stanlaii	309.643	19.245	0.063	0.801	20
Rhinella sternosignata	960.396	31.504	0.021	0.805	100

Rhinella veraguensis	289.82	4.234	0	0.919	19
Sarcohyla arborescandens	779.242	3.783	0.021	0.844	52
Sarcohyla bistincta	799.728	5.252	0.063	0.778	51
Sarcohyla celata	39.653	5.292	0.667	0.563	7
Sarcohyla charadricola	174.711	3.62	0.034	0.74	23
Sarcohyla cyclada	133.413	7.119	0	0.836	27
Sarcohyla hapsa	373.606	11.875	0.042	0.906	43
Sarcohyla pentheter	109.804	38.562	0.125	0.874	9
Scarthyla goinorum	609.833	4.059	0.083	0.72	47
Scarthyla vigilans	1660.195	8.03	0.005	0.848	214
Scinax acuminatus	2132.989	4.997	0.103	0.732	218
Scinax agilis	128.364	16.642	0.167	0.75	7
Scinax altae	254.911	14.065	0.188	0.728	25
Scinax alter	1280.649	11.286	0	0.877	91
Scinax arduous	38.559	5.058	0.333	0.628	7
Scinax argyreornatus	475.1	66.407	0	0.764	23
Scinax auratus	137.556	6.321	0.125	0.844	12
Scinax blairi	126.882	5.383	0.25	0.796	10
Scinax boesemani	1089.046	14.131	0	0.847	140
Scinax boulengeri	1115.047	23.655	0	0.849	246
Scinax caldarum	24.203	5.921	0	0.884	7
Scinax caprarius	196.562	4.887	0.179	0.72	18

Scinax cardosoi	NA	NA	0.5	0.594	7
Scinax catharinae	510.522	5.851	0	0.869	23
Scinax crospedospilus	310.763	1.056	0.125	0.824	44
Scinax cruentomma	1834.645	56.09	0.025	0.857	84
Scinax curicica	71.031	4.87	0.125	0.736	8
Scinax cuspidatus	406.401	11.226	0.107	0.797	42
Scinax duartei	119.899	2.008	0.125	0.837	12
Scinax elaeochroa	1531.266	40.317	0	0.824	388
Scinax eurydice	507.569	3.449	0.083	0.779	42
Scinax flavoguttatus	128.366	0.053	0.125	0.8	12
Scinax funereus	352.789	3.706	0.125	0.715	55
Scinax fuscomarginatus	3623.727	90.296	0.061	0.777	151
Scinax fuscovarius	17110.286	219.374	0.006	0.865	715
Scinax garbei	2609.719	15.239	0.036	0.648	330
Scinax granulatus	2174.33	21.85	0.029	0.682	326
Scinax hayii	736.945	8.449	0	0.851	121
Scinax ictericus	289.156	6.346	0	0.911	25
Scinax imbegue	481.049	3.648	0	0.612	39
Scinax jolyi	93.883	8.945	0.464	0.787	13
Scinax kennedyi	316.899	3.682	0.05	0.819	46
Scinax littoralis	192.52	3.882	0.091	0.866	11
Scinax longilineus	NA	NA	0.2	0.621	7
Scinax luizotavioi	54.604	0.159	0.25	0.831	7

Scinax nasicus	3924.111	31.43	0.006	0.787	427
Scinax nebulosus	785.379	13.221	0.142	0.583	99
Scinax obtriangulatus	100.134	10.172	0.25	0.854	9
Scinax oreites	132.48	15.141	0.304	0.841	13
Scinax pachycrus	276.173	31.602	0	0.804	20
Scinax pedromedinae	535.606	14.017	0.005	0.912	34
Scinax perereca	599.792	5.299	0	0.766	93
Scinax perpusillus	211.955	7.509	0.06	0.872	14
Scinax proboscideus	369.597	24.898	0.036	0.906	30
Scinax quinquefasciatus	699.839	3.734	0.136	0.801	197
Scinax rizibilis	89.529	6.096	0.25	0.625	9
Scinax rostratus	2968.849	20.835	0.005	0.741	326
Scinax ruber	10326.96	196.507	0.005	0.526	1449
Scinax similis	1180.843	30.454	0	0.752	58
Scinax squalirostris	2336.271	8.651	0.107	0.729	211
Scinax staufferi	7986.417	26.495	0	0.738	912
Scinax strigilatus	402.3	6.558	0	0.819	16
Scinax sugillatus	449.741	8.859	0.087	0.776	72
Scinax trapicheiroi	123.728	23.381	0.167	0.895	7
Scinax tsachila	1229.217	6.105	0.109	0.705	93
Scinax tymbamirim	373.46	3.452	0.063	0.825	67
Scinax uruguayus	NA	NA	0.333	0.678	7
Scinax wandae	1353.85	17.089	0.034	0.706	162

Scinax x-signatus	2959.346	4.518	0.017	0.706	372
Smilisca baudinii	3967.752	5.993	0	0.716	3486
Smilisca cyanosticta	966.956	7.542	0.154	0.712	121
Smilisca dentata	264.702	2.187	0	0.797	24
Smilisca fodiens	1589.738	2.988	0.013	0.724	312
Smilisca manisorum	1170.853	78.637	0.011	0.88	93
Smilisca phaeota	2299.438	18.747	0	0.559	1253
Smilisca puma	316.524	9.937	0.007	0.843	44
Smilisca sila	1195.642	35.746	0	0.786	268
Smilisca sordida	1315.471	9.76	0	0.869	296
Sphaenorhynchus caramaschii	443.648	3.595	0.167	0.609	32
Sphaenorhynchus carneus	409.23	6.085	0.1	0.713	33
Sphaenorhynchus dorisae	480.782	3.255	0	0.785	45
Sphaenorhynchus lacteus	1889.57	24.507	0.032	0.763	223
Sphaenorhynchus planicola	280.963	3.303	0	0.942	33
Sphaenorhynchus platycephalus	139.842	19.053	0	0.849	9
Sphaenorhynchus prasinus	177.341	24.393	0.333	0.891	10
Sphaenorhynchus surdus	224.873	2.779	0.083	0.591	21
Tepuihyla exophthalma	39.153	5.867	0.25	0.867	8
Tepuihyla tuberculosa	151.57	3.153	0	0.764	18

Tepuihyla warreni	74.144	6.57	0.125	0.514	7
Tlalocohyla godmani	463.999	6.414	0.02	0.841	44
Tlalocohyla loquax	1707.822	5.006	0.038	0.64	292
Tlalocohyla picta	1767.775	16.633	0.006	0.752	233
Tlalocohyla smithii	2033.508	16.421	0.01	0.815	368
Trachycephalus coriaceus	463.17	4.787	0	0.782	47
Trachycephalus cunauaru	766.442	15.832	0.056	0.86	36
Trachycephalus hadroceps	396.795	11.267	0.012	0.782	35
Trachycephalus imitatrix	169.956	2.013	0.25	0.65	16
Trachycephalus jordani	650.028	14.714	0.037	0.796	190
Trachycephalus macrotis	416.968	12.361	0.237	0.635	39
Trachycephalus mesophaeus	1021.493	16.344	0.011	0.853	216
Trachycephalus nigromaculatus	416.48	2.288	0.083	0.898	44
Trachycephalus quadrangulum	1134.069	0	0.079	0.7	90
Trachycephalus resinifictrix	698.922	19.464	0.063	0.748	82
Trachycephalus typhonius	27098.97	161.772	0.001	0.649	1028
Trachycephalus venulosus	2712.986	16.268	0	0.673	113
Trachycephalus vermiculatus	27365.295	90.776	0.001	0.81	1351
Triprion petasatus	606.165	4.944	0	0.726	261

Triprion spatulatus	891.524	17.616	0.019	0.944	64
Triprion spinosus	788.219	57.492	0.011	0.748	47

Conclusão Geral

As mudanças climáticas representam uma ameaça crescente à biodiversidade, promovendo alterações sem precedentes nos padrões de temperatura e precipitação que afetam diretamente a distribuição e a persistência das espécies. Entre os organismos mais vulneráveis destacam-se os anfíbios, cuja sensibilidade está relacionada a características fisiológicas, ecológicas e funcionais. Esta tese demonstrou que os impactos do clima sobre esses organismos variam conforme atributos biogeográficos e ecológicos, manifestando-se de maneiras distintas em diferentes escalas espaciais e dimensões da diversidade. Os resultados indicam que espécies de maiores altitudes e dependentes de ambientes florestais tendem a perder grande parte de suas áreas climaticamente adequadas, enquanto espécies de habitats mais secos podem expandi-las no futuro. Também observamos que espécies atualmente mais amplamente distribuídas podem ser as que enfrentarão maiores reduções. Esses achados reforçam a noção de que variáveis biogeográficas podem ter maior poder preditivo do que as características de história de vida para antecipar os efeitos das mudanças climáticas na distribuição dos anfíbios.

Outro aspecto explorado nesta tese foi que as diferentes dimensões da diversidade respondem de maneira distinta às mudanças climáticas. As métricas de biodiversidade podem variar no espaço e apresentar alta incongruência espacial devido a mecanismos específicos que modulam suas relações. Por exemplo, a topologia da árvore filogenética e a presença de espécies altamente distintas filogeneticamente influenciam a relação entre diversidade taxonômica e filogenética, reduzindo a correlação entre essas métricas. Nossos resultados indicam regiões onde a diversidade de anuros neotropicais pode ser subestimada quando se considera apenas a diversidade taxonômica, como o sudeste e norte do Brasil, sul do Paraguai, norte da Bolívia, nordeste do Peru, leste da Colômbia, sul da Venezuela e norte da Guiana — áreas-chave para a conservação da diversidade filogenética. Da mesma forma, as Ilhas do Caribe, o México e o norte da Colômbia apresentam endemismo filogenético elevado, apesar da diversidade taxonômica relativamente baixa. A perda de espécies com longos ramos filogenéticos, que representam histórias evolutivas profundas, implica reduções muito mais severas da diversidade evolutiva do que a simples perda de espécies. Conservar o endemismo filogenético é crucial do ponto de vista evolutivo, pois essas áreas podem abrigar linhagens geneticamente distintas, com alto potencial adaptativo às mudanças climáticas. Além disso, podem conter organismos com histórias de vida singulares e sem parentes filogenéticos próximos, ressaltando seu valor insubstituível para a conservação da biodiversidade.

Ao particionar o endemismo filogenético em diferentes categorias (neo, paleo, misto e superendemismo), identificamos áreas onde ocorre exclusivamente apenas um tipo de endemismo. O neoendemismo, por exemplo, concentra-se em pequenas regiões da Mesoamérica, dos Andes e do Escudo das Guianas, enquanto os centros de paleoendemismo são ainda mais restritos, localizando-se na Mata Atlântica, nos Andes e na Mesoamérica. Esses padrões evidenciam a complexidade de definir prioridades de conservação, já que diferentes regiões maximizam diferentes dimensões da diversidade. Além disso, nossos

resultados mostram que áreas protegidas e áreas de vegetação nativa exercem papéis complementares na conservação do endemismo, tanto em cenários atuais quanto futuros. Enquanto os centros de neoendemismo estão situados em regiões com pouca vegetação nativa, mas amplamente inseridos em áreas protegidas, outros tipos de endemismo tendem a ocorrer em locais com maior cobertura de vegetação, porém menos representados dentro da rede de proteção. Esse achado destaca a importância de, além de manter as áreas protegidas já existentes, também expandir sua rede no futuro e garantir a conservação da vegetação nativa remanescente nos Neotrópicos, de modo a sustentar a diversidade evolutiva dos anuros e de outros grupos taxonômicos.

Além das mudanças na diversidade alfa e no endemismo, as alterações climáticas também devem impactar a diversidade beta temporal dos anuros neotropicais. Assim, os efeitos projetados não se restringem ao número de espécies ou à diversidade evolutiva, mas também envolvem a composição das comunidades. Isso significa que a identidade das espécies em cada região deve se modificar substancialmente com o avanço das mudanças climáticas. Áreas como o norte dos Andes, Ilhas do Caribe, Brasil, norte e centro do México, oeste da Colômbia, centro do Equador, Chile e centro-sul da Argentina estão entre as regiões mais propensas a sofrer grandes transformações na composição de espécies. Por outro lado, diversas áreas nos Neotrópicos podem apresentar baixos valores de diversidade beta, indicando um processo de homogeneização biótica, como partes do sul dos Andes. Observamos que as dimensões filogenética e funcional são mais vulneráveis a esse processo do que a dimensão taxonômica, o que levará a comunidades futuras mais similares em termos de traços funcionais e composição evolutiva. A perda de espécies com características únicas pode comprometer serviços ecossistêmicos essenciais. Os anfíbios, em particular, desempenham papéis críticos como predadores e presas, contribuindo para a regulação populacional e o ciclo de nutrientes, de modo que sua redução funcional ameaça diretamente a integridade e o equilíbrio dos ecossistemas.

É importante reconhecer que grande parte dos resultados desta tese se baseia em projeções geradas por modelos que, como qualquer representação empírica, carregam incertezas inerentes. Embora extremamente úteis, esses modelos apresentam limitações decorrentes das premissas adotadas, como assumir que a variação climática atual represente adequadamente os requerimentos climáticos futuros das espécies ou que estas responderão ocupando áreas emergentes compatíveis com suas restrições de nicho e taxas de dispersão. Além disso, pressupostos como o conservadorismo de nicho desconsideram o potencial de adaptação ou plasticidade diante de novas condições climáticas. Ainda assim, entendemos a relevância desses modelos e consideramos que os utilizados nesta tese, baseados em avanços recentes da macroecologia, são suficientemente robustos para capturar as principais relações entre espécies e clima, como já demonstrado em estudos anteriores, oferecendo projeções úteis para análises e decisões de conservação.

Por fim, esta tese contribui metodologicamente com o desenvolvimento do pacote R phyloraster, que integra dados de distribuição de espécies e informações filogenéticas para o cálculo de métricas espaciais de diversidade e endemismo. Demonstramos que o pacote é

mais leve e eficiente do que alternativas existentes, possibilitando análises em alta resolução, de escalas locais a globais, mesmo em computadores com recursos limitados. Ao reduzir barreiras computacionais, o phyloraster amplia o acesso à pesquisa e promove maior equidade científica, favorecendo investigações sobre biodiversidade em diferentes contextos. Em conjunto, os resultados desta tese evidenciam que as mudanças climáticas podem gerar perdas significativas de diversidade taxonômica, funcional e filogenética, além de reduzir padrões de endemismo e intensificar a homogeneização biótica das comunidades de anuros. Também reforçam a necessidade de estratégias de conservação que considerem múltiplas dimensões da biodiversidade, uma vez que cada dimensão responde de forma distinta às mudanças climáticas. Torna-se, assim, urgente o fortalecimento de medidas integradas para mitigar esses impactos e garantir a preservação da diversidade biológica e de seus serviços ecossistêmicos.

General Conclusion

Climate change represents an increasing threat to biodiversity, driving unprecedented alterations in temperature and precipitation patterns that directly affect species distribution and persistence. Among the most vulnerable organisms are amphibians, whose sensitivity is related to physiological, ecological, and functional traits. This thesis demonstrated that the impacts of climate on these organisms vary according to biogeographic and ecological attributes, manifesting differently across spatial scales and dimensions of diversity. The results indicate that high-altitude species and those dependent on forested habitats are likely to lose a large portion of their climatically suitable areas, while species from drier habitats may expand their suitable ranges. We also observed that species currently widely distributed may face the largest reductions in the future. These findings reinforce the notion that biogeographic variables may have greater predictive power than life-history traits in anticipating the effects of climate change on amphibian distributions.

Another aspect explored in this thesis is that different dimensions of diversity respond differently to climate change. Biodiversity metrics can vary spatially and show high spatial incongruence due to specific mechanisms modulating their relationships. For example, phylogenetic tree topology and the presence of highly phylogenetically distinct species influence the relationship between taxonomic and phylogenetic diversity, reducing the correlation between these metrics. Our results highlight regions where Neotropical frog diversity may be underestimated if only taxonomic diversity is considered, such as southeastern and northern Brazil, southern Paraguay, northern Bolivia, northeastern Peru, eastern Colombia, southern Venezuela, and northern Guyana — key areas for the conservation of phylogenetic diversity. Similarly, the Caribbean Islands, Mexico, and northern Colombia exhibit high phylogenetic endemism despite relatively low taxonomic diversity. The loss of species with long phylogenetic branches, representing deep evolutionary histories, implies much more severe reductions in evolutionary diversity than the simple loss of species. Conserving phylogenetic endemism is crucial from an evolutionary perspective, as these areas may harbor genetically distinct lineages with high adaptive potential to climate change. They may also contain organisms with unique life-history traits and no close phylogenetic relatives, emphasizing their irreplaceable value for biodiversity conservation.

By partitioning phylogenetic endemism into different categories (neo-, paleo-, mixed, and superendemism), we identified areas where only one type of endemism occurs exclusively. Neoendemism, for example, is concentrated in small regions of Mesoamerica, the Andes, and the Guiana Shield, while paleoendemism centers are even more restricted, located in the Atlantic Forest, the Andes, and Mesoamerica. These patterns highlight the complexity of setting conservation priorities, as different regions maximize different dimensions of diversity. Moreover, our results show that protected areas and native vegetation areas play complementary roles in conserving endemism under both current and future scenarios. While neoendemism centers are located in regions with low native vegetation cover but largely within protected areas, other types of endemism occur in areas

with higher vegetation cover but are less represented within the protection network. This finding underscores the importance of not only maintaining existing protected areas but also expanding their network in the future and ensuring the conservation of remaining native vegetation in the Neotropics, thereby supporting the evolutionary diversity of amphibians and other taxonomic groups.

Beyond changes in alpha diversity and endemism, climate change is also expected to impact the temporal beta diversity of Neotropical frogs. Thus, projected effects are not limited to species richness or evolutionary diversity but also involve community composition. This implies that species identities in each region are likely to change substantially with ongoing climate change. Areas such as the northern Andes, Caribbean Islands, Brazil, northern and central Mexico, western Colombia, central Ecuador, Chile, and central-southern Argentina are among the regions most likely to experience major shifts in species composition. Conversely, several Neotropical areas may exhibit low beta diversity, indicating potential biotic homogenization, such as parts of the southern Andes. We observed that phylogenetic and functional dimensions are more vulnerable to this process than the taxonomic dimension, resulting in future communities that are more similar in functional traits and evolutionary composition. The loss of species with unique traits can compromise essential ecosystem services. Amphibians, in particular, play critical roles as predators and prey, contributing to population regulation and nutrient cycling, so their functional reduction directly threatens ecosystem integrity and balance.

It is important to acknowledge that much of the results of this thesis are based on model-generated projections, which, like any empirical representation, carry inherent uncertainties. While extremely useful, these models have limitations arising from their assumptions, such as assuming that current climatic variation adequately represents species' future requirements or that species will respond by occupying emerging areas compatible with their niche constraints and dispersal rates. Additionally, assumptions such as niche conservatism overlook the potential for adaptation or plasticity under novel climatic conditions. Nevertheless, we recognize the relevance of these models and consider that those used in this thesis, based on recent advances in macroecology, are sufficiently robust to capture the main species–climate relationships, as demonstrated in previous studies, providing useful projections for analyses and conservation decisions.

Finally, this thesis contributes methodologically through the development of the R package phyloraster, which integrates species distribution and phylogenetic information to calculate spatial metrics of diversity and endemism. We demonstrated that the package is lighter and more efficient than existing alternatives, enabling high-resolution analyses from local to global scales, even on computers with limited resources. By reducing computational barriers, phyloraster broadens research access and promotes greater scientific equity, facilitating biodiversity investigations across diverse contexts. Taken together, the results of this thesis indicate that climate change has the potential to cause significant losses in taxonomic, functional, and phylogenetic diversity, reduce endemism patterns, and intensify biotic homogenization of frog communities. They also reinforce the need for conservation

strategies that consider multiple dimensions of biodiversity, as each dimension responds differently to climate change. It is therefore urgent to strengthen integrated measures to mitigate these impacts and ensure the preservation of biological diversity and its ecosystem services.

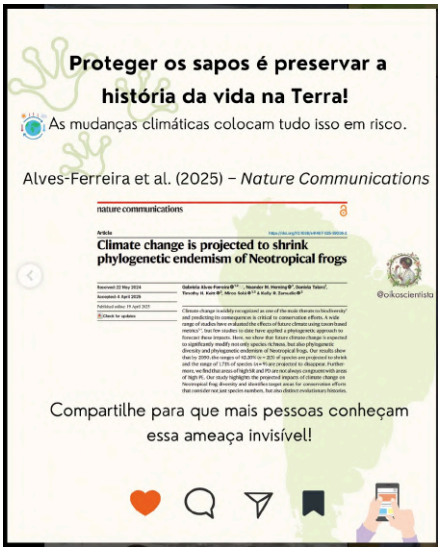
Divulgação científica

Publicação no Instagram n° 1

Publicação em um perfil de divulgação científica no instagram sobre os resultados encontrados no Capítulo 3: https://www.instagram.com/p/DJKlecQuih2/?img_index=1

Publicação no Instagram n° 2

Publicação em um perfil de divulgação científica no instagram sobre os resultados encontrados no Capítulo 3: https://www.instagram.com/p/DItf_49xhCw/?img_index=1



Matéria no Jornal Oeco

O seguinte texto foi publicado no jornal Oeco para divulgação dos resultados do terceiro capítulo e pode ser acessado usando o seguinte link: https://oeco.org.br/noticias/crise-climatica-ira-encolher-o-lar-de-anfibios-na-america-latina/

NOTÍCIAS

Crise climática irá encolher o lar de anfíbios na América Latina

Estudo mostra que até 2050 quase metade das espécies de sapos e rãs deve perder áreas de habitat na região, algumas dela por completo, devido às mudanças do clima

DUDA MENEGASSI

12 de maio de 2025

A perereca-flautinha (Aplastodiscus leucopygius) pode perder todo o seu habitat com as mudanças climáticas. Foto: Renato Gaiga

Especial COP 30 | BELÉM

Biodiversidade | Clima | anfíbios | clima | fauna | mata atlântica | mudanças climáticas | Mata Atlântica

ENTRAR

Os impactos das mudanças climáticas sobre a biodiversidade atingem plantas e animais de diferentes grupos e ambientes. Particularmente sensíveis às alterações de temperatura e umidade, os anfíbios – grupo composto por sapos, rãs e pererecas – estão com seu futuro em xeque. Um estudo recente mostra que 213 espécies da América Latina, quase metade de todos os anfíbios da região, podem perder parte de seu habitat até 2050 e outras nove podem ficar completamente "sem lar".

Os pesquisadores analisaram quase 500 espécies de anfíbios e combinaram dados de clima, genética e distribuição geográfica. O estudo, publicado no periódico Nature Communications, com acesso aberto, revela que a crise climática irá comprometer não apenas a diversidade de espécies, mas também toda história evolutiva de anfíbios na região Neotropical – que equivale aos territórios tropicais da América Latina.

"Anfíbios têm características únicas e vêm se adaptando há milhões de anos. Quando uma dessas espécies some, levam junto uma parte da história da vida na Terra. Além disso, a perda dessas espécies pode levar a perda de serviços essenciais que eles desempenham no ecossistema", explica a ecóloga Gabriela Alves-Ferreira, estudante de doutorado no Programa de Pós graduação em Ecologia e Conservação da Universidade Estadual de Santa Cruz (UESC) e uma das autoras do artigo.

Os resultados da pesquisa mostram que, até 2050, a distribuição de 42,2% dos anfíbios neotropicais irá encolher, o equivalente a 213 espécies impactadas.

Num cenário ainda mais crítico, outras nove espécies perderão por completo seu habitat. Nessa lista preocupante estão cinco anfíbios com ocorrência no Brasil, uma delas exclusiva do país: a perereca-verde ou perereca-flautinha (*Aplastodiscus leucopygius*), que ocorre na Mata

ENTRAR

Atlântica, entre Minas Gerais, São Paulo e Rio de Janeiro. Apesar de atualmente classificada como Menos Preocupante por ter seu habitat distribuído em áreas protegidas, os limites das unidades de conservação nada poderão fazer para deter os impactos das mudanças climáticas.

A ironia se repete para outras espécies, igualmente classificadas como baixo risco de extinção, porém que, diante da crise climática, podem rapidamente desaparecer – vítimas do aumento das temperaturas e alterações no regime de chuvas.

A pesquisadora explica para ((o))eco que, para tentar resguardar os anfíbios, é fundamental investir em políticas e ações de conservação que ajudem a frear os efeitos das mudanças climáticas. Entre as áreas prioritárias para conservação no Brasil, de acordo com o estudo, estão a Serra do Mar, a Serra da Mantiqueira e o sul da Bahia, todas na Mata Atlântica, que poderá ser um refúgio para os anfíbios.

"Também é essencial proteger e restaurar regiões identificadas como áreas-chave para manter a diversidade e a história evolutiva desses animais – como a Serra do Mar, no Brasil, o noroeste e sudeste da Colômbia e o norte do Escudo das Guianas. Preservar esses ambientes não apenas oferece refúgio para as espécies, mas também contribui para mitigar os impactos das mudanças climáticas em escala mais ampla", detalha Gabriela.

Duda Menegassi
Jornalista ambiental especializada em unidades de conservação, montanhismo e divulgação científica. →

Matéria no UTexas News

O seguinte texto foi publicado no UTexas News para divulgação dos resultados do terceiro capítulo e pode ser acessado usando o seguinte link: https://cns.utexas.edu/news/research/nearly-half-latin-american-frogs-and-toads-are-risk

RESEARCH

Nearly Half of Latin American Frogs and Toads Are at Risk

APRIL 25, 2025 • BY GABRIELA ALVES-FERREIRA

A new study shows that nearly half of frog and toad species in Latin America may lose their habitat range by 2050.

Trachycephalus mesophaeus is among the species identified in a new study as likely to lose part of their range due to climate change. Credit: Gabriela Alves-Ferreira

Climate change is expected to drastically reduce the presence of frogs and toads in the wild, especially in the tropical forests of Latin America, according to a new study published in the scientific journal Nature Communications by researchers from Brazil, Germany and the United States. The research shows that nearly half of these species may lose part of their distribution area by 2050, and nine of them may disappear completely.

"Amphibians have unique characteristics and have been adapting for millions of years. When one of these species disappears, it takes with it part of the history of life on Earth. Furthermore, the loss of these species may result in the loss of essential services they perform in the ecosystem," explained ecologist Gabriela Alves-Ferreira, lead author of the study, formerly a visiting scholar at The University of Texas at Austin, and a Ph.D. student in the graduate program in ecology and conservation at the State University of Santa Cruz.

Small frogs and toads, which often go unnoticed, are key components of ecosystems and excellent bioindicators — that is, they are among the first to show that something is wrong in the environment. According to scientists, when amphibians become sick or vanish, it's a sign that nature is at risk.

"With continued climate change, amphibian species will shift their

Share

distributions and the communities of frogs will get scrambled," said Kelly Zamudio, UT professor of integrative biology. "Predictive studies such as this one help us identify areas where most community change will happen and focus on those areas for conservation."

The research analyzed nearly 500 species of frogs and toads and combined climate, phylogenetic and geographical distribution data. The results indicate that with global warming and reduced rainfall, many species will have increasingly smaller habitats — which may lead to the extinction not only of animals but also of millions of years of evolutionary history.

CREDIT: GABRIELA ALVES-FERREIRA

Experts also warn that even species not currently considered at risk may become vulnerable in a short period. Therefore, the criteria for assessing extinction risk must also consider the effects of climate change.

The study helps identify priority areas for conservation, where rare species with long evolutionary histories live.

"Protecting these places could make a difference not only for frogs and toads but for the health of the entire planet," said Alves-Ferreira.

Other authors of the study were UT's Tim Keitt and Universidade Estadual de Santa Cruz's (UESC) Neander Heming, Daniela Talora and Mirco Solé. Funding for the research was provided by the U.S. National Science Foundation, Brazil's Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) and UESC's Pró-Reitoria de Pesquisa e Pós-Graduação.

Tags

Integrative Biology | Biodiversity and Sustainability

RESEARCH

New DNA Evidence Reveals Origins of Finnish, Estonian and Hungarian Languages

JULY 10, 2025 • BY MARC AIRHART

UT BRIDGING DISCIPLINES PROGRAM

Abby Jones' Multifaceted UT Journey

JULY 9, 2025 • BY STAFF WRITER

TACC

Evolutionary Bursts: AI-Driven Research Uncovering Rapid Genomic Shifts in Human Evolution

JUNE 30, 2025 • BY JORGE SALAZAR

Saponilda e o Mistério do Clima Maluco

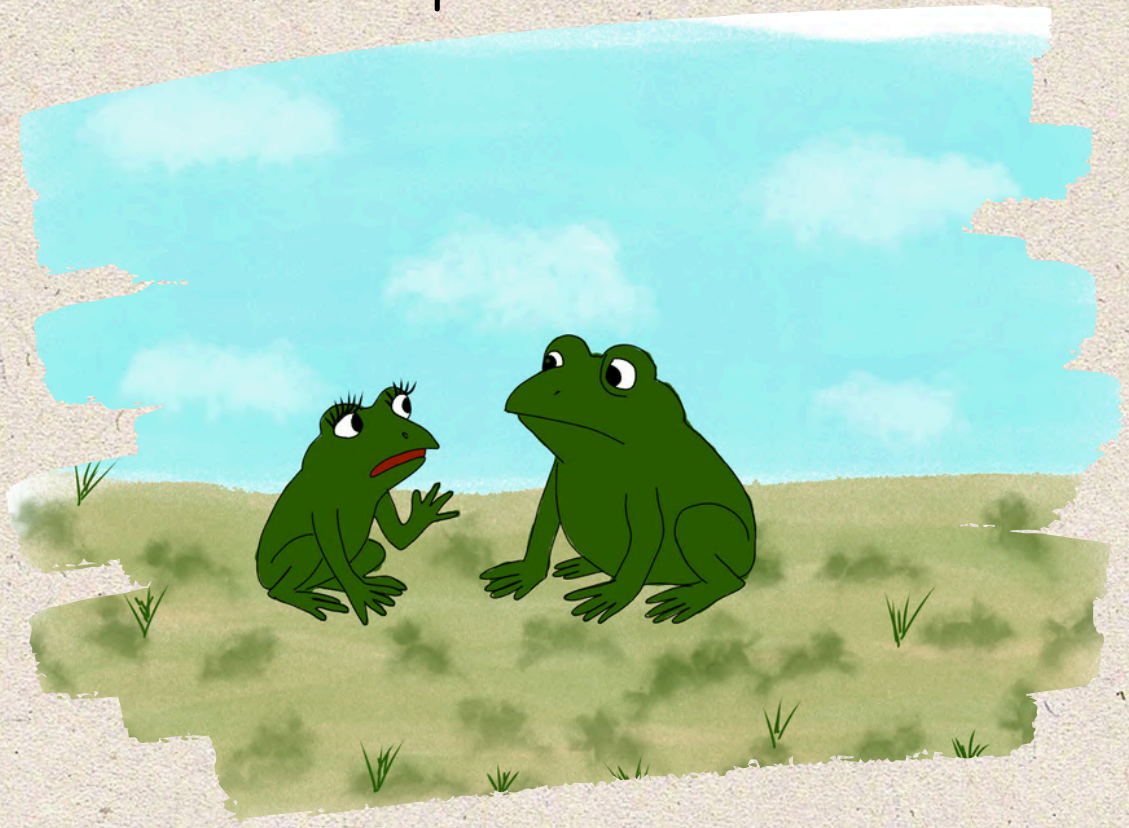
Este livro foi pensado durante meu doutorado para trazer a mensagem sobre as mudanças climáticas para crianças de 9 a 12 anos. A história foi pensada e revisada com a ajuda da minha querida mãezinha, Suelene Alves Pio, que também é autora do livro. Essa ainda não é a versão final do livro, pois pretendo inserir mais desenhos, mas achei pertinente adicionar junto a tese. Abaixo, segue a versão inicial do nosso livro infantil.

SAPONILDA E O MISTÉRIO DO CLIMA MALUCO

Gabriela Alves Ferreira
Suelene Alves Pio

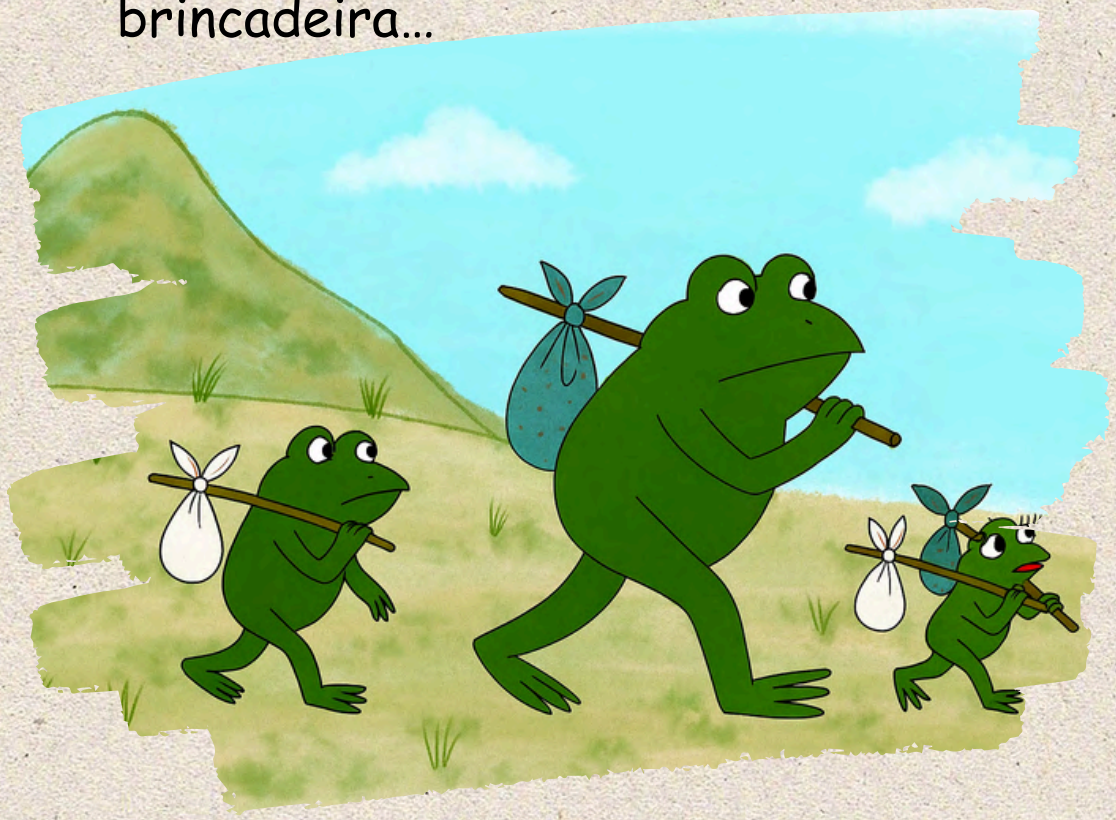
Ilustrações: Gabriela Alves Ferreira

— Ô, Sapo Aldo! Você viu o Jeremias? Sumiu de repente!



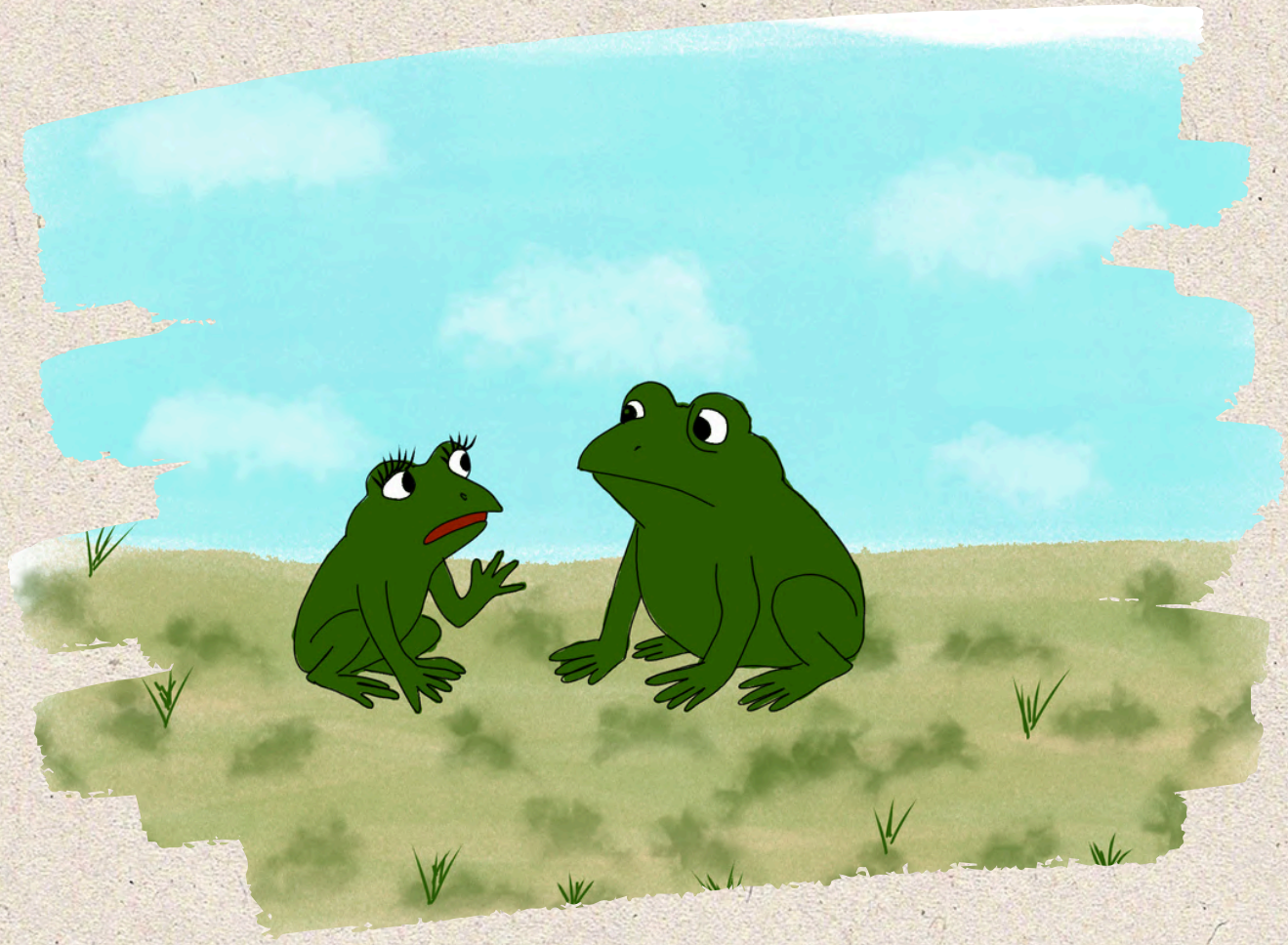
— Uai Saponilda, você não soube? Ele e a esposa se mudaram do Morro da Baleia por causa do calor e da falta de chuva

— Que tristeza, Sapo Aldo!! Tomara que eles estejam bem, pois cruzar esses campos de soja e cana não é brincadeira...

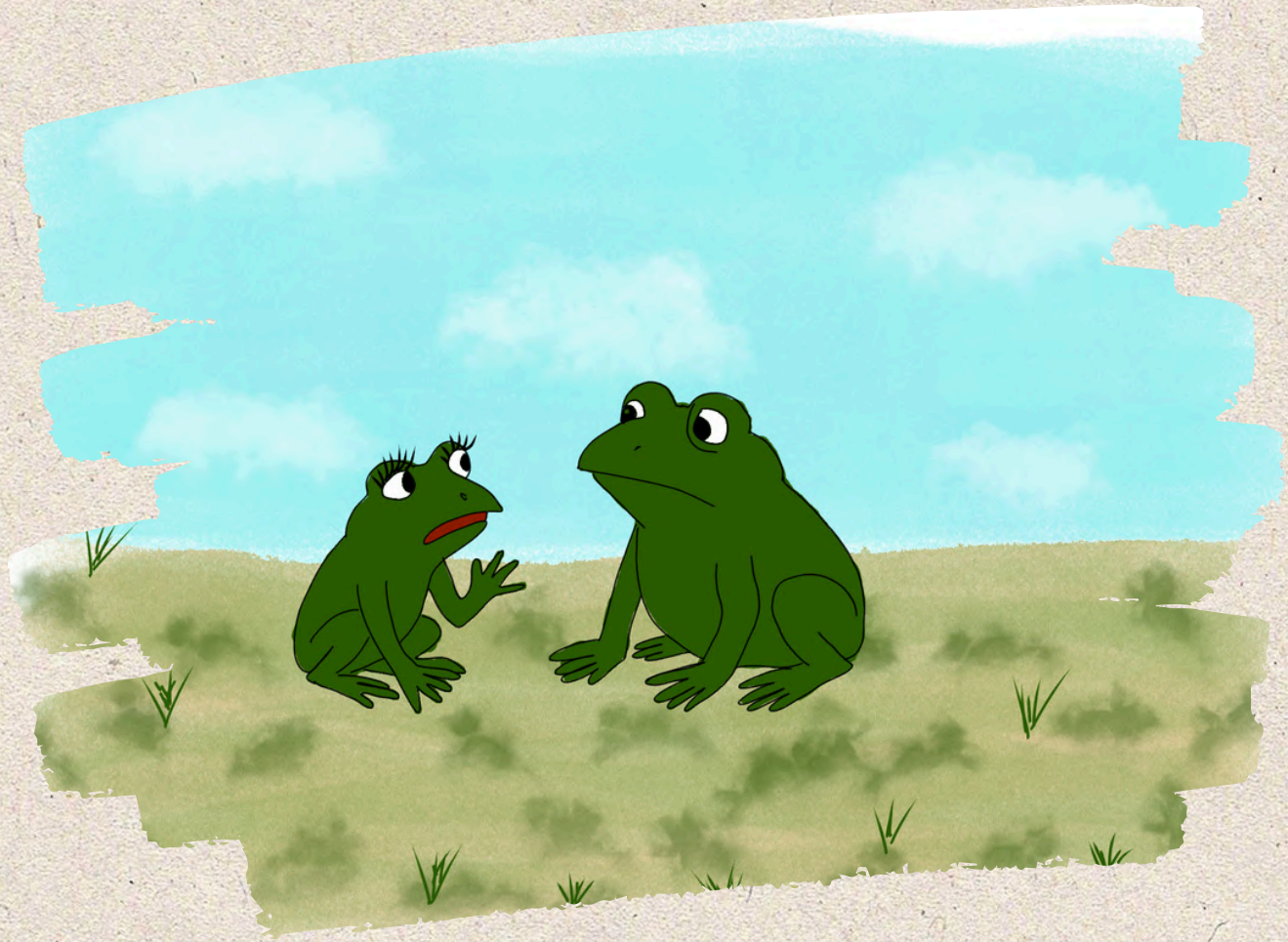


— Pois é, Saponilda... essas mudanças no clima tão afetando todo mundo.

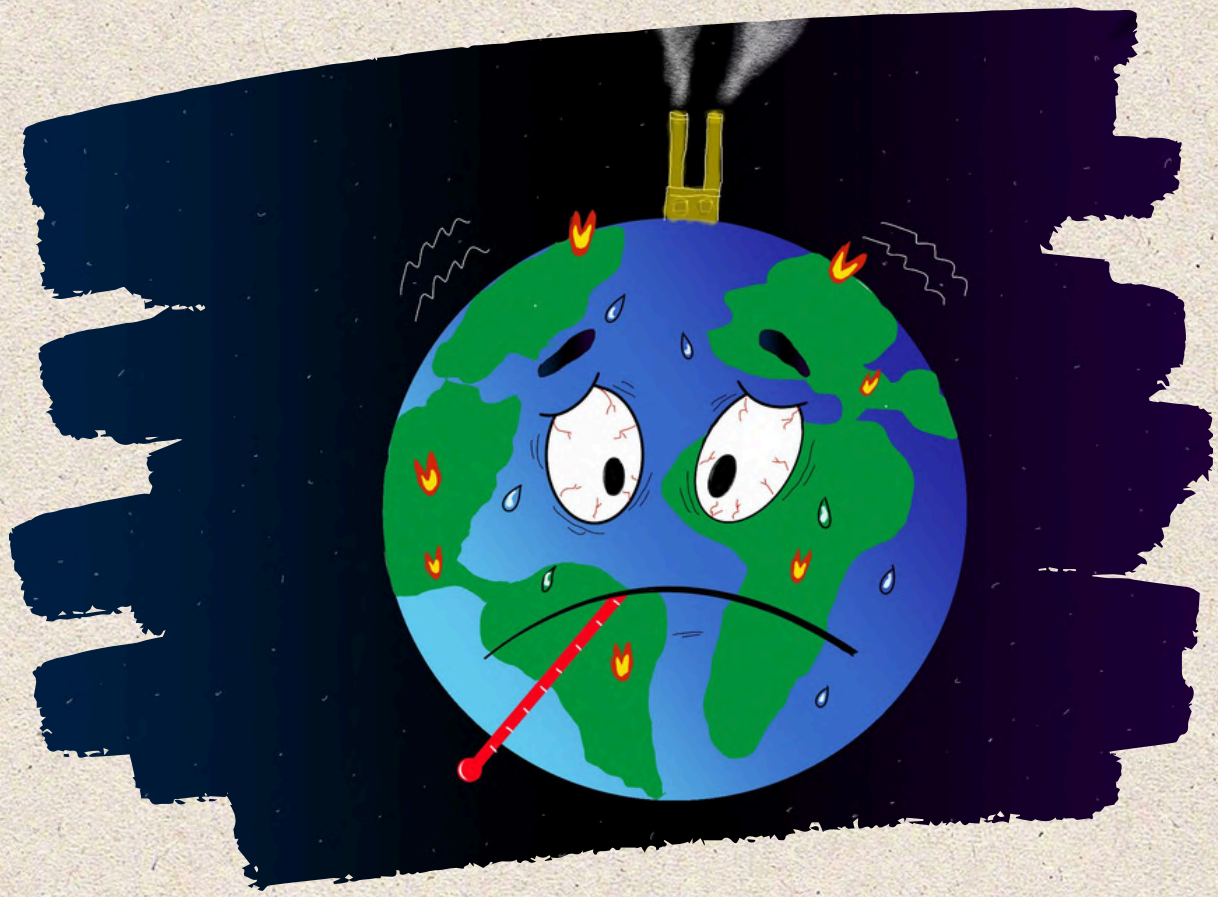
— Mudanças no clima?? Eu achei que isso era só uma temporada ruim que logo iria passar.
Me conta mais sobre isso, Sapo Aldo!



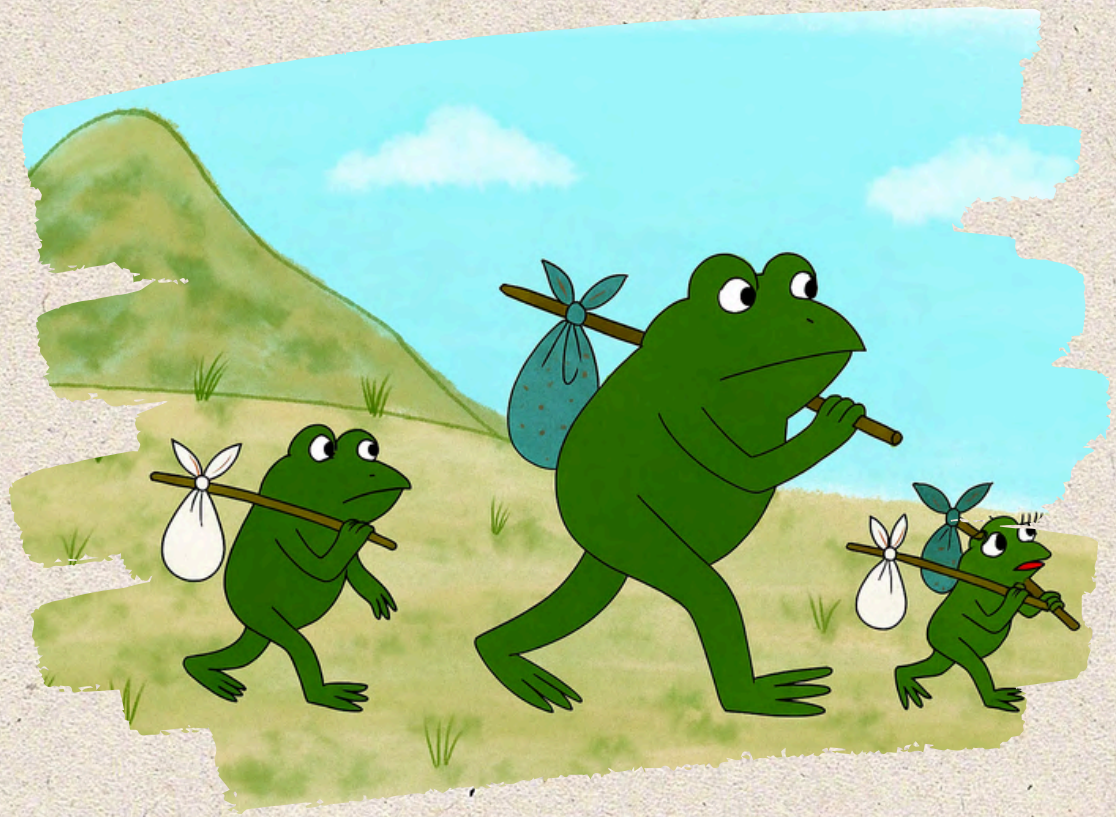
— Quem dera fosse, Saponilda! As mudanças climáticas na verdade acontecem há muitos e muitos anos, e costumavam ser um processo natural do planeta terra.



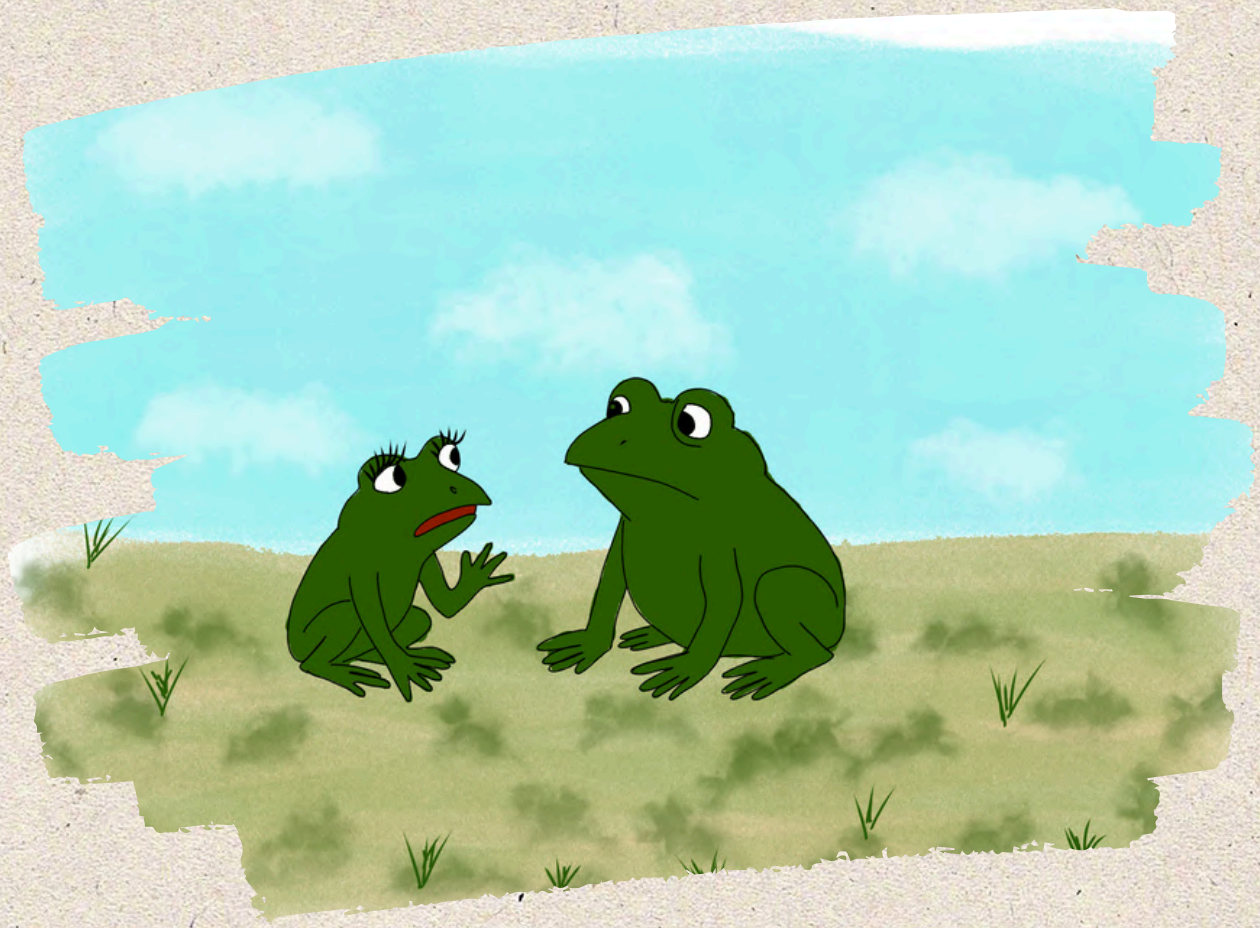
— Só que nos últimos anos, os seres humanos estão aumentando a queima de combustíveis fósseis como carvão e petróleo, e isso está acelerando as mudanças no clima e causando aquecimento global!

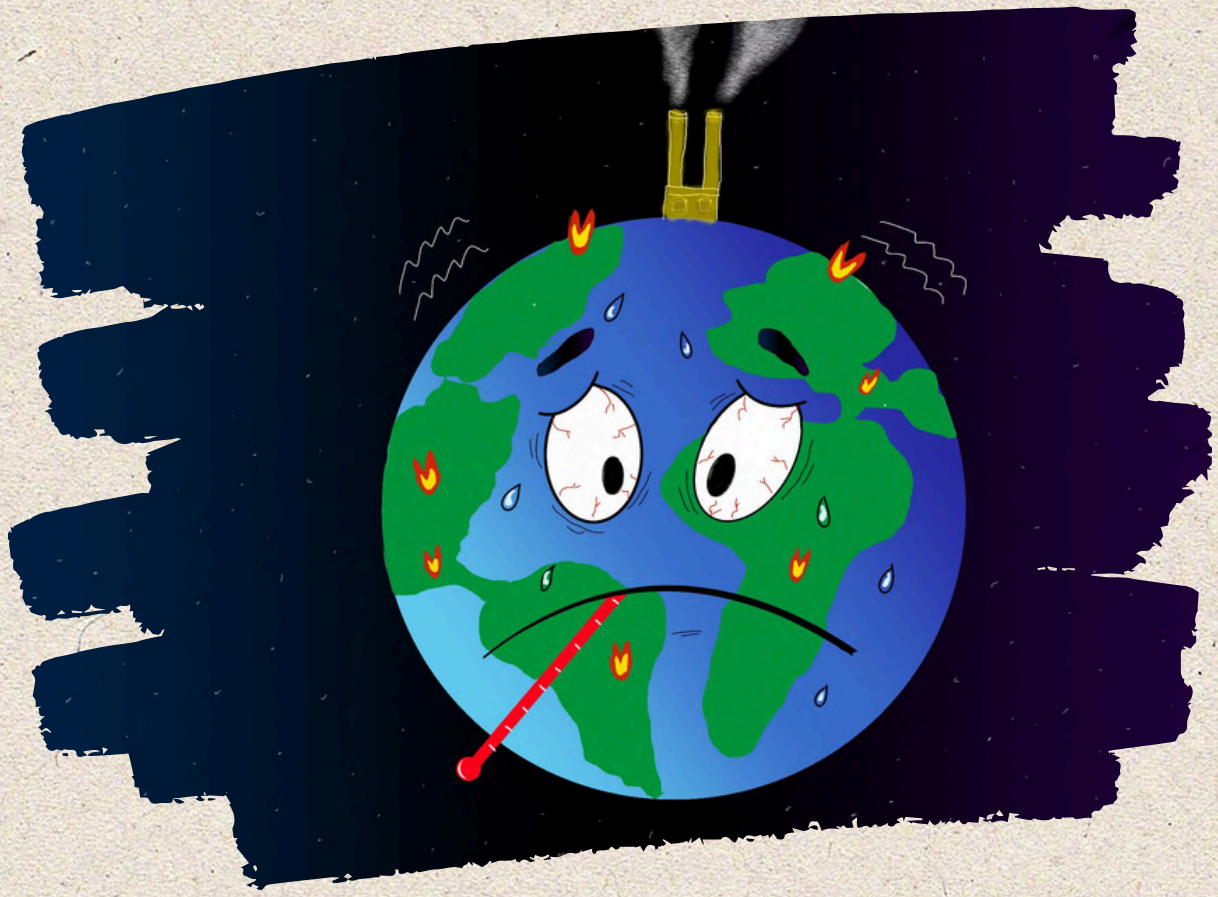


— Como o clima tá mudando muito rápido, Saponilda, não temos tempo de nos adaptar e parentes tão legais como Jeremias, precisam se mudar às pressas em busca de um lugar mais fresquinho e mais chuvoso para criar seus filhos.



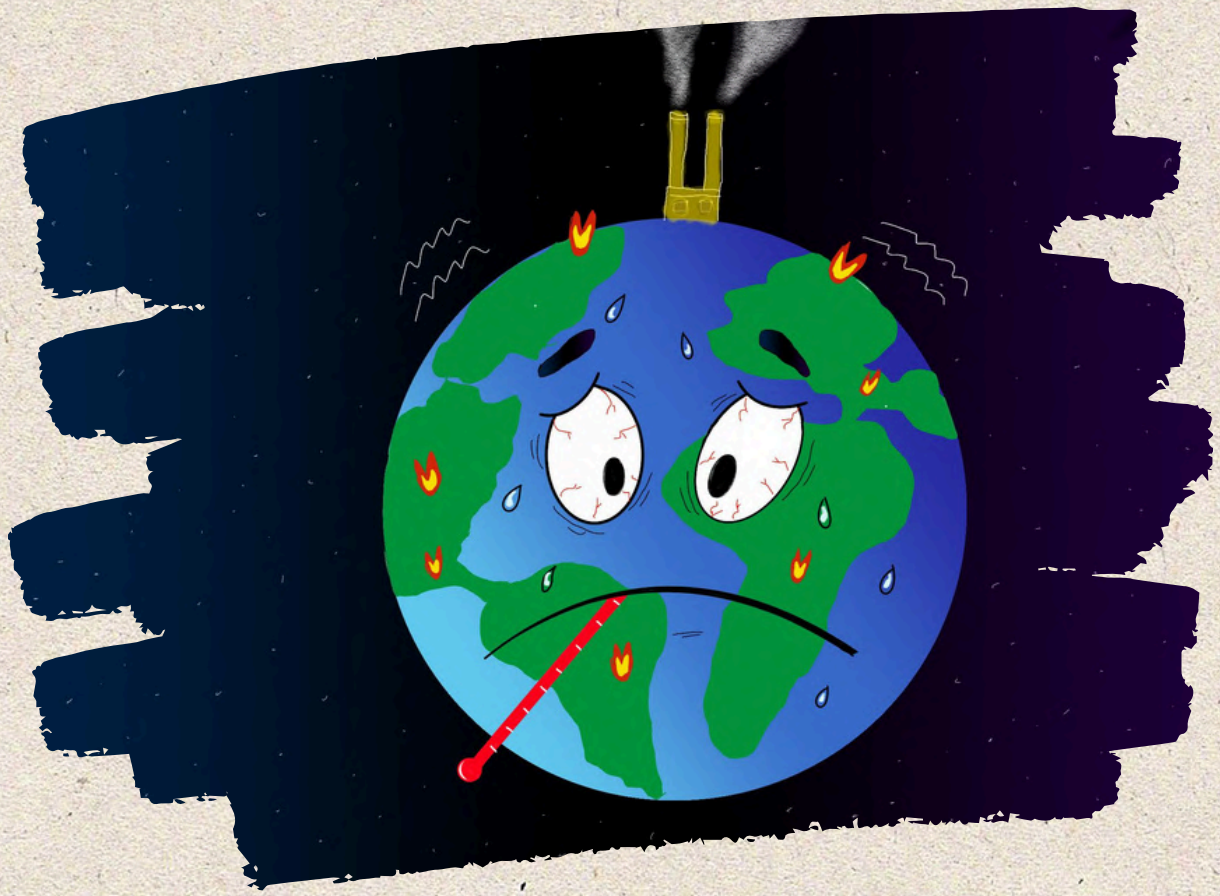
— Parece que o problema é mais complicado do que eu pensava. Que negócio é esse de aquecimento global, Sapo Aldo?



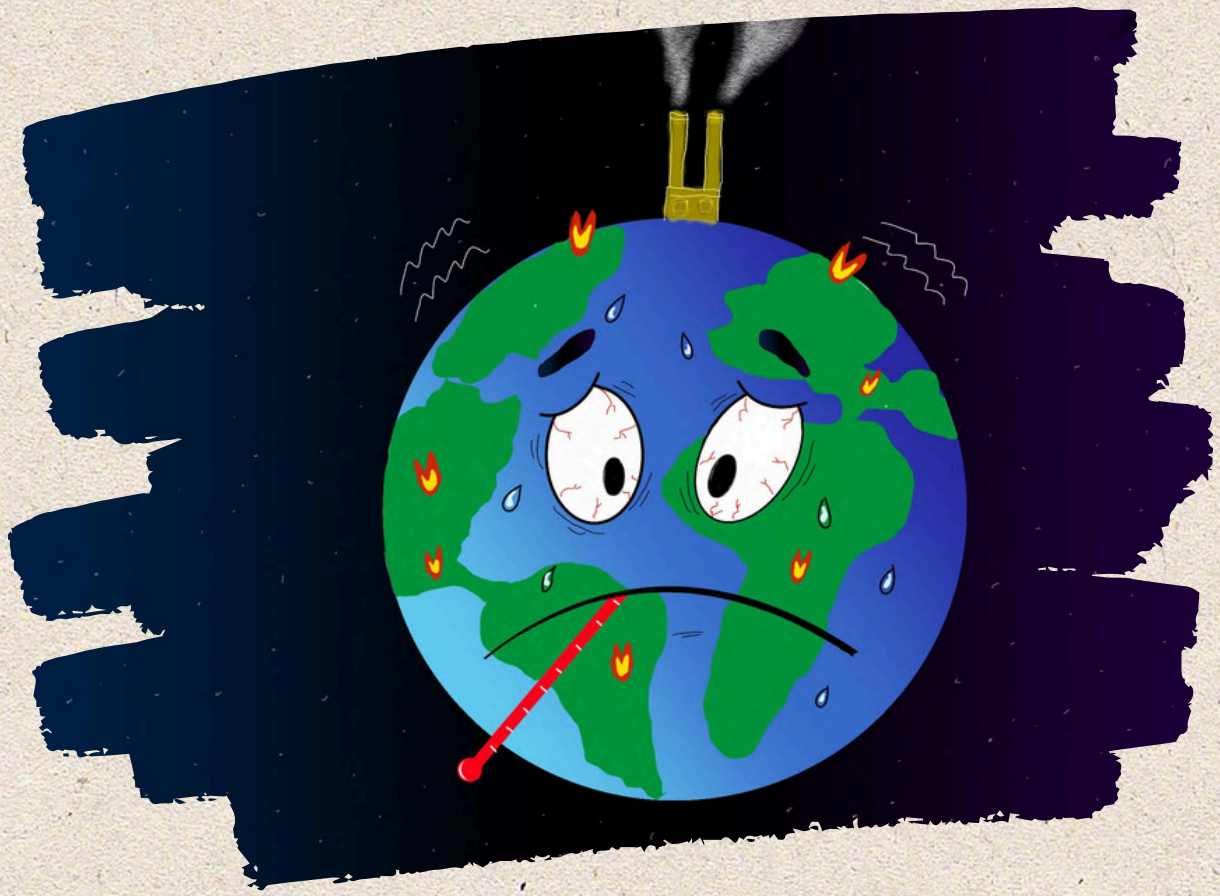


—Uai, Saponilda, aquecimento global é quando a temperatura média da Terra começa a subir. Isso acontece porque os humanos estão liberando muitos gases na atmosfera que fazem o efeito estufa mais forte.

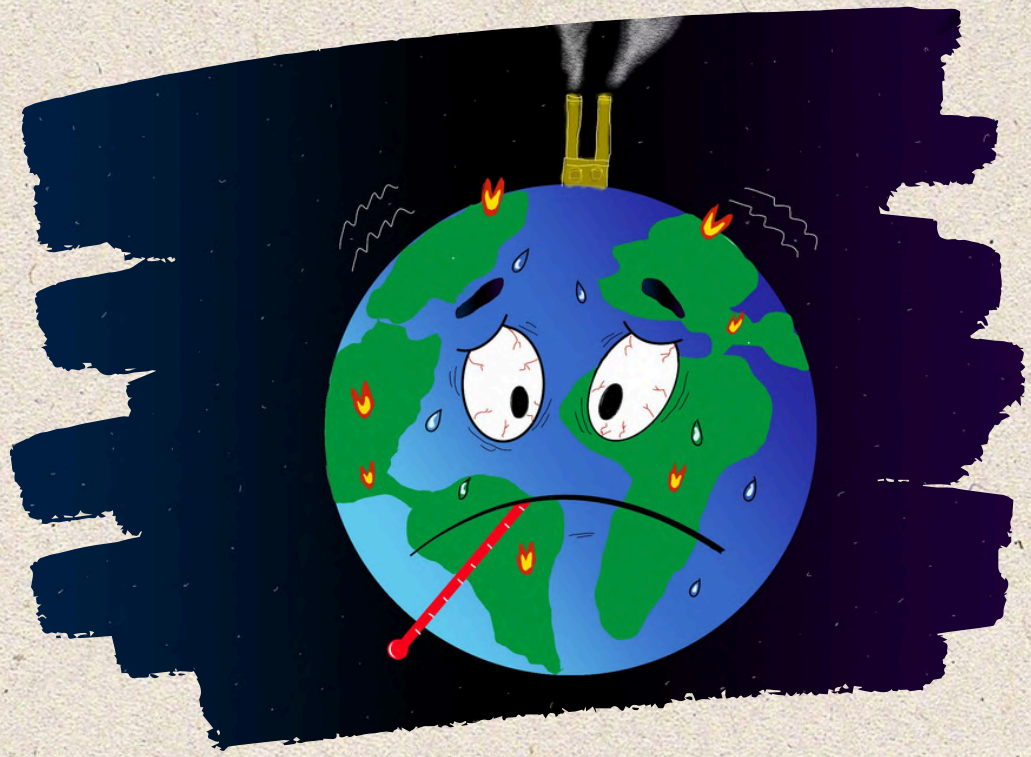
— O efeito estufa é como um cobertorzinho que envolve a Terra, mantendo o planeta quentinho, o que é importante pra gente poder viver aqui.



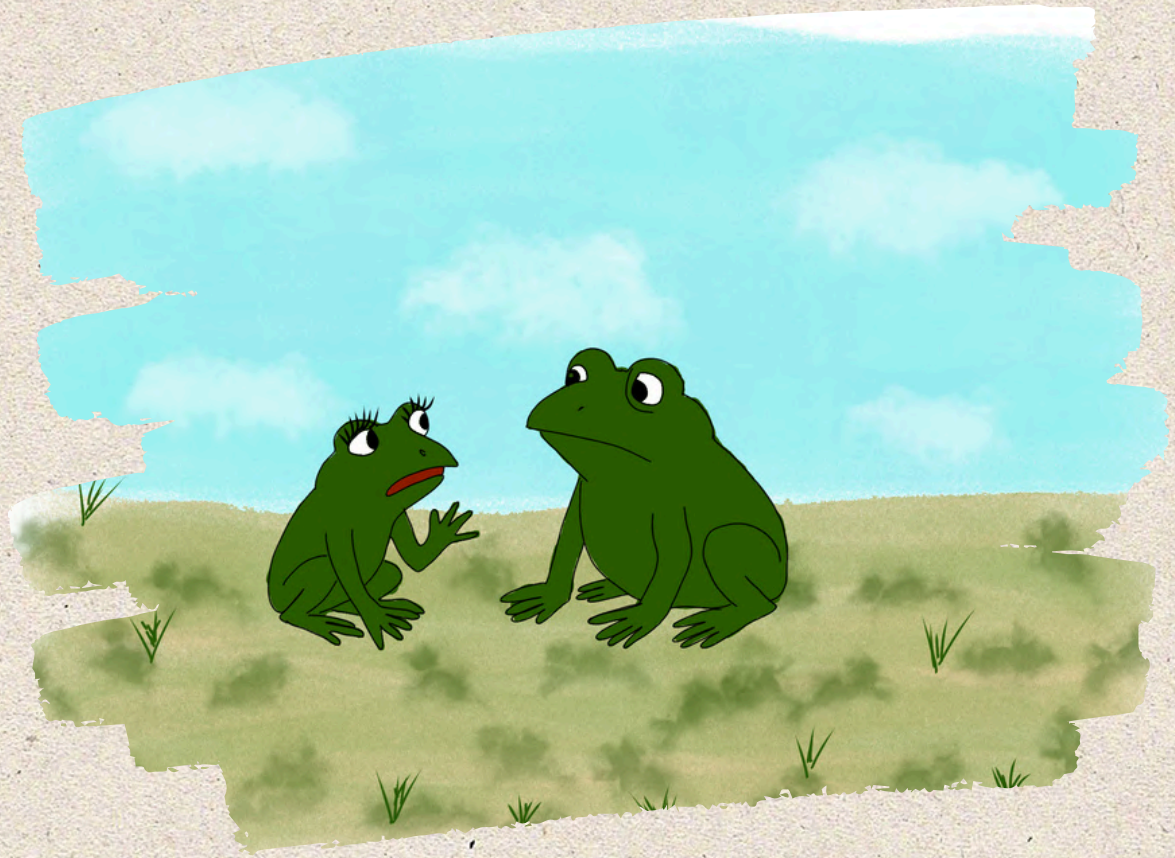
— Mas o problema é que com tanto gás sendo liberado, esse cobertor tá ficando grosso demais, deixando a Terra muuuuuuuuito mais quente, como se estivesse com febre.



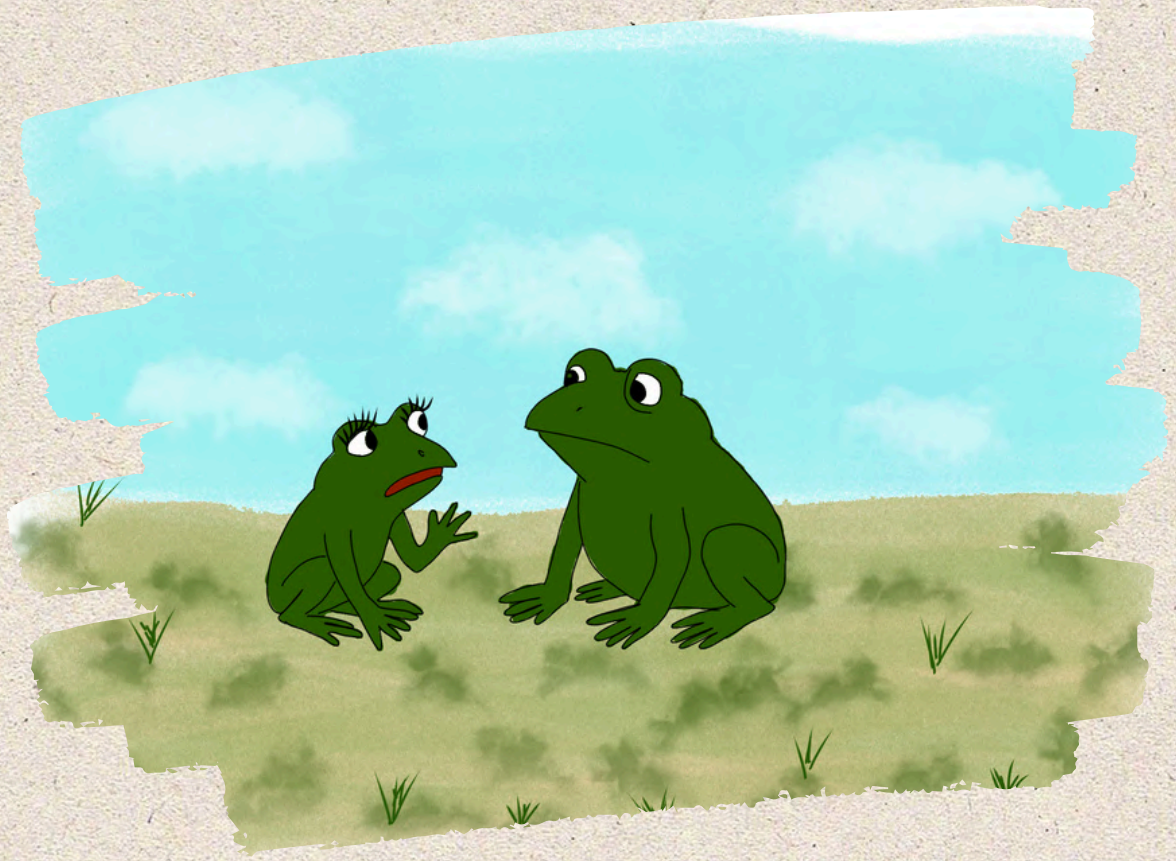
— Essas mudanças no clima tão causando todas essas consequências que a gente tá vendo, como diminuição das chuvas, derretimento das geleiras, calor em excesso em algumas regiões, enchentes e congelamentos em outros lugares



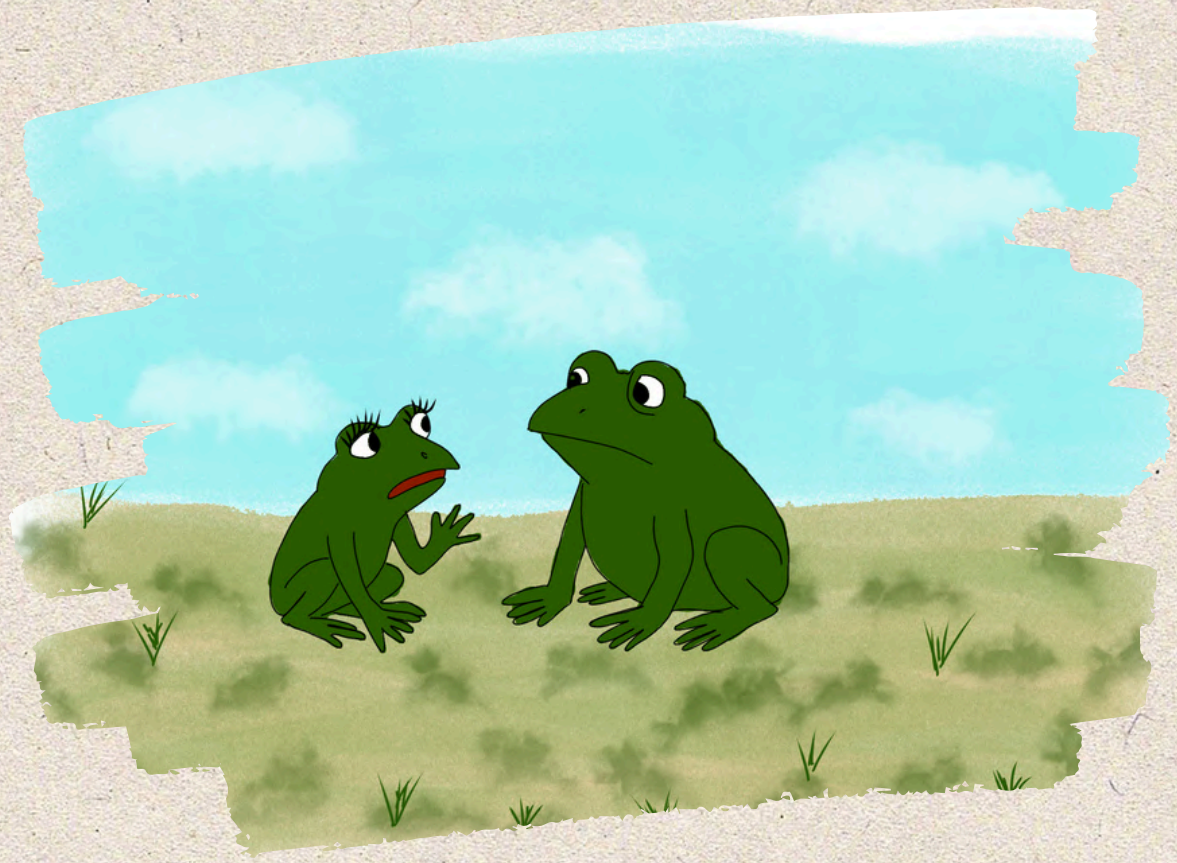
— Ahhhh, Sapo Aldo, agora tudo faz sentido! Então é só parar de liberar esses gases danados, uai! Tá resolvido o problema! Como é que ninguém pensou nisso antes?



— Ô, minha fia, queria que fosse simples assim. Mas a emissão de gases pode vir de um bucado de fontes diferentes. Os carros e os aviões, por exemplo, liberam muito gás carbônico na atmosfera, mas também tem outras fontes de gases como o pum das vacas, a derrubada e queimada de florestas, as fábricas e muitos outros.

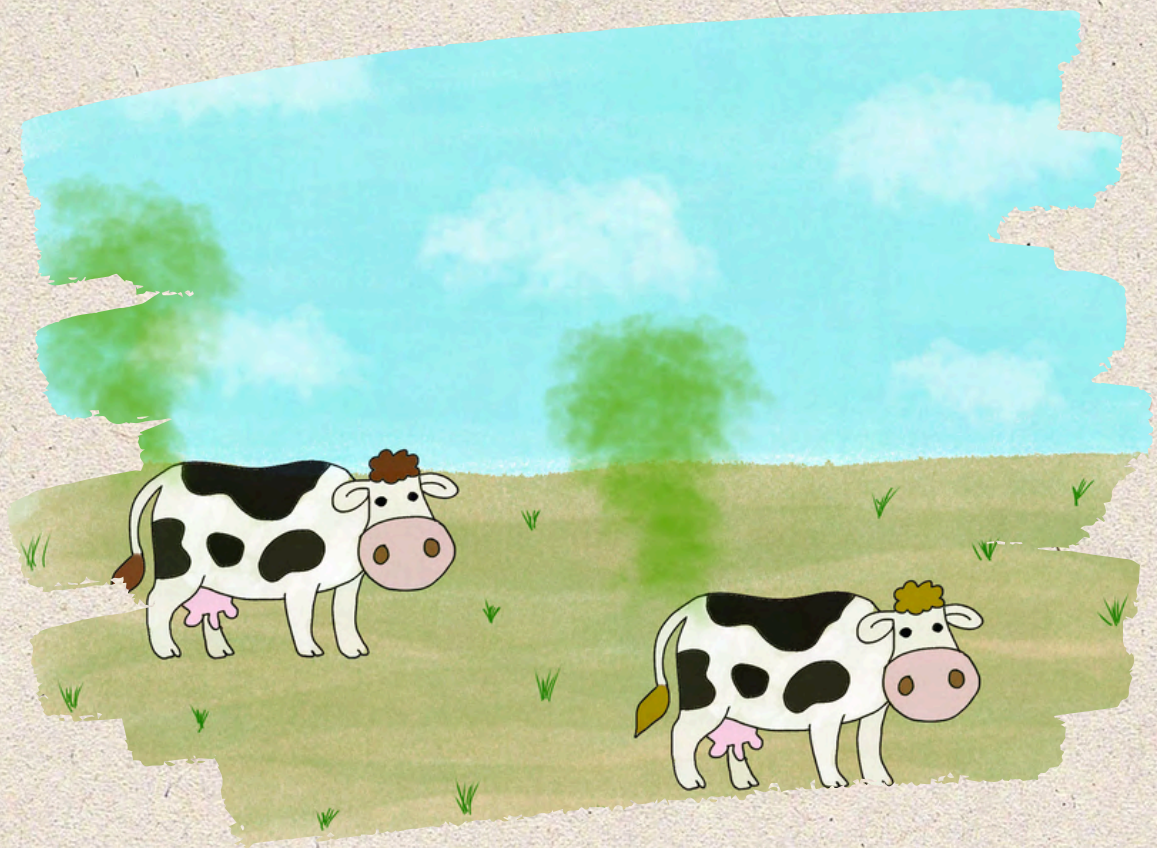


— O pum das vacas? Cê só pode tá de brincadeira, Sapo Aldo!

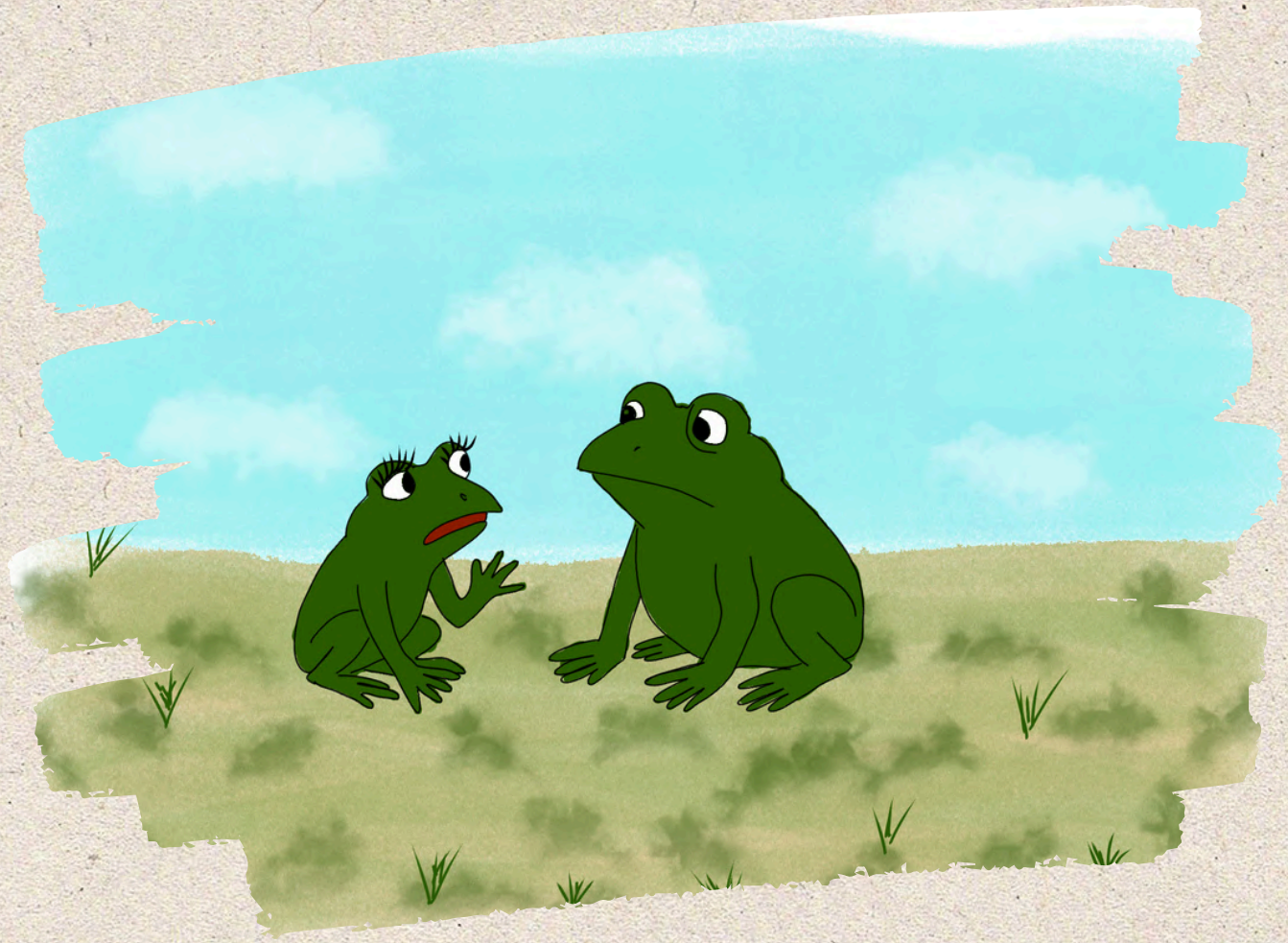


— E eu lá sou homem de brincadeiras, dona Saponilda?

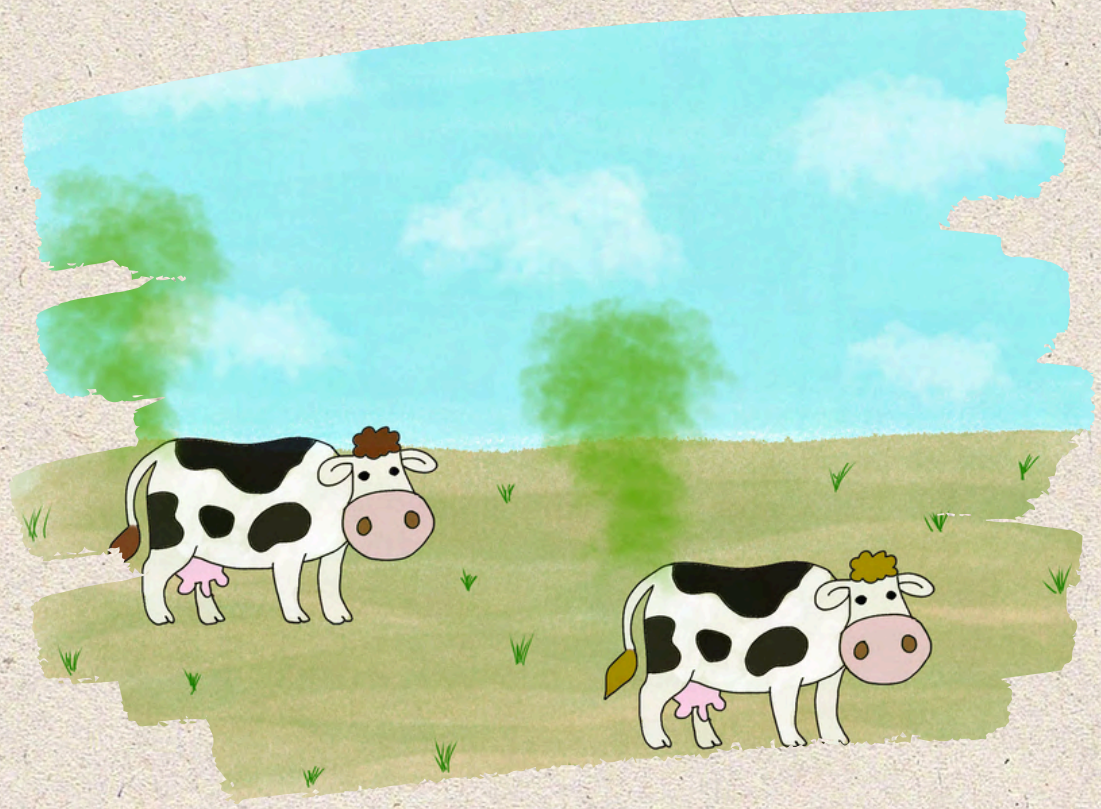
— As vaquinhas criadas nos pastos para virar churrasco e produzir leite pros humanos são um problemão pro meio ambiente! Elas soltam um gás chamado metano quando arrotam e quando soltam pum. E esse tal de metano ajuda a aumentar o efeito estufa e tornar o planeta ainda mais quente.



— Mas gente! Nunca pensei que o pum das vacas podia ser tão perigoso assim!

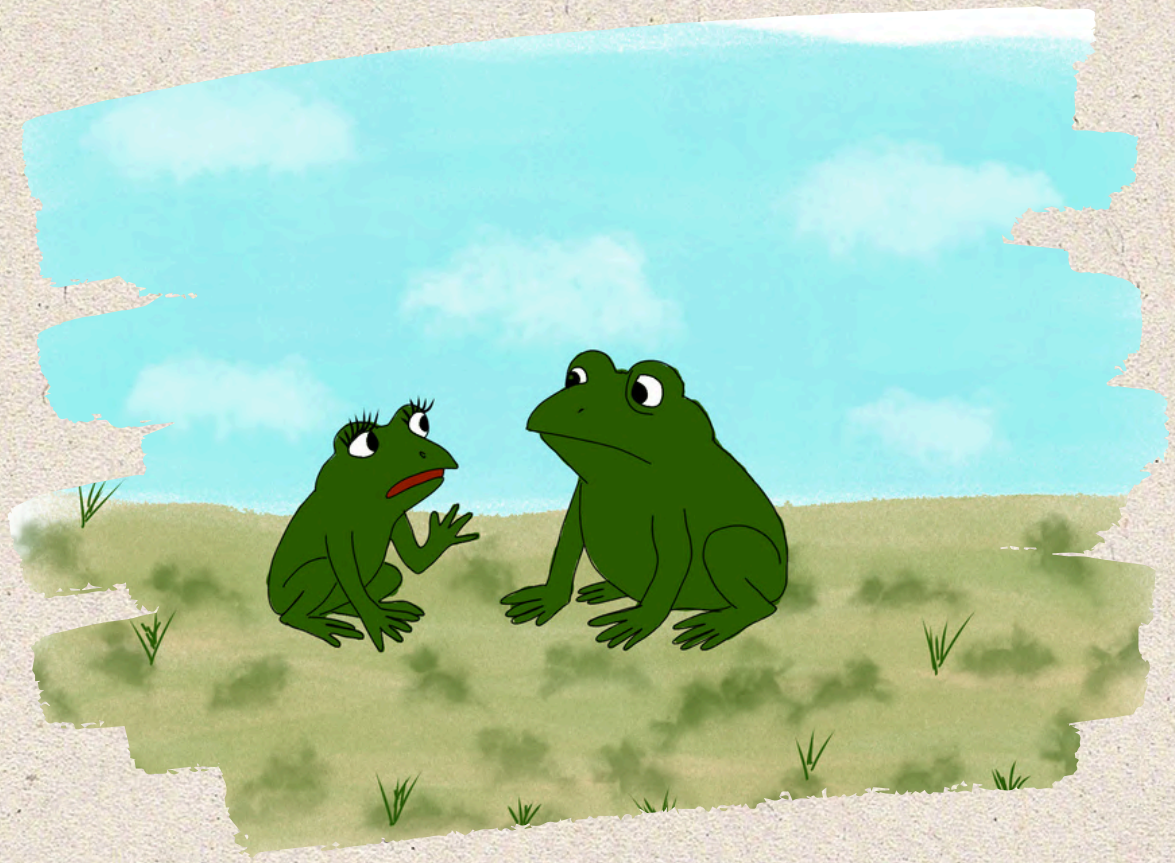


— Pois é, Saponilda. Cada vaquinha pode soltar até 200 litros de gás metano por dia! E como tem milhões de vacas espalhadas pelo mundo, todo esse gás vai subindo pra atmosfera e contribuindo pro aquecimento global. É por isso que precisamos repensar a criação de tanto gado.

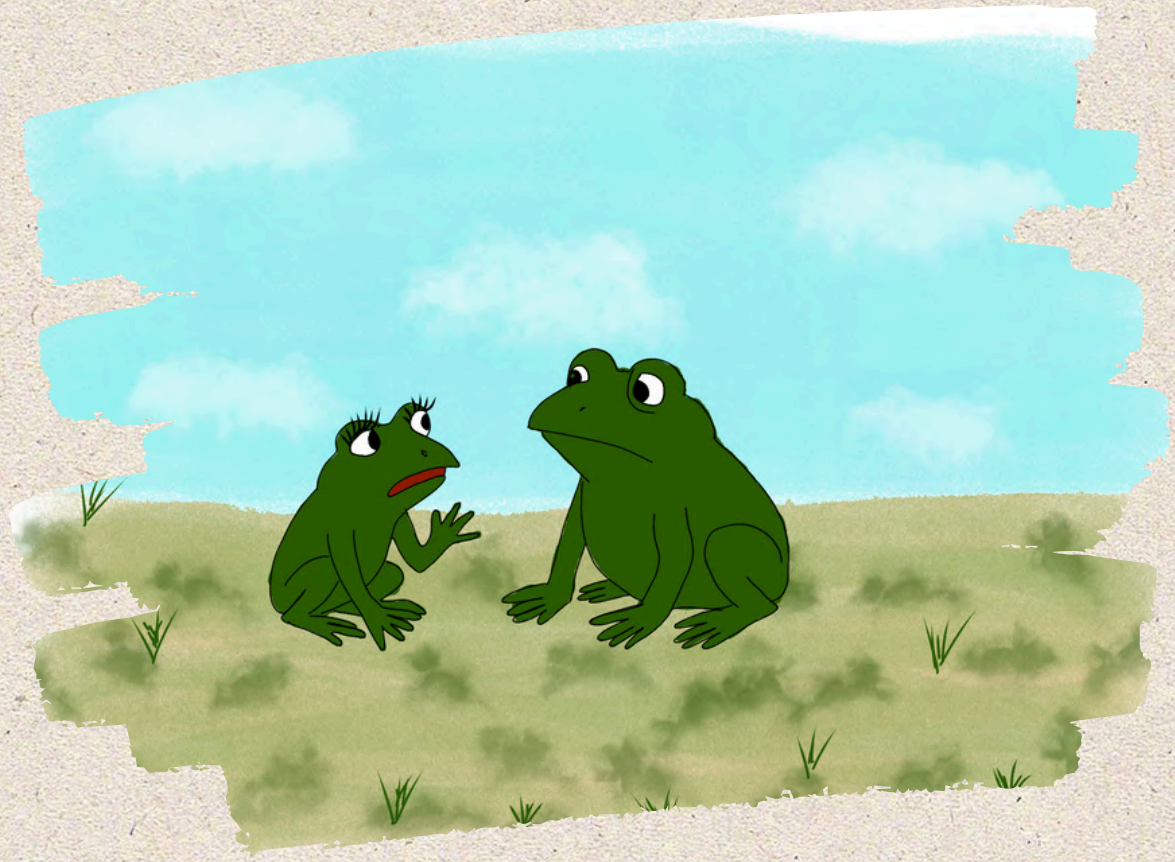


— Eita, nois tá lascado mesmo, ein?! A gente que é sapo parece que fica mais sensível ainda a essas mudanças no clima, eu mesma não posso ver um solzinho que já fico toda ressecada!

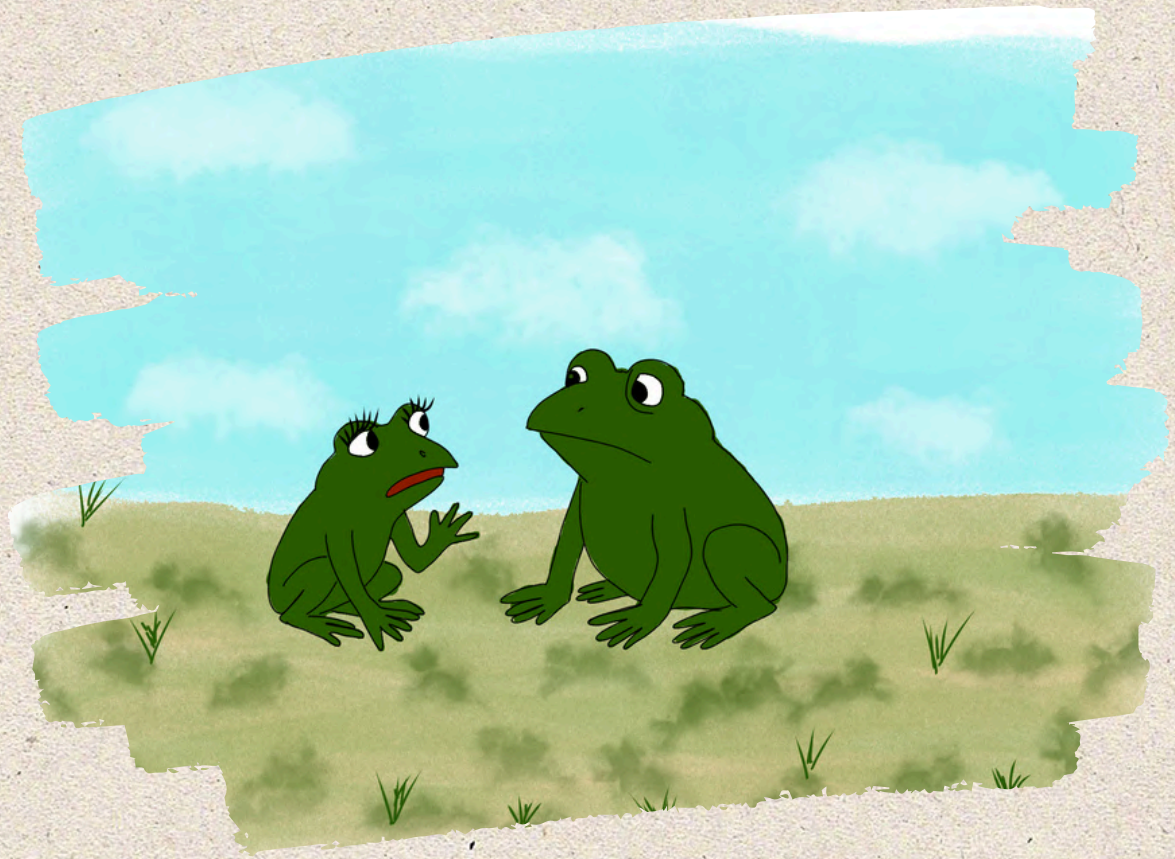
— Sim, Saponilda. Embora as mudanças climáticas afetem todo mundo, tem alguns seres vivos que são mais prejudicados que outros.



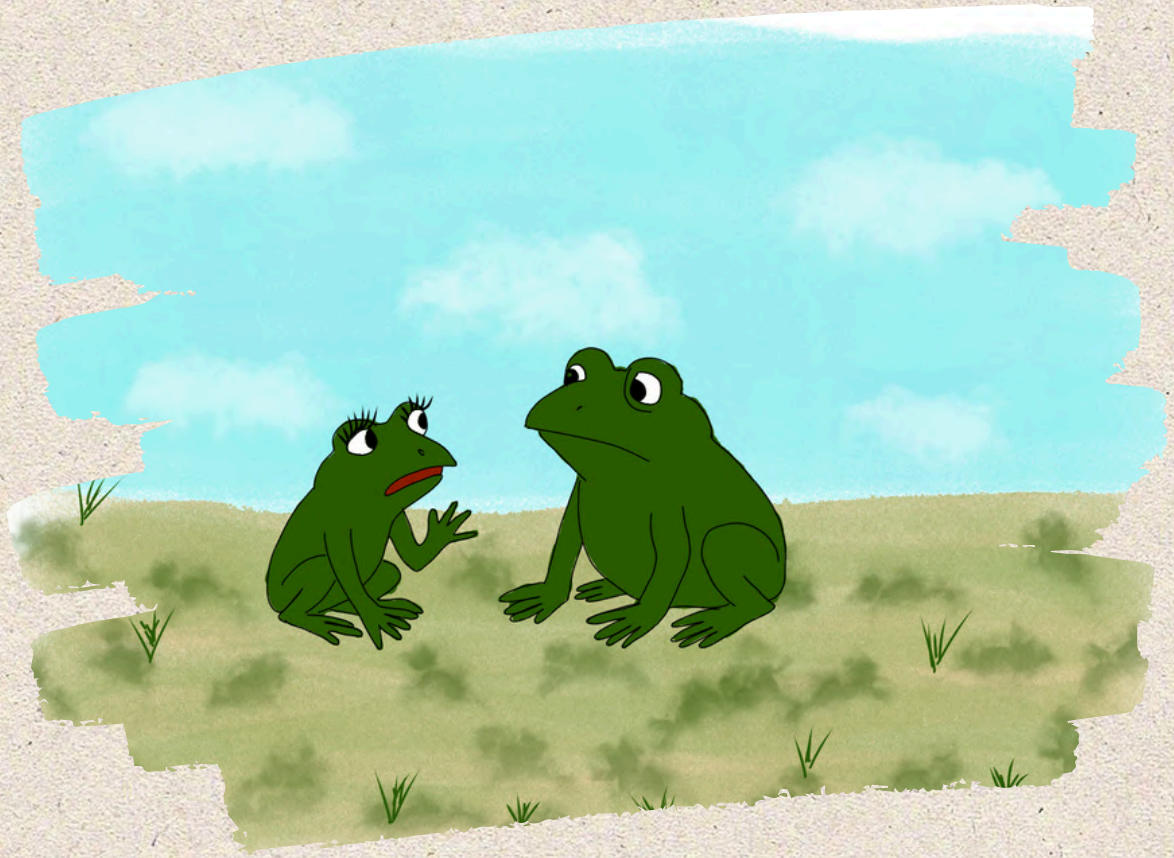
— Os sapos são alguns dos que mais sofrem com as mudanças no clima. Tem alguns parentes que não estão mais conseguindo se reproduzir e cuidar dos filhotinhos como antes por causa da falta de chuva. Com isso, nossas famílias vão ficando cada vez menores e nosso legado vai sendo apagado dessa região.



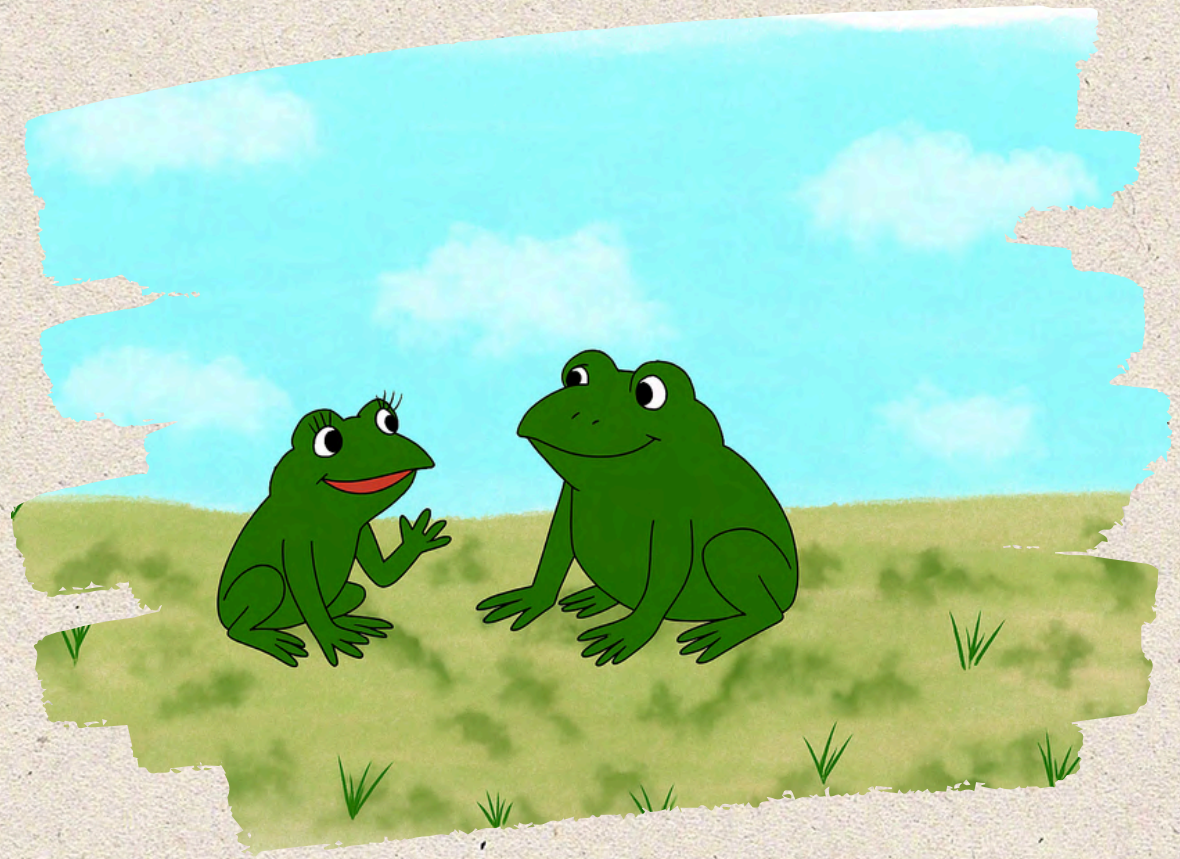
— Poxa... essa conversa me fez perder a vontade de comer meu almoço.



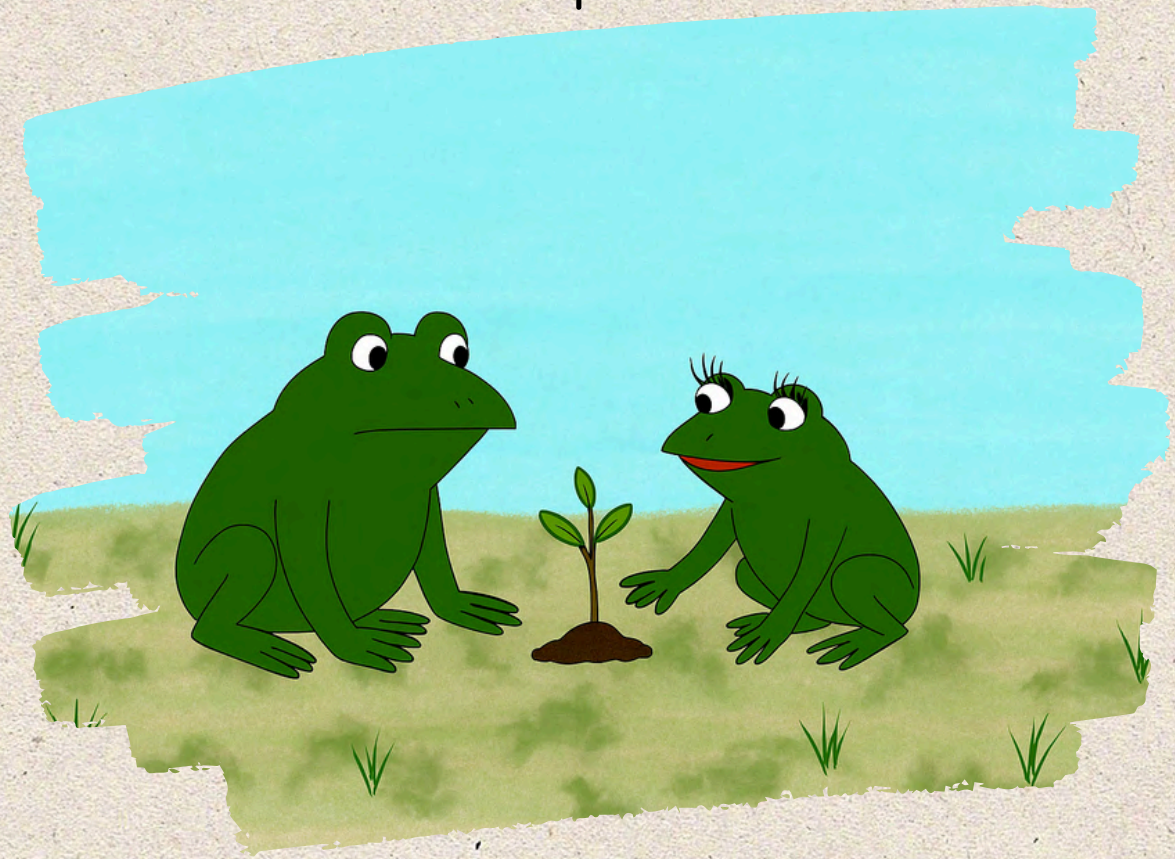
— É, Śaponilda, eu entendo ocê... Tudo isso é muito complicado, mas não dá pra simplesmente desistir do planeta. Como diria um poeta muito sabido: " Ainda há tempo". Eu tenho lido que existe um bucado de soluções para cuidar do planeta, mesmo nessas condições difíceis que tamo enfrentando.



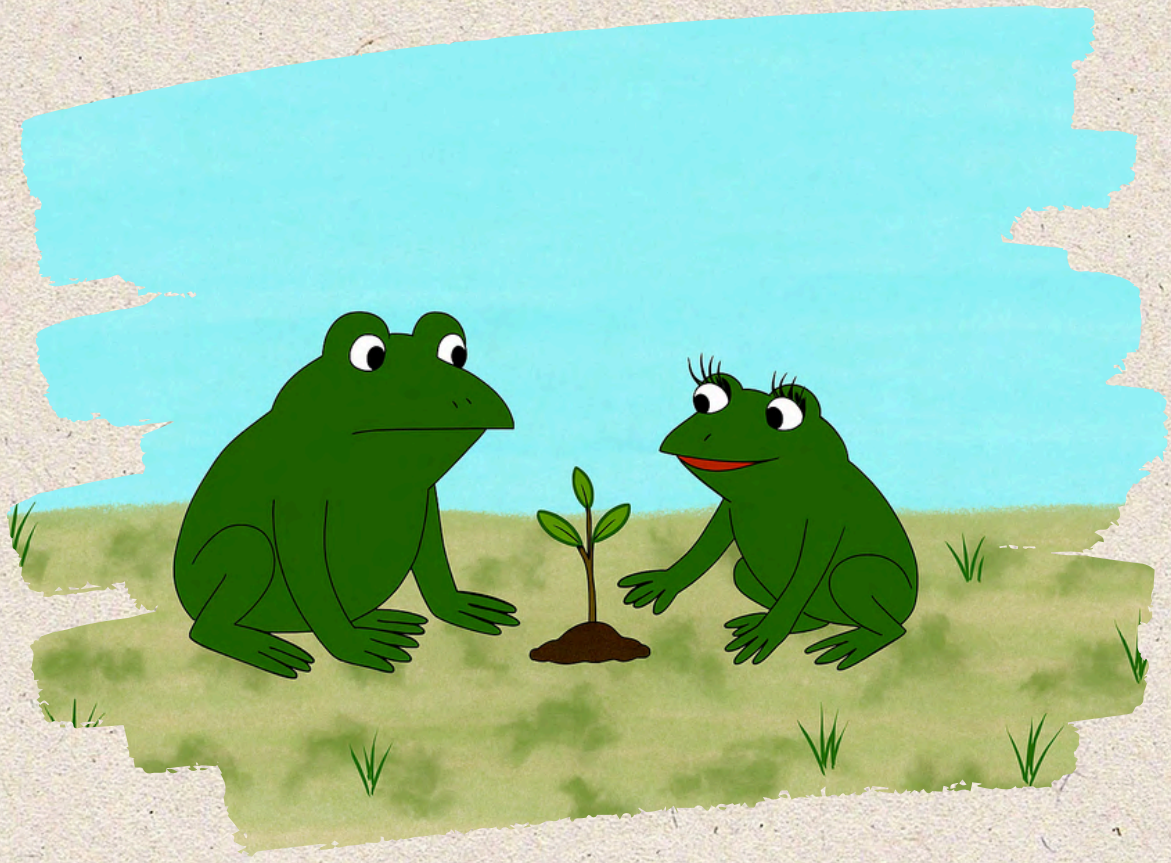
— Tem algumas cidades que estão replantando árvores por toda a cidade e perceberam que a temperatura pode diminuir bastante. Em Medellín, na Colômbia, as ruas foram ocupadas por grandes árvores e a temperatura diminuiu em 2°C!! Isso não é demais?!



— Isso é incrível!!! Agora que cê falou, eu lembrei que sempre achei a Florestinha aqui do lado mais fresca que as pastagens dos gados, onde tudo foi desmatado. Vamos falar com os nossos vizinhos e fazer um mutirão de plantação de árvores, Sapo Aldo!

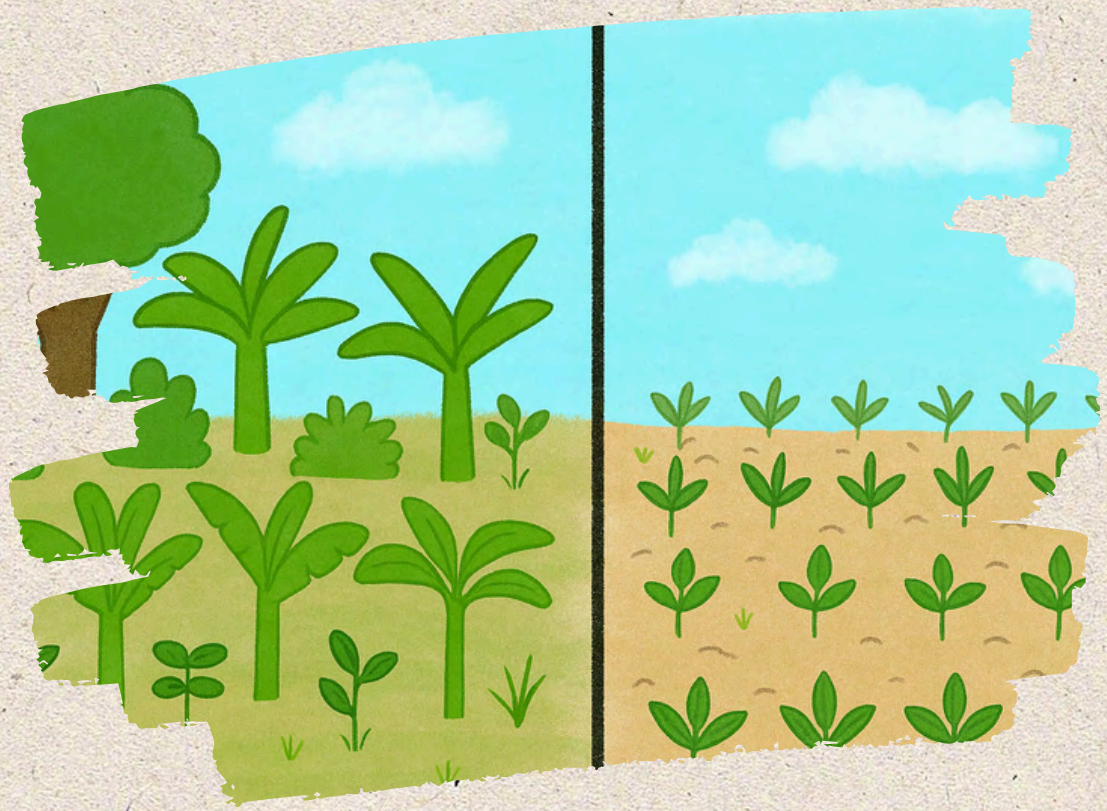


— Que ideia supimpa! Meu nome é "Pronto"!!

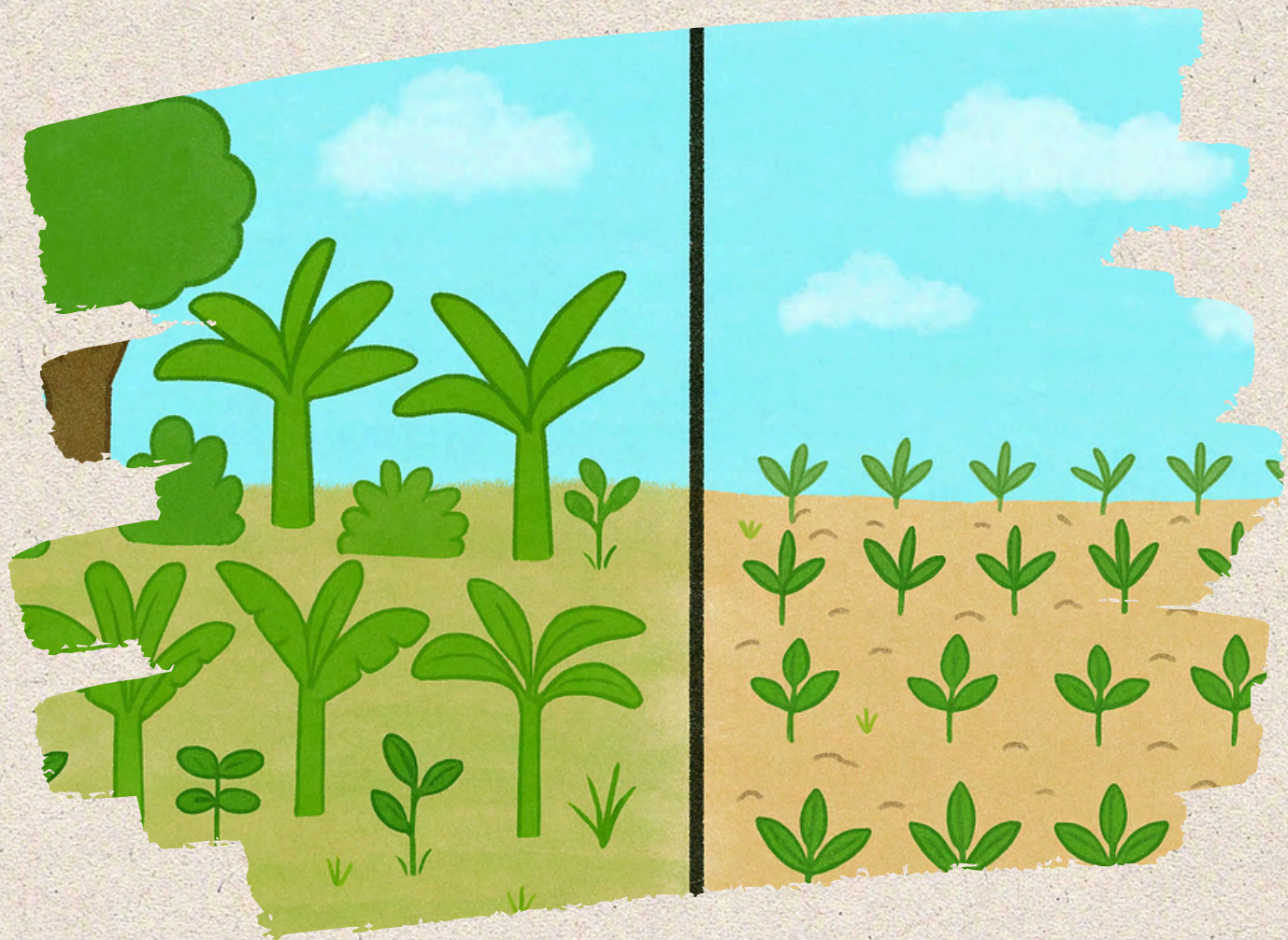


— Existem outras coisas que podemos fazer pra ajudar o planeta a ficar melhor?

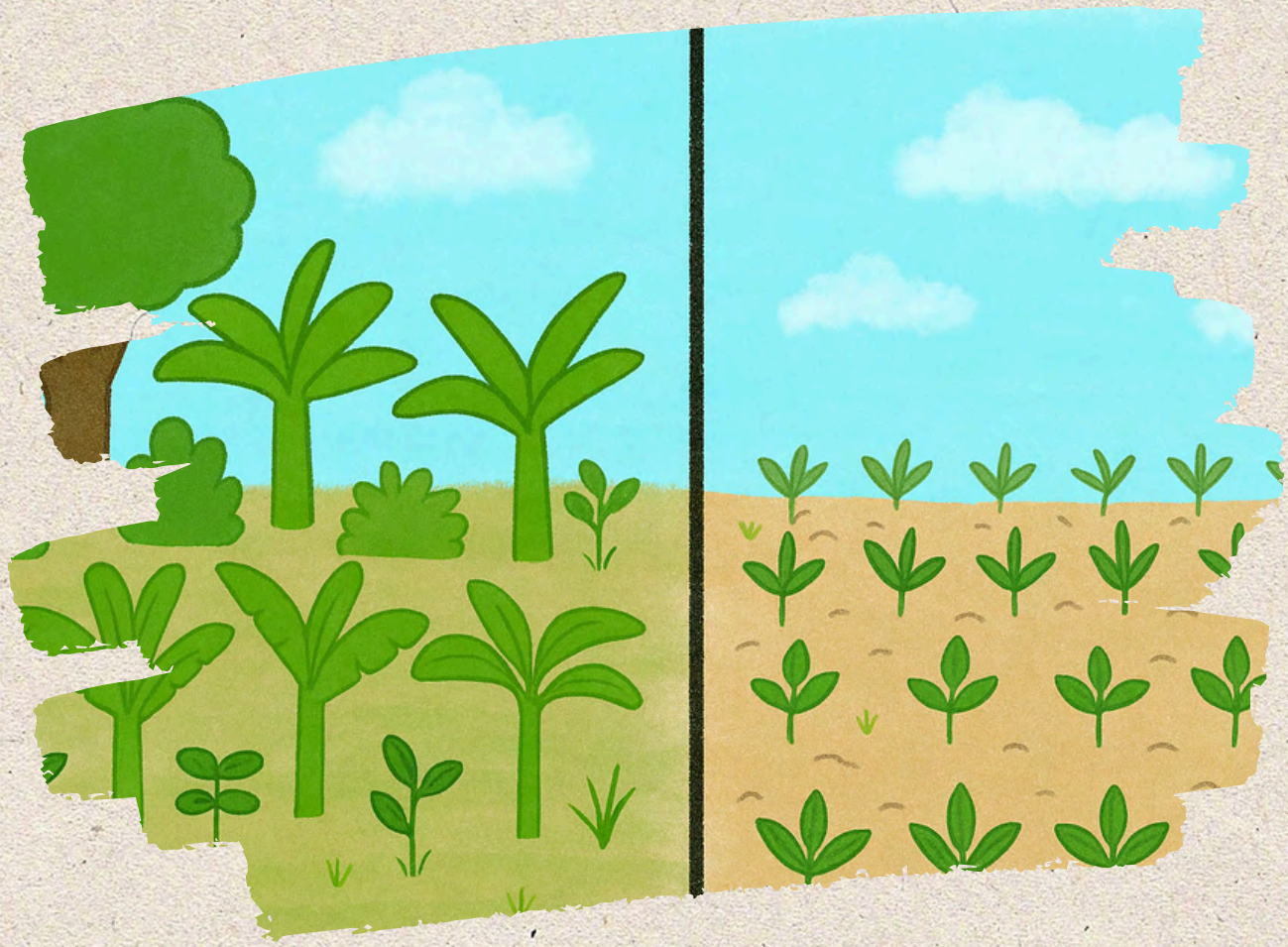
— Sim!! Já ouviu falar das agroflorestas? Elas são plantações muito mais amigáveis para o clima do que as monoculturas que a gente vê por aí. Essas agroflorestas são um tipo de cultura usado há milhares de anos por comunidades tradicionais e são alternativas muito boas para conciliar a plantação de alimentos com a conservação da natureza.



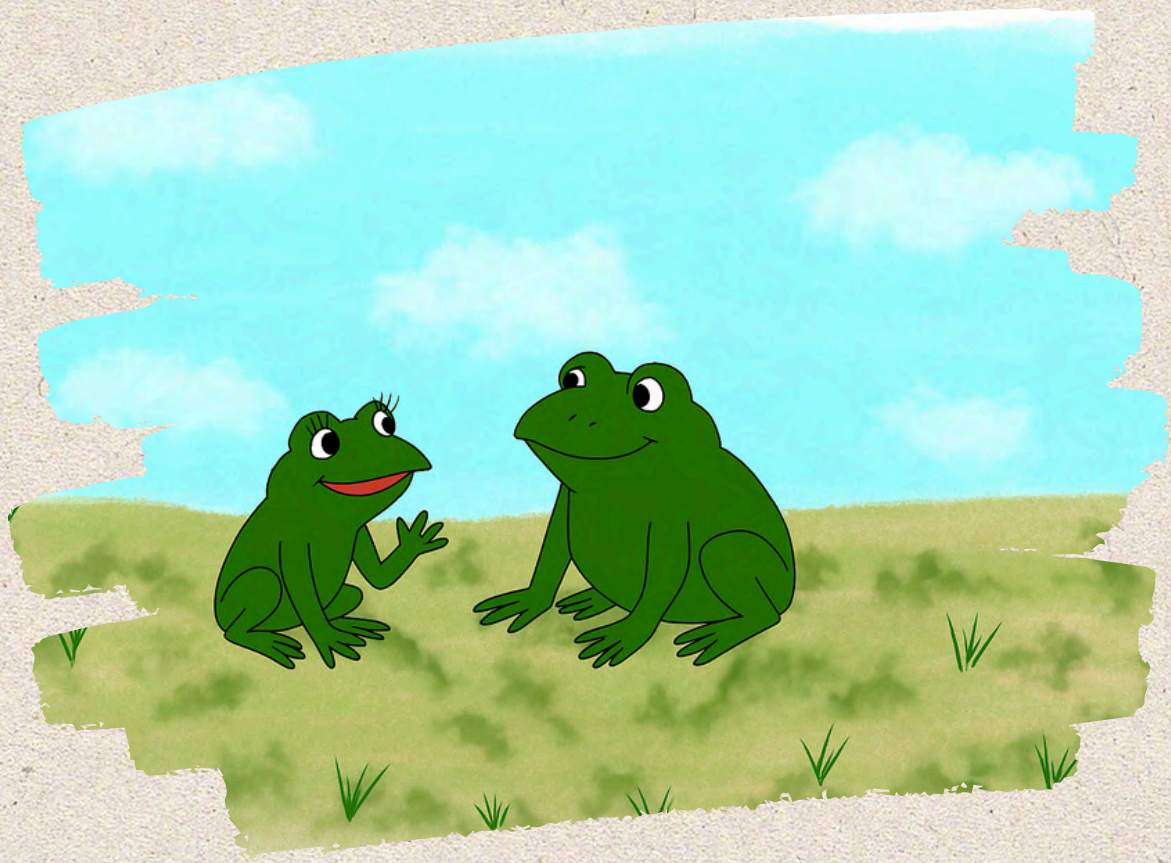
— Essás plantações combinam as árvores nativas da região com outras culturas como cacau e café. As árvores nativas ajudam as culturas a não sofrerem tanto com os impactos das mudanças climáticas como, calor, ventos e enchentes.



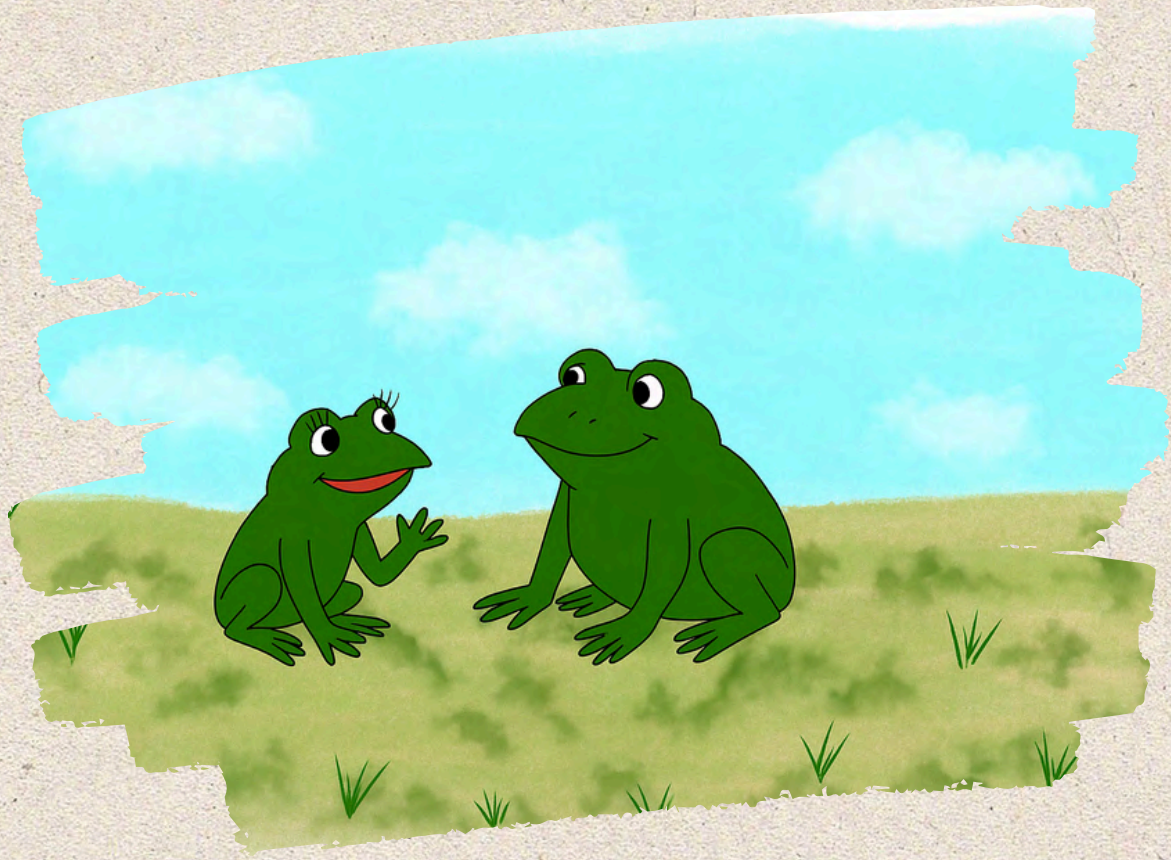
— Além disso, as árvores grandes que ficam nas agroflorestas são uma importante reserva de carbono, que pode ser liberada se as árvores forem desmatadas, contribuindo para o efeito estufa!



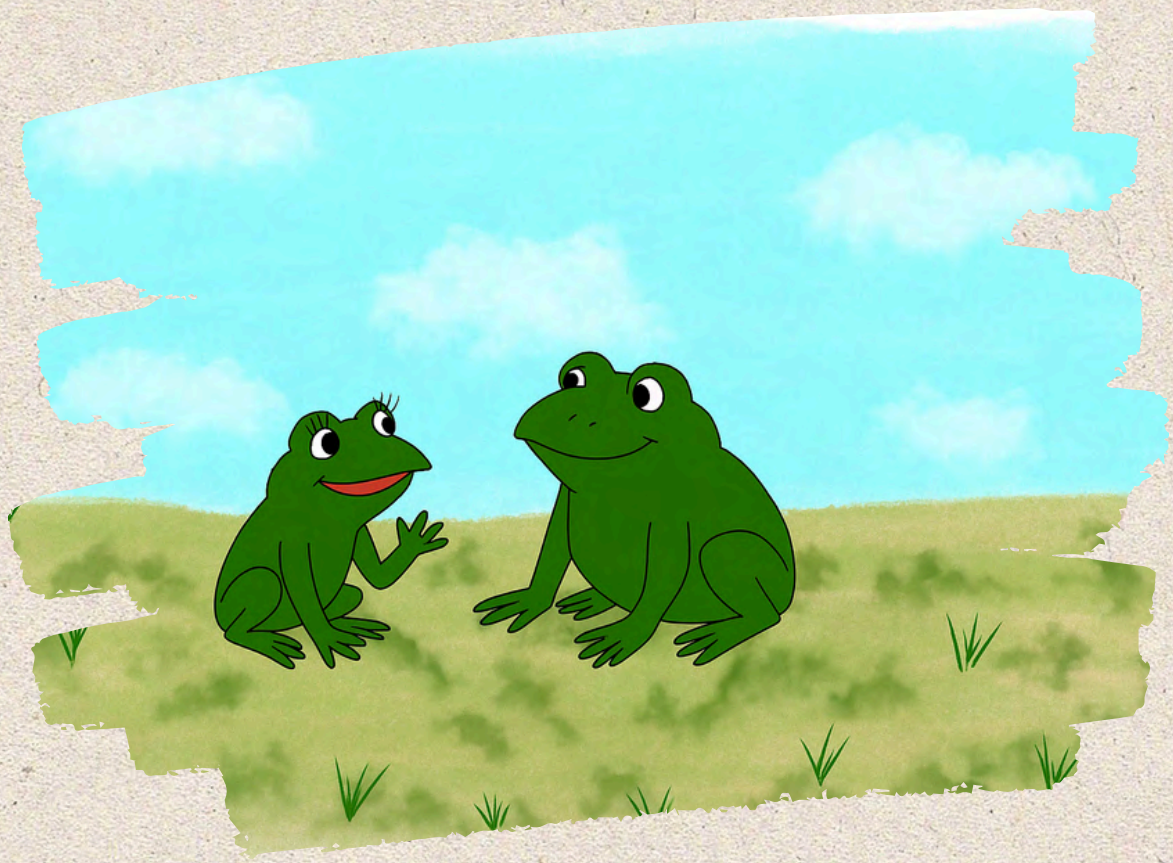
— Que interessante, Sapo Aldo. Pelo visto, nem tudo está perdido…. Temos que contar isso para todo mundo!



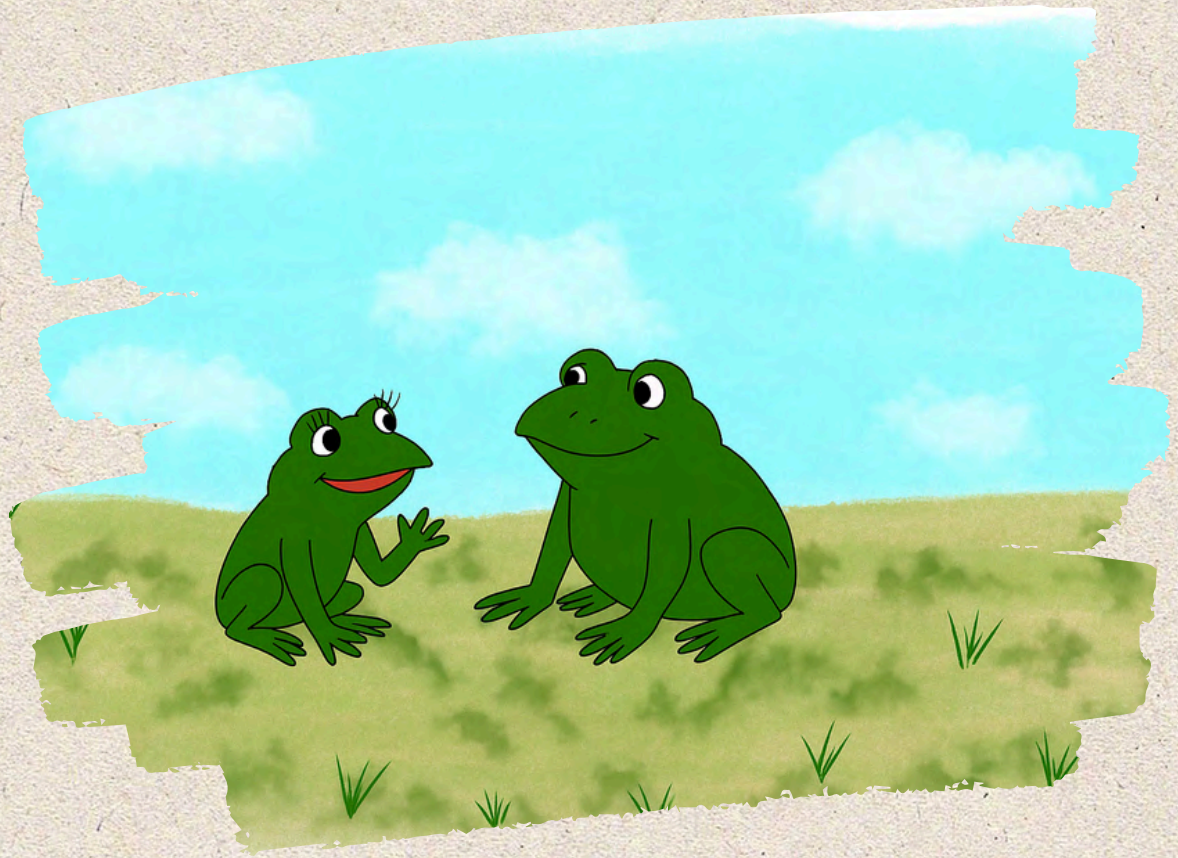
— Sim, Saponilda!! Precisamos mostrar para as pessoas que o aquecimento global realmente existe e já tá afetando os bichos e as plantas. Tem um bucado de gente que ainda acha que isso é história pra boi dormir.



— Mesmo, Sapo Aldo? Então é nossa missão explicar sobre as mudanças climáticas para todos que conhecemos!!



— Isso aí, Saponilda! Com todos trabalhando juntos, podemos criar um ambiente mais resistente às mudanças climáticas e até diminuir seus impactos. E quem sabe, nosso pequeno, mas tão querido brejo, pode inspirar os humanos a cuidarem melhor da Terra também!



FIM

CAÇA-PALAVRAS

Encontre no quadro as palavras destacadas abaixo:

AQUECIMENTO - CLIMA - SAPOALDO - SAPONILDA - PLANETA- BREJO

X	A	E	G	E	E	D	W	T	I	U	H	F	C
V	Q	I	Q	I	I	D	B	R	E	J	O	K	Q
S	U	I	V	E	N	F	I	I	N	G	M	F	I
K	T	U	Y	G	X	D	S	C	A	N	I	C	T
B	S	A	P	O	N	I	L	D	A	R	B	K	Q
P	P	Z	R	L	E	D	Q	Q	A	B	L	H	I
K	Z	Y	F	P	R	C	B	E	A	X	I	P	R
G	A	Q	U	E	C	I	M	E	N	T	O	K	W
V	D	M	T	X	O	Y	X	E	V	G	M	L	N
T	H	P	L	A	N	E	T	A	X	Z	J	F	Y
T	J	Y	Z	F	X	K	L	L	A	Y	Y	B	H
A	Q	V	F	A	O	E	H	V	U	K	T	I	J
L	E	Z	A	O	T	T	A	M	C	L	I	M	A
F	G	L	S	O	B	S	A	P	O	A	L	D	O

LABIRINTO

Vamos ajudar o Jeremias e sua família a cruzar a plantação? Guie o Jeremias para sair do labirinto