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ECOLOGICAL NICHE MODELLING OF THE *LEOPARDUS TIGRINUS* SPECIES COMPLEX (MAMMALIA, FELIDAE) SHEDS LIGHT ON ITS ELUSIVE EVOLUTIONARY HISTORY

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Orientador: Eduardo Eizirik

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Table of Contents

List of Figures

List of Tables

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Resumo

A história evolutiva de *Leopardus tigrinus* tem sido estudada com diferentes abordagens, incluindo análises de estruturação genética e dados de morfologia. Essas análises sugerem que este táxon é um complexo de espécies distribuído na América Central (Costa Rica e Panamá) e América do Sul. Esse tipo de problema taxonômico pode ser abordado também com uma perspectiva ecológica, permitindo conhecer melhor as condições ambientais que favorecem a presença da(s) espécie(s), identificando as adaptações locais das populações e propondo áreas, que devido a suas condições ambientais, podem atuar como barreiras à dispersão, favorecendo a diferenciação genética entre os grupos propostos. Por tanto, os objetivos deste projeto foram: avaliar as diferenças, em nível de nicho ecológico, entre as populações de *L. tigrinus* para determinar a existência de divergência ecológica entre essas; e identificar barreiras ambientais à dispersão da espécie que possam ter contribuído para a diferenciação dos grupos já propostos. Este trabalho propõe quatro barreiras: o centro do Panamá, o Amazonas, os Llanos e a depressão Huancabamba; estas foram avaliadas ao longo de três períodos de tempo: último máximo glacial (LGM), Holoceno médio e o presente para determinar seu efeito ao longo do tempo. Para isto, foram construídos modelos de nicho para o complexo *L. tigrinus* como uma unidade só, para cada grupo proposto dentro dele, e para delimitações hipotéticas das populações que que ocorrem na região do Escudo das Guianas. Foi utilizado o algoritmo de Máxima Entropia implementado no pacote “kuenm” do software R, para a construção dos modelos nos diferentes períodos de tempo, e a taxa de omissão e a área abaixo da curva ROC como métricas de avaliação dos mesmos. A divergência entre os nichos modelados foi avaliada em duas dimensões: no espaço geográfico utilizando o índice D do Schoener no pacote ENMeval; e no espaço ambiental através do mínimo volume do elipsoide (MVE) no software NicheA. Ao nível de diferenças ecológicas, os resultados sugerem que grupos propostos baseados na morfologia apresentam baixa sobreposição tanto no nível geográfico como ambiental. Por outra parte, os grupos andinos sugeridos por análises de DNA mitocondrial genéticos apresentam uma alta sobreposição geográfica e ambiental, mas divergem dos grupos do escudo das Guianas e do NE do Brasil. Com relação às análises exploratórias realizadas para o Escudo das Guianas, foi achada uma alta similaridade ambiental e geográfica com o grupo do NE do Brasil, embora isso possa ser efeito da diferença na quantidade de dados disponíveis para as duas regiões. Quanto às barreiras, os resultados sugerem que a depressão Huancabamba não atua como barreira em nenhum cenário; o Centro do Panamá só para o grupo andino com conectividade no LGM, mas só quando foram incluídos dados da região andina toda e do Escudo das Guianas. A região amazônica se mostrou uma barreira para todos os grupos propostos dentro do complexo, com expansão da distribuição de alguns grupos nesta área no LGM; e os Llanos foram uma barreira sempre para todos os grupos, exceto para o grupo do NE do Brasil. Os resultados deste trabalho sugerem que é pouco provável que tenha existido fluxo gênico entre os grupos da região andina e o leste da América do Sul. O oposto parece ser o caso entre o grupo do Escudo das Guianas e o NE do Brasil, embora sejam requeridos mais dados do escudo das Guianas para testar apropriadamente esse resultado. Esse trabalho identifica que, além das diferenças morfológicas e genéticas já reportadas para *L. guttulus*, a espécie apresenta uma alta divergência ambiental com os outros grupos propostos dentro do complexo *L. tigrinus*. Em conclusão, esse trabalho apoia a existência de diferenças ecológicas e barreiras históricas entre grupos regionais previamente propostos no âmbito do complexo *L. tigrinus*, contribuindo para uma melhor compreensão dos processos evolutivos que levaram à sua diferenciação.

Palavras chaves: Barreiras geográficas, divergência ecológica, gato-do-mato pequeno do Norte, holoceno médio, última glaciação máxima.

Abstract

The evolutionary history of *Leopardus tigrinus* has been studied based on different approaches, including genetic and morphologic data. These analyses have suggested that this taxon is a species complex distributed in Central America (Costa Rica and Panama) and South America. This kind of taxonomic problem can also be approached from an ecological perspective, allowing the assessment of the environmental conditions that allow the presence of the focal species, identifying local adaptations of populations, and proposing areas that, due to their environmental conditions, can act as historical barriers for dispersal, favoring the genetic differentiation among the proposed groups. Therefore, the objectives of this project were: (i) to evaluate the ecological niche differences among regional *L. tigrinus* populations to determine the existence of ecological divergence among them; and (ii) to identify environmental barriers to the historical dispersal of these organisms that could have driven the differentiation among the proposed groups. With respect to the second objective, we have considered four hypothetical barriers: The Panama center, the Amazon, the Llanos e the Huancabamba depression; each of them was evaluated across three time periods, last glacial maximum (LGM), mid-Holocene and present, to determine its potential effect over the time. For this, we constructed niche models for the *L. tigrinus* complex as a whole, for each regional group proposed to comprise it, and for hypothetical delimitations of the populations that occur in the Guiana Shield. We used the Maximum Entropy algorithm implemented in the “kuenm” package of the R software to construct the models for the different time periods, and the omission rate and the area under the ROC curve as metrics for their evaluation. The divergence between the modeled niches was evaluated in two dimensions: in geographic space using Schoener’s D index with the ENMeval package; and in environmental space through the minimum volume of the ellipsoid (MVE) approach implemented in the NicheA software. In terms of ecological differences, the results suggested that the groups proposed on the basis of morphology have low overlap both on the geographic and environmental levels. On the other hand, the Andean groups suggested by mitochondrial DNA data have a high geographic and environmental overlap, but differ from the groups in the Guiana Shield and NE Brazil. Regarding the exploratory analyses carried out for the Guiana Shield, a high environmental and geographical similarity was found with NE Brazil, although this result may have been influenced by the difference in sample size between the two regions. With respect to the barriers, the results suggest that the Huancabamba depression does not act as a barrier in any scenario, the Panama Center is a barrier only for the Andean group, with some connectivity in the LGM, but only when data from the entire Andean region and the Guiana Shield were included. The Amazon region was inferred to be a barrier for all the groups within the complex, with the expansion of the distribution of some groups in this area in the LGM. Finally, the Llanos have always been a barrier for all groups, except for the NE Brazil group. The results of this work indicate that it is unlikely that there is gene flow between groups in the Andean region and eastern South America, however more Guiana shield data are required to properly assess this result. This work further identifies that, in addition to the morphological and genetic differences already reported for *L. guttulus*, the species has a high environmental divergence with the other groups proposed within the *L. tigrinus* complex. In conclusion, this work adds an ecological component that supports the differentiation of groups that have been proposed to comprise the *L. tigrinus* complex, and further identifies areas whose low habitat suitability for these cats have likely contributed to the evolutionary divergence among these regional populations.

Key words: Ecological divergence, geographical barriers, last glaciation maximum, mid-Holocene, Northern tiger cat.

INTRODUCTION

The extant lineages of the cat family (Felidae) descend from a recent diversification process (crown-group age of *ca.* 12 My) (Johnson et al. 2006; Li et al. 2016). In the Neotropics, three of these lineages are presently represented: *Panthera*, *Puma*/*Herpailurus* and *Leopardus* (Johnson et al. 2006; Li et al. 2016), with the latter being endemic to the region and the most diverse genus in the family. This genus includes small to medium-sized felids, which are characterized by having dark spots or rosettes on a grayish, ochre, or yellowish background coat (Nowell and Jackson 1996; Sunquist and Sunquist 2002, 2009; Sanderson and Watson 2011). Considerable intraspecific diversity, and occasional inter-species overlap in pelage features (as well as documented cases of hybridization), have historically posed challenges to accurate species-level delimitation and identification in this group (e.g., Johnson et al. 1999; Nascimento et al. 2020; Nascimento and Feijó 2017; Trigo et al. 2008, 2013). This problem extends to ongoing taxonomic debates affecting the species-level composition of the genus (Kitchener et al. 2017), a topic that has advanced substantially in recent years with the progressive incorporation of more complete molecular and morphological data sets (Johnson et al. 1999; Sicuro 2011; Sakamoto and Ruta 2012; Trigo et al. 2013; Li et al. 2016; Nascimento and Feijó 2017; Nascimento et al. 2020).

One of the foci of taxonomic discussion is the tigrina (*Leopardus tigrinus*) species complex. This species was described in 1775 by Schreber as a small felid from South America, with a type location placed in French Guiana and a distribution that was subsequently proposed to range from Costa Rica to northern Argentina (see Nascimento and Feijó 2017 for a recent review). Recent taxonomic assessments suggested that it comprised four subspecies (e.g., Wozencraft 2005): *L. t. oncilla* in Central America, *L. t. pardinoides* in the Andean region, *L. t. tigrinus* in northern Brazil and the Guiana shield, and *L. t. guttulus* in southern Brazil, Paraguay, and northern Argentina (**Figure 1**). Johnson et al. (1999) presented evidence of strong genetic divergence between *L. t. oncilla* (samples from Costa Rica) and *L. t. guttulus* (samples from southern Brazil), based on mitochondrial DNA (mtDNA) sequences. In that study, a putative distribution of the subspecies was presented, in which *L. t. oncilla* was restricted to Costa Rica and Panamá; *L. t. pardinoides* was distributed in Colombia, Ecuador, northern Peru and western Venezuela; *L. t. guttulus* in southern Brazil, Paraguay, southern Bolivia and northern Argentina; and *L. t. tigrinus* was present in eastern Venezuela, Guiana, French Guiana, Suriname and northern/northeastern

Brazil (**Figure 1A**). However, there was uncertainty with respect to central Venezuela, and the boundaries among these units were not clearly delimited. Still, this proposal was interesting, since it was the only one among recent schemes that considered the existence of *L. t. pardinoides* as a distinct subspecies (**Figure 1**).

Later, Trigo et al. (2013) reported evidence for consistent genetic differentiation and lack of ongoing gene flow between populations of *L. tigrinus* from northeastern and southern/southeastern Brazil, leading them to recognize the latter as a distinct species, *L. guttulus* (i.e., elevating *L. t. guttulus* to a valid species). Taking into account this taxonomic change, the International Union for Conservation of Nature – IUCN presented a proposal for species distribution in which *L. tigrinus* is distributed from Costa Rica to Bolivia and central Brazil, with a gap between eastern Panama and the Andean region in Colombia, and excluding the Llanos region in Colombia and Venezuela, but including the Amazon region (Payan and Oliveira 2016). In its turn, *L. guttulus* would be distributed in southern/southeastern Brazil, Paraguay, and northern Argentina (Oliveira et al. 2016). Moreover, it is noteworthy that, after the recognition of *L. guttulus* as a distinct species, the *L. tigrinus* distribution in South America was provisionally delimited in an arbitrary fashion, as the two species were separated by an almost straight line due to insufficient information on their actual geographic limits (**Figure 1B**).

Recently, Kitchener et al. (2017) recognized *L. guttulus* as a distinct species, and the existence of two subspecies within *L. tigrinus*: *L. t. oncilla* in Central America and *L. t. tigrinus* in South America; they followed the IUCN proposal with respect to the distribution of these species (**Figure 1B**). Those authors mentioned the possibility that Central American tigrinas might represent a distinct species (based on the genetic results presented by Li et al. [2016]), and that those from northwestern South America could also warrant recognition as *L. pardinoides*, but in both cases they concluded that additional analyses were required to settle these questions. In that same year, Nascimento and Feijó (2017), presented a morphological revision of this species complex, in which they recognized three morphotypes that were equated to species (**Figure 1C**): (i) *Leopardus tigrinus*, distributed in Costa Rica, Panama, Colombia, Ecuador, Peru, Bolivia, Venezuela, Guyana, French Guiana, Suriname and Amapá state (Brazil), with records presenting discontinuities in the Llanos of Colombia and Venezuela, in the Amazon region, and in the Panama center; (ii) *Leopardus emiliae*, occurring in eastern South America, mainly in the Caatinga and

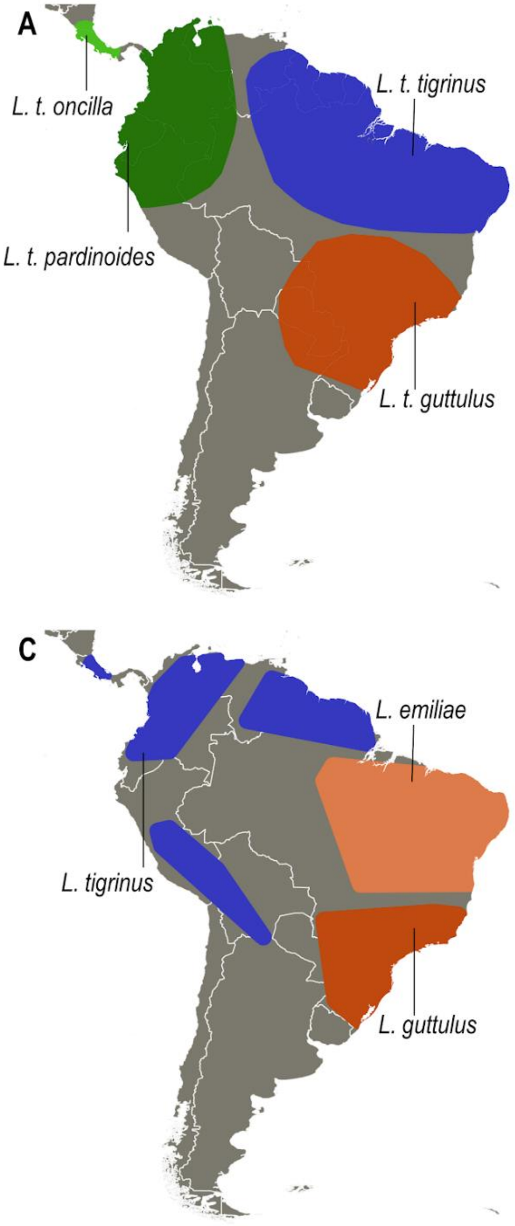


Figure 1: Taxonomic composition of the *Leopardus tigrinus* complex, according to different sources: **A.** Johnson et al. (1999); **B**. Kitchener et al. (2017), in which *L. guttulus* is treated as a separate species; **C.** Polygons created based on occurrence records compiled by Nascimento and Feijó (2017), who used morphological data to propose splitting the complex into three species; **D.** Genetically-identified evolutionary units comprising the complex (Johnson et al. (1999), Trigo et al. (2013), França et al. (*in prep*.), Trindade et al. (*in prep*.)); the Guiana Shield population (which includes the *L. tigrinus* type locality) has not yet been surveyed genetically.

Cerrado biomes in Brazil; and (iii) *Leopardus guttulus*, in southern and southeastern South America, consistent with the results of Trigo et al. (2013).

Finally, a recent genetic analysis using mitochondrial DNA (mtDNA) data revealed notable differences among samples from Central America (C. Am. tigrina), Colombia (N. Andean tigrina) and Peru (S. Andean tigrina), as well as between those and the eastern South American units (*L. guttulus* and samples from northeastern Brazil [herein referred to as 'NE tigrina']); however, they did not include samples from the Guiana Shield, precluding an assessment with respect to the *L. tigrinus* type locality (França et al. *in prep.*). In parallel, an analysis of genome-wide markers (single nucleotide polymorphisms [SNPs]) identified an old divergence between NE tigrina and *L. guttulus*, almost as old as that between *L. guigna* and *L. geoffroyi*, supporting their recognition as distinct species (Trindade et al. *in prep.*). Furthermore, that study revealed that the C. Am. tigrina was placed outside the group comprising the NE tigrina, *L. guttulus*, *L. geoffroyi* and *L. guigna*, indicating paraphyly of the *L. tigrinus* complex. Taken together, these studies suggest that this complex may comprise five different evolutionary units, even allowing for uncertainty regarding the affinities of the Guiana Shield population (**Figure 1D**).

It is clear that the complex is distributed across a broad diversity of environments, while some intervening areas have never been suggested as presenting suitable habitat for these felids. These areas can create barriers that limit historical gene flow among regional populations, leading to potential evolutionary differentiation through time. In addition, there are areas with no recorded occurrence, but in which it is not clear if the complex is really absent or only hard to detect (**Figure 1**). In this context, four putative barriers may be hypothesized: The Panama center, the Llanos of Colombia and Venezuela, the Amazon region and the Huancabamba depression (**Figure 2**). The Panama center, with a mean elevation of 200 m.a.s.l. (Bagley and Johnson 2014) and the lowland Choco-Darien forest could be a barrier between the highland-dwelling populations of Costa Rica/Panama, that are restricted to the Cordillera Talamanca (Payan and Oliveira 2016), and the populations from Colombia, that are restricted to the Andean region (Payán-Garrido and González-Maya 2011). This isolation pattern between these highland regions has already been recorded in other taxonomic groups, such as amphibians and reptiles (Savage 1996; Myers et al. 2007).

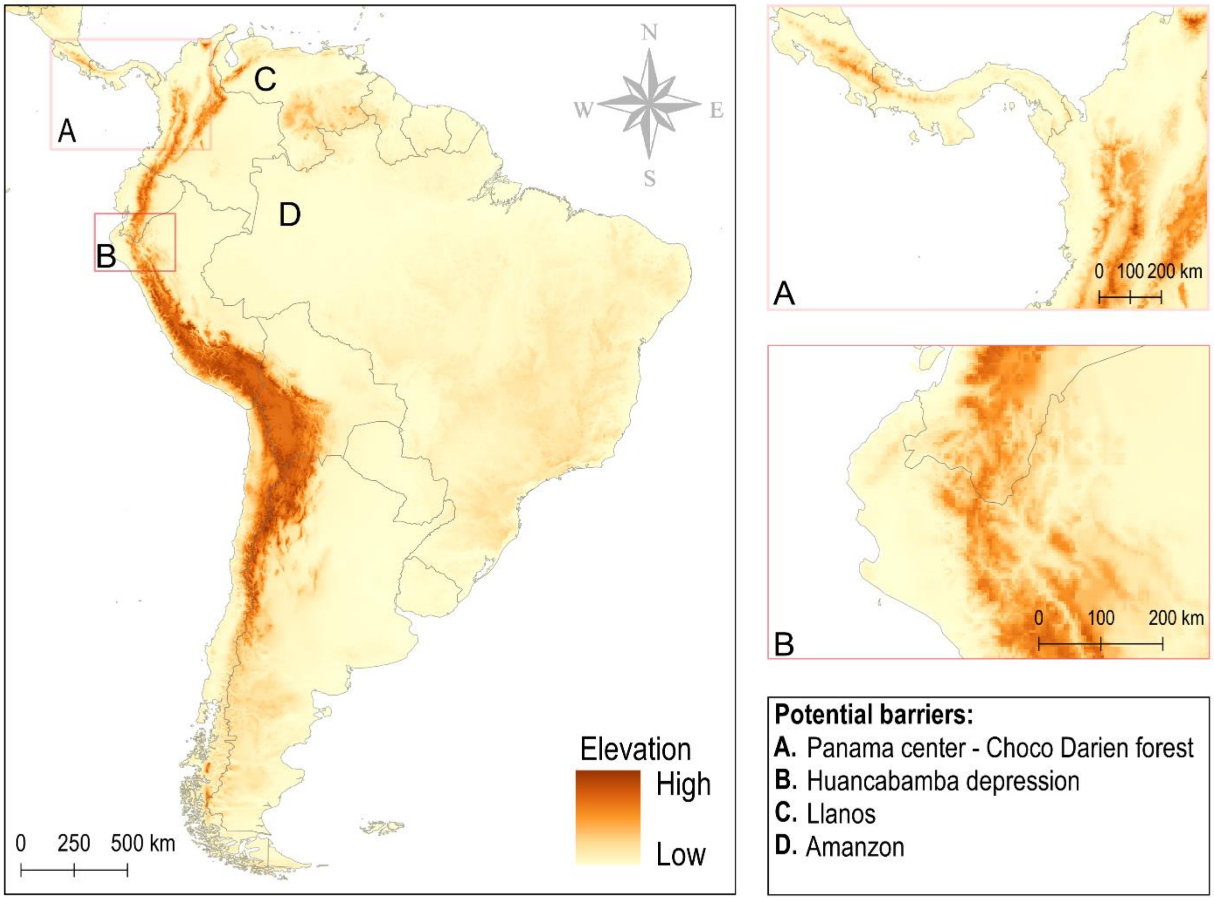


Figure 2: Potential barriers in the *Leopardus tigrinus* complex distribution. **A.** Lowland forests in Panama center and Choco-Darien, **B.** Huancabamba depression, **C.** The Llanos in Colombia and Venezuela and **D.** Amazon region

The Huancabamba depression is a region between southern Ecuador and northern Peru in which the Andes range is partially interrupted by the Rio Chamaya/Rio Marañon system, generating an area with lower altitude (Weigend 2002). This area has been suggested as a barrier for some plants in Peru (Weigend 2002), while it was also found to act as a corridor for some plants in the north-south and west-east directions (Quintana et al. 2017). In this case, although felids have more movement capability than these other taxa, this depression could be assessed as a potential barrier between the Andean populations of Colombia and Peru, given the recent results indicating that they may be genetically distinct (França et al., *in prep*.). While this Andean barrier is putative, the Llanos have never been suggested as a suitable habitat for the species, and even the

IUCN distribution (**Figure 1B**) does not include this area within its potential distribution. The potential distribution of *L. tigrinus* in Colombia, predicted by Payán-Garrido and González-Maya (2011), suggests that the species is strictly Andean. According to Rodríguez and Rojas-Suarez (2008), the species occurs in western Venezuela, between 2800 and 3000 m.a.s.l., continuous with the Colombian distribution. The Llanos are extremely low for the highland populations from Colombia and Venezuela and can limit their dispersal towards the east. In Ecuador and Peru, the species has also been recorded mainly in high Andean regions (Tirira 2001; SERFOR 2018). This suggests that the Amazon could be a barrier to the dispersal of Andean populations. However, one study focusing on the eastern portion of the Amazon suggested that the species occurs there and may be the same population that occurs in the Guiana Shield (de Oliveira 2004).

To understand present distributional patterns, it is important to take into account the species' and genus' evolutionary history. The genus *Leopardus* diverged from other felids 8 million years (My) ago, possibly in North America, and diversified *ca.* 3-4 My ago in South America, after the entry of an ancestral species in this subcontinent during the great American Biotic interchange, induced by the closure of the Panamanian Isthmus (Johnson et al. 2006). Within the genus, some hypotheses have been proposed regarding the biogeography of species-level divergences. For example, *L. pardalis* and *L. wiedii,* the most widely distributed species of the genus, possibly had their origin in northern South America and invaded Central American from south to north. On the other hand, *L. geoffroyi*, *L. guigna* and the *L. colocola* complex apparently evolved in the southern cone of South America (Eizirik 2012). However, for the *L. tigrinus* complex, there is still no hypothesis that addresses its origin and radiation (partly due to the recalcitrant problem of resolving its phylogenetic structure), or the potential impact of recent geo-climatic events such as glacial cycles.

The dynamics of glacial and interglacial periods drove the intermittent contact and isolation of different populations (Barrantes 2009). These dynamics permitted that vegetation from nearby mountainous areas became continuous during glacial periods. This was the case, for example, of the Andes, Serrania del Darien, Baudó, Majé and San Blas, and the Cordillera Talamanca (Bagley and Johnson 2014). Thus, species adapted to high Andean climates could reach similar regions in Central America, to stay isolated again in the interglacial period (Barrantes 2009). Eventually, at the end of the glaciation, some individuals stayed in Central America and others in South America.

So, these changes during the Pleistocene may provide an explanation for the isolation of *L. tigrinus* in Central America relative to the species' distribution in South America. On the other hand, the Amazon Forest reduction, and the savanna expansion during the last glaciation (Behling 2002) could have led to a connection between open biomes as the Caatinga and Cerrado in Brazil with these savannas that regionally replaced the forest at these times. These hypotheses can be tested using niche modelling. The ecological niche is considered a hypervolume in the multidimensional environmental space (*sensu* Hutchinson 1957) that a species requires for survival (Kearney and Porter 2009) and for keeping its population growth positive (Hirzel and Le Lay 2008). The fundamental niche is a term used when only environmental factors are considered, and the realized niche is employed when biotic factors are also considered (Wiens and Graham 2005). Generally, niche modelling is performed only with environmental variables, mainly for two reasons. First, biotic variables are related with environmental variables, and second, the Eltonian noise hypothesis. This hypothesis argues that, on large scales such as regional or global assessments usually conducted with niche modelling, biotic variables are less relevant than environmental variables, while on small scales, biotic variables are more influential (Soberón and Nakamura 2009).

Thus, niche modelling is an important tool that permits exploring geographic and ecological aspects of a given species (Tocchio et al. 2015). Further, the possibility of projecting these models towards the past has allowed scientists to test hypotheses related to the isolation or connectivity of different areas over time, leading to a better understanding of a species' present distribution (Guevara et al. 2018). For example, these analyses could help to test the existence of barriers and the process of connectivity and isolation related with the last glacial maximum. Therefore, comparing the present and past distribution, along with predictions of habitat suitability over time across putative barriers for a species, might help us understand the evolutionary history of this species complex. With this, the objectives of this study were: (i) to determine the ecological divergence, in geographical and environmental space, among the groups previously proposed to comprise the *Leopardus tigrinus* complex on the basis of morphological and/or genetic data; and (ii) to employ ecological niche modelling to identify potential barriers across the overall distribution of the *Leopardus tigrinus* complex that may have induced the evolutionary differentiation among such groups.

MATERIALS AND METHODS

Occurrence data

Due to the taxonomic changes that have recently affected the complex, we used records assigned to both *L. tigrinus* and *L. guttulus*. For *L. tigrinus*, the localities were obtained from the Global Biodiversity Information Facility (GBIF - https://www.gbif.org/) database and were filtered first for the coordinate data associated to the occurrence and second for the record type. Then, human observation, machine recorded, and record type "unknown" were excluded. Thus, only records with high reliability were selected for use. Also, we obtained records from the literature (Pacheco et al. 2001; González-Maya and Schipper 2008; Arias-Alzate et al. 2014; Nascimento and Feijó 2017; Rodgers and Kapheim 2017; Pillco Huarcaya et al. 2019; Bonilla-Sánchez et al. 2020; Mooring et al. 2020). Additionally, we included records from the Oncilla Conservation in Costa Rica and Proyecto Nai, both ongoing projects of Fundación CRWildlife, and camera-trapping records obtained by Antioquia University's mammalogy group. For *L. guttulus*, we used the information reported by Nascimento and Feijó (2017) and the individuals genetically identified by (Sartor et al. 2021). All records included in this study were verified by photo, video or genetic analysis to guarantee their correct identification. We deleted duplicate records and enforced a spatial filter of 25km radius, based on the maximum home range reported for *L. tigrinus* (Payán and Soto 2012), to avoid overprediction in areas with a higher concentration of points due to unequal sampling efforts. The spatial filter was performed using the R package "SpThin" (Aiello-Lammens et al. 2015), that randomly selects all records that comply with the parameter established and remove the others, creating a filtered record set. We created a maximum of 5 record sets that adjust for this distance parameter. This filter was applied to each group set that was modeled in this study.

Environmental data

Environmental information selected for the models included variables related with temperature, evapotranspiration process and terrain (e.g. rugosity) obtained from ENVIREM database (http://envirem.github.io/, Title and Bemmels 2018), (**Table 1**). The variables had a resolution of 2.5 arcseconds, that correspond to approximately 5km^2.

Table 1: Environmental variables of the ENVIREM database used to model the ecological niche of the *L. tigrinus* complex.

Variable	Description	Units
AnnualPET	Annual potential evapotranspiration	mm/year
AridityIndex	Thornthwaite aridity index	
ClimaticMoistureIndex (CMI)	A metric of relative wetness and aridity	
Continentality	Average temp. of warmest month - average temp. of coldest month	°C
GrowingDegDays0 (GDD0)	Sum of mean monthly temperature for months with mean temperature greater than 0°C multiplied by number of days	
GrowingDegDays0 (GDD5)	Sum of mean monthly temperature for months with mean temperature greater than 5°C multiplied by number of days	
MaxTempColdest (MTC)	Maxima temperature of the coldest month	°Cx10
MinTempWarmest(MTW)	Minimum temperature of the warmest month	°Cx10
PETColdestQuarter (PCQ)	Mean monthly PET of coldest quarter	mm/month
PETDriestQuarter (PDQ)	Mean monthly PET of driest quarter	mm/month
PETSeasonality (PSeasonality)	Monthly variability in potential evapotranspiration	mm/month
PETWarmestQuarter (PWQ)	Mean monthly PET of warmest quarter	mm/month
PETWettestQuarter (PWeQ)	Mean monthly PET of wettest quarter	mm/month
Thermicity	Compensated thermicity index	°C
Tri	Terrain roughness index	
TopoWet	Topographic wetness index	

The evaporation is the liquid water transfered from open areas as oceans, lakes and rivers to the atmosphere; and the transpiration is the water lost in plants throughout the stomas. Consequently, the evapotranspiration is the transfer of water from water superficies and plants to the atmosphere (Fisher et al. 2011) and represent the inverse process of precipitation (Thornthwaite 1948). The potential evapotranspiration (PET) is the superficial evapotranspiration rate expected if the ground and vegetation were well watered. (Scheff and Frierson 2014). In ecological research, PET provides a measure of energy regime that reflects the primary production in conditions where the water is not a limiting factor (Fisher et al. 2011). This variable is correlated with temperature in highland environments, as both variables decreases with the elevation (Henning and Henning 1981). The climatic classification of environments into arid or moist requires knowledge of the relationship among precipitation and evapotranspiration (Thornthwaite 1948): arid climates have higher values of PET, because precipitation is lower than evapotranspiration; moisture climates have lower values of PET, because the precipitation is higher than evapotranspiration (Henning and Henning 1981; Fisher et al. 2011; Scheff and Frierson 2014).

The aridity index proposed by Thornthwaite (1948) is calculated as the relation between the precipitation and the PET. High values of AridityIndex indicate climates with high water deficit (Thornthwaite 1948; Lungu et al. 2011; Nastos et al. 2013). The climatic moisture index (CMI) also uses this relation between precipitation and PET to determine if a climate is moist or dry. This index range between -1 and 1, where negative values are associated with dry climates and positive values with moist climates (Vörösmarty et al. 2005). These variables related with environmental aridity and moisture influence the type of vegetation that occurs in a specific area, and consequently determine the habitat type in a large scale (Matheri and Yoshioka 1968; Sohoulande Djebou et al. 2015; Zhao et al. 2021). Due to the broad range of the *L. tigrinus* complex, and the effect of these variables on the vegetation, we consider that they can be important predictors of species distribution in this group.

The Growing Degree Days (GDD) variables are a way to assign a heat value for each day, that allow to predict specific phonological processes in plants (Miller et al. 2001; Marmion et al. 2009). These variables can affect mammal species throughout trophic networks, where the phonologic processes in plants affect directly the herbivore species and consequently the carnivores (Levinsky et al. 2007). For example, in a deer species, *Cervus elaphus*, it was reported changes in the reproductive timing related with changes in GDD values (Boutin and Lane 2014). Other variables like Continentality, that measure the amplitude of annual temperature oscillation (Rivas-Martínez 2004) and maximum temperature in the coldest (MTC) and warmest (MTW) months seem to influence the occurrence of carnivores, probably because the temperature regulates the primary production and consequently the prey offer (Jędrzejewski et al. 2017) The temperature seasonality also plays an important role on species distributions (Anderson and Raza 2010), because extreme temperatures determine the energy expent in thermoregulation and the availability of food resources (Levinsky et al. 2007). thermicity is the temperature variation over the seasons (Barber et al. 2017), and measures the cold intensity, that limits some processes in plants and other organisms. However, as extratropical regions experiment colder periods than tropical regions, the compensate thermicity index weights these periods for the index be comparable. Low values of thermicity correspond to gelid climates, and high values to warm climates (Rivas-Martínez 2004).

Finally, the terrain variables measure two features: the roughness and topographic wetness indexes. The roughness index (tri) determine the terrain irregularity (Sinha and Pathak 2011), and is related with the moisture retained by the terrain. Terrains with high rugosity can retain more moisture than more homogeneous terrains (Valencia et al. 2016). The topographic wetness index (TopoWet) quantify the terrain effect in the generation of run-off (Qin et al. 2011). In this case, it is expected that lowlands have high values of TopoWet (Besnard et al. 2013). These terrain variables can be informative for the species as terrains with high rugosity generate low run-off (Sinha and Pathak 2011), retained water and contribute with the local moisture, and terrains with low values of TopoWet limit the distribution of species that are highly associated with the presence of waterbodies (Besnard et al. 2013). These variables can be particularly informative for some areas as the Llanos, that can accumulate water during the rainfall period (Hamilton et al. 2004), and might act as a barrier for the *L. tigrinus* complex.

Ecological Niche Modelling and barriers identification

Due to the taxonomic instability of the *L. tigrinus* complex, we constructed models for different combinations of geographic units that may comprise it, based on previous genetic and/or morphological studies. We initially modeled the distribution of the complex as whole, assuming two versions of it: (i) a ‘classical’ version (e.g., as assumed by Johnson et al. (1999)) comprising all tigrina units, including *L. guttulus*; and (ii) a more modern version (e.g., as assumed by Kitchener et al. (2017)), already recognizing *L. guttulus* as a distinct species and excluding it from the complex. This initial modelling step aimed to broadly characterize the ecological niche of the *L. tigrinus* complex as whole, and to identify areas of overall low habitat suitability that may have acted as historical barriers among regional units (see below).

A second modelling strategy addressed regional units separately, to characterize their ecological divergence and also to investigate whether their predicted distributions could overlap in the present and/or in the past (see below). For that purpose, we considered two sets of units. One was derived from the morphology-based proposal by Nascimento and Feijó (2017), recognizing *L. tigrinus*, *L. emiliae* and *L. guttulus* as separate species (**Figure 1C**), with each of them being modeled separately. The second set comprised geographic units whose evolutionary distinctiveness have been detected with genetic analyses (Johnson et al. 1999; Trigo et al. 2013; França et al. (*in prep*.); Trindade et al. (*in prep*.); see **Figure 1D**). The *L. guttulus* model was the same for both the morphologically- and genetically-defined sets, and the *L. emiliae* model of the morphologically-defined set was the same for NE tigrina genetically-defined sets.

Finally, we performed several exploratory modelling analyses of the Guiana Shield population. Due to the lack of genetic samples from the Guiana Shield and Amazon region, the few confirmed presence records in the Brazilian Amazon, the possibility that environmental conditions in this area are different from those in the Andes and/or northeastern (NE) Brazil, and the deforestation in the border of the Amazon Forest, we explored different options of treating it separately or grouping it with other units. We explored four different scenarios to determine if the environmental conditions of the presence records from the Guiana Shield are similar to the environmental conditions of the presence records from the Amazon or the Cerrado and Caatinga biome. In order to do that, first, we modeled the ecological niche for the Guiana Shield records including only records from Guiana, French Guiana, Suriname, southern Venezuela and northern Brazilian Amazon (Guiana Shield Strict – Gsstrict, **Figure 3A**). Second, we modeled the ecological niche of Guiana Shield plus records from the entire Amazon biome in Brazil (GSAmaz, **Figure 3B**). Third, we modeled only the records from the Amazon biome in Brazil (Amaz, **Figure 3C**). Finally, we modeled NE tigrina plus records from the Brazilian Amazon (NE tigrina + Amaz, **Figure 3D**). None model from the Guiana Shield exploratory analysis was compared with *L. guttulus* because this species is clearly differentiated from *L. tigrinus* (*sensu* Kitchener et al. 2017), and its affinity with the Guiana Shield population is not relevant for the purpose of these analysis.

For the calibration of the models, we selected different areas according to each assessed scenario, and the delimitation of these areas was conducted following the criterion proposed by Anderson and Raza (2010). For this, we drew the minimum convex polygon plus a buffer of 1° (111.1 km) around the occurrence records. The models were constructed with de Maximum Entropy Algorithm (Phillips and Dudík 2008) employed by the R (R Core Team 2018) package "kuenm" (Cobos et al. 2019). This package allows comparisons among models with different settings, changing the "feature class" (FC), the "regularization multiplier" (RM), and evaluating different variable sets. For all the scenarios, we evaluated the RM between 1 and 4, at 0.5 intervals;

and four FC options: linear (L), quadratic (Q), linear and quadratic (LQ) and hinge and quadratic (HQ), which are the FC options recommended for the amount of records included in this study, according with Phillips and Dudík (2008). The occurrence data was divided into training and test sets by randomly selecting 25% of the total records for training. This process was performed for each record set in each scenario evaluated (Sobek-Swant et al. 2012; Fitzpatrick et al. 2013; Fand et al. 2014; Silva et al. 2019).

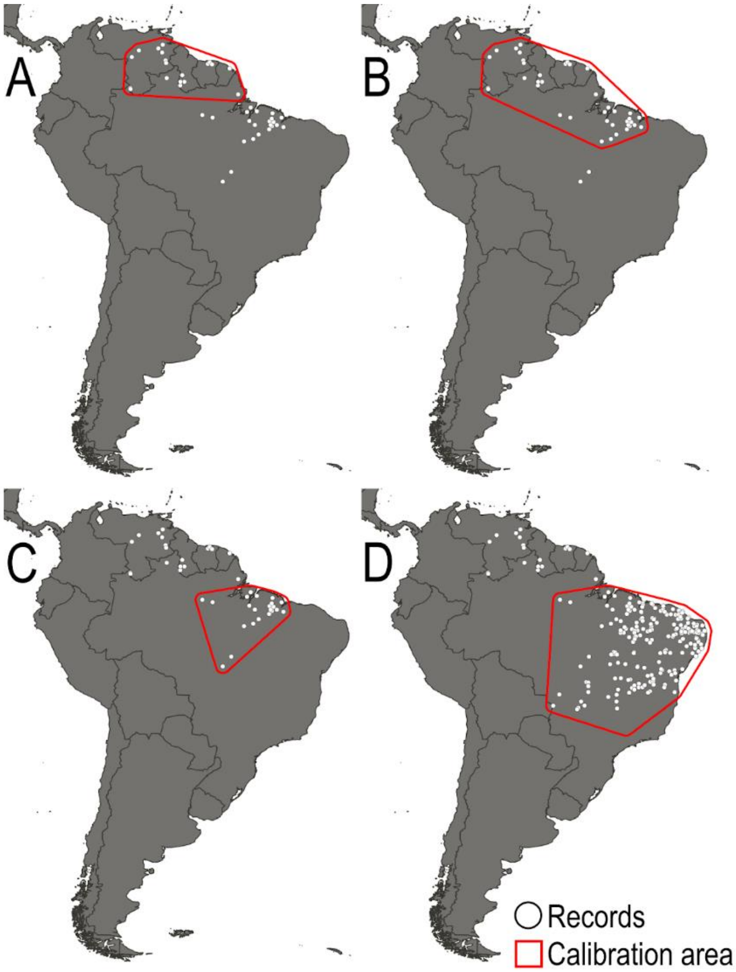


Figure 3 : Calibration areas for the Exploratory analysis for the Guiana Shield. **A.** Guiana Shield strict (GSstrict), **B.** Guiana Shield plus Amazon records (GSAmaz), **C.** Amazon records (Amaz), and **D.** NE tigrina plus Amazon records (NE tigrina + Amaz)

For the evaluation of the candidate models, the package used three metrics. First, it selects the statistically significant models through the area under receiver operating characteristic partial curve (AUC of partial ROC) made based on the training data. This metric is considered better for ecological niche models evaluation (Peterson et al. 2008). Second, it selects the models with the omission rate criterion, using 5% as the maximum omission rate allowed. This metric measures the proportion of localities with occurrence data that are left out of the prediction area. Finally, between the models selected previously, it was calculated the delta of AIC (Akaike Information Criterion) and selected the models with delta of AIC less than 2 to avoid overparameterization (Burnham and Anderson 2002).

For taxonomic approaches with small sample size (less than 25 records) the jackknife approach proposed by Pearson et al. (2007) was used. This approach suggests calibrating models with n-1 occurrences and testing with the record excluded. For each model we determined if the test record was included in the area predicted as present. This data partitioning strategy is included in the R package “ENMeval” (Muscarella et al. 2014). In this case, the best model of each variable set was selected based on a delta of AIC equal to 0. The best model for each record set was selected based on the highest value of AUC_{test} (Warren and Seifert 2011). The final models of all taxonomic approaches were constructed with 10 replicated type bootstraps.

In order to avoid model overfitting, we evaluated sets of independent variables for each of the assessed groups or group sets. To construct these variables sets, first we evaluated a set that included all variables (**Table 1**) and in the best model chosen for this set, variables with “permutation importance” greater than 1 were selected (Cao et al. 2013). Then, we checked the independence of the variables based on the Spearman correlation index, excluding variables highly correlated ($-0.8 \leq r \geq 0.8$). Finally, the construction of the environmental niche models for each taxonomic approach was done from these variables sets. The selected models were projected in three scenarios: present and two periods in the past (mid-Holocene and Last Glacial Maximum (LGM)). The projections were made across Central (Costa Rica and Panama) and South America to determine if in the present scenario the species or units evaluated have suitable habitats in other regions of the continent, and to verify the possibility of occurrence along the barriers proposed. These areas were also evaluated in the past to determine if the connectivity of species distribution changed across the potential barriers in the LGM (ca. 22.000 ya) and in the mid-Holocene (ca. 6000 ya). Finally, we constructed a “consensus model” between the final projections made for each record set by calculating the average of all models.

For the projection of the taxonomic approaches beyond to their calibration areas, we used two methods: free extrapolation (E), where the areas outside the calibration range are predicted depending on the response curve, assuming that the tendency found in this curve is real and is keeping along the variable range; and extrapolation and clamping (EC), where the values outside the calibration range are approximated to the nearest value known. Free extrapolation was only used when the response curves had a normal function-like shape, because this guarantee more accurate predictions. For this, the MaxEnt makes two risks of extrapolation analysis. First, make a multivariate environmental similarity surface (MESS) value in each grid cell. This analysis compares the values included in the calibration with the values in the projection area, and constructs a picture showing the areas where one or more variables are outside the range to be treated with caution. The results of this analysis permit mapping the limiting factors, with which we can deduce what factors limit the ecological and physiological process (Li et al. 2015). The second analysis is derived from MESS leading to finding the most dissimilar variable (MoD). This analysis calculates the pixels with the smallest similarity value, for each variable (Elith et al. 2010). This analysis is important because the method “clamping” treats the values outside of training variables range as if these had the limit value in the range of the training variables, and this might have an effect in the predictions (Phillips 2017).

In addition to the habitat suitability probability map made by MaxEnt, we constructed predictions of potential distribution for the three time periods. For this, we used two thresholds calculated by MaxEnt that were suggested as the best by Cao et al. (2013): the maximum training sensitivity plus specificity (MTSS) and the equal training sensitivity and specificity (ETSS). For each prediction we presented the two maps corresponding with each threshold. Due to several record sets being modeled, the average of each threshold was used for the binary map construction. These maps were used to infer changes in the potential distribution along the time.

Ecological Niche Divergence

The taxonomic groups identified with morphological and genetic data were compared in the geographic and environmental space. However, we only compared groups that do not share records, that is, groups that include records from others, for example *L. tigrinus* morphological and N. Andean tigrina, were not compared. For the geographic space we used three analyses. First, we made a Pearson correlation analysis using the R package ‘raster’ (Hijmans et al. 2019) to determine if there is an association between the models. Second, we made an overlap analysis using a R package ‘ENMeval’ (Muscarella et al. 2014) based on the Schoener’s D index to compare the suitable areas predicted with each model. We used five categories to determine the level of overlap following Rödder and Engler (2011): no overlap or very limited (0 – 0.2), low

(0.21 –0.4), moderate (0.41 –0.6), high (0.61 –0.8), and very high overlap (0.81 –1). We also assumed this categorization for the correlation values. Finally, we compared graphically the predictions obtained, making the subtraction of two predictions.

In the environmental space we used two analyses. First, we made a density profile analysis to compare the density distribution of each group related to each variable. This analysis was made by pairs to obtain a p-value for each comparison with the R package ‘sm’ (Bowman and Azzalini 2018). With this information, density curves were constructed comparing all the groups. This analysis could help to identify if the differences observed in the niche models reflect differences in the underlying distributions, or if they are random (Bowman and Azzalini 1997). Second, we calculated the overlap in the environmental space between the units using the software Niche Analyst (Qiao et al. 2016). This software generates a tridimensional principal component analysis (PCA) of the environmental variables, in which it plots the minimum volume-ellipsoid (MVE) for each unit to estimate the fundamental niche, considering the Grinellian definition that only include environmental variables. These MVEs are compared between units, allowing to identify if there exist similarities in the environmental space between the units proposed in the *L. tigrinus* complex. The comparison is made based on the volume of each ellipsoid and the proportion of each volume that is overlapping with the other.

RESULTS

Ecological divergence among the groups proposed to comprise the *Leopardus tigrinus* complex

Due to the low accuracy in the Guiana Shield Strict models, we did not consider it appropriate to compare any model with the Guiana Shield strict (GSstrict) models in the geographic space. However, the density curves and MVE results were compared. In the environmental space, most pairs of groups compared showed low overlap. However, the comparison between *L. tigrinus* (m) and NE tigrina showed an intermediate overlap, while the comparisons between Guiana Shield exploratory scenarios and NE tigrina presented a high overlap, and the comparison among C. Am. tigrina and N. Andean tigrina showed the highest overlap (**Table 2**). The density kernel analysis demonstrated that *L. tigrinus* (m) and NE tigrina are very divergent, with opposite optimal ranges for all variables, except for potential evapotranspiration seasonality. On the other hand, the curves showed similar optimal ranges for potential evapotranspiration in the wettest quarter and topographic wetness index for NE tigrina and *L. guttulus*. These three groups presented a gradient pattern for the other variables, where each group found its optimal range in different values of these gradients. For example, the lowest values of annual potential evapotranspiration are preferred by *L. tigrinus* (m), the highest values are preferred by NE tigrina, and *L. guttulus* prefers intermediate values. This order was not the same for all variables, and all comparisons between them were statistically different ($p < 0.05$, **Figure 4**)

The density kernel analysis for the highland groups (C. Am. tigrina, N. Andean tigrina and S. Andean tigrina) showed a preference for lower values of topographic wetness index for all of them, ranging between 6 and 10. For annual potential evapotranspiration, maximum temperature in the coldest and driest month, potential evapotranspiration in the coldest and driest quarter and thermicity, the analysis suggested the existence of a gradient, where C. Am. tigrina prefers lower values, N. Andean tigrina intermediate values and S. Andean tigrina higher ones. For continentality and potential evapotranspiration seasonality, we found that C. Am. tigrina and N. Andean tigrina have a marked preference for lower values, whereas S. Andean tigrina did not present a preference. Similarly, for climatic moisture index, only C. Am. tigrina showed a marked preference for lower values, while the Andean groups did not demonstrate any preference. For growing degree days 0 and 5 and potential evapotranspiration in the warmest and wettest quarter, the C. Am. tigrina and N. Andean tigrina preferred lower values, and S. Andean tigrina higher values. Finally, for aridity index, C. Am. tigrina and S. Andean tigrina are more similar to each other than with N. Andean tigrina (**Figure 4**).

The density curves of NE tigrina are very different from C. Am. tigrina and N. Andean tigrina, but they are very close to the ranges of S. Andean tigrina for several variables (annual potential evapotranspiration, climatic moisture index, potential evapotranspiration in the coldest and warmest quarter). This similarity with S. Andean tigrina was also found in the *L. guttulus* curves. For other variables (aridity index, growing degree days 0 and 5, maximum temperature in the coldest and warmest months, potential evapotranspiration in the driest quarter, thermicity and topographic wetness index) NE tigrina seem to prefer more extreme conditions with higher values, whereas the highland groups prefer ranges of lower values. When comparing the highland groups with *L. guttulus*, for several variables (annual potential evapotranspiration, climatic moisture index and maximum temperature in the coldest month), the optimal range of *L. guttulus* was between the optimal range of C. Am./N. Andean tigrina and S. Andean tigrina. However, for aridity index, potential evapotranspiration in the coldest and driest quarter, *L. guttulus* prefers lower values than the highland groups, whereas for continentality, potential evapotranspiration seasonality and topographic wetness index, the species seems to prefer higher values than the highland group (**Figure 4**).

The density kernel analysis for the exploratory scenarios of the Guiana Shield showed high overlap between GSstrict and the NE tigrina + Amaz models. In general terms, all scenarios have density curves very close to the NE tigrina curves. For GSstrict, growing degree days 0 and 5, maximum temperature in the coldest month, potential evapotranspiration in the driest quarter and thermicity had the same range that NE tigrina. For minimum temperature in the warmest month and topographic wetness index, the optimal range of GSstrict was in the most extreme values. Guiana Shield including records from Amazon biome in Brazil (GSAmaz) differed from this pattern for Continentality, that was between the optimal range of N. Andean tigrina and C. Am. tigrina. In the case of the Amaz scenario, the main differences were that the optimal range of the Amaz models for annual potential evapotranspiration and potential evapotranspiration in the wettest quarter were closer to the NE tigrina, while for potential evapotranspiration in the warmest quarter was between *L. guttulus* and NE tigrina/S. Andean tigrina, and for climatic moisture index and Continentality were the same as the GSAmaz scenario. Finally, for NE tigrina + Amaz, the density kernel analysis showed density curves very similar to the NE tigrina ones. However, the optimal range for annual potential evapotranspiration and potential evapotranspiration in the wettest quarter were similar to the Amaz, and the optimal range for growing degree days 0 and 5, maximum temperature in the coldest month, potential evapotranspiration in the driest quarter and thermicity were similar to the GSstrict and GSAmaz.

In the geographic space, the comparisons between highland groups showed a moderate correlation and overlap between S. Andean and the other groups, and high correlation with moderate overlap between C. Am. tigrina and N. Andean tigrina (**Table 3**). The C. Am. tigrina and N. Andean tigrina presented higher suitability across almost the whole Andean region and Central America, except in the eastern region of the southern Andes, where S. Andean tigrina presented higher (**Figure S1**). The comparisons of NE tigrina and NE tigrina + Amaz showed limited correlation and moderate overlap with the Andean groups and *L. tigrinus* (m) and low correlation and low overlap with C. Am. tigrina. Further, NE tigrina showed low correlation and moderate overlap with *L. guttulus*, and high overlap but limited or low correlation with the Guiana Shield models (**Table 3**). In the model subtraction, it is clear that NE tigrina models presented higher habitat suitability in the lowlands, such as Caatinga, Llanos, and Panama Center, than any other group. The Guiana Shield exploratory models, on the other hand, presented higher suitability in lowlands that are not as dry as the Caatinga biome, but areas such as the Cerrado or Amazon Forest. In contrast, *L. tigrinus* (m), highland groups and *L. guttulus* presented higher suitability in highland areas in the Andean region and the Atlantic Forest in Brazil (**Figure S1**).

Table 2: Environmental overlap analysis between the groups proposed within the *L. tigrinus* complex. The upper diagonal shows the overlap value between each pair of groups. The lower diagonal shows the precision of the estimated overlap. The greys cells show the MVE calculated for each group. 'NA' indicates comparisons that were not made due to shared records between the groups, in order to avoid bias (see Materials and Methods).

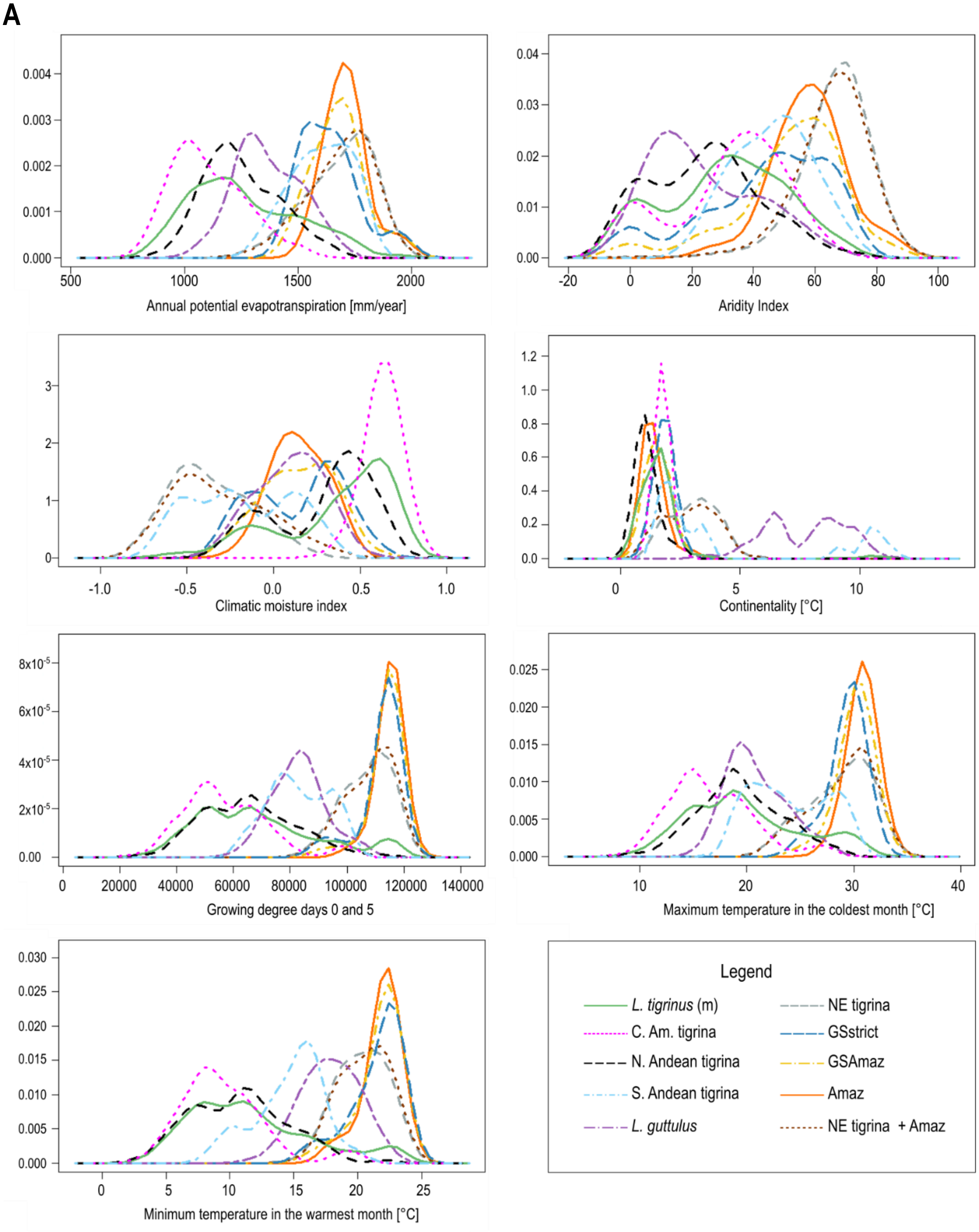
Group	***L. tigrinus* (m)**	**C. Am. Tigrina**	**N. Andean tigrina**	**S. Andean tigrina**	**NE tigrina**	**GS strict**	**GS Amaz**	**Amaz**	**NE tigrina + Amaz**	***L. guttulus***
***L. tigrinus* (m)**	8.022	NA	NA	NA	1.568	NA	NA	0.055	1.567	1.726
C. Am. Tigrina	NA	0.36	0.346	0.059	0.093	0.047	0.054	0	0.093	0.007
N. Andean tigrina	NA	0.004	1.293	0.197	0.164	0.095	0.119	0.005	0.163	0.016
S. Andean tigrina	NA	0.004	0.013	1.733	0.39	0.05	0.069	0	0.388	0.593
NE tigrina	0.026	0.004	0.013	0.017	2.569	0.251	0.506	0.155	NA	0.907
GS strict	NA	0.003	0.003	0.003	0.003	0.262	NA	0.053	0.252	NA
GS Amaz	NA	0.004	0.005	0.005	0.005	NA	0.545	NA	NA	NA
Amaz	0.002	0.002	0.002	0.002	0.002	0.002	NA	0.163	NA	NA
NE tigrina + Amaz	0.026	0.004	0.013	0.017	NA	0.003	NA	NA	2.572	NA
L. guttulus	0.036	0.0036	0.0129	0.017	0.025	NA	NA	NA	NA	3.573

When comparing the highland groups with *L. guttulus*, *L. guttulus* showed high correlation and overlap with N. Andean tigrina, high correlation and moderate overlap with C. Am. tigrina, and moderate correlation and high overlap with S. Andean tigrina. When compared *L. guttulus* with *L. tigrinus* (m) the correlation was moderate, and the overlap was high too (**Table 3**). The mainly differences between the predictions of these groups are the stronger predictions of *L. guttulus* models in the Atlantic Forest, and the C. Am. and Andean tigrina models in the Andean region (**Figure S1**). Finally, the comparison of highland groups and Guiana Shield models showed low correlation and overlap with C. Am. tigrina, and low correlation and moderate overlap with the Andean groups. The comparison of NE tigrina + Amaz and Amaz with *L. tigrinus* (m), presented low correlation and moderate overlap (**Table 3**). The most marked differences are focused on the lowlands predicted by the Guiana Shield models (**Figure S1**).

Table 3: Geographical correlation and overlap analysis between the groups proposed within *L. tigrinus* complex. The upper diagonal shows the Pearson correlation value between each pair of groups. The lower diagonal shows Schoener's D overlap. 'NA' indicates comparisons that were not made due to shared records between the groups, in order to avoid bias (see Materials and Methods).

Group	***L. tigrinus* (m)**	**C. Am. Tigrina**	**N. Andean tigrina**	**S. Andean tigrina**	**NE tigrina**	**GS strict**	**GS Amaz**	**Amaz**	**NE tigrina + Amaz**	***L. guttulus***
***L. tigrinus* (m)**		NA	NA	NA	0.14	NA	NA	-0.40	0.04	0.60
C. Am. Tigrina	NA		0.72	0.48	0.33	NA	-0.27	-0.30	0.27	0.81
N. Andean tigrina	NA	0.52		0.46	0.16	NA	-0.36	-0.53	0.03	0.82
S. Andean tigrina	NA	0.47	0.55		0.09	NA	-0.32	-0.32	0.07	0.51
NE tigrina	0.55	0.36	0.60	0.47		NA	0.31	-0.09	NA	0.21
GS strict	NA	NA	NA	NA	NA		NA	NA	NA	NA
GS Amaz	NA	0.25	0.56	0.44	0.74	NA		NA	NA	NA
Amaz	0.45	0.21	0.46	0.40	0.66	NA	NA		NA	NA
NE tigrina + Amaz	0.53	0.34	0.57	0.46	NA	NA	NA	NA		NA

L. guttulus	0.70	0.60	0.77	0.62	0.55	NA	NA	NA	NA	



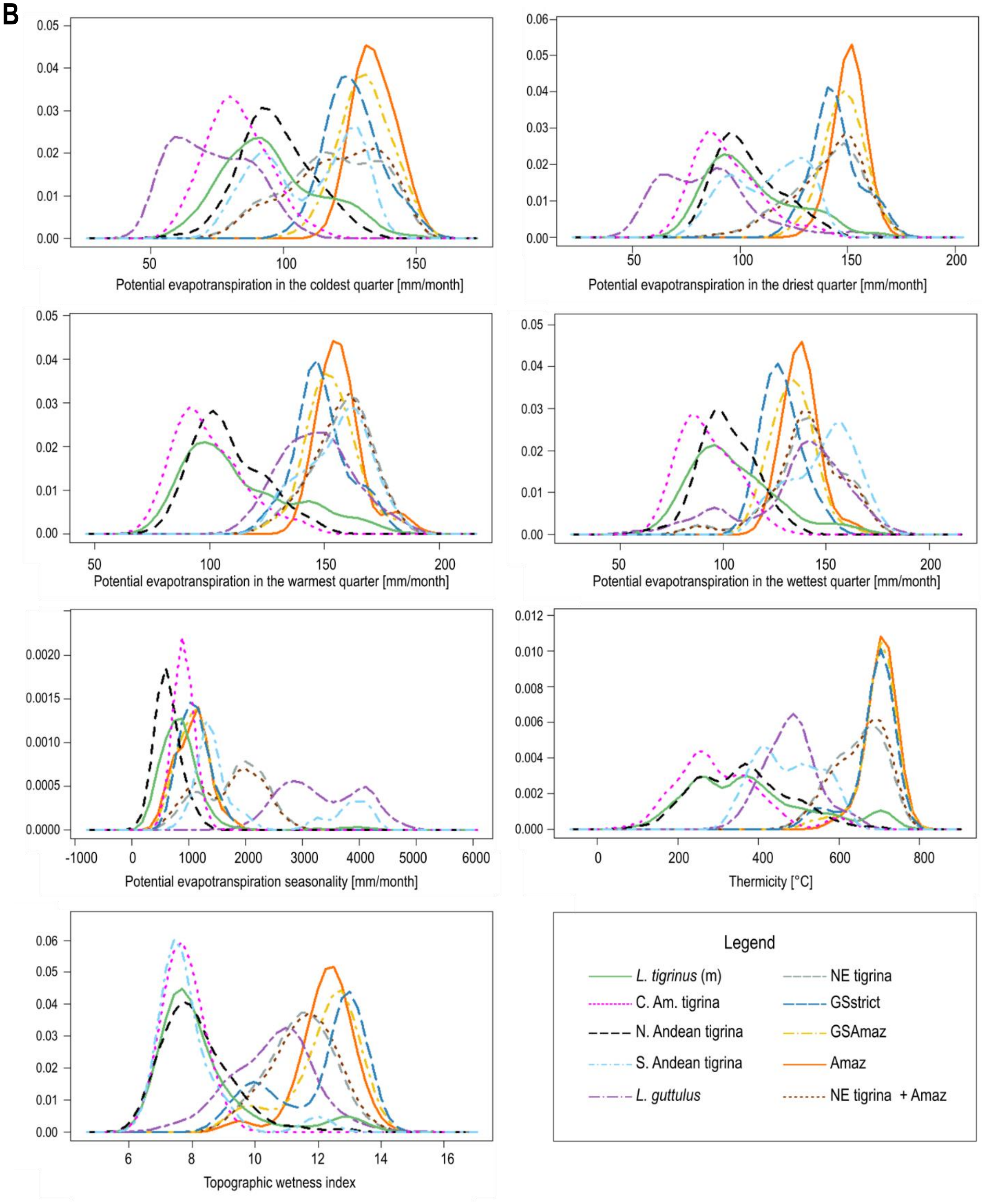


Figure 4: Density kernel analysis for the geographic units comprising the *Leopardus tigrinus* complex across the environmental gradient. The Y axis corresponds to the record density and the X axis to the variables' range. In the panel **A** the Growing degree days 0 and 5 curves are the

same, so only one was included, in the panel **B. t**he topographic wetness index and terrain rugosity index curves are the same, so only one was included.

Potential barriers across the overall distribution of the *Leopardus tigrinus* complex

The models constructed for the *Leopardus tigrinus* complex as a single unit identified a continuity across the highlands from Costa Rica to the Andean region of Colombia, without a barrier in the center of Panama. The predicted distribution in the Andes is also continuous, without a barrier between Ecuador and Peru, in the Huancabamba depression. Still, the Guiana Shield presented small patches of potential distribution for the complex without connectivity with the Andean region or the Caatinga and Cerrado biomes in Brazil. On the other hand, the Amazon region and the Llanos were not suggested as suitable habitat for the complex and were identified as barriers in the three time periods modeled (**Figure 5** and **Figure S2**). However, the *L. tigrinus* complex *sensu* Kitchener et al. (2017) identified the northwestern region of the Llanos as suitable habitat, demonstrating some degree of connectivity between the northeastern portion of the continent and the Andean region throughout the Cordillera de la Costa, in Venezuela (**Figure 5B** and **Figure S2**).

The models of the *L. tigrinus* (m) (proposed by Nascimento and Feijó (2017)) identified the same barriers as the previous models. They presented a continuous distribution across the Cordillera Talamanca and Andean region, without barriers in the Panama Center nor in the Huancabamba depression. On the other hand, the Llanos and Amazon region were identified as barriers between the Andean and Guiana Shield populations (**Figure 6** and **Figure S11**). For the interglacial period and last glacial maximum, the barriers identified in the present were kept despite the expansion of predicted distribution, particularly in the Guiana Shield, during the LGM.

Panama center

The geographical predictions made for C. Am. tigrina and N. Andean tigrina in the three time periods were very similar and suggest the existence of suitable habitat exclusively in highland areas, with a gap in the Panama center (**Figure 7A**), contrary to the results made for the whole *L. tigrinus* complex and *L. tigrinus* (m).

Huancabamba depression

The predictions of N. Andean and S. Andean tigrinas showed a distribution restricted to highland areas, but the potential distribution does not suggest a discontinuity in the Huancabamba depression. The prediction in this region seems to be less broad but show some patches that connect the northern with the southern region (**Figure 7B**). The absence of a barrier in this region is consistent with the results made for the whole *L. tigrinus* complex and *L. tigrinus* (m).

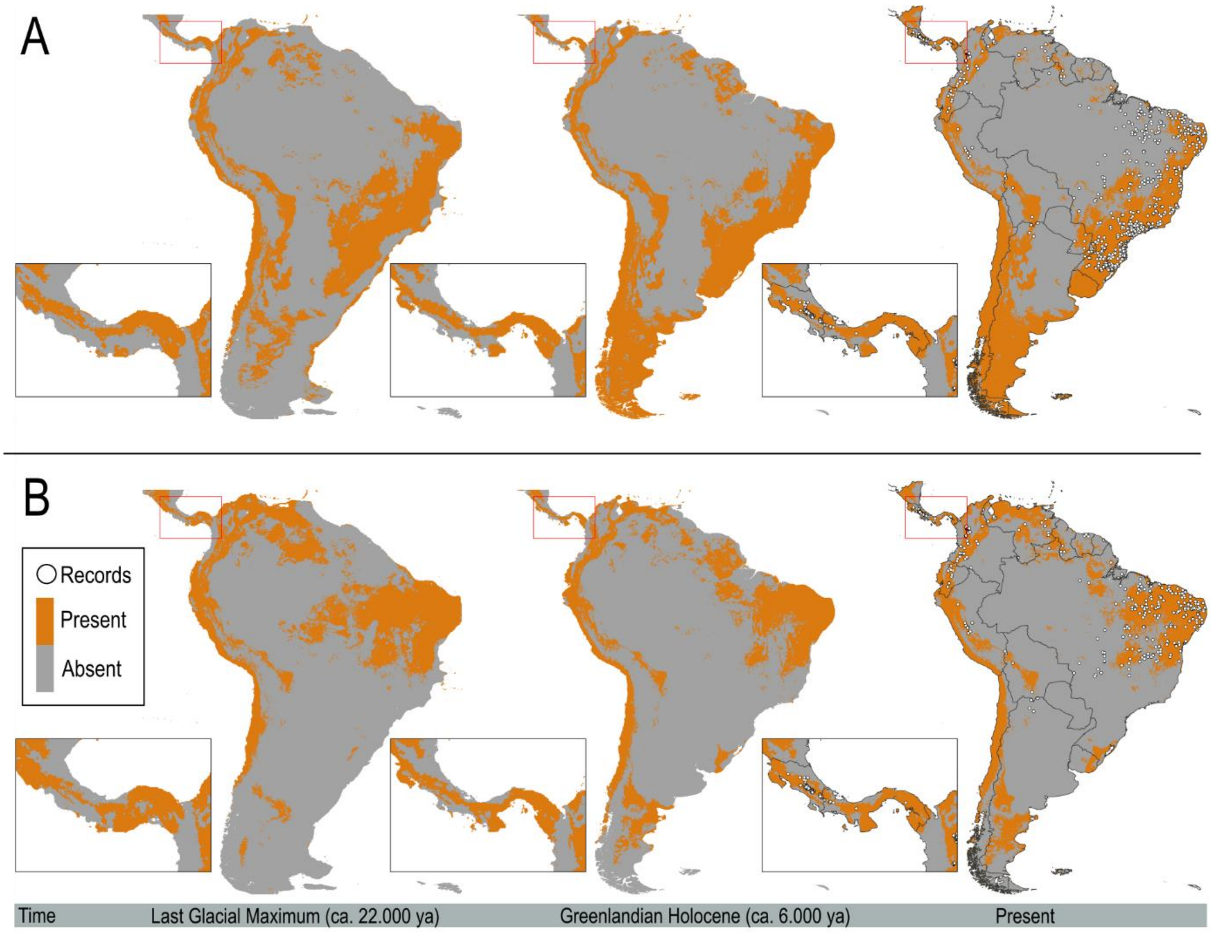


Figure 5: Potential distribution of the *L. tigrinus* complex **A.** *sensu* Jonhson et al (1999) and **B.** *sensu* Kitchener et al. (2017) based on the Equal training sensitivity and specificity (ETSS) threshold. Distributions are shown for three time periods, from left to right: LGM, mid-Holocene, and Present. Presence records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

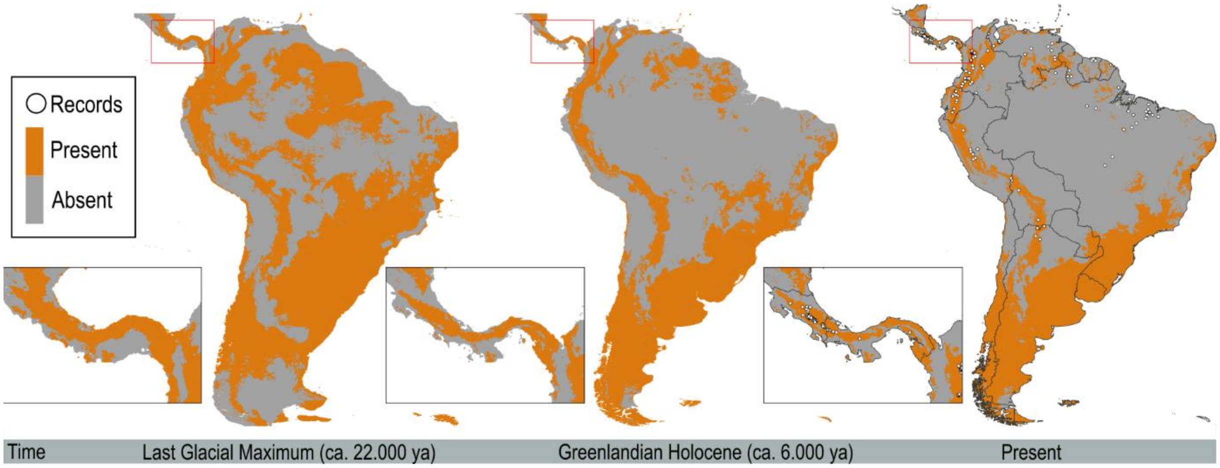


Figure 6: Potential distribution for the *L. tigrinus* (m) based on the Equal training sensitivity and specificity (ETSS) threshold. Distributions are shown for three time periods, from left to right: LGM, mid-Holocene, and Present. Presence records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

<u>Amazon region and Llanos</u>

The Andean groups models predicted a strict distribution in highlands, as mentioned above, identifying the Amazon and the Llanos as barriers for these groups. For the NE tigrina the models predicted small patches of suitable habitat in the border of Amazon region, but not in the center, suggesting that the Amazon region also acts as a barrier to the connectivity of the *L. tigrinus* complex between northwestern-northeastern areas of the continent. However, the Llanos were not identified as barrier to NE tigrina (**Figure 7C**). These results are consistent whit the predictions made for the *L. tigrinus* complex *sensu* Kitchener et al. (2017).

DISCUSSION

The *L. tigrinus* complex is broadly distributed in South and Central America, occurring in different habitat types with considerable diversity in vegetation cover and climatic conditions. This great environmental variety within the distribution of this complex may have led to local adaptations of populations to the environmental conditions of particular areas, limiting their distribution and/or restricting their connectivity. Therefore, considering that populations may be highly adapted to the environmental conditions where they occur, we proposed four barriers that could limit or prevent dispersal across the whole complex distribution. These possible local adaptations were recovered in this work for some taxonomic units proposed within the *L. tigrinus* complex. The environmental preferences of each one allowed the observation of the effects of the proposed geographic barriers across time, from the LGM to the present, identifying changes in potential distribution. These results help us better understand the evolutionary history of the *L. tigrinus* complex and provide important information that may help in the taxonomic reclassification of this taxon.

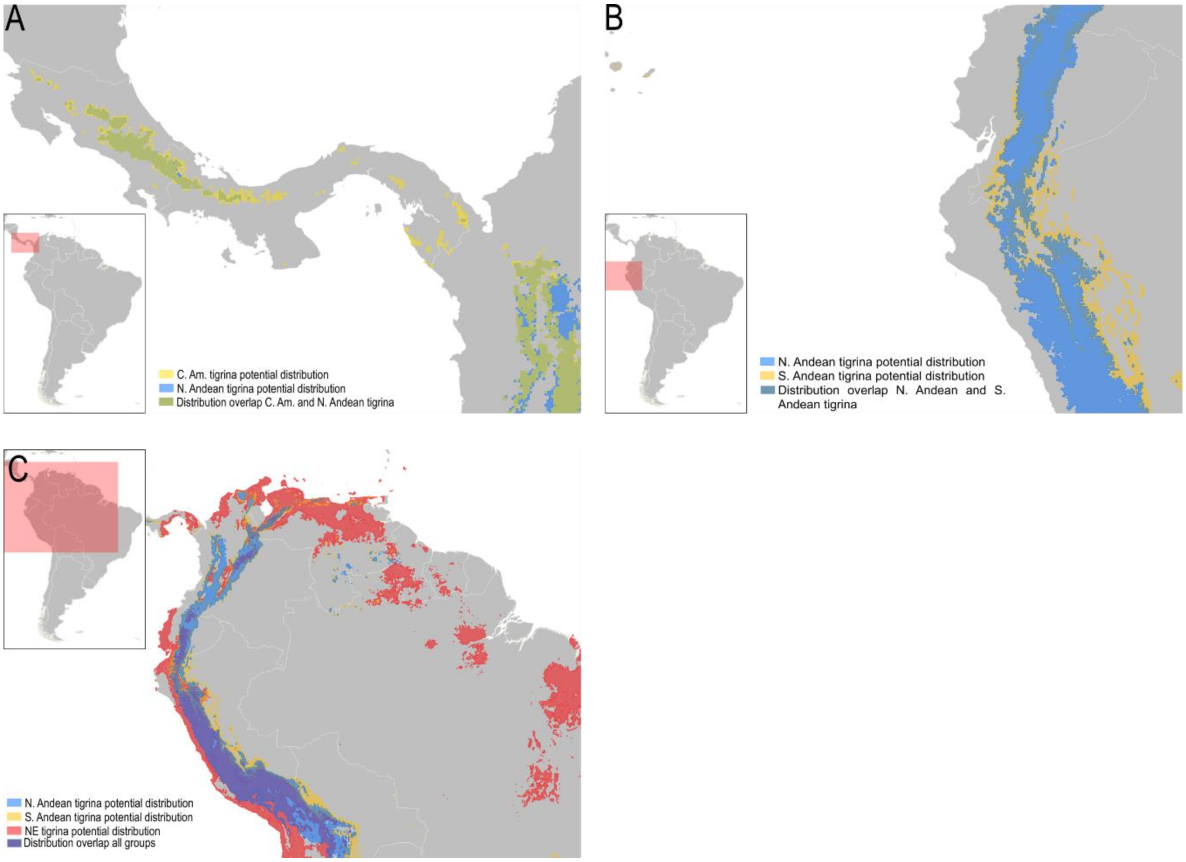


Figure 7. Geographical barriers evaluated for the connectivity of the *L. tigrinus* complex. **A.** Panama center, **B.** Huancabamba depression and **C.** Amazon and Llanos region.

The recognition of *L. guttulus* as a distinct species caused a notable change in the ecological niche and predicted geographic distribution of the *L. tigrinus* complex, reflected especially in the areas of the Atlantic Forest, were *L. guttulus* occurs, predicted only by the *L. tigrinus* complex *sensu* Johnson et al. (1999) models (**Figure 5** and **Figure S2**). The area predicted as suitable for *L. guttulus* in this work is consistent with the results found by Sartor et al. (2021). The environmental conditions of the Atlantic Forest and its differences from other forested areas may explain the significant changes caused by the inclusion/exclusion of *L. guttulus* records in the habitat suitability maps generated for the entire complex. However, when we modeled the distribution of *L. tigrinus* (m), a portion of the Atlantic Forest was predicted as potential for the group (**Figure S11**). Reciprocally, the *L. guttulus* models also predicted some portions of the Andean region (**Figure S8**). This similarity in the geographical predictions of *L. tigrinus* (m) and *L. guttulus* are supported by the similarity in the environmental preferences (**Figure 4**). Therefore, the differences between *L. tigrinus* complex models *sensu* Johnson et al. (1999) and *sensu* Kitchener et al. (2017) must be related with other phenomena, instead of the environmental differences between forested areas. It is clear that NE tigrina have environmental requirements that can be very contrasting with the other highland groups and *L. guttulus* (**Figure 4**). This, in addition to the record quantity, may have influenced the model to predict suitable areas that are more similar to NE tigrina requirements than to *L. tigrinus* (m) in the *L. tigrinus* complex sensu Kitchener et al. (2017) models.

Nevertheless, there are some differences between *L. tigrinus* (m) and *L. guttulus* models that could be related with the seasonality that occurs in southern areas and consequently the Atlantic Forest. The seasonality has been identified as an important factor related with reproductive characteristics in carnivores as gestation length, weaning age and sexual maturity age (Tökölyi et al. 2014). This adaptation to seasonal environments is a marked characteristic of *L. guttulus* if compared with the other groups, which is apparent in the density curves of potential evapotranspiration seasonality and Continentality of the kernel analysis (**Figure 4**). This suggests that the climatic variables have modeled biological aspects of this species that could be less successful or adequate in other environments. Likewise, *L. guttulus* showed some similarities with NE tigrina. This result was unexpected as both groups occupy very distinct habitats. However, as these groups seem to present a continuous distribution in some areas, it is possible that there exist intermediate areas that include environmental conditions that could be favorable for both species. This is visible in the kernel analysis, where for several variables (except potential evapotranspiration in the driest and coldest quarter, and aridity index), the optimal range for *L. guttulus* is followed by the optimal range for NE tigrina (**Figure 4¡Error! No se encuentra el origen de la referencia.**). Another possible explanation is that NE tigrina may be expanding its distribution into fragmented areas of the Atlantic Forest that were once occupied by *L. guttulus*. Future studies with land cover change should enable further analyses this possibility.

The models of the highland groups identified within *L. tigrinus* (m) showed the preference of these groups for highlands and reinforce the role of lowlands forest (Amazon and Panama center) as historical barriers for populations specialized in highland environmental conditions. According to the models, it seems that the high temperatures experienced by lowland forests in the coldest and warmest months limit the distribution of the Andean groups in these areas. Among these groups, the ecological niche models identified a niche conservatism process between C. Am. tigrina and N. Andean tigrina. These group models presented high overlap in the environmental space and predicted the distribution of each other, which is commonly seen in sister taxa generated by allopatric processes (Peterson et al. 1999; Alvarado-Serrano and Knowles 2014), supporting the findings of França et al. (*in prep.*) that identified these two groups as sister-taxa. In addition, the Panama Center acts as a barrier for these groups, even in the LGM. However, the results for *L. tigrinus* (m) for the glacial periods (**Figure S11**) showed connectivity between Cordillera Talamanca and Colombian Andean region. The distributional changes experienced by highland forests in the LGM also suggest a possible connectivity between both groups during these periods (Barrantes 2009; Weir 2009). It is also possible that these two groups still comprise a single species that, despite the lack of connectivity between them, have not differentiated enough due to the similarities of the habitats they occupy or the short time since the interruption of gene flow between them. For the montane forests in the Andean region, it is proposed that during the LGM the forests prevailed, but they were displaced down-slope 1000-1500m below the present range (Ramírez-Barahona and Eguiarte 2013). This down-slope migration was also reported to the montane forest in Costa Rica (Islebe et al. 1995; Islebe and Hooghiemstra 1997), supporting the possibility of gene flow between C. Am. tigrina and N. Andean tigrina during the LGM.

Despite the differences in the environmental requirements between the Andean groups, the Huancabamba depression was never recovered as unsuitable for these groups. Therefore, it is possible that there exists some level of gene flow between these populations that was not recovered by the mitochondrial markers used by França et al. (*in prep.*). On the other hand, the Andean populations could be isolated due to their distinct environmental preferences. In this case, instead of finding suitable habitat across the whole Andean region, each group would be more successful in a particular area. This may be the case, considering the latitudinal change across the Andean region, being more seasonal in the area where S. Andean tigrina occurs. In that sense, the groups identified within *L. tigrinus* (m) may have a specialization to local environmental conditions, which is supported by the differences found in the kernel density analysis (**Figure 4**).

The kernel density analysis also suggests that there are some similarities in the optimal range for some variables between NE tigrina and S. Andean tigrina (**Figure 4**). For example, both prefer drier climates, in contrast to C. Am. tigrina and N. Andean tigrina, which prefer more moist climates, as demonstrated by the climatic moisture index curves. These similarities are clearer when comparing the drylands in the continent and the record distribution. According to the maps included in the work of Prăvălie (2016), the records from Peru and Bolivia included semi-arid and dry sub-humid areas, similar to the environmental type found in the Caatinga and part of Cerrado biomes.

On the other hand, the Guiana Shield exploratory analyses showed that the environmental conditions of this region are very contrasting with the Andean region as the Guiana Shield groups did not predict the Andean region, except for NE tigrina + Amaz. The environmental conditions of the Guiana Shield where *L. tigrinus* occurs are similar to the environmental conditions of the Caatinga and Cerrado biomes, where NE tigrina occurs. Furthermore, the optimal ranges for Guiana Shield records share optimal ranges with S. Andean tigrina. These similarities are supported by the vegetation type of the records in the Guiana Shield. According to Gond et al. (2011) the Guiana Shield includes different vegetation cover that varies from high forest with regular canopy to savanna, and the records for the species in these regions are associated mainly with savanna, grasslands and high forest with disrupted canopy, similar to what is found in the southern portion of the Andes. However, records from the northern Andean region are mainly associated with forest cover. Although *L. tigrinus* (m) models predicted the highlands and high forest with regular canopy in the Guiana Shield as potential distribution for the species, the Guiana Shield tigrina occurs in completely different habitats. In any event, it does not seem possible that the Guiana Shield populations could have maintained historical gene flow with the Andean populations, since the Llanos and Amazon Forest are unsuitable for *L. tigrinus* (m). For the past, the *L. tigrinus* (m) models predicted an expansion of potential distribution along the Amazon region (**Figure S11**). According to Arruda et al. (2018) during the LGM, the forest in Amazonia lowlands was retracted in refuges while other forests with preferences for cold and wet climate expanded in these areas. However, this was not demonstrated by the Andean group models. Thus, we believe that if there was any type of connectivity between the Andean and Guiana Shield populations, it occurred more deeply in the past.

Interestingly, the areas where Guiana Shield tigrina do occur were predicted by NE tigrina models. These patches of open vegetation in the Guiana Shield could be connected with the Caatinga and Cerrado biomes where NE tigrina occurs through the Amazon savanna patches (Sarmiento 1984), suggesting that there may exist some level of historical gene flow between Guiana Shield and NE tigrinas. These savanna patches were recovered by NE tigrina models for the mid-Holocene and present time periods, identifying suitable areas between the northeast region of Brazil and the Guiana Shield (**Figure S23**). Still, it is possible that there exist smaller patches of open habitat within the Amazon Forest that were not recovered here as our environmental variables had a 5km^2 resolution. These smaller areas could work as stepping-stone patches connecting the Guiana Shield with the Cerrado and Caatinga biomes.

This hypothesis is only supported by GSAmaz and NE tigrina + Amaz approaches. The other approaches did not recover this possible connectivity between Guiana Shield and Caatinga/Cerrado biomes. In the GSStrict approach, the selected models are probably overfitted, generating response curves without any pattern, due to the limited number and dispersed distribution of available records. This could explain the low suitability values for areas with records in the calibration area. On the other hand, records from only the Amazon biome in Brazil predicted the center of Amazon Forest and did not predict anything for the past periods. Thus, we highlight the importance of obtaining more records and genetic samples from the Guiana Shield and Amazon Forest, to better analyze the possible connectivity between these regions and NE Brazil. Even so, based on the vegetation coverage and kernel density analysis, it is plausible to hypothesize that as the records of Guiana Shield tigrina are associated with open areas, this group is probably more similar ecologically to NE tigrina than to other groups included in *L. tigrinus* (m).

Another interesting result was that the NE tigrina models also presented high suitability in the eastern region of the Llanos. This prediction suggests that there could exist connectivity between the Llanos and the Andean region in Venezuela. However, this area has been documented as unsuitable or non-occupied by the *L. tigrinus* complex (*sensu* Kitchener et al., 2017) by other authors (de Oliveira 2004; Payán-Garrido and González-Maya 2011; Payan and Oliveira 2016), and the models for the global complex or particular groups always suggested the Llanos as a barrier in all modeled periods of time. This region presents a marked seasonality with dry *vs.* rainy periods, where the latter implies the inundation of a great area between July and September (Hamilton et al. 2004), likely making this area unsuitable for the survival of the species. Finally, the Amazon Forest was also identified as a barrier for the NE tigrina, as it is a very moist forest, and NE tigrina prefers drier climates, such as Caatinga and Cerrado. This preference can be seen in the climatic moisture index density curve (**Figure 4**) and the response curves of selected models (**Figure S22**), where the optimal range is in negative values, associated with drier climates. In addition, contrary to other groups that experienced an expansion in their distribution in the LGM, NE tigrina models showed a small retraction in its distribution in this period (**Figure S23**), probably due to the restriction of dry vegetation to small areas of ecotone (Werneck et al. 2011).

This work supports the ecological differentiation between some groups of the *L. tigrinus* complex. According to our results, we can conclude that almost all groups proposed within the *L. tigrinus* complex present marked local adaptation to the environmental conditions of the region where they occur. The only exception seems to be the C. Am. and N. Andean tigrina, that presented great niche similarities, but seem to be disconnect due to the lowland areas in the center of Panama. The Amazon region and the Llanos are clear barriers for the dispersal of the Andean groups, preventing the connectivity between western and eastern South America. On the other hand, we did not identify any physical barrier that impedes the contact of the Andean populations, and in this case, more records are needed to determine if any barrier exists in that region. Also, more records are necessary from the Guiana Shield to construct better models and to determine the similarities with NE tigrina. We also identified ecological niche differences between *L. guttulus* and the rest of the *L. tigrinus* complex, supporting its recognition as a different species from an ecological perspective (in addition to the genetic and morphological data that have been previously reported). Overall, our results support the view that the evolutionary differences and similarities among regional groups within the *L. tigrinus* complex are probably a product of the vegetation dynamics of glacial and interglacial periods, which has intermittently promoted or inhibited gene flow among populations.

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SUPPLEMENTARY MATERIAL

Ecological niche modelling results

Modelling of the *Leopardus tigrinus* complex as a whole

For this 'classical' version of the *L. tigrinus* complex, (*sensu* Jonhson et al. 1999) including what is now recognized as *L. guttulus* (see **Figure 1A**), we obtained 775 records, of which 477 were retained after the filtering. We constructed four record sets (which retained the maximum number of records) and evaluated two variable sets for each record set. All selected models comply with the omission rate and the AIC criteria (**Table S1**). For the *L. tigrinus* complex *sensu* Kitchener et al. (2017) we obtained 625 records, but only 270 were retained after filtering. The number of variable sets was different for each record set, ranging from 8 to 32 variable sets, and all selected models complied with the AIC and omission criteria (**Table S2**).

The variables with the highest permutation importance in the selected models for *L. tigrinus* complex, *sensu* Jonhson et al. (1999) were annual potential evapotranspiration, topographic wetness index, and potential evapotranspiration in the coldest quarter (**Table S3**). Annual potential evapotranspiration and topographic wetness index, also had high permutation importance for *L. tigrinus* complex *sensu* Kitchener et al (2017) in addition to aridity index, potential evapotranspiration in the warmest quarter, climatic moisture index, maximum temperature in the coldest month and Continentality (**Table S4**). In both approaches all these variables had a negative tendency in the response curve, where low values had the highest habitat suitability probability. Thus, for both approaches of *L. tigrinus* complex, areas with values of annual potential evapotranspiration between 600 and 1000 mm/year, and topographic wetness index reached between 6 and 7, seems to have high suitability probability. The *L. tigrinus* complex, *sensu* Jonhson et al. (1999) models predict as suitable areas with potential evapotranspiration in the coldest quarter between 35 and 60 mm/month. On the other hand, for The *L. tigrinus* complex, *sensu* Kitchener et al. (2017) models, the optimal ranges for the other variables are aridity index around 70-100, potential evapotranspiration in the warmest quarter between 40-100 mm/month, climatic moisture index among -1.2 and -1.0, maximum temperature in the coldest month between 0-20°C, and for Continentality between -1.0 and 0. These patterns were kept for all response curves in all selected models (**Figure S3** and **Figure S4**)

Both models for the present scenario predict the Cordillera Talamanca and the Andean regions in Colombia, Ecuador, Bolivia, and Argentina as highly suitable for the species, as well as the Atlantic Forest and a small portion of the Caatinga biomes in Brazil. However, when are not included the *L. guttulus* records the predictions had a marked absence of the Atlantic Forest as suitable habitat for the complex. Furthermore, much of the extension of the Caatinga and Cerrado biomes are suggested as suitable. The Guiana Shield presents small patches of potential distribution for the complex without connectivity with the Andean region or the Caatinga and Cerrado biomes in Brazil (**Figure 5** and **Figure S2**). In both approaches, the predictions made for the mid-Holocene and LGM are very similar to the present predictions, with expansion in some regions (**Figure 5** and **Figure S2**). The projections also suggested the south cone of South America as suitable for the complex distribution, but the extrapolation risk analysis suggested that this area is out of the calibration range (**Figure S5** and **Figure S6**), so it was not considered. Furthermore, it is known that the *L. tigrinus* complex does not occur in that region of the continent.

Leopardus guttulus

For this species, we obtained 347 records and retained 208 after filtering. In this case, four record sets were generated because only them retained the maximum record number. For each record set were evaluated 10 variable sets, except for the record set 4, for which were evaluated six. However, the selected models from two of four record sets did not comply with the omission rate criterion (<5%, **Table S5**). To determine if the models result of these record set, generate dissimilar predictions that could be change the results, and if it was necessary to exclude these record set models of analysis, we were made a correlation and overlap analysis, using the Pearson coefficient with the R packages “raster” and “ENMeval”, respectively. This analysis was made comparing the final consensus when the models from these record sets were included and excluded. The results of this analysis suggested that the models from these record sets models despite breaking the omission rate criterion, do not have a notable effect in the final consensus (**Table S6**), therefore, it was considered the consensus with the models from record set 1 for the results and analysis of this group.

In the selected models, the variables with higher permutation importance were potential evapotranspiration in the coldest quarter, growing degree days 0 and 5, and annual potential evapotranspiration (**Table S7**). The optimal range of potential evapotranspiration in the coldest quarter for *L. guttulus* ranging between 40 and 60 mm/month. The optimal range of growing degree days 0 and 5 was between 0.5 and 0.7x10^5, and for annual potential evapotranspiration the optimal range for *L. guttulus* was between 1000 and 1200 mm/year. These tendencies of response curves were very similar for all models, with small changes in the curve form (**Figure S7**). For the present projection, the models predict high suitability in the Atlantic Forest biome, in southern Brazil. Still, it predicts as suitable habitat the Andean region in Colombia, Ecuador, Peru, Bolivia, Argentina and Chile, and Cordillera Talamanca in Costa Rica and Panamá. This pattern is similar for the mid-Holocene, and the LGM projections, but in this last period the areas are broader than the present (**Figure S8**). Nevertheless, all predictions have a high extrapolation risk in areas out of the center and southern Brazil, mainly (**Figure S9**).

Leopardus tigrinus (*L. tigrinus* (m))

For the *Leopardus tigrinus* proposed based in morphology (*L. tigrinus* (m)), we obtained 229 records but only 87 were retained after filtering. Further, only three record sets were constructed because they retained the maximum number of records. For the first record set, four variables were evaluated, and for the second and third, eight were evaluated. All selected models comply with the omission rate and AIC criterion (**Table S8**). The variables with more permutation importance in these models were potential evapotranspiration in the coldest quarter, maximum temperature in the coldest month, and potential evapotranspiration seasonality (**Table S9**). These variables showed a response curve with negative tendency, being the lowest values the optimal range for the species. The optimal ranges to potential evapotranspiration in the coldest quarter and maximum temperature in the coldest month were the same that reported previously (PCQ = 35-60 mm/month, MTC = 0-20°C). For potential evapotranspiration seasonality the optimal range was between 0 - 500 mm/month. This tendency was found in all response curves (**Figure S10**).

The present projection suggests the whole Andean region (Colombian, Ecuadorian, Peruvian, and Bolivian) as potential for the species distribution. In the Guiana Shield is suggested small patches being broader in the ETSS threshold map than MTSS (**Figure S11**). Much of the extension of Atlantic Forest is predicted as potential for the species despite this model not including the *L. guttulus* occurrences. For the interglacial period and last glacial maximum, the binary maps suggest a broader distribution in the past than in the present, particularly in the Andean region and in the Guianas Shield in the mid-Holocene. The Andean distribution does not change notably, but the areas in the Guiana Shield and northeastern of Brazil had a high connectivity, in the ETSS threshold map, forming an only patch of habitat suitable in this time, contrary to the observed in the present. Further, the Llanos neither were habitat suitable for the species in this period. The Amazon region seems to be threshold dependent, so with the ETSS threshold were considered some areas of this region as suitable, but with the MTSS threshold do not have occurrence prediction in these areas (**Figure S11**). However, this projection must be taken in account with precaution, because the risk extrapolation analysis shows this area as out of the calibration range for both present and past (**Figure S12**).

Geographic units identified within *L. tigrinus* (m) based on molecular data

Central American tigrina (C. Am. tigrina)

For this group, 74 records were obtained, but only 12 were retained after the filter. Three variable sets were evaluated for the record set 1, one variable set for the record sets 2, 3 and 4; and two for the record set 5 (**Table S10**). In all selected models the variable with higher permutation importance was topographic wetness index (**Table S11**), with the optimal range found between 6 and 7. This tendency was found in the five response curves, with some variations (**Figure S13**). The geographical predictions for the three time periods were very similar and suggest the existence of suitable habitat exclusively in highland areas (**Figure S14**). Andean regions of Colombia, Ecuador, Perú and Central America are considered without extrapolation risk, while projections in the southern Andean region must be taken in account with caution (**Figure S15**).

Northern Andean tigrina (N. Andean tigrina)

For this genetic group, 90 records were obtained and 40 were retained after the filter. For each record set we evaluated between six and eight variable sets. However, the selected models from record set 4 did not comply with the omission criterion (**Table S12**). So, we made the correlation and overlap analysis between the final consensus generated with and without that record set. This analysis suggested that there are no significant differences between the final consensus when the selected models from record set 4 are included or excluded (**Table S13**). Thus, we considered the final consensus with these selected models. The model's results showed that the variables with more permutation importance were minimum temperature in the warmest month, growing degree days 0, thermicity and topographic wetness index (**Table S14**). However, the optimal range for minimum temperature in the warmest month and thermicity was different in each record set model. For example, for minimum temperature in the warmest month the optimal range found for record set 1 models was between -5 and 5°C, whereas for the record set 2 models was between 5 and 10°C, on the other hand, for record set 3 models, was between 2.5 and 7.5 °C. In the case of thermicity, for the record set 1 the optimal range is between -100 and 100 °C, and in the record set 2 is between 100 and 200. For growing degree days 0 all the curves showed the same tendency, with the optimal range in the lowest values between 0.0 and 0.4 x 10^5, and for topographic wetness index the optimal range is between 6 and 7 (**Figure S16**).

The threshold maps for the present showed potential distribution in highlands across the Andean region of Colombia, Ecuador, and Peru and in Cordillera Talamanca in Central America, and discontinuous areas in the Panamá Center. The potential distribution also included a few patches in the Guiana Shield and in the Atlantic Forest biome in Brazil. However, the patch size in these areas is smaller in the ETSS than in the MTSS threshold map (**Figure S17**). The mid-Holocene predictions present the same patterns than the present, with greater connectivity between the Atlantic Forest and the Pampa biome, but only in the MTSS threshold map. The highlands with high habitat suitability probability were also predicted in the LGM, but the threshold maps showed a broader potential distribution. The predictions made in the southern continent (from southern Amazon to southern Chile and Argentina) must be taken in account with caution, because the southern continent presents extrapolation risk (**Figure S18**).

Southern Andean tigrina (S. Andean tigrina)

For this genetic group, we obtained 18 records and 15 were retained after the filtering. For each record set we evaluated between two and six variables set (**Table S15**). The variables with more permutation importance in the selected models were growing degree days 5, topographic wetness index, thermicity and minimum temperature in the warmest month (**Table S16**). The optimal range of growing degree days 5 for this group is between 0.7 and 0.9x10^5, for topographic wetness index the optimal range is between 6 and 7 as in other models, thermicity is around 500 °C, and for minimum temperature in the warmest month is around 15°C. However, the suitability probability for minimum temperature in the warmest month and thermicity is not high, even in the optimal range (**Figure S19**). The geographic predictions showed a restricted highland distribution, but with a small projection in the Atlantic Forest. These predictions are very similar between the three time periods modeled, with a little expansion of the distribution in the LGM (**Figure S20**). In general terms, the projections had low extrapolation risk, only the Andean region in Colombia and Ecuador presented values for potential evapotranspiration seasonality out of calibration range. The other regions with extrapolation risk were not predicted as potential or suitable for the species (**Figure S21**: Extrapolation risk for S. Andean tigrina models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set3 LQ_0.5 constructed with the record set 1, **B.** Extrapolation risk map for the model Set1 LQ_0.5 constructed with the record set 2, and **C.** Extrapolation risk map for the model Set5 LQ_0.5 constructed with the record set 3.).

Northeastern Brazilian tigrina or *L. emiliae* (NE tigrina)

For this unit, 198 records were obtained but 162 were retained after filtering. The number of variable sets evaluated for each record set was variable, ranging between 10 and 18 variable sets. All selected models complied with the omission rate and AIC criterion, except the selected from record set 1, that had an omission rate of 5.8% (**Table S17**). The correlation and overlap analysis suggested that the models from set 1 models in spite of breaking the omission rate criterion, do not have a notable effect in the final consensus (**Table S18**), therefore, it was considered the consensus with the models from record set 1 for the results and analysis of this group. The variables with more permutation importance were annual potential evapotranspiration, climatic moisture index and potential evapotranspiration in the driest quarter (**Table S19**). annual potential evapotranspiration and climatic moisture index showed a response curve with negative tendency, as in previous models, with the optimal range in the lowest values (annual potential evapotranspiration = 1150 -1300 mm/year; climatic moisture index = -0.7 to -0.4). On the other hand, potential evapotranspiration in the driest quarter had a response curve with a positive tendency, with the optimal range between 180-190 mm/month. This tendency was found in all response curves, except for annual potential evapotranspiration in Set1 QH 0.5, with the record set 4 (**Figure S22**).

The binary maps for the present projection presented broader suitable patches in these same areas but with small patches in the Cerrado biome in Brazil, and in the Guiana Shield, connecting with the Caatinga biome. This pattern is very similar for the two threshold maps. The predictions for the mid-Holocene and LGM presented the same pattern than the present projection. For the

LGM, particularly, it was not demonstrated the patches that connect the Guianas Shield with northeastern Brazil (**Figure S23**). Predictions made in the Andean region and southern continent must be taken in account with caution because these areas had the highest extrapolation risk (**Figure S24**).

Exploratory modelling for the Guiana Shield

Guiana Shield strict (GSstrict)

For this scenario, 20 records were obtained and 19 were retained after the filter. As the global models only selected one variable, all variable sets were evaluated for all record sets (**Table S20**). Furthermore, the best models selected with AIC delta criterion had low AUC_{test} values (< 0.5), so, for this scenario only, the best models of each variable set were selected with the highest AUC_{test} values. The selected models also presented a high number of parameters and AUC_{test} values between 0.66 and 0.68, demonstrating the low reliability of the model (**Table S20**). However, due to the importance of the Guiana Shield comparison, we still presented the results for these models, in which the variables with higher permutation importance were aridity index, Continentality, growing degree days 5, potential evapotranspiration in the driest and coldest quarter, climatic moisture index (**Table S21**). Although none of the response curves showed a clear tendency, each one presented a singular pattern that was maintained in all selected models (**Figure S25**).

The predictions did not show a pattern of potential distribution. The binary maps showed as suitable areas small patches in the Guianas Shield that do not include all records and predicted a potential for the species in the Atlantic Forest, southern Cerrado biome, part of Pampa biome, part of Amazon region and other patches without any pattern. Furthermore, the ETSS threshold included areas broader than the MTSS threshold (**Figure S26**). For the mid-Holocene, binary maps included broad areas in the center of the Amazonian region, but the areas predicted in the Guiana Shield are broader than the present. For LGM, the predictions are like the mid-Holocene predictions, with some patches broader (**Figure S26**). These models presented high extrapolation risk in the areas south of the Amazon region, so the predictions made in this area can be unreliable (**Figure S27**). However, the response curves calculated for the variables and the number of parameters included in the selected models, in addition to the AUC_{test} values, suggest that these models may have produced unrealistic predictions.

Guiana Shield including records from Amazon biome in Brazil (GSAmaz)

For this scenario, 45 records were obtained, and 41 were retained after the filter. The two records out of calibration area (**Figure 3**), were considered very extreme and was not consider for the analysis. For each record set we evaluated among two and six variable sets. However, the selected models from record set 1 and 3 had a high omission rate (>5%, **Table S22**), so we made a correlation and overlap analysis between the consensus calculated with and without these selected models. The results showed a high correlation and overlap values, so we used the consensus calculated with the selected models from record set 1 and 3 (**Table S23**). The variables with more permutation importance were aridity index, climatic moisture index, potential evapotranspiration in the coldest and driest quarter, Continentality, and topographic wetness index (**Table S24**). For aridity index and topographic wetness index, the records from GSAmaz showed an optimal range in the highest values of these variables, ranging between 90-100, and between 15 -16, respectively. For potential evapotranspiration in the coldest quarter and Continentality, the optimal range is in lowest values ranging between 80-100 mm/month, and 0.3-0.5 respectively. For climatic moisture index the optimal range is between -0.1 and 0.1 with non-optimal ranges in highest and lowest values. Finally, potential evapotranspiration in the driest quarter presented a quasi-straight line across to the whole range. However, for the last two variables, the optimal range had intermediate values of suitability probability. These variables follow these same tendencies in all selected models (**Figure S28**).

The predictions for the present showed small patches in the Guianas Shield, with small areas connecting these patches with broad area in the northern Cerrado and southern Amazonian biome in Brazil, and the northern Caatinga. Still, this prediction suggested the Llanos as suitable for the species. For the mid-Holocene the predictions are limited to the Llanos and Panama center with small patches in the Cerrado biome. For the LGM, the predictions in the Llanos are maintained, and a small patch in the Guianas Shield, in addition to a broad patch between southern amazon (in Brazil), northern Cerrado and western Caatinga (**Figure S29**). However, according to the extrapolation risk the areas in the Cerrado biome must be taken in account with caution as they have high extrapolation risk (**Figure S30**).

Amazon biome in Brazil (Amaz)

For this scenario 25 records were obtained and 22 were retained after filtering. For each record set we evaluated between four and six variable sets, and the selected models had AUC_{test} values between 0.6944 and 0.7245. In these models the variables with more permutation importance were potential evapotranspiration in the coldest quarter and thermicity (**Table S26**). The potential evapotranspiration in the coldest quarter curve showed a negative tendency, with the optimal range between 112 and 120 mm/month, whereas the thermicity curve showed a positive tendency with the optimal range between 740 and 760 °C. This optimal range was found for all selected models that had thermicity as the most important variable (**Figure S31**). The predictions suggested the central Amazon Forest and lowlands in northern Colombia as suitable for the species (**Figure S32**). These areas do not present extrapolation risk (**Figure S33**). However, these models did not predict suitable areas in the past time periods and consequently, they cannot predict possible distributions in the past.

NE tigrina plus records from the Amazon biome in Brazil (NE tigrina +Amaz)

For this scenario 224 records were obtained and 183 were retained after the filter. Between eight and 16 variable sets were evaluated for each record set. All selected models comply with the omission and AIC criterion (**Table S27**). In these models, the variables with more permutation importance were potential evapotranspiration coldest quarter and climatic moisture index (**Table S28**). Both variables showed a negative tendency, with the optimal range in the lowest values. The optimal range for potential evapotranspiration coldest quarter is between 70 and 80 mm/month. For climatic moisture index, the optimal range is between -0.9 and -0.8. These optimal ranges are the same in all response curves for these variables (**Figure S34**). The predictions were very similar, but broader than the NE tigrina models, including a small part of the Cerrado biome. In the past periods, the potential distribution seems to be little reduced (**Figure S35**). The predictions showed a low extrapolation risk for all time periods (**Figure S36**).

Supplementary Tables

Table S1: All variables set evaluated and selected as the best models for each record set of *Leopardus tigrinus sensu* Johnson et al. (1999). Numbers in bold indicate the variable set (or sets) corresponding to the selected models.

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	**1**	x	x	x	x				x	x		x				x		LQ	1.5	4.3	12
	2	x	x	x	x	x				x		x				x					
2	1	x	x	x	x				x	x	x	x				x					
	2	x	x	x	x	x				x	x	x				x		LQ	0.5	4.2	18
3	**1**	x	x	x					x	x						x		L	4	4.3	6
	2	x	x	x			x			x						x		L	0.5	4.3	6
4	1	x	x	x	x				x	x			x			x					
	2	x	x	x	x		x			x			x			x		QH	3.5	4.2	42

Table S2: All variables set evaluated and selected as the best models for each record set of *Leopardus tigrinus sensu* Kitchener et al. (2017). The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

Variables																		Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	**1**	x	x	x	x		x	x			x		x			x		LQ	5	3.1	15
	2		x	x	x		x	x			x	x	x			x					
	3	x	x	x	x	x		x			x		x			x					
	4		x	x	x	x		x			x	x	x			x					
	5	x	x	x	x		x	x		x			x			x					
	6		x	x	x		x	x		x		x	x			x					
	7	x	x	x	x	x		x		x			x			x					
	8		x	x	x	x		x		x		x	x			x					
	9	x	x	x			x	x			x		x	x		x		LQ	0.5	3.1	16
	10		x	x			x	x			x	x	x	x		x		QH	3.5	4.7	20
	11	x	x	x		x		x			x		x	x		x					
	12		x	x		x		x			x	x	x	x		x		LQ	0.5	3.1	15
	13	x	x	x			x	x		x			x	x		x					
	14		x	x			x	x		x		x	x	x		x					
	15	x	x	x		x		x		x			x	x		x					
	16		x	x		x		x		x		x	x	x		x					
2	1	x	x	x	x		x	x			x		x			x					
	2		x	x	x		x	x			x	x	x			x		LQ	0.5	4.7	14
	3	x	x	x	x	x		x			x		x			x					
	4		x	x	x	x		x			x	x	x			x					
	5	x	x	x	x			x	x		x		x			x					
	6		x	x	x			x	x		x	x	x			x					
	7	x	x	x	x			x			x		x		x	x					
	8		x	x	x			x			x	x	x		x	x					
	9	x	x	x	x		x			x			x			x					
	10		x	x	x		x			x		x	x			x					
	11	x	x	x	x	x				x			x			x					
	12		x	x	x	x				x		x	x			x					
	13	x	x	x	x				x	x			x			x					
	14		x	x	x				x	x		x	x			x					
	15	x	x	x	x					x			x		x	x					
	16		x	x	x					x		x	x		x	x					
	17	x	x	x			x	x			x		x	x		x					
	18		x	x			x	x			x	x	x	x		x		LQ	0.5	4.7	14

								Variables										Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
	19	x	x	x		x		x			x		x	x		x					
	20		x	x		x		x			x	x	x	x		x					
	21	x	x	x				x	x		x		x	x		x					
	22		x	x				x	x		x	x	x	x		x					
	23	x	x	x				x			x		x	x	x	x					
	24		x	x				x			x	x	x	x	x	x					
	25	x	x	x			x			x			x	x		x					
	26		x	x			x			x		x	x	x		x					
	27	x	x	x		x				x			x	x		x					
	28		x	x		x				x		x	x	x		x					
	29	x	x	x					x	x			x	x		x					
	30		x	x					x	x		x	x	x		x					
	31	x	x	x						x			x	x	x	x					
	32		x	x						x		x	x	x	x	x					
3	1		x	x	x		x	x			x		x			x					
	2		x	x	x	x		x			x		x			x					
	3		x	x	x			x			x		x		x	x					
	4		x	x	x		x			x			x			x					
	5		x	x	x	x				x			x			x					
	6		x	x	x					x			x		x	x					
	7		x	x			x	x			x		x	x		x		QH	4	4.4	20
	8		x	x		x		x			x		x	x		x					
	9		x	x				x			x		x	x	x	x					
	10		x	x			x			x			x	x		x					
	11		x	x		x				x			x	x		x					
	12		x	x						x			x	x	x	x					
4	**1**	x		x	x		x	x			x		x			x		L	0.5	3	8
																		L	1	3	8
	2			x	x		x	x			x	x	x			x		L	0.5	1.5	8
																		L	1	1.5	8
	3	x		x	x			x	x		x		x			x					
	4			x	x			x	x		x	x	x			x					
	5	x		x	x		x			x			x			x		L	0.5	3	6
																		L	1	3	6
																		L	1.5	3	6
																		L	2	3	6
	6			x	x		x			x		x	x			x		L	0.5	3	6

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
																		L	1	3	6
																		L	1.5	4.5	6
	7	x		x	x				x	x			x			x		L	0.5	3	6
																		L	1	3	6
	8			x	x				x	x		x	x			x		L	1	3	6
	9	x		x			x	x			x		x	x		x					
	10			x			x	x			x	x	x	x		x		QH	3.5	4.7	20
	11	x		x				x	x		x		x	x		x					
	12			x				x	x		x	x	x	x		x		LQ	0.5	3.1	15
	13	x		x			x			x			x	x		x					
	14			x			x			x		x	x	x		x					
	15	x		x					x	x			x	x		x					
	16			x					x	x		x	x	x		x					
5	**1**		x	x	x		x				x	x	x			x		LQ	0.5	4.5	15
	2		x	x	x				x		x	x	x			x		LQ	0.5	4.5	12
	3		x	x	x		x			x		x	x			x					
	4		x	x	x				x	x		x	x			x					
	5		x	x			x				x	x	x	x		x					
	6		x	x					x		x	x	x	x		x					
	7		x	x			x			x		x	x	x		x					
	8		x	x					x	x		x	x	x		x					

Table S3: Permutation importance of each variable in the selected models for each record set of *Leopardus tigrinus sensu* Johnson et al. (1999). NA indicates that these variables were not included in the variable sets.

Record Set	Variable Set	PCQ	TopoWet	MTW	GDD0	GDD5	CMI	AnnualPET	AridityIndex	PWQ	Continental	PDQ	PWeQ
1	Set 1 LQ 1.5	7.2	21	12	NA	NA	11	40	6.2	0.2	1.6	NA	NA
2	Set 2 LQ 0.5	7.7	16	NA	9.7	NA	6.6	46	5.5	3.4	3.2	1.5	NA
3	Set 1 L 4	19	41	13	NA	NA	5.6	19	3.4	NA	NA	NA	NA
	Set 2 L 0.5	40	29	NA	NA	9.2	2.2	15	4.6	NA	NA	NA	NA
4	Set 2 QH 3.5	28	19	NA	17	NA	7.4	14	11	NA	NA	NA	0.3

Table S4: Permutation importance of each variable in the selected models for each record set of *Leopardus tigrinus sensu* Kitchener et al. (2017). NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	Continentality	PDQ	MTC	GDD5	AnnualPET	TopoWet	CMI	PWeQ	AridityIndex	PSeasonality	PWQ	GDD0	PCQ	MTW
1	Set 1 LQ 0.5	4.2	13.1	6.1	10.8	26.6	14.5	17.4	0.8	6.5	NA	NA	NA	NA	NA
	Set 9 LQ 0.5	NA	17.2	5.7	10.8	27.4	10.9	18.5	2.4	2	5.1	NA	NA	NA	NA
	Set 10 QH 3.5	NA	11.7	5.4	11.5	NA	13.3	15.2	2.1	21.1	2.1	17.5	NA	NA	NA
	Set 12 LQ 0.5	NA	11.6	15.3	NA	NA	14.1	13.4	0.7	8.4	2.1	23.8	10.6	NA	NA
2	Set 2 LQ 0.5	1.7	12.9	12.7	11	NA	9.3	13.7	1.6	8.3	NA	28.8	NA	NA	NA
	Set 18 LQ 0.5	NA	12.4	7.2	11.1	NA	18.4	20.9	1.2	3.1	2.3	23.6	NA	NA	NA
3	Set 7 QH 4	NA	2	5.3	12.4	NA	22.6	15.1	19.1	20.6	3	NA	NA	NA	NA
4	Set 1 L 0.5	11.4	5.3	23.2	10.3	7.2	15.3	26.2	1.1	NA	NA	NA	NA	NA	NA
	Set 1 L 1	11.9	9.8	12.4	10.6	10.7	13.3	28	3.4	NA	NA	NA	NA	NA	NA
	Set 2 L 0.5	12.9	7	24.4	8.9	NA	14	25	1.9	NA	NA	5.8	NA	NA	NA
	Set 2 L 1	5.7	6.2	26	14.5	NA	16.9	21.9	2.6	NA	NA	6.3	NA	NA	NA
	Set 5 L 0.5	22.4	NA	NA	11.3	2	13.9	28.3	6	NA	NA	NA	NA	16.1	NA
	Set 5 L 1	15.5	NA	NA	11.7	3.6	17.9	29.1	8.9	NA	NA	NA	NA	13.2	NA
	Set 5 L 1.5	18.7	NA	NA	12.7	5.2	15.7	32.3	5.2	NA	NA	NA	NA	10.2	NA
	Set 5 L 2	16.4	NA	NA	15.6	1.9	18.1	26.2	12.4	NA	NA	NA	NA	9.5	NA
	Set 6 L 0.5	23	NA	NA	11.6	NA	18	23.6	7.8	NA	NA	1.3	NA	14.7	NA
	Set 6 L 1	15.1	NA	NA	13.7	NA	20.5	30	8.5	NA	NA	1.2	NA	11	NA
	Set 6 L 1.5	15.5	NA	NA	11.8	NA	20.7	31.3	9.5	NA	NA	4.5	NA	6.8	NA
	Set 7 L 0.5	18.7	NA	NA	NA	5.4	18.1	28	7.1	NA	NA	NA	NA	16.2	6.5
	Set 7 L 1	19.8	NA	NA	NA	3.4	21.7	33.6	6.3	NA	NA	NA	NA	4.9	10.2
	Set 8 L 1	14	NA	NA	NA	NA	24.4	32.7	8.2	NA	NA	1.2	NA	9.6	9.9
5	Set 1 LQ 0.5	4.1	13.4	NA	9.8	NA	13.7	16.8	1.1	6.3	NA	34.7	NA	NA	NA
	Set 2 LQ 0.5	3.8	15.2	NA	NA	NA	13.5	18.1	1.4	6.6	NA	32	NA	NA	9.3

Table S5: All variables set evaluated and selected as the best models for each record set of *Leopardus guttulus*. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	1			x		x			x	x	x		x			x					
	2			x			x		x	x	x		x			x					
	3			x					x	x	x		x		x	x		LQ	1.5	5.9	9
	4	x	x	x	x	x			x		x		x			x					
	5	x	x	x	x		x		x		x		x			x					
	6	x	x	x	x				x		x		x		x	x					
	7	x	x	x		x			x		x		x	x		x					
	8	x	x	x			x		x		x		x	x		x					
	9	x	x	x					x		x		x	x	x	x					
	10			x				x	x		x		x			x					
2	1					x			x	x						x					
	2						x		x	x						x					
	3								x	x					x	x					
	4	x			x	x			x							x		Q Q	0.5 1	5.8 5.8	5 4
	5	x			x		x		x							x		Q Q	0.5 1	5.8 5.8	5 4
	6	x			x				x						x	x					
	7	x				x			x					x		x					
	8	x					x		x					x		x					
	9	x							x					x	x	x					
	10							x	x							x					
3	1					x			x	x	x		x			x					
	2						x		x	x	x		x			x					
	3								x	x	x		x		x	x					
	4	x	x		x	x			x		x		x			x		LQ	0.5	3.8	14
	5	x	x		x		x		x		x		x			x		LA	0.5	3.8	14
	6	x	x		x				x		x		x		x	x					
	7	x	x			x			x		x		x	x		x					
	8	x	x				x		x		x		x	x		x					
	9	x	x						x		x		x	x	x	x					
	10							x	x		x		x			x					
4	**1**			x		x			x	x	x	x				x		Q Q	0.5 1	3.8 3.8	7 7

Variables																		Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
																		Q	1.5	3.8	7
																		Q	3	3.8	6
																		Q	3.5	3.8	6
																		Q	0.5	3.8	7
																		Q	1	3.8	7
	2			x			x		x	x	x	x				x		Q	1.5	3.8	7
																		Q	3	3.8	6
																		Q	3.5	3.8	6
	3	x	x	x	x	x			x		x	x				x		Q	3.5	3.8	7
																		Q	4	3.8	6
	4	x	x	x	x		x		x		x	x				x		Q	3.5	3.8	7
																		Q	4	3.8	6
	5	x	x	x		x			x		x	x		x		x		Q	2.5	3.8	8
																		Q	3	3.8	7
																		Q	3.5	3.8	7
																		Q	4	3.8	6
	6	x	x	x			x		x		x	x		x		x		Q	2.5	3.8	8
																		Q	3	3.8	7
																		Q	3.5	3.8	7
																		Q	4	3.8	6

Table S6: Correlation and overlap analysis made with and without record set 1 models to determine the effect of models with high omission rate in the final consensus in *L. guttulus* models. t: value of statistic test, df: degrees of freedom. All correlation estimates had p = $2.2x10^{-16}$

Scenario	**t**	**df**	**Confidence Interval**	**Correlation**	**Overlap (Schoener's D)**
Current	17322	898992	0.9984991 - 0.9985114	0.9985053	0.9867165
Holocene	17161	909632	0.9984529 - 0.9984656	0.9984593	0.9864365
LGM	16528	1055186	0.9980669 - 0.9980816	0.9980743	0.9844301

Table S7: Permutation importance of each variable in the selected models for each record set of *Leopardus guttulus*. NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	AnnualPET	GDD0	MTW	Thermicity	GDD5	Continentality	Pseasonality	AridityIndex	CMI	PDQ	PWeQ	TopoWet	PWQ
1	Set 2 LQ 1.5	28.8	13.8	NA	NA	NA	NA	4.1	2.4	19	9	4.7	18.3	NA
	Set 3 LQ 0.5	26.4	NA	6.2	NA	NA	13.3	NA	3.2	19.3	12.4	4.2	14.9	NA
	Set 3 LQ 1	27.8	NA	11.1	NA	NA	10.7	NA	2.8	18.2	21	1.3	7.1	NA
	Set 3 LQ 1.5	29	NA	2.1	NA	NA	15.3	NA	2.6	27	7.7	2.5	13.7	NA
	Set 4 LQ 1.5	37	NA	4.5	NA	NA	NA	6.4	1.4	20.8	26.1	0.9	2.8	NA
	Set 4 LQ 2	30	NA	11.7	NA	NA	NA	4.1	1.9	19.1	15.8	1.9	15.5	NA
	Set 5 LQ 0.5	43.4	NA	NA	10.2	NA	4.4	NA	2	11.4	19.8	2.8	6.1	NA
	Set 5 LQ 1	37.4	NA	NA	16.7	NA	11.6	NA	1.6	18.9	10.1	0.4	13.3	NA
	Set 5 LQ 1.5	17.7	NA	NA	11.8	NA	10.5	NA	1.9	20.6	15.1	8.3	14	NA
	Set 5 QH 2.5	28.7	NA	NA	12.5	NA	13	NA	2	15.2	11.4	3.4	13.8	NA
	Set 6 LQ 1.5	25.5	NA	NA	6.9	NA	NA	6.8	1.9	24.5	19.8	1.7	12.9	NA
	Set 6 LQ 2	3.4	NA	NA	11.6	NA	NA	3.1	5.9	16.3	18	0.3	12.3	NA
2	Set 1 LQ 0.5	40.8	9.9	NA	NA	NA	7	NA	2.9	11.4	16.9	2	9	NA
	Set 1 LQ 1	43.4	5.6	NA	NA	NA	8	NA	6.2	14.4	15.6	1.2	5.7	NA
	Set 2 LQ 1.5	34.8	7.3	NA	NA	NA	NA	6.5	2.4	16.5	18.8	3.3	10.2	NA
	Set 2 LQ 2	34.7	4.5	NA	NA	NA	NA	7.9	2.5	22.4	15.2	0.7	11.9	NA
	Set 3 LQ 1	31	NA	13.4	NA	NA	7	NA	3.1	16.8	18.2	2.1	8.5	NA
	Set 4 LQ 1.5	23.9	NA	8.7	NA	NA	NA	8	3.6	25.7	14.5	6.6	8.9	NA
	Set 4 LQ 2	28.1	NA	5.2	NA	NA	NA	5	4.4	33.9	10.7	1.4	11.2	NA
	Set 5 LQ 1	41.9	NA	NA	6.6	NA	7.7	NA	2.7	18.7	10.7	1.4	10.3	NA
	Set 6 LQ 2	39.5	NA	NA	14.9	NA	NA	3.3	1.8	19.6	14	1	5.8	NA
	Set 7 LQ 0.5	38.8	NA	NA	NA	6	7.6	NA	2.3	21.2	15.2	1.2	7.8	NA
	Set 7 LQ 1	41.1	NA	NA	NA	8.1	11.3	NA	0.9	17.4	12.5	0.8	7.9	NA
	Set 8 LQ 1.5	37.5	NA	NA	NA	8.5	NA	9	2.7	17	14.6	1.9	9	NA
	Set 8 LQ 2	34.1	NA	NA	NA	7.5	NA	2.6	2.5	25.5	14.5	2.2	11.2	NA
3	Set 2 LQ 1.5	23	NA	12	NA	NA	NA	5	2.1	26.1	16.6	3.6	11.7	NA
	Set 3 LQ 1	28.3	NA	NA	13	NA	10.8	NA	1.3	20.4	14.1	2.2	9.8	NA
4	Set 1 QH 0.5	19.9	NA	11.5	NA	NA	18.7	NA	4.4	13.1	13.4	5.5	13.4	NA
5	Set 7 L 4	NA	NA	NA	NA	NA	0.5	NA	1.3	20.3	37.7	NA	10.4	29.6

Table S8: All variables set evaluated and selected as the best modelsfor each record set of *Leopardus tigrinus* (m). The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

Variables																		Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	**1**		x	x	x			x	x	x	x			x		x		LQ	1	4.5	2
	2		x	x	x	x		x		x	x			x		x					
	3		x	x	x		x	x		x	x			x		x		LQ	1	4.5	14
	4		x	x	x			x		x	x			x	x	x					
2	**1**	x	x	x	x			x	x	x	x		x	x		x		LQ	1	4.5	13
																		LQ	2	4.5	12
	2		x	x	x			x	x	x	x	x	x	x		x		LQ	1	4.5	13
																		LQ	2	4.5	12
	3	x	x	x	x	x		x		x	x		x	x		x		LQ	1	4.5	2
	4		x	x	x	x		x		x	x	x	x	x		x		LQ	1	4.5	12
	5	x	x	x	x		x	x		x	x		x	x		x		LQ	1	4.5	13
																		LQ	2	4.5	12
	6		x	x	x		x	x		x	x	x	x	x		x		LQ	1	4.5	13
																		LQ	2	4.5	12
	7	x	x	x	x			x		x	x		x	x	x	x		LQ	1	4.5	13
																		LQ	2	4.5	12
	8		x	x	x			x		x	x	x	x	x	x	x		LQ	1	4.5	13
																		LQ	2	4.5	12
3	**1**	x	x	x	x			x	x	x	x		x	x		x		LQ	1	4.5	12
	2		x	x	x			x	x	x	x	x	x	x		x		LQ	1	4.5	12
																		QH	3	4.5	12
																		QH	4	4.5	10
	3	x	x	x	x	x		x		x	x		x	x		x					
	4		x	x	x	x		x		x	x	x	x	x		x					
	5	x	x	x	x		x	x		x	x		x	x		x					
	6		x	x	x		x	x		x	x	x	x	x		x					
	7	x	x	x	x			x		x	x		x	x	x	x					
	8		x	x	x			x		x	x	x	x	x	x	x					

Table S9: Permutation importance of each variable in the selected models for each record set of *Leopardus tigrinus* (m). NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	MTW	TopoWet	MTC	CMI	AridityIndex	Pseasonality	Continentality	PDQ	PCQ	GDD5	PWeQ	AnnualPET	PWQ	GDD0	Thermicity
1	Set 1 LQ 1	5.9	9.6	20.7	3.4	3.9	17.5	5.4	6	27.7	NA	NA	NA	NA	NA	NA
	Set 3 LQ 0.5	NA	5.4	32.7	1.9	3.3	21.1	10.7	4.5	10.4	9.9	NA	NA	NA	NA	NA
2	Set 1 LQ 1	7.8	7.8	18.2	1.4	2.2	23.1	7.6	4.7	20.4	NA	1.4	5.4	NA	NA	NA
	Set 1 LQ 1.5	10.4	14.2	23.7	2.8	2.2	17.2	8.3	5.7	7.3	NA	0.6	7.6	NA	NA	NA
	Set 2 LQ 1	8.5	13.8	16.7	2.9	2.3	21.4	7	6.3	16.8	NA	2.3	NA	1.8	NA	NA
	Set 2 LQ 1.5	8.3	8.3	45	2.2	2.2	15.8	5.9	4.5	4.5	NA	2.8	NA	0.5	NA	NA
	Set 3 LQ 1	NA	5.1	20.2	2.5	3.2	23	11.3	5.1	16.5	NA	1.6	4.2	NA	10.5	NA
	Set 4 LQ 1	NA	5.2	25.7	2.3	1.5	16.1	8.1	7.9	14.2	NA	1.1	NA	4.5	13.6	NA
	Set 5 LQ 1	NA	8.2	27.5	1.9	2.1	20.7	8.5	7.3	14.5	7.9	1	0.3	NA	NA	NA
	Set 5 LQ 1.5	NA	7	24.8	4	1	21.2	7.3	4.8	14.9	13	0.3	1.6	NA	NA	NA
	Set 6 LQ 1	NA	9.1	14	5.3	0.9	19.7	11.2	5.6	13.6	14	0.7	NA	6.3	NA	NA
	Set 6 LQ 1.5	NA	17.6	29.5	3.4	1.5	10.8	9	3.1	3.7	15	2.2	NA	4.3	NA	NA
	Set 7 LQ 1	NA	8.3	31.3	1.1	3	20.8	8.9	7	10.2	NA	0.6	1	NA	NA	7.8
	Set 7 LQ 1.5	NA	8.5	24.6	2.5	1.5	12.2	9.8	7.5	11.2	NA	0.3	10.5	NA	NA	11.3
	Set 8 LQ 1	NA	5.4	19.6	2.1	1.4	30	8.2	6	18.4	NA	0.7	NA	0.4	NA	7.8
	Set 8 LQ 1.5	NA	3.1	41.4	0.9	2.1	20.9	6.4	2.6	15.4	NA	0.2	NA	0.4	NA	6.7
3	Set 1 LQ 1	8	8	27.6	5	1.5	18.1	10.1	7	9.5	NA	1	4.3	NA	NA	NA
	Set 2 LQ 1	11.7	5.1	25.3	2.4	3.1	18.2	4.5	4.2	21.2	NA	1.3	NA	3	NA	NA
	Set 2 QH 3	17.4	16.3	30.3	11.7	5.1	0.2	3.5	2.8	5.2	NA	4	NA	3.6	NA	NA
	Set 2 QH 3.5	15.6	25.2	26.9	9.1	3.3	2.3	1.1	1.6	1.6	NA	11.7	NA	1.6	NA	NA

Table S10: All variables set evaluated and selected as the best models for each record set of C. Am. tigrina. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	AUC$_{test}$	Parameters
1	**1**				x					x						x		LQ	0.5	0.940	2
	2				x	x				x											
	3				x		x			x											
2	**1**				x					x						x		LQ	0.5	0.940	2
3	**1**				x					x						x		Q	0.5	0.936	2
4	**1**				x				x	x						x		LQ	0.5	0.925	2
5	**1**				x					x						x		HQ	1.5	0.932	2
	2				x		x			x											

Table S11: Permutation importance of each variable in the selected models for each record set of C. Am. tigrina. NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	PCQ	TopoWet	MTW	Continentality
1	Set1 LQ 0.5	36.4	62.5	NA	1.2
2	Set1 LQ 0.5	41.8	56.7	NA	1.4
3	Set 1 Q 05	27.2	70.4	NA	2.4
4	Set1 LQ 0.5	33.9	40.2	24.2	1.6
5	Set1 HQ 1.5	42.2	56.1	NA	1.8

Table S12: All variables set evaluated and selected as the best models for each record set of N. Andean tigrina. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

								Variables										Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	**1**		x	x					x	x				x				Q	2	0	4
																		Q	2.5	0	4
																		LQ	3.5	0	3
																		Q	3.5	0	3
																		LQ	4	0	3
																		Q	4	0	3
	2		x	x	x				x	x								Q	1	0	4
																		LQ	2	0	4
																		LQ	2.5	0	3
																		LQ	3	0	3
																		Q	3	0	2
																		LQ	3.5	0	2
																		Q	3.5	0	2
																		LQ	4	0	2
																		Q	4	0	2
	3		x	x		x				x				x				QH	4	0	4
	4		x	x	x	x				x								Q	1	0	4
																		LQ	1.5	0	4
																		LQ	2	0	4
	5		x	x				x		x				x							
	6		x	x	x			x		x											
	7		x	x						x				x	x			Q	0.5	0	5
																		LQ	4	0	3
																		Q	4	0	3
	8		x	x	x					x					x			Q	0.5	0	5
																		LQ	1.5	0	5
																		Q	1.5	0	4
																		LQ	2	0	4
																		LQ	2.5	0	4
																		LQ	3	0	3
																		Q	3.5	0	2
																		Q	4	0	2
2	**1**		x						x					x				LQ	0.5	0	4
	2		x		x				x									LQ	0.5	0	5

									Variables									Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
																		LQ	1	0	3
	3		x											x	x						
	4		x		x										x			LQ LQ	0.5 1	0 0	5 3
	5		x											x		x					
	6		x		x											x					
3	1		x	x					x		x			x							
	2		x	x	x				x		x							LQ	1.5	0	3
	3		x	x	x							x									
	4		x	x							x			x		x					
	5		x	x	x						x					x					
	6		x	x										x	x						
	7		x	x	x										x			LQ	1	0	5
4	1		x	x					x		x		x	x							
	2		x	x	x				x		x		x								
	3		x	x				x					x	x							
	4		x	x	x			x					x								
	5		x	x								x	x	x		x		L L	0.5 1	10 10	6 6
	6		x	x									x	x	x						
	7		x	x	x								x		x						
	8		x	x	x						x		x			x		L L L	3 3.5 4	10 10 10	4 4 4
5	1		x	x					x		x			x							
	2		x	x	x				x		x							QH	4	0	4
	3		x	x										x	x						
	4		x	x	x										x			QH	2	0	8
	5		x	x							x			x		x					
	6		x	x	x						x					x					

Table S13: Correlation and overlap analysis made with and without record set 4 models to determine the effect of models with high omission rate in the final consensus of N. Andean tigrina models. t: value of statistic test, df: degrees of freedom. All correlation estimates had p = 2.2x10^{-16}

Scenario	**t**	**df**	**Confidence Interval**	**cor**	**Overlap (Shoener's D)**
Current	6885.3	898992	0.9906127 – 0.9906896	0.9906512	0.9590296
Holocene	6748.3	909632	0.9901196 – 0.9902001	0.9901399	0.9628075
LGM	4740.7	1055186	0.9772346 – 0.9774058	0.9773203	0.965966

Table S14: Permutation importance of each variable in the selected models for each record set of N. Andean. tigrina. NA indicates that these variables were not included in these variable sets.

Record set	Variable Set	MTW	PCQ	Pseasonality	AridityIndex	CMI	Continentality	GDD0	Thermicity	PWQ	PWeQ	TopoWet	PDQ
1	Set 1 Q 2	77.7	0.5	14.2	7.1	0.4	NA	NA	NA	NA	NA	NA	NA
	Set 1 Q 2.5	83.6	0.4	14.1	1.2	0.7	NA	NA	NA	NA	NA	NA	NA
	Set 1 Q 3.5	88.2	0.6	9.2	1.8	0.2	NA	NA	NA	NA	NA	NA	NA
	Set 1 LQ 3.5	86.4	0.4	8.3	1.5	3.4	NA	NA	NA	NA	NA	NA	NA
	Set 1 Q 4	86.1	0	8.7	1.9	3.3	NA	NA	NA	NA	NA	NA	NA
	Set 1 LQ 4	81.9	0.5	14.2	2.7	0.7	NA	NA	NA	NA	NA	NA	NA
	Set 2 Q 1	94.5	1.4	NA	1.6	0.8	1.7	NA	NA	NA	NA	NA	NA
	Set 2 LQ 2	90.5	2.8	NA	0.6	0.8	5.4	NA	NA	NA	NA	NA	NA
	Set 2 LQ 2.5	94.9	0.2	NA	2.6	0.9	1.5	NA	NA	NA	NA	NA	NA
	Set 2 Q 3	92.3	0	NA	3.2	4.5	0	NA	NA	NA	NA	NA	NA
	Set 2 LQ 3	87	0	NA	7.3	1.7	4	NA	NA	NA	NA	NA	NA
	Set 2 Q 3.5	89.3	0	NA	5.5	0.4	4.8	NA	NA	NA	NA	NA	NA
	Set 2 LQ 3.5	95	0.4	NA	1.7	2.5	0.5	NA	NA	NA	NA	NA	NA
	Set 2 Q 4	93	0	NA	4.2	0.1	2.8	NA	NA	NA	NA	NA	NA
	Set 2 LQ 4	96.1	0	NA	3.6	0.1	0.3	NA	NA	NA	NA	NA	NA
	Set 3 QH 4	NA	0.6	11	1.2	1.9	85.3	NA	NA	NA	NA	NA	NA
	Set 4 Q 1	NA	1.2	NA	3.1	0.1	2.2	93.4	NA	NA	NA	NA	NA
	Set 4 LQ 1.5	NA	1.9	NA	4.3	1	1.5	91.3	NA	NA	NA	NA	NA
	Set 4 LQ 2	NA	3	NA	6.5	1	1.8	87.7	NA	NA	NA	NA	NA
	Set 7 Q 0.5	NA	0.9	8.8	5.7	1.7	NA	NA	82.9	NA	NA	NA	NA
	Set 7 Q 4	NA	0.2	27.3	2.3	0.5	NA	NA	70	NA	NA	NA	NA
	Set 7 LQ 4	NA	0.3	8.3	6.8	1.8	NA	NA	82.9	NA	NA	NA	NA
	Set 8 Q 0.5	NA	5.3	NA	6.7	1.8	1.7	NA	84.5	NA	NA	NA	NA
	Set 8 Q 1.5	NA	2.5	NA	0.6	2.5	0.6	NA	93.7	NA	NA	NA	NA

Record set	Variable Set	MTW	PCQ	Pseasonality	AridityIndex	CMI	Continentality	GDD0	Thermicity	PWQ	PWeQ	TopoWet	PDQ
	Set 8 LQ 1.5	NA	2.4	NA	1.4	1.7	2.5	NA	92	NA	NA	NA	NA
	Set 8 LQ 2	NA	1.7	NA	1.9	1.1	1	NA	94.2	NA	NA	NA	NA
	Set 8 LQ 2.5	NA	1	NA	5	1.5	1.5	NA	90.8	NA	NA	NA	NA
	Set 8 LQ 3	NA	0.1	NA	1.2	4.3	4	NA	90.4	NA	NA	NA	NA
	Set 8 Q 3.5	NA	0	NA	6.7	0.7	1	NA	91.6	NA	NA	NA	NA
	Set 8 Q 4	NA	0.1	NA	1.3	0.4	4.4	NA	93.8	NA	NA	NA	NA
2	Set 1 LQ 0.5	92	NA	3.4	4.7	NA	NA	NA	NA	NA	NA	NA	NA
	Set 2 LQ 0.5	87.5	NA	NA	3.1	NA	9.4	NA	NA	NA	NA	NA	NA
	Set 2 LQ 1	89.3	NA	NA	4.1	NA	6.6	NA	NA	NA	NA	NA	NA
	Set 4 LQ 0.5	NA	NA	NA	7.9	NA	8.8	NA	83.3	NA	NA	NA	NA
	Set 4 LQ 1.5	NA	NA	NA	6	NA	2.6	NA	91.4	NA	NA	NA	NA
3	Set 2 LQ 1.5	91.3	3.1	NA	0.9	1.4	3.2	NA	NA	NA	NA	NA	NA
	Set 7 LQ 1	NA	NA	NA	1.8	2.3	2.6	NA	93.3	NA	NA	NA	NA
4	Set 5 L 0.5	NA	NA	37	2.7	3.1	NA	NA	NA	6.1	2.7	48.4	NA
	Set 5 L 1	NA	NA	14	4.2	1.7	NA	NA	NA	23.7	8.4	4.8	NA
	Set 8 L 3.5	NA	NA	NA	0.8	0.5	2.2	NA	NA	NA	6.9	71	18.7
	Set 8 L 3	NA	NA	NA	4.1	2	3.4	NA	NA	NA	6.1	72	12.4
	Set 8 L 4	NA	NA	NA	1.3	0.7	6.6	NA	NA	NA	8.6	74.8	8
5	Set 2 QH 4	92.2	NA	NA	5.6	0.4	0.4	NA	NA	NA	NA	NA	1.4
	Set 4 QH 2	NA	NA	NA	10.7	1.2	1.8	NA	NA	NA	NA	NA	86.3

Table S15: All variables set evaluated and selected as the best models for each record set of S. Andean tigrina. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

	Variables																	Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	AUC_{test}	Parameters
1	1			x					x							x					
	2			x					x								x				
	3			x			x									x		LQ	0.5	0.863	4
	4			x			x										x				
2	**1**			x					x					x		x		LQ	0.5	0.881	5
	2			x			x							x		x					
3	1				x				x							x					
	2								x					x		x					
	3				x		x									x					
	4						x							x		x					
	5				x										x	x		LQ	0.5	0.878	4
	6													x	x	x					
4	1			x	x				x							x					
	2			x					x					x		x		LQ	0.5	0.895	5
	3			x	x		x									x					
	4			x			x							x		x					
5	1			x	x				x							x					
	2			x					x					x		x		LQ	0.5	0.894	5
	3			x	x		x									x					
	4			x			x							x		x					

Table S16: Permutation importance of each variable in the selected models for each record set of S. Andean tigrina. NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	GDD5	TopoWet	CMI	PSeasonality	MTW	Thermicity	Continentality
1	Set3 LQ 0.5	19	30.4	50.6	NA	NA	NA	NA
2	Set1 LQ 0.5	NA	58.2	6.6	13.5	21.6	NA	NA
3	Set5 LQ 0.5	NA	40.5	NA	NA	NA	51.8	7.8
4	Set2 LQ 0.5	NA	37.1	9.6	NA	41.4	NA	11.9
5	Set2 LQ 0.5	NA	51	19.1	NA	18.9	NA	11

Table S17: All variables set evaluated and selected as the best models for each record set of NE tigrina. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	1	x	x	x	x	x					x		x			x					
	2	x	x	x		x					x		x	x		x		LQ	1.5	5.8	8
	3	x	x	x	x				x		x		x			x		LQ	0.5	5.8	11
																		LQ	1	5.8	10
																		LQ	1.5	5.8	10
	4	x	x	x					x		x		x	x		x		LQ	1.5	5.8	8
																		LQ	2	5.8	8
	5	x	x	x	x						x		x		x	x		LQ	0.5	5.8	11
																		LQ	1	5.8	10
																		LQ	1.5	5.8	10
																		LQ	2.5	5.8	12
	6	x	x	x							x		x	x	x	x		LQ	1.5	5.8	8
																		LQ	2	5.8	8
	7		x	x	x			x			x	x	x			x					
	8		x	x				x			x	x	x	x		x					
	9		x	x	x	x				x	x	x	x			x					
	10		x	x		x				x	x	x	x	x		x					
	11		x	x	x				x	x	x	x	x			x					
	12		x	x					x	x	x	x	x	x		x					
	13		x	x	x					x	x	x	x		x	x					
	14		x	x						x	x	x	x	x	x	x					
2	**1**	x	x	x	x	x					x		x			x		LQ	0.5	4.9	10
																		LQ	1	4.9	10
	2	x	x	x		x					x		x	x		x		LQ	1.5	4.9	8
																		LQ	2	4.9	8
	3	x	x	x	x				x		x		x			x		LQ	1	4.9	10
	4	x	x	x					x		x		x	x		x		LQ	1.5	4.9	8
																		LQ	2	4.9	8
	5	x	x	x	x						x		x		x	x		LQ	1	4.9	10
	6	x	x	x							x		x	x	x	x		LQ	2	4.9	8
	7	x	x	x	x		x				x		x			x		LQ	0.5	4.9	10
																		LQ	1	4.9	10
	8	x	x	x			x				x		x	x		x		LQ	1.5	4.9	8
																		LQ	2	4.9	8
	9		x	x	x			x			x	x	x			x					

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
	10		x	x				x			x	x	x	x		x					
	11		x	x	x	x				x	x	x	x			x					
	12		x	x		x				x	x	x	x	x		x					
	13		x	x	x				x	x	x	x	x			x					
	14		x	x					x	x	x	x	x	x		x					
	15		x	x	x					x	x	x	x		x	x					
	16		x	x						x	x	x	x	x	x	x					
	17		x	x	x		x			x	x	x	x			x					
	18		x	x			x			x	x	x	x	x		x					
3	1	x	x	x	x				x		x		x			x					
	2	x	x	x					x		x		x	x		x		LQ	1	4.9	3
	3	x	x	x	x						x		x		x	x		LQ	1.5	2.4	2
	4	x	x	x							x		x	x	x	x					
	5		x	x	x			x			x	x	x			x					
	6		x	x				x			x	x	x	x		x					
	7		x	x	x				x	x	x	x	x			x					
	8		x	x					x	x	x	x	x	x		x					
	9		x	x	x					x	x	x	x		x	x					
	10		x	x						x	x	x	x	x	x	x					
4	**1**	x	x	x	x				x		x		x			x		QH	0.5	2.4	102
	2	x	x	x					x		x		x	x		x					
	3	x	x	x	x						x		x		x	x					
	4	x	x	x							x		x	x	x	x					
	5		x	x	x			x			x	x	x			x					
	6		x	x				x			x	x	x	x		x					
	7		x	x	x				x	x	x	x	x			x					
	8		x	x					x	x	x	x	x	x		x					
	9		x	x	x					x	x	x	x		x	x					
	10		x	x						x	x	x	x	x	x	x					
5	1	x	x	x	x	x					x					x					
	2	x	x	x		x					x			x		x					
	3	x	x	x	x				x		x					x					
	4	x	x	x					x		x			x		x					
	5	x	x	x	x						x				x	x					
	6	x	x	x							x			x	x	x					
	7		x	x	x						x	x				x		L	4	4.9	5
	8		x	x							x	x		x		x					

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
	9		x	x	x	x				x	x	x				x					
	10		x	x		x				x	x	x		x		x					
	11		x	x	x				x	x	x	x				x					
	12		x	x					x	x	x	x		x		x					
	13		x	x	x					x	x	x			x	x					
	14		x	x						x	x	x		x	x	x					

Table S18: Correlation and overlap analysis made with and without record set 1 models to determine the effect of models with high omission rate in the final consensus in NE tigrina models. t: value of statistic test, df: degrees of freedom. All correlation estimates had $p = 2.2 \times 10^{-16}$

Scenario	**t**	**df**	**Confidence Interval**	**Correlation**	**Overlap (Schoener's D)**
Current	17322	898992	0.9984991- 0.9985114	0.9985053	0.9867165
Holocene	17161	909632	0.9984529- 0.9984656	0.9984593	0.9864365
LGM	16528	1055186	0.9980669- 0.9980816	0.9980743	0.9844301

Table S19: Permutation importance of each variable in the selected models for each record set of NE tigrina. NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	AnnualPET	GDD0	MTW	Thermicity	GDD5	Continentality	Pseasonality	AridityIndex	CMI	PDQ	PWeQ	TopoWet	PWQ
1	Set 2 LQ 1.5	28.8	13.8	NA	NA	NA	NA	4.1	2.4	19	9	4.7	18.3	NA
	Set 3 LQ 0.5	26.4	NA	6.2	NA	NA	13.3	NA	3.2	19.3	12.4	4.2	14.9	NA
	Set 3 LQ 1	27.8	NA	11.1	NA	NA	10.7	NA	2.8	18.2	21	1.3	7.1	NA
	Set 3 LQ 1.5	29	NA	2.1	NA	NA	15.3	NA	2.6	27	7.7	2.5	13.7	NA
	Set 4 LQ 1.5	37	NA	4.5	NA	NA	NA	6.4	1.4	20.8	26.1	0.9	2.8	NA
	Set 4 LQ 2	30	NA	11.7	NA	NA	NA	4.1	1.9	19.1	15.8	1.9	15.5	NA
	Set 5 LQ 0.5	43.4	NA	NA	10.2	NA	4.4	NA	2	11.4	19.8	2.8	6.1	NA
	Set 5 LQ 1	37.4	NA	NA	16.7	NA	11.6	NA	1.6	18.9	10.1	0.4	13.3	NA
	Set 5 LQ 1.5	17.7	NA	NA	11.8	NA	10.5	NA	1.9	20.6	15.1	8.3	14	NA
	Set 5 QH 2.5	28.7	NA	NA	12.5	NA	13	NA	2	15.2	11.4	3.4	13.8	NA
	Set 6 LQ 1.5	25.5	NA	NA	6.9	NA	NA	6.8	1.9	24.5	19.8	1.7	12.9	NA
	Set 6 LQ 2	3.4	NA	NA	11.6	NA	NA	3.1	5.9	16.3	18	0.3	12.3	NA
2	Set 1 LQ 0.5	40.8	9.9	NA	NA	NA	7	NA	2.9	11.4	16.9	2	9	NA
	Set 1 LQ 1	43.4	5.6	NA	NA	NA	8	NA	6.2	14.4	15.6	1.2	5.7	NA
	Set 2 LQ 1.5	34.8	7.3	NA	NA	NA	NA	6.5	2.4	16.5	18.8	3.3	10.2	NA
	Set 2 LQ 2	34.7	4.5	NA	NA	NA	NA	7.9	2.5	22.4	15.2	0.7	11.9	NA
	Set 3 LQ 1	31	NA	13.4	NA	NA	7	NA	3.1	16.8	18.2	2.1	8.5	NA
	Set 4 LQ 1.5	23.9	NA	8.7	NA	NA	NA	8	3.6	25.7	14.5	6.6	8.9	NA
	Set 4 LQ 2	28.1	NA	5.2	NA	NA	NA	5	4.4	33.9	10.7	1.4	11.2	NA
	Set 5 LQ 1	41.9	NA	NA	6.6	NA	7.7	NA	2.7	18.7	10.7	1.4	10.3	NA
	Set 6 LQ 2	39.5	NA	NA	14.9	NA	NA	3.3	1.8	19.6	14	1	5.8	NA
	Set 7 LQ 0.5	38.8	NA	NA	NA	6	7.6	NA	2.3	21.2	15.2	1.2	7.8	NA
	Set 7 LQ 1	41.1	NA	NA	NA	8.1	11.3	NA	0.9	17.4	12.5	0.8	7.9	NA
	Set 8 LQ 1.5	37.5	NA	NA	NA	8.5	NA	9	2.7	17	14.6	1.9	9	NA
	Set 8 LQ 2	34.1	NA	NA	NA	7.5	NA	2.6	2.5	25.5	14.5	2.2	11.2	NA
3	Set 2 LQ 1.5	23	NA	12	NA	NA	NA	5	2.1	26.1	16.6	3.6	11.7	NA
	Set 3 LQ 1	28.3	NA	NA	13	NA	10.8	NA	1.3	20.4	14.1	2.2	9.8	NA
4	Set 1 QH 0.5	19.9	NA	11.5	NA	NA	18.7	NA	4.4	13.1	13.4	5.5	13.4	NA
5	Set 7 L 4	NA	NA	NA	NA	NA	0.5	NA	1.3	20.3	37.7	NA	10.4	29.6

Table S20: All variables set evaluated and selected as the best modelsfor each record set of Guianas Shield strict. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	Record Set	FC	RM	AUC_{test}	Parameters
1	x	x	x	x			x	x		x			x		x						
2	x	x	x	x			x	x			x		x		x						
3	x	x	x	x	x					x			x		x						
4	x	x	x	x	x						x		x		x						
5	x	x	x	x		x				x			x		x						
6	x	x	x	x		x					x		x		x						
7	x	x	x	x						x			x	x	x						
8	x	x	x	x							x		x	x	x						
9		x	x	x			x	x	x	x			x		x		5	HQ	0.5	0.681	63
10		x	x	x			x	x	x		x		x		x						
11		x	x	x	x				x	x			x		x						
12		x	x	x	x				x		x		x		x						
13		x	x	x		x			x	x			x		x						
14		x	x	x		x			x		x		x		x						
15		x	x	x					x	x			x	x	x						
16		x	x	x					x		x		x	x	x						
17		x	x	x				x				x	x		x						
18		x	x	x	x					x		x	x		x						
19		x	x	x	x						x	x	x		x						
20		x	x	x		x				x		x	x		x		2 4	HQ HQ	0.5 0.5	0.669 0.674	67 77
21		x	x	x		x					x	x	x		x						
22		x	x	x						x		x	x	x	x		1 3	HQ HQ	0.5 0.5	0.667 0.668	68 65
23		x	x	x							x	x	x	x	x						

Table S21: Permutation importance of each variable in the selected models for each record set of GSstrict. NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	PWeQ	GDD5	Thermicity	PDQ	AridityIndex	CMI	Continentality	Pseasonality	TopoWet	PCQ	MTC	MTW
1	Set 22 HQ 0.5	6	NA	10.3	9.4	20.7	18.6	20.2	9.2	5.6	NA	NA	NA
2	Set 20 HQ 0.5	7.1	27.3	NA	19.4	9.8	23	2.1	5.5	5.9	NA	NA	NA
3	Set 22 HQ 0.5	7.5	NA	13.1	24.9	12.9	13	13.2	8.1	7.3	NA	NA	NA
4	Set 20 HQ 0.5	13.1	9	NA	17.7	18.8	18.3	6.7	10.8	5.6	NA	NA	NA
5	Set 9 HQ 0.5	NA	NA	NA	17.9	5.3	7.2	6.4	7.8	10.2	20.8	14.3	10

Table S22: All variables set evaluated and selected as the best models for each record set of GSAmaz. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

									Variables									Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	**1**		x	x	x			x		x	x	x		x		x		L	0.5	20	8
																		L	1.5	20	7
																		Q	2	20	6
																		Q	2.5	20	6
																		QH	2.5	20	6
																		QH	3.5	20	5
	2	x	x	x	x			x			x	x		x		x		QH	4	20	4
	3		x	x	x			x			x	x	x	x		x		L	1.5	20	5
																		QH	4	20	4
2	1		x		x			x	x	x	x			x		x					
	2		x		x	x		x		x	x			x		x		Q	0.5	0	7
	3	x	x		x			x	x		x			x		x					
	4	x	x		x	x		x			x			x		x					
	5		x		x			x	x		x		x	x		x					
	6		x		x	x		x			x		x	x		x					
3	1		x	x	x					x	x			x		x		Q	0.5	20	6
																		Q	1	20	6
	2		x	x	x						x		x	x		x					
4	**1**		x	x	x			x	x	x	x	x		x		x		L	2	0	6
	2		x	x	x	x		x		x	x	x		x		x		L	2	0	6
	3	x	x	x	x			x	x		x	x		x		x					
	4	x	x	x	x	x		x			x	x		x		x					
	5		x	x	x			x	x		x	x	x	x		x					
	6		x	x	x	x		x			x	x	x	x		x					
5	**1**		x	x	x			x	x	x	x	x		x		x		Q	1.5	0	6
																		Q	2	0	5
																		Q	2.5	0	5
																		QH	2.5	0	5
	2		x	x	x	x		x		x	x	x		x		x		Q	1.5	0	6
																		Q	2	0	5
																		Q	2.5	0	5
	3	x	x	x	x			x	x		x	x		x		x		Q	4	0	3
																		QH	4	0	3
	4	x	x	x	x	x		x			x	x		x		x		Q	4	0	3
																		QH	4	0	3

Variables																		Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
	5		x	x	x			x	x		x	x	x	x		x		L	1.5	0	5
																		Q	1	0	5
																		Q	4	0	3
																		QH	4	0	3
	6		x	x	x	x		x			x	x	x	x		x		L	1	0	5
																		L	1.5	0	5
																		Q	1	0	5
																		Q	4	0	3
																		QH	4	0	3

Table S23: Correlation and overlap analysis made with and without models of record sets 1 and 3 to determine the effect of models with high omission rate in the final consensus. t: value of statistic test, df: degrees of freedom. All correlation estimates had $p = 2.2 \times 10^{-16}$

Scenario	**t**	**df**	**Confidence Interval**	**Cor**	**Overlap (Schoener's D)**
Current	3868	898992	0.9711288 – 0.9713632	0.9712462	0.9711501
Holocene	4525.9	909632	0.9784215 – 0.9785963	0.9785091	0.9718003
LGM	4868.1	1055186	0.9783727 – 0.9785354	0.9784542	0.9684902

Table S24: Permutation importance of each variable in the selected models for each record set of GSAmaz. NA indicates that these variables were not included in these variable sets.

Record Set	Variable Set	AridityIndex	TopoWet	Continentality	Pseasonality	CMI	PDQ	MTC	PWQ	PCQ	AnnualPET	PWeQ	GDD0	MTW
1	Set 1 L 0.5	33	0.7	7.4	16.6	1.5	4.4	2	10.1	24.3	NA	NA	NA	NA
	Set 1 L 1.5	444.6	5.2	17.8	4.3	4.6	2.4	2.4	7.7	11.2	NA	NA	NA	NA
	Set 1 Q 2	37.1	10.7	4.6	1	34	3.3	0.1	0	9.1	NA	NA	NA	NA
	Set 1 Q 2.5	27.9	13.9	5.6	0.1	15.6	2.6	1.5	4.5	28.3	NA	NA	NA	NA
	Set 1 QH 2.5	46.3	3.8	5.4	3.2	30.6	2.7	0.8	0.2	7.2	NA	NA	NA	NA
	Set 1 QH 3.5	52.8	2.7	7.7	4.8	7.9	9.5	4.6	0.8	9.2	NA	NA	NA	NA
	Set 2 QH 4	61.8	17.7	0	0.6	10.4	3.7	0.1	0	NA	5.7	NA	NA	NA
	Set 3 L 1.5	54	8.6	7.1	2.8	6.1	6	2.7	8.9	NA	NA	3.8	NA	NA
	Set 3 QH 4	35	9.9	1.6	0.6	33	15.8	1.2	2.4	NA	NA	0.5	NA	NA
2	Set 2 Q 0.5	37.6	1.8	31.9	5.1	NA	4.5	6.2	NA	8.4	NA	NA	4.5	NA
3	Set 1 Q 0.5	46.1	17.5	2.2	6.5	2.4	7.2	NA	NA	18.1	NA	NA	NA	NA
	Set 1 Q 1	18.3	23.2	8.3	6.9	5.4	4.1	NA	NA	33.7	NA	NA	NA	NA
4	Set 1 L 2	33.8	4.4	15.7	2.7	0.1	8.4	4.1	1.3	27.2	NA	NA	NA	2.4
	Set 2 L 2	42.5	3.8	5.8	3.6	7.8	6.5	0.2	0.9	25.6	NA	NA	3.3	NA
5	Set 1 Q 1.5	35.8	6.9	11.3	1.9	16.4	3.7	2.2	0.6	14.5	NA	NA	NA	6.7
	Set 1 Q 2	50.1	3.5	3.6	4.2	12.7	2.9	2.6	1.1	16.1	NA	NA	NA	3.2
	Set 1 Q 2.5	36.2	13.9	12.5	1.6	6.6	2.3	1.7	0	25.1	NA	NA	NA	0
	Set 1 QH 2.5	30.2	7.5	8.8	3.8	8.9	2.8	0.7	11.5	23.7	NA	NA	NA	2.1
	Set 2 Q 1.5	31.4	3.8	7.2	1.4	23.3	13	0.1	0.5	19.1	NA	NA	0	NA
	Set 2 Q 2	40.3	6.1	2	2	19.8	6	1.3	0.6	19.6	NA	NA	2.4	NA
	Set 2 Q 2.5	45.7	0.8	1.3	2.2	29.7	6.1	0.1	0.3	12.4	NA	NA	1.3	NA
	Set 3 Q 4	70.7	3.8	4.8	0.6	1	11.7	1.2	0	NA	3.4	NA	NA	2.8
	Set 3 QH 4	58.5	12.3	14.6	1.3	1.3	9.8	0	1.6	NA	0.5	NA	NA	0
	Set 4 Q 4	40	22.2	9.6	2.4	5	13.5	0	0	NA	2	NA	5.4	NA
	Set 4 QH 4	58.6	14.7	4.8	1.9	6.4	8.1	0	0	NA	1.8	NA	3.7	NA
	Set 5 L 1.5	35.7	15.9	3.3	1	6.2	13.1	5.1	2.9	NA	NA	6.2	NA	10.8
	Set 5 Q 1	32.3	21.7	18.7	5.7	7.3	6.2	2.6	1.7	NA	NA	0.7	NA	3.1
	Set 5 Q 4	54.7	16.7	3	0.2	9.6	6	0	9.1	NA	NA	0.3	NA	0.4
	Set 5 QH 4	57.1	10.2	1.3	12.1	2.6	5.4	0.3	2.3	NA	NA	7.2	NA	1.6
	Set 6 L 1	39.9	1.3	5.1	5.5	3.3	10	0.9	11.1	NA	NA	7.3	3.9	NA
	Set 6 L 1.5	59.2	4.7	4.2	5	5.1	11.2	3	1.7	NA	NA	2.4	3.3	NA
	Set 6 Q 1	20.1	20.3	5.1	6.6	14.8	10.9	4.4	3.6	NA	NA	7	7.1	NA
	Set 6 Q 4	50.5	16.3	6.8	4.3	5.3	11.2	0.2	2.2	NA	NA	2.8	0	NA
	Set 6 QH 4	45.3	8.3	2.7	9	13	12.4	0	1.8	NA	NA	0.6	6.9	NA

Table S25: All variables set evaluated and selected as the best models for each record set of Amaz. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	AUC_{test}	Parameters
1	1				x					x					x						
	2				x	x				x								LQ	0.5	0.725	3
	3				x								x		x						
	4				x	x							x								
2	**1**				x					x				x	x			Q	2	0.694	2
	2				x	x				x				x							
	3				x								x	x	x						
	4				x	x							x	x							
	5	x			x								x	x	x						
	6	x			x	x							x	x							
3	1				x					x				x	x						
	2				x	x				x				x							
	3				x								x	x	x						
	4				x	x							x	x							
	5	x			x								x	x	x			Q	1.5	0.698	1
	6	x			x	x							x	x							
4	**1**				x					x				x	x			L	1	0.712	3
	2				x	x				x				x							
	3				x								x	x	x						
	4				x	x							x	x							
	5	x			x								x	x	x						
	6	x			x	x							x	x							
5	**1**				x					x					x			LQ	0.5	0.722	3
	2				x	x				x											
	3				x								x		x						
	4				x	x							x								

Table S26: Permutation importance of each variable in the selected models for each record set of Amaz. NA indicates that these variables were not included in these variable sets.

Record Set	Variable set	PCQ	GDD0	Continentality	Thermicity	Pseasonality	AnnualPET
1	Set 2 LQ 0.5	52	17.7	30.4	NA	NA	NA
2	Set 1 Q 2	24	NA	13.1	61.6	1.3	NA
3	Set 5 Q 1.5	NA	NA	25.6	70.1	3.3	0.9
4	Set 1 L 1	22.5	NA	16.5	51	10	NA
5	Set 1 LQ 0.5	19.3	NA	27.7	53	NA	NA

Table S27: All variables set evaluated and selected as the best models for each record set of NE tigrine + Amaz. The numbers in bold font indicate the variable set (or sets) corresponding to the selected models.

		Variables																Selected Models			
Record Set	Variable set	AnnualPET	AridityIndex	CMI	Continentality	GDD0	GDD5	MTC	MTW	PCQ	PDQ	PWQ	PWeQ	Pseasonality	Thermicity	TopoWet	tri	FC	RM	Omission (%)	Parameters
1	1	x	x	x	x	x				x	x		x			x					
	2	x	x	x	x				x	x	x		x			x					
	3	x	x	x	x					x	x		x		x	x					
	4	x	x	x		x				x	x		x	x		x					
	5	x	x	x					x	x	x		x	x		x		L	1	2.2	7
																		L	1.5	2.2	7
	6	x	x	x						x	x		x	x	x	x		L	0.5	4.4	7
	7		x	x	x	x		x			x	x	x			x					
	8		x	x	x			x	x		x	x	x			x					
	9		x	x	x			x			x	x	x		x	x					
	10		x	x		x		x			x	x	x	x		x					
	11		x	x				x	x		x	x	x	x		x					
	12		x	x				x			x	x	x	x	x	x					
2	1	x	x	x	x	x				x	x		x			x					
	2	x	x	x	x				x	x	x		x			x					
	3	x	x	x	x					x	x		x		x	x		QH	3.5	4.4	13
	4	x	x	x	x		x			x	x		x			x					
	5	x	x	x		x				x	x		x	x		x					
	6	x	x	x					x	x	x		x	x		x					
	7	x	x	x						x	x		x	x	x	x					
	8	x	x	x			x			x	x		x	x		x					
	9		x	x	x	x		x			x	x	x			x					
	10		x	x	x			x	x		x	x	x			x					
	11		x	x	x			x			x	x	x		x	x					
	12		x	x	x		x	x			x	x	x			x					
	13		x	x		x		x			x	x	x	x		x					
	14		x	x				x	x		x	x	x	x		x					
	15		x	x				x			x	x	x	x	x	x					
	16		x	x			x	x			x	x	x	x		x					
3	1	x	x	x	x				x	x	x		x			x					
	2	x	x	x	x					x	x		x		x	x					
	3	x	x	x					x	x	x		x	x		x					
	4	x	x	x						x	x		x	x	x	x		L	1.5	4.4	8
																		L	2	4.4	8

																	L L	2.5 3	4.4 4.4	8 8
	5		x	x	x			x	x		x		x			x				
	6		x	x	x			x			x		x		x	x				
	7		x	x				x	x		x		x	x		x				
	8		x	x				x			x		x	x	x	x				
4	1	x	x	x	x	x				x	x		x			x				
	2	x	x	x	x				x	x	x		x			x				
	3	x	x	x	x					x	x		x		x	x				
	4	x	x	x		x				x	x		x	x		x	L L	1 1.5	2.2 2.2	7 7
	5	x	x	x					x	x	x		x	x		x	L L	1.5 2	2.2 2.2	7 7
	6	x	x	x						x	x		x	x	x	x	L L	0.5 1	4.4 2.2	8 7
	7		x	x	x	x		x			x	x	x			x				
	8		x	x	x			x	x		x	x	x			x				
	9		x	x	x			x			x	x	x		x	x				
	10		x	x		x		x			x	x	x	x		x				
	11		x	x				x	x		x	x	x	x		x				
	12		x	x				x			x	x	x	x	x	x				
5	1	x	x	x	x				x	x	x					x				
	2	x	x	x	x					x	x				x	x				
	3	x	x	x	x	x				x	x					x				
	4	x	x	x					x	x	x			x		x				
	5	x	x	x						x	x			x	x	x	L L	0.5 1	4.3 4.3	8 8
	6	x	x	x		x				x	x			x		x	L	0.5	4.3	8
	7		x	x	x			x	x		x					x				
	8		x	x	x			x			x				x	x				
	9		x	x	x	x		x			x					x				
	10		x	x				x	x		x			x		x				
	11		x	x				x			x			x	x	x				
	12		x	x		x		x			x			x		x				

Table S28: Permutation importance of each variable in the selected models for each record set NE tigrina +Amaz. NA indicates that these variables were not included in these variable sets.

Record Set	Varible Set	AnnualPET	PCQ	Pseasonality	MTW	Thermicity	AridityIndex	CMI	PDQ	PWeQ	TopoWet	Continentality	GDD0
1	Set 5 L 1	2.1	29.9	19.2	5.4	NA	0.5	23.6	13	1.5	4.7	NA	NA
	Set 5 L 1.5	3.6	26.9	20.4	5	NA	1.7	20.6	12.8	0.7	8.1	NA	NA
	Set 6 L 0.5	2.6	33	13.3	NA	7.8	1.4	27.5	8	1	5.5	NA	NA
2	Set 3 QH 3.5	12.8	14.4	NA	NA	13.8	4.5	32.5	5.2	4.4	6	6.2	NA
3	Set 4 L 1.5	0.8	35	17.7	NA	9.4	1.3	21.9	9.9	0.9	3.1	NA	NA
	Set 4 L 2	5.4	28.5	17	NA	9.3	1.4	22.7	8.7	0.9	6.1	NA	NA
	Set 4 L 2.5	2.6	26.3	19.5	NA	12.2	0.7	26.3	9.1	0	3.4	NA	NA
	Set 4 L 3	5	23.9	11.7	NA	13.1	2.6	30.3	5.9	1.3	6.2	NA	NA
4	Set 4 L 1	3.2	33.2	17.3	NA	NA	0.7	21	14.4	0.7	3.6	NA	5.9
	Set 4 L 1.5	3.5	27.6	20	NA	NA	1	19.7	16	0.8	4.7	NA	8.6
	Set 5 L 1.5	2.6	32.2	19.1	5.5	NA	1.7	19.2	15	0.6	4.1	NA	NA
	Set 5 L 2	3.8	28.6	13.4	8.5	NA	3.5	23.4	9.8	3.2	6	NA	NA
	Set 6 L 0.5	2.5	31.6	21.2	NA	8.1	0.6	22.3	9.4	2.3	2	NA	NA
	Set 6 L 1	3	28	15.3	NA	4.7	0.7	25.8	16.1	0.4	6	NA	NA
5	Set 5 L 0.5	2.6	NA	18.7	NA	9.6	0.3	26.9	8.6	NA	3.4	NA	NA
	Set 5 L 1	3.2	NA	18.8	NA	6.7	2.5	22.9	9.3	NA	5.5	NA	NA
	Set 6 L 0.5	5.7	NA	18.5	NA	NA	2.1	20.4	10.1	NA	3.6	NA	5.2

Table S29: Correlation and overlap analysis between the groups included in the morphological proposal. t: value of statistic test. All correlation estimates had p- = 2.2x10^{-16} and df: degrees of freedom = 898992

Comparison	**t**	**Confidence interval**	**Correlation**	**Overlap (Shoener's D)**
L. tigrinus (m) x NE tigrina	130.72	0.1345482 – 0.1386053	0.1365773	0.5492314
NE tigrina x *L. guttulus*	206.98	0.2112997 – 0.215246	0.2132737	0.552702
L. tigrinus (m) x *L. guttulus*	704.8	0.5952413 – 0.5979042	0.5965744	0.6954478

Table S30: Correlation and overlap analysis between taxonomic units identified within *L. tigrinus* (m) based on molecular data. t: value of statistic test. All correlation estimates had p = 2.2×10^{-16} and df: degrees of freedom = 898992

Comparison	t	Confidence inteverval	Correlation	Overlap (Schoerner's D)
C. Am. tigrina x N. Andean tigrina	995.75	0.7232182 – 0.7251842	0.7242027	0.522278
C. Am. tigrina x S. Andean tigrina	511.84	0.4734295 – 0.4766308	0.4750317	0.4696297
N. Andean x S. Andean tigrina	495.79	0.4617476 – 0.4649941	0.4633724	0.5474774

Table S31: Correlation and overlap analysis between taxonomic units identified within *L. tigrinus* (m) based on molecular data and NE tigrina. t: value of statistic test. All correlation estimates had p = 2.2×10^{-16} and df: degrees of freedom = 898992

Comparison	t	Confidence interval	Correlation	Overlap (Shoener's D)
C. Am. Tigrina x NE tigrina	329.26	0.3261987 – 0.3298881	0.3280446	0.3623553
N. Andean tigrina x NE tigrina	152.78	0.1570652 – 0.1610949	0.1590807	0.6022076
S. Andean tigrina x NE tigrina	90.132	0.09258512 – 0.09668237	0.09463414	0.4746387

Table S32: Correlation and overlap analysis between taxonomic units identified within *L. tigrinus* (m) based on molecular data and *L. guttulus*. t: value of statistic test. All correlation estimates had p = 2.2×10^{-16} and df: degrees of freedom = 898992

Comparison	t	Confidence interval	Correlation	Overlap (Schoener's D)
C. Am. Tigrina x *L. guttulus*	1319.6	0.8114078 – 0.8128154	0.8121128	0.6039331
N. Andean tigrina x *L. guttulus*	1368.4	0.8212968 – 0.8226368	0.8219684	0.7692888
S. Andean tigrina x *L. guttulus*	569.5	0.5133805 – 0.5164187	0.5149012	0.6228729

Table S33: Correlation and overlap analysis between GSAmaz and the other taxonomic units proposed within *L. tigrinus* complex. t: value of statistic test. All correlation estimates had p = 2.2x10^{-16} and df: degrees of freedom = 898992

Comparison	**t**	**Confidence Interval**	**Correlation**	**Overlap (Schoener's D)**
GSAmaz x NE tigrina	305.75	0.3050292 – 0.3087741	0.3069028	0.73859
GSAmaz x C. Am. tigrina	-266.85	-0.2728348 – -0.2690039	-0.2709204	0.2484195
GSAmaz x N. Andean tigrina	-370.92	-0.3661065 – -0.362521	-0.3643151	0.561466
GSAmaz x S. Andean tigrina	-323.63	-0.3248796 – -0.3211767	-0.3230294	0.4383456

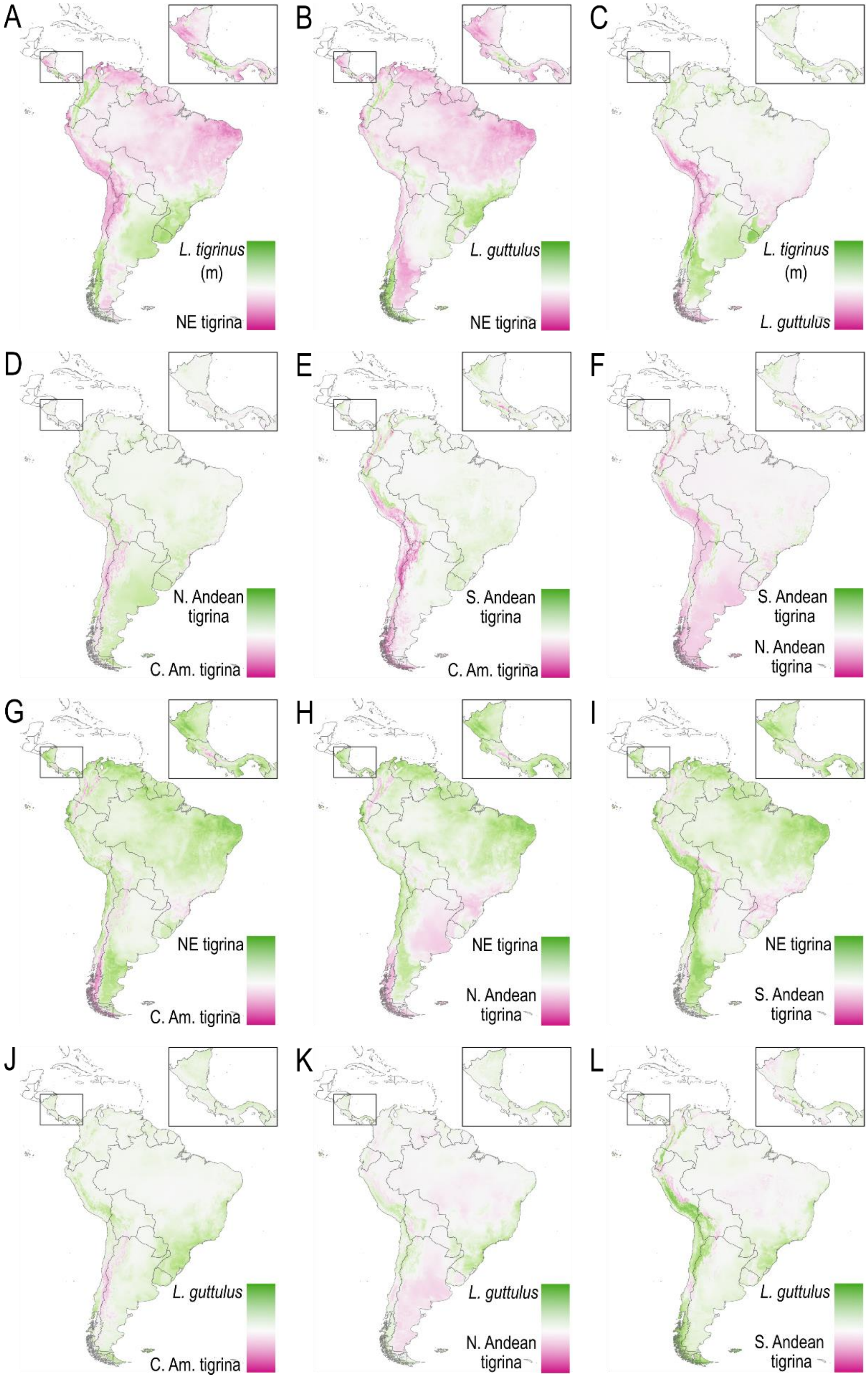
Table S34: Correlation and overlap analysis between Amazonian biome and the other taxonomic units proposed within *L. tigrinus* complex t: value of statistic test. All correlation estimates had p = 2.2x10^{-16} and df: degrees of freedom = 898992

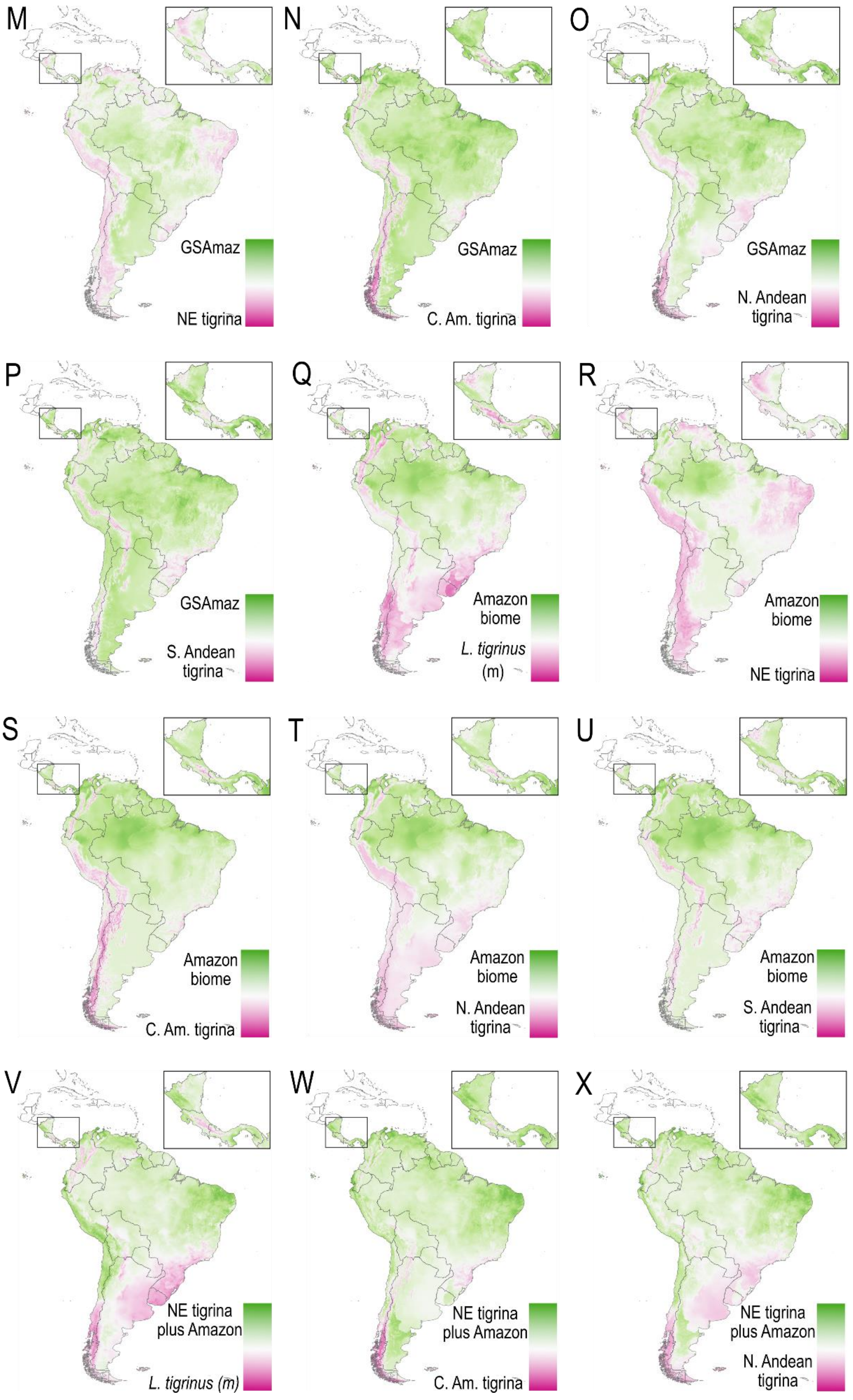
Comparison	**t**	**Confidence Interval**	**Correlation**	**Overlap (Schoener's D)**
Amaz x *L. tigrinus* (m)	-412.06	-0.4003141 – -0.3968367	-0.3985768	0.4521104
Amaz x NE tigrina	-86.375	-0.09277217 – -0.08867192	-0.09072243	0.6641277
Amaz x C. Am. tigrina	-301.28	-0.3047112 – -0.3009561	-0.3028349	0.2102924
Amaz x N. Andean tigrina	-595.2	-0.5331518 – -0.5301861	-0.5316706	0.4641241
Amaz x S. Andean tigrina	-323.5	-0.3247587 – -0.3210555	-0.3229083	0.3997591

Table S35: Correlation and overlap analysis between NE tigrine + Amaz and the other taxonomic units proposed within *L. tigrinus* complex. t: value of statistic test. All correlation estimates had p = 2.2×10^{-16} and df: degrees of freedom = 898992

Comparison	**t**	**Confidence Interval**	**Correlation**	**Overlap (Schoener's D)**
NE tigrina + Amaz x *L. tigrinus* (m)	41.4	0.04155928 – 0.04568569	0.04362267	0.528711
NE tigrina + Amaz x C. Am. tigrina	270.76	0.2726791 – 0.275017	0.2745915	0.338997
NE tigrina + Amaz x N. Andean tigrina	32.559	0.03225443 – 0.03638384	0.03431928	0.5739896
NE tigrina + Amaz x S. Andean tigrina	62.658	0.06388244 – 0.06799874	0.06594087	0.4600662

Supplementary Figures




M
GSAmaz
NE tigrina
N
GSAmaz
C. Am. tigrina
O
GSAmaz
N. Andean tigrina
P
GSAmaz
S. Andean tigrina
Q
Amazon biome
L. tigrinus (m)
R
Amazon biome
NE tigrina
S
Amazon biome
C. Am. tigrina
T
Amazon biome
N. Andean tigrina
U
Amazon biome
S. Andean tigrina
V
NE tigrina plus Amazon
L. tigrinus (m)
W
NE tigrina plus Amazon
C. Am. tigrina
X
NE tigrina plus Amazon
N. Andean tigrina

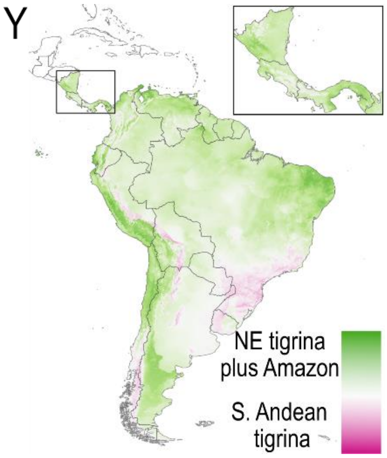


Figure S1: Geographical divergence between predictions made for taxonomic units included in the morphological proposal. The maps show the models subtraction. Darker colors indicate areas where one of the taxonomic groups have higher occurrence probability than the other, whereas lighter colors indicate similar suitability values between the compared groups. **A.** is the comparison between *L. tigrinus* (m) and NE tigrina, **B.** between *L. guttulus* and NE tigrina, and **C.** between *L. tigrinus* (m) and *L. guttulus*, **D.** between C. Am. tigrina and N. Andean tigrina, **E.** between C. Am. tigrina and S. Andean tigrina, **F.** between N. Andean tigrina and S. Andean tigrina **G.** between NE tigrina and C. Am. tigrina, **H.** between NE tigrina and N. Andean tigrina, **I.** between NE tigrina and S. Andean tigrina, **J.** between *L. guttulus* and C. Am. tigrina, **K.** between *L. guttulus* and N. Andean tigrina, **L.** between *L. guttulus* and S. Andean tigrina, **M.** between GSAmaz and NE tigrina, **N.** between GSAmaz and C. Am. tigrina, **O.** between GSAmaz and N. Andean tigrina, **P.** between GSAmaz and S. Andean tigrina, **Q.** between Amaz and *L. tigrinus* (m), **R.** between Amaz and NE tigrina, **S.** between Amaz and C. Am. tigrina, **T.** between Amaz and N. Andean tigrina, **U.** between Amaz and S. Andean tigrina, **V.** between NE tigrina + Amaz and *L. tigrinus* (m), **W.** between NE tigrina + Amaz and C. Am. tigrina, **X.** between NE tigrina + Amaz and N. Andean tigrina, **Y.** between NE tigrina + Amaz and S. Andean tigrina,

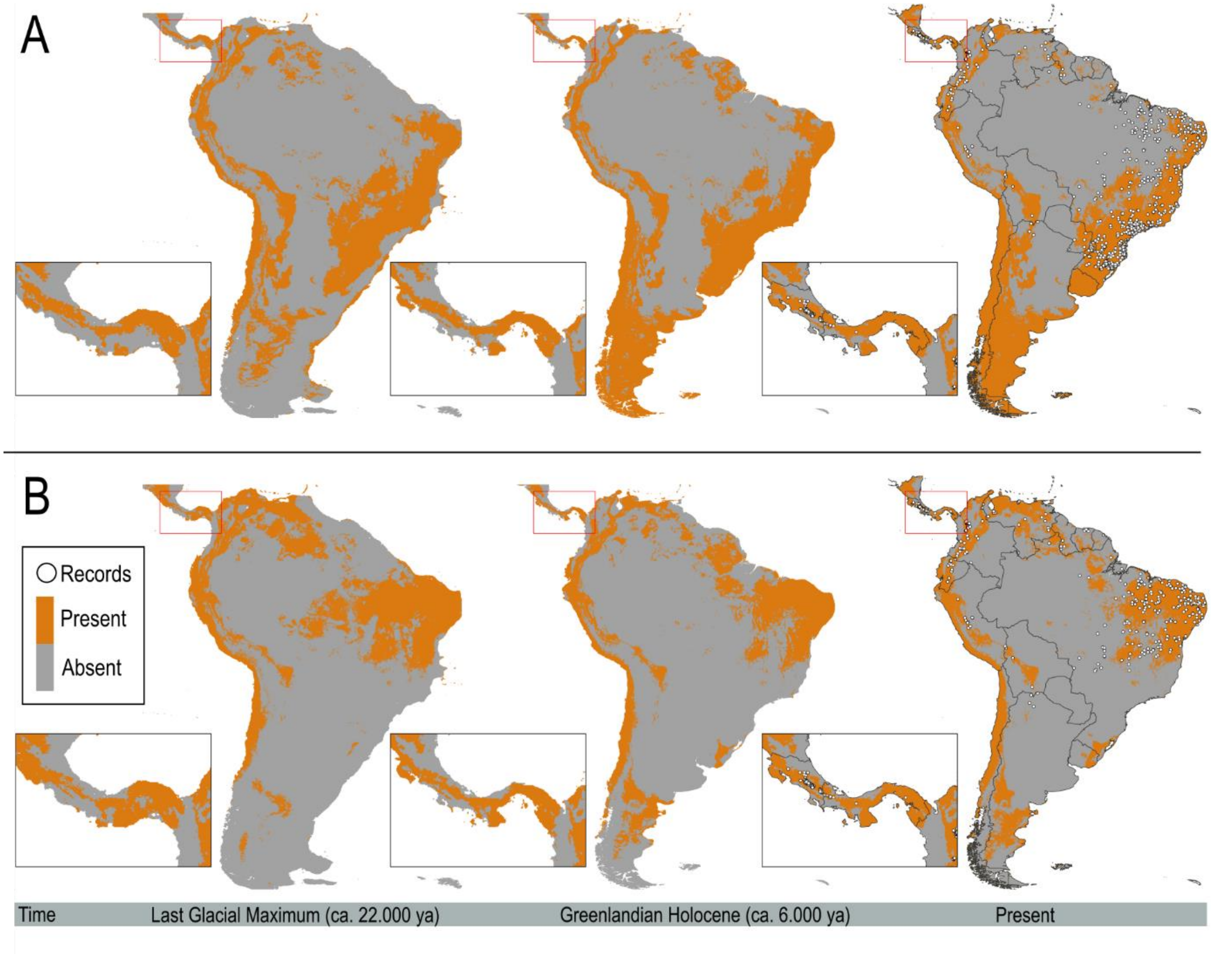


Figure S2: Potential distribution for the *L. tigrinus* complex **A.** *sensu* Jonhson et al (1999) and **B.** *sensu* Kitchener et al. (2017) based on Maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: LGM, mid-Holocene, and Present. Presence records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

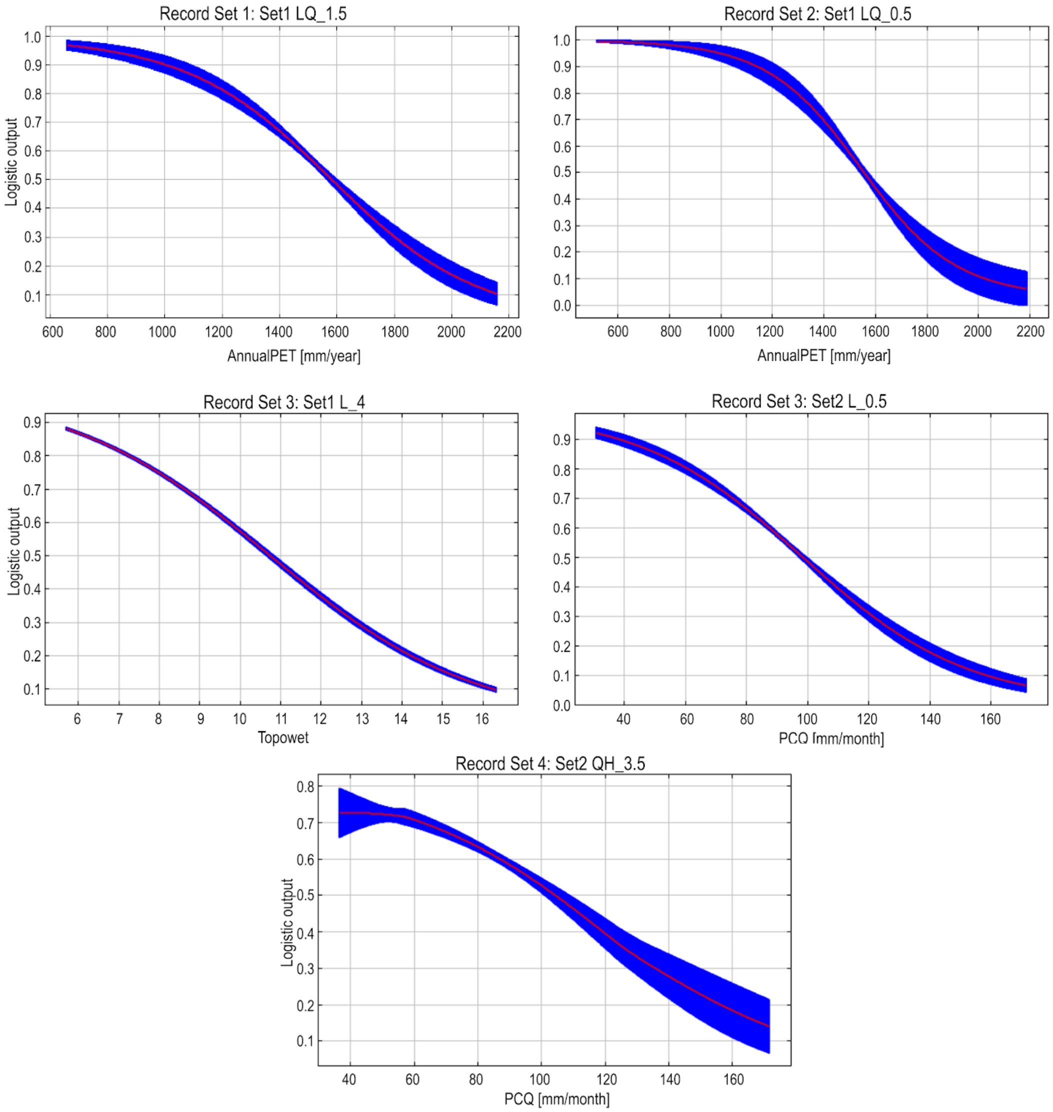


Figure S3: Response curves of variables with highest permutation importance in the selected models for each record set of Leopardus tigrinus sensu Johnson et al. (1999). The curves show the mean response of the 10 replicate Maxent runs (red) and the mean +/- standard deviation (blue).

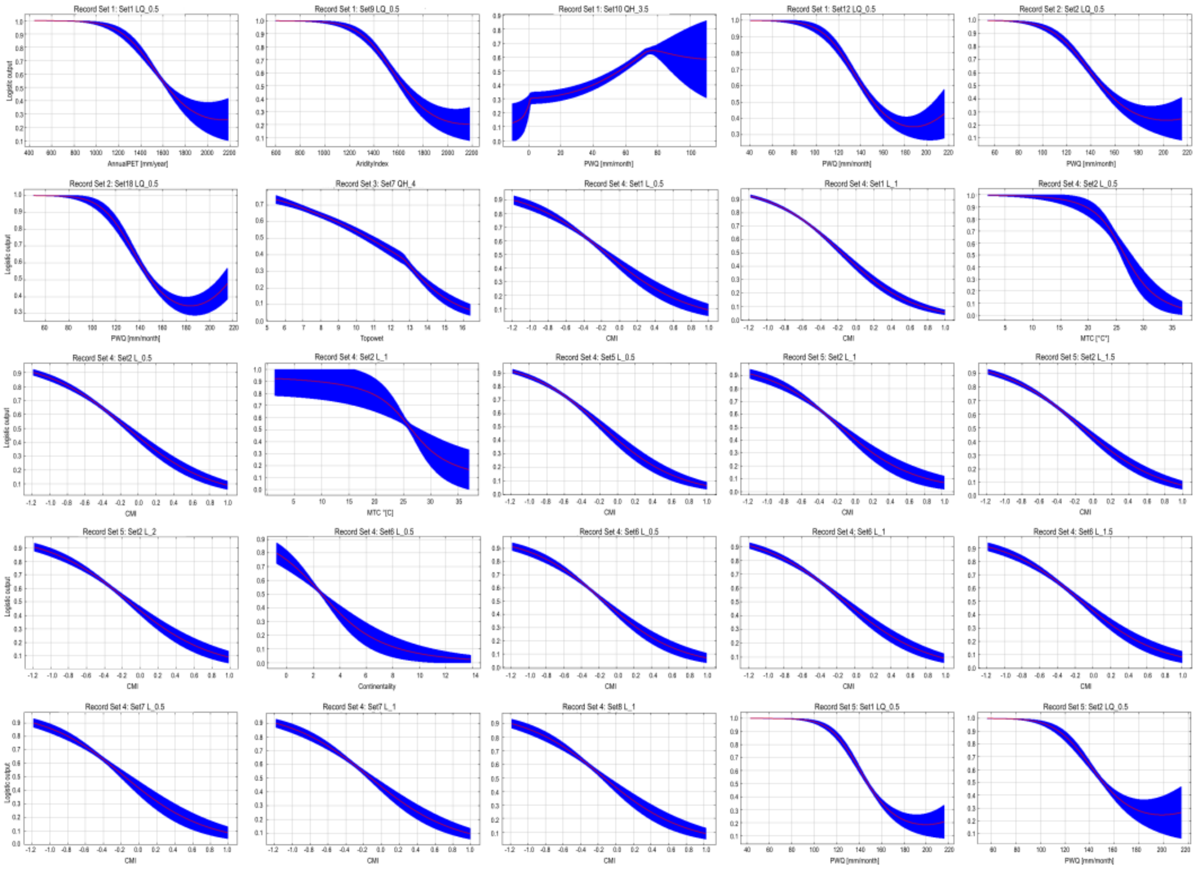


Figure S4: Response curves of variables with highest permutation importance in the selected models for each record set of *Leopardus tigrinus* sensu Kitchenet et al. (2017).

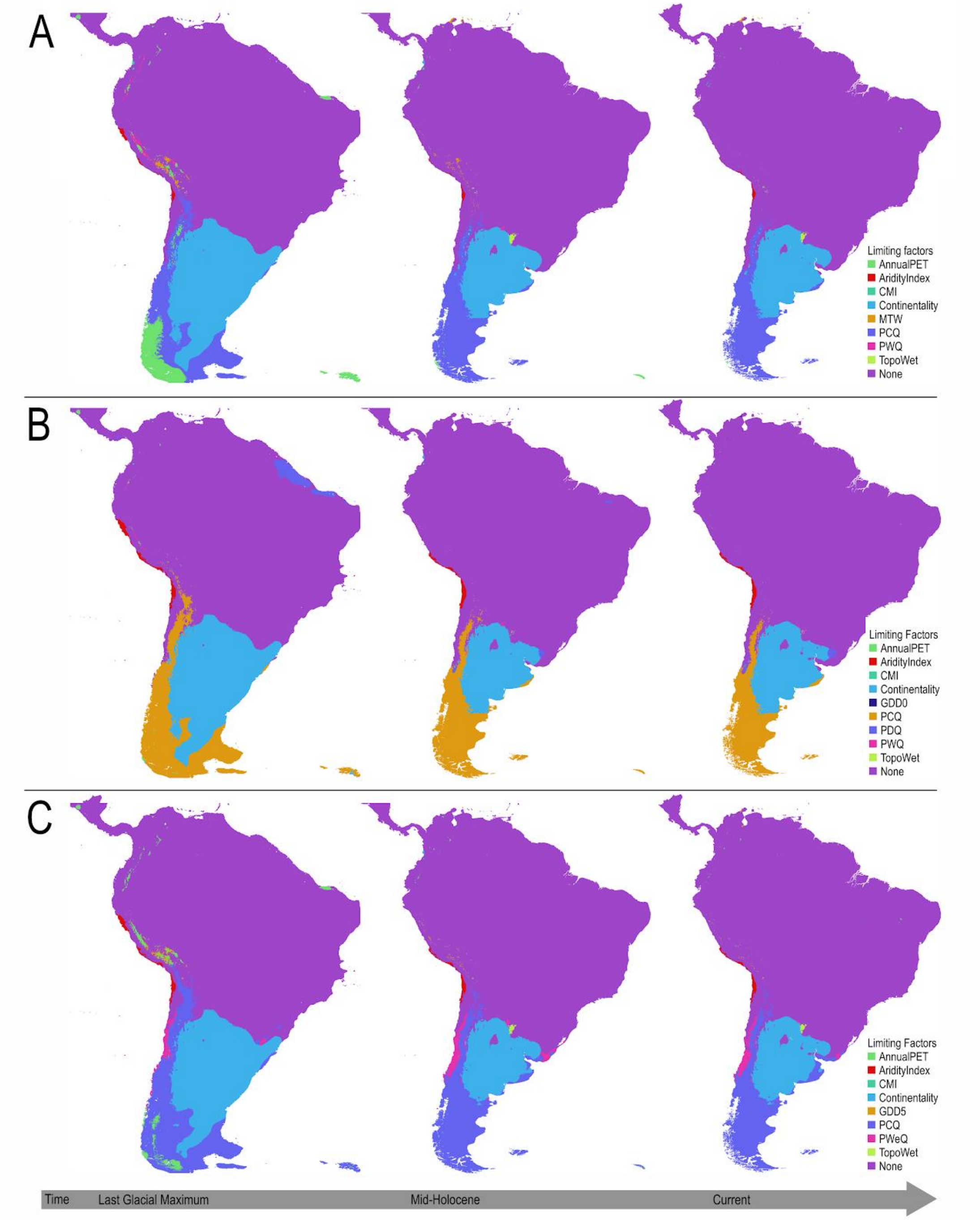


Figure S5: Extrapolation risk of variables for *L. tigrinus* complex sensu Johnson et al. (1999) models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set1 LQ_1.5 constructed with the record set 1. **B.** Extrapolation risk map for the model Set2 LQ_0.5 constructed with the record set 2, and **C.** Extrapolation risk map for the model Set2H_3.5 constructed with the record set 4.

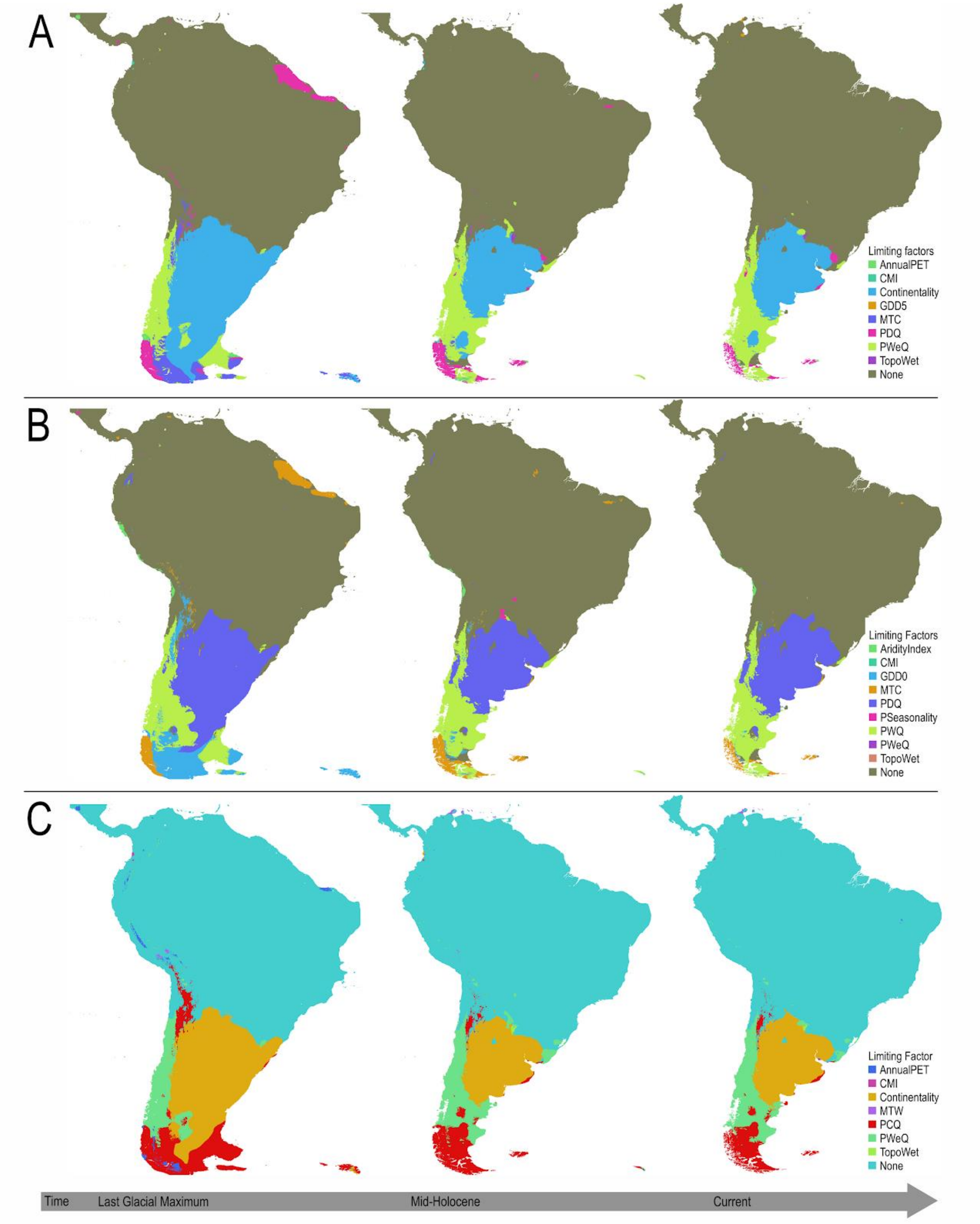


Figure S6: Extrapolation risk of the *L. tigrinus* complex *sensu* Kitchener et al. (2007). Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set1 LQ_0.5, **B.** Extrapolation risk map for the model Set12 LQ_0.5 constructed with the record set 1, and **C.** Extrapolation risk map for the model Set7 LQ_0.5 constructed with the record set 4.

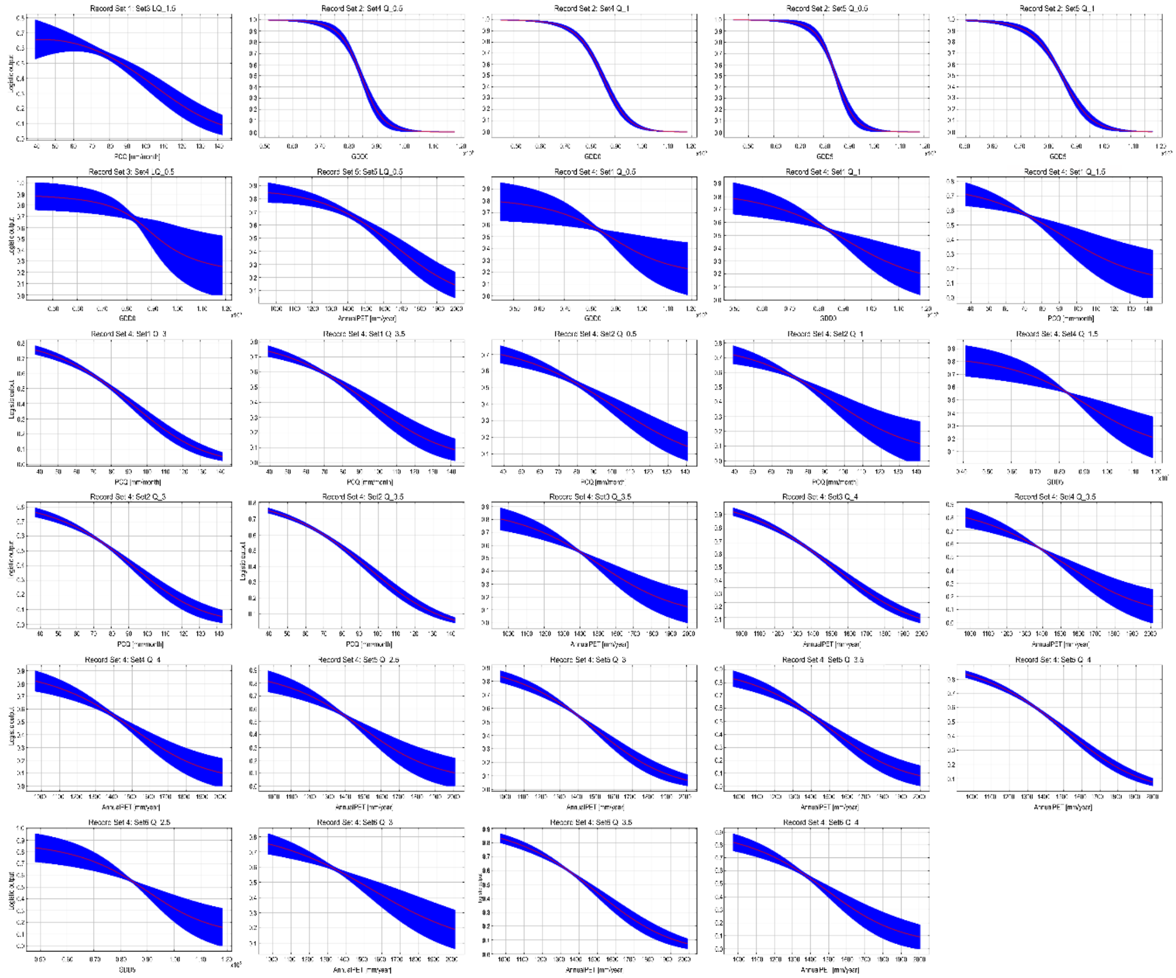


Figure S7: Response curves of variables with highest permutation importance in the selected models for each record set of *Leopardus guttulus*.

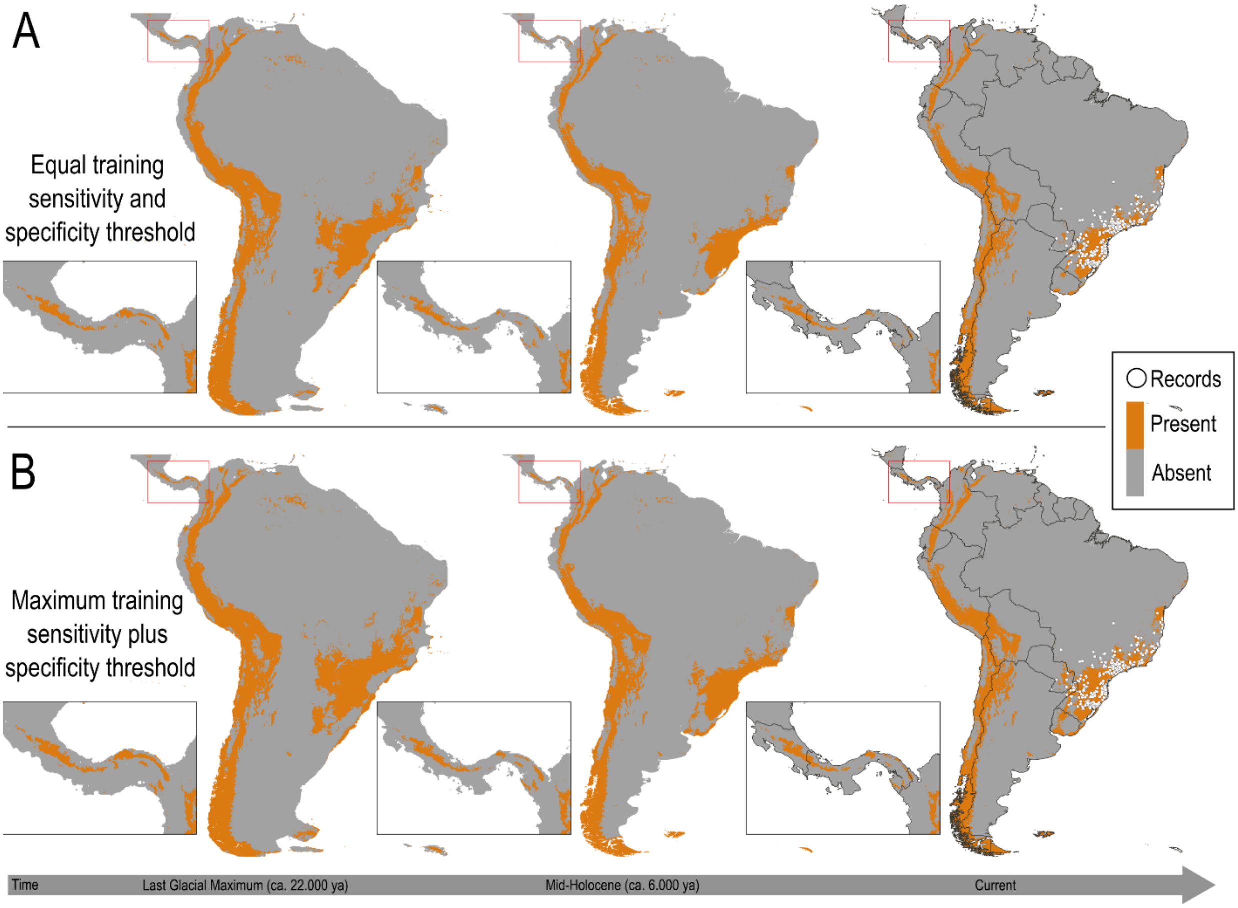


Figure S8: Potential distribution of *L. guttulus* based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

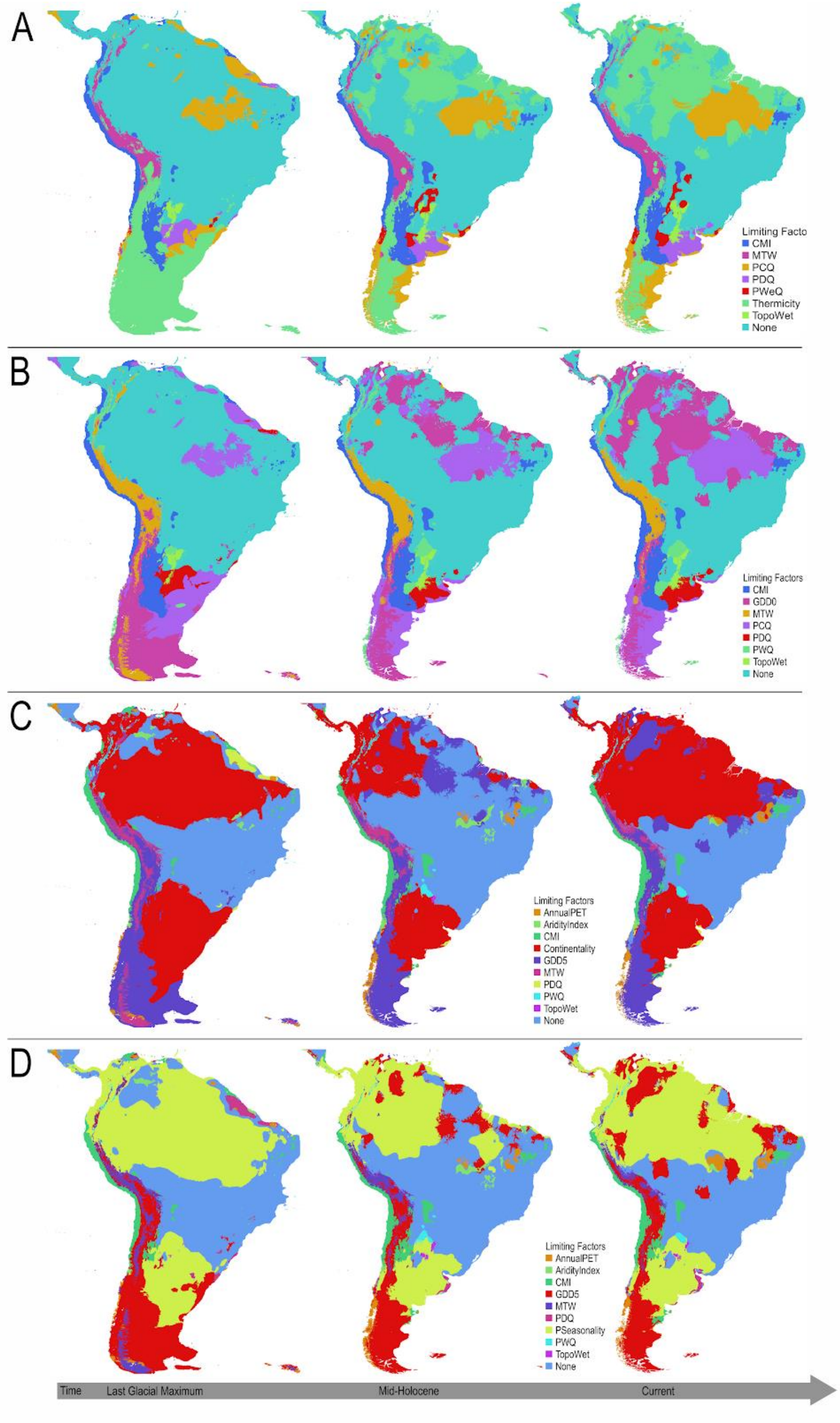

A
Limiting Facto
CMI
MTW
PCQ
PDQ
PWeQ
Thermicity
TopoWet
None
B
Limiting Factors
CMI
GDD0
MTW
PCQ
PDQ
PWQ
TopoWet
None
C
Limiting Factors
AnnualPET
AridityIndex
CMI
Continentality
GDD5
MTW
PDQ
PWQ
TopoWet
None
D
Limiting Factors
AnnualPET
AridityIndex
CMI
GDD5
MTW
PDQ
PSeasonality
PWQ
TopoWet
None
Time
Last Glacial Maximum
Mid-Holocene
Current

Figure S9: Extrapolation risk for *L. guttulus* models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set3 LQ_1.5 constructed with the record set 1, **B.** Extrapolation risk map for the model Set1 Q_0.5 **C.** Extrapolation risk map for the model Set4 Q_3.5, and **D.** Extrapolation risk map for the model Set6 Q_3 constructed with the record set 4.

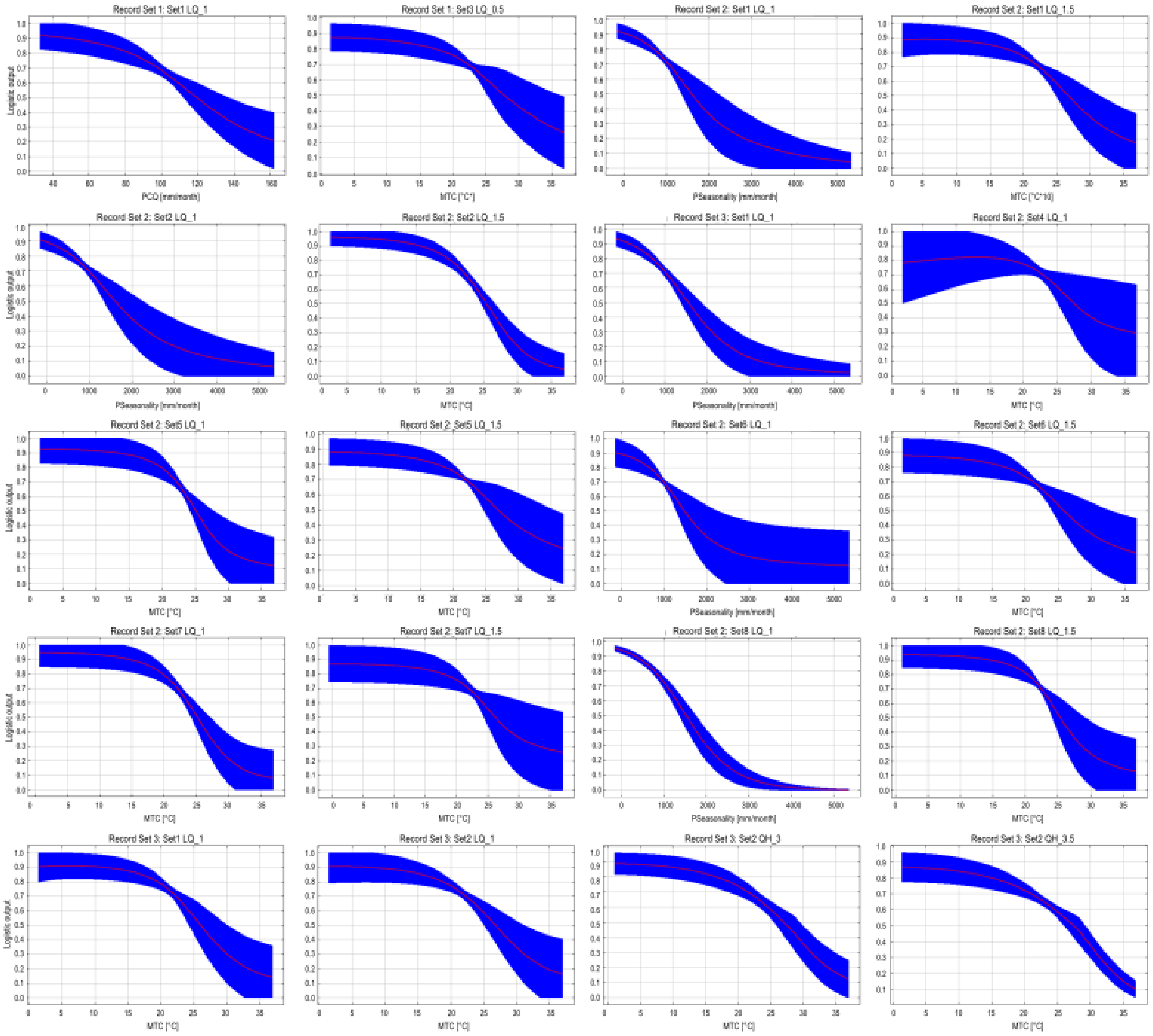


Figure S10: Response curves of variables with highest permutation importance in the selected models for each record set of *L. tigrinus* (m).

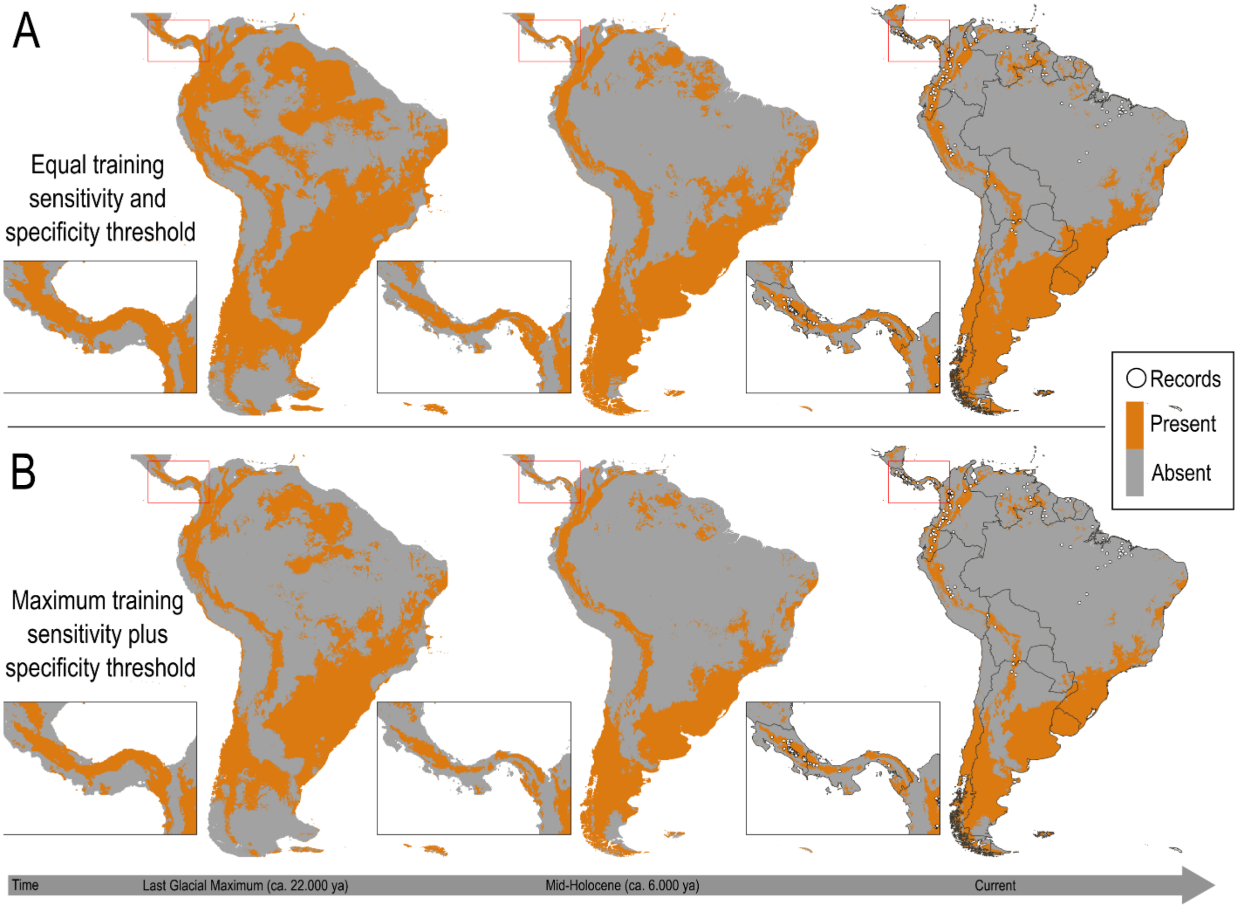


Figure S11: Potential distribution of *L. tigrinus* (m) based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

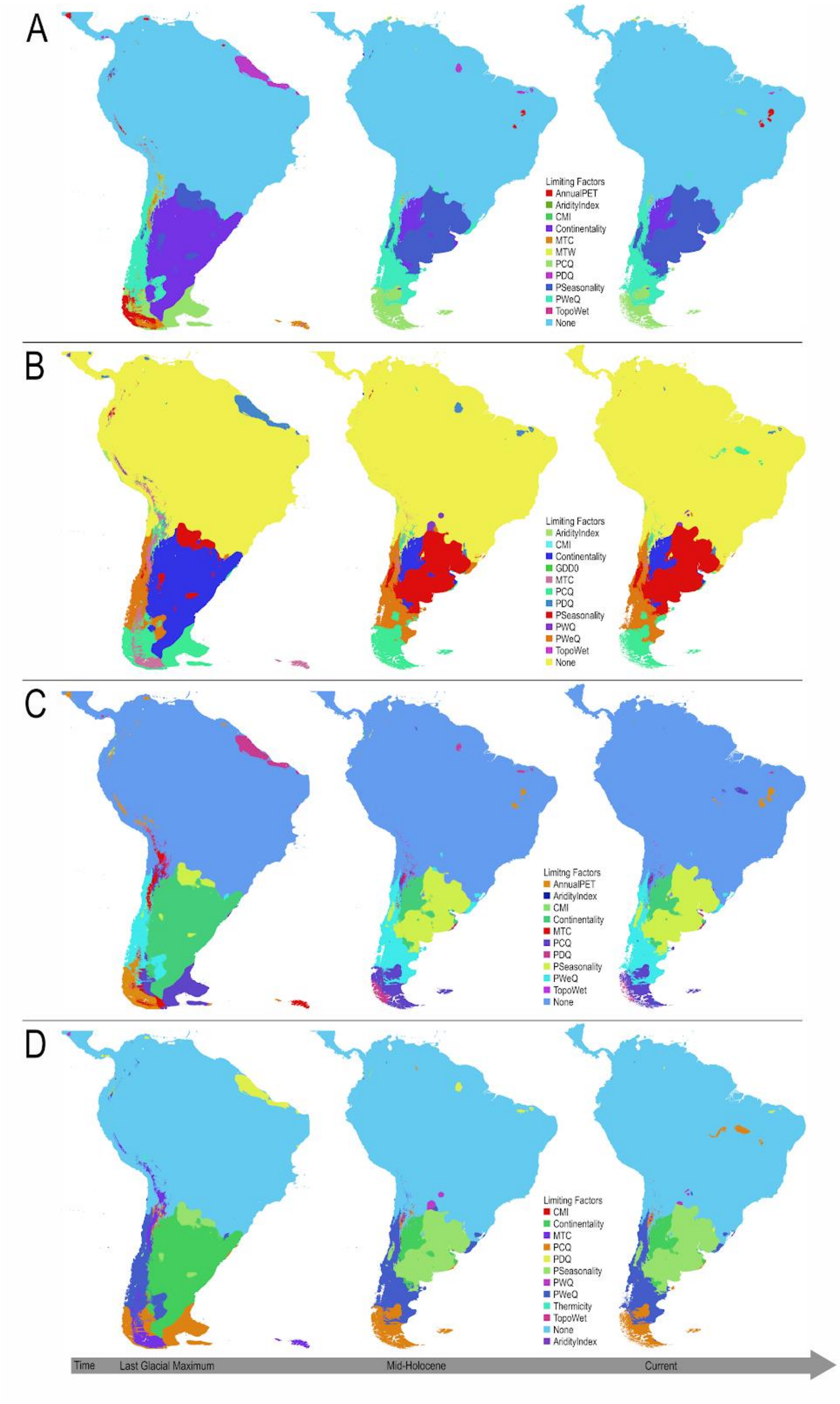

A
Limiting Factors
AnnualPET
AridityIndex
CMI
Continentality
MTC
MTW
PCQ
PDQ
PSeasonality
PWeQ
TopoWet
None
B
Limiting Factors
AridityIndex
CMI
Continentality
GDD0
MTC
PCQ
PDQ
PSeasonality
PWQ
PWeQ
TopoWet
None
C
Limitng Factors
AnnualPET
AridityIndex
CMI
Continentality
MTC
PCQ
PDQ
PSeasonality
PWeQ
TopoWet
None
D
Limiting Factors
CMI
Continentality
MTC
PCQ
PDQ
PSeasonality
PWQ
PWeQ
Thermicity
TopoWet
None
AridityIndex
Time
Last Glacial Maximum
Mid-Holocene
Current

Figure S12: Extrapolation risk for *L. tigrinus* (m) models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set1 LQ_1, **B.** Extrapolation risk map for the model Set4 LQ_1 constructed with the **C.** Extrapolation risk map for the model Set5 LQ_1, and **D.** Extrapolation risk map for the model Set8 LQ_1 constructed with the record set 2.

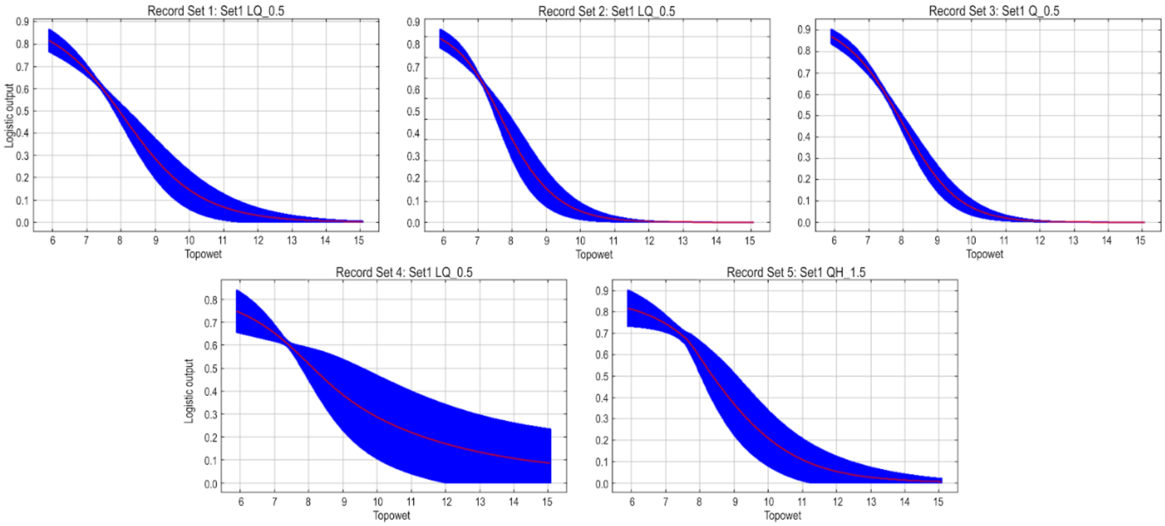


Figure S13: Response curves of variables with highest permutation importance in the selected models for each record set of C. Am. tigrina. The curves show the mean response of the 10 replicate Maxent runs (red) and the mean +/- one standard deviation (blue).

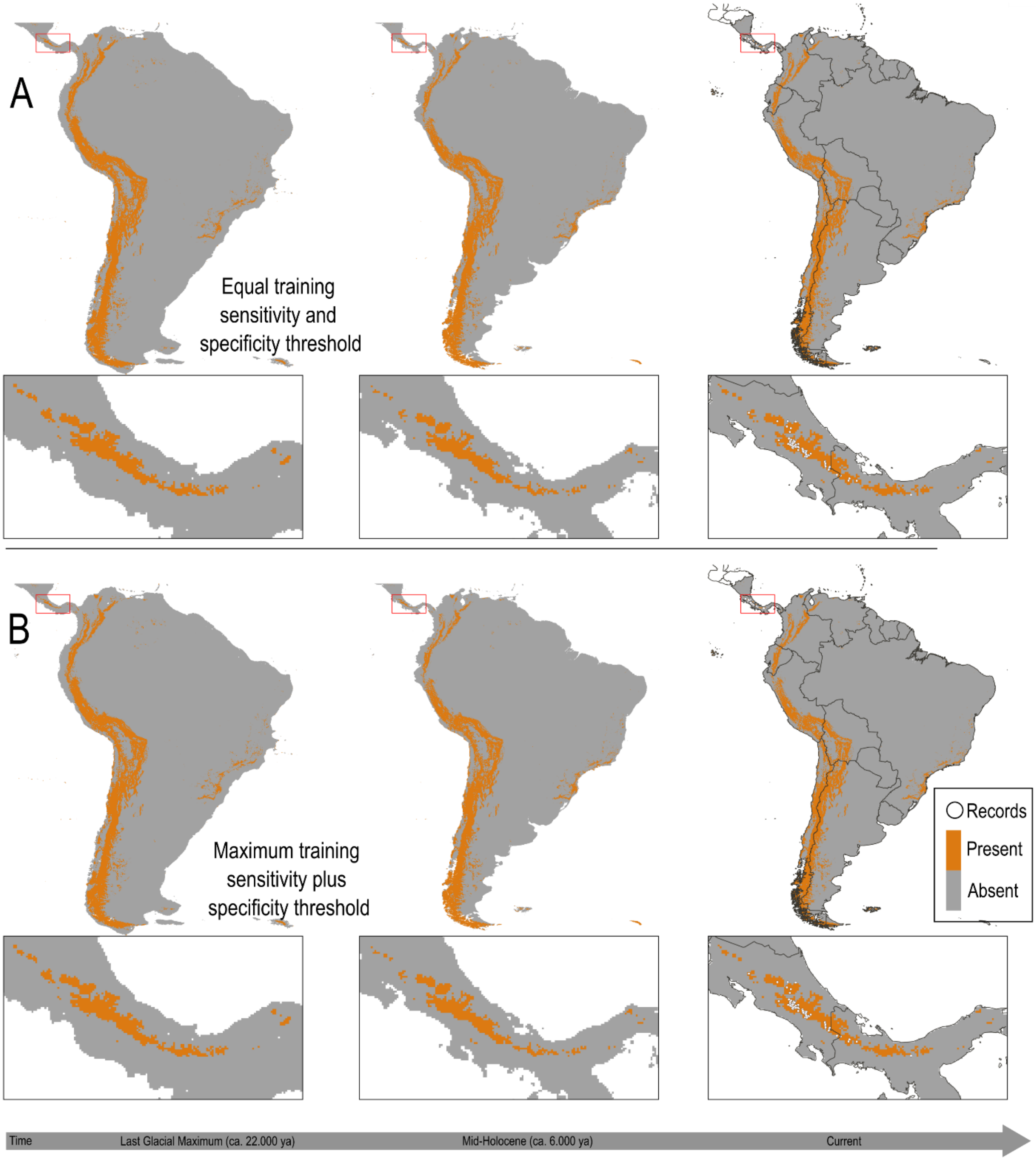


Figure S14: Potential distribution of C. Am. tigrina based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

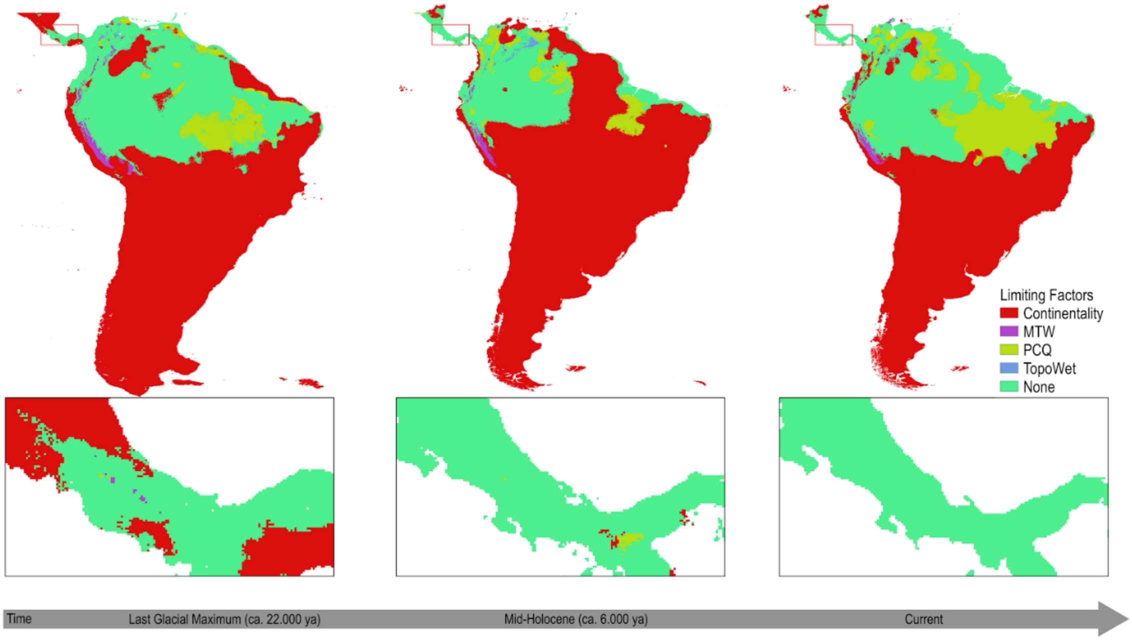


Figure S15: Extrapolation risk for the C. Am. tigrina selected model.

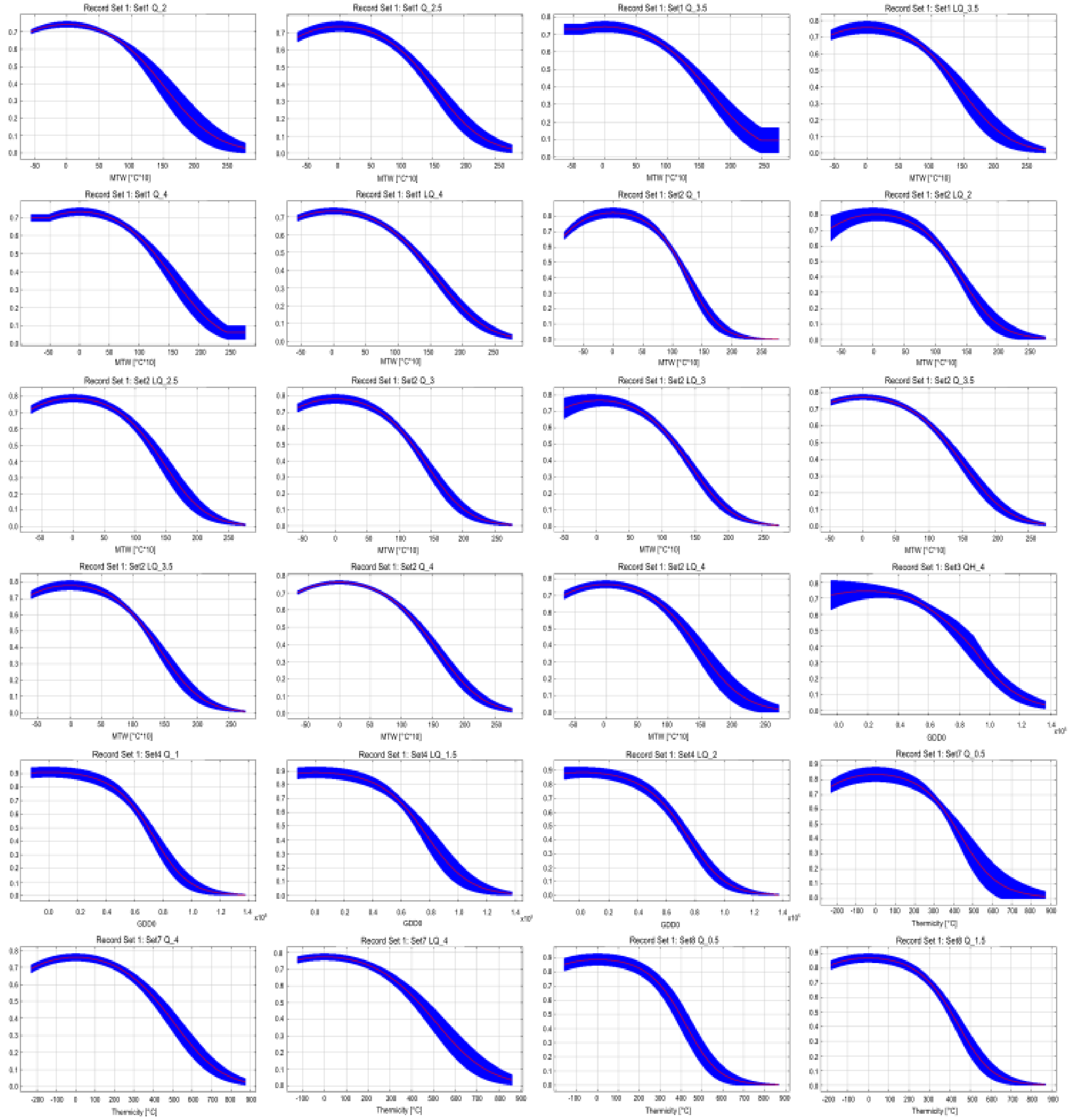


Figure S16-1: Response curves of variables with highest permutation importance in the selected models for each record set of N. Andean tigrina.

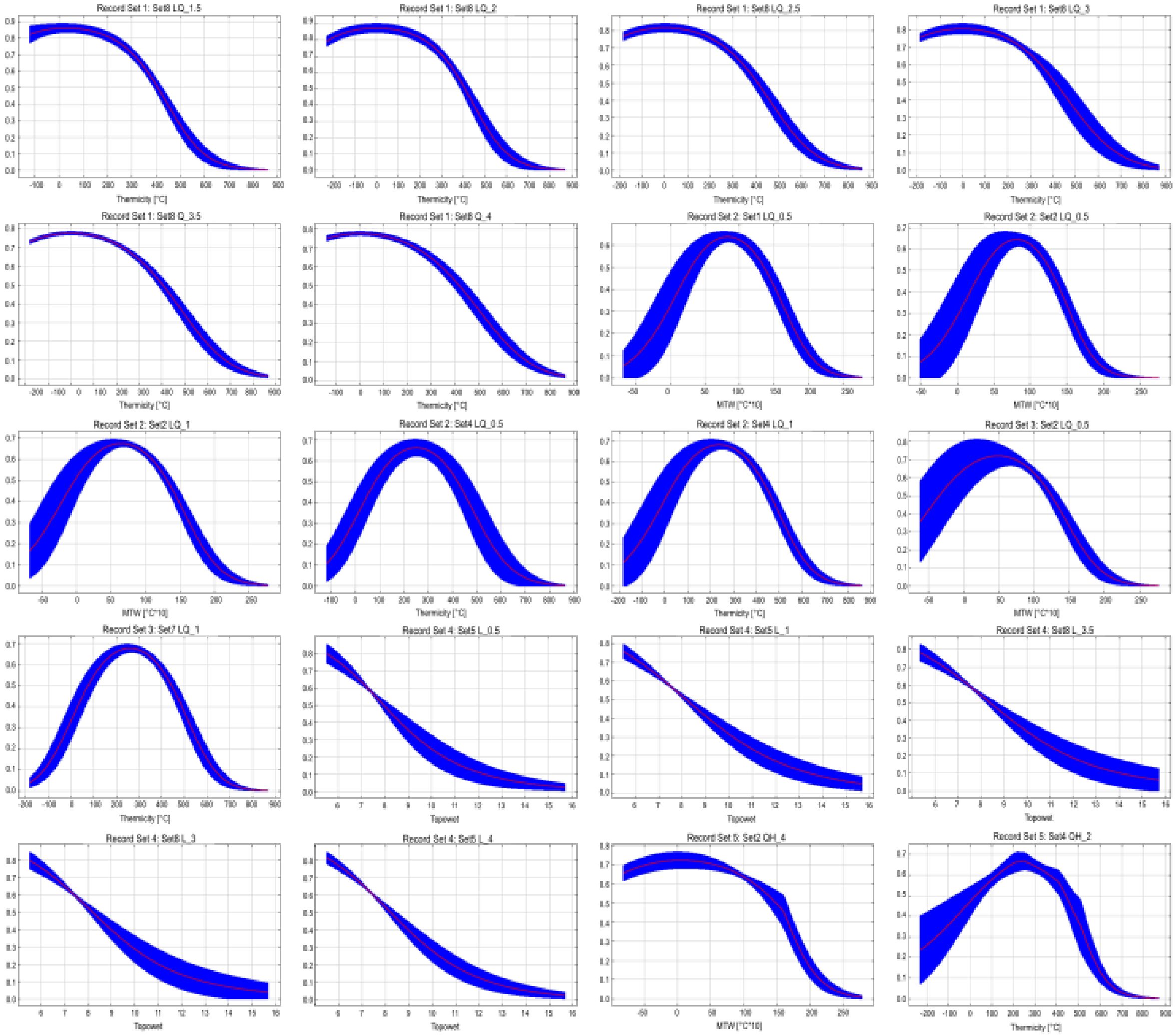


Figure S15-2: Response curves of variables with highest permutation importance in the selected models for each record set of N. Andean tigrina.

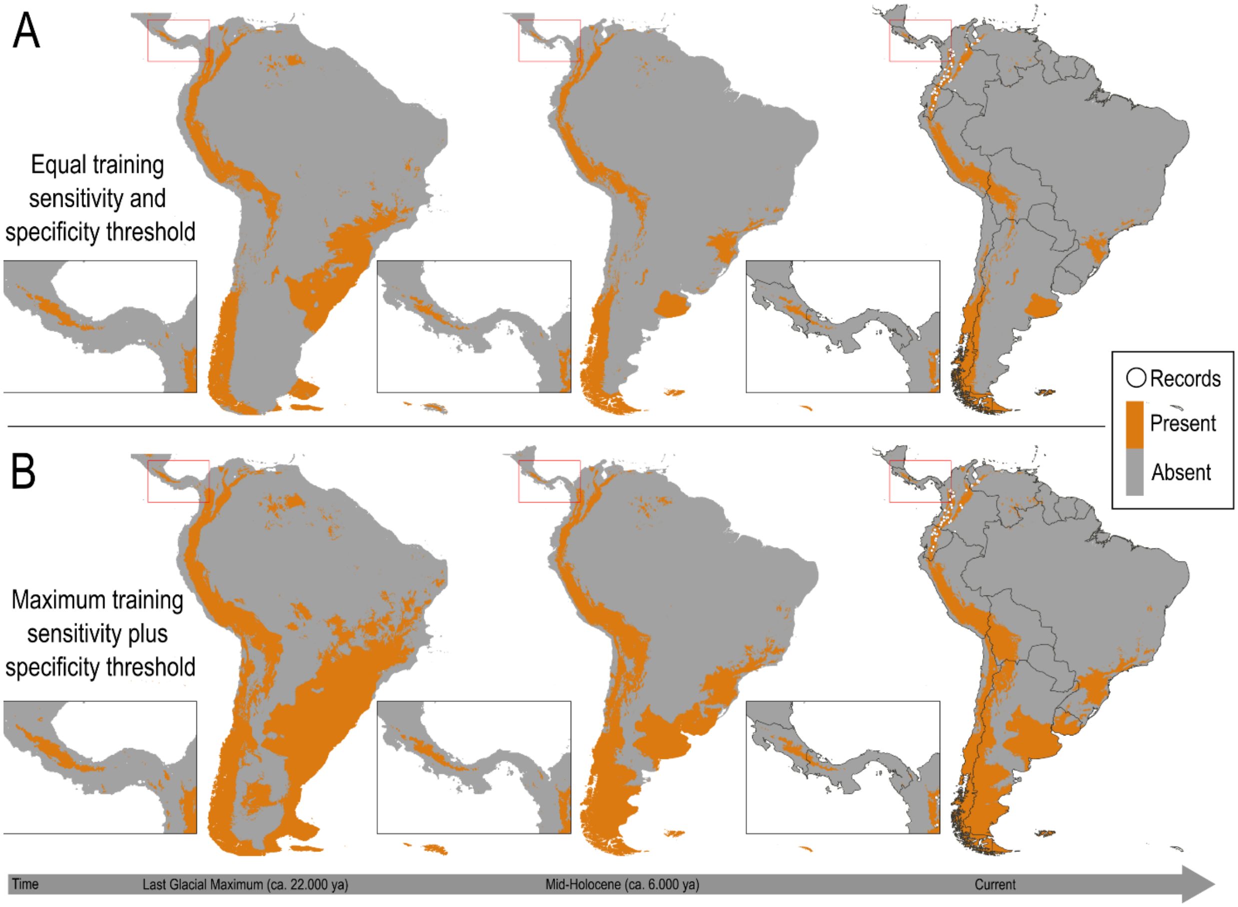


Figure S17: Potential distribution of N. Andean tigrina based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.


A
Limiting Factors
AridityIndex
CMI
GDD0
PCQ
PSeasonality
None
B
Limiting Factors
AridityIndex
CMI
Continentality
MTW
PDQ
None
C
Limiting Factors
AridityIndex
CMI
Continentality
Thermicity
None
D
Limiting Factors
AridityIndex
CMI
PSeasonality
PWQ
PWeQ
TopoWet
None
Time
Last Glacial Maximum
Mid-Holocene
Current

Figure S18: Extrapolation risk for N. Andean tigrina models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set3 QH_4 constructed with the record set 1, **B.** Extrapolation risk map for the model Set2 LQ_1.5 **C.** Extrapolation risk map for the model Set7 LQ_1 constructed with the record set 3, and **D.** Extrapolation risk map for the model Set5 L_0.5 constructed with the record set 5.

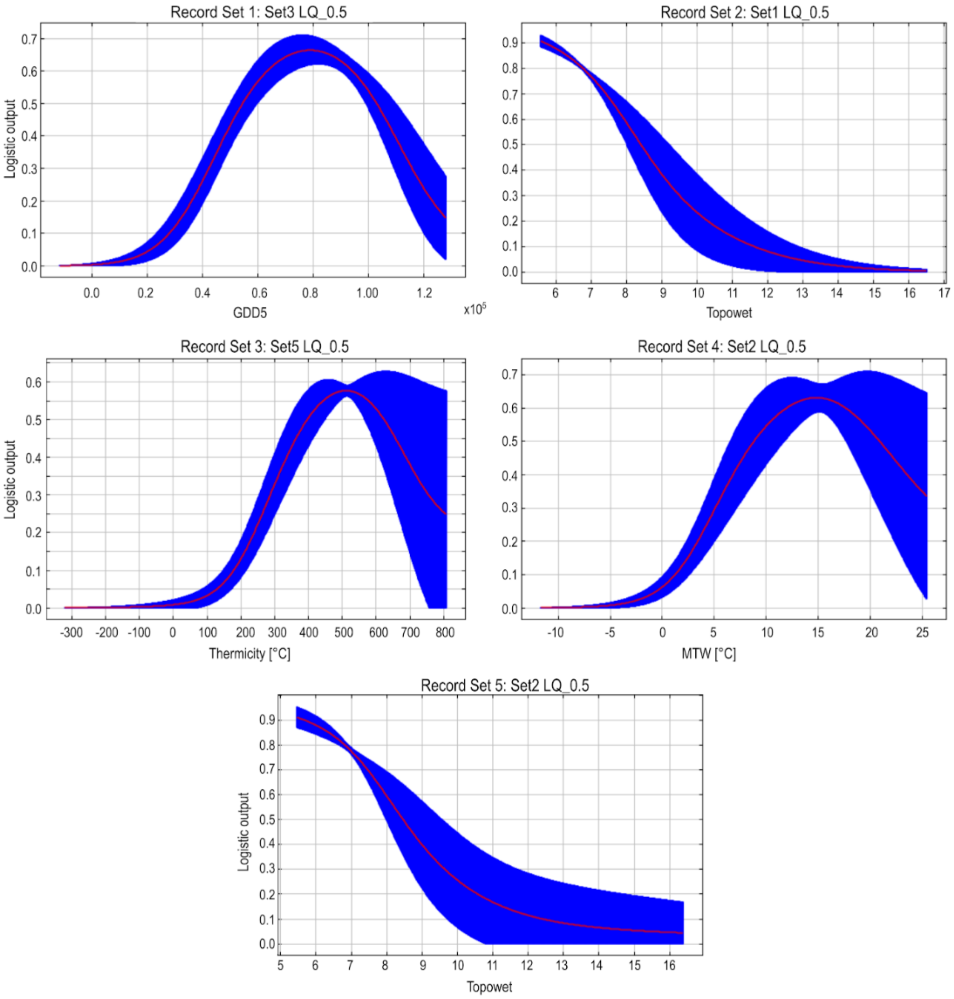


Figure S19: Response curves of variables with highest permutation importance in the selected models for each record set of S. Andean tigrina. The curves show the mean response of the 10 replicate Maxent runs (red) and the mean +/- standard deviation (blue).

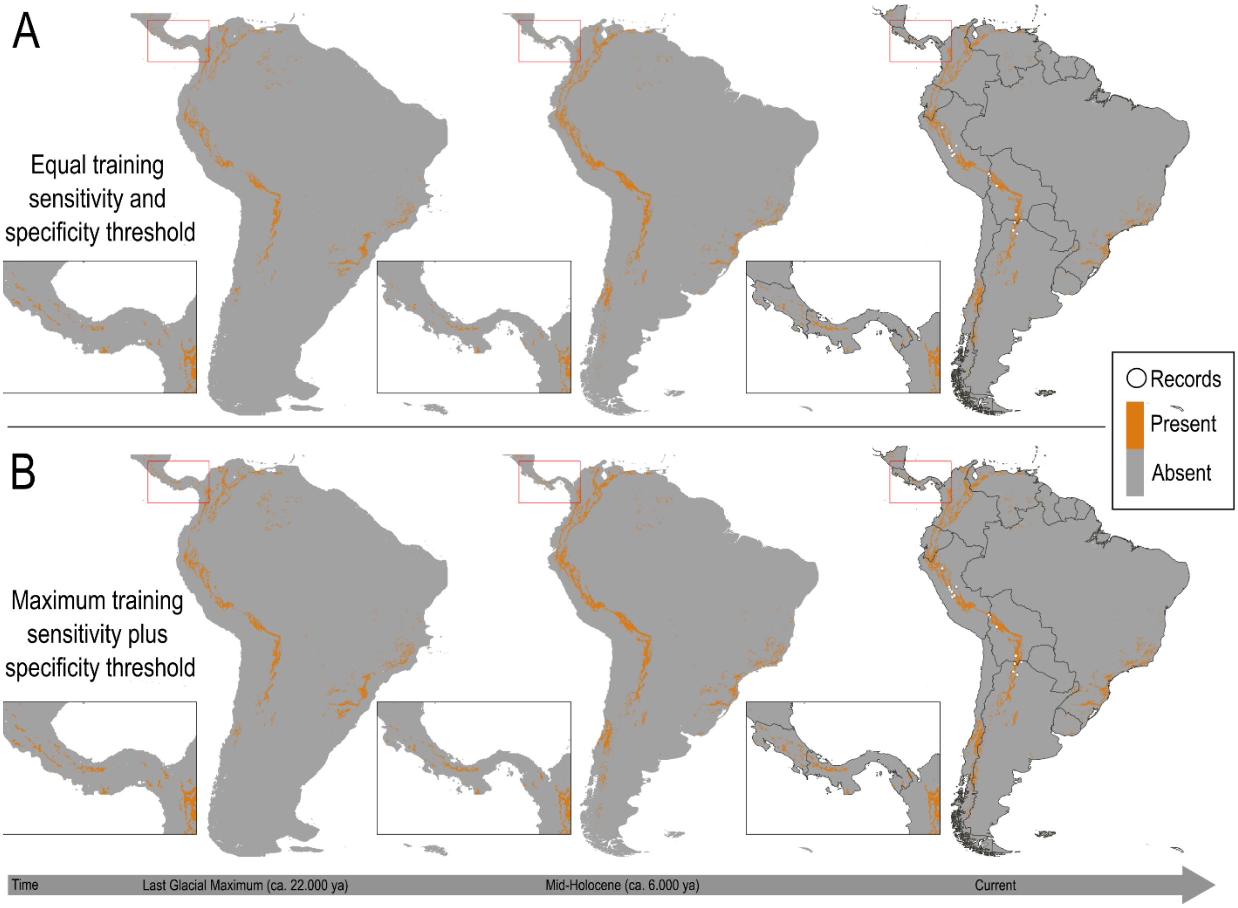


Figure S20: Potential distribution of S. Andean tigrina based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

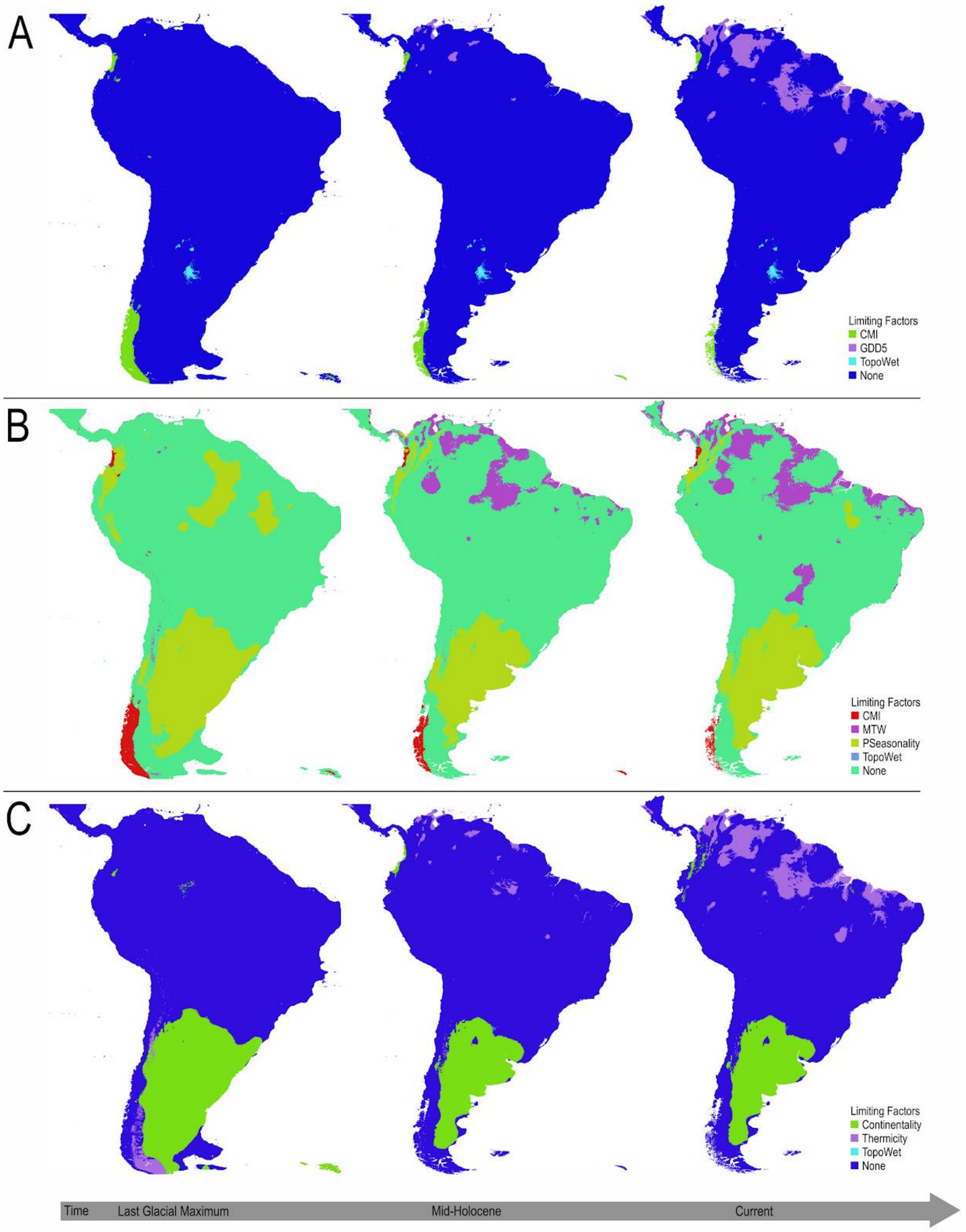


Figure S21: Extrapolation risk for S. Andean tigrina models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set3 LQ_0.5 constructed with the record set 1, **B.** Extrapolation risk map for the model Set1 LQ_0.5 constructed with the record set 2, and **C.** Extrapolation risk map for the model Set5 LQ_0.5 constructed with the record set 3.

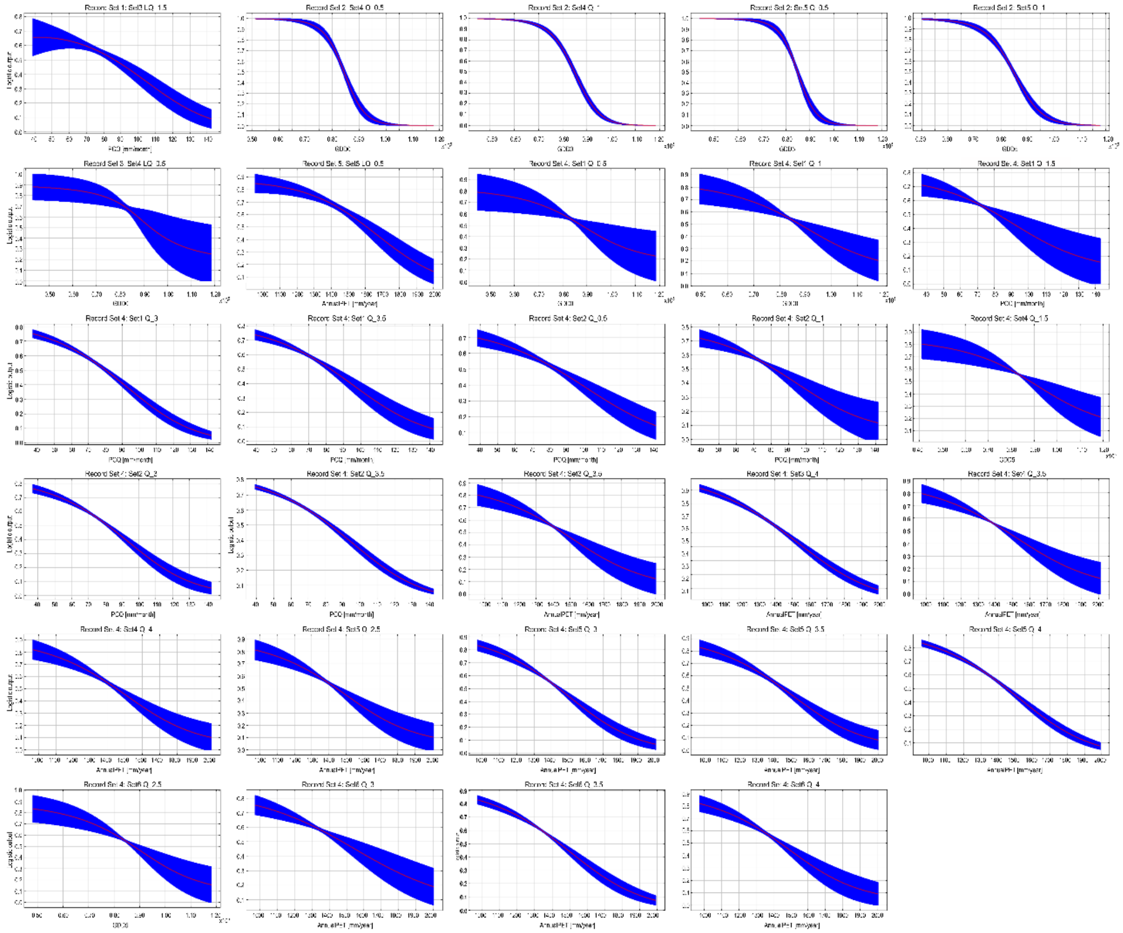


Figure S22: Response curves of variables with highest permutation importance in the selected models for each record set of NE tigrina.

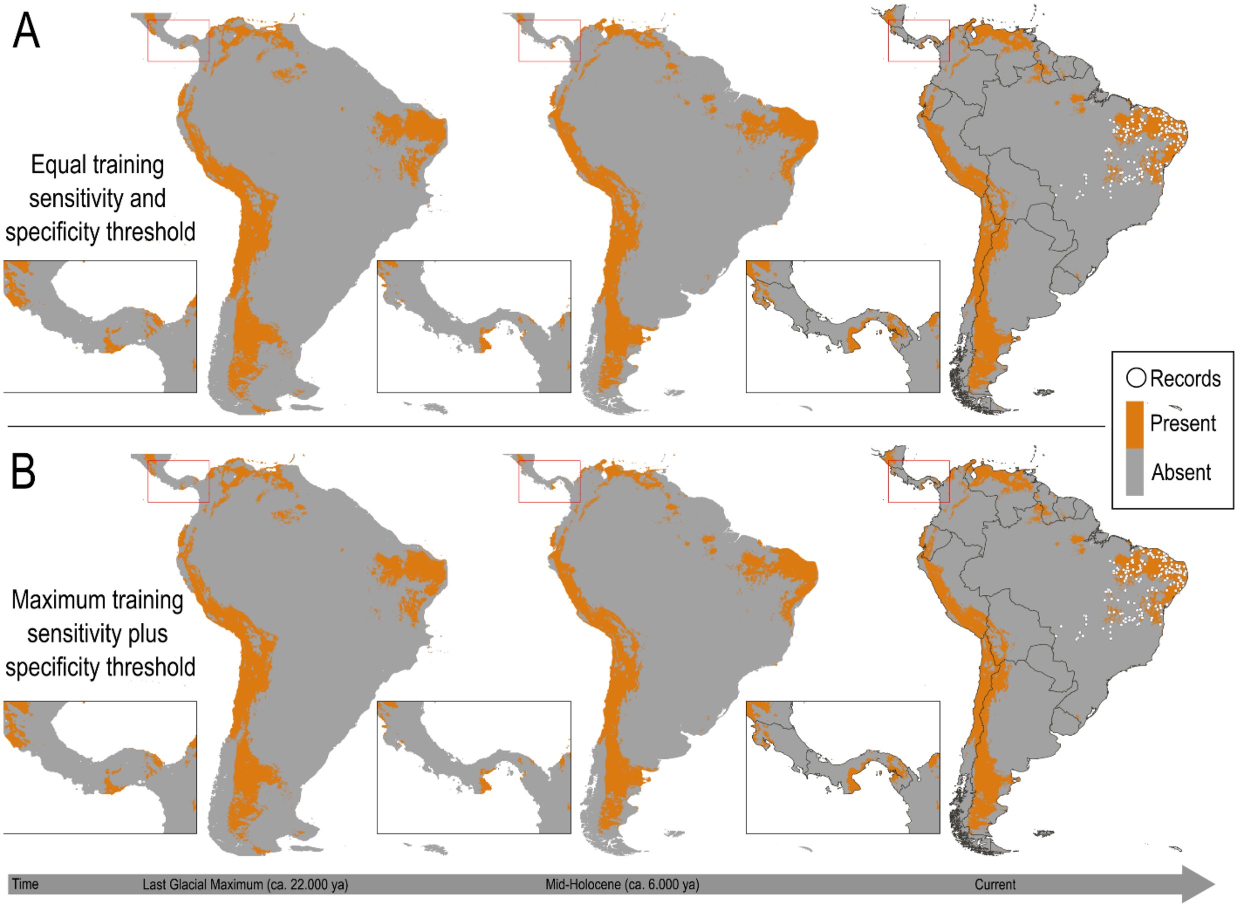


Figure S23: Potential distribution of NE tigrina based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

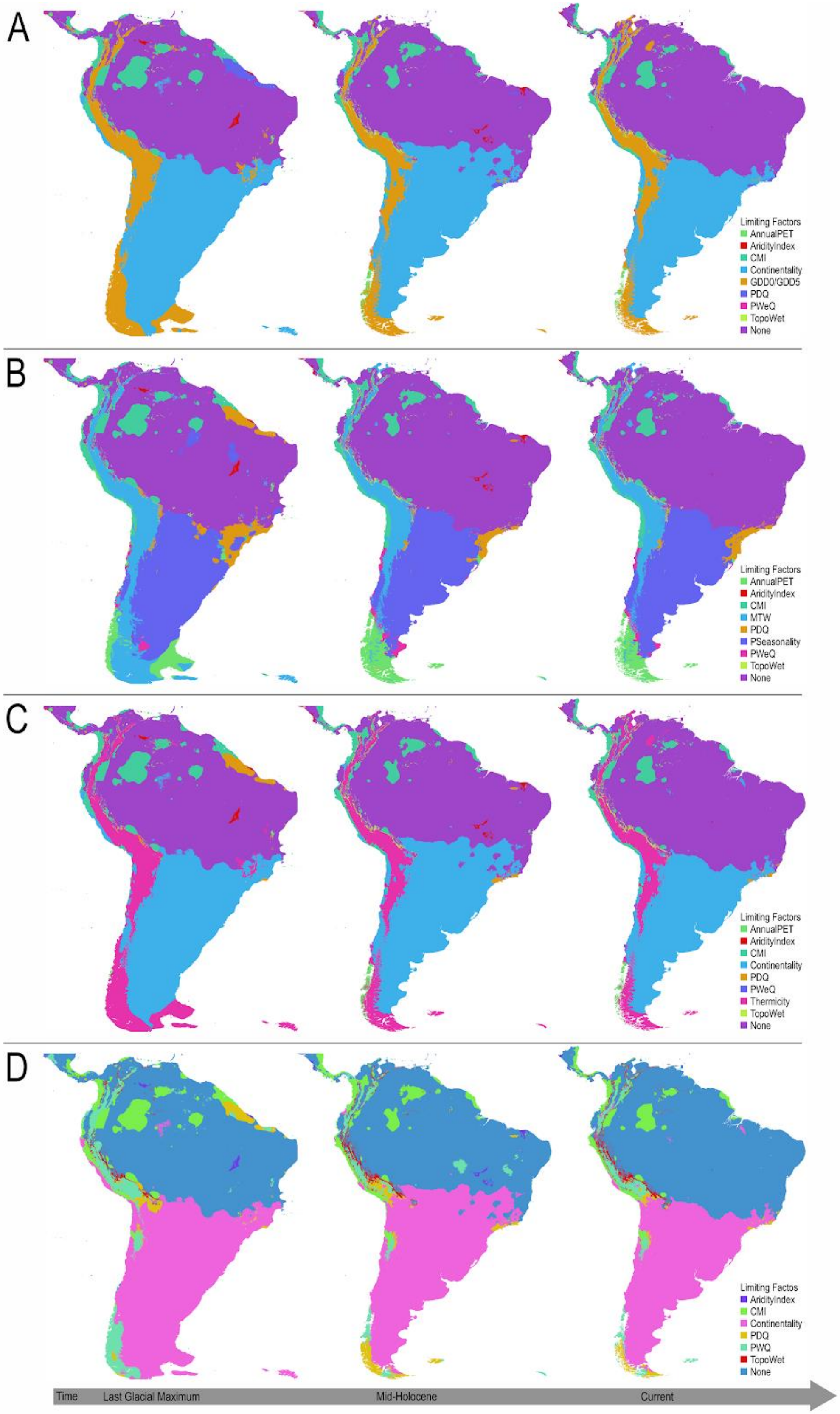

A
Limiting Factors
AnnualPET
AridityIndex
CMI
Continentality
GDD0/GDD5
PDQ
PWeQ
TopoWet
None
B
Limiting Factors
AnnualPET
AridityIndex
CMI
MTW
PDQ
PSeasonality
PWeQ
TopoWet
None
C
Limiting Factors
AnnualPET
AridityIndex
CMI
Continentality
PDQ
PWeQ
Thermicity
TopoWet
None
D
Limiting Factos
AridityIndex
CMI
Continentality
PDQ
PWQ
TopoWet
None
Time
Last Glacial Maximum
Mid-Holocene
Current

Figure S24: Extrapolation risk for NE tigrina models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set1 LQ_1, **B.** Extrapolation risk map for the model Set4 LQ_1, **C.** Extrapolation risk map for the model Set5 LQ_1, and **D.** Extrapolation risk map for the model Set8 LQ_1 constructed with the record set 2.

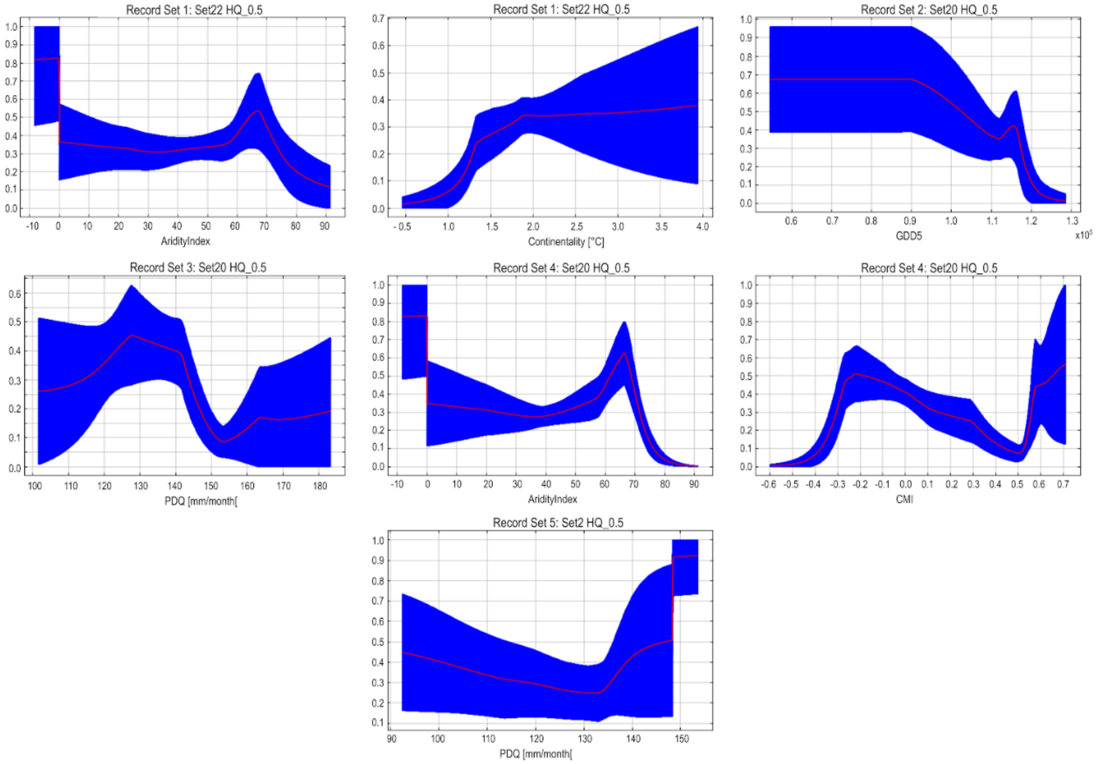


Figure S25: Response curves of variables with highest permutation importance in the selected models for each record set of GSstrict. The curves show the mean response of the 10 replicate Maxent runs (red) and the mean +/- standard deviation (blue).

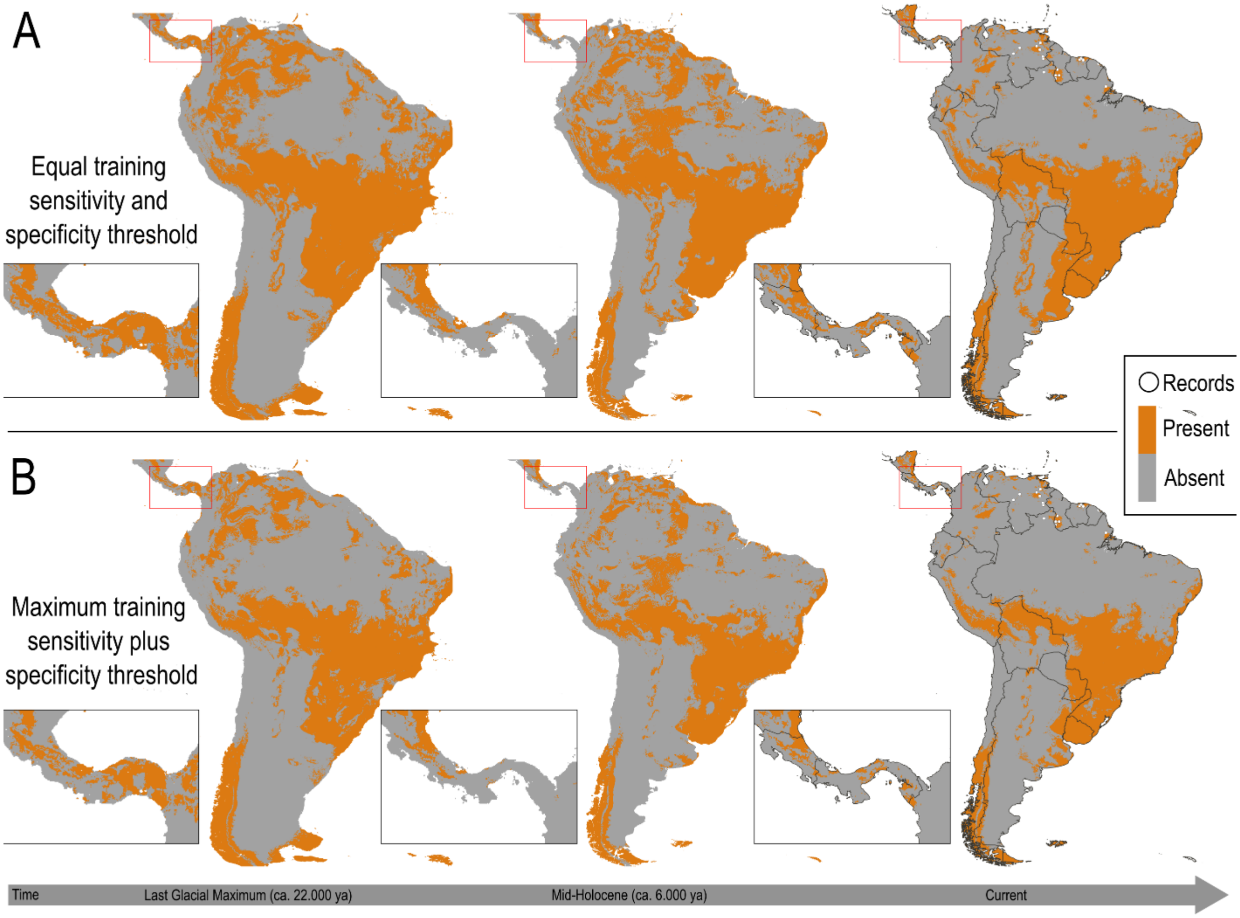


Figure S26: Potential distribution for the GSstrict based on on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

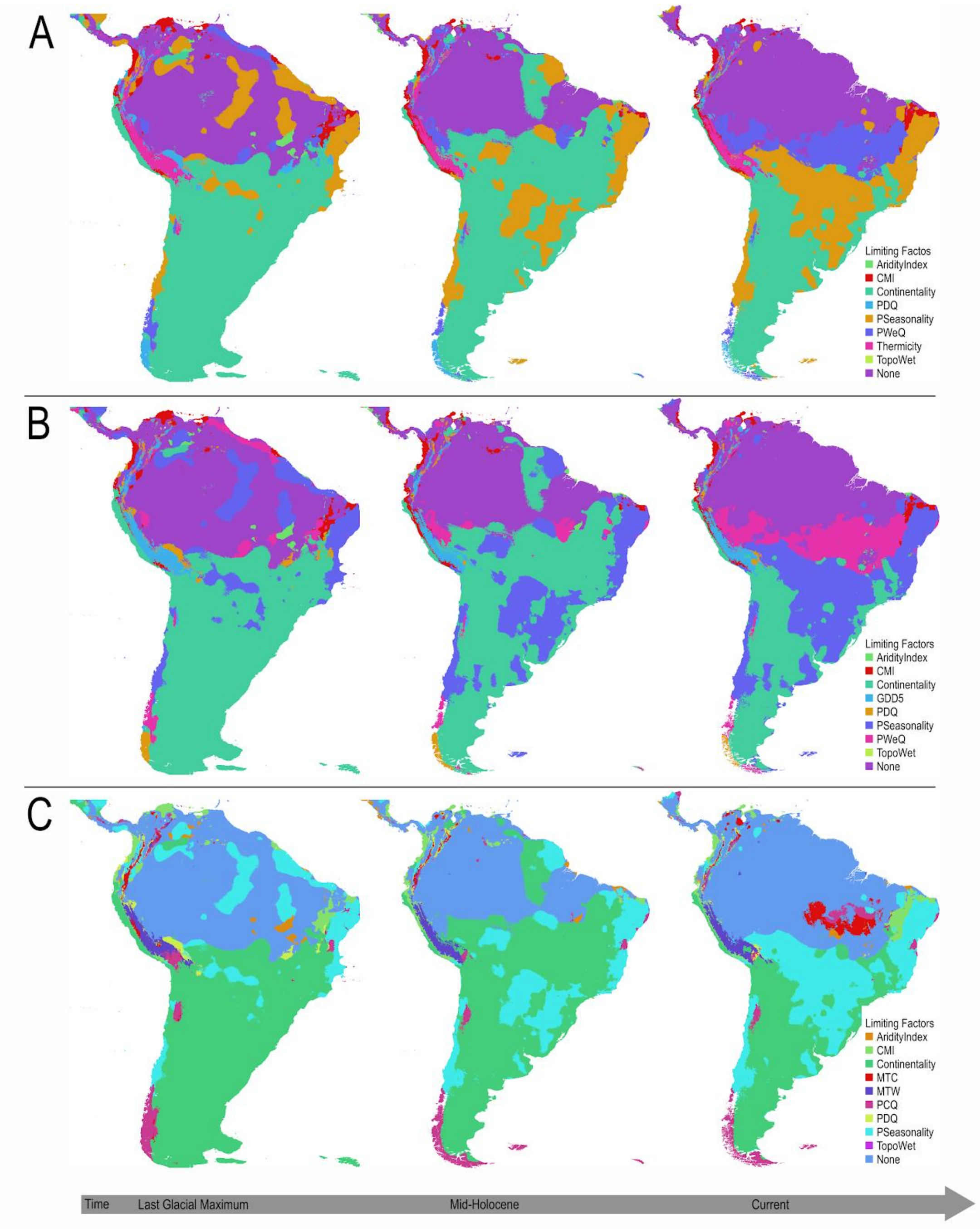


Figure S27: Extrapolation risk for GSstrict models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set3 LQ_0.5 constructed with the record set 1, **B.** Extrapolation risk map for the model Set1 LQ_0.5 constructed with the record set 2, and **C.** Extrapolation risk map for the model Set5 LQ_0.5 constructed with the record set 3.

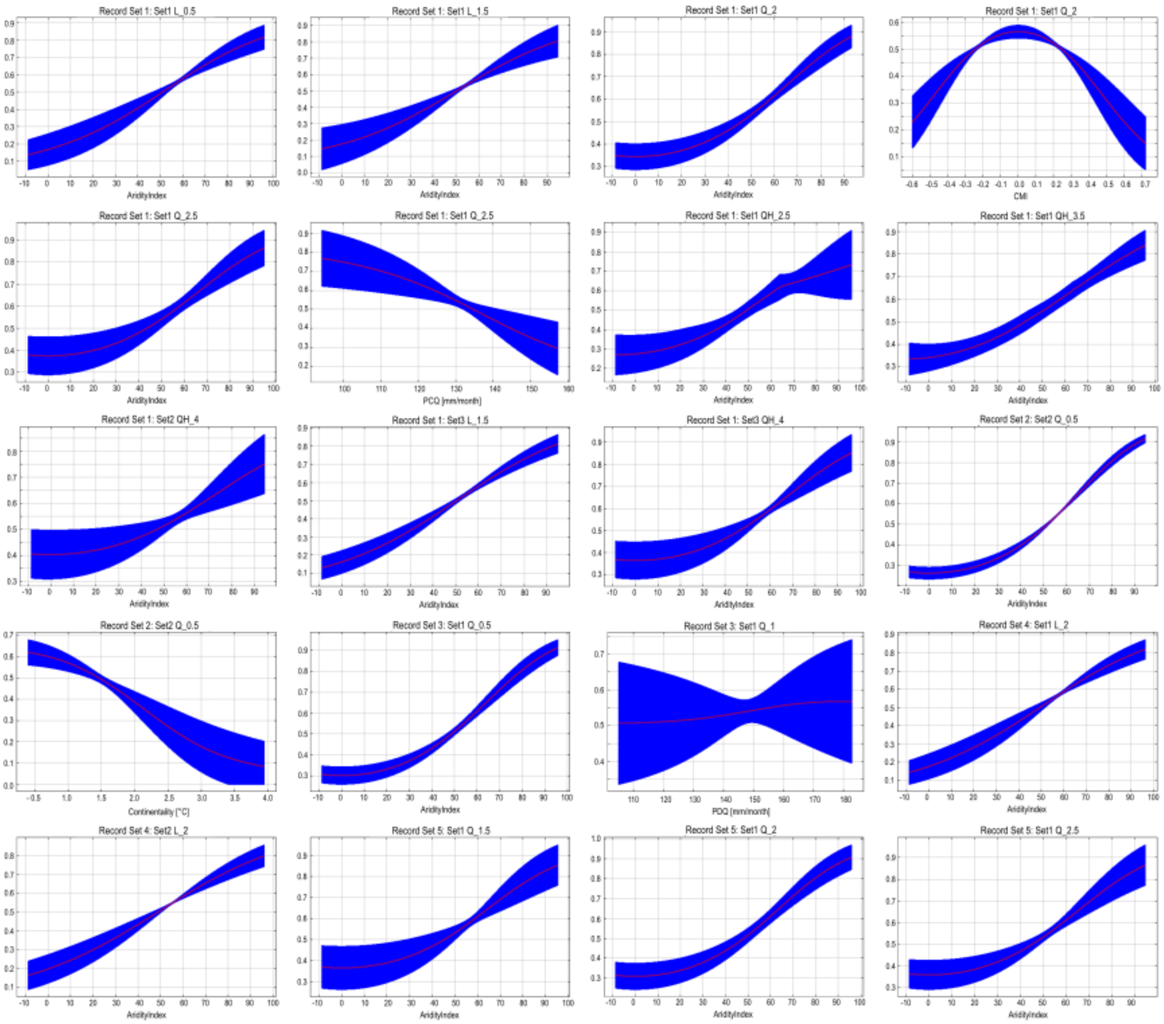


Figure S28-1: Response curves of variables with highest permutation importance in the selected models for each record set of GSAmaz.

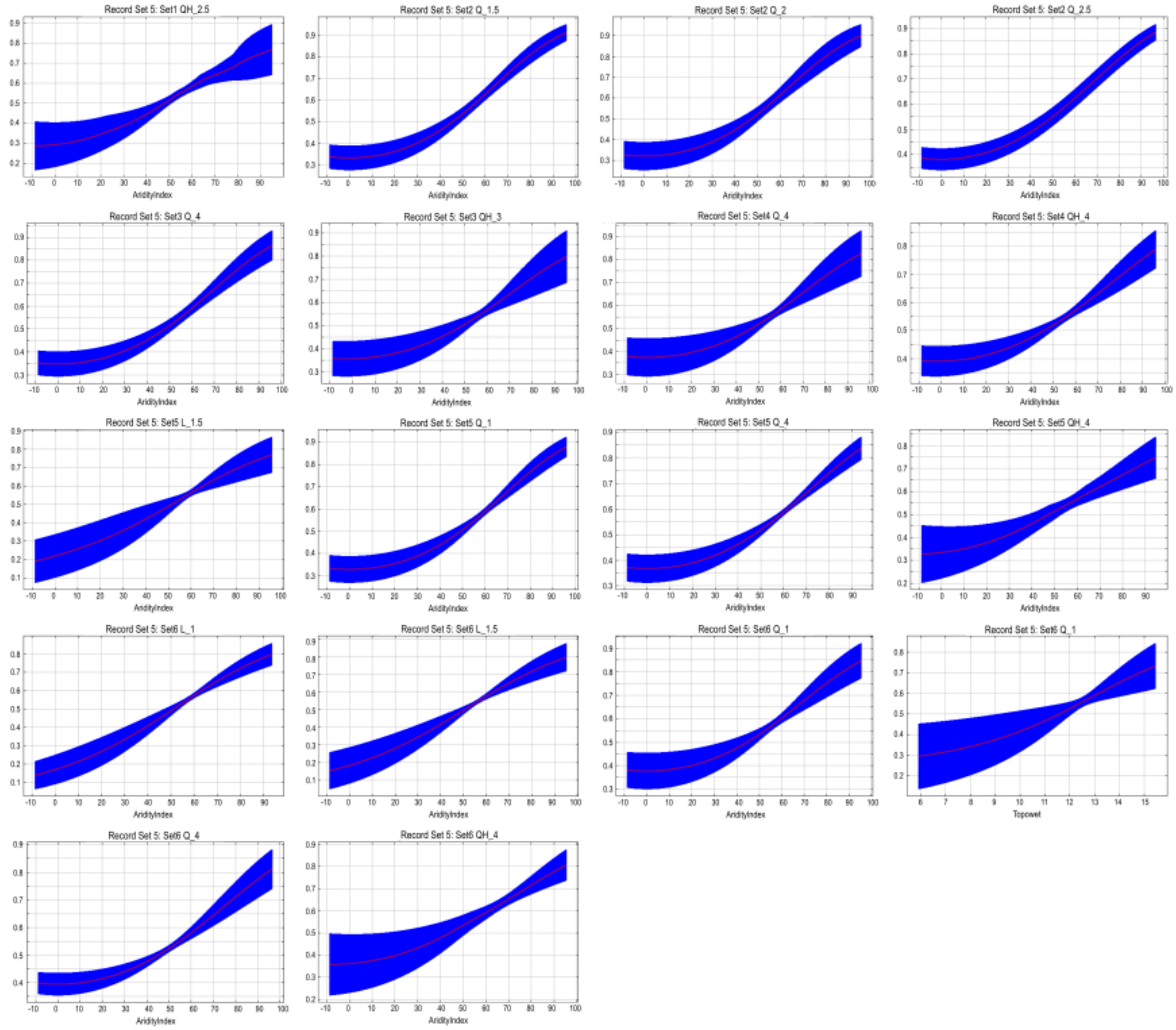


Figure S27-2: Response curves of variables with highest permutation importance in the selected models for each record set of GSAmaz.

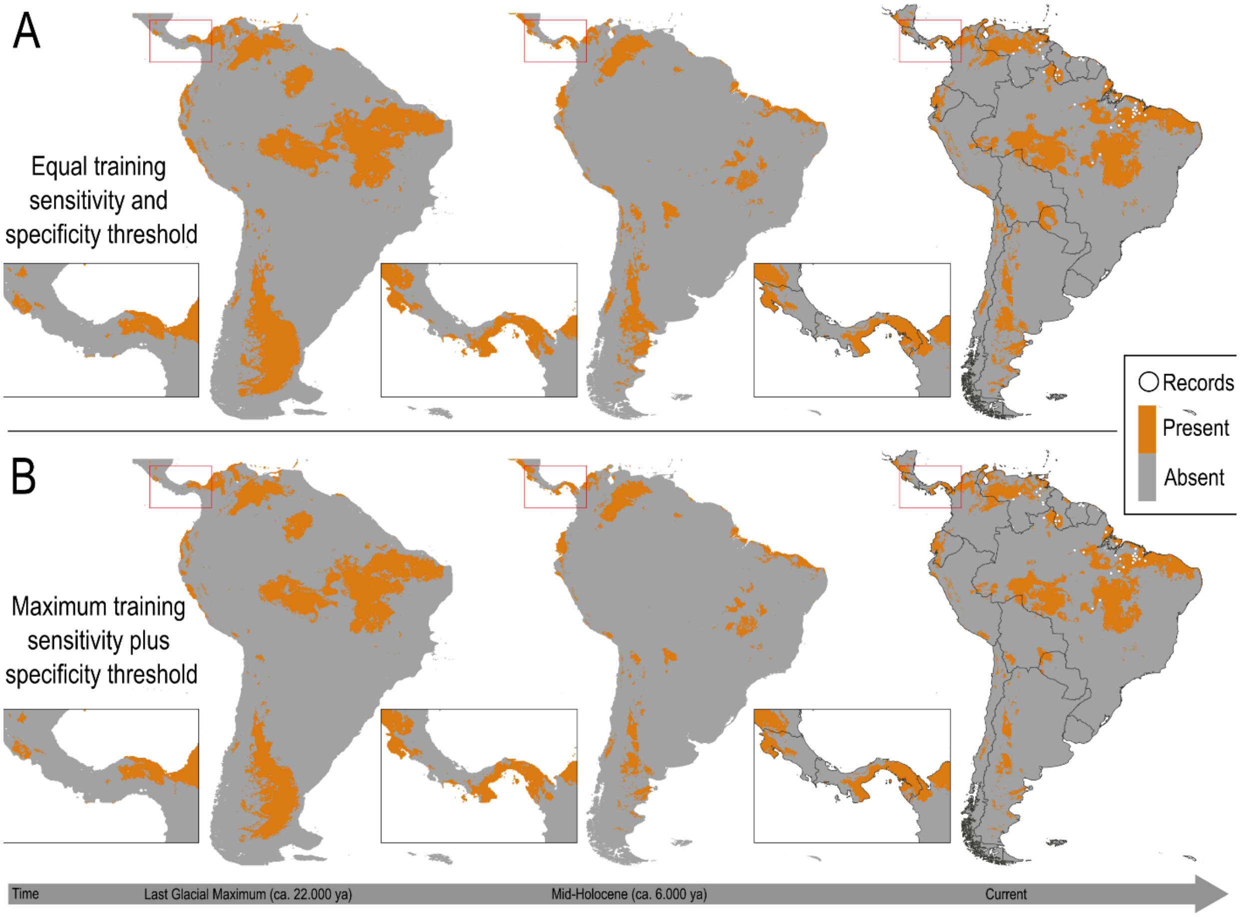


Figure S29: Potential distribution for the GSAmaz based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

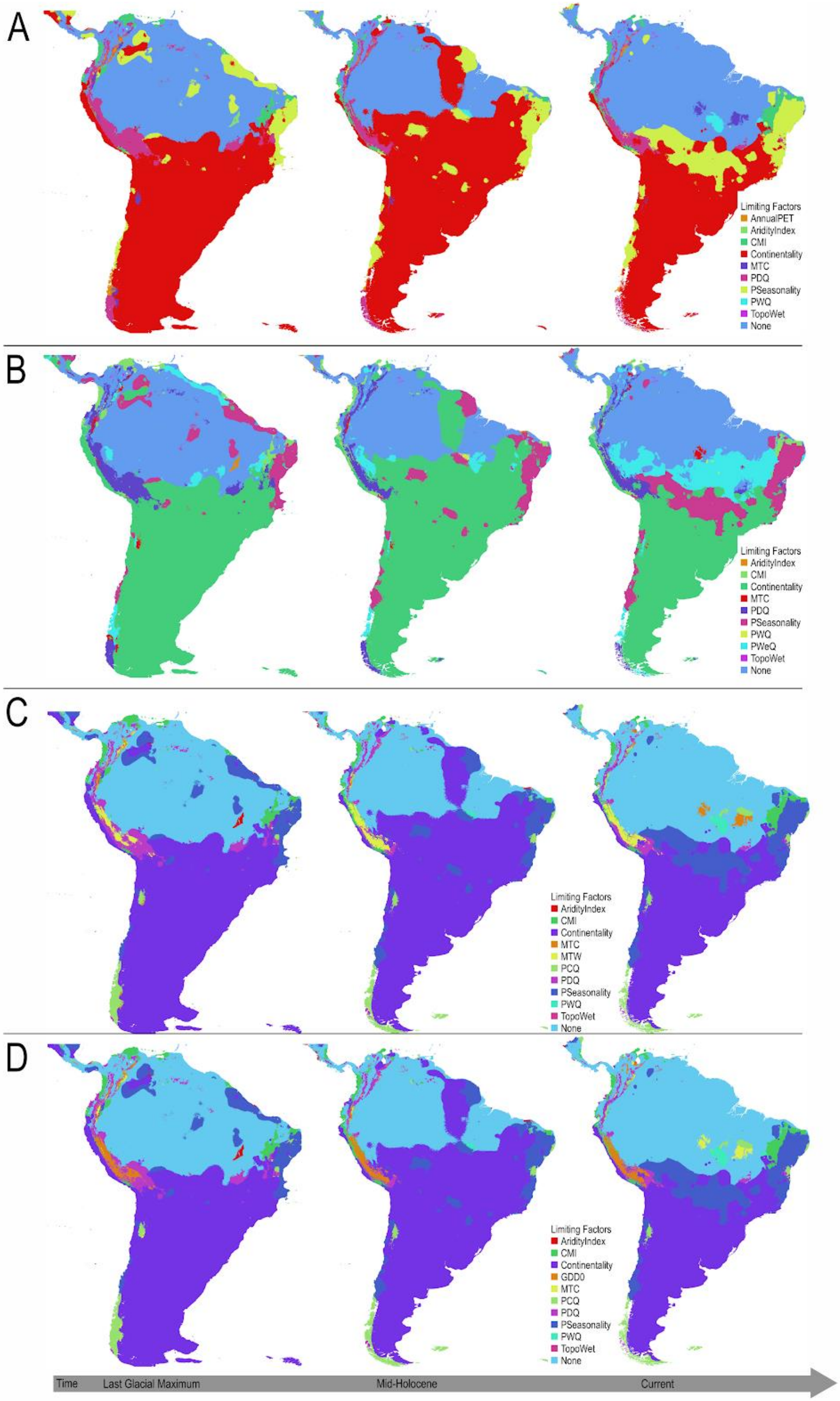

A
Limiting Factors
AnnualPET
AridityIndex
CMI
Continentality
MTC
PDQ
PSeasonality
PWQ
TopoWet
None
B
Limiting Factors
AridityIndex
CMI
Continentality
MTC
PDQ
PSeasonality
PWQ
PWeQ
TopoWet
None
C
Limiting Factors
AridityIndex
CMI
Continentality
MTC
MTW
PCQ
PDQ
PSeasonality
PWQ
TopoWet
None
D
Limiting Factors
AridityIndex
CMI
Continentality
GDD0
MTC
PCQ
PDQ
PSeasonality
PWQ
TopoWet
None
Time
Last Glacial Maximum
Mid-Holocene
Current

Figure S30: Extrapolation risk for GSAmaz models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set2 QH_4, **B.** Extrapolation risk map for the model Set3 L_1.5 constructed with the record set 1, **C.** Extrapolation risk map for the model Set1 L_2, and **D.** Extrapolation risk map for the model Set2 L_2, constructed with the record set 4.

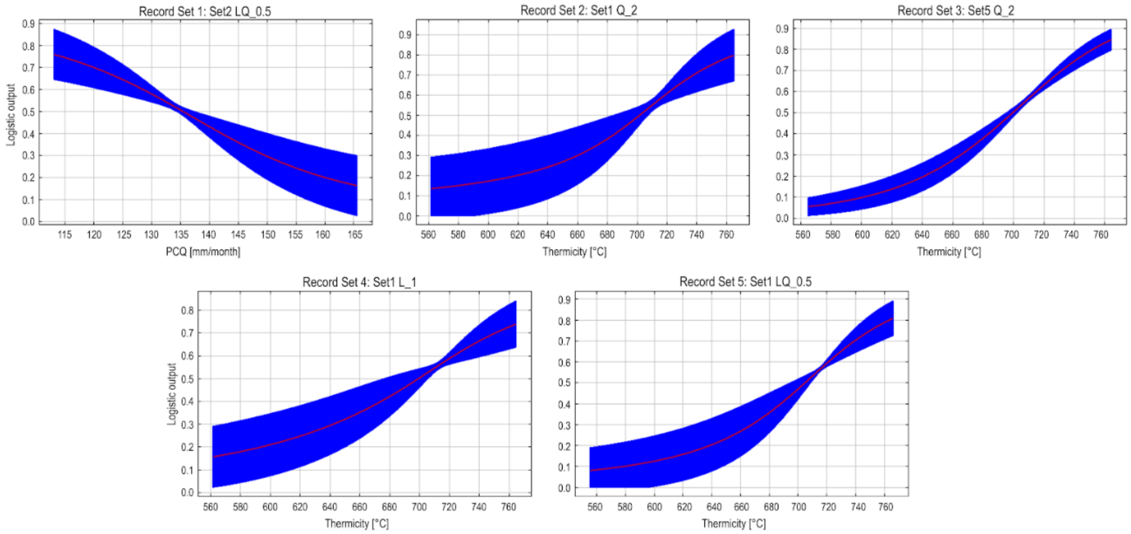


Figure S31: Response curves of variables with highest permutation importance in the selected models for each record set of Amaz. The curves show the mean response of the 10 replicate Maxent runs (red) and the mean +/- standard deviation (blue).

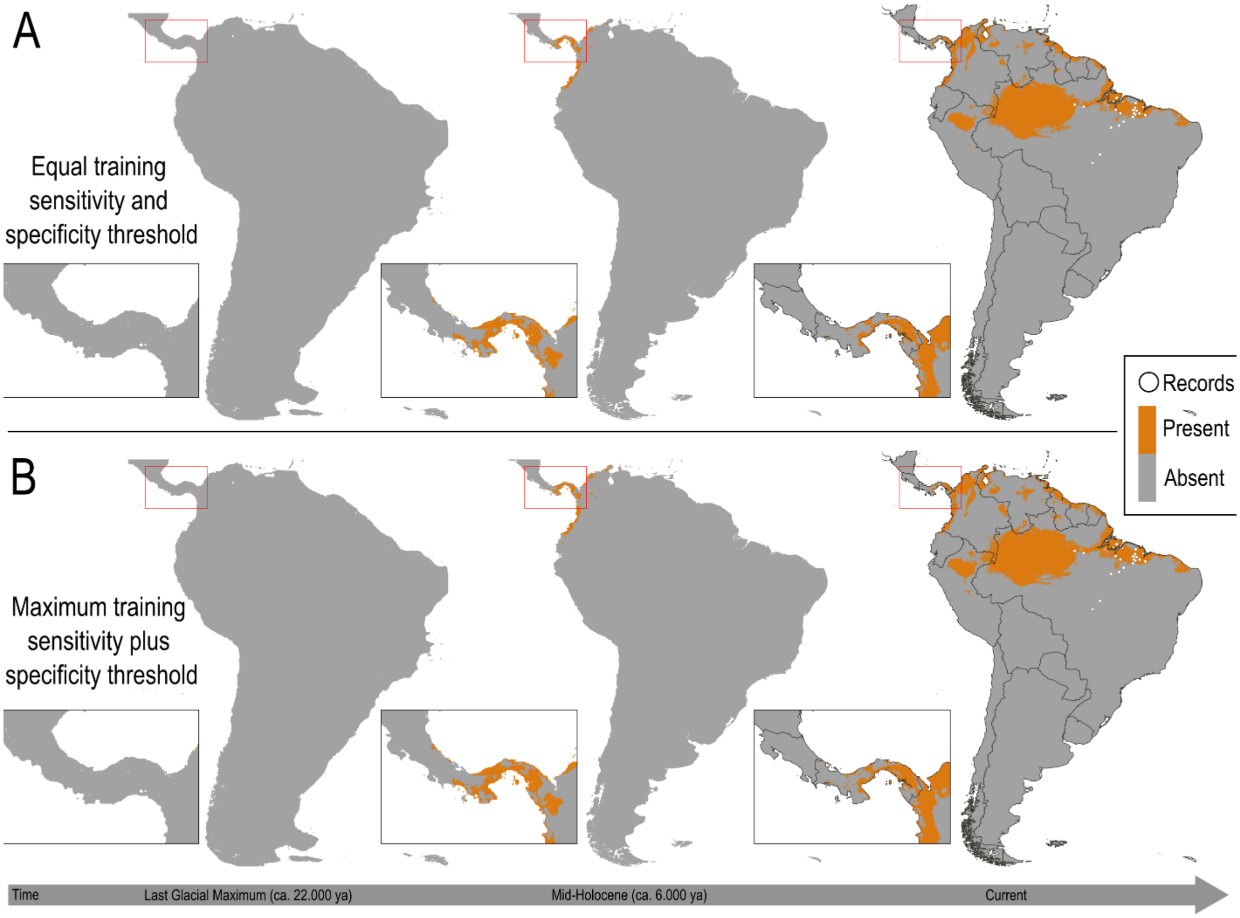


Figure S32: Potential distribution for the Amaz based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

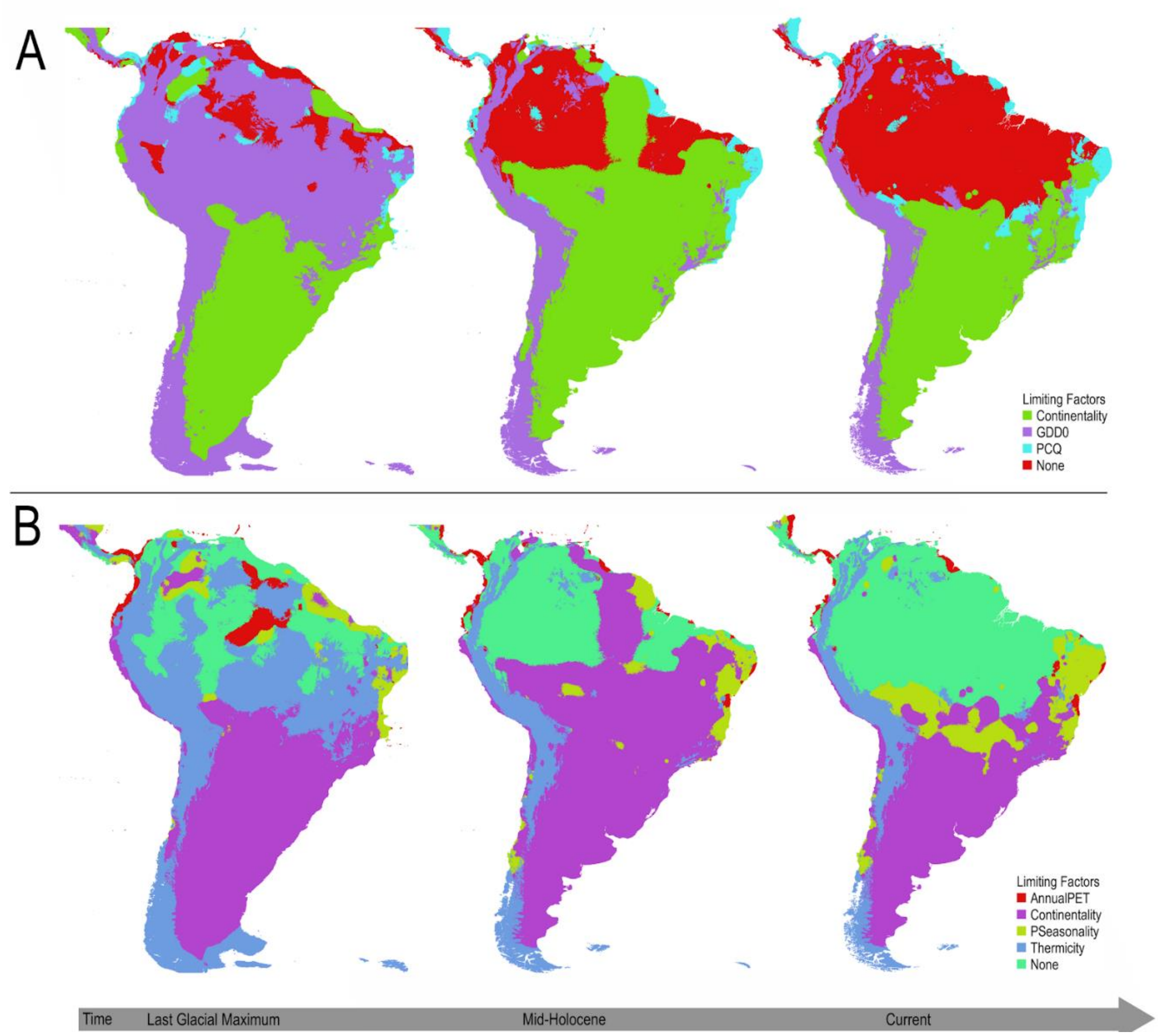


Figure S33: Extrapolation risk for Amaz models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set2 LQ_0.5 constructed with the record set 1, **B.** Extrapolation risk map for the model Set5 Q_1.5 constructed with the record set 3.

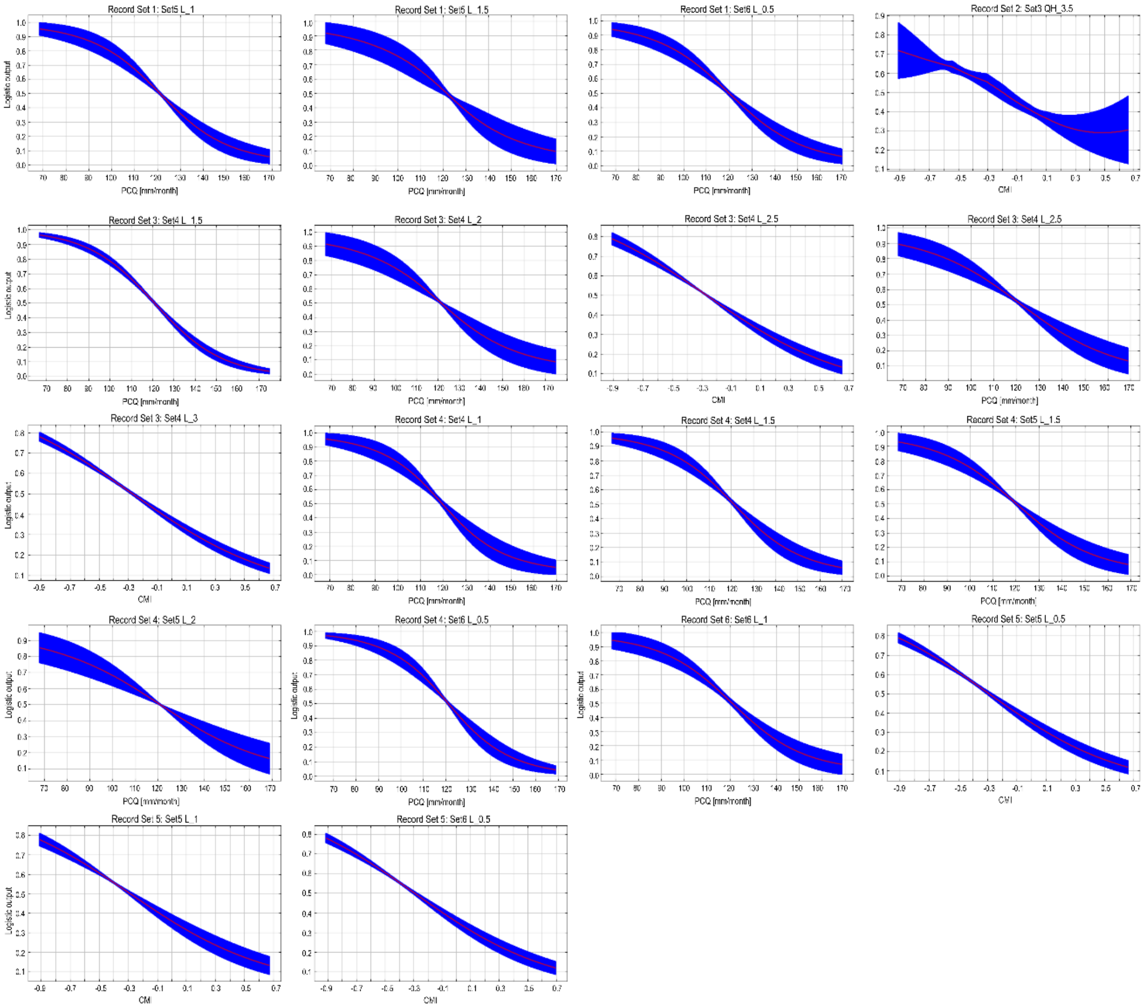


Figure S34: Response curves of variables with highest permutation importance in the selected models for each record set of NE tigrina + Amaz.

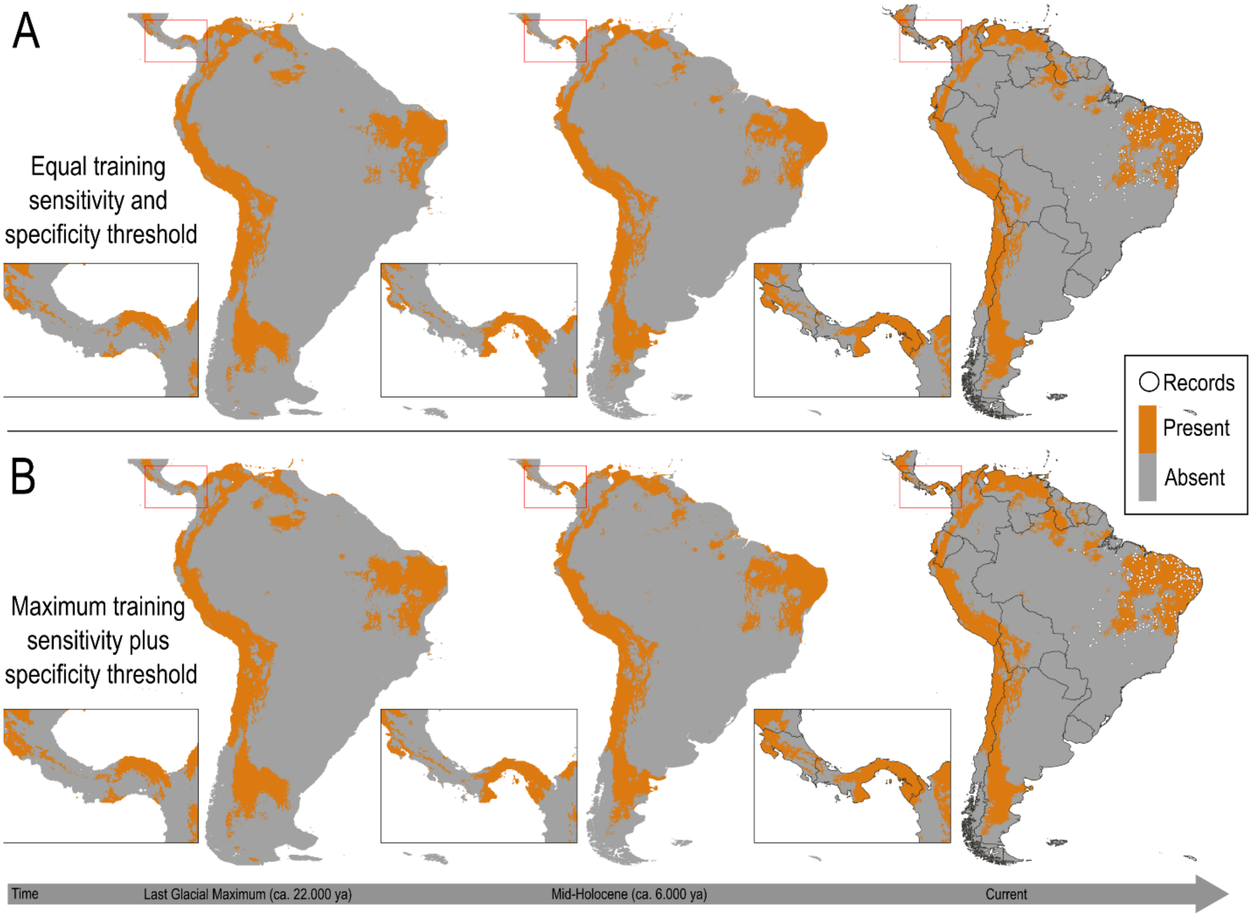


Figure S35: Potential distribution for the NE tigrina + Amaz based on **A.** Equal training sensitivity and specificity (ETSS) threshold **B.** maximum training sensitivity plus specificity (MTSS) threshold. Distributions are shown for three time periods, from left to right: Last Glacial Maximum, Mid-Holocene, and Present. Location records are shown on the map for the Present. The inset shows a close-up image of southern Central America.

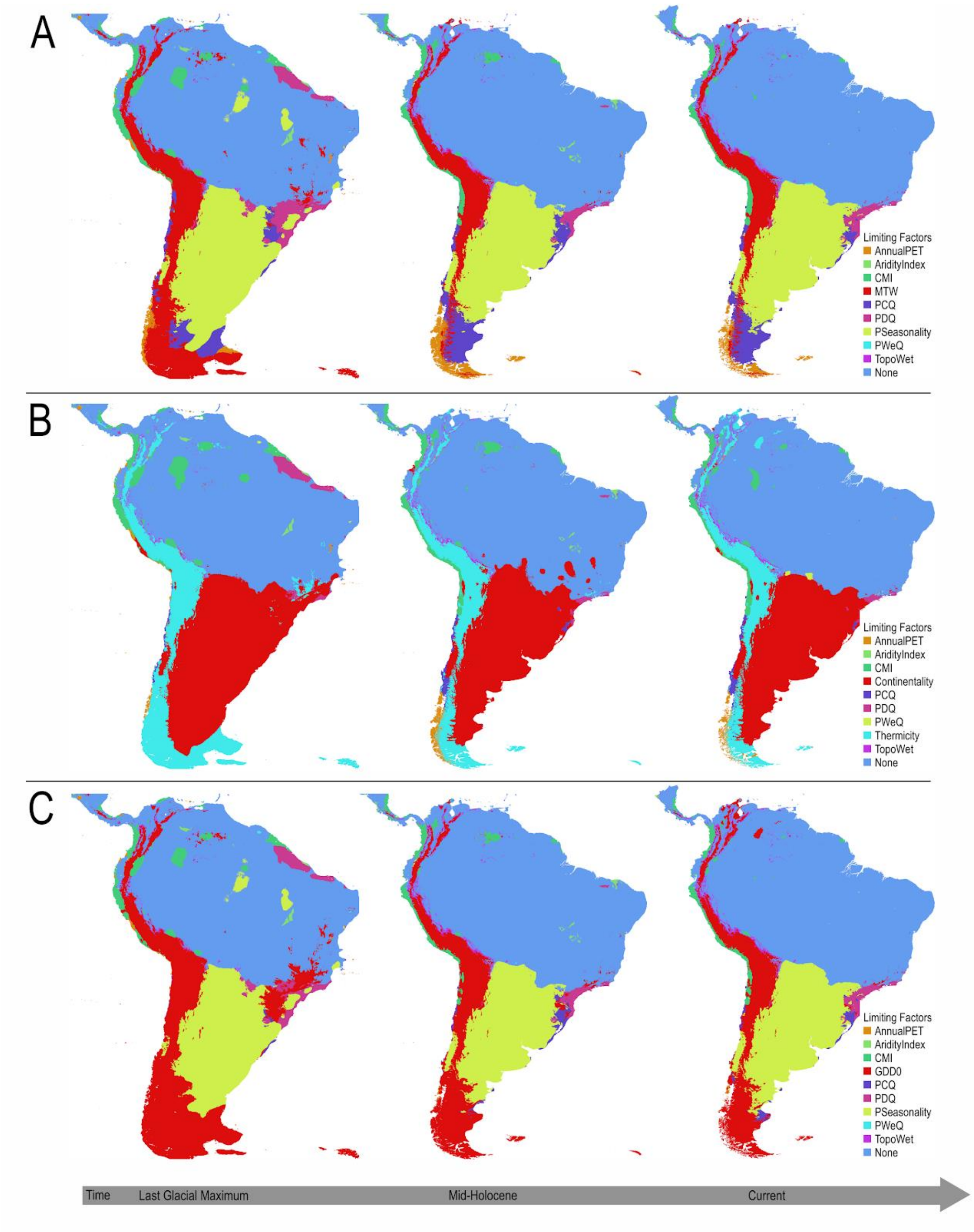


Figure S36: Extrapolation risk for NE tigrina + Amaz models. Extrapolation risk maps are included for several models, which allow visualizing the extrapolation risk of all variables included in the selected models. **A.** Extrapolation risk map for the model Set5 L_1 constructed with the record set 1, **B.** Extrapolation risk map for the model Set3 QH_3.5 constructed with the record set 2, and **C.** Extrapolation risk map for the model Set4 L_1 constructed with the record set 4.