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**A importância das interações bióticas e atributos na distribuição
das espécies e estruturação das comunidades ecológicas**

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MÁRCIA NEUNSWANDER KURTZ

**A importância das interações bióticas e atributos na distribuição
das espécies e estruturação das comunidades ecológicas**

Tese apresentada ao programa de pós-graduação em Ecologia e Evolução do Departamento de Ecologia do Instituto de Ciências Biológicas da Universidade Federal de Goiás como parte das exigências para a obtenção do título de Doutora em Ecologia e Evolução.

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ATA DE DEFESA DE TESE

Ata Nº 103 da sessão de Defesa de Tese de **Márcia Neunschwander Kurtz** que confere o título de Doutora em **Ecologia e Evolução**, na área de concentração em **Ecologia e Evolução**.

Aos **trinta dias do mês de novembro de dois mil e vinte (30/11/2020)**, a partir das **08h00min**, por **webconferência**, **segundo portaria CAPES no. 36 de 16 de março de 2020 e recomendação da UFG**, realizou-se a sessão pública de Defesa de Tese intitulada “**A importância das interações bióticas e atributos na distribuição das espécies e estruturação das comunidades ecológicas**”. Os trabalhos foram instalados pelo Orientador, **Prof. Dr. Marcus Vinicius Cianciaruso (Depto de Ecologia/UFG)**, com a participação dos demais membros da Banca Examinadora: **Profa. Dra. Levi Carina Terribile (Depto. Ciências Biológicas/UFJ)**, membro titular interno; **Prof. Dr. Joaquin Hortal Munoz (Depto. de Ecologia/UFG)**, membro titular interno; **Profa. Dra. Héliida Ferreira da Cunha (RENAC/UEG)**, membro titular externo; e **Dr. Lucas Lacerda Caldas Zanini Jardim (DTI PosDoc Depto. de Ecologia/UFG)**, membro titular externo. Durante a argüição os membros da banca [**não fizeram**] sugestão de alteração do título do trabalho [**(em caso de sugestão conforme explicitado abaixo)**]. A Banca Examinadora reuniu-se em sessão secreta a fim de concluir o julgamento da tese, tendo sido a candidata [**aprovada**] pelos seus membros. Proclamados os resultados pelo **Prof. Dr. Marcus Vinicius Cianciaruso**, Presidente da Banca Examinadora, foram encerrados os trabalhos e, para constar, lavrou-se a presente ata que é assinada pelos Membros da Banca Examinadora, ao(s) **trinta dias do mês de novembro de dois mil e vinte (30/11/2020)**.

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Resumo geral

As perturbações estruturais e climáticas criadas direta ou indiretamente pela atividade humana atuam profundamente sobre os organismos e são responsáveis pela crescente mudança na biodiversidade. Tais mudanças estão associadas a alterações relevantes na abundância relativa, extinção e habilidade invasiva das espécies. Nesse contexto de mudanças iminentes, é cada vez mais urgente a necessidade de descrever os padrões e entender os processos que regem a biodiversidade, a fim de prever e mitigar as mudanças atuais e futuras. Uma forma de fazer isso é através dos modelos de distribuição de espécies, que são geralmente construídos apenas com preditores abióticos já que a importância das interações bióticas é considerada irrelevante em grandes escalas espaciais (hipótese do ruído Eltoniano). Para testar a hipótese do ruído Eltoniano, nós modelamos a distribuição de várias espécies de beija-flores distribuídas através do continente americano e avaliamos o efeito das interações bióticas no desempenho dos modelos e nas previsões espaciais (**Capítulo 1**). Nós encontramos que a adição das interações bióticas teve pouco efeito sobre a performance dos modelos e a adequabilidade ambiental predita, mas alterou a distribuição geográfica estimada das espécies. Essa dissimilaridade espacial não melhorou o modelo, o que sugere que os modelos de distribuição de espécies podem ser sensíveis a inclusão de variáveis preditoras, especialmente em grandes extensões espaciais. Além disso, a fim de entender os processos que regem a montagem e manutenção das comunidades, investigamos o papel da partição de recursos para a coexistência das espécies. Para isso, avaliamos quais atributos associados a aquisição de recursos tróficos podem explicar a coexistência de espécies similares nas comunidades (**Capítulo 2**). Concluimos que comunidades com maior sobreposição de espécies são, na verdade, particionadas em fina escala, associadas ao comportamento de forrageio das espécies. Por fim, sabendo que informações sobre as espécies são essenciais para estudar a biodiversidade, propomos avaliar o tamanho e as relações causais associadas à lacuna Raunkiaerana de aves (**Capítulo 3**). Identificamos que a lacuna de conhecimento sobre os atributos investigados é maior principalmente para espécies de regiões tropicais e com pequena distribuição geográfica, mas também mostramos que a maior disponibilização e mobilização de dados pode ampliar significativamente nosso conhecimento atual.

Palavras-chave: Bases de dados, Completude de informação, Co-ocorrência de espécies, Diagrama BAM, Interações positivas, Sobreposição de nicho, Trochilidae.

General abstract

Structural and climatic disturbances created directly or indirectly by human activity have a profound effect on organisms and are responsible for the increasing changes in biodiversity. Such changes are associated with relevant modification in the relative abundance, extinction and invasive ability of the species. In this context of imminent changes, there is an increasingly urgent need to describe patterns and understand processes that govern biodiversity, in order to predict and mitigate current and future changes. One way of doing this is through species distribution models, which are generally built only with abiotic predictors since the importance of biotic interactions is considered irrelevant at large spatial scales (Eltonian noise hypothesis). To test the Eltonian noise hypothesis, we modeled the distribution of several species of hummingbirds distributed across the American continent and evaluated the effect of biotic interactions on model performance and spatial predictions (Chapter 1). We found that the addition of biotic interactions had little effect on model performance and predicted environmental suitability, but altered the estimated geographic distribution of the species. This spatial dissimilarity did not improve the model, what suggests that species distribution models might be sensitive to the inclusion of predictor variables, especially in large spatial extents. Moreover, in order to understand the processes that govern the assembly and maintenance of communities, we investigated the role of resource partition for species coexistence. Specifically, we evaluated which traits associated with the acquisition of trophic resources can explain the coexistence of similar species in the communities (Chapter 2). We conclude that communities with more overlapping species are, in fact, partitioned on a fine scale, associated with the species' foraging behavior. Finally, knowing that information about species are essential for biodiversity studies, we propose to assess the size and the sources of the Raunkiaeran shortfall of birds (Chapter 3). We show that the knowledge gap on the investigated traits is large mainly for small-ranged species from tropical regions, but we also show that data sharing and mobilization can significantly expand our current knowledge.

Key-words: BAM diagram, Data base, Information completeness, Niche overlap, Positive interactions, Species co-occurrence, Trochilidae.

Introdução geral

O ser humano tem causado impactos substanciais no planeta Terra, que resultaram no surgimento do antropoceno (Steffen *et al.* 2011). As transformações que estão ocorrendo na superfície terrestre, como por exemplo a perda e fragmentação de habitats devido ao uso da terra, e alteração da composição do solo e da atmosfera através da deposição de substâncias nitrogenadas e liberação de carbono (Lewis & Maslin 2015) são rápidas e persistentes. Tais perturbações estruturais e climáticas criadas direta ou indiretamente pela atividade humana atuam profundamente sobre os organismos nos ambientes afetados e são responsáveis pela crescente mudança na biodiversidade. Essas alterações na biodiversidade estão associadas a alterações drásticas na abundância relativa, extinção e habilidade invasiva das espécies (Hermoso *et al.* 2011; Pyron 2018), o que resulta na desestabilização das interações biológicas (Tylianakis *et al.* 2008). Todas essas alterações podem modificar os padrões e reduzir os processos ecológicos essenciais realizados pelas comunidades e ecossistemas, incluindo serviços necessários ao bem-estar humano (e.g. serviços ecossistêmicos, Knapp 2019). Nesse contexto de mudanças iminentes, é cada vez mais urgente a necessidade de descrever e entender, da melhor forma possível, os padrões e processos que regem a biodiversidade, além de identificar a lacuna de dados faltantes, para tentar prever e mitigar as mudanças na biodiversidade que estão ocorrendo e que ocorrerão nas próximas décadas.

Biodiversidade não é um conceito simples, ela abrange múltiplos elementos da variabilidade biótica, como a diversidade taxonômica, genética, funcional e de interações (Maier 2012; Pereira *et al.* 2013). Essas diferentes formas de acessar a biodiversidade refletem diferentes objetivos que contribuem para entender melhor os padrões e processos como um todo, em escala local e global. Os estudos clássicos em ecologia frequentemente descrevem a biodiversidade em termos de identidade das espécies, enquanto os outros componentes da biodiversidade são geralmente subestimados (Díaz & Cabido 2001; van der

Plas 2019). O fato de a riqueza de espécies e medidas relacionadas serem mais populares está provavelmente associado a restrição de dados (Pereira *et al.* 2013; Schneider *et al.* 2019). Apesar da lacuna nos dados de biodiversidade ser bastante expressiva, especialmente em animais, diversos esforços têm sido realizados para compilação e ampliação dos conjuntos de dados disponíveis livremente (Wilman *et al.* 2014; Rodrigues *et al.* 2019; Gallagher *et al.* 2020; Ortega *et al.* 2020). Nesse sentido, a investigação de outros elementos associados a variabilidade biológica, como a pesquisa baseada em atributos funcionais e o uso de interações bióticas, vem ganhando bastante espaço na literatura (Heikkinen *et al.* 2007; Freitas & Mantovani 2018; Gherghel *et al.* 2018). Essas duas facetas da biodiversidade têm auxiliado na identificação de padrões e processos que moldam a distribuição das espécies e a associação entre as espécies nas comunidades, e portanto, são fundamentais para compreender melhor como as comunidades e os ecossistemas são estruturados, e como podem responder às mudanças globais atuais e futuras.

De modo geral, a distribuição das espécies no planeta pode ser determinada pela interação de três processos: barreiras físicas que limitam seu movimento (M), condições abióticas (A) adequadas aos seus requisitos fisiológicos e condições bióticas (B) formadas por interações favoráveis à sua ocorrência. Tais processos foram reunidos conceitualmente no diagrama BAM (Soberón 2007). Um ou mais desses componentes de tolerância das espécies são frequentemente combinados a dados de presença para, através de algoritmos correlativos (Urbina-Cardona *et al.* 2019), gerar modelos de distribuição que podem ser subsequentemente projetados para o espaço geográfico devido a “dualidade de Hutchinson” (Hutchinson 1957; Colwell & Rangel 2009; Peterson *et al.* 2011; Peterson & Soberón 2012).

Em geral é aceito que os processos associados ao diagrama BAM operam concomitantemente de forma hierarquia através das escalas espaciais. É esperado que as variáveis abióticas e aquelas associadas a dispersão dos organismos exerçam um papel

dominante na distribuição das espécies em escalas regionais e continentais, enquanto as interações bióticas devem desempenhar um papel importante em escalas locais (Pearson & Dawson 2003; Peterson *et al.* 2011). Essa abordagem assume que as espécies ocorrem em todos os locais acessíveis e dentro da sua tolerância climática (Kearney & Porter 2009), e, conseqüentemente, essa distribuição será mais ampla que a área hipoteticamente ocupada pela espécie, i.e., aquela que leva em consideração as outras limitações à ocorrência das espécies (Soberón *et al.* 2017). A suposição de que o impacto relativo das interações bióticas pode se tornar insignificante ao considerar escalas espaciais maiores é conhecida como hipótese do ruído Eltoniano (Soberón 2007). Esse pressuposto, associado a baixa disponibilidade de dados de interações bióticas, tem levado a maioria dos estudos a concentrarem seus esforços nos efeitos das condições abióticas sobre a distribuição das espécies. Só recentemente o crescente número de evidências tem demonstrado que as interações das espécies podem ser importantes em maiores escalas geográficas. Contudo, a maioria desses estudos são limitados a um pequeno conjunto de espécies (Araújo & Luoto 2007; Heikkinen *et al.* 2007; Atouchi *et al.* 2018; Palacio & Girini 2018; Raath *et al.* 2018), ou a uma área geográfica restrita (Meier *et al.* 2010; Pellissier *et al.* 2010; da Cunha *et al.* 2018; Kass *et al.* 2020). Além disso, ainda falta uma investigação da influência de predadores bióticos para além do desempenho do modelo, incluindo também análises espaciais associadas a mudanças nas projeções geográficas e estimativas das áreas de distribuição (Simões & Peterson 2018). Por isso, no **Capítulo 1** nós avaliamos a importância das interações bióticas para estimar a distribuição de várias espécies de beija-flores distribuídas sobre todo o continente americano usando tanto as medidas de desempenho dos modelos quanto análises de similaridade espacial.

O pressuposto hierárquico citado acima também representa um processo de filtragem ambiental que, conseqüentemente, seleciona em um local espécies que contém atributos

funcionais mais similares que o esperado ao acaso (Petchey *et al.* 2007). Contudo, a teoria da competição assume que para as espécies coexistirem elas devem apresentar alguma limitação às suas similaridades, de modo que as comunidades sejam compostas por espécies com características complementares em pelo menos uma dimensão do nicho (Hutchinson 1961; MacArthur & Levins 1967). Assim, é esperado que a coexistência entre espécies troficamente similares seja impulsionada principalmente pela disponibilidade de recursos alimentares e/ou partição de nicho nas comunidades, como por exemplo diferenças morfológicas ou comportamentais. No entanto, estudos que inferem a partição de nicho têm evidências conflitantes (Gómez *et al.* 2010; Hidasi-Neto *et al.* 2012). Por isso, no **Capítulo 2** propomos o uso de informações ecológicas detalhadas, como as contidas em redes de interações ecológicas, para quantificar a sobreposição de nicho e atributos associados a partição do nicho trófico como preditores da coexistência de espécies similares nas comunidades, a fim de entender melhor os mecanismos associados a coexistência entre espécies semelhantes.

Ao realizar os dois estudos anteriores, observamos que tanto as informações de atributos quanto de interações bióticas enfrentam fortes restrições ou ausência de dados. Enquanto algumas medidas, como os registros de ocorrência das espécies, por exemplo, tornaram-se mais populares e acessíveis nos últimos anos, outras ainda permanecem pouco conhecidas. As principais lacunas existentes na área de biodiversidade foram catalogadas por Hortal *et al.* (2015), mas ainda são poucos os estudos que quantificam essas lacunas. Apesar do grande esforço dos pesquisadores em coletar e disponibilizar os mais variados dados relacionados à biodiversidade, ainda estamos longe de ter um conjunto de informações robusto (Cornwell *et al.* 2019). Nessa linha, uma das lacunas que tem sido pouco explorada é a Raunkiaerana. Até recentemente não tínhamos nenhuma noção da dimensão dessa lacuna. Apenas nos últimos anos é que alguns estudos iniciaram a tarefa de tentar quantificá-la e propor soluções para reduzi-la (Etard *et al.* 2020; Gallagher *et al.* 2020). Contudo, ainda não

existem critérios bem estabelecidos sobre quais atributos são importantes de serem avaliados, principalmente para os grupos animais, e quais os fatores socioambientais associados a essa lacuna. Sabendo que a lacuna de conhecimento sobre os dados de atributos pode afetar o desenvolvimento dos estudos em biodiversidade, no **Capítulo 3** nós quantificamos a lacuna Raunkiaerana para aves. Especificamente, nós sintetizamos os atributos considerados ecologicamente relevantes de acordo com seu uso na literatura, avaliamos a completude de dados abertamente acessíveis para cada atributo, e mapeamos a completude média de cada região com base na distribuição das espécies. Com isso, avaliamos os fatores socioambientais que podem influenciar a existência de dados para aves e que podem, potencialmente, afetar também outros taxa.

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CAPÍTULO 1

Biotic interactions do not improve species distribution models
for hummingbirds¹

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Biotic interactions do not improve species distribution models for hummingbirds

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Abstract

Species distribution models (SDMs) are an important tool in ecology, biogeography and conservation planning. However, these models generally include only abiotic variables to access the environmental suitability and the potential distribution of the species in the geographic space. This occurs because the influence of biotic interactions in species distributions is assumed to decrease with the coarse resolution of the models (i.e. the Eltonian noise hypothesis). Although many studies have shown that the addition of biotic predictors can indeed increase the predictability of the models, these studies are generally limited in terms of number of species and spatial extent. In addition, these studies rarely evaluate the effect of biotic predictors on the spatial output of the models. In this study, we tested whether incorporating information about species interactions affects the quality and prediction of SDMs for 100 hummingbird species distributed throughout the New World. For each species, we generated two models: the first SDM was based only on climatic variables, while the second SDM included both the climatic variables and the environmental suitability of the main plant species visited by each hummingbird. Then, we compared the models' performance, spatial projection and geographic range estimation. Overall, we found that models purely abiotic and those combining biotic predictors showed similar performance values and indistinguishable projections of environmental suitability. Only the estimated geographic range of the species changed after including biotic predictors, especially for species occurring in large areas. However, this spatial dissimilarity did not improve the models, which can indicate a sensibility of SDMs to variables addition under large extents rather than a positive effect of biotic interactions. Thus, our study suggests that the inclusion of biotic interactions has little effect on the performance and spatial predictions of SDMs of hummingbirds. However, additional tests using different modelling techniques are still necessary to confirm the generality of these results.

Key-words: BAM diagram, Eltonian niche, Niche models, Positive interactions, Trochilidae.

Introduction

Species distribution models (SDMs) have become increasingly important to predict the impacts of anthropic threats and the current climate changes. In recent years, a number of SDM studies have been published focusing mostly on conservation planning and biological invasions (Guisan *et al.* 2013; Urbina-Cardona *et al.* 2019). These models are often built using correlative algorithms that combine points of occurrence and one or more predictor variable to define the niche space for a given species and subsequently project into the geographic space the regions that are suitable for its survival and population growth (Urbina-Cardona *et al.* 2019). The choice of the predictor variables should then represent those factors most likely affecting the species distribution.

In general, the distribution of the species depends on several factors that are currently represented in a simplified way by the “BAM diagram”. The diagram is based on a theoretical framework that lists three main components (Biotic, Abiotic and Mobility) that causally determine the distribution area of a species. Biotic conditions (B) are based on the concept of Eltonian niche (Elton 1927), which deals with biological interactions between organisms. These interactions can be of several types, so that they can facilitate or inhibit the persistence of a species in a given environment. Abiotic conditions (A) are based on the concept of Grinnellian niche (*sensu* Soberón 2007), which are associated with environmental variables that limit species physiologically. Mobility (M), on the other hand, represents the restriction to species dispersion and it is linked to the species' ability to disperse in areas favorable to their existence (Soberón & Peterson 2005). Although biotic, abiotic and mobility components represent a set of complementary conditions that enable the survival and permanence of the species in certain places, most models are based only on the abiotic needs of the species and rarely include the role of mobility and, specially, biotic interactions (Peterson *et al.* 2011; Record *et al.* 2018). The non-consideration of biotic interaction in

SDM is endorsed by the Eltonian noise hypothesis, which state that at large-spatial scales abiotic variables and dispersion restrictions should have a greater influence on species distribution than biotic interactions (Sóberon & Nakamura 2009).

However, no organism exists in absolute isolation in nature and, therefore, its interactions with other organisms are inevitable and fundamental for its survival and for the functioning of the ecosystem. These ecological interactions can be defined as the effects that an organism has on another one and are differentiated by the type of relationship that the organisms maintain with each other. These relationships either facilitate or limit the presence of species in favorable abiotic environments (Araújo & Rozenfeld 2014). For example, species that provide trophic or reproductive requirements for other species, can affect population growth and consequently the presence of the dependent species, directly influencing their geographic distribution at different scales (Abrams 1983; Heikkinen *et al.* 2007; Araújo & Rozenfeld 2014; da Cunha *et al.* 2018; Gherghel *et al.* 2018). Therefore, when a given species depends, to some degree, on another to survive, it must necessarily occur within the geographic range of its biotic resources (Cohen 1977; da Cunha *et al.* 2018; Gherghel *et al.* 2018).

Studies that use and assess the influence of biotic variables on modeling performance over large spatial scales have increased considerably in the last years (Heikkinen *et al.* 2007; Araújo & Rozenfeld 2014; da Cunha *et al.* 2018; Kass *et al.* 2020 and others). So far, these studies have shown that the inclusion of biotic variables increases the performance of SDMs. However, the inclusion of biotic variables in SDMs has still being a challenge due to the insufficient data availability on geographical distribution and biotic interactions for most species (i.e. Wallacean and Eltonian shortfall, Hortal *et al.* 2015), besides the dynamic nature of interactions in the temporal and spatial scope (Sóberon & Nakamura 2009; Peterson *et al.* 2011). In this sense, most analyses have been limited to a small set of focal and interactors

species (Araújo & Luoto 2007; Heikkinen *et al.* 2007; Gianini *et al.* 2013; Atauchi *et al.* 2018; Palacio & Girini 2018; Raath *et al.* 2018), or in a restricted geographical area such as one country or biome (Meier *et al.* 2010; Pellissier *et al.* 2010; da Cunha *et al.* 2018; Kass *et al.* 2020). Even for the few studies that evaluate a large number of species or species distributed over a wide geographic extent (Belmaker *et al.* 2015; Ilsøe *et al.* 2017), it is still lacking an investigation of the influence of biotic predictors beyond model performance, including also analyses of spatial changes in geographical projections and size/position of range estimates (Simões & Peterson 2018).

In this study, we assessed the importance of biotic interactions to estimate the distribution of hummingbird species on a large spatial scale. Hummingbirds have an obligatory relationship with nectar-producing plants, since 90% of their diet is based on nectar (Gass & Montgomerie 1981). In addition, they are considered highly specialized at the community level (Maglianesi *et al.* 2014). Since hummingbirds are a popular group, there are many studies on their distribution and ecology, so records of spatial occurrence and interactions records with nectar-producing plants are gradually becoming more available over time (Wolf 1970; Stiles 1985; Sazima *et al.* 1996; Rodríguez Flores 2009; Las-Casas *et al.* 2012; Tinoco *et al.* 2017). We compiled this data and constructed SDMs for the plants that interact with each hummingbird species and included them as biotic predictors for the construction bird's distribution model, combining abiotic and biotic variables. Finally, we compared the performance and prediction of these SDMs with those generated in function of purely abiotic predictors.

Methods

To assess the influence of biotic interactions on the performance and prediction of SDMs, we built two types of models for each hummingbird species: a) Abiotic Model, it was

generated in a standard way, using the occurrence of the hummingbird species and climatic variables as predictors; b) Combined Model, it was similar to the Abiotic Model but here we also included the environmental suitability of the plants that interact with the hummingbird as predictors. To project the environmental suitability of the plants we generate for each species a standard SDM using climatic and soil variables as environmental predictors (Velazco *et al.* 2017). According to Anderson (2017), the method described above is the most appropriated for including biotic predictors in SDMs as long as the distribution of the interacting species (here, the plants) does not depend exclusively on the focal species (hummingbirds). Since even plant species commonly visited by hummingbirds, such as Bromeliaceae, can be pollinated by insects and other vertebrates, not depending then exclusively on one hummingbird species (Fumero-Cabán & Meléndez-Ackerman 2007; Scrok & Varassin 2011), we considered this method adequate to our purpose.

Interaction records

In order to identify the plants consumed by each hummingbird, we first compiled data on the trophic ecology of different hummingbird species from the literature and from databases of ecological interactions. Specifically, we searched for quantitative interaction networks in the Web of Science database from 1945 to January 2020 with the following combinations of keywords: (hummingbird AND pollination) OR (hummingbird AND interaction) OR Trochilidae. In addition, we included data from scientific articles, theses and dissertations obtained only through Google Scholar®, the CAPES thesis and dissertations catalog (catalogodeteses.capes.gov.br), Web of Life (www.web-of-life.es), and the Interaction Web Database (iwdb.nceas.ucsb.edu). We selected only quantitative interaction networks with a minimum sampling period of eight months, covering the main annual climatic variations, as we consider that these networks present a sufficient sampling effort to describe the species' diet. Our search resulted in a total of 58 networks derived from 43

different sources. We then checked the taxonomic nomenclature of the species of hummingbirds and plants, respectively, in the HBW & BirdLife International (2019) and The Plant List (www.theplantlist.org). After correcting for synonyms, this initial dataset was composed by 2,060 unique interactions between 124 hummingbird and 637 plant species.

We assume that not all plants visited by a hummingbird species have a determining role in its distribution. That is, while the high consumption of a given plant should indicate a great dependence on this resource, sporadic consumption could reflect a resource independence, and including these sporadic interactions may not improve the distribution model (de Araújo *et al.* 2014). Therefore, we selected the most relevant plants in the diet of each hummingbird species based on the index proposed by de Araújo *et al.* (2014). According to this index, the most important plant species in the hummingbird's diet are the ones with high consumption over a broad area. So, we first calculated for each hummingbird species the proportion of visits to each plant recorded in each study. We then standardized this value so that the importance of each plant for a given hummingbird in each study varied from 0 to 1. Finally, we summed the standardized values of each plant across the interaction networks to find the most important plants for each hummingbird species. We selected for using as biotic variables, for each hummingbird species, plants with an importance value ≥ 0.9 . This value was chosen to ensure that each hummingbird species would have at least one biotic predictor in the model (de Araújo *et al.* 2014). After this process our data set was reduced to 488 unique interactions and 257 plant species.

Occurrence records and data cleaning procedures

The occurrence data for all selected species of hummingbirds and plants were obtained from the Global Biodiversity Information Facility database (www.gbif.org). After retrieving the data, we eliminated records: without coordinates information, made by machine or unknown sources, repeated geographical coordinates and outside the American continent.

To avoid using records outside the native range of the species due to misidentification, taxonomic change, geographical errors or introduced/cultivated distribution, we checked manually if the filtered records lay inside the countries where the species are naturally distributed. We used country limits to validate species occurrence because that was the only information easily accessible to compare the available occurrence records with the native distribution of the plants. For hummingbirds, this procedure was conducted consulting the species distribution in the BirdLife International (www.birdlife.org/). For plants, we consulted the Plants of the world online (www.plantsoftheworldonline.org), PLANTS Database (plants.sc.egov.usda.gov/java) and Invasive Specie Compendium (www.cabi.org/isc); when necessary we also checked the “Flora del Conosur” (www.darwin.edu.ar/Proyectos/FloraArgentina/fa.htm), “Flora do Brasil” (floradobrasil.jbrj.gov.br/) and “Catálogo de plantas y líquenes de Colombia” (catalogoplantasdecolombia.unal.edu.co). Any record classified as introduced or unclassified records with no evidence of natural distribution were removed and species of plants classified as exotic in the continent were completely excluded. Finally, we removed outliers by eliminating records >500 km from other records of the species using the “CoordinateCleaner” package (Zizka *et al.* 2019). We chose this distance because it performed best to our data in a previous visual examination. After this rigorous cleaning process, we selected only species occurring in 10 or more cells of our spatial grid in order to avoid biases caused by low number of occurrences (see Wisz *et al.* 2008). We also removed hummingbirds for which the total distribution of all interacting plants do not cover at least 90% of its occurrence records and disregarded interactions for which the plant species do not cover at least 25% of the focal species occurrence. We recognize that these overlap thresholds are arbitrary, but we considered that using hummingbirds for which the area occupied by the plants available cover only a small fraction of their occurrence records could bias our modelling results.

Therefore, our final data set was composed by 362 unique interactions between 100 hummingbirds and 202 plant species (Table S1), with a median of three and a maximum of 20 plant interaction per hummingbird species (see Fig. S1 in Supplementary Material for the distribution of the species).

Environmental variables

To characterize the climatic variation across the American continent, we used the CHELSA v1.2 database (Karger *et al.* 2017). This database provides 19 bioclimatic variables obtained from downscaling temperature and precipitation outputs from a global circulation model based on a statistical approach that includes the influence of local scale terrain features (topography, wind fields, etc.) and bias corrections using climatologic stations. Variables related to physical and chemical soil properties were obtained from the SoilGrids database (soilgrids.org/). SoilGrids provides nine variables for six different soil depths, totalizing 54 layers. Both climatic and edaphic variables were obtained at very high resolution (CHELSA: 30 arc-seconds; SoilGrids: 7.5 arc-seconds) and upscaled to the average value at 0.1° (5 arc-minutes). For a complete list of the variables used, see Table S2 of the Supplementary Material.

To avoid multicollinearity among predictors variables and overfitting of SDMs, we reduced the dimensionality of the predictors through a principal component analysis (PCA). This procedure extracts the dominant patterns from a group of predictor variables and summarizes this information in new uncorrelated predictors, the principal components (PCs). For each species, we selected the PCs that captured 95% of the total variation found in the original variables (i.e. climate and climate plus plant's suitability for abiotic and combined models, respectively) to calibrate the species' distribution models. The number of predictors used for each hummingbird species varied from an average of 5.52 ± 0.66 (mean \pm SD) in abiotic to 7.53 ± 2.15 in combined models (Supplementary Material Table S3).

Species modelling

To build the SDMs we used MaxEnt, a machine learning algorithm based on principles of maximum entropy that calculates the probability of presence of a species along the study background (Phillips *et al.* 2006). The definition of the geographical background (the extent of the study area) is a key point that can affect the performance and prediction of niche models (Acevedo *et al.* 2012). Therefore, we restricted the background region to areas that are potentially accessible for species. To do so, we first circumscribed the occurrence records of each species using a convex hull. Then, we selected the ecoregions (Olson *et al.* 2001) encompassed by this convex hull. Since both birds and plants show strong fidelity to ecoregions boundaries (Smith *et al.* 2018), our background represents a proxy for the species' historical dispersal area (see also Cooper & Soberón 2020). Then, a maximum of 10,000 background cells were randomly sampled from predictor layers.

To reduce the spatial autocorrelation between training and test records in each model, we used the 'block' method. This method partitions data into four bins based on the lines of latitude and longitude that divide occurrence localities as equally as possible in geographic (and environmental) space. Then, four models are run iteratively using three bins for training and the remaining one for testing. Metrics of model evaluation are then summarized across the 4 iterations (Muscarella *et al.* 2014). In addition, we optimized the models' performance by selecting among models with different combinations of features classes (Linear, Linear Quadratic, Hinge, Linear Quadratic Hinge, Linear Quadratic Hinge Product and, Linear Quadratic Hinge Product and Threshold) and regularization multiplier values (RM: 0.5, 1, 1.5, 2). The set of configurations that calibrated the ideal model was defined by the Akaike information criterion corrected for small sample sizes (AICc). The use of AICc for the comparison of SDMs represents a trade-off between the quality of the fit and the complexity of the model (Warren & Seifert 2011). In general, the optimized models are expected to be

less overfitted and exhibit lower omission rates than MaxEnt default models (Muscarella *et al.* 2014). All the models were run using the “*dismo*” (Hijmans *et al.* 2017) and “*ENMeval*” (Muscarella *et al.* 2014) R packages.

Model evaluation

To test the importance of including plants used as a trophic resource in the modeling of hummingbird species, we selected two different metrics, widely used in the literature, that capture different aspects associated with performance of the SDMs to compare purely abiotic and combined models: Sensitivity and Specificity (Fielding & Bell 1997; Jiménez-Valverde 2014). Sensitivity and Specificity quantify, respectively, the errors of omission and commission, that is, the proportion of presence and absence records correctly classified (Jiménez-Valverde 2014). To calculate these threshold-based metrics, we converted continuous predictions into binary maps using a threshold that maximizes the sum of sensitivity and specificity for each model. This method has proven to be robust for use with both presence/absence and presence-only data (Liu *et al.* 2005; Liu *et al.* 2016).

Data analysis

The overall performance of purely abiotic and combined models was compared with the Wilcoxon matched-pairs test, using each hummingbird species as a sample. We used the Wilcoxon test because our data did not meet the assumptions necessary for the parametric analysis. We also assessed the best fit between the two models comparing their second-order Akaike information criterion (AICc; Burnham & Anderson 2002). To evaluate the possible changes in spatial predictions when biotic variables are included, we also calculated the spatial similarity in environmental suitability and geographic range projection between results from abiotic and combined models. The degree of similarity in environmental suitability was estimated using the Schoener’s D index (Warren *et al.* 2008), which ranges from 0 (suitability

completely divergent) to 1 (identical suitability) and has been widely used in species distribution modelling studies. Geographical range similarity was measured using the Jaccard index after converting the continuous suitability estimates to binary presence/absence maps by applying the maximum sensitivity plus specificity threshold, that is, area hypothetically occupied by species according to the models. Specifically, we compared for each species whether its set of grid cells occupied according to the abiotic model is similar to the set of grid cells that are occupied according to the combined model. We evaluated both the total dissimilarity and the fraction resulting from turnover and nestedness component using the “*betapart*” package (Baselga *et al.* 2018).

Finally, using a linear regression, we evaluated whether differences in environmental suitability and estimated geographical range between abiotic to combined models can be influenced by the geographic extent (number of grid cells within the area occupied by the species), number of records (number of grid cells comprising the species record) and number of interactions. In all regression models, the predictor variables were log-transformed to increase normality and a weighted regression using fitted values from the estimated variance as weights was adopted when we detected heteroscedasticity. All analyzes were conducted in the R programming environment version 3.6.0 (R Core Team 2019) using the packages cited above.

Results

Model performance

Metrics of SDM performance for each hummingbird species showed, on average, high values with little variation, regardless of whether the predictor was abiotic or combined (Table 1). Sensitivity and Specificity mean values were ≥ 0.83 (Table 1), indicating that both abiotic and combined models have adequate performance, correctly predicting most of the

presence and absence of hummingbird species. The AICc criterion was lower for most models that included both abiotic and biotic predictors (73%) compared to those that included only abiotic predictors (27%, see Table S3 of the Supplementary Material).

Table 1. Average values of performance metrics of species distribution models for hummingbird species using abiotic and combined predictors. We also report the mean values, standard deviation and results of the Wilcoxon matched-pairs test between the two models.

	Abiotic model		Combined model		es	Wilcoxon	p-value
	Mean	s.d.	Mean	s.d.			
Se	0.87	0.1	0.88	0.08	0.01	1629	0.13
Sp	0.83	0.08	0.83	0.09	<0.01	2380	0.62

Sensitivity (Se) and Specificity (Sp), degrees of freedom (df), es (effect size).

Spatial predictions

Our spatial prediction comparisons revealed a high overlap between environmental suitability estimated by purely abiotic and combined models (median = 0.97; Figure 1 and Table S4 of the Supplementary Material). This high similarity did not change with the number of interactions of the hummingbird species ($R^2_{\text{interactions}} < 0.07$; $p > 0.05$), number of occurring cells ($R^2_{\text{occurrence}} = 0.01$; $p > 0.05$) or geographic extent ($R^2_{\text{geog.exten.}} = 0.01$; $p > 0.05$). On the other hand, the geographic range estimation after converting continuous projections to binary presence/absence maps showed only a moderate and variable similarity between the two models, with a median of 0.69 (Figure 1). Changes in geographic similarity were not affected by the number of interactions ($R^2_{\text{interactions}} = 0.04$; $p > 0.05$) or number of occurring cells ($R^2_{\text{occurrence}} = 0.03$; $p > 0.05$), but it was influenced by geographic extent ($R^2_{\text{geog.exten.}} = 0.16$; $p < 0.01$). Overall, we found that the geographic similarity of the binary maps decreases with the increasing geographic extent (Figure 2). We also found that the contribution of turnover is greater than that of nestedness to the total geographic dissimilarity between the models ($t = 4.83$, $df = 198$, $p < 0.01$), and the number of cells designated as a

potential presence did not vary between the models (paired $t = -0.16$, $df = 99$, $p > 0.05$). This predominance of the turnover component in the geographic dissimilarity of the two models indicates that there is a spatial shift in the binary maps of the hummingbird species instead of a reduction in the number of occupied cells when biotic variables are added to the models.

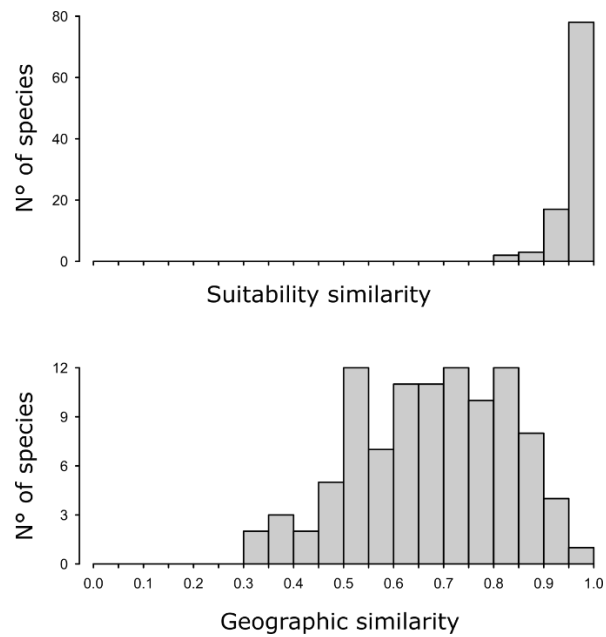


Figure 1. Histograms showing the distribution of similarity in environmental suitability (top) and binary geographic projection (bottom) between models including only abiotic and combined (abiotic + biotic) predictors. Environmental suitability similarity was calculated using Schoener's D index estimations, and geographic similarity was calculated using Jaccard similarity to compare the cells potentially occupied by the species after converting continuous projection into binary presence/absence maps.

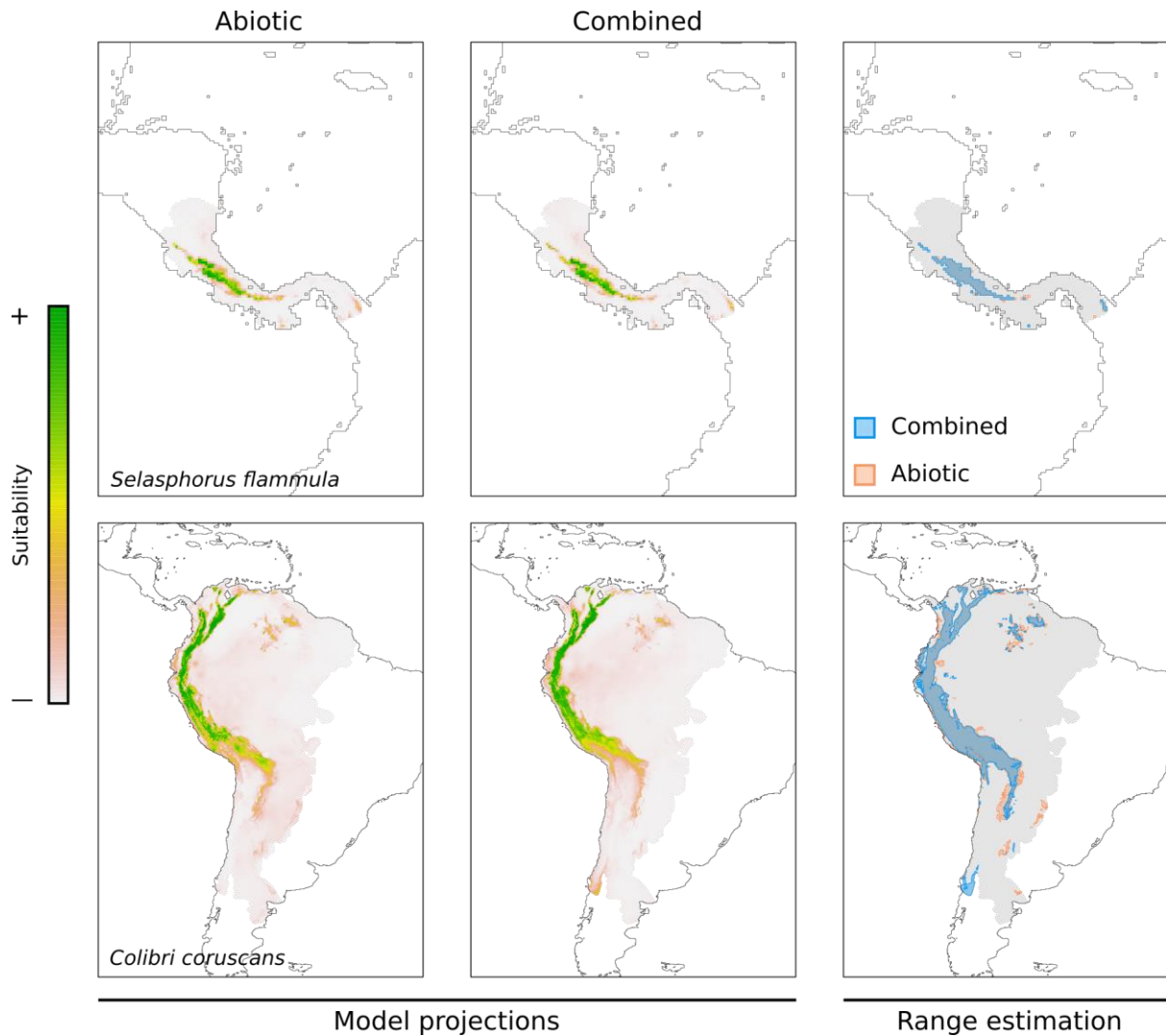


Figure 2. Example of the difference in model projection and range estimation for two hummingbird species with different geographical extent. Species distribution models were generated using only abiotic or the combined (abiotic + biotic) predictor variables and the estimated range were defined based on the maximum sensitivity plus specificity threshold.

Discussion

In this study, we evaluated the importance of including biotic interactions in SDMs (specifically MaxEnt), a step generally neglected in models at large geographic scales (Sóberon & Nakamura 2009). We found that the inclusion of biotic predictors improves model fit (AICc), but the accuracy of the model is not affected. Our results show that the addition of biotic interactions in SDMs can noticeably modify only the estimated range of the

widely distributed species after binarizing model's output to presence/absence maps. However, as we explain below, considering the overall results, this geographic dissimilarity seems to support rather than contradict the Eltonian noise hypothesis.

Generally, the inclusion of biotic predictors tends to increase the complexity of the models through greater overfitting and omission errors (false absences; Radosavljevic & Anderson 2014). However, we found that both the sensitivity and specificity values do not change significantly, indicating that the accuracy of the models is not altered by the inclusion of biotic interactions. Despite this result, most models still showed better fit (AICc). At first glance, this could indicate an influence of biotic interaction on large-scale geographic distributions, in line with the growing number of studies which show that different types of biotic interactions significantly improve SDMs predictions over a wide range of taxa (Heikkinen *et al.* 2007; Meier *et al.* 2010; Atauchi *et al.* 2018; Gherghel *et al.* 2018; Kass *et al.* 2020). However, we consider that the difference in projections between models that include combined predictors (i.e., abiotic and biotic) and those only abiotic is too small to contest the Eltonian noise hypothesis.

Most of the studies that assess the influence of biotic predictors have evaluated species that have a strong relationship with their interactors, being it trophic or related to reproductive dependence (Heikkinen *et al.* 2007; da Cunha *et al.* 2018; Gherghel *et al.* 2018; Palacio *et al.* 2018; Atauchi *et al.* 2018). For this reason, it has been suggested that the importance of biotic interactions for SDMs may be linked to the level of ecological dependence of the focal species (Araújo & Rozenfeld 2014). Although we have selected only the most relevant plant species to act as predictors of the occurrence of hummingbirds, these strong interactions are not necessarily exclusive and, as showed by our data, less frequent visits also occurred in other plants. In addition, it is not totally clear if the number of interactions of the local specialists would not increase at a regional scale (Gaston *et al.* 1997).

For these species, interactions can be too complex and dynamic to be accurately represented by a static model (Peterson *et al.* 2011; Anderson 2017). Therefore, the lack of exclusive relationships across scales may be the main reason why we did not find influence of biotic interactions on the hummingbirds' SDMs.

Although environmental suitability was highly similar between models using abiotic and combined predictors, our results revealed that the projected ranges were spatially variable. Generally, studies that do not support the Eltonian noise hypothesis also find some spatial changes resulting from a reduction in the size of the potential range (Cunha *et al.* 2018; Gherghel *et al.* 2018). The inclusion of biotic predictors reduces the overestimation of the geographic distribution generated based solely on abiotic predictors (da Cunha *et al.* 2018; Raath *et al.* 2018), and brings the projection closer to the realized distribution of the species (occupied area, *sensu* Soberón *et al.* 2017). This pattern is in line with the hierarchical niche structure proposed by Soberón (2007), which suggests that large-scale environmental conditions determine all the potentially suitable areas that meet the physiological requirements of a species (i.e. the Grinnellian niche), but biotic interactions are necessary to determine the subset of these areas that remain ecologically habitable (i.e. the Eltonian niche). However, we did not find a reduction in the size of the estimated range of the species as in previous studies. Conversely, the geographic dissimilarity identified here was associated mainly to turnover, indicating that there is some degree of spatial change in the location of the estimated geographic ranges after including biotic predictors.

The variability of the estimated range was not affected by the number of interactions or number of occurrence cells, but by the geographic extent of the area occupied by the species. According to visual inspections, this dissimilarity seems to be result from the spatial mismatch of the potentially occupied cells at the edges of the estimated ranges (i.e. noise, Figure. 2). The perception of this noise becomes more evident for species with large

geographic extent, when the edge mismatch increases to consistent patches of spatial displacement. Considering that these outputs are not better in terms of sensitivity and specificity estimates than those generated by models using climate-only predictors, this result shows that adding interactions changed the projected distribution without necessarily improving it. Therefore, the spatial displacement found here does not seem robust to reject the Eltonian noise hypothesis. Instead, it seems indicate a higher sensibility of SDMs to model changes under large extents. Larger ranges generally encompass greater environmental heterogeneity, which could lead to higher uncertainty in the occurrence-environment relationship for wide compared to narrow-ranging species (McPherson & Jetz 2007). Other studies have already shown that the addition of predictor variables had only minor effects in the spatial output of range-restricted species (Bucklin *et al.* 2015), and that these species produce models with better performance than those widely distributed (McPherson & Jetz 2007; Tessarolo *et al.* 2014). Range projections of environmentally restricted species are also more spatially consistent even when comparing outputs from different algorithms, which tends to decrease as species become environmentally more generalist (Grenouillet *et al.* 2011). However, further studies are needed to investigate how sensible are the SDMs' outputs to the addition of predictor variables under different geographic extents.

In summary, our study shows that the inclusion of biotic interactions does not increase the performance and spatial predictions of SDMs for hummingbirds, at least not using the MaxEnt algorithm. Specifically, our study suggests that the scale at which biotic interactions remain important may depend on the exclusive dependence of the focal consuming species on their resource species, in addition to the type of interaction studied (Araújo & Rozenfeld 2014). Therefore, future studies should investigate how the changes in the interaction dependence (not only interaction strength) affect the performance and output of distribution models. We also highlight that projections of species with large geographic range tend to be

more sensitive to the addition of predictor variables, though such effects are noticed only when continuous projections are converted to binary maps. Overall, the small influence of biotic variables detected in our study may be seen as the representation of the Eltonian noise. Therefore, although several studies have reported evidence contrary to the Eltonian noise hypothesis, our result indicates that the relevance of biotic interactions in SDMs is more nuanced than previously expected. However, additional tests using different methods to model the distribution of species are still necessary to confirm the generality of these results.

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CAPÍTULO 2

Availability of resources shapes niche overlap in
hummingbird communities

² Kurtz, M.N., Almeida Neto, M, Cianciaruso, M.V. Availability of resources shapes niche overlap in hummingbird communities. *Manuscript in preparation.*

Availability of resources shapes niche overlap in hummingbird communities

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Abstract

The limiting similarity theory predicts that ecological communities should be formed by species with complementary traits in at least one niche dimension. However, studies using morphological traits to infer niche partitioning have conflicting evidences regarding the relationship between coexistence and species trait similarity. In this study, we used ecological information of hummingbird-plant ecological networks to quantify niche overlap. Then, we evaluated the effect of hummingbird morphological traits linked to resource acquisition and foraging behavior on the niche overlap. In addition, we quantified the availability and diversity of resources as control variables. We found a positive relationship between niche overlap and dominant behavior of species and a negative relationship with bill length variation and availability of resources. Thus, communities where species share more resources are those localized in less productive regions with morphologically less specialized species. Although this composition may intensify competition among species, it is offset by differences in the dynamics of foraging behavior. On the other hand, highly productive communities allows hummingbirds to optimize resource acquisition through less defensive behaviors and the selection of the resource based on their aptitude for consumption, reducing niche overlap. Thus, the niche partition through the foraging behavior justifies the coexistence of ecologically similar species, in communities with scarce resources. While communities with abundant resources do not seem to depend heavily on the partition of resources due to relaxation of competitive interactions.

Key-words: Net Primary Productivity (NPP), Mean Pairwise Distance (MPD), Wing Disc Loading (WDL), competitive ability, co-occurring species, dominant and subordinate behavior, theory of optimal foraging.

Introduction

A central goal in community ecology is to understand the main processes that control the assembly and maintenance of ecological communities (Hutchinson 1957; Hubbell 2001). Niche-based theories assume that communities are assembled by environmental filtering and by interspecific competition (Keddy 1992; Díaz *et al.* 1999; McGill *et al.* 2006). If environmental filtering is strong, then co-occurring species should be functionally more similar than expected by chance (Petchey *et al.* 2007). However, competition theory assumes that there is a limiting similarity among co-occurring species, so that communities should consist of species with complementary traits in at least one niche dimension (Hutchinson 1961; MacArthur & Levins 1967). For instance, the coexistence of species that compete for some limiting resource is expected to be facilitated if the competing species show some level of morphological dissimilarity (Chesson & Case 1986; Leibold 1998). Non-random dissimilarity in morphological traits within ecological communities have been interpreted as an indirect evidence of the importance of competition (Young *et al.* 2010, Abrahamczyk & Kessler 2015, Guterres *et al.* 2020). For vertebrates, such evidence arises through the analysis of different traits, such as head length in lizards, dental morphology in rodents, and bill size in birds (e.g., Huey 1974; Dayan & Simberloff 1994; Maglianesi *et al.* 2014, Sottas *et al.* 2020).

Food resources are one of the most relevant niche dimensions for the stable coexistence of species, because it is directly linked to the growth and reproduction of the organisms. A greater amount of energy can lead to higher availability of trophic resources, thus supporting a greater number of individuals and species, i.e. high niche overlap, due to the relaxation of the competition (Wright 1983; Evans *et al.* 2006; Pigot *et al.* 2016). On the other hand, a lower amount of energy will lead to greater competition for trophic resources, promoting morphological and behavioral divergences between species (Kelt & Brown 1999;

Maglianesi *et al.* 2015a,b; Lattanzio & Miles 2016), i.e. high partition of the trophic niche. The availability and diversity of food resources are especially important for trophically specialized guilds, such as hummingbirds, in which floral nectar usually comprise more than 85% of their diet (Gass & Montgomerie 1981). The combination of dietary specialization and high metabolic rates (Schuchmann 1999) makes constant access to food indispensable for hummingbirds. Thus, the segregation of the trophic niche can be particularly important for species coexistence in hummingbird communities. In general, a higher phenotypic specialization to feeding nectar is expected to facilitate the resource sharing among coexisting hummingbird species (Maglianesi *et al.* 2014).

The close morphological matching between traits of hummingbirds and plants is widely documented, especially the matching between bill and corolla length (Sazima *et al.* 1996; Walther & Brieschke 2001; Maglianesi *et al.* 2014). More specialized hummingbirds are generally slightly larger and have a longer and often curved bill (Feinsinger *et al.* 1982; Cotton 1998a; Maglianesi *et al.* 2014), feeding regularly on flowers that have a long corolla whose flowers store more nectar (Snow & Snow 1972; Cotton 1998a). On the other hand, species with a straight bill and medium to short length are generally smaller and can efficiently use small flowers (Snow & Snow 1972; Araujo & Sazima 2003; Dalsgaard *et al.* 2009). These species are adapted to use many plant species, being classified as less specialized (Snow & Snow 1972; Cotton 1998a; Walther & Brieschke 2001). The high degree of matching between the morphological characteristics of hummingbirds and consumed flowers is advantageous for the bird species as it increases the acquisition of nectar due to the fast and efficient ingestion, which contributes to increase their fitness (Temeles 1996; Dohzono *et al.* 2011; Maglianesi *et al.* 2014). This food segregation reduces interspecific competition in communities and facilitates resource allocation (Feinsinger & Colwell 1978; Lara 2006).

Behavioral differences in foraging activities also contribute to the species segregation in the trophic niche, increasing hummingbird coexistence (Lyon 1976; del Rio & Eguarte 1987; Walther & Brieschke 2001; Ornelas *et al.* 2002; Lara *et al.* 2011). Hummingbird species usually adopt a dominant or a subordinate behavioral strategy during their foraging activities. Dominant species are territorial, i.e. their individuals defend a territory containing food resources against potential competitors (Feinsinger 1976; Feinsinger & Colwell 1978; Cotton 1998b), with more aggressive defense on areas with higher quality or quantity of nectar (Temeles *et al.* 2005; Justino *et al.* 2012). The subordinate species, in turn, explore their resources without exhibiting territorial behavior (Feinsinger & Colwell 1978; Rios *et al.* 2010; Tello-Ramos *et al.* 2015). Because the dominant species feed on resource-rich, the subordinate species are forced to explore areas less rich in nectar (Lara *et al.* 2009; Abrahamczyk & Kessler 2010).

Niche partitioning is widely used in the literature to explain the coexistence of species (Safi *et al.* 2011; Hidasi-Neto *et al.* 2012; Sobral *et al.* 2016), where competitive exclusion and limiting similarity should favor the coexistence of functionally different species, promoting the exploitation of different resources (Pianka 1974, Schoener 1974). However, some studies have shown that species richness may not necessarily be associated with an increase in trait dissimilarity and may even be associated with an increase in trait similarity (Gómez *et al.* 2010; Hidasi-Neto *et al.* 2012). In this sense, the use of interaction networks and functional traits of species can help us to better understand the coexistence of species. Here, we investigate how resource partitioning, a broad concept of resource acquisition that includes different dimensions of the niche, like consuming slightly different resources or consuming the same resource at different locations, interfere in the overlapping of the trophic niche of hummingbird communities. Based on networks of plant-hummingbird trophic interactions, we quantified niche overlapping and the mean and variation of morphological

and behavioral traits of hummingbirds related to resource acquisition. We expect that communities with greater niche overlap will have competition attenuated by different ways of obtaining and foraging on the resources, especially in communities that have less resource availability. On the other hand, communities with high resource availability will have relaxed competition interactions and coexistence will be independent of bill morphological or foraging behavior.

Methods

Data collection

Our study units were flower-visiting networks composed of hummingbirds and plants. To gather hummingbird-plant networks, we performed a search on the ISI Web of Science with the following keywords: (hummingbird OR trochilidae) AND (communit* OR pollinat* OR interact* OR visit*). In addition, we compiled data from published scientific articles not included in the ISI Web of Science database, dissertation and theses using Google Scholar®, the CAPES thesis and dissertation catalog (<https://catalogodeteses.capes.gov.br/catalogodeteses>), the NCEAS Interaction Web Database (www.nceas.ucsb.edu/interactionweb) and Web of Life (www.web-of-life.es). Among the 92 plant-hummingbird networks we found in the literature, we selected 43 that meet the requirements mentioned below (details in Appendix A).

In order to minimize potential biases, some criteria were established for the inclusion of the networks in this study: i) only networks in which all species of hummingbird and plants visited by hummingbirds were potentially sampled in the same location, i.e. include legitimate (with pollination) and illegitimate (without pollination) visits. Studies that focused only on a particular group or species of hummingbirds or plants, or on a particular type of visit were excluded; ii) only networks with a minimum sampling period of six months and

that contemplated the annual seasonal variation were included, in order to avoid the influence of the sampling effort and seasonal variations (Cotton 2007; Vizentin-Bugoni *et al.* 2016); and iii) only networks with little or no anthropic influence were selected to avoid potential biases on the results (Mason *et al.* 2011; Hidasi-Neto *et al.* 2012).

We evaluated the degree of niche overlap (NO) among hummingbird species in each network by using the Morisita-Horn index (Horn 1966), which measures the similarity in the pattern of interactions among the species of the same guild. Thus, communities with many specialist species will have a low value of niche overlap ($NO \cong 0$, i.e., high resource partitioning), while communities with a predominance of generalists will have a higher value of niche overlap ($NO \cong 1$, i.e., low resource partitioning).

For each community, we also compiled hummingbird trait data that reflect resource use and partitioning. The morphology of the bill varies widely among hummingbird species and is strongly related to the morphological characteristics of the flowers (Walther & Brieschke 2001; Maglianesi *et al.* 2014). Here, we used bill length (BL) as it can directly influences resource obtaining and the foraging efficiency (Dalsgaard *et al.* 2009; Temeles *et al.* 2009; Maglianesi *et al.* 2014). Additionally, we compiled body mass and wing length data to calculate the wing disc-loading index. Higher wing disc-loading index values promote greater speed and maneuverability that provide greater competitive ability, these characteristics are associated with the territorial dominance and, consequently, the resources dominance in hummingbird species (Feinsinger & Chaplin 1975; Feinsinger & Colwell 1978 (Table 1 and details in Appendix B). That is why in our study the wing disc loading (WDL) was considered a surrogate of defense behavior.

Table 1. Specifications of the traits used.

Traits	Definition	Unity
Bill length (BL)	Measure efferent to exposed culmen. Length from beginning of feathers to tip of beak.	cm
Wing disc loading (WDL)	Calculated by the formula $WDL = BM/\pi * (2.5 * WL/2)^2$, where BM is body mass (g), and WL is wing length (cm) (Feinsinger & Chaplin 1975). WL can be defined as wing chord and were measured as the distance from the carpus to the tip of the longest primary feather (Stiles & Altshuler 2004).	g/cm ²

For each community (i.e., plant-hummingbird network) we generated a Euclidean distance trait matrix to calculate the average dissimilarity between the trait's values of the species (mean pairwise distance), which was calculated separately for BL and WDL. These measure reflect niche differences among species independent of species richness (de Bello *et al.* 2016). In each community, the index was standardized by its maximum distance to vary between 0-1 ranges, from communities with functionally similar species (mean pairwise distance $\cong 0$; low dissimilarity) to functionally unique species (mean pairwise distance $\cong 1$; high dissimilarity). Communities with lower functional similarity among species indicate greater specialization and consequently greater resource partitioning. In addition to the mean pairwise distance, we also evaluate the average values of the BL and WDL across communities. The NO index was calculated with the "bipartite" package version 2.15 (Dormann *et al.* 2009) and the mean pairwise distance with the "melodic" function (de Bello *et al.* 2016).

The Net Primary Productivity (NPP) at each community was extracted from the Moderate Resolution Imaging Spectroradiometer (MODIS) data, MOD17A3 data set (Running *et al.* 2017). We averaged the daily estimates between the years 2000 and 2017 and

extracted the NPP values of the cells where the studied communities were located using *raster* package (Hijmans & Etten 2019). High NPP values are associated with high energy availability. In tropical forests, reproductive structures (flowers and fruits) represent about 6-15% of total NPP and have small spatial variation (Malhi *et al.* 2011). Therefore, we assumed that NPP is positively associated with the number of available flowers and consequently the greater availability of nectar resources. In addition, we used the ratio between the species richness of hummingbirds and plants as an indicative of potential competition, where the higher values of the ratio reflect a higher number of species of hummingbirds visiting the same plants, that is, potentially sharing the same resources.

Data Analysis

To test if niche overlap could be explained by the predictor variables, we used a multiple linear regression analysis. To assess the extent of collinearity between the explanatory variables included in the model, we kept only variables with variation inflation factors (VIFs) < 5 (Zuur *et al.* 2010). Because our tests revealed collinearity between the mean value of BL and the mean pairwise distance of BL, we opted to remove mean BL from the model. Thus, the global model to explain variation in niche overlap was composed of mean pairwise distance of WDL, mean pairwise distance of BL, mean value of WDL, NPP and the ratio between hummingbird richness and plant richness. The last two variables were added as control variables, as they can affect network structure and consequently species coexistence. When necessary, the variables were transformed by $\log_{(x + 1)}$ to meet the normality assumption.

We used all possible combinations of predictive variables, and compared the models adjusted by maximum likelihood. Each model was ranked according to its value determined by Akaike's information criterion (AIC) corrected for small sample size (AICc: Second-order Akaike Information Criterion; Burnham & Anderson 2002) and the best model was selected

(Table S1). In addition, we measured the relative importance of each predictor variable with the method LMG, which calculates the r-squared contribution averaged over orderings among regressors. Finally, based on geographical coordinates of each locality, we also evaluated the existence of spatial autocorrelation in the model's residuals using the Moran's I index. Overall, no evidence of spatial autocorrelation was detected (Moran's $I = -0.10$, p-value = 0.47). All analyses were performed in the software R (R Development Core Team, 2019) with package “*MuMIn*” (Bartoń 2018), “*relaimpo*” (Grömping 2006), “*ape*” (Paradis & Schliep 2019) and “*fields*” (Nychka *et al.* 2017).

Results

Among the 43 analyzed flower-visiting networks (Fig. S1), the species richness of hummingbirds and plants in each community varied from 2 to 24 (mean \pm SD: 8.2 ± 4.1) and from 5 to 68 (22 ± 14), respectively. The number of plant-hummingbird interactions ranged from 1 to 34 (6.7 ± 6.5) across communities. No hummingbird species occurred in more than eight communities and almost half (45%) of the hummingbird species occurred in a single community.

Overall, niche overlap varied widely among communities from 0.07 to 0.91, but cases of low niche overlap were more prevalent (mean \pm SD: 0.3 ± 0.2 , Fig. S2). Among all possible models, the best model explaining changes in niche overlap among hummingbird species was composed by mean WDL, mean pairwise distance of BL and NPP, that together explain 28.6% of niche overlap (see all models in Table S1). Each variable contributed, respectively, with 45%, 29% and 26%, of the explained variation in niche overlap.

Mean WDL value was positively related to niche overlap, while mean pairwise distance of BL values and NPP were negatively related to species' niche overlap (Table S2). This means that the niche overlap was greater in communities where hummingbirds have

higher mean WDL values, lower BL variation and in places with lower productivity. On the other hand, communities with lower niche overlap have, on average, low WDL values and high variation in BL values, in addition to high NPP.

Discussion

Here we investigate the relationship between niche overlap and functional traits in local hummingbird communities. Our results demonstrated that the level of trophic niche overlap in hummingbird communities is partially explained by mean wing disc loading values, bill length variation and net primary productivity. Niche overlap was higher in communities with less resource availability (i.e. local productivity) and negatively related to the variation in the ability to obtain resources (i.e. bill length). Moreover, it is positively related to morphological traits associated to hummingbird defensive behavior. These findings show that hummingbird communities with greater niche overlap are also those with low resource availability, in which most species have greater dominance behavior over the food territory to avoid functionally similar species.

The variable that best explained niche overlap within hummingbird communities was mean WDL, a proxy for defensive behavior in hummingbirds. A dominant behavior occurs in hummingbirds species when they defend a territory, while subordinated species do not defend their territory. Species with subordinate behavior can act in two ways: i) foraging only on resources that are outside the territories defended by dominant species; or ii) foraging over resources that are defended by dominant species. In this last case, the intruder remains in the protected area looking for food until it is expelled by territorial dominant (Feinsinger & Colwell 1978; Ornelas 1994; Barbosa-Filho & de Araujo 2013). The defense of the territory carried out by hummingbird species with dominant behavior involves great energy expenditure that is compensated by the nectar provided by the protected plants (i.e. positive

cost-benefit). Thus, the size of the territory can vary according to the availability of resources but it is restricted to the limit where the defense becomes energetically expensive (Justino *et al.* 2012). That is, in conditions of low availability of resources, communities can present a great number of territorial species, as we found here, but these species tend to have more extensive protected territory (Fonseca *et al.* 2015). The larger the size of a territory, the lower its efficiency in defending it, facilitating the occurrence of intrusive behavior and increasing trophic niche overlap, especially reported on the periphery of the territory (Walther & Brieschke 2001).

Although we found that hummingbirds consume similar resources in communities with low productivity, in general, they prefer to consume flowers that have characteristics that correspond to their bill morphology, as these flowers provide high foraging efficiency; that is, they can consume more nectar in less time, increasing their fitness (Temeles 1996; Dohzono *et al.* 2011; Maglianesi *et al.* 2014). However, this is not a mandatory relationship. It is known that hummingbird species feed on a variety of plant species. In this context, our results indicate that the use of a given resource may depend on its availability. According to Temeles *et al.* (2002), the scarcity of hummingbird 'favorite flowers combined with competition for these resources can result in the incorporation of new flowers into the diet, even though these flowers have little correspondence with the foraging morphology. It is quite common to observe hummingbirds that regularly visit flowers that are not morphologically suitable for them to feed (Feinsinger *et al.* 1982; Arizmendi 2001; Dziedziuch *et al.* 2003; Lara *et al.* 2009; Maruyama *et al.* 2013, 2015; Fonseca *et al.* 2015). These flowers can contribute to the acquisition of a considerable part of the hummingbirds' diet. *Phaethornis ruber*, for example, can have approximately 30% of its diet composed of them (Maruyama *et al.* 2015), and this percentage can be higher in communities with low availability of resources. In this context, our results suggest that species that are highly

specialized in a given resource would have difficulty in acquiring the amount of resources sufficient to supply their energy needs in communities with low availability of resources and strong competitive interactions.

On the other hand, we found that communities with low niche overlap have less territorial species, and the hummingbirds tend to have more dissimilar bill morphology (i.e. ability to obtain different resources) and more resource available. It is expected that species will have interspecific interactions reduced in communities with greater abundance of resources, facilitating their coexistence (Abrahamczyk & Kessler 2010; Malhi *et al.* 2011). In this scenario, the energy needs of all species that make up the community are met, which reduces competitive interactions, and keeps niche overlap low. In addition, species with different bill morphology tend to consume flowers that provide a better cost-benefit balance, while territorial species, with less occurrence, tend to defend smaller areas, which in this case are sufficient to meet their energy costs (as discussed earlier). Species with subordinate behavior, that are majority, also follow a similar pattern, where the increase in available resources allows species to take smaller areas to acquire resources (Tello-Ramos *et al.* 2015), which can make the intrusive behavior reduced or non-existent. In a context of high availability of resources, hummingbirds can focus on plant species and behaviors that increase their fitness, but without increasing the risk of confrontation with other species, reducing interspecific competition. This is in line with the Optimal Foraging Theory (MacArthur & Pianka 1966), which assumes that animals tend to maximize their fitness through the way they forage, that is, they select their diet and structure their foraging activities to maximize gain and minimize energy losses per unit of time, which increases the efficiency of foraging (Charnov 1976; Pyke *et al.* 1977). In hummingbirds, the net energy gain depends on the energy value of the flower nectar, the time used to handle the flowers and ingest the nectar (handling time), the time to fly from flower to flower and the presence

of negative interspecific interactions during foraging. Thus, to optimize foraging, hummingbirds can use information contained in the environment to restrict their effort to those flowers that offer a greater net amount of energy. Flowers that have higher volume and concentration/quality of nectar as well as those with shorter handling times (Maglianesi *et al.* 2014; Temeles *et al.* 2016, 2017) can be selected by the morphological characteristics of the flowers, such as length and corolla curvature, angle of inclination of the flower and number of inflorescences per plant (Sandlin 2000; Sapir & Dudley 2013; Maglianesi *et al.* 2014; Temeles *et al.* 2016; Weinstein & Graham 2017), which makes foraging faster and compensatory.

In summary, hummingbird communities with high dietary overlap are mainly structured by territorial behavior, which is directly affected by the low availability of resources. Although several studies have found that the differences in bill morphology can be determinant for the partition of food resources among hummingbirds due to correspondence with the specific floral morphology (Araujo 1996; Temeles *et al.* 2009; Maglianesi *et al.* 2014), our study shows that, contrary to our theoretical expectation, bill's morphology contributed to increase niche overlap in communities with less resources available. In productive communities, on the other hand, the species will not depend heavily on the niche partition. The partition occurs naturally due to the foraging restricted to small areas and the preference of hummingbirds for the consumption of flowers that optimize their fitness, without increasing energy expenditure, which reduces the trophic niche overlap.

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CAPÍTULO 3

A global synthesis on the Raunkiaeran shortfall for birds³

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A global synthesis on the Raunkiaeran shortfall for birds

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Abstract

Broad and accessible biodiversity-related knowledge is essential to understand the impacts of biodiversity loss and to make appropriate conservation decisions in the face of ongoing global changes. To guide global actions for data mobilization, many efforts have been made to identify gaps in species geographic distribution. However, knowledge gaps in digital accessible information regarding key species traits (i.e. Raunkiaeran shortfall) remain critically limited. Using birds as a study system, here we revise the literature to identify the ecologically most relevant traits and combine >97,000 records from public datasets to quantify and map their Raunkiaeran shortfall. We find that only 62% of the information about the possible species-trait combinations are freely available in published datasets. Major gaps exists for seabirds and small-ranged species from tropical countries, especially regarding morphological traits. Including two additional large data sources that did not meet our initial inclusion criteria reduces massively the shortfall but do not change the main gaps location, which may indicate important predictors of data limitation for less studied taxa. Our study provides a simple and intuitive approach for evaluating trait information that can be applied to study other clades, and highlights important data voids that will demand scientific cooperation and data management to effectively reduce the Raunkiaeran shortfall.

Key-words: Data availability, Information coverage, Functional traits, Knowledge bias, Maps of ignorance.

Introduction

Improvement of biodiversity-related knowledge is essential to understand patterns and processes that occur at different spatial and temporal scales and for making appropriate conservation decisions, so that the development of an advanced and shared biodiversity knowledge base is one of the global conservation targets (Aichi Target 19 - Convention on Biological Diversity; <https://www.cbd.int/sp/targets/>). Syntheses of information availability are therefore required to estimate the amount of knowledge that remains unknown and to comprehend how these data limitation may bias the interpretation of ecological processes or affect conservation initiatives. Relative progress to identify these knowledge gaps have been observed especially in terms of estimating the number of species that remain to be described (i.e. Linnean shortfall; Bini *et al.* 2006; Brown & Lomolino 1998; Mora *et al.* 2011) and estimating uncertainty in species' geographic distribution (i.e. Wallacean shortfall; Bini *et al.* 2006; Lomolino 2004; Menegotto & Rangel 2018). However, despite the growing number of studies with functional diversity due to its wide use in several research fields (Freitas & Mantovani 2018), the dimension of how much we don't know in terms of species traits, i.e. the dimension of the Raunkiaeran shortfall, remains relatively little explored (but see a few examples below).

The Raunkiaeran shortfall is defined as the lack of knowledge about species traits that are ecologically relevant, including the lack of knowledge about the variation of traits within and among species, the ecological function resulting from each trait, how these functions are affected by interactions with other traits, and which traits work together to perform ecosystem functions (Hortal *et al.* 2015). Quantifying how much information about relevant traits is already known for a determined set of species represents then a good starting point to evaluate the dimension of the Raunkiaeran shortfall, but quantifying scientific information is not a trivial task. After two centuries of biodiversity inventories with thousands of new

publications each year, biological researchers have produced a tremendous amount of data dispersed over multiple small datasets (Oliveira *et al.* 2017). Without a proper data management and mobilization, this vast pool of high-value data could remain difficult to find or access by potential users or by anyone willing to quantify the raw product of the individual scientific effort (Hampton *et al.* 2013; Heidorn 2008; Nelson & Ellis 2018). For this reason, estimations of the biodiversity shortfalls usually rely on large and publicly open datasets (Conde *et al.* 2019; Cornwell *et al.* 2019; Etard *et al.* 2020; Meyer *et al.* 2015). On one hand, this choice implies that when estimating the biodiversity knowledge available there will be some degree of underestimation due to the fraction of scientific data that may continue hidden or inaccessible (i.e. the dark data; Heidorn 2008), indistinguishable in a practical sense from an unknown information (the unknown knowns *sensu* Hortal *et al.* 2015). On the other hand, quantifying the information that anyone in the community can easily find, access without restrictions, integrate and re-use (following the FAIR Data Principles; Wilkinson *et al.* 2016) reveals the amount of – and the gaps in the – data at the disposal of researchers and policy makers, which is more in accordance with the international targets.

There is a great effort by plant ecologists to collect, measure and make data on functional attributes available. Since 2003, there are protocols for measurement of plant functional traits that gather traits known to be functional in a standardized way (Cornelissen *et al.* 2003; Pérez-Harguindeguy *et al.* 2013), as well as a database of functional traits that concentrate most of the information available in the literature (TRY - Plant trait database, Kattge *et al.* 2011). Yet, estimates show that we do not know any functional traits for 64.5% of the plant species (Cornwell *et al.* 2019). For most animal groups, the main limitations that prevent us from determining the dimension of the Raunkiaeran shortfall are the lack of definition about the most relevant set of traits and a unified database where trait data can be aggregated and shared (Brousseau *et al.* 2018; Schneider *et al.* 2019, but see recent initiatives

in Gallagher *et al.* 2020; Kissling *et al.* 2018; Moretti *et al.* 2017; Oliveira *et al.* 2017; Parr *et al.* 2016). Five categories of species traits have been suggested recently as essential biological variables for detecting and reporting biodiversity changes (morphology, movement, phenology, physiology, and reproduction; Kissling *et al.* 2018), but a narrower definition about which traits should be assessed for each biological group still does not exist. Consequently, estimates of gaps in trait availability are mainly restricted to a region (Tiler *et al.* 2012) and/or to a specific trait (Freitas *et al.* 2020). The broadest gap estimation until the moment was with a subset of traits that are transversal to terrestrial tetrapods (Etard *et al.* 2020). This study revealed an average trait completeness higher than 84% for birds and mammals species, but lower than 50% for amphibians and reptiles. A similar taxonomic bias have also been observed in tetrapods by population ecologists regarding public availability of demographic information (Conde *et al.* 2019). Although transversal traits are highly important to conduct studies combining different taxa, they may not necessarily represent the most ecologically relevant traits for specific groups, i.e. those that ecologists actually use to evaluate functional changes. Therefore, the amount of information about relevant species traits that is freely available to scientists and practitioners still remains unknown for most, if not all, animal clades.

Here, we provide, as a case study, an overview of the Raunkiaeran shortfall for birds considering only datasets published as data papers or deposited in public data repositories. Birds are among the most well-studied organisms and, therefore, the large set of existing data for this group may indicate an upper bound of the knowledge available for other animal clades. To achieve this goal, we first revised the literature to identify the most used traits in studies of bird functional ecology. By doing so, we assumed that the most used traits are also the most relevant ones to test ecological hypotheses. Then, we searched for digital accessible information about each identified trait in public datasets. After compiling the information

freely available, we estimated the proportion of species for which trait data are available (trait coverage Etard *et al.* 2020). Finally, we mapped the lack of trait data using worldwide species distribution range maps to identify regions where this knowledge is more scarce and to investigate the underlying causes of such geographic bias. Specifically, we evaluated the influence of different socio-environmental variables on trait knowledge gaps based on the hypotheses that information coverage should increase in regions with relatively few species, regions composed by widely distributed species, regions with higher potential for funding scientific activities, and easily accessible regions close to major cities (Meyer *et al.* 2015).

Methods

Defining literature traits

To identify the most used bird traits in functional diversity studies, we first searched in Web of Science for trait-based articles published over the last 20 years (1999-12/12/2019). We searched for articles containing the words “functional diversity” AND (aves OR avian OR bird*) in the title, abstract, or keywords, and selected only those in the ecology subarea. The search was carried out in this way with the aim of restricting the terms found to those used in studies focusing on functional diversity. The literature search yielded 235 articles, of which 87 were disregarded as they were not dealing with birds or were outside of the search scope (n = 148; see a detailed list in Appendix A). After screening, we identified 55 different traits used in functional diversity studies with birds, from which only 14 were frequently used ($\geq 10\%$ of the studies): diet (78%), body mass (76%), foraging strategy (66%), nesting strategy (30%), migratory status (28%), clutch size (25%), wing length (24%), bill length (23%), habitat preference (18%), tarsus length (16%), bill width (14%), activity period (13%), tail length (12%), and Kipp’s distance (10%). Foraging strategy was commonly used to describe the location and/or the method used by the species to obtain their food,

representing two different traits (López-Ordoñez *et al.* 2015). Therefore, we converted foraging strategy into foraging stratum and foraging mode (see Appendix B for the standardized list of traits terms and definitions). We also eliminated habitat preference because the definition of habitat varied widely in the literature, depending totally on the objective of the study. Researchers obtained data for these traits from 325 different data sources, composed mainly by books (64% of the studies), articles (51%), web sites (32%), museums (14%), unpublished data (5%), and field collected data (3%). Data from mobile applications, other online resources, private collections, and dissertations accounted for less than 1%. Overall, 94% of the studies used secondary data sources and only 18% collected primary data (9% did not inform the origin of some or all the used traits).

Searching for trait data

To assess the availability of the 14 traits investigated here we first searched for data papers on bird traits. We searched for (“functional diversity” OR traits) AND (avian OR bird*) in Web of Science, selecting only data papers. We also screened journals that publish biodiversity-related data papers using the same search terms (see <https://www.gbif.org/en/data-papers>). We found 13 datasets that compile species traits for birds. Datasets presented from 2 to 9 (6 ± 2) of the selected traits, with an average information coverage of 92.12% ($\pm 7.50\%$). The geographic coverage of the datasets varied from regional to global scale, ranging from 95 to 9844 species (Table S1). Overall, they totaled 28,807 records for 10,274 of the 10,949 species evaluated here. We also searched for trait data in the public repositories Dryad, Zenodo, Figshare, Pangea and Senckenberg (search in January 2020), as well as in the supplemental material of the 148 articles investigated from Web of Science. This additional search resulted in a total of 324 datasets with 68,338 records for 10,226 species.

Because our initial goal of estimating knowledge gaps considering only datasets published as data papers or in data repositories may be too restrictive, we also accounted for the contribution of two large and available datasets in independent analyses: Pigot *et al.* (2020) and the Handbook of Birds of the World (del Hoyo *et al.* 1992-2011). The first one assemble data on all the seven morphological traits considered in our analyses for 9,810 bird species (90% of our species after synonyms verification), while the second one provides description of body mass, clutch size, diet, forage mode, forage stratum, migratory status and nesting strategy for all species over the world. Regarding the Handbook, some species may still have a few traits undescribed. Therefore, the results of this exercise should be seen as an overestimated extrapolation.

We standardized all scientific names to the species level following the nomenclature accepted by Handbook of the Birds of the World & BirdLife International (2019) taxonomic checklist. For this purpose, we developed an algorithm to search for synonyms of unaccepted names in The World Bird Database (Avibase; Lepage *et al.* 2014), and used the R packages ‘*taxize*’ (Chamberlain & Szocs 2020) and ‘*rredlist*’ (Chamberlain 2020) to verify ambiguous names not corrected by our algorithm. Then we removed all names considered invalid, names of hybrid species and species already extinct (including those extinct in the wild and potentially extinct). After nomenclature correction, our merged dataset totaled information on 10,328 species of the 10,949 species with mapped range on BirdLife International & Handbook of the Birds of the World (2019) (94%; see details below).

Estimating the Raunkiaerian shortfall

To evaluate the extent of the Raunkiaerian shortfall, we first calculate the trait coverage, i.e. percentage of species for which trait information is available. Then, we used the species range available in BirdLife (BirdLife International & Handbook of the Birds of the World, 2019) to map this knowledge estimation by substituting the presence information

of each species by its respective trait coverage and calculating the average coverage of each cell. For this purpose, we converted the range maps into a presence-absence matrix using a global grid of 1° resolution. We selected only ranges where the species are native, extant, resident throughout the year or during the breeding season. From a total of 11,145 species with range available on BirdLife, our map ended up with 10,949 species, which represents the total number of species in all subsequent analyses presented here. We did not include non-breeding ranges to avoid overestimating the trait coverage of regions that receive temporary species coming for well-studied regions, though the inclusion of these ranges does not alter our main results (see Fig. S1). It is also noteworthy that selecting or not non-breeding ranges produces a similar total number of mapped species, with the exception of two birds that have their known distribution reduced to non-breeding ranges (*Acrocephalus sorghophilus* and *Leucocarbo carunculatus*). The whole procedure was conducted in the software R (R, Core Team 2019) using the packages ‘*raster*’ (Hijmans 2019), ‘*rgdal*’ (Bivand *et al.* 2019) and ‘*letsR*’ (Vilela & Villalobos 2015).

Statistical analyses

We analyzed the relationship of four biologic, geographic and economic factors with trait coverage. We considered as biologic variables (i) the number of species and (ii) the average range size of the species in a cell, used here as a measure of endemism. The range size of a species was defined as its number of occupied cells in the world grid map. (iii) As geographic variable we used the on-ground accessibility, included here as the time required to travel to the nearest urban center (population > 50,000; Weiss *et al.* 2018). This variable also includes topographic features, such as slope angle and elevation. (iv) Finally, we used regional GDP per capita, an economic variable, as a proxy of research investment. Data referent to 2015 was obtained from a gridded global dataset at one-twelfth-degree resolution and averaged within 1° cells (Kummu *et al.* 2018).

To investigate the effects of the predictor variables on the Raunkiaerian shortfall we conducted a multiple regression analysis ($n = 15,492$ cells). However, we removed species diversity from the model due to its collinearity with average range size. All predictor variables were transformed by $\log_{(x+1)}$ before analysis to meet the normality assumption. Because we detected spatial autocorrelation in the model's residuals (Moran's $I = 0.17$, p -value < 0.01), we incorporated spatial predictors into our model using the principal coordinates of neighbor matrices (PCNM) approach (Borcard & Legendre 2002; Dray *et al.* 2006). To overcome the challenge of conducting the PCNM for such large dataset, we used the method proposed by Paula-Souza & Diniz-Filho (2020), which consists in to randomly sample the matrix thousands of times and evaluate the statistical distribution of parameters to be estimated. We tested the regression with different sample sizes, from 50 to 2000 grid cells, in order to find the smallest sample size that represents the coverage traits pattern. In our study case, the distribution of the parameters remained relatively stable after 1000 grid cells (Fig. S2; similar to Paula-Souza & Diniz-Filho, 2020). Finally, we calculated the variance partition component to estimate the relative contribution of each predictor variable using the package 'vegan' (Oksanen *et al.* 2020).

Results

Based on a search conducted in January 2020, we found a moderate but variable knowledge deficit in bird traits, with information about only $62 \pm 27\%$ (mean \pm standard deviation) of the 14 traits explored in the 10,949 bird species investigated here. Surprisingly, we found more information for traits related to life history ($70\% \pm 25\%$) than morphology ($54\% \pm 35\%$). Most complete traits, i.e. with information available for more than 90% of the species, were migratory status, body mass and period of activity, while Kipp's distance, foraging mode and bill width had the lowest information coverage (Table 1). A large amount

of the data available was already present in a few data papers (46%), with additional resources found on data repositories and some supplementary materials accounting for 16% of new information – only two datasets accounted for 6% and the ten most important datasets accounted for 12% of new information. These additional data contributed with information mostly related to migratory status (increment of 79%), nesting strategy (26%) and foraging mode (20%; Table 1). An analysis of the frequency that unique species-trait combinations are available revealed that 26% of the combinations appeared only once in our data search, while 36% of the combinations presented some level of redundancy, i.e. appeared in more than one data source (Fig. 1). Traits with redundant information were mainly body mass (85% of the species), migratory status (72%) and diet (64%; Fig. 1). These are the same traits with higher coverage, indicating that the redundancy of information tends to increase for more complete traits ($r = 0.76$).

Despite our focus on public information, we also calculated trait coverage after virtually including records from two large data sources currently available, but that did not meet our initial inclusion criteria, in order to better estimate the scientific knowledge accumulated so far (del Hoyo *et al.* 1992-2011; Pigot *et al.* 2020; see details in the Methods). According to our results, this addition greatly improves coverage estimate, reaching to an impressive value of $95\% \pm 14\%$. Remaining gaps would still occur for nearly 10% of the species, especially in morphological traits (Table 1).

Table 1. Summary description of all the 14 bird traits investigated in our study showing their classification by trait type (LH: life history; M: morphological) and their estimated coverage based only on the 13 data papers currently available for birds traits, based on a robust search in public data repositories, the total completeness based on these digital accessible information, and the total completeness estimated after accounting for information from relatively restricted data sources. We also estimated the average and the maximum number of times that each trait was found for the same species in the public datasets (considering only those species for which the trait was found more than once). Estimates for additional traits are available in Table S2.

Trait	Type	Coverage				Redundancy	
		Data papers	Repositories	Total (DAI)	Total (estimated)	Mean	Max
Activity period	LH	89.86	15.40	90.04	90.04	2.76	9
Bill length	M	46.75	35.07	58.88	91.05	3.01	12
Bill width	M	23.61	32.66	38.28	90.53	2.87	13
Body mass	M	88.36	79.62	91.88	100	6.72	61
Clutch size	LH	61.25	61.23	70.99	100	4.06	36
Diet	LH	72.15	69.42	85.63	100	4.17	37
Foraging mode	LH	3.44	19.86	23.14	100	3.12	13
Foraging	LH	87.57	31.10	88.2	100	2.95	20
Kipp's distance	M	5.43	11.43	14.79	89.89	2.44	5
Migratory	LH	14.49	92.96	93.05	100	3.84	30
Nesting	LH	14.07	36.46	39.68	100	3.78	22
Tail length	M	44.35	31.86	53.89	90.98	2.82	15
Tarsus length	M	45.91	35.88	58.63	91.02	2.93	17
Wing length	M	48.41	37.39	60.76	91.06	3.05	17

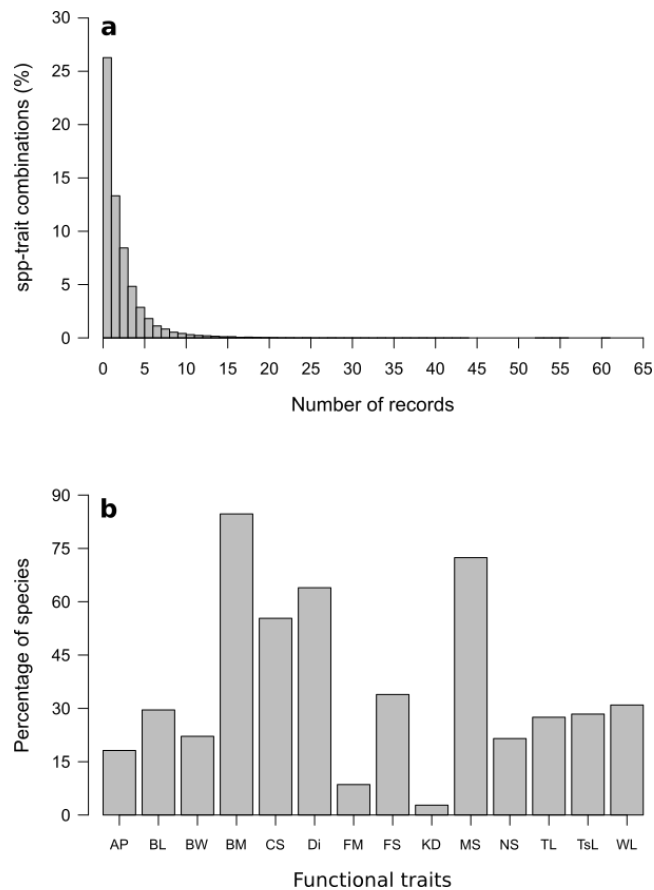


Fig. 1. Redundancy of information in bird traits available in the literature. (a) Histogram showing the frequency that information for unique species-trait combination appears in different datasets. (b) Percentage of species with information appearing more than once for each trait. AP: Activity period; BL: Bill length; BW: Bill width, BM: Body mass; CS: Clutch size; Di: Diet; FM: Foraging mode; FS: Foraging stratum; KD: Kipp’s distance; MS: Migratory status; NS: Nesting strategy; TL: Tail length; TsL: Tarsus length; WL: Wing length.

The amount of trait information available for birds was also highly variable through the space. On average, trait coverage was higher for species in the northern hemisphere, with the highest values in Europe, extending to West Asia, and east of North America. Conversely, the Neotropic (especially Amazon and Andes), Afrotropic and Indo-Malaya regions exhibited lower coverage values, with the lowest estimates in Southeast Asia (Fig. 2; see Fig. S3 for the spatial distribution of the coverage estimation for each trait). Coverage was also strongly reduced for seabirds compared to continental birds, with the lowest values in the Pacific east

coast, Sargasso Sea, Bay of Bengal and in the Sea of Japan (Fig. S1). Despite the different estimates of life history and morphological traits, we found a very similar geographical pattern between both trait categories, either considering the entire domain ($r = 0.87$ and $r = 0.97$, respectively; Fig. S4) or only the continental realm ($r = 0.90$; Fig. 2). Species without any trait information ($n = 625$) were more common in the tropics, especially in the Amazon rain forest and in the Andes (Fig. 3a). Together with the Southeast Asia, these are also the regions where probably are the poorest known species in terms of functional traits, i.e. species with information still incomplete even after considering the inclusion of other large additional data sources (Fig. 3b).

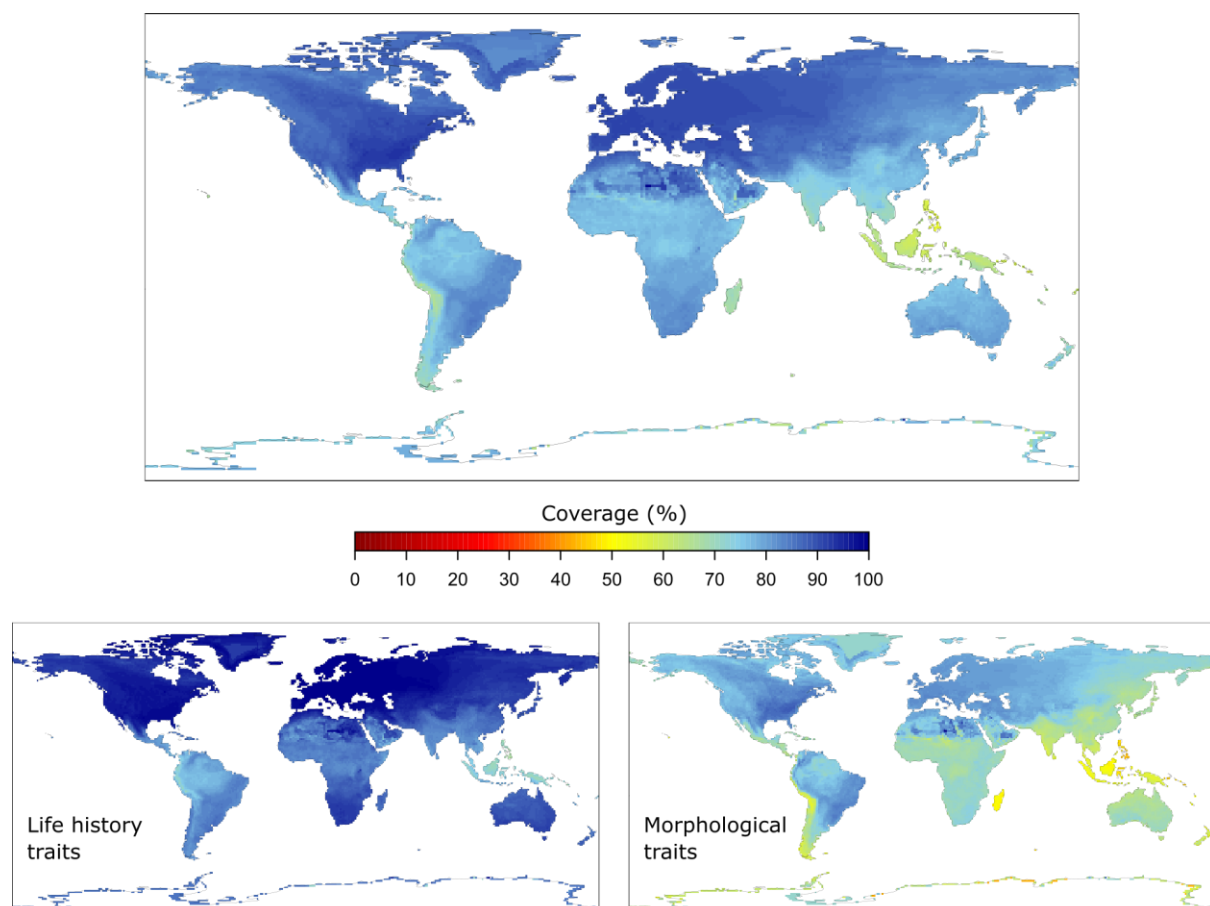


Fig. 2. Spatial variation of average trait coverage in birds considering all the 14 bird traits evaluated in our study (top), only life history traits (bottom-left), and only morphological traits (bottom-right).

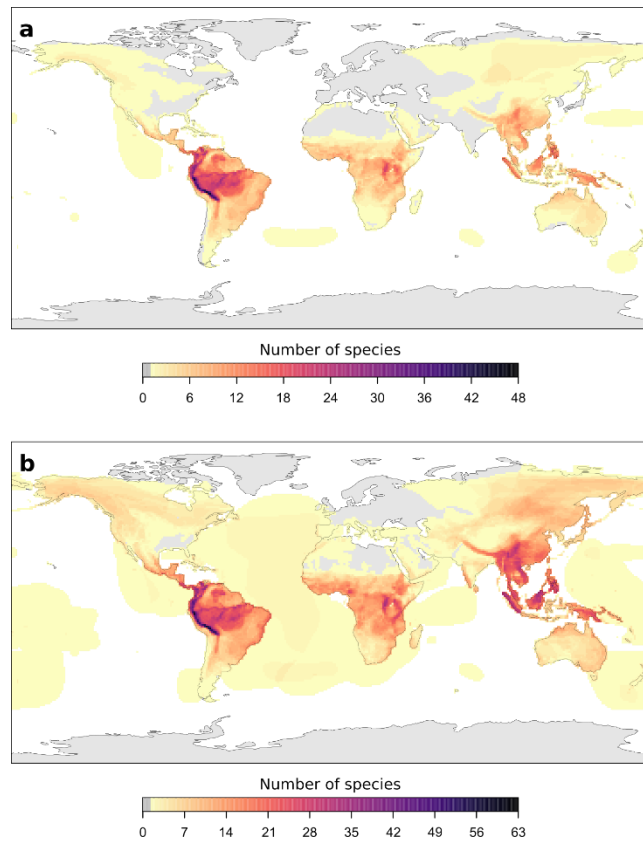


Fig. 3. Global distribution of the species of birds for which digital information about all the 14 traits investigated in our study remain unknown or inaccessible (a), and the species for which at least one trait information would still be missing after accounting for data of Pigot *et al.* (2020) and the Handbook of Birds of the World (del Hoyo *et al.* 1992-2011) (b).

To understand what could explain the spatial variation in trait coverage, we used a multiple regression analysis to identify its main geographic and economic drivers. Our initial predictors were species diversity, average range size of the species, regional Gross Domestic Product (GPD) per capita and on-ground accessibility. However, we excluded species diversity because of its collinearity with average range size. Our results showed that the predictors explained 54% of the spatial variation in trait coverage, and that this pattern is highly structured in geographic space. Pure spatial fraction still accounted for additional 32% of the total explained variation (see Fig. S2c). Average range size was the most important predictor variable, accounting alone for 30% of the explained fraction (Fig. S2d). GDP per capita was the second most important predictor, and similar to the average range size, it was

positively associated with trait coverage. Distance to major cities, as expected, was negatively associated with trait coverage, but accounted for only 8% of the total variation. It is noteworthy that distance to major cities did not exhibit any relationship with traits coverage when analyzed individually ($R^2 < 0.001$), contributing only to the full model. The increase in coverage after including information from other large additional data sources reduces its spatial variability and, consequently, the explanatory power of socio-environmental predictors ($R^2 = 0.16$). But since the regions and species with most gaps remain practically the same, average range size continued as the main predictor of information gaps (Fig. S5).

Discussion

In our evaluation of the Raunkiaeran shortfall we found that birds have, overall, a high information coverage. However, contrary to previous estimates (Etard *et al.* 2020), the public data about bird traits accounts for only 62% of the expected information. More importantly, we show here that this knowledge deficit is not equally distributed through the globe, species and even between trait categories. Despite the increasing interest in functional ecology (Freitas & Mantovani 2018), as far as we know only few studies have ventured to assess the extent of the Raunkiaeran shortfall (Tiler *et al.* 2012; Cornwell *et al.* 2019; Etard *et al.* 2020; Freitas *et al.* 2020). Such studies represent important advances in the field, but they are still limited in terms of geographic extent or number of traits analyzed. In line with the guiding steps for achieving international targets on biodiversity knowledge, our approach contributes to the identification of important data voids across different regions, species, and key functional traits.

All 14 traits investigated here were classified as morphological, those that are measured directly on the body of the organism, and as life history, when they are defined by observing the characteristics of organisms in the field over time. Considering that

morphological traits may be obtained from preserved museum specimens while the record of life history traits demands *in situ* observation and monitoring effort, one would expect a higher information completeness for morphological traits. Curiously, our results revealed the opposite. Information for life history traits were more complete in both data papers and data repositories (Table 1). We suspect that this pattern arise due to the historical compilation of such traits by large-scale guidebooks through the last decades, subsequently available in a machine readable format for a large number of species as published datasets (e.g. Wilman *et al.* 2014). Guidebooks and data papers providing different morphological traits also exist, but they are commonly restricted to specific continents (Hockey *et al.* 2005), biogeographic regions (Cramp *et al.* 1977-1994), countries (Montoya *et al.* 2018) or biomes (Rodrigues *et al.* 2019). In support of this hypothesis, an analysis of the sources used in the functional diversity studies revised here showed that, on average, 93% of the studies that used life history traits gathered data from secondary sources and only 3% collected the data (Table S3). Most of these data were retrieved exactly from a few guidebooks and large data papers (Table S4). Conversely, an average of only 40% of the studies that used morphological traits gathered data from secondary sources, while 58% collected primary data. This fraction is even higher for traits not commonly present in guidebooks such as Kipp's distance and bill width, and lowest for body mass, commonly present in secondary data sources (Table S3). Assembling a large dataset of morphological traits from preserved specimens worldwide is a challenging but not impossible task (Pigot *et al.* 2020), important to increase findability and accessibility of birds data. Fortunately, the necessity for such information is stimulating the collection and sharing of morphological traits in these last years (Table S1), reducing the knowledge gaps in the freely accessible information.

One of the most important outcomes of our analyses was how the global unevenness in publicly accessible trait information may affect ecological investigations in the

biodiversity richest regions of the world. Similar to previous studies (González-Suárez *et al.* 2012; Etard *et al.* 2020), mapping the average information of trait coverage revealed a clear spatial pattern with higher knowledge level in the northern hemisphere and relatively less information about species in tropical regions. Even after expanding the analysis to include records from Pigot *et al.* (2020) and the Handbook of Birds of the World (del Hoyo *et al.* 1992-2011), the tropics were the regions still presenting the remaining data gaps. Among the variables evaluated to explain this variation in traits coverage, the average range size of the species was the most important one, accounting for nearly 48% of the total explained variation. This result is not surprising as research effort in birds is strongly related to the range size of the species (Ducatez & Lefebvre 2014). Species with wide distribution can be studied by different research groups and, consequently, will integrate different datasets sharing traits description. Considering that each dataset may focus on specific sets of traits, these species will have most of their traits measured and shared somewhere. In the data papers investigated here, for example, we observe that even datasets compiled for a specific territory such as Japan (Takagawa *et al.* 2011) are composed by many species occurring all over Eurasia, and even species from other regions all over the world (Fig. S6). Therefore, regions that accumulate widely distributed species such as the high latitudes in the northern hemisphere will necessarily be more complete, especially if they have relatively reduced species richness. The second most important variable was GDP per capita, which accounted for 30% of the explained variation in traits completeness. It is not new that research funding is directly correlated to the level of knowledge in biodiversity, especially for birds (Meyer *et al.* 2015; Titley *et al.* 2017). Consequently, biodiversity research is commonly carried out by institutions of developed countries, particularly in western Europe (Titley *et al.* 2017). Developing countries, on the other hand, have relatively fewer resources to invest in research, which limits local scientific activities and local data availability exactly in those regions of

elevated biodiversity and number of endemic species since most of them are located in the tropics (Orme *et al.* 2005). Such poor data availability for small-ranged species in regions of high diversity is not a phenomenon restricted to birds or traits (González-Suárez *et al.* 2012; Etard *et al.* 2020; Moura & Jetz 2020), but probably a general tendency in biodiversity knowledge limitation that may guide future endeavors in data collection and mobilization. Finally, on-ground accessibility from cities exhibited only a modest contribution. Its relatively low importance makes sense given that traits may be collected at any place across the species range, independent of the distance to major urban centers. However, it is interesting to note that the contribution of accessibility increases in the model including average range size and GDP per capita, suggesting that distance to major cities may still constrain field collections and data availability once other important variables are held constant. This importance could probably be higher than estimated here if only the distance to the research institutions were considered (Meyer *et al.* 2015).

It is noteworthy that we only quantified here the presence of information about each trait. We did not evaluate qualitatively how much the traits are comparable among datasets (i.e. due to differences in how morphological traits are measured and categorical traits are defined), which certainly may reduce or even inhibit the aggregation of different data sources in studies encompassing large scales (Kissling *et al.* 2018). This problem becomes more evident when we observe the low frequency with which records for most species-trait combinations appear in the data compilation, indicating that alternatives to how some traits are measured or categorized may probably not be available for a large number of species and many different traits. Protocols are important exactly to reduce this information incompatibility (Cornelissen *et al.* 2003; Pérez-Harguindeguy *et al.* 2013; Moretti *et al.* 2017; Dawson *et al.* 2019). Aggregating trait data from multiple sources requires not only comprehensive definitions of measurement protocols but also standardized lists of trait terms

or controlled vocabularies (Kissling *et al.* 2018). However, such comprehensive definitions are still missing or remain little-known even for birds (López-Ordoñez *et al.* 2015). We also would like to emphasize that there is no definitive list or ranking of which traits must be used in functional ecology, even because the choice of traits should depend on the research question (Brousseau *et al.* 2018), but our approach allowed us to identify those traits considered most relevant by the peers. Accordingly, all morphological traits identified here are recognized as those well-connected to important niche structures of ecological bird communities (Pigot *et al.* 2020). To investigate how the inclusion of other important traits would impact our results, we included into our data search the set of traits proposed in a regional bird survey protocol (López-Ordoñez *et al.* 2015). As would be expected, increasing the number of traits reduces the overall completeness estimate ($47\% \pm 23\%$; Table S2) but, on the other hand, it does not change our spatial result ($r = 0.94$; Fig. S1), indicating a consistently poor trait availability for regions of reduced information coverage.

In conclusion, our results reveal important limitations in the public information of key traits for birds. The prevalence of gaps for small-ranged species from tropical regions in these well-studied groups (González-Suárez *et al.* 2012; Ducatez & Lefebvre 2014; Etard *et al.* 2020), even after including information from other large data sources available highlights the need for major efforts to acquire and compile traits for other taxa that commonly receive less attention in the literature. Reducing the Raunkiaeran shortfall will demand great effort and cooperation of the scientific community both in collecting primary information and by sharing existing datasets following the FAIR principles of scientific data management (Findability, Accessibility, Interoperability, and Reusability; Wilkinson *et al.* 2016). Such effective data mobilization is of central importance, especially in the current scenario, where traits are essential to understand ecological patterns and processes in different fields of

ecology (Freitas & Mantovani 2018), including our ability to manage and conserve species in the face of climate change.

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Conclusão geral

Essa tese contribui para compreender melhor como diferentes metodologias podem afetar a distribuição das espécies e os fatores que estruturam as comunidades. Além disso, ampliamos também o diagnóstico da lacuna Raunkiaeriana para aves e os fatores que a influenciam.

No primeiro capítulo mostramos que o poder preditivo e a acurácia dos modelos de distribuição de espécies são pouco afetados pela adição de preditores bióticos. No entanto, encontramos que a adição de preditores pode influenciar o range estimado das espécies, principalmente daquelas amplamente distribuídas. Nós argumentamos que para o nosso sistema de estudo (i.e. beija-flores como espécies focais e plantas produtoras de néctar como espécies interatoras) a influência dos preditores bióticos representa apenas um ruído no *output* dos modelos de espécies espacialmente restritas, mas que pode gerar uma dissimilaridade espacial considerável em espécies com ampla distribuição devido a um possível efeito estatístico. Portanto, apesar de diversos estudos suportarem a relevância de preditores bióticos para modelar a distribuição das espécies (contrário a hipótese do ruído Eltoniano), o resultado do nosso estudo indica que a força de interação pode não ser suficiente para representar a importância de preditores bióticos, e que algum nível de dependência entre a espécie foco e a interatora pode ser necessário para afetar a distribuição das espécies em grandes escalas.

No segundo capítulo mostramos que a partição de nicho das espécies de beija-flores em comunidades tidas como sobrepostas de acordo com as redes de interações tróficas podem apresentar partição dos recursos, principalmente a partir de características funcionais mais finas e difíceis de detectar, como por exemplo o comportamento de forrageio. Esse resultado destaca que a partição de nicho pode ocorrer de forma sutil, e a aquisição e disponibilização

de dados de história de vida pode ser essencial para melhor compreensão da estruturação das comunidades.

No terceiro capítulo mostramos que, para aves, cerca de 38% dos dados de atributos continuam inacessíveis ou desconhecidos, principalmente para espécies de regiões tropicais e com pequena distribuição geográfica. Nesse estudo utilizamos inicialmente apenas dados irrestritos, mas analisamos também a dimensão da lacuna Raunkiaerana considerando grandes conjuntos de dados que são conhecidos pela ciência mas que continuam com acesso restrito e/ou imobilizados. Encontramos que a disponibilização aberta desses dados geraria uma completude de 95%. Mesmo assim, nosso resultado mostrou que a distribuição das espécies com algum dado desconhecido se mantém nas mesmas condições (i.e. regiões tropicais com predomínio de espécies com limitada distribuição geográfica). A consistência desse resultado e sua similaridade com outros estudos sugere que o mesmo padrão pode ser esperado para outros grupos de animais, mas isso ainda precisa ser avaliado no futuro próximo.

Capítulo 1: Additional Information

Supplementary Material

Table S1. Unique interactions between 100 hummingbirds and 202 plant species.

Hummingbirds	Plants
<i>Adelomyia melanogenys</i>	<i>Bomarea multiflora</i>
<i>Adelomyia melanogenys</i>	<i>Guzmania gracilior</i>
<i>Adelomyia melanogenys</i>	<i>Palicourea lineata</i>
<i>Adelomyia melanogenys</i>	<i>Tropaeolum deckerianum</i>
<i>Aglaeactis cupripennis</i>	<i>Barnadesia spinosa</i>
<i>Aglaeactis cupripennis</i>	<i>Monnina salicifolia</i>
<i>Aglaeactis cupripennis</i>	<i>Oreocallis grandiflora</i>
<i>Agelaiocercus coelestis</i>	<i>Guzmania jaramilloi</i>
<i>Amazilia beryllina</i>	<i>Penstemon roseus</i>
<i>Amazilia beryllina</i>	<i>Phaseolus coccineus</i>
<i>Amazilia beryllina</i>	<i>Salvia iodantha</i>
<i>Amazilia beryllina</i>	<i>Salvia mexicana</i>
<i>Amazilia brevirostris</i>	<i>Calliandra guildingii</i>
<i>Amazilia fimbriata</i>	<i>Bauhinia forficata</i>
<i>Amazilia fimbriata</i>	<i>Ceiba speciosa</i>
<i>Amazilia fimbriata</i>	<i>Erythrina speciosa</i>
<i>Amazilia fimbriata</i>	<i>Esterhazyia splendida</i>
<i>Amazilia fimbriata</i>	<i>Genipa americana</i>
<i>Amazilia fimbriata</i>	<i>Geissomeria schottiana</i>
<i>Amazilia fimbriata</i>	<i>Helicteres brevispira</i>
<i>Amazilia fimbriata</i>	<i>Hippeastrum stylosum</i>
<i>Amazilia fimbriata</i>	<i>Ipomoea hederifolia</i>
<i>Amazilia fimbriata</i>	<i>Palicourea crocea</i>
<i>Amazilia fimbriata</i>	<i>Psittacanthus cucullaris</i>
<i>Amazilia fimbriata</i>	<i>Sinningia douglasii</i>
<i>Amazilia fimbriata</i>	<i>Stachytarpheta gesnerioides</i>
<i>Amazilia lactea</i>	<i>Abutilon bedfordianum</i>
<i>Amazilia lactea</i>	<i>Anisacanthus brasiliensis</i>
<i>Amazilia lactea</i>	<i>Erythrina speciosa</i>
<i>Amazilia lactea</i>	<i>Palicourea rigida</i>
<i>Amazilia lactea</i>	<i>Stachytarpheta glabra</i>
<i>Amazilia leucogaster</i>	<i>Heliconia richardiana</i>
<i>Amazilia rutila</i>	<i>Combretum farinosum</i>
<i>Amazilia rutila</i>	<i>Crusea coccinea</i>
<i>Amazilia rutila</i>	<i>Lobelia laxiflora</i>
<i>Amazilia rutila</i>	<i>Psittacanthus ramiflorus</i>
<i>Amazilia rutila</i>	<i>Salvia iodantha</i>
<i>Amazilia rutila</i>	<i>Salvia mexicana</i>
<i>Amazilia versicolor</i>	<i>Aechmea cylindrata</i>

<i>Amazilia versicolor</i>	<i>Aechmea nudicaulis</i>
<i>Amazilia versicolor</i>	<i>Erythrina falcata</i>
<i>Amazilia versicolor</i>	<i>Justicia ramulosa</i>
<i>Amazilia versicolor</i>	<i>Macrocarpaea rubra</i>
<i>Amazilia versicolor</i>	<i>Vriesea altodaserrae</i>
<i>Amazilia violiceps</i>	<i>Salvia iodantha</i>
<i>Amazilia violiceps</i>	<i>Salvia mexicana</i>
<i>Anopetia gounellei</i>	<i>Anisacanthus brasiliensis</i>
<i>Anopetia gounellei</i>	<i>Lychnophora salicifolia</i>
<i>Anthracothonax aurulentus</i>	<i>Cordia rickseckeri</i>
<i>Anthracothonax nigricollis</i>	<i>Citharexylum myrianthum</i>
<i>Anthracothonax nigricollis</i>	<i>Erythrina fusca</i>
<i>Anthracothonax nigricollis</i>	<i>Handroanthus chrysotrichus</i>
<i>Anthracothonax nigricollis</i>	<i>Jacaranda puberula</i>
<i>Anthracothonax nigricollis</i>	<i>Norantea guianensis</i>
<i>Aphantochroa cirrochloris</i>	<i>Ceiba speciosa</i>
<i>Aphantochroa cirrochloris</i>	<i>Ruellia angustiflora</i>
<i>Aphantochroa cirrochloris</i>	<i>Vriesea procera</i>
<i>Atthis heloisa</i>	<i>Salvia elegans</i>
<i>Atthis heloisa</i>	<i>Salvia lavanduloides</i>
<i>Augastes scutatus</i>	<i>Stachytarpheta glabra</i>
<i>Boissonneaua flavescens</i>	<i>Aetanthus nodosus</i>
<i>Boissonneaua flavescens</i>	<i>Palicourea lineata</i>
<i>Calothorax lucifer</i>	<i>Bouvardia ternifolia</i>
<i>Calothorax lucifer</i>	<i>Castilleja tenuiflora</i>
<i>Calothorax lucifer</i>	<i>Fouquieria splendens</i>
<i>Calothorax lucifer</i>	<i>Myrtillocactus geometrizans</i>
<i>Campylopterus largipennis</i>	<i>Palicourea crocea</i>
<i>Chalcostigma herrani</i>	<i>Brachyotum lindenii</i>
<i>Chlorostilbon lucidus</i>	<i>Aechmea distichantha</i>
<i>Chlorostilbon lucidus</i>	<i>Bauhinia unguolata</i>
<i>Chlorostilbon lucidus</i>	<i>Buddleja brasiliensis</i>
<i>Chlorostilbon lucidus</i>	<i>Citharexylum myrianthum</i>
<i>Chlorostilbon lucidus</i>	<i>Corymborkis flava</i>
<i>Chlorostilbon lucidus</i>	<i>Coussarea hydrangeifolia</i>
<i>Chlorostilbon lucidus</i>	<i>Fridericia speciosa</i>
<i>Chlorostilbon lucidus</i>	<i>Helicteres brevispira</i>
<i>Chlorostilbon lucidus</i>	<i>Inga vera</i>
<i>Chlorostilbon lucidus</i>	<i>Ipomoea hederifolia</i>
<i>Chlorostilbon lucidus</i>	<i>Lychnophora salicifolia</i>
<i>Chlorostilbon lucidus</i>	<i>Pyrostegia venusta</i>
<i>Chlorostilbon lucidus</i>	<i>Stachytarpheta glabra</i>
<i>Chlorostilbon lucidus</i>	<i>Styrax ferrugineus</i>
<i>Chlorostilbon lucidus</i>	<i>Vochysia emarginata</i>
<i>Chlorostilbon lucidus</i>	<i>Vochysia tucanorum</i>
<i>Chlorostilbon mellisugus</i>	<i>Palicourea crocea</i>

<i>Chlorostilbon notatus</i>	<i>Bomarea edulis</i>
<i>Chlorostilbon notatus</i>	<i>Calliandra guildingii</i>
<i>Chlorostilbon notatus</i>	<i>Erythrina fusca</i>
<i>Chlorostilbon notatus</i>	<i>Gurania acuminata</i>
<i>Chrysuronia oenone</i>	<i>Besleria aggregata</i>
<i>Chrysuronia oenone</i>	<i>Combretum llewelynii</i>
<i>Chrysuronia oenone</i>	<i>Palicourea crocea</i>
<i>Clytolaema rubricauda</i>	<i>Fuchsia regia</i>
<i>Clytolaema rubricauda</i>	<i>Inga sessilis</i>
<i>Clytolaema rubricauda</i>	<i>Siphocampylus sulfureus</i>
<i>Clytolaema rubricauda</i>	<i>Spirotheca rivieri</i>
<i>Coeligena iris</i>	<i>Barnadesia arborea</i>
<i>Coeligena iris</i>	<i>Fuchsia vulcanica</i>
<i>Coeligena iris</i>	<i>Oreocallis grandiflora</i>
<i>Coeligena lutetiae</i>	<i>Fuchsia corollata</i>
<i>Coeligena torquata</i>	<i>Aetanthus nodosus</i>
<i>Coeligena torquata</i>	<i>Bomarea multiflora</i>
<i>Coeligena torquata</i>	<i>Psammisia columbiensis</i>
<i>Coeligena wilsoni</i>	<i>Aetanthus nodosus</i>
<i>Coeligena wilsoni</i>	<i>Mezobromelia capituligera</i>
<i>Coeligena wilsoni</i>	<i>Psammisia ulbrichiana</i>
<i>Colibri coruscans</i>	<i>Castilleja fissifolia</i>
<i>Colibri coruscans</i>	<i>Macleania rupestris</i>
<i>Colibri coruscans</i>	<i>Palicourea demissa</i>
<i>Colibri coruscans</i>	<i>Salvia corrugata</i>
<i>Colibri serrirostris</i>	<i>Helicteres velutina</i>
<i>Colibri serrirostris</i>	<i>Inga vera</i>
<i>Colibri serrirostris</i>	<i>Lobelia fistulosa</i>
<i>Colibri serrirostris</i>	<i>Sinningia elatior</i>
<i>Colibri serrirostris</i>	<i>Stachytarpheta gesnerioides</i>
<i>Colibri serrirostris</i>	<i>Stachytarpheta glabra</i>
<i>Colibri serrirostris</i>	<i>Vochysia cinnamomea</i>
<i>Colibri serrirostris</i>	<i>Vochysia tucanorum</i>
<i>Colibri serrirostris</i>	<i>Zeyheria montana</i>
<i>Cynanthus latirostris</i>	<i>Castilleja toluccensis</i>
<i>Cynanthus latirostris</i>	<i>Cylindropuntia imbricata</i>
<i>Cynanthus latirostris</i>	<i>Ipomoea wolcottiana</i>
<i>Doryfera ludovicae</i>	<i>Cavendishia bracteata</i>
<i>Doryfera ludovicae</i>	<i>Guzmania gracilior</i>
<i>Doryfera ludovicae</i>	<i>Palicourea acetosoides</i>
<i>Ensifera ensifera</i>	<i>Brugmansia sanguinea</i>
<i>Ensifera ensifera</i>	<i>Passiflora mixta</i>
<i>Ensifera ensifera</i>	<i>Tristerix longebracteatus</i>
<i>Eriocnemis derbyi</i>	<i>Barnadesia spinosa</i>
<i>Eriocnemis luciani</i>	<i>Barnadesia arborea</i>
<i>Eriocnemis luciani</i>	<i>Oreocallis grandiflora</i>

<i>Eriocnemis mosquera</i>	<i>Brachyotum lindenii</i>
<i>Eriocnemis vestita</i>	<i>Vaccinium floribundum</i>
<i>Eugenes fulgens</i>	<i>Bouvardia ternifolia</i>
<i>Eugenes fulgens</i>	<i>Calliandra grandiflora</i>
<i>Eugenes fulgens</i>	<i>Cirsium ehrenbergii</i>
<i>Eugenes fulgens</i>	<i>Fuchsia fulgens</i>
<i>Eugenes fulgens</i>	<i>Penstemon gentianoides</i>
<i>Eugenes fulgens</i>	<i>Phaseolus coccineus</i>
<i>Eugenes fulgens</i>	<i>Salvia mexicana</i>
<i>Eupetomena macroura</i>	<i>Anisacanthus brasiliensis</i>
<i>Eupetomena macroura</i>	<i>Bauhinia unguolata</i>
<i>Eupetomena macroura</i>	<i>Erythrina falcata</i>
<i>Eupetomena macroura</i>	<i>Erythrina speciosa</i>
<i>Eupetomena macroura</i>	<i>Esterhazyia splendida</i>
<i>Eupetomena macroura</i>	<i>Handroanthus chrysotrichus</i>
<i>Eupetomena macroura</i>	<i>Heliconia psittacorum</i>
<i>Eupetomena macroura</i>	<i>Inga vera</i>
<i>Eupetomena macroura</i>	<i>Lobelia fistulosa</i>
<i>Eupetomena macroura</i>	<i>Lundia cordata</i>
<i>Eupetomena macroura</i>	<i>Mandevilla guanabaria</i>
<i>Eupetomena macroura</i>	<i>Psittacanthus cordatus</i>
<i>Eupetomena macroura</i>	<i>Stachytarpheta glabra</i>
<i>Eupetomena macroura</i>	<i>Vochysia tucanorum</i>
<i>Eupetomena macroura</i>	<i>Vriesea procera</i>
<i>Eupetomena macroura</i>	<i>Zeyheria montana</i>
<i>Eupherusa nigriventris</i>	<i>Psychotria elata</i>
<i>Eutoxeres aquila</i>	<i>Centropogon granulatus</i>
<i>Florisuga fusca</i>	<i>Aechmea nudicaulis</i>
<i>Florisuga fusca</i>	<i>Aechmea pectinata</i>
<i>Florisuga fusca</i>	<i>Ceiba speciosa</i>
<i>Florisuga fusca</i>	<i>Erythrina speciosa</i>
<i>Florisuga fusca</i>	<i>Inga sessilis</i>
<i>Florisuga fusca</i>	<i>Schwartzia brasiliensis</i>
<i>Florisuga fusca</i>	<i>Pavonia viscosa</i>
<i>Florisuga mellivora</i>	<i>Erythrina fusca</i>
<i>Florisuga mellivora</i>	<i>Isertia hypoleuca</i>
<i>Florisuga mellivora</i>	<i>Norantea guianensis</i>
<i>Florisuga mellivora</i>	<i>Palicourea demissa</i>
<i>Florisuga mellivora</i>	<i>Warszewiczia coccinea</i>
<i>Glaucis dohrnii</i>	<i>Centropogon cornutus</i>
<i>Glaucis hirsutus</i>	<i>Besleria aggregata</i>
<i>Glaucis hirsutus</i>	<i>Centropogon cornutus</i>
<i>Glaucis hirsutus</i>	<i>Heliconia bihai</i>
<i>Glaucis hirsutus</i>	<i>Heliconia richardiana</i>
<i>Glaucis hirsutus</i>	<i>Palicourea crocea</i>
<i>Haplophaedia aureliae</i>	<i>Elleanthus aurantiacus</i>

<i>Haplophaedia lugens</i>	<i>Drymonia tenuis</i>
<i>Heliactin bilophus</i>	<i>Lychnophora salicifolia</i>
<i>Heliactin bilophus</i>	<i>Sacoila lanceolata</i>
<i>Heliangelus exortis</i>	<i>Aetanthus nodosus</i>
<i>Heliangelus exortis</i>	<i>Guzmania gracilior</i>
<i>Heliangelus mavors</i>	<i>Vaccinium floribundum</i>
<i>Heliangelus mavors</i>	<i>Vallea stipularis</i>
<i>Heliangelus strophianus</i>	<i>Palicourea lineata</i>
<i>Heliangelus viola</i>	<i>Gaultheria tomentosa</i>
<i>Heliangelus viola</i>	<i>Oreocallis grandiflora</i>
<i>Heliangelus viola</i>	<i>Salvia corrugata</i>
<i>Heliodoxa imperatrix</i>	<i>Guzmania jaramilloi</i>
<i>Heliodoxa imperatrix</i>	<i>Tropaeolum deckerianum</i>
<i>Heliodoxa jacula</i>	<i>Centropogon solanifolius</i>
<i>Heliodoxa jacula</i>	<i>Heliconia lankesteri</i>
<i>Heliodoxa jacula</i>	<i>Pitcairnia brittoniana</i>
<i>Heliomaster constantii</i>	<i>Ceiba aesculifolia</i>
<i>Heliomaster squamosus</i>	<i>Costus spiralis</i>
<i>Heliomaster squamosus</i>	<i>Erythrina speciosa</i>
<i>Heliomaster squamosus</i>	<i>Tacinga palmadora</i>
<i>Heliomaster squamosus</i>	<i>Qualea parviflora</i>
<i>Hylocharis chrysur</i>	<i>Aechmea distichantha</i>
<i>Hylocharis chrysur</i>	<i>Handroanthus chrysotrichus</i>
<i>Hylocharis chrysur</i>	<i>Inga vera</i>
<i>Hylocharis chrysur</i>	<i>Lepidagathis floribunda</i>
<i>Hylocharis chrysur</i>	<i>Luehea divaricata</i>
<i>Klais guimeti</i>	<i>Hamelia patens</i>
<i>Lafresnaya lafresnayi</i>	<i>Barnadesia spinosa</i>
<i>Lafresnaya lafresnayi</i>	<i>Macleania rupestris</i>
<i>Lafresnaya lafresnayi</i>	<i>Tristerix longibracteatus</i>
<i>Lampornis amethystinus</i>	<i>Phaseolus coccineus</i>
<i>Lampornis amethystinus</i>	<i>Salvia elegans</i>
<i>Lampornis clemenciae</i>	<i>Bouvardia ternifolia</i>
<i>Lampornis clemenciae</i>	<i>Castilleja toluccensis</i>
<i>Lampornis clemenciae</i>	<i>Cirsium nivale</i>
<i>Lampornis clemenciae</i>	<i>Penstemon gentianoides</i>
<i>Lampornis clemenciae</i>	<i>Penstemon roseus</i>
<i>Lampornis clemenciae</i>	<i>Salvia mexicana</i>
<i>Lampornis hemileucus</i>	<i>Psychotria elata</i>
<i>Leucochloris albicollis</i>	<i>Erythrina speciosa</i>
<i>Leucochloris albicollis</i>	<i>Fuchsia regia</i>
<i>Leucochloris albicollis</i>	<i>Handroanthus chrysotrichus</i>
<i>Leucochloris albicollis</i>	<i>Inga sessilis</i>
<i>Leucochloris albicollis</i>	<i>Mutisia speciosa</i>
<i>Leucochloris albicollis</i>	<i>Pyrostegia venusta</i>
<i>Leucochloris albicollis</i>	<i>Siphocampylus sulfureus</i>

<i>Lophornis chalybeus</i>	<i>Aechmea nudicaulis</i>
<i>Lophornis chalybeus</i>	<i>Erythrina speciosa</i>
<i>Lophornis chalybeus</i>	<i>Inga luschnathiana</i>
<i>Lophornis chalybeus</i>	<i>Spirotheca rivieri</i>
<i>Lophornis magnificus</i>	<i>Helicteres brevispira</i>
<i>Lophornis magnificus</i>	<i>Qualea multiflora</i>
<i>Lophornis magnificus</i>	<i>Styrax pohlii</i>
<i>Lophornis magnificus</i>	<i>Vochysia tucanorum</i>
<i>Metallura baroni</i>	<i>Saracha quitensis</i>
<i>Metallura tyrianthina</i>	<i>Aetanthus nodosus</i>
<i>Metallura tyrianthina</i>	<i>Berberis lutea</i>
<i>Metallura tyrianthina</i>	<i>Disterigma codonanthum</i>
<i>Metallura tyrianthina</i>	<i>Echeveria bicolor</i>
<i>Metallura tyrianthina</i>	<i>Elleanthus aurantiacus</i>
<i>Metallura tyrianthina</i>	<i>Gaiadendron punctatum</i>
<i>Metallura tyrianthina</i>	<i>Gaultheria erecta</i>
<i>Metallura tyrianthina</i>	<i>Gaultheria tomentosa</i>
<i>Metallura tyrianthina</i>	<i>Salvia corrugata</i>
<i>Metallura tyrianthina</i>	<i>Viola arguta</i>
<i>Oxypogon lindenii</i>	<i>Castilleja fissifolia</i>
<i>Panterpe insignis</i>	<i>Cavendishia bracteata</i>
<i>Panterpe insignis</i>	<i>Macleania rupestris</i>
<i>Phaethornis bourcieri</i>	<i>Aphelandra macrostachya</i>
<i>Phaethornis bourcieri</i>	<i>Besleria aggregata</i>
<i>Phaethornis bourcieri</i>	<i>Gurania rhizantha</i>
<i>Phaethornis bourcieri</i>	<i>Monotagma secundum</i>
<i>Phaethornis eurynome</i>	<i>Aechmea distichantha</i>
<i>Phaethornis eurynome</i>	<i>Aegiphila obducta</i>
<i>Phaethornis eurynome</i>	<i>Alstroemeria inodora</i>
<i>Phaethornis eurynome</i>	<i>Camptosema scarlatinum</i>
<i>Phaethornis eurynome</i>	<i>Canistrum cyathiforme</i>
<i>Phaethornis eurynome</i>	<i>Collaea speciosa</i>
<i>Phaethornis eurynome</i>	<i>Erythrina speciosa</i>
<i>Phaethornis eurynome</i>	<i>Hippeastrum puniceum</i>
<i>Phaethornis eurynome</i>	<i>Justicia brasiliiana</i>
<i>Phaethornis eurynome</i>	<i>Justicia carnea</i>
<i>Phaethornis eurynome</i>	<i>Lobelia fistulosa</i>
<i>Phaethornis eurynome</i>	<i>Mutisia speciosa</i>
<i>Phaethornis eurynome</i>	<i>Nidularium marigoii</i>
<i>Phaethornis eurynome</i>	<i>Sinningia cooperi</i>
<i>Phaethornis eurynome</i>	<i>Sinningia douglasii</i>
<i>Phaethornis eurynome</i>	<i>Siphocampylus westinianus</i>
<i>Phaethornis guy</i>	<i>Cavendishia bracteata</i>
<i>Phaethornis guy</i>	<i>Heliconia atropurpurea</i>
<i>Phaethornis guy</i>	<i>Heliconia bihai</i>
<i>Phaethornis hispidus</i>	<i>Aechmea contracta</i>

<i>Phaethornis hispidus</i>	<i>Besleria aggregata</i>
<i>Phaethornis hispidus</i>	<i>Costus scaber</i>
<i>Phaethornis hispidus</i>	<i>Palicourea crocea</i>
<i>Phaethornis idaliae</i>	<i>Aechmea nudicaulis</i>
<i>Phaethornis idaliae</i>	<i>Quesnelia quesneliana</i>
<i>Phaethornis idaliae</i>	<i>Tillandsia gardneri</i>
<i>Phaethornis longirostris</i>	<i>Renealmia cernua</i>
<i>Phaethornis longuemareus</i>	<i>Palicourea crocea</i>
<i>Phaethornis malaris</i>	<i>Isertia hypoleuca</i>
<i>Phaethornis pretrei</i>	<i>Aechmea distichantha</i>
<i>Phaethornis pretrei</i>	<i>Ananas ananassoides</i>
<i>Phaethornis pretrei</i>	<i>Geissomeria schottiana</i>
<i>Phaethornis pretrei</i>	<i>Centropogon cornutus</i>
<i>Phaethornis pretrei</i>	<i>Dicliptera squarrosa</i>
<i>Phaethornis pretrei</i>	<i>Geissomeria longiflora</i>
<i>Phaethornis pretrei</i>	<i>Heliconia psittacorum</i>
<i>Phaethornis pretrei</i>	<i>Helicteres velutina</i>
<i>Phaethornis pretrei</i>	<i>Hololepis pedunculata</i>
<i>Phaethornis pretrei</i>	<i>Ipomoea hederifolia</i>
<i>Phaethornis pretrei</i>	<i>Lepidagathis floribunda</i>
<i>Phaethornis pretrei</i>	<i>Lobelia fistulosa</i>
<i>Phaethornis pretrei</i>	<i>Lundia cordata</i>
<i>Phaethornis pretrei</i>	<i>Manettia cordifolia</i>
<i>Phaethornis pretrei</i>	<i>Neoregelia bahiana</i>
<i>Phaethornis pretrei</i>	<i>Opuntia monacantha</i>
<i>Phaethornis pretrei</i>	<i>Ruellia angustiflora</i>
<i>Phaethornis pretrei</i>	<i>Ruellia brevifolia</i>
<i>Phaethornis pretrei</i>	<i>Sinningia rupicola</i>
<i>Phaethornis pretrei</i>	<i>Vriesea procera</i>
<i>Phaethornis ruber</i>	<i>Erythrina speciosa</i>
<i>Phaethornis ruber</i>	<i>Gurania acuminata</i>
<i>Phaethornis ruber</i>	<i>Ischnosiphon lasiocoleus</i>
<i>Phaethornis ruber</i>	<i>Palicourea crocea</i>
<i>Phaethornis ruber</i>	<i>Passiflora speciosa</i>
<i>Phaethornis squalidus</i>	<i>Aechmea ornata</i>
<i>Phaethornis squalidus</i>	<i>Geissomeria schottiana</i>
<i>Phaethornis squalidus</i>	<i>Passiflora speciosa</i>
<i>Phaethornis squalidus</i>	<i>Ruellia brevifolia</i>
<i>Phaethornis squalidus</i>	<i>Vriesea rodigasiana</i>
<i>Phaethornis striigularis</i>	<i>Gurania coccinea</i>
<i>Phaethornis striigularis</i>	<i>Renealmia cernua</i>
<i>Phaethornis syrmatophorus</i>	<i>Centropogon solanifolius</i>
<i>Phaethornis yaruqui</i>	<i>Columnnea mastersonii</i>
<i>Phaethornis yaruqui</i>	<i>Heliconia griggsiana</i>
<i>Pterophanes cyanopterus</i>	<i>Barnadesia arborea</i>
<i>Pterophanes cyanopterus</i>	<i>Macleania rupestris</i>

<i>Pterophanes cyanopterus</i>	<i>Oreocallis grandiflora</i>
<i>Pterophanes cyanopterus</i>	<i>Puya clava-herculis</i>
<i>Pterophanes cyanopterus</i>	<i>Tristerix longebracteatus</i>
<i>Ramphodon naevius</i>	<i>Erythrina speciosa</i>
<i>Ramphodon naevius</i>	<i>Vriesea ensiformis</i>
<i>Ramphodon naevius</i>	<i>Vriesea incurvata</i>
<i>Ramphodon naevius</i>	<i>Vriesea vagans</i>
<i>Ramphomicron microrhynchum</i>	<i>Gaiadendron punctatum</i>
<i>Selasphorus flammula</i>	<i>Disterigma humboldtii</i>
<i>Selasphorus flammula</i>	<i>Fuchsia microphylla</i>
<i>Selasphorus sasin</i>	<i>Prunella vulgaris</i>
<i>Selasphorus scintilla</i>	<i>Disterigma humboldtii</i>
<i>Stephanoxis lalandi</i>	<i>Aechmea distichantha</i>
<i>Stephanoxis lalandi</i>	<i>Buddleja brasiliensis</i>
<i>Stephanoxis lalandi</i>	<i>Cestrum corymbosum</i>
<i>Stephanoxis lalandi</i>	<i>Collaea speciosa</i>
<i>Stephanoxis lalandi</i>	<i>Nematanthus fornix</i>
<i>Stephanoxis lalandi</i>	<i>Salvia arenaria</i>
<i>Stephanoxis loddigesii</i>	<i>Aechmea distichantha</i>
<i>Stephanoxis loddigesii</i>	<i>Bougainvillea glabra</i>
<i>Stephanoxis loddigesii</i>	<i>Gaylussacia brasiliensis</i>
<i>Stephanoxis loddigesii</i>	<i>Lantana camara</i>
<i>Thalurania furcata</i>	<i>Besleria aggregata</i>
<i>Thalurania furcata</i>	<i>Dicliptera squarrosa</i>
<i>Thalurania furcata</i>	<i>Gurania rhizantha</i>
<i>Thalurania furcata</i>	<i>Gurania spinulosa</i>
<i>Thalurania furcata</i>	<i>Heliconia psittacorum</i>
<i>Thalurania furcata</i>	<i>Helicteres brevispira</i>
<i>Thalurania furcata</i>	<i>Palicourea marcgravii</i>
<i>Thalurania furcata</i>	<i>Psychotria platypoda</i>
<i>Thalurania furcata</i>	<i>Ruellia brevifolia</i>
<i>Thalurania glaucopis</i>	<i>Abutilon bedfordianum</i>
<i>Thalurania glaucopis</i>	<i>Aechmea nudicaulis</i>
<i>Thalurania glaucopis</i>	<i>Geissomeria schottiana</i>
<i>Thalurania glaucopis</i>	<i>Erythrina speciosa</i>
<i>Thalurania glaucopis</i>	<i>Fuchsia regia</i>
<i>Thalurania glaucopis</i>	<i>Psychotria nuda</i>
<i>Thalurania glaucopis</i>	<i>Spirotheca rivieri</i>
<i>Threnetes leucurus</i>	<i>Cuphea melvilla</i>
<i>Threnetes leucurus</i>	<i>Erythrina fusca</i>
<i>Threnetes leucurus</i>	<i>Heliconia stricta</i>
<i>Threnetes leucurus</i>	<i>Passiflora quadriglandulosa</i>
<i>Threnetes ruckeri</i>	<i>Calathea inocephala</i>
<i>Tilmatura dupontii</i>	<i>Salvia iodantha</i>
<i>Tilmatura dupontii</i>	<i>Salvia mexicana</i>
<i>Topaza pyra</i>	<i>Isertia hypoleuca</i>

Table S2. Abiotic variables used to build the species distribution models.

Climatic properties	Soil properties*
Annual Mean Temperature	Bulk density
Mean Diurnal Range	Clay content
Isothermality	Coarse fragments
Temperature Seasonality	Sand
Maximum Temperature of Warmest Month	Silt
Minimum Temperature of Coldest Month	Cation exchange capacity (at pH 7)
Temperature Annual Range	Nitrogen
Mean Temperature of Wettest Quarter	Soil organic carbon
Mean Temperature of Driest Quarter	pH water
Mean Temperature of Warmest Quarter	
Mean Temperature of Coldest Quarter	
Annual Precipitation	
Precipitation of Wettest Month	
Precipitation of Driest Month	
Precipitation Seasonality	
Precipitation of Wettest Quarter	
Precipitation of Driest Quarter	
Precipitation of Warmest Quarter	
Precipitation of Coldest Quarter	

* Each soil property has data for six different soil depths (0-5, 5-15, 15-30, 30-60, 60-100, 100-200 cm).

Table S3. Results of the species distribution models generated using only abiotic variables and combined variables (abiotic and biotic), and the best fit of each model according to the second-order Akaike information criterion (AICc) for all 100 hummingbird species evaluated. NP: number of predictors, Se: Sensitivity, Sp: Specificity

Species	Abiotic				Combined			
	NP	AICc	Se	Sp	NP	AICc	Se	Sp
<i>Glaucis dohrnii</i>	4	283.70	1.00	0.84	5	286.83	1.00	0.84
<i>Oxyopogon lindenii</i>	5	106.68	1.00	0.92	5	107.34	1.00	0.92

<i>Metallura baroni</i>	4	121.60	1.00	0.98	6	635.43	1.00	0.84
<i>Stephanoxis lalandi</i>	6	1074.42	0.99	0.91	5	112.55	1.00	0.99
<i>Eriocnemis derbyi</i>	5	1227.63	0.98	0.88	5	1229.14	0.99	0.86
<i>Ramphodon naevius</i>	6	3586.69	0.97	0.93	8	4766.12	0.99	0.82
<i>Stephanoxis loddigesii</i>	6	4697.52	0.97	0.85	7	3564.97	0.98	0.93
<i>Lophornis chalybeus</i>	6	1426.37	0.97	0.94	5	5231.18	0.97	0.88
<i>Coeligena torquata</i>	6	10652.44	0.97	0.86	7	1358.78	0.97	0.96
<i>Lafresnaya lafresnayi</i>	6	8727.31	0.97	0.87	8	2535.38	0.97	0.87
<i>Lampornis hemileucus</i>	5	643.35	0.96	0.85	12	9383.80	0.97	0.87
<i>Panterpe insignis</i>	5	916.15	0.96	0.88	10	18536.77	0.96	0.86
<i>Heliangelus exortis</i>	5	5226.94	0.96	0.85	7	937.49	0.96	0.87
<i>Eriocnemis vestita</i>	5	5251.33	0.96	0.89	5	699.98	0.96	0.90
<i>Ensifera ensifera</i>	5	7143.74	0.96	0.89	6	5243.58	0.96	0.86
<i>Aglaeactis cupripennis</i>	6	9896.79	0.96	0.88	6	4056.38	0.96	0.92
<i>Boissonneaua flavescens</i>	5	5260.31	0.96	0.86	7	1869.39	0.96	0.89
<i>Chalcostigma herrani</i>	5	2091.57	0.96	0.81	10	18097.36	0.96	0.91
<i>Eriocnemis mosquera</i>	5	1948.33	0.96	0.86	6	777.66	0.96	0.83
<i>Selasphorus flammula</i>	5	721.17	0.96	0.90	6	725.37	0.96	0.90
<i>Heliodoxa imperatrix</i>	5	1212.83	0.96	0.85	9	16430.83	0.95	0.80
<i>Ramphomicron microrhynchum</i>	5	4121.54	0.95	0.90	6	9410.99	0.95	0.75
<i>Haplophaedia aureliae</i>	5	5422.83	0.95	0.80	7	2171.40	0.95	0.88
<i>Metallura tyrianthina</i>	5	18068.39	0.95	0.90	6	5196.66	0.95	0.86
<i>Coeligena lutetiae</i>	5	3108.77	0.95	0.88	7	10619.17	0.95	0.87
<i>Haplophaedia lugens</i>	5	588.86	0.95	0.86	7	8736.13	0.95	0.89
<i>Colibri coruscans</i>	6	34921.41	0.95	0.84	7	9933.81	0.95	0.89
<i>Leucochloris albicollis</i>	6	16556.66	0.95	0.81	6	639.54	0.95	0.88
<i>Atthis heloisa</i>	5	4054.11	0.94	0.81	6	5329.85	0.95	0.81
<i>Phaethornis eurynome</i>	6	9330.28	0.94	0.90	7	3802.59	0.95	0.77
<i>Selasphorus scintilla</i>	5	1134.79	0.94	0.85	8	6353.34	0.94	0.91
<i>Clytolaema rubricauda</i>	6	3978.32	0.94	0.89	6	7116.28	0.94	0.92
<i>Pterophanes cyanopterus</i>	5	6390.23	0.94	0.90	8	3850.47	0.94	0.91
<i>Phaethornis squalidus</i>	6	2601.23	0.94	0.92	6	3076.44	0.94	0.89
<i>Augastes scutatus</i>	6	610.20	0.93	0.93	6	1135.67	0.94	0.88
<i>Heliangelus viola</i>	5	1951.61	0.93	0.88	8	1475.26	0.94	0.75
<i>Coeligena iris</i>	5	2190.08	0.93	0.87	9	11844.85	0.94	0.88
<i>Heliangelus mavors</i>	5	695.17	0.92	0.94	7	7921.23	0.94	0.87
<i>Thalurania glaucopis</i>	6	18768.98	0.92	0.88	8	1041.40	0.93	0.94
<i>Doryfera ludovicae</i>	5	9525.65	0.92	0.89	6	1235.01	0.92	0.90
<i>Heliomaster constantii</i>	7	14833.31	0.92	0.77	6	4044.03	0.92	0.83
<i>Adelomyia melanogenys</i>	5	18896.39	0.92	0.88	6	2084.94	0.92	0.86
<i>Phaethornis yaruqui</i>	5	3885.45	0.92	0.73	6	1204.83	0.92	0.90
<i>Eupherusa nigriventris</i>	5	782.81	0.91	0.87	8	34731.76	0.92	0.87
<i>Tilmatura dupontii</i>	6	5907.10	0.91	0.74	7	7215.08	0.92	0.84
<i>Phaethornis syrmatophorus</i>	6	7949.53	0.91	0.89	6	1925.82	0.91	0.91
<i>Amazilia beryllina</i>	7	21307.34	0.91	0.75	9	21275.93	0.91	0.74

<i>Eriocnemis luciani</i>	5	1260.61	0.90	0.92	8	17158.15	0.91	0.86
<i>Florisuga fusca</i>	6	15228.00	0.90	0.82	8	19191.18	0.91	0.87
<i>Calothorax lucifer</i>	6	9974.84	0.90	0.71	7	9395.43	0.91	0.90
<i>Amazilia rutila</i>	6	35109.29	0.89	0.77	7	14886.68	0.91	0.77
<i>Agelaiocercus coelestis</i>	6	2461.37	0.89	0.82	7	5885.12	0.90	0.75
<i>Phaethornis idaliae</i>	4	673.11	0.89	0.82	10	23622.26	0.90	0.80
<i>Anopetia gounellei</i>	6	1477.70	0.89	0.78	9	34960.34	0.90	0.79
<i>Phaethornis guy</i>	6	17789.65	0.89	0.81	10	15010.29	0.89	0.86
<i>Phaethornis longuemareus</i>	6	2037.08	0.89	0.83	7	9581.22	0.88	0.82
<i>Amazilia lactea</i>	6	11948.47	0.89	0.92	7	602.01	0.88	0.97
<i>Chrysuronia oenone</i>	5	9666.80	0.88	0.81	11	11666.25	0.87	0.84
<i>Lampornis amethystinus</i>	6	6404.92	0.88	0.82	6	9289.60	0.87	0.80
<i>Lampornis clemenciae</i>	6	14463.49	0.88	0.81	6	2400.39	0.87	0.87
<i>Aphantochroa cirrochloris</i>	6	7275.14	0.88	0.85	8	5119.01	0.87	0.78
<i>Cynanthus latirostris</i>	6	44048.25	0.87	0.86	6	585.60	0.87	0.83
<i>Florisuga mellivora</i>	6	45817.76	0.87	0.65	7	29051.93	0.87	0.72
<i>Topaza pyra</i>	6	1402.07	0.86	0.72	8	44393.90	0.87	0.85
<i>Eutoxeres aquila</i>	5	7604.91	0.86	0.77	9	9830.42	0.87	0.76
<i>Glaucis hirsutus</i>	6	32535.52	0.86	0.56	9	14341.62	0.85	0.83
<i>Phaethornis hispidus</i>	5	12862.87	0.86	0.67	8	3639.26	0.84	0.74
<i>Hylocharis chrysura</i>	6	35120.81	0.85	0.77	8	35076.00	0.84	0.76
<i>Coeligena wilsoni</i>	5	1914.86	0.84	0.87	8	5989.18	0.84	0.72
<i>Colibri serrirostris</i>	6	11797.65	0.84	0.88	17	25449.93	0.84	0.79
<i>Heliomaster squamosus</i>	6	5998.25	0.84	0.75	6	20390.40	0.84	0.76
<i>Phaethornis longirostris</i>	6	20525.83	0.83	0.77	7	6383.23	0.84	0.83
<i>Phaethornis pretrei</i>	6	25676.39	0.82	0.80	6	13730.29	0.84	0.75
<i>Heliangelus strophianus</i>	5	765.39	0.82	0.89	8	19121.01	0.84	0.87
<i>Chlorostilbon lucidus</i>	6	86188.77	0.82	0.71	6	7565.61	0.83	0.81
<i>Amazilia leucogaster</i>	6	3998.60	0.82	0.92	14	86098.10	0.83	0.70
<i>Phaethornis malaris</i>	5	13686.35	0.82	0.78	6	2056.59	0.83	0.90
<i>Heliodoxa jacula</i>	6	5118.05	0.82	0.82	8	8248.15	0.83	0.67
<i>Selasphorus sasin</i>	6	24238.34	0.82	0.91	6	741.90	0.82	0.89
<i>Amazilia violiceps</i>	7	19176.42	0.82	0.87	15	40327.70	0.82	0.81
<i>Phaethornis striigularis</i>	6	29571.01	0.81	0.74	7	1940.02	0.82	0.89
<i>Urostitte benjamini</i>	6	1390.18	0.81	0.81	8	3053.19	0.81	0.86
<i>Klais guimeti</i>	6	9739.67	0.81	0.82	6	3727.29	0.81	0.82
<i>Eupetomena macroura</i>	5	41386.73	0.81	0.78	7	1411.77	0.81	0.73
<i>Amazilia brevirostris</i>	5	3717.20	0.80	0.84	9	31808.20	0.80	0.60
<i>Lophornis magnificus</i>	6	3101.12	0.80	0.88	8	12681.97	0.80	0.78
<i>Eugenes fulgens</i>	6	23802.17	0.79	0.84	14	49517.48	0.80	0.59
<i>Chlorostilbon notatus</i>	5	13948.15	0.77	0.74	6	1391.79	0.80	0.83
<i>Threnetes ruckeri</i>	6	9618.18	0.77	0.82	9	13599.50	0.79	0.78
<i>Heliactin bilophus</i>	6	3702.52	0.76	0.77	7	4021.53	0.78	0.94
<i>Threnetes leucurus</i>	5	7115.98	0.73	0.89	6	24437.23	0.78	0.72
<i>Phaethornis bourcierii</i>	6	8241.18	0.71	0.73	9	44521.87	0.77	0.83
<i>Phaethornis ruber</i>	5	32259.45	0.69	0.69	9	31542.76	0.77	0.78

<i>Anthracothorax aurulentus</i>	3	853.17	0.69	0.43	6	16588.33	0.75	0.69
<i>Campylopterus largipennis</i>	5	16584.08	0.69	0.76	7	24771.30	0.75	0.93
<i>Chlorostilbon mellisugus</i>	5	24600.80	0.66	0.76	7	7031.61	0.75	0.88
<i>Thalurania furcata</i>	6	43777.51	0.62	0.70	3	853.24	0.68	0.44
<i>Amazilia versicolor</i>	5	23169.66	0.61	0.86	9	22925.07	0.67	0.82
<i>Amazilia fimbriata</i>	6	49976.70	0.56	0.79	11	43338.93	0.67	0.69
<i>Anthracothorax nigricollis</i>	6	63355.81	0.54	0.84	8	62058.78	0.61	0.84

Table S4. Results of the spatial similarity in environmental suitability and binary geographic projection between the species distribution models generated using only abiotic variables and those with abiotic and biotic variables for all 100 hummingbird species evaluated.

Species	Suitability Similarity	Geographic Similarity
<i>Anthracothorax aurulentus</i>	1.00	0.98
<i>Oxygogon lindenii</i>	1.00	0.92
<i>Glaucis dohrnii</i>	1.00	0.93
<i>Eriocnemis vestita</i>	1.00	0.94
<i>Anopetia gounellei</i>	1.00	0.85
<i>Eriocnemis derbyi</i>	1.00	0.81
<i>Boissonneaua flavescens</i>	1.00	0.94
<i>Heliomaster constantii</i>	1.00	0.88
<i>Urostitte benjamini</i>	1.00	0.84
<i>Topaza pyra</i>	1.00	0.89
<i>Tilmatura dupontii</i>	0.99	0.87
<i>Chalcostigma herrani</i>	0.99	0.73
<i>Hylocharis chrysur</i>	0.99	0.82
<i>Amazilia brevirostris</i>	0.99	0.68
<i>Selasphorus flammula</i>	0.99	0.88
<i>Chlorostilbon mellisugus</i>	0.99	0.57
<i>Amazilia rutila</i>	0.99	0.79
<i>Heliangelus exortis</i>	0.99	0.89
<i>Heliangelus mavors</i>	0.99	0.64
<i>Aglaeactis cupripennis</i>	0.99	0.83
<i>Campylopterus largipennis</i>	0.99	0.57
<i>Phaethornis malaris</i>	0.99	0.73
<i>Coeligena torquata</i>	0.99	0.84
<i>Atthis heloisa</i>	0.99	0.79
<i>Phaethornis syrmatophorus</i>	0.98	0.79
<i>Amazilia violiceps</i>	0.98	0.75
<i>Amazilia beryllina</i>	0.98	0.85

<i>Heliodoxa jacula</i>	0.98	0.72
<i>Phaethornis longirostris</i>	0.98	0.78
<i>Lampornis amethystinus</i>	0.98	0.77
<i>Coeligena lutetiae</i>	0.98	0.85
<i>Ensifera ensifera</i>	0.98	0.77
<i>Thalurania furcata</i>	0.98	0.49
<i>Phaethornis ruber</i>	0.98	0.51
<i>Heliomaster squamosus</i>	0.98	0.73
<i>Lophornis magnificus</i>	0.98	0.65
<i>Lampornis clemenciae</i>	0.98	0.76
<i>Stephanoxis loddigesii</i>	0.98	0.85
<i>Heliactin bilophus</i>	0.98	0.68
<i>Lampornis hemileucus</i>	0.98	0.81
<i>Doryfera ludovicae</i>	0.98	0.74
<i>Amazilia leucogaster</i>	0.98	0.60
<i>Eriocnemis mosquera</i>	0.98	0.62
<i>Phaethornis bourcieri</i>	0.98	0.63
<i>Lafresnaya lafresnayi</i>	0.98	0.80
<i>Calothorax lucifer</i>	0.98	0.64
<i>Eupherusa nigriventris</i>	0.98	0.73
<i>Chlorostilbon notatus</i>	0.98	0.54
<i>Panterpe insignis</i>	0.97	0.77
<i>Eugenes fulgens</i>	0.97	0.65
<i>Aphantochroa cirrochloris</i>	0.97	0.67
<i>Phaethornis hispidus</i>	0.97	0.50
<i>Haplophaedia aureliae</i>	0.97	0.75
<i>Metallura tyrianthina</i>	0.97	0.84
<i>Leucochloris albicollis</i>	0.97	0.81
<i>Coeligena wilsoni</i>	0.97	0.70
<i>Amazilia fimbriata</i>	0.97	0.35
<i>Threnetes leucurus</i>	0.97	0.52
<i>Selasphorus scintilla</i>	0.97	0.82
<i>Florisuga fusca</i>	0.97	0.61
<i>Chrysuronia oenone</i>	0.97	0.63
<i>Pterophanes cyanopterus</i>	0.97	0.83
<i>Amazilia versicolor</i>	0.96	0.48
<i>Eriocnemis luciani</i>	0.96	0.74
<i>Phaethornis striigularis</i>	0.96	0.69
<i>Heliodoxa imperatrix</i>	0.96	0.61
<i>Chlorostilbon lucidus</i>	0.96	0.77
<i>Anthracothorax nigricollis</i>	0.96	0.37
<i>Colibri serrirostris</i>	0.96	0.67
<i>Thalurania glaucopis</i>	0.96	0.71
<i>Coeligena iris</i>	0.96	0.71
<i>Colibri coruscans</i>	0.96	0.72
<i>Cynanthus latirostris</i>	0.96	0.68

<i>Florisuga mellivora</i>	0.96	0.42
<i>Phaethornis yaruqui</i>	0.96	0.68
<i>Glaucis hirsutus</i>	0.96	0.43
<i>Amazilia lactea</i>	0.95	0.59
<i>Ramphomicron microrhynchum</i>	0.95	0.69
<i>Phaethornis squalidus</i>	0.95	0.53
<i>Agelaiocercus coelestis</i>	0.95	0.57
<i>Heliangelus strophianus</i>	0.95	0.55
<i>Phaethornis pretrei</i>	0.94	0.65
<i>Eutoxeres aquila</i>	0.94	0.50
<i>Eupetomena macroura</i>	0.94	0.53
<i>Heliangelus viola</i>	0.93	0.73
<i>Adelomyia melanogenys</i>	0.93	0.63
<i>Phaethornis longuemareus</i>	0.93	0.47
<i>Threnetes ruckeri</i>	0.93	0.57
<i>Ramphodon naevius</i>	0.93	0.52
<i>Clytolaema rubricauda</i>	0.92	0.68
<i>Stephanoxis lalandi</i>	0.92	0.54
<i>Selasphorus sasin</i>	0.92	0.49
<i>Augastes scutatus</i>	0.91	0.38
<i>Phaethornis guy</i>	0.91	0.54
<i>Phaethornis eurynome</i>	0.91	0.61
<i>Lophornis chalybeus</i>	0.89	0.52
<i>Haplophaedia lugens</i>	0.89	0.53
<i>Phaethornis idaliae</i>	0.88	0.48
<i>Klais guimeti</i>	0.84	0.37
<i>Metallura baroni</i>	0.83	0.35

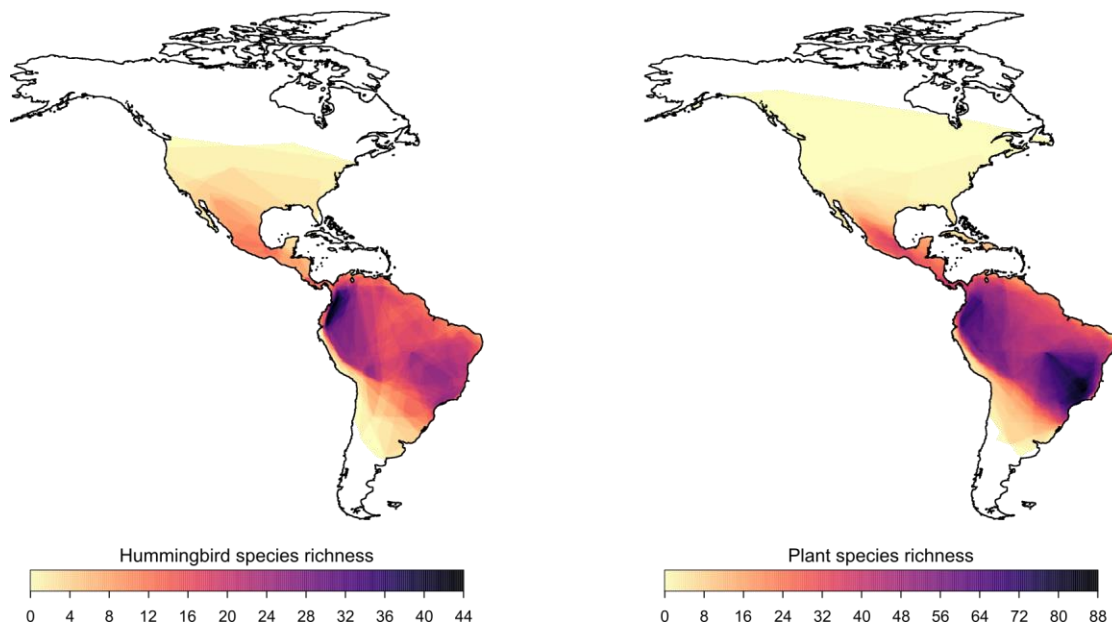


Fig. S1. Distribution of hummingbird and plant species analyzed in our study.

Capítulo 2: Additional Information

Supplementary Material

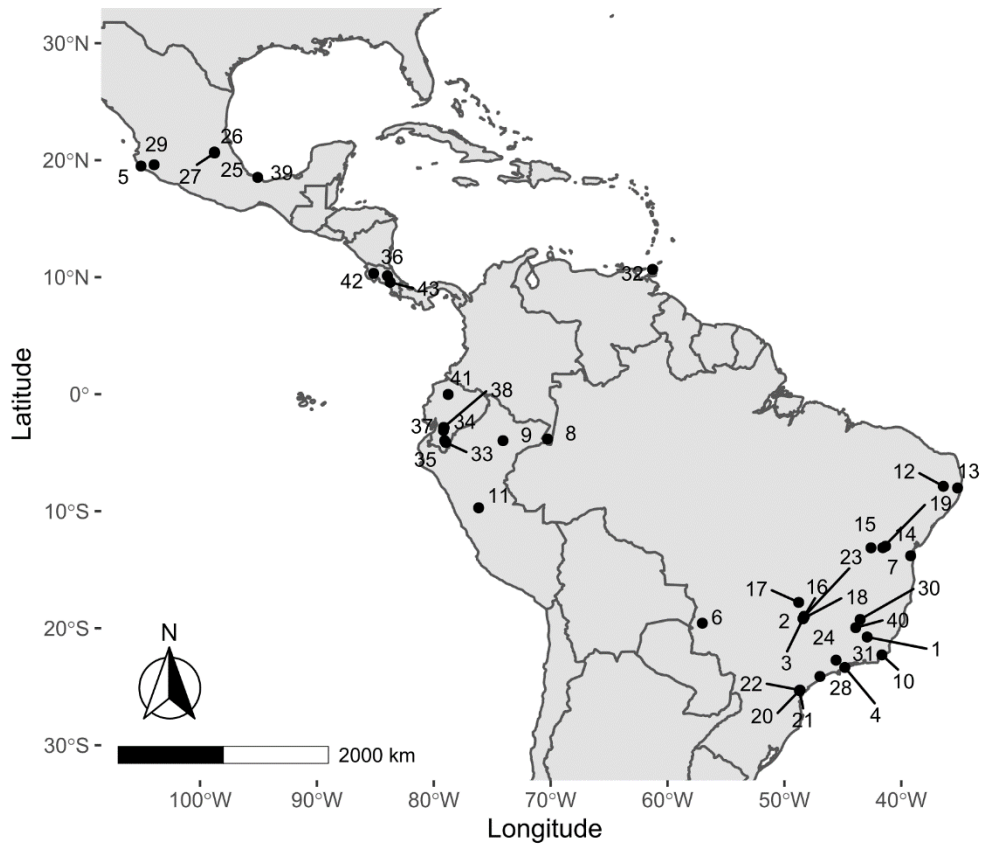


Fig. S1. Location map of the hummingbird-plant interaction networks used in this study. See Table A1 for codes meaning and references.

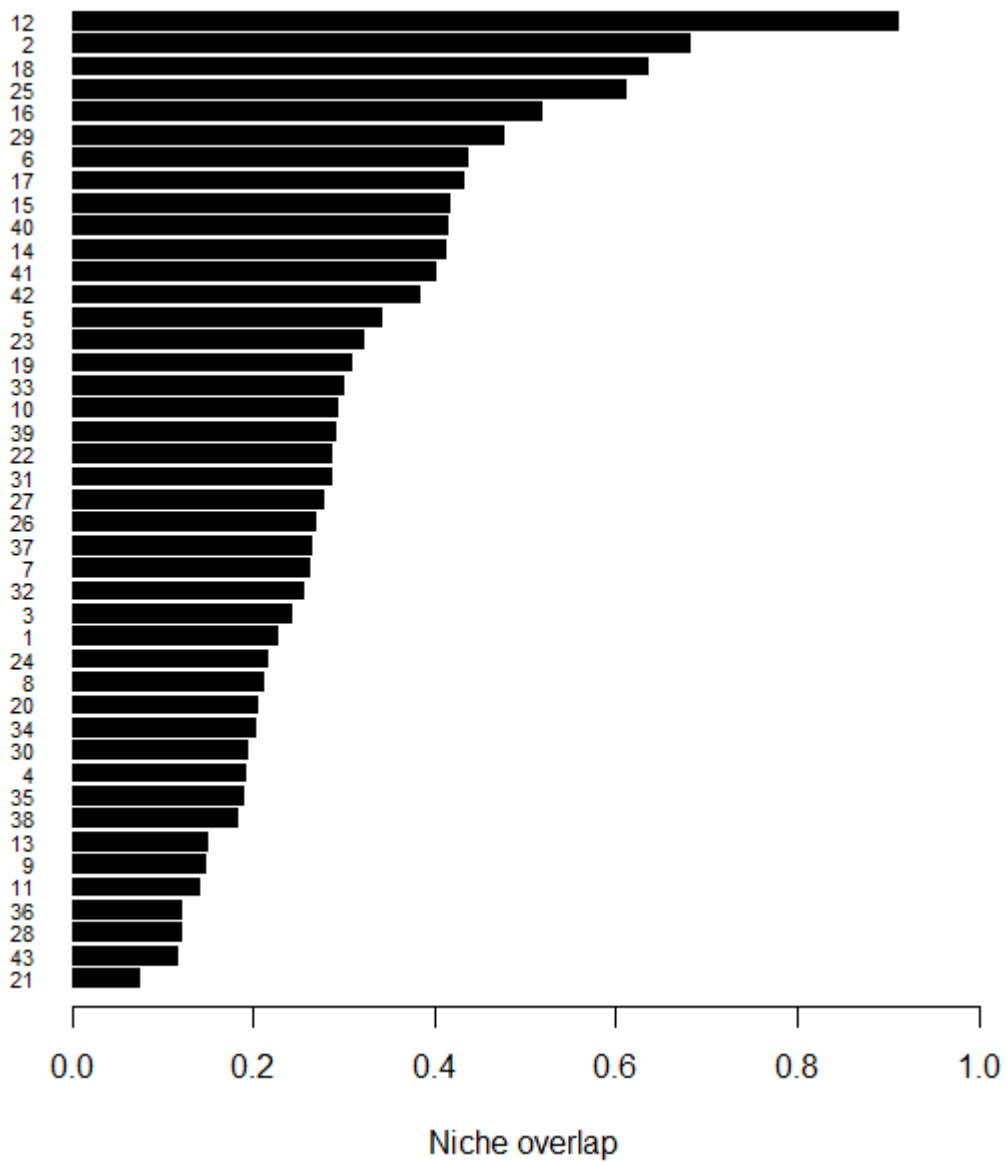


Fig. S2. Overlap values in each community. To access the code with the name of the networks, see Appendix A.

Table S1. All regression models generated. Net Primary Productivity (NPP), Mean Wing Disc Loading (\bar{x} WDL), Mean Pairwise Distance of the Bill Length (MPD.BL) and ratio between the species richness of hummingbirds and plants (RAT).

Models	df	AICc	Δ AICc	R ²
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(NPP+1)	5.0	-34.0	0.00	0.29
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1)	4.0	-33.0	1.00	0.22
NO ~ Log _(\bar{x}WDL+1)	3.0	-33.0	1.10	0.18
NO ~ Log _(MPD.BL+1) + Log _(NPP+1)	4.0	-33.0	1.60	0.21
NO ~ Log _(\bar{x}WDL+1) + Log _(NPP+1)	4.0	-32.0	2.00	0.21
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(NPP+1) + Log _(RAT+1)	6.0	-32.0	2.20	0.29
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(NPP+1) + Log _(MPD.WDL+1)	6.0	-32.0	2.40	0.29
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(RAT+1)	5.0	-32.0	2.40	0.24
NO ~ Log _(\bar{x}WDL+1) + Log _(RAT+1)	4.0	-32.0	2.50	0.20
NO ~ Log _(\bar{x}WDL+1) + Log _(MPD.WDL+1)	4.0	-31.0	3.30	0.18
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(MPD.WDL+1)	5.0	-31.0	3.40	0.23
NO ~ Log _(MPD.BL+1) + Log _(NPP+1) + Log _(RAT+1)	5.0	-31.0	3.50	0.23
NO ~ Log _(\bar{x}WDL+1) + Log _(NPP+1) + Log _(RAT+1)	5.0	-30.0	4.00	0.22
NO ~ Log _(MPD.BL+1) + Log _(NPP+1) + Log _(MPD.WDL+1)	5.0	-30.0	4.10	0.21
NO ~ Log _(\bar{x}WDL+1) + Log _(NPP+1) + Log _(MPD.WDL+1)	5.0	-30.0	4.20	0.21
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(NPP+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	7.0	-30.0	4.50	0.30
NO ~ Log _(MPD.BL+1) + Log _(\bar{x}WDL+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	6.0	-30.0	4.60	0.25
NO ~ Log _(\bar{x}WDL+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	5.0	-29.0	5.00	0.20
NO ~ Log _(NPP+1)	3.0	-28.0	5.90	0.08
NO ~ Log _(MPD.BL+1)	3.0	-28.0	5.90	0.08
NO ~ Log _(MPD.BL+1) + Log _(NPP+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	6.0	-28.0	6.00	0.23
NO ~ Log _(MPD.BL+1) + Log _(RAT+1)	4.0	-28.0	6.40	0.12
NO ~ Log _(\bar{x}WDL+1) + Log _(NPP+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	6.0	-28.0	6.50	0.22
NO ~ Log _(NPP+1) + Log _(MPD.WDL+1)	4.0	-28.0	6.80	0.11
Intercept	2.0	-27.0	7.20	0.00
NO ~ Log _(NPP+1) + Log _(RAT+1)	4.0	-27.0	7.40	0.10
NO ~ Log _(RAT+1)	3.0	-27.0	7.60	0.04
NO ~ Log _(MPD.WDL+1)	3.0	-26.0	8.30	0.03
NO ~ Log _(MPD.BL+1) + Log _(MPD.WDL+1)	4.0	-26.0	8.40	0.08
NO ~ Log _(MPD.BL+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	5.0	-25.0	8.80	0.12
NO ~ Log _(NPP+1) + Log _(RAT+1) + Log _(MPD.WDL+1)	5.0	-25.0	8.90	0.12
NO ~ Log _(RAT+1) + Log _(MPD.WDL+1)	4.0	-25.0	9.30	0.06

Table S2: Coefficient values of the regression model used in our study ($\text{niche.overlap} \sim \log(\text{MPD.BL} + 1) + \log(\bar{\text{xWDL}} + 1) + \log(\text{NPP} + 1)$). Mean Wing Disc Loading ($\bar{\text{xWDL}}$), Mean Pairwise Distance of the Bill Length (MPD.BL) and Net Primary Productivity (NPP).

	Estimate	Std. Error	t-value
MPD.BIL	-0.30	0.15	-2.09
$\bar{\text{xWDL}}$	0.29	0.15	1.99
NPP	-0.28	0.15	-1.84

Appendix A

Appendix A: Details on the interaction networks used.

Table A1. Network data used in the study.

Code	Latitude	Longitude	Humming-bird richness	Plant richness	NPP	Data Source Reference
1	-20.75	-42.92	8	14	114.38	(Abreu & Vieira 2004)
2	-18.99	-48.3	6	5	84.01	(de Araújo <i>et al.</i> 2011)
3	-19.18	-48.4	7	36	84.28	(Araújo <i>et al.</i> 2013)
4	-23.35	-44.83	12	44	150.78	(Araújo 1996)
5	19.5	-105.05	5	23	129.52	(Arizmendi & Ornelas 1990)
6	-19.57	-57.02	3	15	94.35	(Bogiani 2012)
7	-13.81	-39.2	13	18	150.17	(Coelho 2013)
8	-3.82	-70.27	14	29	145.77	(Cotton 1998)
9	-3.97	-74.08	24	63	153.52	(Dziedzioch <i>et al.</i> 2003)
10	-22.28	-41.66	3	10	122.11	(Fonseca <i>et al.</i> 2015)
11	-9.71	-76.16	12	27	65.83	(Gonzalez & Loiselle 2016)
12	-7.87	-36.4	5	31	88.22	(Las-Casas <i>et al.</i> 2012)
13	-8.02	-35.18	8	27	103.47	(Lopes & Sazima 2002)
14	-12.99	-41.34	7	36	90.92	(Machado <i>et al.</i> 2007)
15	-13.13	-42.59	7	29	83.7	(Machado 2009)
16	-18.98	-48.3	10	10	84.01	(Machado 2012)
17	-17.79	-48.78	8	12	87.27	(Machado 2012)
18	-19.17	-48.39	6	17	84.28	(Machado 2012)
19	-13.12	-41.58	8	10	86.52	(Machado 2014)
20	-25.32	-48.71	7	13	139.81	(Malucelli 2014)
21	-25.32	-48.71	4	13	139.81	(Malucelli 2014)
22	-25.29	-48.66	4	13	139.81	(Malanotte 2018)
23	-18.99	-48.3	7	9	84.01	(Maruyama <i>et al.</i> 2013)
24	-19.17	-48.4	6	17	84.28	(Maruyama <i>et al.</i> 2013)
25	20.68	-98.76	3	7	158.21	(Martínez-García & Ortiz-Pulido 2014)

26	20.69	-98.77	2	9	158.21	(Martínez-García & Ortiz-Pulido 2014)
27	20.61	-98.76	5	11	158.21	(Martínez-García & Ortiz-Pulido 2014)
28	-24.12	-46.96	13	38	151.62	(Rocca de Andrade 2006)
29	19.61	-103.93	11	14	120.34	(Rodríguez Flores 2009)
30	-19.25	-43.52	6	45	120.53	(Rodrigues & Rodrigues 2014)
31	-22.73	-45.58	4	23	147.71	(Sazima <i>et al.</i> 1996)
32	10.67	-61.28	9	58	100.38	(Snow & Snow 1972)
33	-4.13	-78.97	7	16	183.1	(Sonne <i>et al.</i> 2019)
34	-3.1	-79.17	8	17	93.58	(Sonne <i>et al.</i> 2019)
35	-3.97	-79.07	9	13	93.58	(Sonne <i>et al.</i> 2019)
36	10.12	-83.97	13	51	153.76	(Stiles 1985)
37	-2.87	-79.12	8	20	72.79	(Tinoco <i>et al.</i> 2017)
38	-2.84	-79.16	12	19	72.79	(Tinoco <i>et al.</i> 2017)
39	18.53	-95.07	10	18	98.87	(Toledo 1975)
40	-19.95	-43.9	6	10	120.53	(Vasconcelos & Lombardi 1999)
41	-0.02	-78.77	13	28	94.51	(Walther & Brieschke 2001)
42	10.33	-85.15	9	11	89.67	(Wolf 1970)
43	9.57	-83.73	4	18	134.86	(Wolf <i>et al.</i> 1976)

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Appendix B

Appendix B: Details about the collected traits.

The species traits were obtained from 25 different sources (references below). We prioritized obtaining data that contained information for both female and male adult individuals. Most of the acquired data presented these characteristics, 95% for bill length values and 96% for mass and wing length values. The rest of the values were filled with data from adult males. The species *Lophornis magnificus*, *Phaethornis subochraceus* and *Oxygogon lindenii*, were excluded from the interaction networks, as some of their traits were not available in the literature.

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Capítulo 3: Additional Information

Supplementary Material

Table S1. Basic description about the 13 data papers found with bird traits. These 13 datasets together account for 46% of all information available for the 10,949 species investigated here (see the main text). S: number of 10,949 species that are present in the dataset; N° Traits: number of morphological (M) and life history (H) traits evaluated in this study that are present in the dataset; Dataset completeness: percentage of information completeness considering the number of species (S) and traits (N° Traits) in the dataset; Dataset contribution: percentage of information completeness in the dataset considering the total number of species and traits evaluated in this study. See Appendix A for references.

Reference	S	N° Traits (M - H)	Dataset coverage (%)	Dataset contribution (%)
Burgio <i>et al.</i> 2019	394	5 - 3	96.86	1.99
Garnett <i>et al.</i> 2015	930	1 - 4	83.76	2.54
Lislevand <i>et al.</i> 2007	3729	5 - 1	75.48	11.02
Montoya <i>et al.</i> 2018	604	7 - 0	98.30	2.71
Myhrvold <i>et al.</i> 2015	9435	1 - 1	83.83	10.32
Razafindratsima <i>et al.</i> 2018	242	1 - 6	95.81	1.06
Renner & van Hoesel 2017	98	6 - 2	90.94	0.47
Ricklefs 2017	1684	5 - 0	100	5.49
Rodrigues <i>et al.</i> 2019	763	6 - 0	89.30	2.67
Storchová & Horák 2018	497	5 - 4	99.73	2.91
Takagawa <i>et al.</i> 2011	492	1 - 4	92.68	1.49
Willians <i>et al.</i> 2010	95	1 - 3	99.47	0.25
Wilman <i>et al.</i> 2014	9844	1 - 3	91.34	23.46

Table S2. Summary description of eight additional traits investigated here to evaluate the consistency of our results. These traits integrate a list of 19 bird functional traits (most already present in our initial list based on ecologists preference) suggested by a regional bird survey protocol (López-Ordoñez *et al.* 2015). See Table 1 for caption and the main text for reference.

Trait	Type	Coverage Data papers	Coverage Repositories	Coverage Total	Mean redundancy	Max redundancy
Bill curvature	M	0	0.80	0.80	0	0
Bill height	M	23.55	31.24	37.25	2.63	9
Hallux length	M	19.8	7.11	24.72	2.03	3
Nesting behavior	H	12.46	45.79	47.05	3.02	13
Social behavior	H	10.69	19.99	25.64	2.48	7
Tail graduation	M	4.2	9.78	13.62	2.02	3
Wing area	M	1.83	3.55	4.89	2.02	3
Wingspan	M	1.74	6.78	7.74	2.07	3

Table S3. Relative contribution of primary (field and museum) and secondary (articles, books, etc.) data sources for each one of the 14 traits most frequently used in the ecological literature. To calculate this source contribution, we considered only those articles that explicitly cited the data source of each trait (86% of the 148 analyzed articles). Note that an article can use more than one source for the same trait, and, for this reason, the sum of the columns may be higher than 100%.

Life history traits	Primary Source	Secondary Source	No Reference
Activity period	0.12	1.00	0
Clutch size	0	0.93	0.07
Diet	0.02	0.96	0.04
Foraging strategy	0.02	0.95	0.05
Habitat preference	0	0.81	0.19
Migratory status	0.03	0.93	0.03
Nesting strategy	0	0.94	0.06
<i>Average</i>	<i>0.03</i>	<i>0.93</i>	<i>0.06</i>
Morphological traits	Primary Source	Secondary Source	No Reference
Body mass	0.08	0.91	0.05
Bill length	0.58	0.39	0.06
Bill width	0.95	0.05	0.05
Kipp's distance	0.93	0	0.07
Tail length	0.53	0.47	0.06
Tarsus length	0.50	0.45	0.09
Wing length	0.47	0.50	0.06
<i>Average</i>	<i>0.58</i>	<i>0.40</i>	<i>0.06</i>

Table S4. Relative contribution of the five most cited data sources for each one of the 14 traits most frequently used in the ecological literature. To calculate this source contribution, we considered only those articles that explicitly cited the data source of each trait (86% of the 148 analyzed articles). Note that an article can use more than one source for the same trait, and, for this reason, the sum of the rows may be higher than 100%. See references of the data sources below.

Source	AP	BL	BW	BM	CS	Di	FS	HP	KD	MS	NS	TL	TsL	WL
Batisteli <i>et al.</i> 2018								0.06						
Garnett <i>et al.</i> 2015					0.07			0.12		0.1				0.06
BoA		0.06										0.12	0.09	0.06
BTO		0.03											0.05	
BWP	0.18			0.07	0.14	0.12	0.11			0.13	0.24			
BirdsNA	0.12					0.07	0.11			0.13	0.06	0.06		
HBW	0.24			0.1	0.14	0.18	0.17				0.09	0.06		
Devictor <i>et al.</i> 2010	0.12				0.11					0.1	0.09			
HABM				0.22										
HANZAB								0.12						0.06
BoSA		0.12		0.12	0.14	0.13	0.1	0.19		0.17	0.27	0.12	0.14	0.18
Matthews <i>et al.</i> 2017			0.05						0.07					
Museum		0.55	0.9						0.86			0.47	0.45	0.44
No reference		0.06	0.05					0.19	0.07				0.09	
Particular collection			0.05						0.07					
Trisos <i>et al.</i> 2014			0.05											
Wilman <i>et al.</i> 2014	0.35			0.22		0.24	0.28							

AP: Activity period; BL: Bill length; BW: Bill width, BM: Body mass; CS: Clutch size; Di: Diet; FS: Forage strategy; HP: Habitat preference; KD: Kipp’s distance; MS: Migratory status; NS: Nesting strategy; TL: Tail length; TsL: Tarsus length; WL: Wing length.

BoA: The Birds of Africa (Brown *et al.* 1982-2013); BTO: British Trust for Ornithology (“BTO - British Trust for Ornithology”); BWP: The Birds of Western Palearctic (Cramp *et al.* 1977-1994); BirdsNA: The Birds of North America (Rodewald 2019); HBW: Handbook of the Birds of the World (del Hoyo *et al.* 1992-2013); HABM: Handbook of Avian Body Mass (Dunning 2007); HANZAB: Handbook of Australian, New Zealand and Antarctic Birds (Marchant *et al.* 1990-2006); BoSA: Birds of Southern Africa (Hockey *et al.* 2005).

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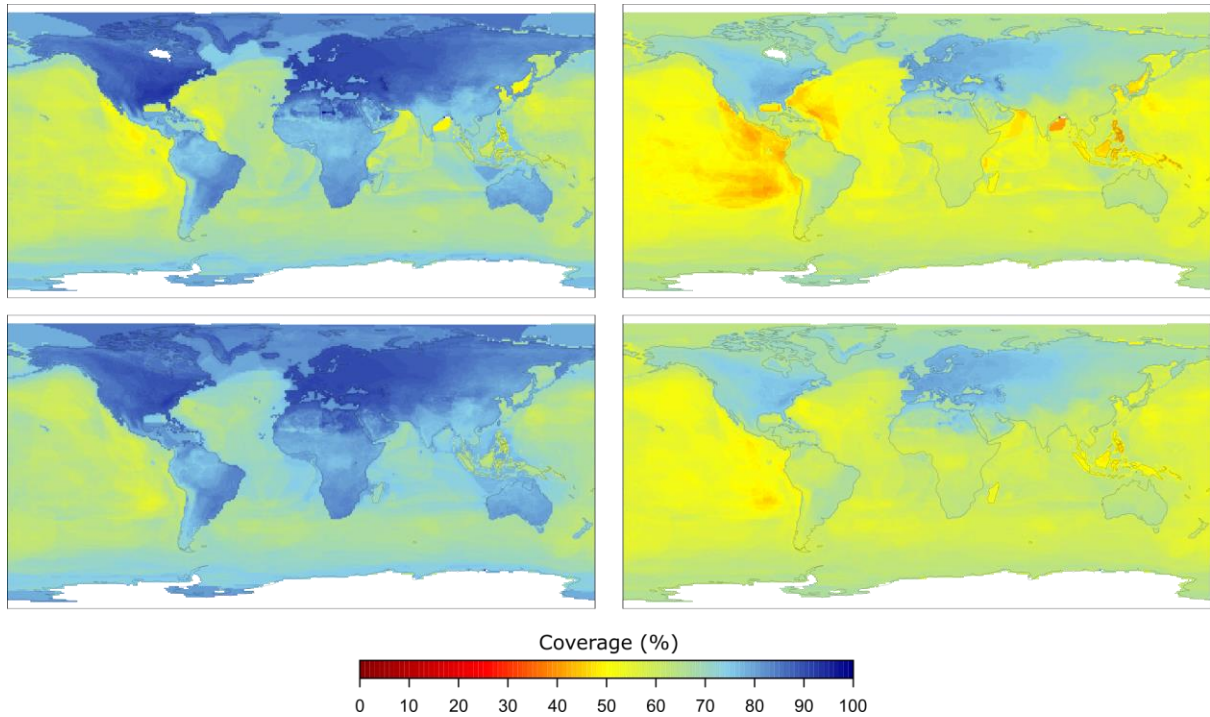


Fig. S1. Spatial variation of average trait completeness in birds considering only breeding ranges to map species distribution (top), the option adopted in our study, and including non-breeding ranges (bottom), for our initial list with the 14 most relevant functional traits according to the ecological literature (left) and after the addition of eight traits proposed by López-Ordoñez *et al.* (2015) (right). See the main text for reference.

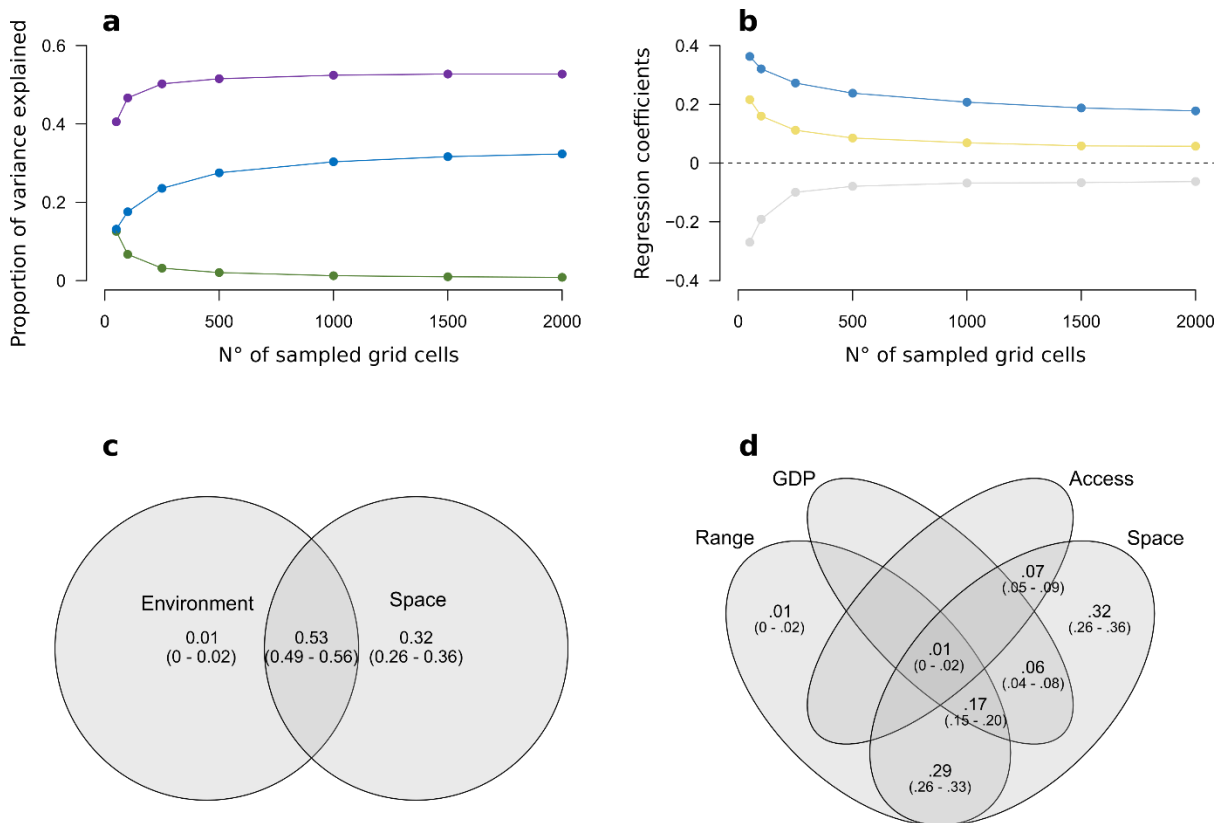


Fig. S2. Results of the resampling approach used to estimate the statistical distribution of the variation partitioning components and the multiple regression coefficients of the model explaining trait information coverage for birds considering only public datasets. a) Tendency lines of variance partitioning components: median values for unique environmental (or socio-environmental, green line), shared (purple line), and unique geographical (blue line) effects on birds trait coverage worldwide at different samples sizes. b) Tendency lines of the standardized regression coefficients: median values for average range size (blue line), GDP (yellow line) and accessibility (grey line) at different samples sizes. c) Variance partitioning of the effects of environmental and geographical variables on birds trait coverage, with median values and 95% CI limits for the 1000 samples. d) Variance partitioning of the effects of average range size, GDP per capita, on-ground accessibility and geographical variables, with median values and 95% CI limits for the 1000 samples (values < 0.01 are not shown). The median value and 95% CI limits of the standardized regression coefficients at the sample size of 1000 grid cells was 0.19 (0.04, 0.32) for average range size, 0.06 (-0.01, 0.16) for GDP per capita and -0.07 (-0.13, 0) for on-ground accessibility.

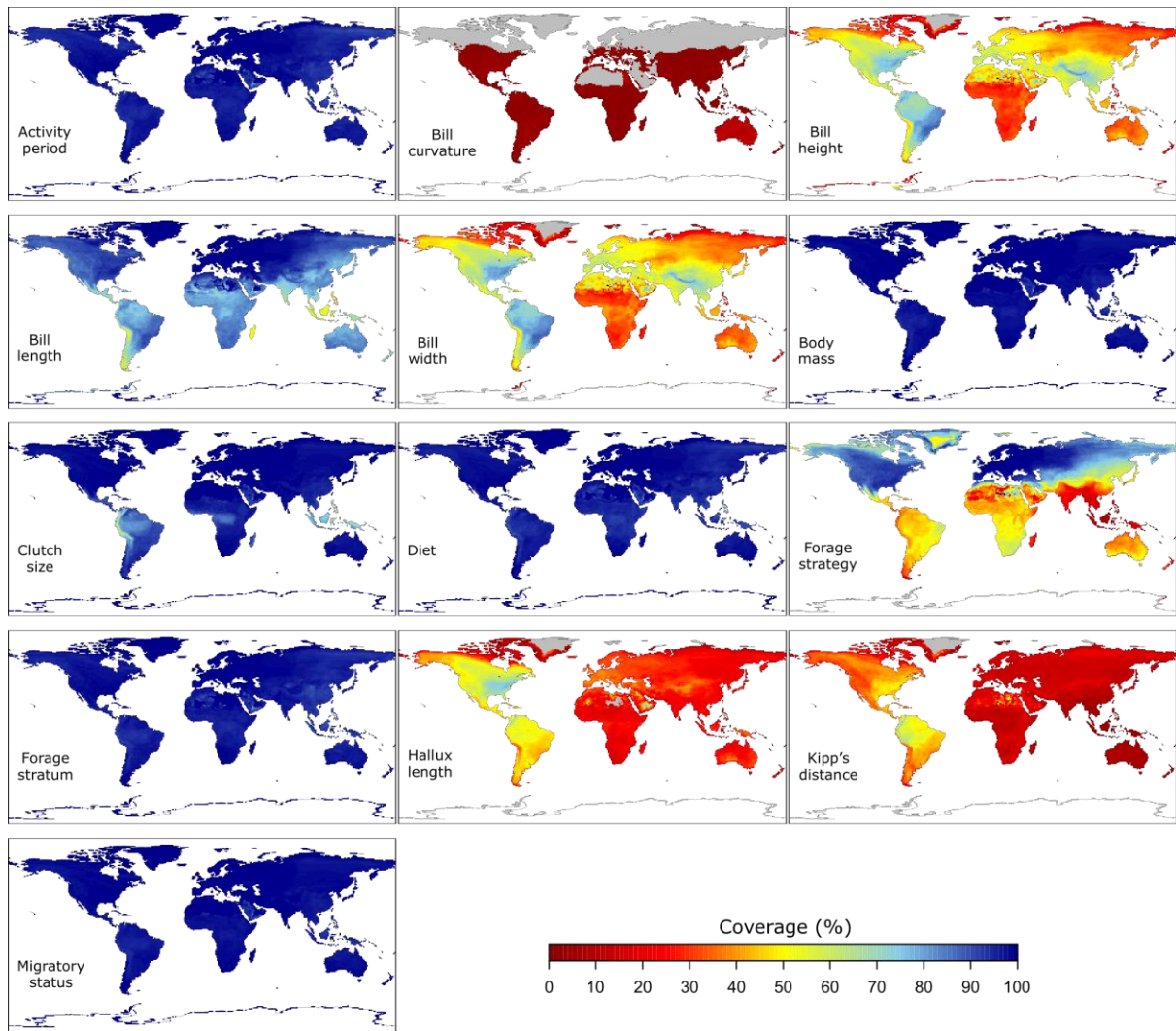


Fig. S3. Spatial variation of average coverage for each bird trait investigated in our study. Grey cells indicate regions where the trait remains unknown for all species. Figure continues to the next page.

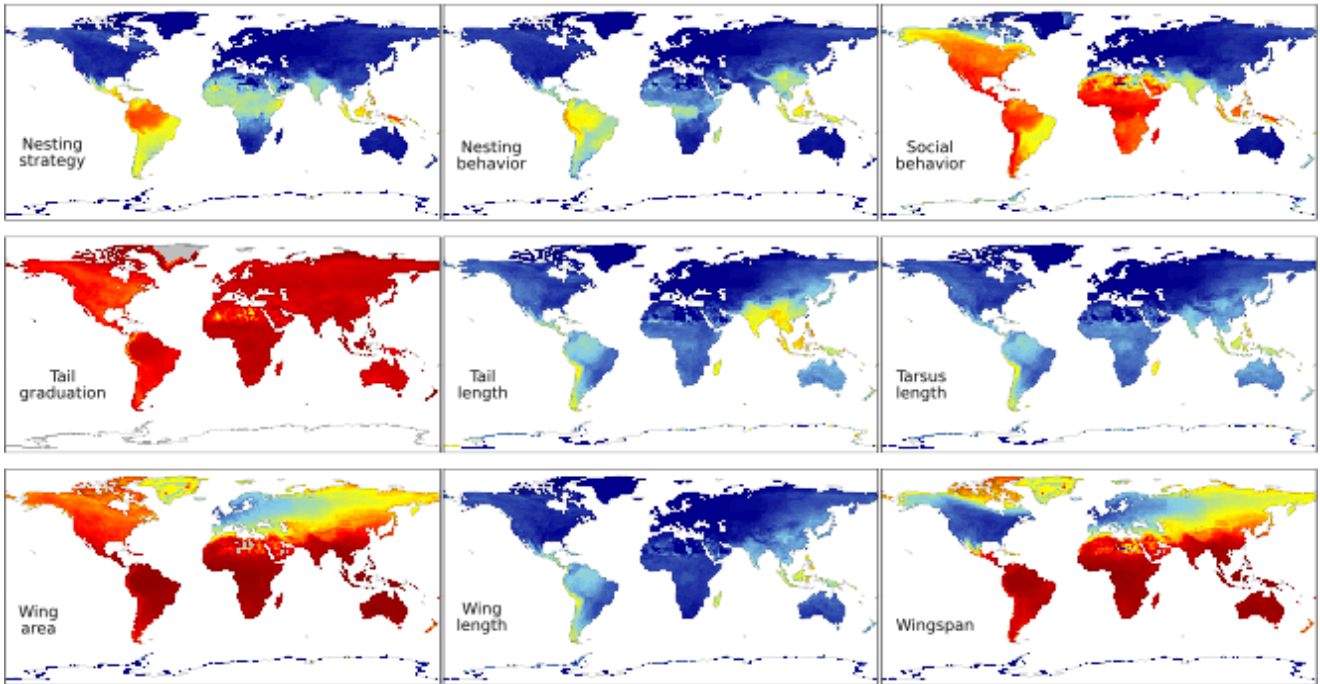


Fig. S3. Continued.

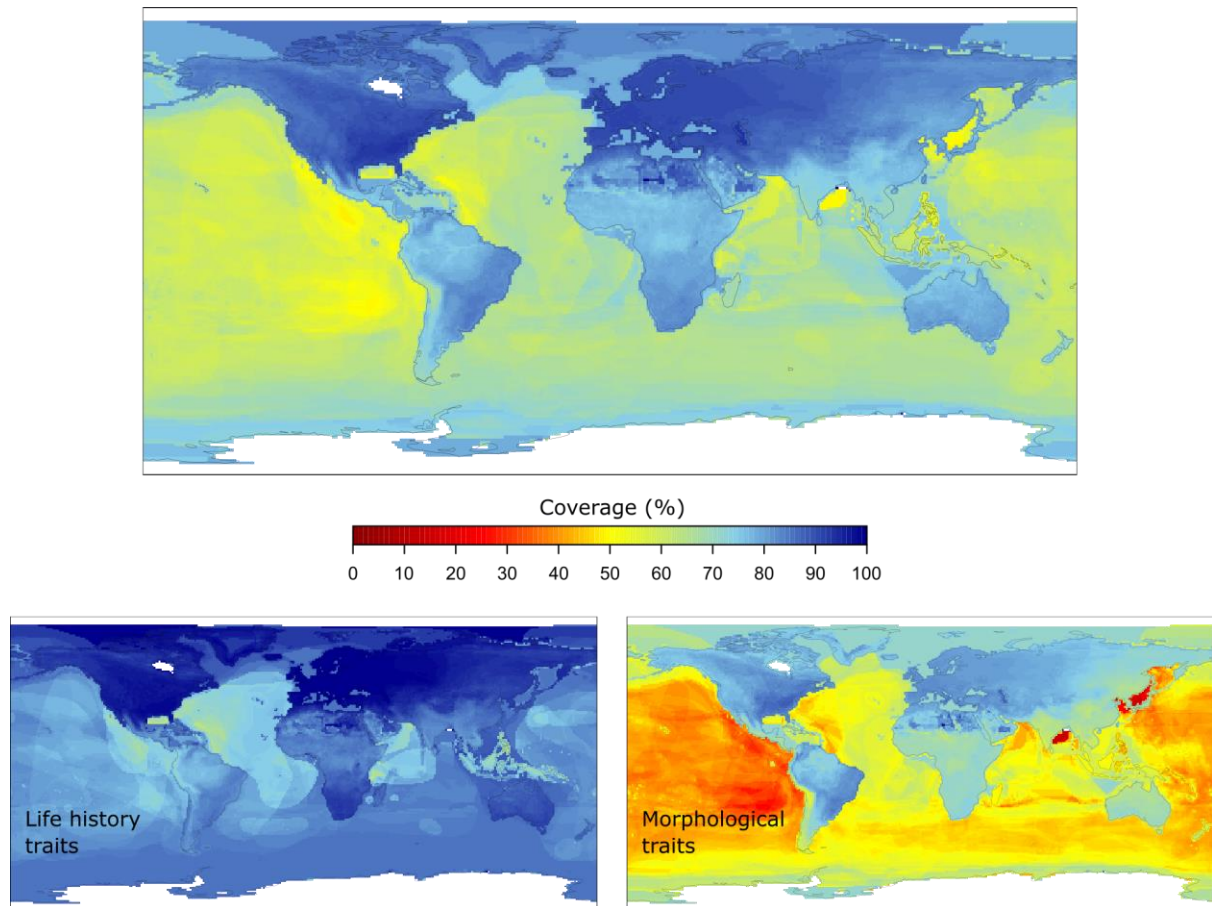


Fig. S4. Spatial variation of average trait coverage in birds considering all the 14 functional traits evaluated in our study (top), only life history traits (bottom-left), and only morphological traits (bottom-right) without masking ocean grid cells.

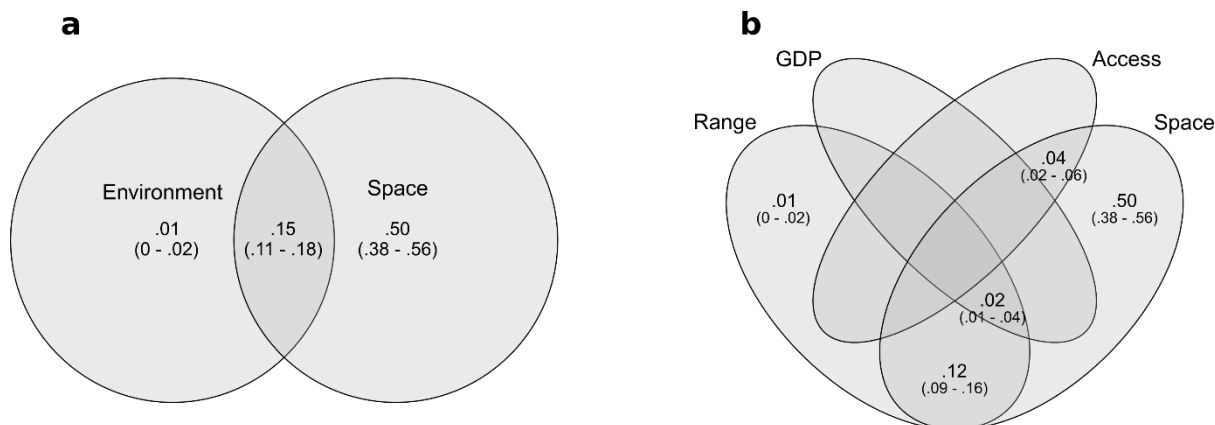


Fig. S5. Results of the resampling approach used to estimate the statistical distribution of the variation partitioning components and the multiple regression coefficients of the model explaining trait information coverage for birds considering public datasets plus the additional information from the Handbook of Birds of the World (del Hoyo et al. 1992-2011) and Pigot *et al.* (2020). a) Variance partitioning of the effects of environmental and geographical variables on birds trait coverage, with median values and 95% CI limits for the 1000 samples. d) Variance partitioning of the effects of average range size, GDP per capita, on-ground accessibility and geographical variables, with median values and 95% CI limits for the 1000 samples (values < 0.01 are not shown). The median value and 95% CI limits of the standardized regression coefficients at the sample size of 1000 grid cells was 0.14 (0.02, 0.29) for average range size, -0.01 (-0.10, 0.09) for GDP per capita and -0.05 (-0.14, 0.04) for on-ground accessibility.

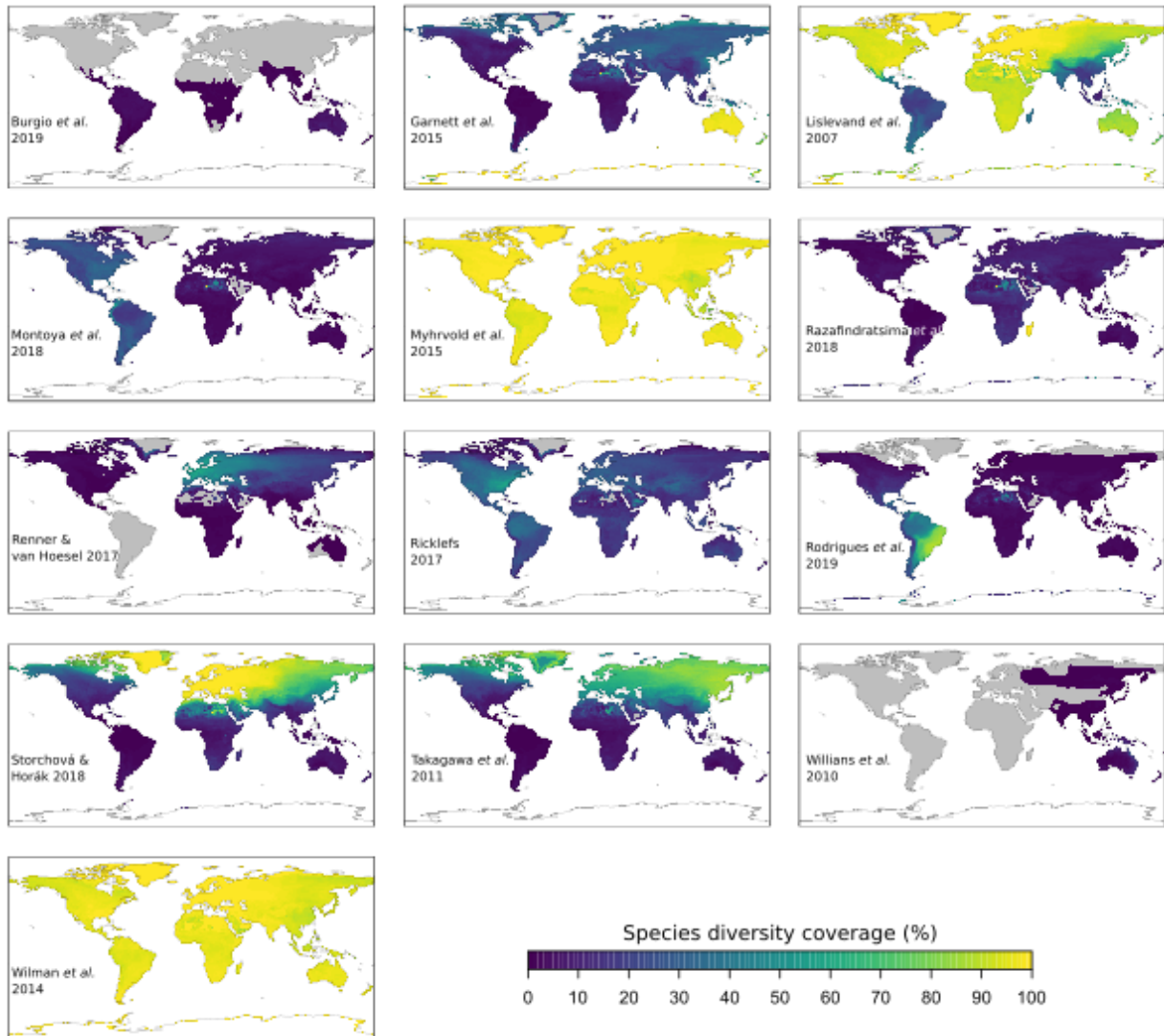


Fig. S6. Spatial diversity coverage of 13 data papers with bird traits. Grey cells indicate regions not covered by the data paper.

Appendix A

Appendix A1. List of the 148 references reviewed in this study to select the most relevant functional traits according to the ecological literature.

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Appendix A2. Data papers with birds functional traits found in our data search.

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the Australian Wet Tropics. *Ecology*, 91, 2493. <https://doi.org/10.1890/09-1069.1>.

Wilman, H., Belmaker, J., Simpson, J., de la Rosa, C., Rivadeneira, M.M. & Jetz, W. (2014). EltonTraits 1.0: Species-level foraging attributes of the world's birds and mammals. *Ecology*, 95, 2027.

Appendix A3. Datasets published in public repositories with birds functional traits found in our data search.

Acker, P., Grégoire, A., Rat, M., Spottiswoode, C.N., van Dijk, R.E., Paquet, M., et al. (2015). Disruptive viability selection on a black plumage trait associated with dominance. *Dryad*. Dataset. <https://doi.org/10.5061/dryad.b5837>.

Adamkova, M., Bilkova, Z., Tomasek, O., Simek, Z., Simek, Z. & Albrecht, T. (2019). Feather steroid hormone concentrations in relation to age, sex, and moulting time in a long distance migratory passerine. *Dryad*. v2. Dataset. <https://doi.org/10.5061/dryad.v4bf803>.

Araya-Ajoy, Y.G., Ranke, P.S.S., Kvalnes, T., Rønning, B., Holand, H., Myhre, A.M., et al. (2020). Characterizing morphological (co)variation using structural equation models: body size, allometric relationships and evolvability in a house sparrow metapopulation. *Dryad*. v2. Dataset. <https://doi.org/10.5061/dryad.s654mf6>.

Armstrong, C., Richardson, D.S., Hipperson, H., Horsburgh, G.J., Kuepper, C., Percival-Alwyn, L., et al. (2018). Genomic associations with bill length and disease reveal drift and selection across island bird populations. *Dryad*. Dataset. <https://doi.org/10.5061/dryad.9642b>.

Arnold, S.J. & Houck, L.D. (2016). Can the Fisher-Lande process account for birds of paradise and other sexual radiations?. *Dryad*. v2. Dataset. <https://doi.org/10.5061/dryad.66ft5>.

Atwell, J.W., Cardoso, G.C., Whittaker, D.J., Price, T.D. & Ketterson, E.D. (2014). Hormonal, behavioral, and life-history traits exhibit correlated shifts in relation to population establishment in a novel environment. *Dryad*. Dataset. <https://doi.org/10.5061/dryad.b6h36>.

Badás, E.P., Autor, A., Martínez, J., Rivero-de Aguilar, J. & Merino, S. (2020). Individual quality and extra-pair paternity in the blue tit: sexy males bear the costs. *Dryad*. v3. Dataset. <https://doi.org/10.5061/dryad.pzgmsbcgf>.

Balasubramaniam, P. & Rotenberry, J.T. (2017). Elevation and latitude interact to drive life-history variation in precocial birds: a comparative analysis using Galliformes. *Dryad*. Dataset. <https://doi.org/10.5061/dryad.38s8g>.

Barbaro, L., Allan, E., Ampoorter, E., Castagneyrol, B., Charbonnier, Y., De Wandeler, H., et al. (2018). Biotic predictors complement models of bat and bird responses to climate

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- Bentz, A.B., Andreassen, V.A. & Navara, K.J. (2018). An experimental test of the relationship between yolk testosterone and the social environment in a colonial passerine. *Dryad*. Dataset. <https://doi.org/10.5061/dryad.42tv030>.
- Bertrand, J.A.M., Delahaie, B., Bourgeois, Y.X.C., Duval, T., García-Jiménez, R., Cornuault, J., *et al.* (2016). The role of selection and historical factors in driving population differentiation along an elevational gradient in an island bird. *Dryad*. Dataset. <https://doi.org/10.5061/dryad.50b93>.
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Appendix B

Appendix B. List of the standardized definition for traits used in this study. Of which 14 bird were compiled from literature (†) and 8 suggested by a regional bird survey protocol (§, López-Ordoñez *et al.* 2015).

Trait	Description
Activity period (†)	Main period to which the individual restricts its activities: diurnal, crepuscular, nocturnal or cathemeral (i.e. irregularly active at any time of night or day; Wilman <i>et al.</i> 2014; Razafindratsima <i>et al.</i> 2018).
Bill curvature (§)	Bill shape can be classified as down curved, straight, up curved and flat (de Arruda Almeida <i>et al.</i> 2017; López-Ordoñez <i>et al.</i> 2015).
Bill height (§)	This measurement is taken as the length of an imaginary line perpendicular to the longitudinal axis of the bill, between the culmen and the lower jaw, with the bill completely closed. This measurement can be taken on the proximal end of operculum or in the most distal part of the nostrils (López-Ordoñez <i>et al.</i> 2015; Matthews <i>et al.</i> 2017; Oliveira <i>et al.</i> 2019).
Bill length (†,§)	Can be measured as the distance, from the closed bill and straight, from the tip of the bill to the base of the skull (i.e. total culmen), to the point at which the forehead feathers begin (i.e. exposed culmen; (López-Ordoñez <i>et al.</i> 2015; Pigot <i>et al.</i> 2016; Matthews <i>et al.</i> 2017), for the previous edge of the nostrils (Pigot <i>et al.</i> 2016; Matthews <i>et al.</i> 2017), or for the commissural point (i.e. gape length, Vollstädt <i>et al.</i> 2017).
Bill width (†,§)	Measured by the length between the commissures (corners located between the base of the maxilla and mandible, i.e. gape width; López-Ordoñez <i>et al.</i> 2015) or the bill width at proximal end of operculum (Oliveira <i>et al.</i> 2019; López-Ordoñez <i>et al.</i> 2015).
Body mass (†, §)	Body weight (Wilman <i>et al.</i> 2014; López-Ordoñez <i>et al.</i> 2015).
Clutch size (†)	Number of eggs or offspring produced in a single reproductive event/clutch (Lislevand <i>et al.</i> 2007; Williams <i>et al.</i> 2010; Myhrvold <i>et al.</i> 2015).

Diet (†, §)	Main food resources a bird consumes most of its life (López-Ordoñez <i>et al.</i> 2015). It can be divided into diet categories (i.e. seeds, fruits, nectar, invertebrates, vertebrates and others; Dias 2016), food guilds (i.e. Nectivore, granivore, frugivore, folivore, insectivore, carnivore, omnivore, among others; López-Ordoñez <i>et al.</i> 2015; Pringle <i>et al.</i> 2019) or trophic position, estimated using stable isotope analysis (Edwards <i>et al.</i> 2013).
Foraging strategy (†)	Foraging strategy can be defined as the vertical stratum (foraging stratum) that the species occupies in vegetation during foraging (i.e. aquatic, semi-aquatic, ground, grassland, understory, midstrata, canopy; Wilman <i>et al.</i> 2014; López-Ordoñez <i>et al.</i> 2015; Prescott <i>et al.</i> 2016; Zhang <i>et al.</i> 2019), through the type of specific substrate (foraging substrate) in which the species usually seeks food (aquatic, trunk / bark, soil / litter, foliage or Air: prey items caught in the air; Prescott <i>et al.</i> 2016), or as the method used by species to find food (foraging mode) such as: Pursuit, Gleaning, Pouncing, Grazing, Digging, Scavenging, Probing (López-Ordoñez <i>et al.</i> 2015; Li <i>et al.</i> 2018). These three foraging strategies description are overlapping in the literature so, for simplicity, they were considered the same trait during the review and converted posteriorly in “Foraging mode” and “Foraging stratum”.
Foraging mode (†, §)	Defined as the method or mode used by species to find food (i.e. Pursuit, Gleaning, Pouncing, Grazing, Digging, Scavenging, Probing; López-Ordoñez <i>et al.</i> 2015; Li <i>et al.</i> 2018)
Foraging stratum (†, §)	Defined as the stratum (i.e. aquatic, ground, understory, canopy, air) or type of substrate (i.e. trunk / bark, soil / litter or foliage) on which species usually search for food (Wilman <i>et al.</i> 2014; López-Ordoñez <i>et al.</i> 2015; Prescott <i>et al.</i> 2016).
Hallux length (§)	Length of the nail present in the finger 1 (López-Ordoñez <i>et al.</i> 2015; Oliveira <i>et al.</i> 2019).
Kipp’s distance (†, §)	Linear distance from the tip of the longest primary feather to the longest secondary feather (López-Ordoñez <i>et al.</i> 2015; Phillips <i>et al.</i> 2018).

Migratory status (†, §)	Migration types can be grouped according to the geographic coverage of the trips. The main categories are: Altitudinal migration (species remain all year round in the same region, but move between different altitudinal ranges); local migration (species have a wide distribution, but a given population makes a cyclical movement within the same latitudinal belt in response to habitat availability or the presence of resources); continental migration (species migrate latitudinally each year; Residents: species that do not perform any type of migratory movement López-Ordoñez <i>et al.</i> 2015; Ehlers Smith <i>et al.</i> 2019).
Nesting behavior (§)	It is defined as the type of reproductive strategy, this includes several aspects such as the construction of the nest, surveillance, feeding and parental care of juveniles of the species. It can be divided into two categories. Colonial, where cooperative participation exists between individuals of the same species for the creation of juveniles. Individual, where species build nests and raise juveniles individually or in pairs (López-Ordoñez <i>et al.</i> 2015).
Nesting strategy (†)	The nest can be classified by type (e.g. open, built cavity, natural cavity, cavity in human constructions, closed, nest parasite), location (e.g. ground, rock, shrub, tree) or both (e.g. Open on ground, Open in tree; (Devictor <i>et al.</i> 2010; Leitão <i>et al.</i> 2016; White <i>et al.</i> 2018).
Social behavior (§)	Defined as the association behavior of an individual with others of the same or other species, to perform activities related to food and rest. Taking into account the number of species that make up the group and the number of individuals of each species, the main categories are: monoespecific flocking (groups of individuals of the same species that forage for a specific resource), mix flocking (groups of individuals of different species that forage together for food), association (individuals of different species that gather around a specific site, this is usually related to an environment, e.g. waterbirds associated with an estuary), solitary (species observed solitary most of the time) or in pairs (species that forage in pairs; Karp <i>et al.</i> 2012; López-Ordoñez <i>et al.</i> 2015).
Tail graduation (§)	It refers to the shape of the tail and can be measured by the difference in the length of the longest and shortest rectrix (López-Ordoñez <i>et al.</i> 2015).
Tail length (†, §)	Distance from the tip of the longest rectrix to the base of the tail (point at which the two central rectrices protrude from the skin; Pigot <i>et al.</i> 2016).

Tarsus length (†, §)	Distance between the back of the intertarsal joint and the lower front edge of the last undivided scale before the beginning of the fingers (Eck <i>et al.</i> 2011; López-Ordoñez <i>et al.</i> 2015; Oliveira <i>et al.</i> 2019).
Wing area (§)	Area occupying the maximum wing extension limits (López-Ordoñez <i>et al.</i> 2015; Tinoco <i>et al.</i> 2018).
Wing length (§)	Length of the carpal (carpal junction) to the tip of the largest primary wing feather, measured with the wing closed (e.i. Wing chord; López-Ordoñez <i>et al.</i> 2015; Renner & Hoesel 2017; Storchová & Hořák 2018).
Wingspan (†, §)	Length between the tip of the largest left primary feather to the right, measured with flattened and stretched wings over a plane (López-Ordoñez <i>et al.</i> 2015; Renner & Hoesel 2017).

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