

# Mismatch between IUCN range maps and species interactions data illustrated using the Serengeti food web

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**Abstract: Background.** Range maps are a useful tool to describe the spatial distribution of species. However, they need to be used with caution, as they essentially represent a rough approximation of a species' suitable habitats. When stacked together, the resulting communities in each grid cell may not always be realistic, especially when species interactions are taken into account. Here we show the extent of the mismatch between range maps, provided by the International Union for Conservation of Nature (IUCN), and species interactions data. More precisely, we show that local networks built from those stacked range maps often yield unrealistic communities, where species of higher trophic levels are completely disconnected from primary producers. **Methodology.** We used the well-described Serengeti food web of mammals and plants as our case study, and identify areas of data mismatch within predators' range maps by taking into account food web structure. We then used occurrence data from the Global Biodiversity Information Facility (GBIF) to investigate where data is most lacking. **Results.** We found that most predator ranges comprised large areas without any overlapping distribution of their preys. However, many of these areas contained GBIF occurrences of the predator. **Conclusions.** Our results suggest that the mismatch between both data sources could be due either to the lack of information about ecological interactions or the geographical occurrence of preys. We finally discuss general guidelines to help identify defective data among distributions and interactions data, and we recommend this method as a valuable way to assess whether the occurrence data that are being used, even if incomplete, are ecologically accurate.

# 1 Introduction

2 Finding a species in a certain location is like finding an encrypted message that traveled through  
3 time. It carries the species' evolutionary history, migration patterns, as well as any direct and  
4 indirect effects generated by other species (some of which we may not even know exist). Ecolo-  
5 gists have been trying to decode this message with progressively more powerful tools, from their  
6 field notes to highly complex computational algorithms. However, to succeed in this challenge  
7 it is important to have the right clues in hand. There are many ways we can be misled by data - or  
8 the lack of it: taxonomic errors (e.g., due to updates in the taxonomy of a species), geographic  
9 inaccuracy (e.g., approximate coordinates or lack of documentation about their accuracy), or  
10 sampling biases (e.g., data clustered near roads or research centers) (Ladle and Hortal 2013;  
11 Hortal et al. 2015; Poisot et al. 2021). One way to identify - and potentially fix - these errors  
12 is to combine many different pieces of information about the occurrence of a species, so agree-  
13 ments and mismatches can emerge. Although previous studies have combined different types  
14 of occurrence data to measure the accuracy of datasets (Hurlbert and Jetz 2007; Hurlbert and  
15 White 2005; Ficetola et al. 2014), none have used different types of information so far (i.e., eco-  
16 logical characteristics other than geographical distribution). Here we suggest jointly analysing  
17 species occurrence (range maps and point occurrences) and ecological interactions to identify  
18 mismatches between datasets and areas of data deficit.

19 Interactions form complex networks that shape ecological structures and maintain the essential  
20 functions of ecosystems, such as seed dispersal, pollination, and biological control (Albrecht  
21 2018; Fricke et al. 2022) that ultimately affect the composition, richness, and successional pat-  
22 terns of communities across biomes. Yet, the connection between occurrence and interaction  
23 data is a frequent debate in ecology (Blanchet, Cazelles, and Gravel 2020; Wisz et al. 2013). For  
24 instance, macroecological models are often used with point or range occurrence data in order  
25 to investigate the dynamics of a species with its environment. However, these models do not  
26 account for ecological interactions, although it has been demonstrated that they might largely  
27 affect species distribution (Abrego et al. 2021; Afkhami, McIntyre, and Strauss 2014; Araújo,  
28 Marcondes-Machado, and Costa 2014; Godsoe et al. 2017; Godsoe and Harmon 2012; Gotelli,  
29 Graves, and Rahbek 2010; Wisz et al. 2013). Some researchers argue that occurrence data can

30 also capture real-time interactions (see Roy et al. 2016; Ryan et al. 2018), and, because of that,  
31 it would not be necessary to include ecological interaction dynamics in macroecological mod-  
32 els. On the other hand, many mechanistic simulation models in ecology have considered the  
33 effect of competition and facilitation in range shifts. For example, Gotelli *et al.* (2010) demon-  
34 strate how conspecific attraction might be the main factor driving the distribution of migratory  
35 birds; Afkhami *et al.* (2014) explores how mutualistic fungal endophytes are responsible for  
36 expanding the range of native grass; many other examples are discussed in Wisz *et al.* (2013).  
37 Although interactions across trophic levels are demonstrated to determine species range (Wisz  
38 *et al.* 2013), the use of these interactions in mechanistic simulation models in macroecology  
39 remains insufficient (as discussed in Cabral, Valente, and Hartig 2017).

40 A significant challenge in this debate is the quality and quantity of species distribution and eco-  
41 logical data (Boakes et al. 2010; Ronquillo et al. 2020; Meyer, Weigelt, and Kreft 2016) -  
42 a gap that can lead to erroneous conclusions in macroecological research (Hortal et al. 2008).  
43 Amongst the geographical data available are the range maps provided by the International Union  
44 for the Conservation of Nature (IUCN). Such maps consist of simplified polygons, often created  
45 as alpha or convex hulls around known species locations, refined by expert knowledge about the  
46 species (IUCN Red List Technical Working Group 2019). These maps can be used in macroeco-  
47 logical inferences in the lack of more precise information (Fourcade 2016; Alhajeri and Fourcade  
48 2019), but it has been recommended that they are used with caution since they tend to under-  
49 estimate the distribution of species that are not well-known (Herkt, Skidmore, and Fahr 2017)  
50 (especially at fine scale resolutions; Hurlbert and Jetz (2007); Hurlbert and White (2005)), do  
51 not represent spatial variation in species occurrence and abundance (Dallas, Pironon, and Santini  
52 2020), and can include inadequate areas within the estimated range. Another source of species  
53 distribution information is the Global Biodiversity Information Facility (GBIF), which is an on-  
54 line repository of georeferenced observational records that come from various sources, including  
55 community science programs, museum collections, and long-term monitoring schemes. A great  
56 source of bias in these datasets is the irregular sampling effort, with more occurrences originat-  
57 ing from attractive and accessible areas and observation of charismatic species (Alhajeri and  
58 Fourcade 2019). As for ecological data, a complete assessment is difficult and is aggravated by

59 biased sampling methods, data aggregation (Poisot et al. 2020; Hortal et al. 2015) and by the  
60 fact that interactions are very often events that occur in a narrow window of time. Nevertheless,  
61 we have witnessed an increase in the availability of biodiversity data in the last decades, includ-  
62 ing those collected through community science projects (Callaghan et al. 2019; Pocock et al.  
63 2015) and dedicated databases, such as Mangal (Poisot et al. 2016). This provides an opportu-  
64 nity to merge species distribution and ecological interaction data to improve our predictions of  
65 where a species may be found across large spatial scales.

66 It has been demonstrated that the agreement between range maps and point data varies geograph-  
67 ically (Hurlbert and Jetz 2007; Hurlbert and White 2005; Ficetola et al. 2014). Adding ecolog-  
68 ical interaction data to this comparison might help to elucidate where these (dis)agreements are  
69 more likely to be true and which dataset better represent the actual distribution of a species. In  
70 this context, we elaborate a method that allows us to detect areas of potential misestimation of  
71 species' distribution data (more precisely range maps) based on interaction data. This method is  
72 based on the assumption that organisms cannot persist in an area unless they are directly or in-  
73 directly connected to a primary producer within their associated food web (Power 1992). Thus,  
74 given that herbivores are the main connection between plant resources (directly limited by en-  
75 vironmental conditions) and predators (Dobson 2009; Scott et al. 2018), the range of a predator  
76 (omnivore or carnivore) depends on the overlapping ranges of its herbivore preys. If sections of  
77 a predator's range do not overlap with at least one of its prey it will become disconnected from  
78 primary producers, and therefore we would not expect the predator to occur in this area.

79 This mismatch can be the result of different mechanisms, like the misestimation of both the  
80 predator's and the preys' ranges (Ladle and Hortal 2013; Rondinini et al. 2006), taxonomic  
81 errors (Isaac, Mallet, and Mace 2004; Ladle and Hortal 2013), or the lack of information about  
82 trophic links (i.e., the lack of connection between the ranges of a predator and a primary producer  
83 may be due a third species we don't know is connected to both). Here in this proof of concept,  
84 we investigate the disagreements between available data for species that compose a well-known  
85 food web in the African continent, discuss the mechanisms that can lead to this, and reinforce  
86 the importance of open geographically explicit interaction data.

## 87 **Methods**

88 We identified areas of data deficits within the ranges of predators based on a simple rule: any  
89 part of a predator's range that did not intersect with the range of at least one prey herbivore  
90 species, which in turn is directly connected to a primary producer (plants), was considered data  
91 deficient. To do that, we used a Serengeti food web dataset (Baskerville et al. 2011) (which  
92 comprises carnivores, herbivores, and plants from Tanzania) and its species ranges from IUCN.  
93 Then, we calculated the difference in range sizes between the original IUCN ranges of predators  
94 and those without the areas where they would be disconnected from their food webs, based on  
95 species interaction data. Finally, we added the GBIF occurrence points for the Serengeti species  
96 to investigate whether the results would be different if we used another source of distribution  
97 data.

## 98 **Data**

99 We investigated the mismatch between savannah species ranges and interactions in Africa (fig. 1).  
100 These ecosystems host a range of different species, including the well-characterized predator-  
101 prey dynamics between iconic predators (e.g., lions, hyenas, and leopards) and large herbivores  
102 (e.g., antelopes, wildebeests, and zebras), as well as a range of herbivorous and carnivorous  
103 small mammals. The Serengeti ecosystem has been extensively studied and its food web is one  
104 of the most complete we have to date, including primary producers identified to the species level.  
105 Here we focus on six groups of herbivores and carnivores from the Serengeti Food Web Data Set  
106 (Baskerville et al. 2011). These species exhibit direct antagonistic (predator-prey) interactions  
107 with one another and are commonly found across savannah ecosystems on the African continent  
108 (McNaughton 1992). Plants in the network were included indirectly in our analyses as we do  
109 not expect the primary producers to significantly influence the range of herbivores for several  
110 reasons. Firstly, many savannah plants are functionally similar (i.e., grasses, trees and shrubs)  
111 and cooccur across the same habitats (Baskerville et al. 2011). Secondly, herbivores in the net-  
112 work are broadly generalists feeding on a wide range of different plants across habitats. Indeed,  
113 out of 129 plants in our dataset, herbivores ( $n = 23$ ) had a mean out degree (mean number of

114 preys) of around 22 (std = 17.5). There is also an absence of global range maps for many plant  
115 species (Daru 2020), which prevents their direct inclusion in our analysis. Therefore, we as-  
116 sume that plants consumed by herbivores are present across their ranges, and as such the ranges  
117 of herbivores are not expected to be significantly constrained by the availability of food plants.  
118 From the wider ecological network presented in Baskerville (2011), we sampled interaction data  
119 for herbivores and carnivores. This subnetwork contained 32 taxa (23 herbivores and 9 carni-  
120 vores) and 84 interactions and had a connectance of 0.08. Although self-loops are informative,  
121 we removed these interactions to allow for the original IUCN ranges of predators with canni-  
122 balistic interactions to be adjusted. We treated this overall network as a metaweb since it *should*  
123 contain all potential species interactions between mammalian taxa occurring across savannah  
124 ecosystems such as the Serengeti.

125 We compiled IUCN range maps for the 32 species included in the metaweb from the Spatial Data  
126 Download portal ([www.iucnredlist.org/resources/spatial-data-download](http://www.iucnredlist.org/resources/spatial-data-download)), which we rasterized  
127 at a 0.5 degrees resolution (~50 km at the equator). We restricted the rasters to a spatial extent  
128 comprised between latitudes 35°S and 40°N and longitudes 20°W and 55°E. We then combined  
129 interaction data from the metaweb and cooccurrence data generated from species ranges to create  
130 networks for each raster pixel. This generated a total of 11,308 pixel-level networks. These  
131 networks describe potential predation, not actual interactions: the former is derived information  
132 from the metaweb, and the latter is contingent on the presence of herbivores.

### 133 **Range overlap measurement**

134 We calculated the geographical overlap, i.e. the extent to which interacting predator and prey  
135 species co-occurred across their ranges, as  $a/(a + c)$ , where  $a$  is the number of pixels where  
136 predator and prey cooccur and  $c$  is the number of pixels where only the focal species occur.  
137 This index of geographical overlap can be calculated with prey or predators as the focal species.  
138 Values vary between 0 and 1, with values closer to 1 indicating that there is a large overlap in  
139 the ranges of the two species and values closer to 0 indicating low cooccurrence across their  
140 ranges. For each predator species, we calculated its generality to understand whether the level  
141 of trophic specialization (i.e., number of prey items per predator) affects the extent to which the

142 ranges of the species comprised areas of data deficits. One would assume that predators with a  
143 greater number of prey taxa (i.e., a higher generality) are less likely to have large areas of data  
144 mismatch within their range as it is more likely that at least one prey species is present across  
145 most of their range.

## 146 **Validation**

147 For each species in the dataset we collated point observation data from GBIF ([www.gbif.org](http://www.gbif.org)).  
148 We used the GBIF download API to retrieve all species occurrences on November 22nd 2022  
149 (GBIF.org 2022). We restricted our query to the data with spatial coordinates and which were  
150 inside the spatial extent of our rasters. A few observations were localized in the ocean near lat-  
151 itude 0° and longitude 0°. We assumed these were errors and removed all observations falling  
152 in the extent between latitudes 2°S and 2°N and longitudes 2°W and 2°E to keep only mainland  
153 sites. We did not use any additional geographical filters to retrieve as much data as possible.  
154 Being mindful of the recent and remarkable anthropogenic impact on African megafauna, we  
155 decided to restrict the occurrences used on the validation step to those recorded after the year  
156 2000 (and, therefore, only records with date information). This decision was made after evalu-  
157 ating the overall temporal distribution of the GBIF records.

158 We then converted the occurrence data into raster format by determining which pixels had at  
159 least one GBIF occurrence. This allowed us to remove the effect of repeated sampling in some  
160 locations. These data were used to validate the areas identified as being ecologically unrealistic  
161 based on species interactions and occurrence data (see beginning of Methods section). To do  
162 so, we calculated the proportion of GBIF presence pixels occurring within both the original  
163 IUCN species range and the adjusted one (i.e., the one without unrealistic food webs). We then  
164 compared these proportions for all predators to verify if the areas of data mismatch contained  
165 locations with GBIF observations, hence likely true habitats.



## 166 **Software**

167 We performed all analyses using *Julia* v1.7.2 (Bezanson et al. 2017). We used the packages  
168 `SimpleSDMLayers.jl` (Dansereau and Poisot 2021) to manipulate the raster layers, `EcologicalNetworks.jl`  
169 (Poisot et al. 2019) to construct and manipulate the interaction networks, and `GBIF.jl` (Dansereau  
170 and Poisot 2021) to reconcile species names with the GBIF backbone taxonomy (GBIF Secre-  
171 tariat 2021). We also used *GDAL* (GDAL/OGR contributors 2021) to rasterize the IUCN range  
172 maps (initially available as shapefiles from the Spatial Data Download portal). All the scripts  
173 required to reproduce the analyses are available at <https://doi.org/10.5281/zenodo.6842861>.

## 174 **Results**

175 Mammal species found in the Serengeti food web are widespread in Africa, especially in grass-  
176 lands and savannahs (panel (a) of fig. 1). From our analysis, most local networks (69.07%) built  
177 using the original IUCN range maps had at least one mammal species with a path to a primary  
178 producer (panel (b) of fig. 1), which reinforces that the interactions we observe in the Serengeti  
179 food web is representative of the interactions for these mammals in the whole African continent.  
180 On average, local food webs had almost half of their mammal species disconnected from basal  
181 species (mean = 46.2%, median = 33.3%). In addition, 16.6% of the networks only had discon-  
182 nected mammals, and the number of mammal species varied from 1 to 28, with a mean of 6.7.  
183 As expected, the proportion of carnivores with a path to a primary producer was conditional on  
184 the total number of mammal species in each local network (third panel of fig. 1).

185 [Figure 1 about here.]

## 186 **Specialized predators have higher rates of range mismatch**

187 [Figure 2 about here.]

188 If we consider that we can not use areas where there are no superposition between predators and  
189 prey on ecological analyses, we lose more range area for predators with fewer prey (fig. 2). For

190 instance, both *Leptailurus serval* and *Canis mesomelas* have only one prey in the Serengeti food  
191 web (tbl. 1), each of them with a very small range compared to those of their predator. This  
192 discrepancy between range sizes promotes significant range loss. On the other hand, predators  
193 of the genus *Panthera* are some of the most connected species, and they also lose the least  
194 proportion of their ranges. This mismatch between predators and preys can also be a result of  
195 taxonomic disagreement between the geographical and ecological data. Although *Canis aureus*  
196 has the same number of prey as *Caracal caracal*, none of the prey taxa of the former occurs  
197 inside its original range (tbl. 1), which results in complete range loss.

198 [Figure 3 about here.]

199 There was a high variation in the overlap of predator and prey ranges (fig. 3). The high density of  
200 points on the left-hand side of fig. 3 indicates that most preys have small ranges in comparison to  
201 those of the set of carnivores in the networks, resulting in either low overlap between both ranges  
202 (bottom) or high overlap of ranges because much of that of the prey is within predators' range  
203 (top). The top-right side of the plot encompasses situations where the ranges of both predator  
204 and prey are similar and overlapping, while the bottom-right part of the plot represents a situation  
205 where the range of the predator is smaller than that of its prey and much of it occurs within the  
206 preys' range. For example, *Panthera pardus* had many preys occurring inside its range, with  
207 highly variable levels of overlap (tbl. 1). In general, species exhibited more consistent values of  
208 prey-predator overlap, than predator-prey overlap – indicated by the spread of points along the  
209 x-axis, yet more restricted variation on the y-axis (fig. 3). There was also no overall relationship  
210 between the two metrics, or for any predator species.

Table 1: List of species analysed, their out and in degrees, total original range size (in pixels), and proportion of their ranges occupied by their preys and predators (values between 0 and 1). Species are sorted according to the groups identified by Baskerville et al. (2011). Notice how some species are isolated in the network (*Loxodonta africana*) and how *Canis aureus*'s range does not overlap with any of its preys.

Species	Number of preys	Number of predators	Total range size	Proportion of range occupied by preys	Proportion of range occupied by predators
<b>Large carnivores</b>					
<i>Acinonyx jubatus</i>	8	1	9250	0.437	0.618
<i>Crocuta crocuta</i>	12	1	4822	0.844	0.253
<i>Lycaon pictus</i>	14	0	427	0.918	-
<i>Panthera leo</i>	18	0	1274	0.935	-
<i>Panthera pardus</i>	22	0	7563	0.766	-
<b>Small carnivores</b>					
<i>Canis aureus</i>	4	1	816	0.000	0.782
<i>Canis mesomelas</i>	1	1	2201	0.190	0.994
<i>Caracal caracal</i>	4	0	5239	0.833	-
<i>Leptailurus serval</i>	1	1	4319	0.011	0.978
<b>Small herbivores</b>					
<i>Damaliscus lunatus</i>	0	4	626	-	1
<i>Hippopotamus amphibius</i>	0	0	419	-	-
<i>Kobus ellipsiprymnus</i>	0	4	2961	-	1
<i>Ourebia ourebi</i>	0	5	2484	-	1
<i>Pedetes capensis</i>	0	2	1318	-	1
<i>Phacochoerus africanus</i>	0	5	3331	-	1
<i>Redunca redunca</i>	0	5	1935	-	1
<i>Rhabdomys pumilio</i>	0	5	53	-	1

Species	Number of preys	Number of predators	Total range size	Proportion of range occupied by preys	Proportion of range occupied by predators
<i>Tragelaphus oryx</i>	0	2	2316	-	0.990
<i>Tragelaphus scriptus</i>	0	3	3999	-	0.985
<b>Large grazers</b>					
<i>Aepyceros melampus</i>	0	5	1167	-	1
<i>Alcelaphus buselaphus</i>	0	4	2307	-	1
<i>Connochaetes taurinus</i>	0	6	1074	-	1
<i>Equus quagga</i>	0	5	786	-	1
<i>Eudorcas thomsonii</i>	0	6	51	-	1
<i>Nanger granti</i>	0	6	261	-	1
<b>Hyraxes</b>					
<i>Heterohyrax brucei</i>	0	1	1961	-	0.973
<i>Procavia capensis</i>	0	1	5312	-	0.647
<b>Others</b>					
<i>Giraffa camelopardalis</i>	0	1	607	-	0.473
<i>Loxodonta africana</i>	0	0	1078	-	-
<i>Madoqua kirkii</i>	0	7	443	-	1
<i>Papio anubis</i>	0	1	2571	-	0.937
<i>Syncerus caffer</i>	0	1	2808	-	0.251

## 211 **Validation with GBIF occurrences**

212 The proportion of GBIF pixels (pixels with at least one GBIF occurrence) matching the IUCN  
213 ranges varied a lot for species with small ranges and way less for species with large ranges (fig. 4,  
214 left). This means that species with large ranges had more area where their datasets for ecolog-  
215 ical and geographical information agreed. The lowest proportions of GBIF pixels occurred for  
216 species with small ranges. Amongst herbivores, *Rhabdomys pumilio* has a proportion of 25.6%  
217 of its presence pixels within its IUCN range, while predators have this proportion above 47%  
218 (such as *Lycaon pictus*, with 47.6%, and *Panthera leo*, with 49.3%). Nevertheless, some species  
219 with smaller ranges showed high data overlap (such as *Canis mesomelas*, with 94.1%, and many  
220 herbivores). Overall, predators and preys displayed similar overlap variations, and species with  
221 median and large ranges had higher proportions of agreement between GBIF, IUCN and inter-  
222 action datasets.

223 The proportion of GBIF pixels in revised ranges can only be equal to or lower than that of  
224 the original ranges, as our analysis removes pixels from the original range and does not add  
225 new ones. Rather, the absence of a difference between the two types of ranges indicates that  
226 no pixels with GBIF observations, hence likely true habitats, were removed by our analysis.  
227 Here this proportion was mostly similar to that of the original IUCN ranges for most predator  
228 species (fig. 4). Two species showed no difference in proportion (*Lycaon pictus* and *Panthera*  
229 *leo*) while four species showed only small differences (*Crocuta crocuta* lost 0.4% of the original  
230 data overlap; *Caracal caracal* lost 3.4%; *Acinonyx jubatus* and *Panthera pardus* lost 6.2%).

231 On the other hand, three species, *Canis aureus*, *Canis mesomelas*, and *Leptailurus serval* showed  
232 very high differences, with overlaps lowered by 100%, 58.4%, and 100% respectively. These  
233 last two species are also the only predators with a single prey in our metaweb. *Canis aureus*  
234 has four preys, but it has one of the smallest ranges in IUCN, which is not covered by any of  
235 its preys. This result reinforces the concern raised in the literature on the use of IUCN range  
236 maps for species that are not well known (Herkt, Skidmore, and Fahr 2017), demonstrating how  
237 small range species are likely to have their distribution underestimated in the IUCN database.  
238 Additionally, the fact that *Canis aureus* had such a conspicuous discrepancy between its original  
239 IUCN range and those of its preys, and between GBIF and IUCN data, may indicate a taxonomic

240 incongruency between the three databases used here, which we explore in the Discussion section.  
241 Our results delineate how a mismatch between GBIF and IUCN databases differ greatly with  
242 small changes in herbivore species ranges, and it is somewhat positively related to range size  
243 for predator species. Moreover, we show that accounting for interactions does not necessarily  
244 aggravates this dissimilarity, but it is relevant for species about which we have little ecological  
245 information or for specialists groups.

246 [Figure 4 about here.]

## 247 Discussion

248 Here we identify areas of data mismatch between species range maps by using ecological in-  
249 teraction data (predator-prey interactions within food webs). Our results did show a significant  
250 mismatch in the IUCN range areas of specialized and generalist predatory organisms and their  
251 prey, which highlights the importance of accounting for species interactions when estimating  
252 the range of a species. Although this type of data mismatch can be result of actual ecological  
253 processes, outdated occurrence data, taxonomic errors and more, we argue that, here, they rather  
254 indicate a lack of interaction sampling data.

255 The case of the golden jackal (*Canis aureus*) is a good illustration of how the taxonomic, geo-  
256 graphical and ecological data can be used to validate one another. The jackal is a widespread  
257 taxon in northern Africa, Europe, and Australasia, generally well adapted to local conditions  
258 due to its largely varied diet (Tsunoda and Saito 2020; Krofel et al. 2021). Because of that,  
259 we expected that the *Canis* species in our dataset would be the ones losing the least amount  
260 of range, with a higher value of the proportion of GBIF pixels within their IUCN range maps.  
261 However, the taxonomy of this group is a matter of intense discussion, as molecular and mor-  
262 phological data seem to disagree in the clustering of species and subspecies (Krofel et al. 2021;  
263 Stoyanov 2020). This debate probably influenced our results: with originally only 64.9% of  
264 the GBIF pixels of the golden jackal overlapping with its IUCN data, we suspect that many of  
265 the GBIF occurrences refer to other *Canis* species, and that its taxonomic identification in the  
266 network database is probably outdated. This led to a complete exclusion of *Canis aureus* from

267 its original range in our analysis, despite the fact that this species has four documented preys in  
268 our metaweb.

## 269 **Geographical mismatch and data availability**

270 The lack of superposition between IUCN range maps and GBIF occurrences in our results sug-  
271 gests that we certainly miss geographical information about the distribution of either the prey or  
272 the predator. On the other hand, if both GBIF and IUCN occurrences tended to superpose and  
273 the species was still locally removed, this indicates that we don't have information about all its  
274 interactions (e.g., predators may be feeding on different species than the ones in our dataset out-  
275 side the Serengeti ecosystem). This rationale can be illustrated with three types of mismatches  
276 identified in our results.

277 First, *Panthera leo* was one of the species with no difference between ranges before and after  
278 our analysis, but 50.7% of its GBIF pixels did not superpose with the IUCN range (fig. 4). In  
279 this particular case, the IUCN maps seem to agree with species interaction data. However, the  
280 disagreement between the IUCN and the GBIF databases is concerning and suggests that the  
281 IUCN maps might underestimate the lion's distribution.

282 On the other hand, *Leptailurus serval* and *Canis mesomelas* are two of the three species that  
283 have the higher proportion of mismatched range due to the lack of paths to a herbivore, but are  
284 also some of the species with the higher proportion of GBIF occurrences inside their original  
285 IUCN range maps (fig. 4). This indicates that the information we are missing for these two  
286 species is related to either an additional interaction or to the presence of external interacting  
287 species. To illustrate that, we mapped the GBIF data for the prey of *Leptailurus serval*, with  
288 a mobility buffer around each point (fig. 5). When considering GBIF data, approximately 36%  
289 of the prey's occurrences are within the portion of the predator's range that was divergent from  
290 its original IUCN data. With the buffer area, this corresponds to 5.57% of the mismatched  
291 area. By adding GBIF information for the prey, we could therefore reduce the discrepancy of  
292 the range (or information) for the predator by 5.57% since its distribution is conditional on the  
293 occurrence of its preys. In other words, the range mismatch was exaggerated because we were  
294 missing information on the presence of an interacting species (i.e., this also indicates that there

295 is a mismatch - or complementarity - between the IUCN and GBIF data for their prey).

296 [Figure 5 about here.]

297 Finally, the extreme case of *Canis aureus* illustrates a lack of both geographical and ecological  
298 information: only half of its GBIF presence pixels and none of its preys occur inside its IUCN  
299 range. We believe, therefore, that the validation of species distribution based on ecological inter-  
300 action is a relevant method that can further fill in information gaps. Nevertheless, it is imperative  
301 that more geographically explicit data about ecological networks and interactions become avail-  
302 able. This would help clarify when cooccurrences can be translated into interactions (Windsor  
303 et al. 2022) and help the development of more advanced validation methods for occurrence data.

#### 304 **Next steps**

305 Here we demonstrated how we can detect areas of data deficit in species distribution data us-  
306 ing ecological interactions. Knowing where questionable occurrence data are can be crucial in  
307 ecological modelling (Hortal 2008; Ladle and Hortal 2013), and accounting for these errors can  
308 improve model outputs by diminishing the error propagation (Draper 1995). For instance, we  
309 believe our method is a way to account for ecological interactions in habitat suitability models  
310 without making the models more complex, but by making sure (not assuming) that the input data  
311 - the species occurrence - actually accounts for ecological interactions. Another application of  
312 this method is mapping areas where data are deficient, thus helping to identify priority sampling  
313 locations for interaction data, which can, in turn, reduce uncertainty in network prediction. For  
314 example, if a certain pixel confirms the presence of a species both with IUCN and GBIF data,  
315 but lacks connection between species, this pixel has a high potential to hide an unobserved in-  
316 teraction and should therefore be a priority sampling location.

317 It is important to notice, however, that the quality and usefulness of this method are highly corre-  
318 lated with the amount and quality of data available about species' occurrences **and** interactions.  
319 With this paper, we hope to add to the collective effort to decode the encrypted message that  
320 is the occurrence of a species in space and time. A promising avenue that adds to our method  
321 is the prediction of networks and interactions at large scales (Strydom et al. 2021; Windsor et



322 al. 2022), for they can add valuable information about ecological interactions where they are  
323 missing. Additionally, in order to achieve a robust modelling framework towards actual species  
324 distribution models we should invest in efforts to collect and combine open data on species oc-  
325 currence and interactions (Windsor et al. 2022), especially because we may be losing ecological  
326 interactions at least as fast as we are losing species (Valiente-Banuet et al. 2015).

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## 332 **References**

- 333 Abrego, Nerea, Tomas Roslin, Tea Huotari, Yinqiu Ji, Niels Martin Schmidt, Jiaxin Wang, Dou-  
334 glas W. Yu, and Otso Ovaskainen. 2021. “Accounting for Species Interactions Is Necessary  
335 for Predicting How Arctic Arthropod Communities Respond to Climate Change.” *Ecogra-*  
336 *phy* 44 (6): 885–96. <https://doi.org/10.1111/ecog.05547>.
- 337 Afkhami, Michelle E., Patrick J. McIntyre, and Sharon Y. Strauss. 2014. “Mutualist-Mediated  
338 Effects on Species’ Range Limits Across Large Geographic Scales.” *Ecology Letters* 17  
339 (10): 1265–73. <https://doi.org/10.1111/ele.12332>.
- 340 Albrecht, Jörg. 2018. “Plant and Animal Functional Diversity Drive Mutualistic Network As-  
341 sembly Across an Elevational Gradient.” *NATURE COMMUNICATIONS*, 10.
- 342 Alhajeri, Bader H, and Yoan Fourcade. 2019. “High Correlation Between Species-Level En-  
343 vironmental Data Estimates Extracted from IUCN Expert Range Maps and from GBIF Oc-  
344 currence Data.” *Journal of Biogeography*, 13. <https://doi.org/10.1111/jbi.13619>.
- 345 Araújo, Carlos B. de, Luiz Octavio Marcondes-Machado, and Gabriel C. Costa. 2014. “The  
346 Importance of Biotic Interactions in Species Distribution Models: A Test of the Eltonian

347 Noise Hypothesis Using Parrots.” *Journal of Biogeography* 41 (3): 513–23. [https://doi.](https://doi.org/10.1111/jbi.12234)  
348 [org/10.1111/jbi.12234](https://doi.org/10.1111/jbi.12234).

349 Baskerville, Edward B., Andy P. Dobson, Trevor Bedford, Stefano Allesina, T. Michael An-  
350 derson, and Mercedes Pascual. 2011. “Spatial Guilds in the Serengeti Food Web Re-  
351 vealed by a Bayesian Group Model.” *PLOS Computational Biology* 7 (12): e1002321.  
352 <https://doi.org/10.1371/journal.pcbi.1002321>.

353 Bezanson, Jeff, Alan Edelman, Stefan Karpinski, and Viral B. Shah. 2017. “Julia: A Fresh  
354 Approach to Numerical Computing.” *SIAM Review* 59 (1): 65–98. [https://doi.org/10.](https://doi.org/10.1137/141000671)  
355 [1137/141000671](https://doi.org/10.1137/141000671).

356 Blanchet, F. Guillaume, Kevin Cazelles, and Dominique Gravel. 2020. “Co-Occurrence Is Not  
357 Evidence of Ecological Interactions.” *Ecology Letters* 23 (7): 1050–63. [https://doi.org/](https://doi.org/10.1111/ele.13525)  
358 [10.1111/ele.13525](https://doi.org/10.1111/ele.13525).

359 Boakes, Elizabeth H., Philip J. K. McGowan, Richard A. Fuller, Ding Chang-qing, Natalie E.  
360 Clark, Kim O’Connor, and Georgina M. Mace. 2010. “Distorted Views of Biodiversity:  
361 Spatial and Temporal Bias in Species Occurrence Data.” *PLOS Biology* 8 (6): e1000385.  
362 <https://doi.org/10.1371/journal.pbio.1000385>.

363 Cabral, Juliano Sarmento, Luis Valente, and Florian Hartig. 2017. “Mechanistic Simulation  
364 Models in Macroecology and Biogeography: State-of-Art and Prospects.” *Ecography* 40  
365 (2): 267–80. <https://doi.org/10.1111/ecog.02480>.

366 Callaghan, Corey T., Jodi J. L. Rowley, William K. Cornwell, Alistair G. B. Poore, and Richard  
367 E. Major. 2019. “Improving Big Citizen Science Data: Moving Beyond Haphazard Sam-  
368 pling.” *PLOS Biology* 17 (6): e3000357. [https://doi.org/10.1371/journal.pbio.](https://doi.org/10.1371/journal.pbio.3000357)  
369 [3000357](https://doi.org/10.1371/journal.pbio.3000357).

370 Dallas, Tad, Samuel Pironon, and Luca Santini. 2020. “The Abundant-Centre Is Not All That  
371 Abundant: A Comment to Osorio-Olvera Et Al. 2020,” 2020.02.27.968586. [https://doi.](https://doi.org/10.1101/2020.02.27.968586)  
372 [org/10.1101/2020.02.27.968586](https://doi.org/10.1101/2020.02.27.968586).

373 Dansereau, Gabriel, and Timothée Poisot. 2021. “SimpleSDMLayers.jl and GBIF.jl: A Frame-  
374 work for Species Distribution Modeling in Julia.” *Journal of Open Source Software* 6 (57):

375 2872. <https://doi.org/10.21105/joss.02872>.

376 Daru, Barnabas H. 2020. “GreenMaps: A Tool for Addressing the Wallacean Shortfall in the  
377 Global Distribution of Plants.” *bioRxiv*, 2020.02.21.960161. [https://doi.org/10.1101/  
378 2020.02.21.960161](https://doi.org/10.1101/2020.02.21.960161).

379 Dobson, Andy. 2009. “Food-Web Structure and Ecosystem Services: Insights from the Serengeti.”  
380 *Philosophical Transactions of the Royal Society B: Biological Sciences* 364 (1524): 1665–  
381 82. <https://doi.org/10.1098/rstb.2008.0287>.

382 Draper, D. 1995. “Assessment and Propagation of Model Uncertainty.” *Journal of the Royal  
383 Statistical Society Series B-Statistical Methodology* 57 (1): 45–97. [https://doi.org/10.  
384 1111/j.2517-6161.1995.tb02015.x](https://doi.org/10.1111/j.2517-6161.1995.tb02015.x).

385 Ficetola, Gentile Francesco, Carlo Rondinini, Anna Bonardi, Vineet Katariya, Emilio Padoa-  
386 Schioppa, and Ariadne Angulo. 2014. “An Evaluation of the Robustness of Global Am-  
387 phibian Range Maps.” *Journal of Biogeography* 41 (2): 211–21. [https://doi.org/10.  
388 1111/jbi.12206](https://doi.org/10.1111/jbi.12206).

389 Fourcade, Yoan. 2016. “Comparing Species Distributions Modelled from Occurrence Data  
390 and from Expert-Based Range Maps. Implication for Predicting Range Shifts with Climate  
391 Change.” *Ecological Informatics* 36: 8–14. [https://doi.org/10.1016/j.ecoinf.2016.  
392 09.002](https://doi.org/10.1016/j.ecoinf.2016.09.002).

393 Fricke, Evan C., Alejandro Ordonez, Haldre S. Rogers, and Jens-Christian Svenning. 2022.  
394 “The Effects of Defaunation on Plants’ Capacity to Track Climate Change.” *Science*. [https:  
395 //doi.org/10.1126/science.abk3510](https://doi.org/10.1126/science.abk3510).

396 GBIF.org. 2022. “GBIF Occurrence Download.” The Global Biodiversity Information Facility.  
397 <https://doi.org/10.15468/DL.PF4586>.

398 GBIF Secretariat. 2021. “GBIF Backbone Taxonomy.” <https://doi.org/10.15468/39omei>.

399 GDAL/OGR contributors. 2021. *GDAL/OGR Geospatial Data Abstraction Software Library*.  
400 Manual. Open Source Geospatial Foundation.

- 401 Godsoe, William, and Luke J. Harmon. 2012. "How Do Species Interactions Affect Species Dis-  
402 tribution Models?" *Ecography* 35 (9): 811–20. [https://doi.org/10.1111/j.1600-0587.](https://doi.org/10.1111/j.1600-0587.2011.07103.x)  
403 [2011.07103.x](https://doi.org/10.1111/j.1600-0587.2011.07103.x).
- 404 Godsoe, William, Jill Jankowski, Robert D. Holt, and Dominique Gravel. 2017. "Integrating  
405 Biogeography with Contemporary Niche Theory." *Trends in Ecology and Evolution* 32 (7):  
406 488–99. <https://doi.org/10.1016/j.tree.2017.03.008>.
- 407 Gotelli, Nicholas J., Gary R. Graves, and Carsten Rahbek. 2010. "Macroecological Signals  
408 of Species Interactions in the Danish Avifauna." *Proceedings of the National Academy of*  
409 *Sciences* 107 (11): 5030–35. <https://doi.org/10.1073/pnas.0914089107>.
- 410 Herkt, K. Matthias B., Andrew K. Skidmore, and Jakob Fahr. 2017. "Macroecological Conclu-  
411 sions Based on IUCN Expert Maps: A Call for Caution." *Global Ecology and Biogeography*  
412 26 (8): 930–41. <https://doi.org/10.1111/geb.12601>.
- 413 Hortal, Joaquín. 2008. "Uncertainty and the Measurement of Terrestrial Biodiversity Gradi-  
414 ents." *Journal of Biogeography* 35 (8): 1335–36. [https://doi.org/10.1111/j.1365-2699.](https://doi.org/10.1111/j.1365-2699.2008.01955.x)  
415 [2008.01955.x](https://doi.org/10.1111/j.1365-2699.2008.01955.x).
- 416 Hortal, Joaquín, Francesco de Bello, José Alexandre F. Diniz-Filho, Thomas M. Lewinsohn,  
417 Jorge M. Lobo, and Richard J. Ladle. 2015. "Seven Shortfalls That Beset Large-Scale  
418 Knowledge of Biodiversity." *Annual Review of Ecology, Evolution, and Systematics* 46 (1):  
419 523–49. <https://doi.org/10.1146/annurev-ecolsys-112414-054400>.
- 420 Hortal, Joaquín, Alberto Jiménez-Valverde, José F. Gómez, Jorge M. Lobo, and Andrés Baselga.  
421 2008. "Historical Bias in Biodiversity Inventories Affects the Observed Environmental  
422 Niche of the Species." *Oikos* 117 (6): 847–58. [https://doi.org/10.1111/j.0030-1299.](https://doi.org/10.1111/j.0030-1299.2008.16434.x)  
423 [2008.16434.x](https://doi.org/10.1111/j.0030-1299.2008.16434.x).
- 424 Hurlbert, Allen H., and Walter Jetz. 2007. "Species Richness, Hotspots, and the Scale Depen-  
425 dence of Range Maps in Ecology and Conservation." *Proceedings of the National Academy*  
426 *of Sciences* 104 (33): 13384–89. <https://doi.org/10.1073/pnas.0704469104>.
- 427 Hurlbert, Allen H., and Ethan P. White. 2005. "Disparity Between Range Map- and Survey-  
428 Based Analyses of Species Richness: Patterns, Processes and Implications." *Ecology Letters*

429 8 (3): 319–27. <https://doi.org/10.1111/j.1461-0248.2005.00726.x>.

430 Isaac, Nick J. B., James Mallet, and Georgina M. Mace. 2004. “Taxonomic Inflation: Its Influ-  
431 ence on Macroecology and Conservation.” *Trends in Ecology & Evolution* 19 (9): 464–69.  
432 <https://doi.org/10.1016/j.tree.2004.06.004>.

433 IUCN Red List Technical Working Group. 2019. “Mapping Standards and Data Quality for  
434 IUCN Red List Spatial Data.” Prepared by the Standards and Petitions Working Group of  
435 the IUCN SSC Red . . . .

436 Krofel, M., J. Hatlauf, W. Bogdanowicz, L. a. D. Campbell, R. Godinho, Y. V. Jhala, A. C.  
437 Kitchener, et al. 2021. “Towards Resolving Taxonomic Uncertainties in Wolf, Dog and  
438 Jackal Lineages of Africa, Eurasia and Australasia.” *Journal of Zoology* n/a (n/a): 1–14.  
439 <https://doi.org/10.1111/jzo.12946>.

440 Ladle, Richard, and Joaquín Hortal. 2013. “Mapping Species Distributions: Living with Un-  
441 certainty.” *Frontiers of Biogeography* 5 (1): 4–6.

442 McNaughton, S. J. 1992. “The Propagation of Disturbance in Savannas Through Food Webs.”  
443 *Journal of Vegetation Science* 3 (3): 301–14. <https://doi.org/10.2307/3235755>.

444 Meyer, Carsten, Patrick Weigelt, and Holger Kreft. 2016. “Multidimensional Biases, Gaps and  
445 Uncertainties in Global Plant Occurrence Information.” *Ecology Letters* 19 (8): 992–1006.  
446 <https://doi.org/10.1111/ele.12624>.

447 Pocock, Michael J. O., Helen E. Roy, Chris D. Preston, and David B. Roy. 2015. “The Biological  
448 Records Centre: A Pioneer of Citizen Science.” *Biological Journal of the Linnean Society*  
449 115 (3): 475–93. <https://doi.org/10.1111/bij.12548>.

450 Poisot, Timothée, Benjamin Baiser, Jennifer A Dunne, Sonia Kéfi, François Massol, Nicolas  
451 Mouquet, Tamara N Romanuk, Daniel B Stouffer, Spencer A Wood, and Dominique Gravel.  
452 2016. “Mangal - Making Ecological Network Analysis Simple.” *Ecography* 39 (4): 384–90.

453 Poisot, Timothée, Gabriel Bergeron, Kevin Cazelles, Tad Dallas, Dominique Gravel, Andrew  
454 MacDonald, Benjamin Mercier, Clément Violet, and Steve Vissault. 2021. “Global Knowl-  
455 edge Gaps in Species Interaction Networks Data.” *Journal of Biogeography* 48 (7): 1552–  
456 63. <https://doi.org/10.1111/jbi.14127>.

457 Poisot, Timothée, Gabriel Bergeron, Kevin Cazelles, Tad Dallas, Dominique Gravel, Andrew  
458 Macdonald, Benjamin Mercier, Clément Violet, and Steve Vissault. 2020. “Environmental  
459 Biases in the Study of Ecological Networks at the Planetary Scale.” *bioRxiv*, 2020.01.27.921429.  
460 <https://doi.org/10.1101/2020.01.27.921429>.

461 Poisot, Timothée, Zachary Bélisle, Laura Hoebeke, Michiel Stock, and Piotr Szefer. 2019. “Eco-  
462 logicalNetworks.jl: Analysing Ecological Networks of Species Interactions.” *Ecography* 42  
463 (11): 1850–61. <https://doi.org/10.1111/ecog.04310>.

464 Power, Mary E. 1992. “Top-Down and Bottom-Up Forces in Food Webs: Do Plants Have  
465 Primacy.” *Ecology* 73 (3): 733–46. <https://doi.org/10.2307/1940153>.

466 Rondinini, Carlo, Kerrie A. Wilson, Luigi Boitani, Hedley Grantham, and Hugh P. Possingham.  
467 2006. “Tradeoffs of Different Types of Species Occurrence Data for Use in Systematic  
468 Conservation Planning.” *Ecology Letters* 9 (10): 1136–45. [https://doi.org/10.1111/  
469 j.1461-0248.2006.00970.x](https://doi.org/10.1111/j.1461-0248.2006.00970.x).

470 Ronquillo, Cristina, Fernanda Alves-Martins, Vicente Mazimpaka, Thadeu Sobral-Souza, Bruno  
471 Vilela-Silva, Nagore G. Medina, and Joaquín Hortal. 2020. “Assessing Spatial and Tempo-  
472 ral Biases and Gaps in the Publicly Available Distributional Information of Iberian Mosses.”  
473 *Biodiversity Data Journal* 8: e53474. <https://doi.org/10.3897/BDJ.8.e53474>.

474 Roy, Helen E., Elizabeth Baxter, Aoine Saunders, and Michael J. O. Pocock. 2016. “Focal  
475 Plant Observations as a Standardised Method for Pollinator Monitoring: Opportunities and  
476 Limitations for Mass Participation Citizen Science.” *PLOS ONE* 11 (3): e0150794. [https:  
477 //doi.org/10.1371/journal.pone.0150794](https://doi.org/10.1371/journal.pone.0150794).

478 Ryan, S. F., N. L. Adamson, A. Aktipis, L. K. Andersen, R. Austin, L. Barnes, M. R. Beasley,  
479 et al. 2018. “The Role of Citizen Science in Addressing Grand Challenges in Food and  
480 Agriculture Research.” *Proceedings of the Royal Society B: Biological Sciences* 285 (1891).  
481 <https://doi.org/10.1098/rspb.2018.1977>.

482 Scott, Abigail L., Paul H. York, Clare Duncan, Peter I. Macreadie, Rod M. Connolly, Megan T.  
483 Ellis, Jessie C. Jarvis, Kristin I. Jinks, Helene Marsh, and Michael A. Rasheed. 2018. “The  
484 Role of Herbivory in Structuring Tropical Seagrass Ecosystem Service Delivery.” *Frontiers*

485       in *Plant Science* 9: 127. <https://doi.org/10.3389/fpls.2018.00127>.

486 Stoyanov, S. 2020. “Cranial Variability and Differentiation Among Golden Jackals (*Canis Au-*  
487       *reus*) in Europe, Asia Minor and Africa.” *ZooKeys*. [https://doi.org/10.3897/zookeys.](https://doi.org/10.3897/zookeys.917.39449)  
488       917.39449.

489 Strydom, Tanya, Michael D. Catchen, Francis Banville, Dominique Caron, Gabriel Dansereau,  
490       Philippe Desjardins-Proulx, Norma R. Forero-Muñoz, et al. 2021. “A Roadmap Towards  
491       Predicting Species Interaction Networks (across Space and Time).” *Philosophical Trans-*  
492       *actions of the Royal Society B: Biological Sciences* 376 (1837): 20210063. [https://doi.](https://doi.org/10.1098/rstb.2021.0063)  
493       [org/10.1098/rstb.2021.0063](https://doi.org/10.1098/rstb.2021.0063).

494 Tsunoda, Hiroshi, and Masayuki U. Saito. 2020. “Variations in the Trophic Niches of the Golden  
495       Jackal *Canis Aureus* Across the Eurasian Continent Associated with Biogeographic and An-  
496       thropogenic Factors.” *Journal of Vertebrate Biology* 69 (4): 20056.1. [https://doi.org/](https://doi.org/10.25225/jvb.20056)  
497       [10.25225/jvb.20056](https://doi.org/10.25225/jvb.20056).

498 Valiente-Banuet, Alfonso, Marcelo A. Aizen, Julio M. Alcántara, Juan Arroyo, Andrea Cocucci,  
499       Mauro Galetti, María B. García, et al. 2015. “Beyond Species Loss: The Extinction of  
500       Ecological Interactions in a Changing World.” Edited by Marc Johnson. *Functional Ecology*  
501       29 (3): 299–307. <https://doi.org/10.1111/1365-2435.12356>.

502 Windsor, Fredric M., Johan van den Hoogen, Thomas W. Crowther, and Darren M. Evans. 2022.  
503       “Using Ecological Networks to Answer Questions in Global Biogeography and Ecology.”  
504       *Journal of Biogeography* n/a (n/a). <https://doi.org/10.1111/jbi.14447>.

505 Wisz, Mary Susanne, Julien Pottier, W Daniel Kissling, Loïc Pellissier, Jonathan Lenoir, Chris-  
506       tian F Damgaard, Carsten F Dormann, et al. 2013. “The Role of Biotic Interactions in  
507       Shaping Distributions and Realised Assemblages of Species: Implications for Species Dis-  
508       tribution Modelling.” *Biological Reviews of the Cambridge Philosophical Society* 88 (1):  
509       15–30. <https://doi.org/10.1111/j.1469-185X.2012.00235.x>.

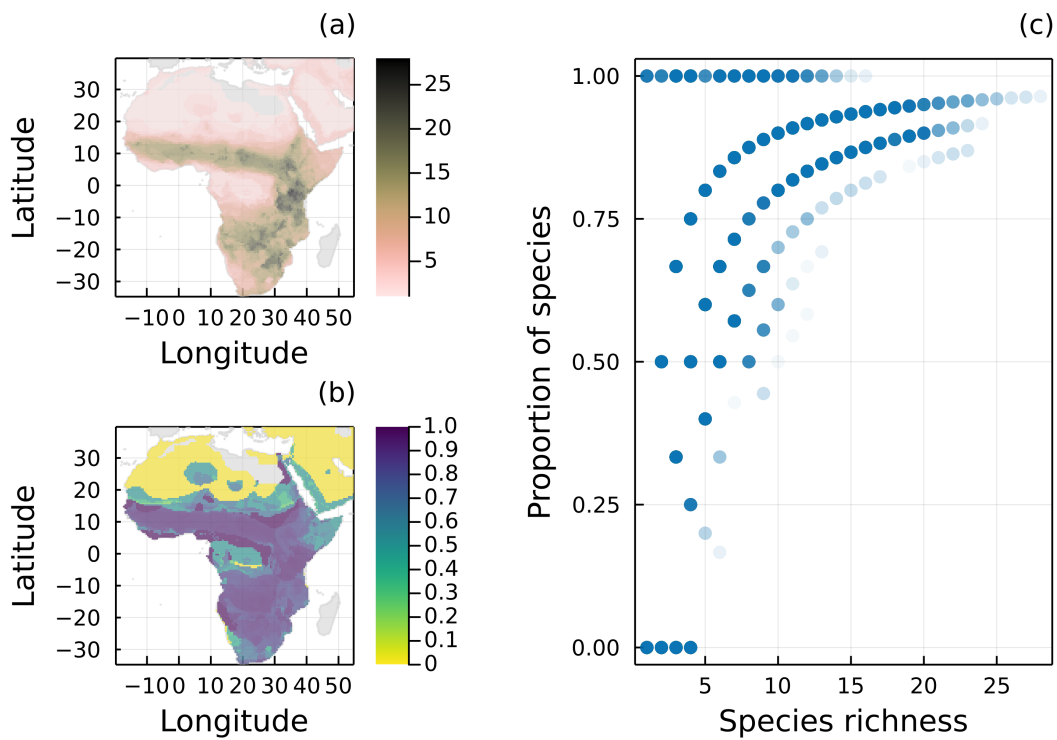


Figure 1: (a) Spatial distribution of species richness according to the original IUCN range maps of all 32 mammal species of the Serengeti food web. (b) Proportion of mammal species remaining in each local network (i.e., each pixel) after removing all species without a path to a primary producer. (c) Proportion of mammal species remaining in each local network as a function of the number of species given by the original IUCN range maps.



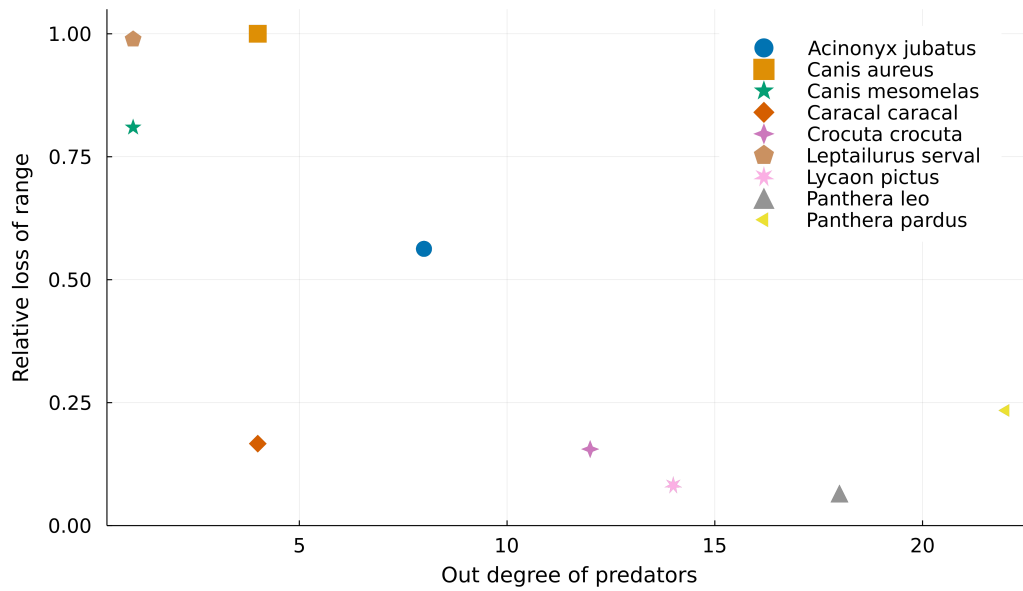


Figure 2: Negative relationship between the out degree of predator species and their relative range mismatch. More specialized predators “lose” a higher proportion of their ranges due to mismatches with the ranges of their preys.

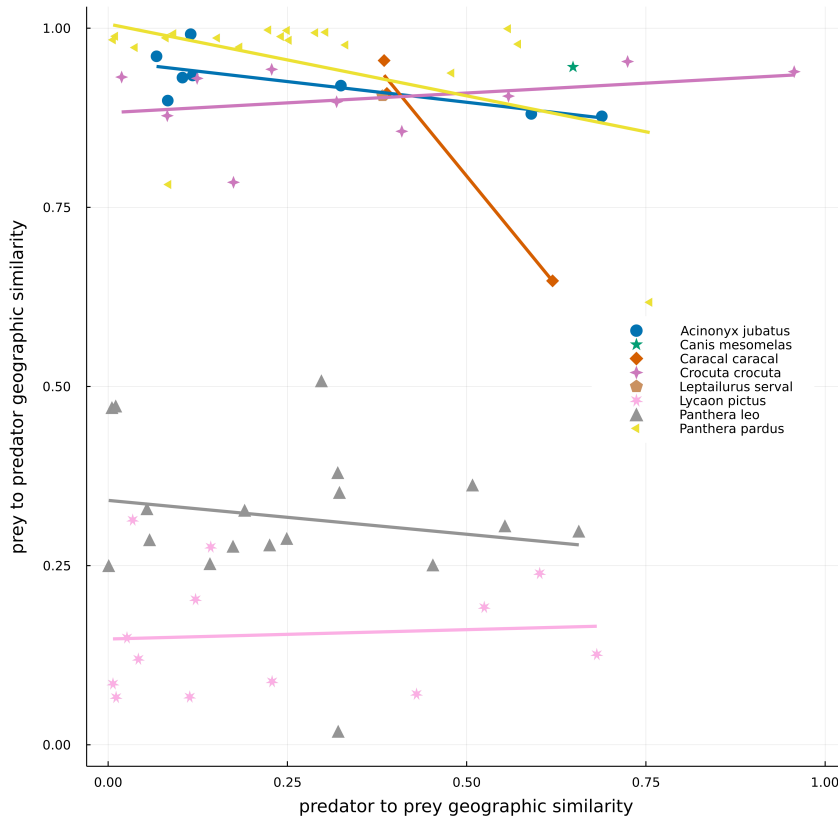


Figure 3: Geographical similarity between the original IUCN range maps of predators and preys. Dots represent predator-prey pairs, with different symbols corresponding to different predators. For a given pair of species, the number  $c$  of pixels where the focal species is present but not the other and the number  $a$  of pixels where the predator and prey cooccur, were calculated. Geographic similarities were given by  $a/(a + c)$ , with the predator being the focal species in the predator to prey similarity (x-axis), while the prey is the focal one in the prey to predator similarity (y-axis). One of the predators, *Canis aureus*, is not represented in the image because it is an extreme case (where all its range is suppressed by the absence of preys) and it would make the interpretation of the data more difficult.

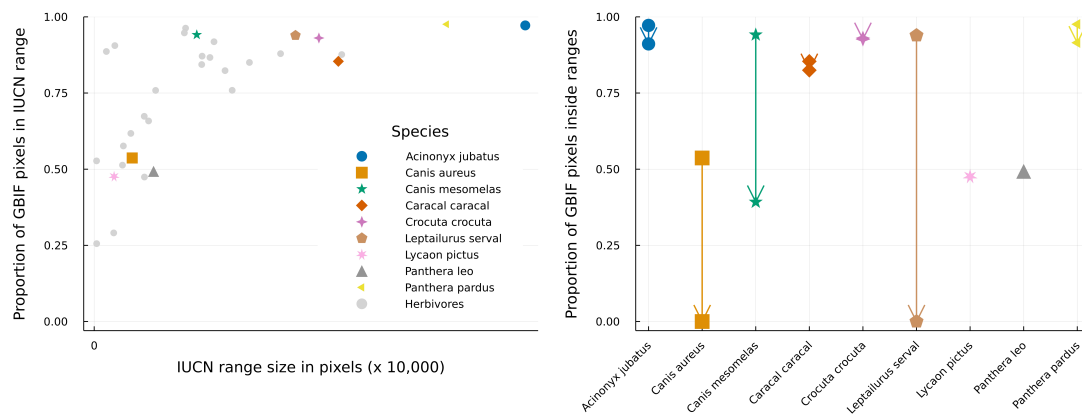


Figure 4: Left panel: Distribution of the proportion of GBIF pixels (pixels with at least one occurrence in GBIF) superposed by the IUCN range data for different range sizes. Right panel: Differences between the proportion of GBIF pixels matching the original and cropped IUCN range maps for every predator species. Arrows go from the proportion inside the original range to the proportion inside the revised range, which can only be equal or lower. Overlapping markers indicate no difference between the types of layers. Species markers are the same on both figures, with predators presented in distinct colored markers and all herbivores grouped in a single grey marker. Pixels represent a resolution of 0.5 degrees.

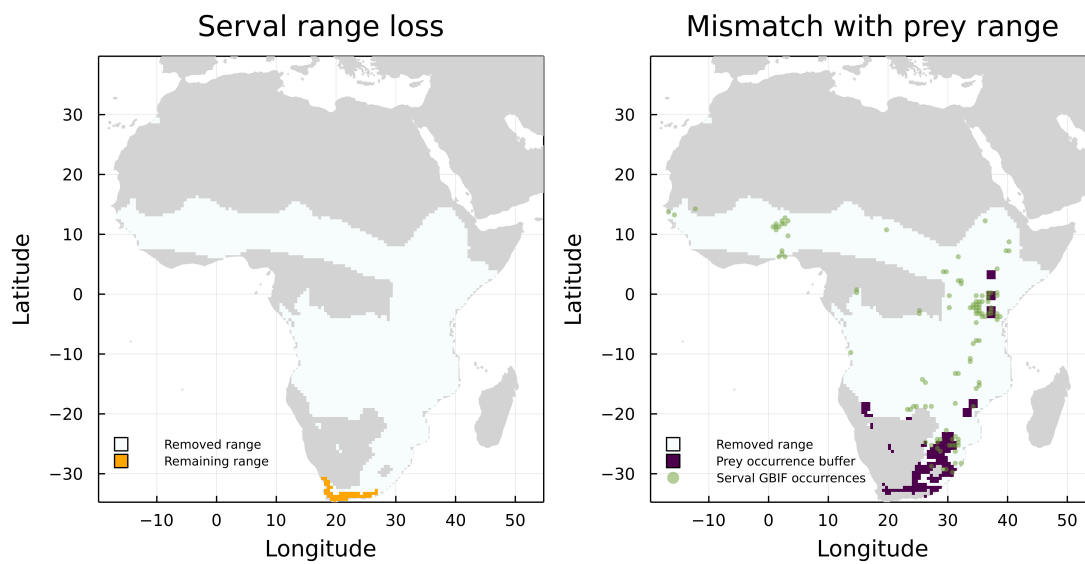


Figure 5: Mismatch between servals' range loss and GBIF occurrence of its prey. The left panel shows the reduction of servals' range when we consider the IUCN data of its prey. On the right panel, we added GBIF data on both serval and its prey, with a buffer for the prey to account for species mobility.