

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

Gracielle T Higino^{Corresp., 1}, Francis Banville^{2, 3, 4}, Gabriel Dansereau^{3, 4}, Norma Rocio Forero Muñoz^{3, 4}, Fredric Windsor⁵, Timothée Poisot^{Corresp. 3, 4}

¹ Biodiversity Research Centre, University of British Columbia, Vancouver, British Columbia, Canada

² University of Sherbrooke, Sherbrooke, Québec, Canada

³ University of Montreal, Montréal, Québec, Canada

⁴ Quebec Centre for Biodiversity Science, Montréal, Québec, Canada

⁵ School of Natural and Environmental Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom

Corresponding Authors: Gracielle T Higino, Timothée Poisot

Email address: graciellehigino@gmail.com, timothee.poisot@umontreal.ca

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 provide updated range maps for all predators 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.

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Gracielle T. Higinio¹ Francis Banville^{2,3,4} Gabriel Dansereau^{2,4} Norma R. Forero-Muñoz^{2,4}
Fredric M. Windsor⁵ Timothée Poisot^{2,4}

¹ Biodiversity Research Centre, University of British Columbia ² Université de Montréal ³ Université de Sherbrooke ⁴ Quebec Centre for Biodiversity Science ⁵ School of Natural and Environmental Sciences, Newcastle University

Correspondance to:

Gracielle T. Higinio — graciellehiginio@gmail.com

Timothée Poisot — timothee.poisot@umontreal.ca

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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 provide updated range maps for all predators 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). Ecol-
5 ogists have been trying to decode this message with progressively more powerful tools, from
6 their field notes to highly complex computational algorithms. However, to succeed in this chal-
7 lenge it is important to have the right clues in hand. There are many ways we can be misled
8 by data - or the lack of it: taxonomic errors (e.g., due to updates in the taxonomy of a species),
9 geographic inaccuracy (e.g., approximate coordinates or lack of documentation about their ac-
10 curacy), or sampling biases (e.g. data clustered near roads or research centers) (Ladle and Hortal
11 2013; Hortal et al. 2015; Poisot et al. 2021). One way to identify - and potentially fix - these
12 errors is to combine many different pieces of information about the occurrence of a species, so
13 agreements and mismatches can emerge. Although previous studies have combined different
14 types of occurrence data to measure the accuracy of datasets (Hurlbert and Jetz 2007; Hurlbert
15 and White 2005; Ficetola et al. 2014), none have used different types of information so far
16 (i.e., ecological characteristics other than geographical distribution). Here we suggest jointly
17 analysing species occurrence (range maps and point occurrences) and ecological interactions to
18 identify mismatches between datasets.

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 and data aggregation (Poisot et al. 2020; Hortal et al. 2015). Never-
60 theless, we have witnessed an increase in the availability of biodiversity data in the last decades,
61 including those collected through community science projects (Callaghan et al. 2019; Pocock et
62 al. 2015) and dedicated databases, such as Mangal (Poisot et al. 2016). This provides an oppor-
63 tunity to merge species distribution and ecological interaction data to improve our predictions
64 of where a species may be found across large spatial scales (e.g., continental and global).

65 It has been demonstrated that the agreement between range maps and point data varies geograph-
66 ically (Hurlbert and Jetz 2007; Hurlbert and White 2005; Ficetola et al. 2014). Adding ecolog-
67 ical interaction data to this comparison might help to elucidate where these (dis)agreements are
68 more likely to be true and which dataset better represent the actual distribution of species. In
69 this context, we elaborate a method that allows us to refine distribution data (more precisely
70 range maps) based on interaction data, considering the basic assumption that predators can only
71 be present in regions where they are connected to at least one herbivore - and thus indirectly
72 connected to primary producers. We used a Serengeti food web dataset (Baskerville et al. 2011)
73 (which comprises carnivores, herbivores, and plants from Tanzania) to demonstrate how a mis-
74 match between occurrence and interaction data can highlight significant uncertainty areas in
75 IUCN range maps. Finally, we add the GBIF occurrence points for the Serengeti species to the
76 investigation, discuss the mechanisms that can lead to the lack of agreement between data, and
77 build from that a vision for the next steps, reinforcing the importance of geographically explicit
78 interaction data.

79 **Methods**

80 Organisms cannot persist unless they are directly or indirectly connected to a primary producer
81 within their associated food web (Power 1992). Therefore, the range of a predator (omnivore or
82 carnivore) depends on the overlapping ranges of its preys. If sections of a predator's range does
83 not overlap with at least one of its prey it will become disconnected from primary producers,
84 and therefore we would not expect the predator to occur in this area. This mismatch can be
85 the result of different mechanisms, like the misestimation of both the predator's and the preys'

86 ranges (Ladle and Hortal 2013; Rondinini et al. 2006), taxonomic errors (Isaac, Mallet, and
87 Mace 2004; Ladle and Hortal 2013), or the lack of information about trophic links (i.e., the
88 lack of connection between the ranges of a predator and a primary producer may be due a third
89 species we don't know is connected to both). Thus, given that herbivores are the main connection
90 between plant resources (directly limited by environmental conditions) and predators (Dobson
91 2009; Scott et al. 2018), here we adjusted the ranges of predators based on a simple rule: we
92 removed any part of a predator's range that did not intersect with the range of at least one prey
93 herbivore species. So, unless the range of the predator overlapped with at least one prey item,
94 which in turn is directly connected to a primary producer (plants), we removed that section of
95 the predator's range. Finally, we calculated the difference in range size between the original
96 IUCN ranges and those adjusted based on species interaction data.

97 **Data**

98 We investigated the mismatch between savannah species ranges and interactions in Africa (fig. 1).
99 These ecosystems host a range of different species, including the well-characterized predator-
100 prey dynamics between iconic predators (e.g., lions, hyenas, and leopards) and large herbivores
101 (e.g., antelopes, wildebeests, and zebras), as well as a range of herbivorous and carnivorous
102 small mammals. The Serengeti ecosystem has been extensively studied and its food web is one
103 of the most complete we have to date, including primary producers identified to the species level.
104 Here we focus on six groups of herbivores and carnivores from the Serengeti Food Web Data Set
105 (Baskerville et al. 2011). These species exhibit direct antagonistic (predator-prey) interactions
106 with one another and are commonly found across savannah ecosystems on the African continent
107 (McNaughton 1992). Plants in the network were included indirectly in our analyses as we do
108 not expect the primary producers to significantly influence the range of herbivores for several
109 reasons. Firstly, many savannah plants are functionally similar (i.e., grasses, trees and shrubs)
110 and cooccur across the same habitats (Baskerville et al. 2011). Secondly, herbivores in the net-
111 work are broadly generalists feeding on a wide range of different plants across habitats. Indeed,
112 out of 129 plants in our dataset, herbivores ($n = 23$) had a mean out degree (mean number of
113 preys) of around 22 (std = 17.5). There is also an absence of global range maps for many plant

114 species (Daru 2020), which prevents their direct inclusion in our analysis. Therefore, we as-
115 sume that plants consumed by herbivores are present across their ranges, and as such the ranges
116 of herbivores are not expected to be significantly constrained by the availability of food plants.

117 From the wider ecological network presented in Baskerville (2011), we sampled interaction data
118 for herbivores and carnivores. This subnetwork contained 32 taxa (23 herbivores and 9 carni-
119 vores) and 84 interactions and had a connectance of 0.08. Although self-loops are informative,
120 we removed these interactions to allow for the original IUCN ranges of predators with canni-
121 balistic interactions to be adjusted. We treated this overall network as a metaweb since it *should*
122 contain all potential species interactions between mammalian taxa occurring across savannah
123 ecosystems such as the Serengeti.

124 We compiled IUCN range maps for the 32 species included in the metaweb from the Spatial Data
125 Download portal (www.iucnredlist.org/resources/spatial-data-download), which we rasterized
126 at 10 arc-minute resolution (~18 km at the equator). We restricted the rasters a spatial extent
127 comprised between latitudes 35°S and 40°N and longitudes 20°W and 55°E. We then combined
128 interaction data from the metaweb and cooccurrence data generated from species ranges to create
129 networks for each raster pixel. This generated a total of 84,244 pixel-level networks. These
130 networks describe potential predation, not actual interactions: the former is derived information
131 from the metaweb, and the latter is contingent on the presence of herbivores.

132 **Range overlap measurement**

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

142 prey taxa (i.e., a higher generality) are less likely to have significant changes in their range as it
143 is more likely that at least one prey species is present across most of their range.

144 **Validation**

145 For each species in the dataset we collated point observation data from GBIF (www.gbif.org).
146 We restricted our queries to the data with spatial coordinates and which were inside the spatial
147 extent of our rasters. We did not use continental or date filters to retrieve as much data as possible.
148 However, a few observations were localized in the ocean near latitude 0° and longitude 0° . We
149 assumed these were errors and removed all observations falling in the extent between latitudes
150 2°S and 2°N and longitudes 2°W and 2°E to keep only mainland sites.

151 We then converted the occurrence data into raster format by determining which pixels had a
152 least one GBIF occurrence. This allowed us to remove the effect of repeated sampling in some
153 locations. These data were used to validate the range adjustments made based on species in-
154 teractions (see beginning of Methods section). To do so, we calculated the proportion of GBIF
155 presence pixels occurring within both the original IUCN species range and the adjusted one. We
156 then compared these proportions for the predators to verify if the range adjustments removed
157 locations with GBIF observations, hence likely true habitats.

158 **Software**

159 We performed all analyses using *Julia* v1.7.2 (Bezanson et al. 2017). We used the packages
160 `SimpleSDMLayers.jl` (Dansereau and Poisot 2021) to manipulate the raster layers, `EcologicalNetworks.jl`
161 (Poisot et al. 2019) to construct and manipulate the interaction networks, and `GBIF.jl` (Dansereau
162 and Poisot 2021) to retrieve the species occurrences from GBIF. We also used *GDAL* (GDAL/OGR
163 contributors 2021) to rasterize the IUCN range maps (initially available as shapefiles from the
164 Spatial Data Download portal). All the scripts required to reproduce the analyses are available
165 at <https://doi.org/10.5281/zenodo.6842861>.

166 **Results**

167 Mammal species found in the Serengeti food web are widespread in Africa, especially in grass-
168 lands and savannahs (first panel of fig. 1). However, most local networks (83.2%) built using the
169 original IUCN range maps had at least one mammal species without a path to a primary pro-
170 ducer (second panel of fig. 1). On average, local food webs had almost the third of their mammal
171 species (mean = 30.5%, median = 14.3%) disconnected from basal species. In addition, many
172 networks (16.6%) only had disconnected mammals; these networks however all had a very low
173 number of mammal species, specifically between 1 and 4 (from a total of 32). As expected, the
174 proportion of carnivores with a path to a primary producer was conditional on the total number
175 of mammal species in each local network (third panel of fig. 1).

176 [Figure 1 about here.]

177 **Specialized predators lose more range**

178 [Figure 2 about here.]

179 Predators with fewer prey lose more range with our method (fig. 2). For instance, both *Leptail-*
180 *urus serval* and *Canis mesomelas* have only one prey in the Serengeti food web (tbl. 1), each
181 of them with a very small range compared to those of their predator. This discrepancy between
182 range sizes promotes significant range loss. On the other hand, predators of the genus *Panthera*
183 are some of the most connected species, and they also lose the least proportion of their ranges.
184 This mismatch between predators and preys can also be a result of taxonomic disagreement be-
185 tween the geographical and ecological data. Although *Canis aureus* has the same number of
186 prey as *Caracal caracal*, none of the prey taxa of the former occurs inside its original range
187 (tbl. 1), which results in complete range loss.

188 [Figure 3 about here.]

189 There was a high variation in the overlap of predator and prey ranges (fig. 3). The high density of
190 points on the left-hand side of fig. 3 indicates that most preys have small ranges in comparison to

191 those of the set of carnivores in the networks, resulting in either low overlap between both ranges
 192 (bottom) or high overlap of ranges because much of that of the prey is within predators' range
 193 (top). The top-right side of the plot encompasses situations where the ranges of both predator
 194 and prey are similar and overlapping, while the bottom-right part of the plot represents a situation
 195 where the range of the predator is smaller than that of its prey and much of it occurs within the
 196 preys' range. For example, *Panthera pardus* had many preys occurring inside its range, with
 197 highly variable levels of overlap (tbl. 1). In general, species exhibited more consistent values of
 198 prey-predator overlap, than predator-prey overlap – indicated by the spread of points along the
 199 x-axis, yet more restricted variation on the y-axis (fig. 3). There was also no overall relationship
 200 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
Large carnivores					
<i>Acinonyx jubatus</i>	8	1	15540	0.560	0.670
<i>Crocuta crocuta</i>	12	1	43307	0.848	0.252
<i>Lycaon pictus</i>	14	0	3873	0.916	-
<i>Panthera leo</i>	18	0	11384	0.934	-
<i>Panthera pardus</i>	22	0	68137	0.766	-
Small carnivores					
<i>Canis aureus</i>	4	1	7358	0.000	0.780
<i>Canis mesomelas</i>	1	1	19872	0.190	0.995
<i>Caracal caracal</i>	4	0	47243	0.832	-

Species	Number of preys	Number of predators	Total range size	Proportion of range occupied by preys	Proportion of range occupied by predators
<i>Leptailurus serval</i>	1	1	38856	0.011	0.979
Small herbivores					
<i>Damaliscus lunatus</i>	0	4	5567	-	1
<i>Hippopotamus amphibius</i>	0	0	3695	-	-
<i>Kobus ellipsiprymnus</i>	0	4	26705	-	1
<i>Ourebia ourebi</i>	0	5	22380	-	1
<i>Pedetes capensis</i>	0	2	11901	-	1
<i>Phacochoerus africanus</i>	0	5	29963	-	0.999
<i>Redunca redunca</i>	0	5	17465	-	1
<i>Rhabdomys pumilio</i>	0	5	465	-	0.998
<i>Tragelaphus oryx</i>	0	2	20852	-	0.991
<i>Tragelaphus scriptus</i>	0	3	36011	-	0.984
Large grazers					
<i>Aepyceros melampus</i>	0	5	10579	-	1
<i>Alcelaphus buselaphus</i>	0	4	20761	-	1
<i>Connochaetes taurinus</i>	0	6	9650	-	1
<i>Equus quagga</i>	0	5	7070	-	1
<i>Eudorcas thomsonii</i>	0	6	463	-	1
<i>Nanger granti</i>	0	6	2303	-	1
Hyraxes					
<i>Heterohyrax brucei</i>	0	1	17728	-	0.972
<i>Procavia capensis</i>	0	1	47697	-	0.647

Species	Number of preys	Number of predators	Total range size	Proportion of range occupied by preys	Proportion of range occupied by predators
Others					
<i>Giraffa camelopardalis</i>	0	1	5418	-	0.470
<i>Loxodonta africana</i>	0	0	9654	-	-
<i>Madoqua kirkii</i>	0	7	4002	-	1
<i>Papio anubis</i>	0	1	23171	-	0.938
<i>Syncerus caffer</i>	0	1	25223	-	0.250

201 Validation with GBIF occurrences

202 The proportion of GBIF pixels (pixels with at least one GBIF occurrence) falling within the
 203 IUCN ranges varied from low to high depending on the species (fig. 4, left). The lowest pro-
 204 portions occurred for species with small ranges. Amongst herbivores, *Rhabdomys pumilio* has
 205 a proportion of 22.6% of its presence pixels within its IUCN range, while predators have this
 206 proportion above 55% (such as *Lycaon pictus*, with 55.1%, and *Canis aureus*, with 56.2%). Nev-
 207 ertheless, some species with smaller ranges showed high data overlap (such as *Canis mesomelas*,
 208 with 94.9%, and many herbivores). Overall, predators and preys displayed similar overlap vari-
 209 ations, and species with median and large ranges had higher proportions of occurrences falling
 210 into their IUCN range.

211 The proportion of GBIF pixels in updated ranges can only be equal to or lower than that of
 212 the original ranges, as our analysis removes pixels from the original range and does not add
 213 new ones. Rather, the absence of a difference between the two types of ranges indicates that
 214 no pixels with GBIF observations, hence likely true habitats, were removed by our analysis.
 215 Here this proportion was mostly similar to that of the original IUCN ranges for most predator
 216 species (fig. 4). Two species showed no difference in proportion while four species showed only

217 small differences (*Crocuta crocuta* lost 1.3% of the original data overlap; *Acinonyx jubatus* lost
218 1.9%; *Panthera pardus* lost 8.8%; and *Caracal caracal* lost 12.3%). On the other hand, three
219 species, *Canis aureus*, *Canis mesomelas*, and *Leptailurus serval* showed very high differences,
220 with overlaps lowered by 100%, 57.4%, and 100% respectively. These last two species are also
221 the only predators with a single prey in our metaweb. *Canis aureus* has four preys, but it has one
222 of the smallest ranges in IUCN, which is not covered by any of its preys. This result reinforces
223 the concern raised in the literature on the use of IUCN range maps for species that are not well
224 known (Herkt, Skidmore, and Fahr 2017), demonstrating how small range species are likely to
225 have their distribution underestimated in the IUCN database. Additionally, the fact that *Canis*
226 *aureus* had such a conspicuous mismatch between both the original and updated IUCN range
227 maps, and between GBIF and IUCN data, may indicate a taxonomic incongruency between the
228 three databases used here, which we explore in the Discussion section. Our results delineate how
229 a mismatch between GBIF and IUCN databases differ greatly with small changes in herbivore
230 species ranges, and it is somewhat positively related to range size for predator species. Moreover,
231 we show that accounting for interactions does not necessarily aggravates this dissimilarity, but
232 it is relevant for species with little ecological information or specialists.

233 [Figure 4 about here.]

234 Discussion

235 The jackal is a widespread taxon in northern Africa, Europe, and Australasia, generally well
236 adapted to local conditions due to its largely varied diet (Tsunoda and Saito 2020; Krofel et
237 al. 2021). Because of that, we expected that the *Canis* species in our dataset would be the
238 ones losing the least amount of range, with a higher value of the proportion of GBIF pixels
239 within their IUCN range maps. However, the taxonomy of this group is a matter of intense
240 discussion, as molecular and morphological data seem to disagree in the clustering of species
241 and subspecies (Krofel et al. 2021; Stoyanov 2020). This debate probably influenced our results:
242 with originally only 56.2% of the GBIF pixels of the golden jackal (*Canis aureus*) overlapping
243 with the IUCN data, we suspect that many of the GBIF occurrences refer to other *Canis* species,

244 and that its taxonomic identification in the network database is probably outdated. This led to
245 a complete exclusion of *Canis aureus* from its original range in our analysis, despite the fact
246 that this species has four documented preys in our metaweb. This example illustrates how the
247 taxonomic, geographical and ecological data can be used to validate one another.

248 Here we show that when ecological interaction data (predator-prey interactions within food
249 webs) are used to refine species range maps, there are significant reductions in the IUCN range
250 size of predatory organisms. Despite showing the potential importance of accounting for species
251 interactions when estimating the range of a species, it remains unclear the extent to which the
252 patterns observed represent ecological processes or a lack of data.

253 **Connectivity, diversity and range preservation**

254 In the Serengeti food web there is a positive relationship between the out degrees of predators
255 and the size of their ranges. Here, we showed that there is a negative relationship between the
256 relative loss of predators' ranges and their number of preys, reinforcing the idea that generalist
257 species can preserve their distributions longer while losing interactions. The factors limiting the
258 geographical range of a species in a community can vary with connectivity and richness (Sven-
259 ning et al. 2014). Younger communities may be more affected by environmental limitations
260 because they are dominated by generalist species, while older metacommunities are probably
261 affected in different ways in the center of the distribution, at the edge of ranges, and in sink and
262 source communities (Svenning et al. 2014; Godsoe et al. 2017; Cazelles et al. 2016; Bullock
263 et al. 2000). Additionally, it is likely that species with larger ranges of distribution and those
264 that are more generalists would co-occur with a greater number of other species (Dáttilo et al.
265 2020), while dispersal capacity of competitive species modulate their aggregation in space and
266 the effect of interactions on their range limits (Godsoe et al. 2017).

267 **Geographical mismatch and data availability**

268 The geographical mismatch between predators and preys has ecological consequences such as
269 loss of ecosystem functioning and extinction of populations (Anderson et al. 2016; Dáttilo and

270 Rico-Gray 2018; Pringle et al. 2016; Young et al. 2013). Climate change is one of the causes
271 of this, leading, for instance, to the decrease of plant populations due to the lack of pollination
272 (Bullock et al. 2000; Afkhami, McIntyre, and Strauss 2014; Godsoe et al. 2017). However,
273 this mismatch can also be purely informational. When the distribution of predators and preys
274 does not superpose, it can mean we lack information about the distribution of either species or
275 about their interactions (e.g., predators may be feeding on different species than the ones in our
276 dataset outside the Serengeti ecosystem). Here we addressed part of this problem by comparing
277 the IUCN range maps with GBIF occurrences, which helped us clarify what is the shortfall for
278 each species.

279 The lack of superposition between IUCN range maps and GBIF occurrences suggests that we
280 certainly do miss geographical information about the distribution of a certain species, but this is
281 not an indicator of the completeness of the information about ecological interactions. However,
282 if both GBIF and IUCN occurrences tend to superpose and still the species is locally removed,
283 this indicates we don't have information about all its interactions. The combination of this ratio-
284 nale with our method of updating range maps based on ecological interactions allows us to have
285 a clearer idea of which information we are missing. For example, the lion (*Panthera leo*) was
286 one of the species with no difference between the original and the updated ranges, but 40.7% of
287 the GBIF occurrences for this species fell outside its IUCN range (fig. 4). In this particular case,
288 the IUCN maps seem to agree with species interaction data. However, the disagreement between
289 the IUCN and the GBIF databases is concerning and suggests that the IUCN maps might un-
290 derestimate the lion's distribution. On the other hand, *Leptailurus serval* and *Canis mesomelas*
291 are two of the three species that lose the higher proportion of range due to the lack of paths to
292 a herbivore, but are also some of the species with the higher proportion of GBIF occurrences
293 inside IUCN range maps (fig. 4). This indicates that the information we are missing for these
294 two species is related to either the occurrence of an interaction or the presence of interacting
295 species. To illustrate that, we mapped the GBIF data for the prey of *Leptailurus serval*, with a
296 mobility buffer around each point (fig. 5). When considering GBIF data, approximately 42% of
297 the prey's occurrences are within the portion of the serval's range that was lost. With the buffer
298 area, this corresponds to 15% of the lost range. This means that by adding GBIF information,

299 we would reduce the loss of range (or information) for the predator by 15% since its distribution
300 is conditional on the occurrence of its preys.

301 [Figure 5 about here.]

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

309 **Next steps**

310 Here we demonstrated how we can detect uncertainty in species distribution data using ecolog-
311 ical interactions. Knowing where questionable occurrence data are can be crucial in ecological
312 modelling (Hortal 2008; Ladle and Hortal 2013), and accounting for these errors can improve
313 model outputs by diminishing the error propagation (Draper 1995). For instance, we believe
314 this is a way to account for ecological interactions in habitat suitability models without making
315 the models more complex, but by making sure (not assuming) that the input data - the species
316 occurrence - actually accounts for ecological interactions. It is important to notice, however,
317 that the quality and usefulness of this method are highly correlated with the amount and quality
318 of data available about species' occurrences **and** interactions. With this paper, we hope to add
319 to the collective effort to decode the encrypted message that is the occurrence of a species in
320 space and time. A promising avenue that adds to our method is the prediction of networks and
321 interactions in large scales (Strydom et al. 2021; Windsor et al. 2022), for they can add valu-
322 able information about ecological interactions where they are missing. Additionally, in order to
323 achieve a robust modelling framework towards actual species distribution models we should in-
324 vest in efforts to collect and combine open data on species occurrence and interactions (Windsor

325 et al. 2022), especially because we may be losing ecological interactions at least as fast as we
326 are losing species (Valiente-Banuet et al. 2015).

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Figure 1

Geographical distribution of species richness and removal of predators.

(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.

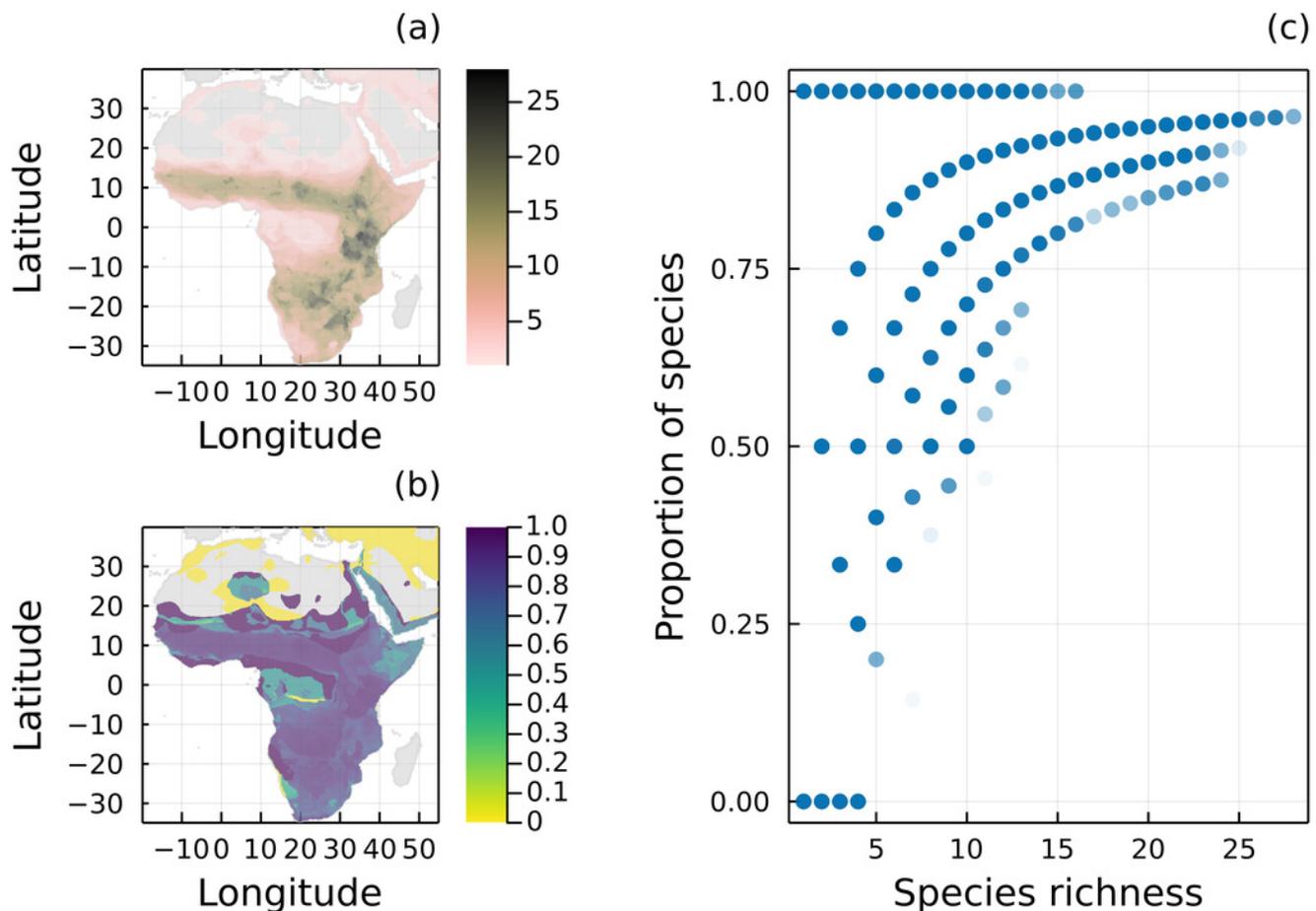


Figure 2

Relationship between the number of preys of each predator and their relative range loss.

Negative relationship between the out degree of predator species and their relative range loss. More specialized predators lose a higher proportion of their ranges due to mismatches with the ranges of their preys.

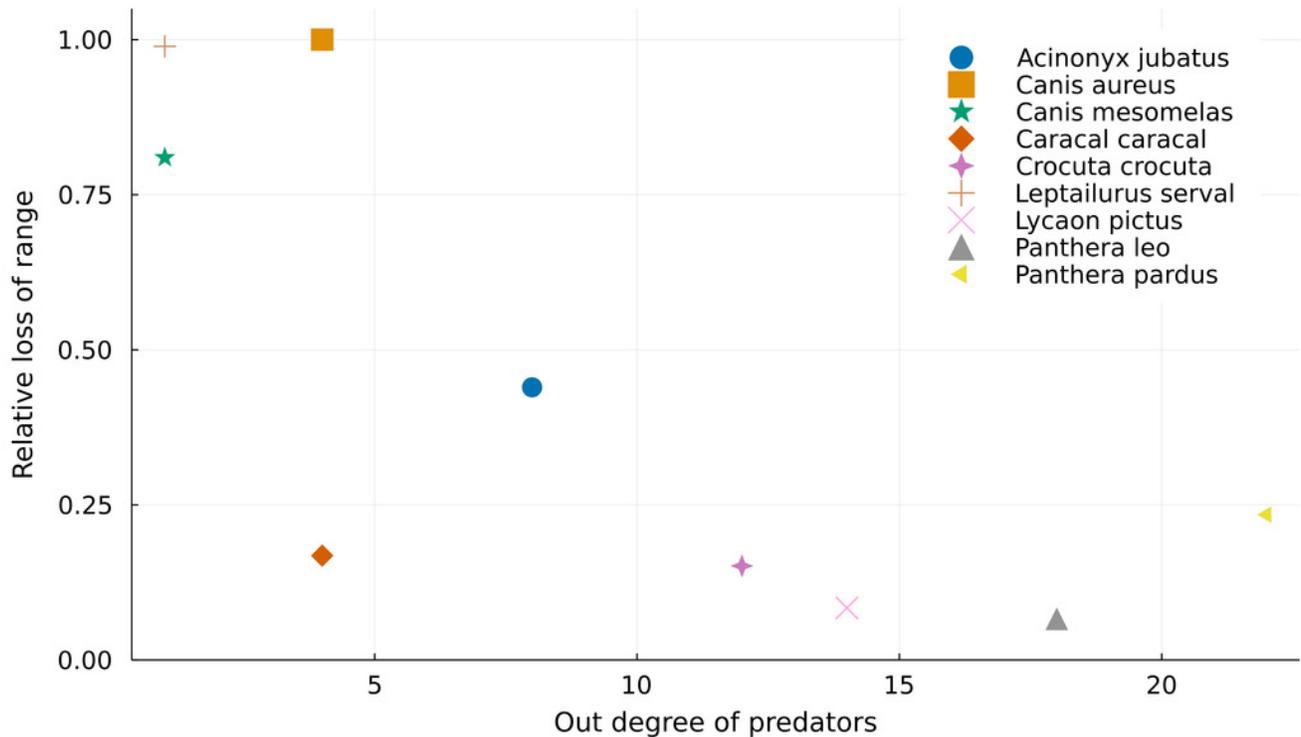


Figure 3

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.

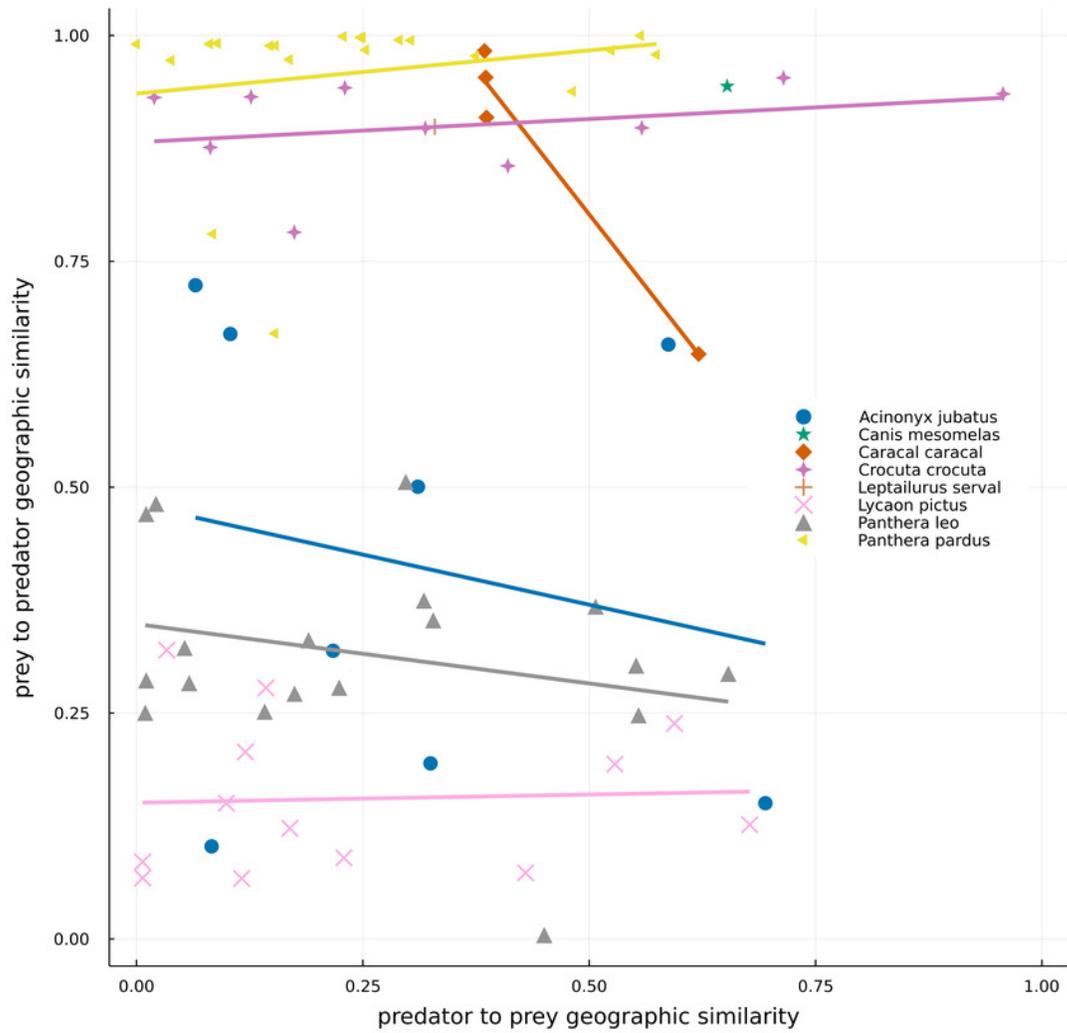


Figure 4

Distribution of GBIF and IUCN mismatch between different range sizes.

Left panel: Distribution of the proportion of GBIF pixels (pixels with at least one occurrence in GBIF) falling into the IUCN range for different range sizes. Right panel: Differences between the proportion of GBIF pixels falling into the IUCN and the updated ranges for every predator species. Arrows go from the proportion inside the original range to the proportion inside the updated 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 10 arc-minutes.

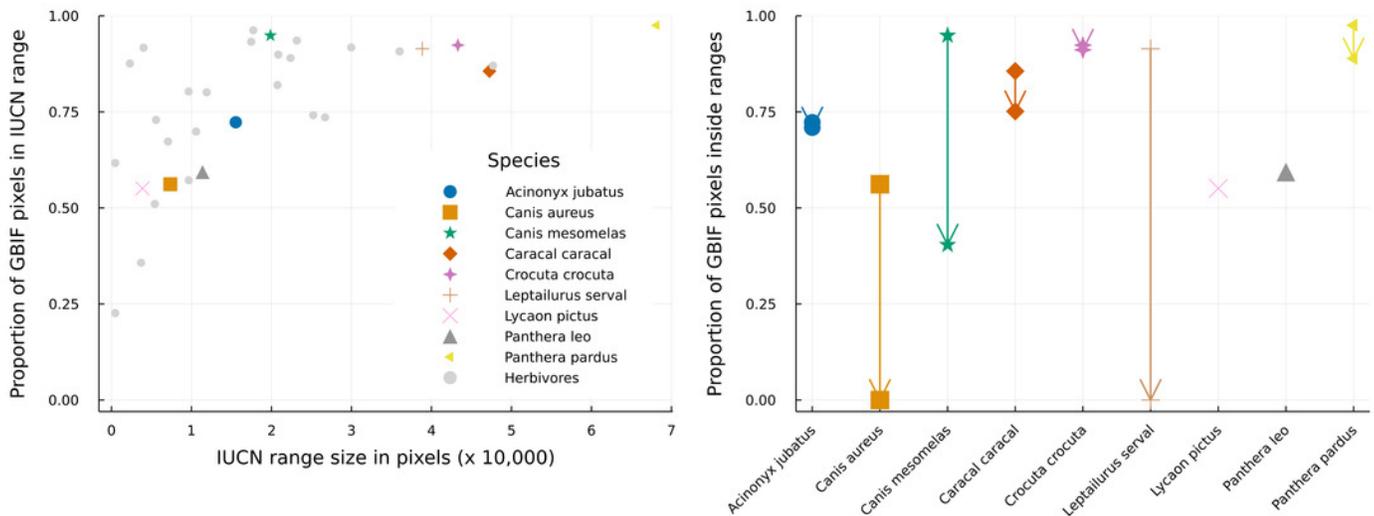


Figure 5

Comparison between the serval's IUCN range loss and its mismatch with GBIF data.

Mismatch between serval's range loss and GBIF occurrence of its prey. The left panel shows the reduction of serval's range when we consider the IUCN data on 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.

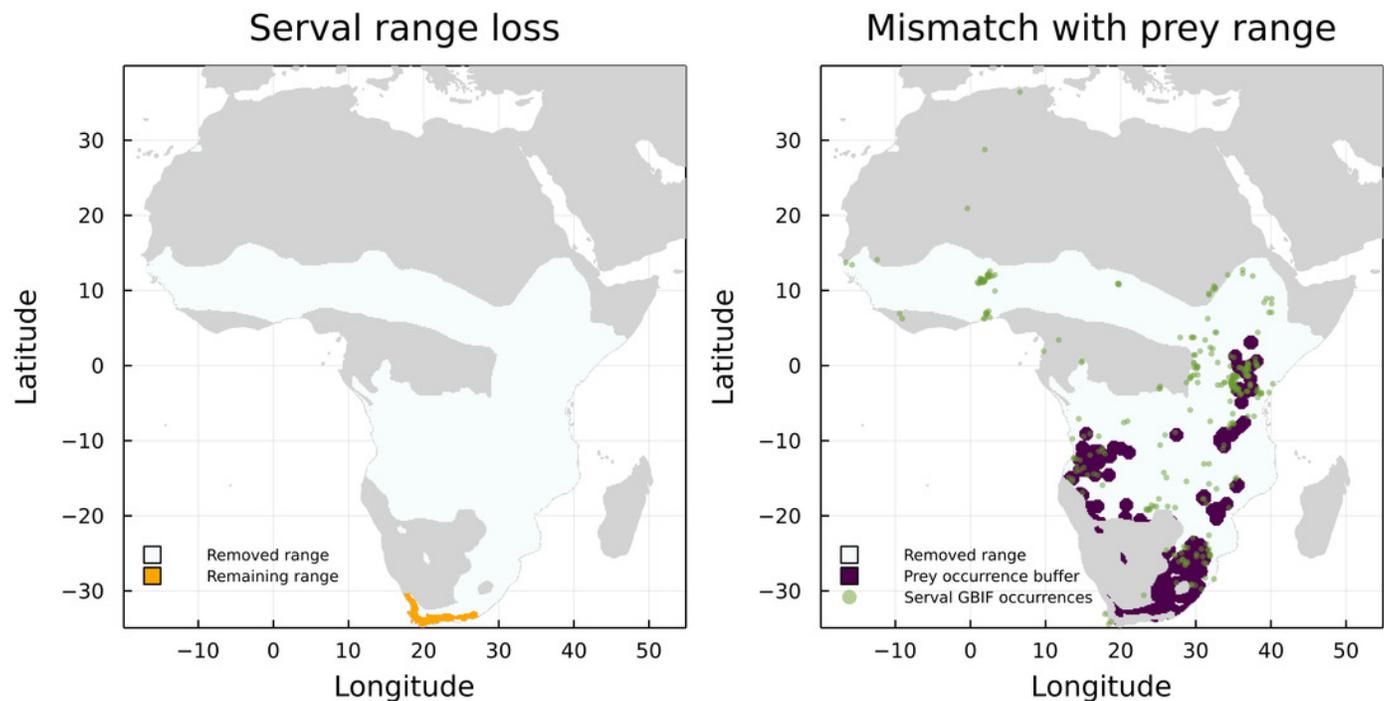


Table 1 (on next page)

List of species in the network, their ranges, degrees and overlap with prey's ranges.

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
Large carnivores					
Acinonyx jubatus	8	1	15540	0.560	0.670
Crocuta crocuta	12	1	43307	0.848	0.252
Lycaon pictus	14	0	3873	0.916	-
Panthera leo	18	0	11384	0.934	-
Panthera pardus	22	0	68137	0.766	-
Small carnivores					
Canis aureus	4	1	7358	0.000	0.780
Canis mesomelas	1	1	19872	0.190	0.995
Caracal caracal	4	0	47243	0.832	-
Leptailurus serval	1	1	38856	0.011	0.979
Small herbivores					
Damaliscus lunatus	0	4	5567	-	1
Hippopotamus amphibius	0	0	3695	-	-
Kobus ellipsiprymnus	0	4	26705	-	1
Ourebia ourebi	0	5	22380	-	1
Pedetes capensis	0	2	11901	-	1
Phacochoerus africanus	0	5	29963	-	0.999
Redunca redunca	0	5	17465	-	1
Rhabdomys pumilio	0	5	465	-	0.998
Tragelaphus oryx	0	2	20852	-	0.991
Tragelaphus scriptus	0	3	36011	-	0.984

Large grazers

Aepyceros melampus	0	5	10579	-	1
Alcelaphus buselaphus	0	4	20761	-	1
Connochaetes taurinus	0	6	9650	-	1
Equus quagga	0	5	7070	-	1
Eudorcas thomsonii	0	6	463	-	1
Nanger granti	0	6	2303	-	1

Hyraxes

Heterohyrax brucei	0	1	17728	-	0.972
Procavia capensis	0	1	47697	-	0.647

Others

Giraffa camelopardalis	0	1	5418	-	0.470
Loxodonta africana	0	0	9654	-	-
Madoqua kirkii	0	7	4002	-	1
Papio anubis	0	1	23171	-	0.938
Syncerus caffer	0	1	25223	-	0.250