Supplementary Information

Overcoming the disconnect between interaction networks and biodiversity conservation and management

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Extended methods

Our study was focused on all terrestrial tetrapods present across all European countries, Turkey, Georgia and European Russia (hereafter 'Europe'), for which we had information on potential prey, habitat preferences and geographical distribution. This information was summarised into four different matrices (the metaweb, species x habitat, pixel x habitats and pixel x species matrices), which we detail separately before explaining how local networks were calculated across Europe, the scenarios climate change and IUCN extinctions, and the workflow of our simulation experiment – available in CeresBarros/TrophicNetRobWF (Barros, 2024b) with accompanying data hosted at Zenodo (Barros, 2024a), and accessed automatically during the workflow. All analyses were done at 10 Km^2 resolution.

The metaweb – potential trophic interactions between all pan-European vertebrates

A trophic metaweb is a species x species square matrix containing all potential binary trophic interactions between *n* rows of prey and *n* columns of predators, *n* being the number of vertebrate species. We used the metaweb by Maiorano et al. (2020) and adapted it for the purpose of this work. This metaweb contains binary information on potential pairwise trophic interactions between 1151 tetrapods per life stage (juvenile, adult and carrion, with carrion life stages only being prey) plus whether they consume any of 11 diet categories (Algae, Mosses/Lichens, Mushrooms, Fruits, Grains/Nuts/Seeds, Other Plant Parts, Insects, Fish, Domestic Animals, Faeces and Detritus), collected from available literature and expert knowledge on species' feeding ecology.

From this initial metaweb, we excluded species that had a large enough geographical distribution (at least 20 pixels at 10km scale). Links between juvenile reptiles and diet categories (DC) were ignored if not present in the adult diet; for birds and mammals, links with DC were removed if the species' diet was composed of <50% of non-vertebrate items and fish (with reference to EltonTraits 1.0 diet categories; Wilman et al., 2014). This resulted in a total of 94 species being considered exclusively as carnivores (0 amphibians, 42 birds, 19 mammals and 33 reptiles). Links with carrion life stages were removed for all amphibian and reptile species, under the assumption that these species either rely on DC items or actively hunt. For birds and mammals, links with carrion life stages were kept for species that relied on scavenging for ≥50% of their diet (with reference to EltonTraits 1.0), resulting in a total of 7 scavengers. All life stages were later collapsed by species into a binary matrix.

We are aware that the thresholds we used to filter species dietary requirements are arbitrary. Unfortunately, it was not possible to obtain information on the proportion of tetrapod vertebrate items required to ensure the survival of the >1000 species in our metaweb. Hence, we opted to use a neutral threshold of 50% that does not assume a species to be more or less dependent on terrestrial vertebrates than on other dietary items.

Our (filtered) metaweb was then comprised of 1099 species (91 amphibians, 504 birds, 283 mammals and 221 reptiles) plus the initial 11 DC. Diet categories never prey on any species or other DC, and so zeros were assigned to all DC columns.

Regional species x habitat matrix – species' habitat preferences

Species' habitat preferences were obtained from Maiorano *et al.* (2013), who assigned a value of habitat suitability to each of the 46 land-cover classes from GlobCover V2.2, following expert-based knowledge and available literature. Maiorano *et al.* (2013) classified land-cover classes as 2 if they were optimal habitats for a species (i.e. where the species is able to persist), 1 if they constituted secondary habitat for the species (i.e. where the species can be present, but will not persist in the absence of optimal habitat), and 0 if they were unsuitable habitat for the species. For the present study, we considered secondary and optimal habitats equally, in order to maintain a maximum degree of potentiality in our analyses.

Table S1. *GlobCover v2.2 habitat classes and their description.*

Class	Description
40	Closed to open (>15%) broad-leaved evergreen or semi-deciduous forest (> 5m)
41	Closed (>40%) broad-leaved evergreen and/or semi-deciduous forest
50	Closed (>40%) broad-leaved deciduous forest (>5m)
60	Open (15-40%) broad-leaved deciduous forest/woodland (>5m)
70	Closed (>40%) needle-leaved evergreen forest (>5m)
90	Open (15-40%) needle-leaved deciduous or evergreen forest (>5m)
91	Open (15-40%) needle-leaved deciduous forest (>5m)
92	Open (15-40%) needle-leaved evergreen forest (>5m)
100	Closed to open (>15%) mixed broad-leaved and needle-leaved forest
101	Closed (>40%) mixed broad-leaved and needle-leaved forest
110	Mosaic forest or shrubland (50-70%) and grassland (20-50%)
130	Closed to open (>15%) (broad-leaved or needle-leaved)
131	Closed to open (>15%) broad-leaved or needle-leaved evergreen shrubland (<5m)
132	Closed to open (>15%) broad-leaved evergreen shrubland (<5m)
133	Closed to open (>15%) needle-leaved evergreen shrubland (<5m)
134	Closed to open (>15%) broad-leaved deciduous shrubland (<5m)
136	Open (15-40%) broad-leaved deciduous shrubland (<5m)
120	Mosaic grassland (50-70%) and forest or shrubland (20-50%)
140	Closed to open (>15%) herbaceous vgt (grassland)
141	Closed (>40%) grassland
144	Open (15-40%) grassland with sparse (<15%) trees or shrubs
150	Sparse (<15%) vegetation
151	Sparse (<15%) grassland
152	Sparse (<15%) shrubland

200	Bare areas
201	Consolidated bare areas (hardpans)
202	Non-consolidated bare areas (sandy desert)
203	Salt hardpans
180	Closed to open (>15%) grassland or woody vegetation on regularly flooded or waterlogged soil
185	Closed to open (>15%) grassland on regularly flooded or waterlogged soil
11	Post-flooding or irrigated croplands (or aquatic)
13	Post-flooding or irrigated herbaceous crops
14	Rainfed croplands
15	Rainfed herbaceous crops
16	Rainfed shrub or tree crops (cashcrops)
20	Mosaic cropland (50-70%) / vegetation (grassland/shrubland/forest) (20-50%)
21	Mosaic cropland (50-70%) / grassland or shrubland (20-50%)
30	Mosaic vegetation (grassland/shrubland/forest) (50-70%) / cropland (20-50%)
32	Mosaic forest (50-70%) / cropland (20-50%)
210	Water bodies
220	Permanent snow and ice
190	Artificial surfaces and associated areas (Urban areas >50%)

Pixel x habitats matrix – habitat maps

As in Maiorano *et al.* (2013), we used the GlobCover v2.2 land-cover map as the "habitats map" to build both the baseline networks and networks projected under scenarios of change. The GlobCover land-cover layer is originally at 200 m resolution and so we calculated the proportion of each a given land-cover type per 10x10 Km pixel. The final pixel x habitat matrix then contained the proportion of each land-cover class present in each 10x10 Km pixel. Any given species habitat was considered "available" if its land-cover type had > 0% cover in that pixel.

Baseline and future pixel x species matrices – species distributions

Species' geographical distributions came from species distribution model (SDMs) projections. These models aim to establish the statistical link between species' presences (and absences) and climate. Species presence/absence information was obtained from Maiorano *et al.* (2013) and rescaled from 300 m resolution to 10 Km resolution using a potential presence perspective. This is, a species was considered present in a 10 Km^2 pixel if it was detected in at least one 300 m^2 pixel of secondary or optimal habitat. After rescaling, species whose distributions were smaller than twenty 10 Km^2 pixels were excluded from further analyses, since low sample size would result in poor SDM accuracy. Baseline and future species distributions were then obtained by projecting species presences/absences in function of four bioclimatic variables from WordClim v1.4 (annual mean temperature, Bio1, temperature seasonality, Bio4, annual precipitation, Bio12, and precipitation seasonality, Bio15) at 10' resolution – available at https://www.worldclim.org/version1). These variables adequately represent dominant N-S and E-W climatic gradients in Europe and are known to directly or indirectly affect species distributions across Europe (Braga et al., 2019; Currie, 1991; Mouchet et al., 2015; Svenning et al., 2011). 'Baseline' species distributions were projected the climate normals period of 1960-1990. Future species distributions were obtained using climate projections for 2050 (average for 2041-2060), using the HadGEM2-AO global circulation model from the CMIP5 database and an extreme high emissions scenario (RCP 8.5, equivalent to CMIP6 SSP5-8.5; IPCC, 2014). Random forest models (RFs) were used to fit and predict species presences/absences as a function of the four bioclimatic variables. For each species, the model fitting and evaluation process was repeated 5 times. Each repetition was calibrated using 70% of the total presence/absence dataset and evaluated on the remaining 30% (using random data splitting). Repetitions were evaluated by calculating the TSS (true skill statistics) and the area under the curve (AUC) of the receiver operating characteristic (ROC) algorithms. TSS reflects how well the model predicts presences and absences, being calculated as the difference between the sensitivity (the ratio between true presences and predicted presences) and specificity (the ratio of true absences and predicted absences) of the model minus 1. TSS values range from -1, no agreement, to +1, perfect agreement, with 0 meaning a random fit. AUC summarises model accuracy by evaluating the rate of true presences *vs.* false absences. AUC values range from 0, all predictions are false, to 1, all predictions are true, with 0.5 indicating a random fit. Final projections were obtained using a weighted average ensemble forecasting method. This is, the final distribution of each species was built by averaging individual model replicates weighted proportionally to their TSS score. Only the replicates with TSS > 0.4 were used for ensemble forecasting, except for species B155 for which we had to lower the threshold to 0.35. A second set of ensemble projections was calculated using committee averaging (Araújo & New, 2007), but later discarded as model performance (measured by TSS and AUC scores) was worse than when using weighted averaging. Final distributions were later converted to binary values using a threshold maximizing the TSS statistics. The weighted average ensemble model fit was overall very good, with mean TSS and AUC scores across species being 0.897 (± 0.138) and 0.973 (± 0.046) respectively. All species distributions (baseline and future) were later aggregated into pixel x species binary matrices. All SDM fitting, evaluation and predictions were computed using the *biomod2 R* package (Thuiller et al., 2009).

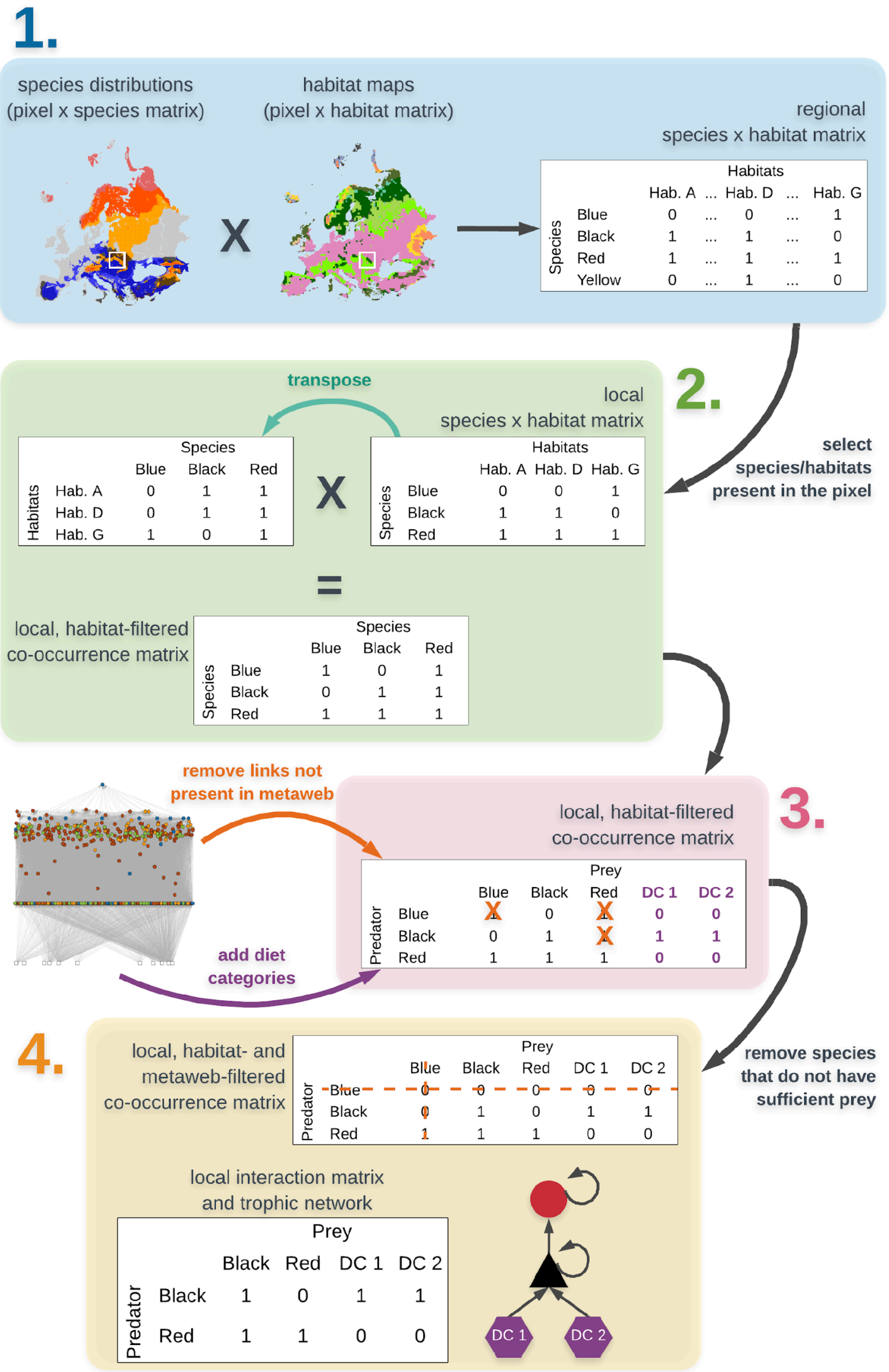
Building local networks

Local networks were built per 10 Km^2 pixel by conditioning species presences to the presences of their prey, with which they needed to share at least one common habitat type. This involved the following steps:

1. Listing the species and habitats present in the pixel, using the pixel x species and pixel x habitats matrices described above;
2. Building a local, habitat-filtered species co-occurrence matrix, by filtering the regional species x habitat matrix to the species and habitats found in 1) and then multiplying this filtered matrix by its transpose. The obtained species co-occurrence matrix is the first form of the local interaction matrix. For instance, if species 'Black' only uses

habitats ‘A’ and ‘D’ and species ‘Blue’ only uses habitat ‘G’, the two species are locally present but will not interact (Fig. S1, panel 2);

3. Building a local, habitat- and metaweb-filtered species co-occurrence matrix, by adding links between species and DC, and removing links between species that do not exist in the metaweb.
4. Building the final interaction matrix (and local trophic network), by iteratively removing species that have insufficient prey items (according to the threshold of extinction; see *Extinction thresholds and sensitivity analysis* below), since removing one prey-less species can cause another to become prey-less as well. Note that DC were ubiquitously present across the landscape.



Species	Habitats				
	Hab. A	...	Hab. D	...	Hab. G
Blue	0	...	0	...	1
Black	1	...	1	...	0
Red	1	...	1	...	1
Yellow	0	...	1	...	0

Habitats	Species		
	Blue	Black	Red
Hab. A	0	1	1
Hab. D	0	1	1
Hab. G	1	0	1

Species	Habitats		
	Hab. A	Hab. D	Hab. G
Blue	0	0	1
Black	1	1	0
Red	1	1	1

Species	Species		
	Blue	Black	Red
Blue	1	0	1
Black	0	1	1
Red	1	1	1

Predator	Prey				
	Blue	Black	Red	DC 1	DC 2
Blue	~~1~~	0	~~1~~	0	0
Black	0	1	~~1~~	1	1
Red	1	1	1	0	0

Predator	Prey				
	~~Blue~~	Black	Red	DC 1	DC 2
~~Blue~~	~~0~~	~~0~~	~~0~~	~~0~~	~~0~~
Black	~~0~~	1	0	1	1
Red	~~1~~	1	1	0	0

Predator	Prey			
	Black	Red	DC 1	DC 2
Black	1	0	1	1
Red	1	1	0	0

Figure S1. *Building local trophic networks. Schematic representation of the four steps involved in building local trophic networks at 10 Km*^{2} *resolution, based on species distributions, species habitat preferences and habitat maps, and the metaweb. Note that the pixel representation is not to scale and that transparent areas in maps represent areas excluded from the analyses (e.g. large lakes, the Black Sea).*

A first set of baseline networks was calculated based on baseline species distributions and assuming that a species only required one prey item to colonise a given pixel ('no threshold of extinction'). This resulted in a total of 972 species across all local networks, 86 amphibians, 478 birds, 261 mammals and 147 reptiles. However, assuming that all species only require one prey item is quite unrealistic, so we re-built baseline networks by constraining species presences with a minimum number of prey defined on a species-by-species basis, i.e. species-specific 'extinction thresholds'. These extinction thresholds were obtained by calculating the 10% quantile value of each species' prey distributions – the distribution of the number of prey across all baseline networks built without a threshold of extinction. The quantile value of 10% was chosen based on a sensitivity analysis (see *Extinction thresholds and sensitivity analysis* below). By using the same percentile across species, we assumed all species required the same proportion of their dietary niche to survive. Although it can be argued that specialist species require larger proportions of their dietary niche than generalist species, a constant threshold ensured that we did not select against specialist species when building our baseline networks. The total numbers of species, amphibians, birds, mammals and reptiles did not change after imposing the threshold on baseline networks.

Calculating robustness of European trophic networks to scenarios of change

We explored the robustness of the baseline networks to two extreme scenarios of change: climate change under a high emissions scenario (climate change scenario) and the loss of all Critically Endangered, Endangered and Vulnerable species across Europe (IUCN extinctions scenario). For the climate change scenario, we rebuilt all trophic webs using future species occurrences obtained from SDM projections using climate projections for 2050 (see *Baseline and future pixel x species matrices – species geographical distributions* above). For the IUCN extinctions scenario, all species that whose IUCN status was Critically Endangered, Endangered or Vulnerable were removed from their entire range.

For each scenario, we recalculated all trophic networks using the same species-specific minimum prey thresholds used for calculating baseline networks. This way, we guaranteed that changes in species composition were only due to climate effects or targeted species removals, rather than changes in species minimum dietary requirements. Species were then considered primarily extinct if they were predicted to be absent from a pixel due to future climatic conditions (i.e. range changes), and secondarily extinct when they could be present in terms of climate and habitat suitability but had too few prey items. Note that basal species (species that feed only on DC) could not go secondarily extinct as DC were ubiquitous and unchangeable across Europe. Network robustness was then measured as:

$$Robustness = 1 - \frac{no.\ secondary\ extinctions}{initial\ no.\ secondary\ consumers} \quad \text{(Eq. 1)}$$

where *no. sec. extinctions* is the number of secondary extinctions and the *initial no. secondary consumers* is the number of secondary consumers present in the baseline network (which can be calculated as network species richness minus the number of basal species). Robustness values were bound between 0 (complete loss of secondary species, no robustness) and 1 (no secondary extinctions, highest robustness).

Extinction thresholds and sensitivity analysis

We tested the sensitivity of baseline networks properties to changes in quantile values of the extinction thresholds. After calculating all baseline networks assuming a conservative approach (i.e. a species was present in a local network as long as it had at least one prey item), we extracted the distribution of the number of prey items across pixels for each species (‘species prey distributions’). We then calculated the minimum, median and 10%, 25%, 75% and 90% quantile values of number of prey items from each species prey distribution and re-built all baseline local networks using these values as species-specific extinction thresholds.

Using a threshold equal to the minimum number of prey per species did not cause baseline networks to change, as would be expected. Increasing this threshold to the 10% quantile value caused relatively small changes in the distribution of network properties, and thresholds equal to or larger than the 25% quantile values caused large changes to baseline network properties (Fig. S2). Quantile values above 25% also resulted in a large loss of analysable networks because they became disconnected, which rendered link-based network properties meaningless. Hence, we chose to use the 10% quantile for our simulations, since it provided a more realistic representation of species abilities to survive in a given pixel, relatively to assuming that all species survive with at least one prey item, without significantly disrupting baseline networks.

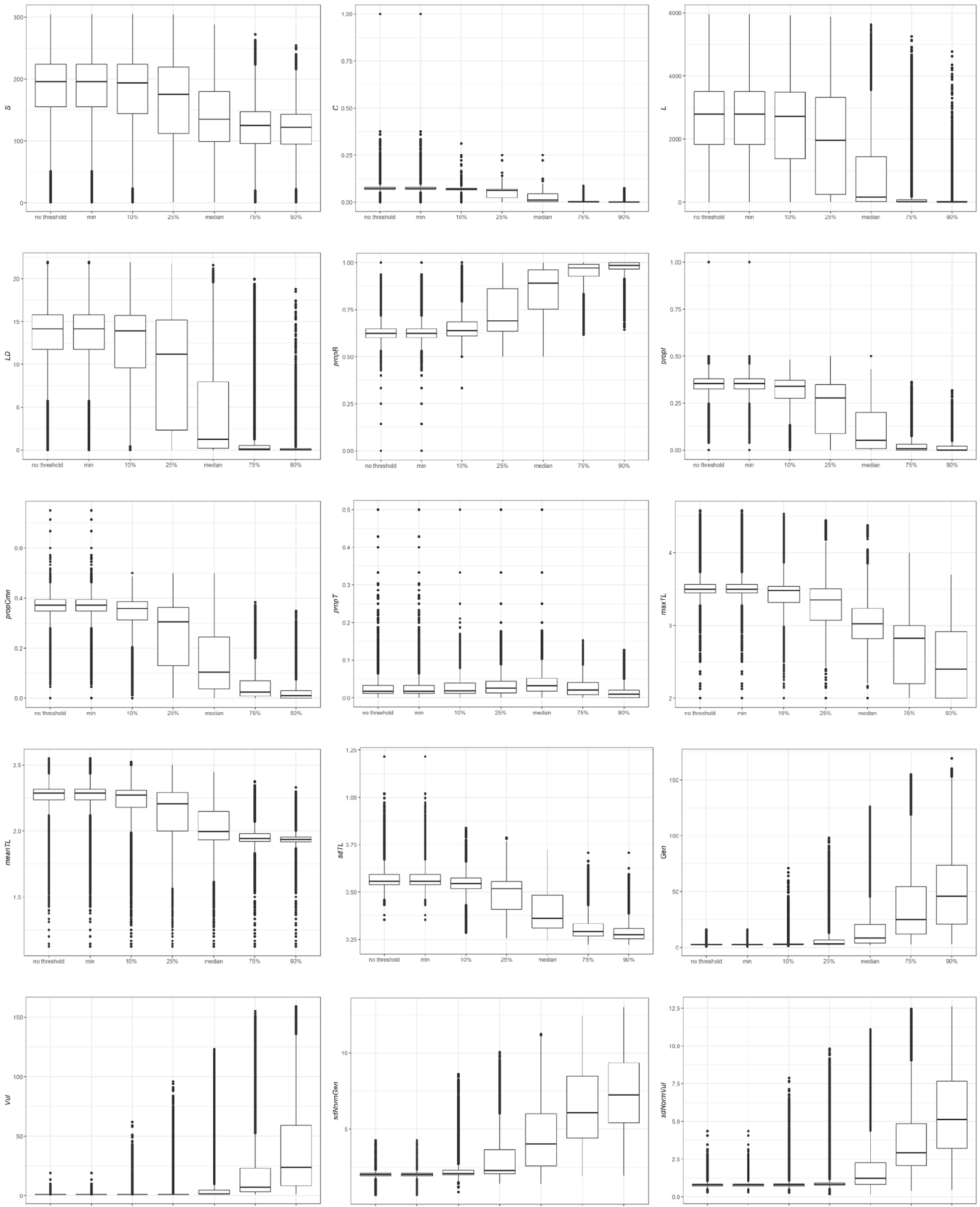


Figure S2. *Sensitivity analysis of baseline network properties to changing species' quantile thresholds of no. of prey. Thresholds were calculated per species as the mininum, median and 10%, 25%, 75% and 90% quantile values of the distribution of number of prey items across all baseline networks built using a conservative approach (i.e. species only required one prey item – 'no threshold' – to be present in a given pixel's network). See Table S2 for the list of abbreviations of network properties.*

Table S2. *List of baseline network properties measured, their abbreviations and, where appropriate, formulas for their calculation. Omnivory was calculated as the proportion of omnivore species, with omnivore species being those whose prey differed in trophic level. Trophic levels were calculated based on prey-averaged trophic levels, using the PreyAveragedTrophicLevel function available in the cheddar R package.*

Network property	Abbreviation
Species richness (= number of nodes)	*S*
Number of links	*L*
Link density	*LD*
Connectance (L/S^2)	*C*
Standard deviation generality (normalised by LD)§	*sdNormGen*
Standard deviation vulnerability (normalised by LD)§	*sdNormVul*
Proportion of basal species (species with no vertebrate prey)	*propB*
Proportion of intermediate species	*propI*
Proportion of top species (species with no predators)	*propT*
Omnivory	*propOmn*
Mean trophic level	*meanTL*
Maximum trophic level	*maxTL*
Standard deviation of trophic level	*sdTL*

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