Supplementary information

Ecological network complexity scales with area

In the format provided by the authors and unedited

SUPPLEMENTARY INFORMATION:

Ecological network complexity scales with area

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Supplementary Text 1. Dataset specification. Description of different aspects of the datasets used to build networks across spatial scales (i.e. Network-Area Relationships), including locations, area sizes, and sampling methodologies. Datasets are presented grouped into the spatial categories used in the main text: regional and biogeographical. The name that has been assigned to each dataset is given in brackets and that will be used in the appendices which follow.

REGIONAL SPATIAL DOMAIN

1-3. Plant-pollinator and host-parasite interaction networks in Mediterranean scrubland in the Garraf Natural Park, Catalunya, Spain. (Garraf PP, Garraf PP2, Garraf HP)

Three independent datasets were collected within this same area. These are identified by numbers in each section. 1 & 2 = Plant-pollinator networks, $3 =$ Host-parasite networks.

- **Study area:** Garraf Natural Park, Catalunya, Spain
- **Interaction types:** Plant-pollinator and host-parasite (Cavity-nesting bee/wasps and their cleptoparasites, parasitoids and nest predators) interactions.
- **Type of system:** Mediterranean scrubland.
- **Number and extent of replicated patches:**

1) 40 local patches of the same size (40x30 m) within a homogeneous landscape connected through dispersal. Total area: 40 km^2 . Distance between patches: 520 to 1440 m.

2) 21 local patches of the same size (40x40 m) within a homogeneous landscape connected through dispersal. Total area: 32 km^2 . Distance between patches: 585 to 1345 m.

3) 25 local patches. Total area: 33 km². Distance between patches: 585 to 1354 m.

- **Number of networks:** 1 plant-pollinator or 1 host-parasitoid network per patch. This yields a total of 86 networks
- **Type of networks:** Bipartite.
- **Taxonomic resolution of the nodes:** Species level.
- **Total number of species and links at the regional scale:**

1) 170 pollinator and 24 plant species. 3577 individual contacts spread across a total of 325 interspecific interactions.

2) 303 pollinator and 23 plant species. However, information on interactions available only for 200 species. 900 interactions.

3) 41 host and 26 parasite species. 654 individuals parasitized spread across a total 72 interspecific interactions.

• **Sampling procedure (of species and interactions):**

Plant-pollinator interactions:

1) Counted number of visits per open flower by each pollinator species.

2) Sampled pollinator and plant species. Interactions inferred from interactions observed during four years in other plots within the same landscape.

Host-parasite interactions:

3) Nests of bees and wasps collected with trap-nests. Hosts and parasites reared from each nest. Interactions quantified as the number of cells of each host species attacked by each parasite species.

Publication references:

1) Reverté S., Bosch J., Arnan X., Roslin T., Stefanescu C., Calleja J. A., Molowny-Horas R., Hernández-Castellano C., Rodrigo A. 2019. Spatial variability in a plant-pollinator community across a continuous habitat: high heterogeneity in the face of apparent uniformity. *Ecography* 42: 1–11, 2019. doi: 10.1111/ecog.04498

2) Unpublished.

3) A. Torné-Noguera, X. Arnan, A. Rodrigo, J. Bosch. 2020. Spatial variability of hosts, parasitoids and their interactions across a homogeneous landscape. *Ecology & Evolution* 10: 3696-3705.

4. Host-parasite interaction networks within a mosaic of forest/agricultural landscape in Olot, Catalunya, Spain. (Olot)

- **Study area:** Olot, Catalunya, Spain
- **Interaction types:** Host-parasite (Cavity-nesting bee/wasps and their associated parasites) interactions
- **Type of system:** Mosaic landscape of mixed forest and extensive agricultural land
- Number and extent of replicated patches: 14 local patches. Total area: 100 km². Distance between patches 1.4 to 13 km.
- **Number of networks:** 1 host-parasite network per patch. This yields a total of 14 networks
- **Type of networks:** Bipartite
- **Taxonomic resolution of the nodes:** Species level.
- **Total number of species and links at the regional scale:** 29 host and 20 parasitoid species. 1695 contacts (cells parasitized) spread across a total of 80 inter-specific interactions.

• **Sampling procedure (of species and interactions):** Nests of bees and wasps collected with trapnests. Hosts and parasites reared from each nest. Interactions quantified as the number of cells of each host species attacked by each parasite species.

Publication reference:

S. Osorio, X. Arnan, E. Bassols, N. Vicens, J. Bosch. 2015. Local and landscape effects in a host–parasitoid interaction network along a forest–cropland gradient. *Ecological Applications* 25: 1869–1879.

5. Plant-pollinator interaction networks within dense forest in Montseny Natural Park, Catalunya, Spain. (Montseny)

- **Study area:** Montseny Natural Park, Catalunya, Spain
- **Interaction types:** Plant-pollinator interactions
- **Type of system:** Local patches (clearings) within a dense forest matrix
- **Number and extent of replicated patches:** 18 local patches of the same size (25x25 m). Total area: 18.7 km². Distance between patches 550 to 2050 m.
- **Number of networks:** 1 plant-pollinator network per patch. This yields a total of 18 networks
- **Type of networks:** Bipartite.
- **Taxonomic resolution of the nodes:** Species level.
- **Total number of species and links at the regional scale:** 194 pollinator and 61 plant species. 8605 individual flower visits distributed among a total 873 unique inter-specific interactions.
- **Sampling procedure (of species and interactions):** Counted number of visits per open flower by each pollinator species.
- **Publication reference:** C. Hernández-Castellano, A. Rodrigo, J. M. Gómez, C. Stefanescu, J. A. Calleja, S. Reverté, J. Bosch. 2020. A new native plant in the neighborhood: effects on plantpollinator networks, pollination and plant reproductive success. *Ecology* doi.org/10.1002/ecy.3046

6. Plant-pollinator networks in Nahuel Huapi National Park, Argentina. (Nahuel)

- **Study area:** Nahuel Huapi National Park and surrounding areas in Neuquén and Río Negro provinces, Argentina
- **Interaction types:** Plant-pollinator interactions (flower visits).
- **Type of system:** Eight sites with native temperate forest, four grazed with domestic cattle and four ungrazed, located in an area of ca. 20x50 km.
- **Number and extent of replicated patches:** Eight sites of 6-12 ha.
- **Number of networks:** 8, one per site.
- **Type of networks:** Bipartite
- **Taxonomic resolution of the nodes:** Species level
- **Total number of species and links at the regional scale:** 14 plants, 90 pollinators, 164 links, 5285 flower visits.
- Sampling procedure (of species and interactions): Data were collected throughout one flowering season, with weekly sampling of each site (a pair of sites per day), with multiple 5 min observation periods per site and date. Interactions were determined by observed visits to flowers. Links are quantified as the total number of visits recorded in the study.
- **Publication reference:** Vázquez, D. P. & Simberloff, D. 2003. Changes in interaction biodiversity induced by an introduced ungulate Ecology Letters, 6, 1077-1083

7. Trophic marine intertidal networks in the Sanak Archipelago, Alaska. (Sanak)

- **Study area:** The Sanak Archipelago lies in the Eastern Aleutian Islands, south of the Alaska Peninsula, in the North Pacific Ocean.
- **Interaction types:** Trophic interactions.
- **Type of system:** The coastline contains a mix of semi-exposed rocky intertidal habitats interspersed with protected sedimented and boulderstrewn shores.
- **Number and extent of replicated patches:** The data used consists of 339 quadrants of 0.25m² along 39 transects that were laid across the intertidal zones around the Sanak Islands. Transects spanned the entire intertidal zone, and were placed perpendicular to the shoreline at 300m intervals.
- **Number of networks:** 1 food web per quadrant (i.e. 339 local food webs).
- **Type of networks:** Food webs.
- **Taxonomic resolution of the nodes:** Nodes span the entire range from species to phyla. Taxa were identified to the lowest possible resolution in the field. Some taxa were lumped into groups.
- **Total number of species and links at the regional scale:** 100 species and 502 links.
- **Sampling procedure (of species and interactions):** direct observation of the species presences. To determine interactions between species, mixture of direct observation, gut content analysis, stable isotope analysis, literature searches and discussion with experts.
- **Publication reference:** Wood, S. A., Russell, R., Hanson, D., Williams, R. J., & Dunne, J. A. (2015). Effects of spatial scale of sampling on food web structure. *Ecology and evolution*, *5*(17), 3769-3782.

8. Trophic marine intertidal networks in the Bristol Channel, UK. (Bristol)

- **Study area:** Four study sites composed by archipelagos of salt marsh islands located in the intertidal mudflats along the Bristol Channel in the southwest of England.
- **Interaction types:** Plant-pollinator, plant-herbivore, predator-prey interactions.
- **Type of system:** salt marsh islands located in four archipelagos on intertidal mudflats.
- **Number and extent of replicated patches:** 39 small salt marsh islands of $0.2-2$ m² in size. Larger islands were excluded to be able to treat the data as replicates of the same size.
- **Number of networks:** 1 food web per island (i.e. 39 food webs)
- **Type of networks:** Food webs.
- **Taxonomic resolution of the nodes:** Species level.
- **Total number of species and links at the regional scale:** 57 species and 175 links.
- **Sampling procedure (of species and interactions):** direct observation of the species presences. To determine interactions between species, mixture of direct observation, gut content analysis, stable isotope analysis, literature searches and discussion with experts.
- **Publication reference:** Montoya, D., Yallop, M. L., & Memmott, J. (2015). Functional group diversity increases with modularity in complex food webs. *Nature communications*, *6*, 7379.

9. Host-specific gallers and leaf-miners in pedunculate oaks in Finland. (Quercus)

- **Study area:** natural communities of specialist insect-herbivores and their natural enemies on the pedunculate oak, *Quercus robur* in the southwest coast of Finland.
- **Interaction types:** Host-parasitoid interactions (host-specific gallers and leaf-miners in pedunculate oaks)
- **Type of system:** Naturally fragmented landscape of oak trees in the archipelago of SW Finland.
- **Number and extent of replicated patches:** 22 oak trees.
- **Number of networks:** 1 per tree (i.e. 22 networks).
- **Type of networks:** Bipartite.
- **Taxonomic resolution of the nodes:** Species level.
- **Total number of species and links at the regional scale:** 85 species and 135 links.
- **Sampling procedure (of species and interactions):** sampling was conducted three times in 2006: in May-June, in late July, and in September in 2006. During each sampling event, a standardized volume of foliage (30 half-meter branches per tree) was collected with the aid of a pole pruner, and all galls and leaf-mines present were recorded. Interactions were quantified by rearing of predators.
- **Publication reference:** Kaartinen, R., & Roslin, T. (2011). Shrinking by numbers: landscape context affects the species composition but not the quantitative structure of local food webs. *Journal of Animal Ecology*, *80*(3), 622-631.

10-16. Soil food webs (Soil 1-7)

- **Study area:** managed agroecosystems on sandy soils across The Netherlands. Seven independent datasets were collected within this same area.
- **Interaction types:** Trophic interactions.
- **Type of system:**
	- 19 Scots pine forests, used for traditional agroforestry.
	- 10 certified organic grasslands (including mixed and bio-dynamic regimes), using compost/farmyard manure and no biocides, averaging 60 ha.
	- 19 conventional farms, using mineral fertilisers, with a much smaller amount of farmyard manure, averaging 45 ha.
	- 20 semi-intensive farms, using both organic and mineral fertilisers, averaging 25 ha.
	- 19 intensive farms, using biocides and fertilisers, averaging 20 ha.
	- 28 multi-cropping fields, averaging 63 ha.
	- 10 abandoned meadows.
- **Number and extent of replicated patches:** see above.
- **Number of networks:** 1 network per site: 125 networks.
- **Type of networks:** Soil food webs.
- **Taxonomic resolution of the nodes:** genus level.
- **Total number of species and links at the regional scale:**
	- 130 species; 2647 links
	- 181 species; 5174 links
	- 136 species; 3609 links
	- 144 species; 3888 links
	- 103 species; 2177 links
	- 101 species; 2002 links
	- 102 species; 2044 links

• **Sampling procedure (of species and interactions):**

Microarthropods were collected in a randomized block design and their four-fold cores (diameter 5.8×5 cm) were kept separate until behavioural extraction using the Tullgren high-gradient canister method with a low wattage bulb.

Enchytraeids were sampled using six-fold cores (diameter 5.8×15 cm, 6 rings of 2.5 cm height each), extracted using wet funnel extraction, identified, measured and counted. Lumbricids were recovered manually, identified, weighted and counted.

Nematodes were extracted from 100 g soil using elutriation, sieving and cottonwool extraction. All individuals within two clean 10 ml water suspensions were screened, counted with a stereomicroscope and fixed in 4% formaldehyde. Per sample, at least 150 individuals were identified at genus level by light microscopy (400–600×) and assigned to feeding habits.

Soil community structure was described using food-web data with M (dry body mass in μ g), N (*animals/m²*) and *B* (dry biomass in μ g/ m^2 , i.e. $\log(B) = \log(N) + \log(M)$). A guild-lumped web was established for each site by taking the sub-predation-matrix determined by the trophic guilds that were present. The presence or absence, but not the quantitative extent, of consumer–resource links was established using additional information from the literature.

• **Publication reference:** Mulder C, Den Hollander HA, Hendriks AJ (2008) Aboveground herbivory shapes the biomass distribution and flux of soil invertebrates. PLoS ONE 3(10): e3573. https://doi.org/10.1371/journal.pone.0003573

17-18. Plant-pollinator and host-parasitoid interaction networks on fragmented calcareous grasslands of Germany. (Gottin PP, Gottin HP)

Two independent datasets were collected within this same area.

- **Study area:** Göttingen, central Germany
- **Interaction types:** Plant-pollinator and host-parasitoid interactions
- **Type of system:** Calcareous grassland. Semi-natural habitat of high conservation value due to their high biodiversity (plants and insects in particular). These grasslands are heavily fragmented due to agricultural landscape simplification and intensification.
- **Number and extent of fragments:** 11 fragments. Area size of fragments ranged from 314–1,133 m². Extra available sites of varying sizes were excluded to be able to treat the data as replicates of the same size.
- **Number of networks:** 1 plant-pollinator and 1 host-parasitoid network per fragment. This yields a total of 22 networks.
- **Type of networks:** Bipartite
- **Taxonomic resolution of the nodes:** Species level in most cases (some hosts or parasitoids identified to genus level and then assigned to morphospecies).
- **Total number of species and links at the regional scale:** 227 plant-pollinator interactions among 119 species. 55 host-parasitoid interactions among 48 parasitoid species.
- **Sampling procedure (of species and interactions):**

Plant-pollinator networks: Flower visitors (wild bees and hoverflies; assumed to be pollinators of visited plants) were sampled via four five-minute-transect walks six times from April to September 2004 within a 4 m corridor. Data from the 5-min-transects of all six sampling events were pooled per grassland fragment. Specimens were either identified on the wing or caught with a net and identified in the lab. The plant species visited was recorded for each specimen.

Host-parasitoid networks: Parasitoids/parasites and hosts were sampled using trap nests at the same sites. Trap nests consisted of bundles of reed internodes of common reed *Phragmites australis* (about 150–180 reed internodes of 2–10 mm diameter in plastic tubes of 10 cm diameter per trap nest) exposed at a height of 100–120 cm. Depending on the fragment size, 4–6 wooden posts with 2 trap nests each were used: 4 posts (8 trap nests) in 11 small fragments, 5 posts (10 trap nests) in 13 medium fragments, 6 posts (12 trap nests) in eight large fragments. The trap nests were spread regularly over study sites and exposed at the beginning of the flowering period (mid-April) until autumn (beginning October). Afterwards, trap nests were stored in a climate chamber at 4°C and occupied reed internodes were opened. For each nest, the number of brood cells and number of parasitized cells were recorded. We identified host and parasitoid identities to genus or species level as far as possible using larvae and nest characteristics. Because *Osmia rufa* overwinter as adults, these cocoons were opened to check for parasitoids. All other nests were stored separately in test tubes closed with a wad of cotton wool. Tubes were exposed to room temperature (ca. 20°C) to end diapause. Reared adults were identified to species level.

• **Publication reference:** Grass, I., Jauker, B., Steffan-Dewenter, I., Tscharntke, T., & Jauker, F. (2018). Past and potential future effects of habitat fragmentation on structure and stability of plant–pollinator and host–parasitoid networks. *Nature ecology & evolution*, 1.

19. Plant-leafminer-parasitoid networks from central Argentina. (Chaco)

- **Study area:** Chaco Serrano District in Argentina, belonging to the most extensive dry forest in South America. The characteristic vegetation is low, open woodland, with a tree layer, shrubs, herbs and grasses, and many vines and epiphytic bromeliads.
- **Interaction types:** Plant-herbivore-parasitoid interactions
- **Type of system:** Woodland sites in a fragmented semi-natural landscape. The woodlands are mainly used for cattle grazing, and are embedded in an agricultural matrix largely dominated by wheat in winter and soy or maize in summer.
- **Number and extent of sites:** 12 woodland sites ranging in area size from 0.13ha to 3.58ha. Extra available sites of varying sizes were excluded to be able to treat the data as replicates of the same size.
- **Number of networks:** 12 networks, one per site.
- **Type of networks:** Unipartite.
- **Taxonomic resolution of the nodes:** Species level.
- **Total number of species and links at the regional scale:** 349 species and 753 links.
- **Sampling procedure (of species and interactions):** At each site, all mined leaves detected were collected along five 50 long, 2 m wide and 2 m high transects (100 m2) in two occasions (November-December 2002 and February-March 2003) within peak period of leafminer activity. Mined leaves were taken to the laboratory and reared adult leafminers and parasitoids, which were identified and counted.

• **Publication reference:** Cagnolo, L., Salvo, A., & Valladares, G. (2011). Network topology: Patterns and mechanisms in plant-herbivore and host-parasitoid food webs. *Journal of Animal Ecology, 80*(2), 342-351. Retrieved from http://www.jstor.org/stable/41059064

BIOGEOGRAPHICAL SPATIAL DOMAIN

1-2. Plant-herbivore and host-parasitoid interactions observed on willow tree species (*Salix* **spp.) across Europe (Kopelke et al. Ecology 2017) (Salgal, Galpar)**

- **Study area:** Europe from Italy in the south to Northern Norway
- **Interaction types:** Plant-herbivore and host-parasitoid interactions
- **Type of system:** Different habitats where species belonging to the Salix genus are found
- **Number and extent of sites:** 641 sites. Area size of sites varied between 0.01 and 1 ha depending on the size of individual trees
- **Number of networks:** 1 plant-herbivore and 1 host-parasitoid network per tree. This yields a total of 641 networks of each type.
- **Type of networks:** Bipartite
- **Taxonomic resolution of the nodes:** Trees and herbivores are resolved to the species level. All trees belong to the Salix genus. All herbivores are galling sawflies. Parasitoids are sometimes resolved to the genus level.
- **Total number of species and links at the regional scale:** 52 species of trees from the Salix genus, 96 species of sawflies (herbivores), and 126 parasitoid taxa.
- **Sampling procedure (of species and interactions):** Collection and counting of galls produced by the galling sawflies on the trees to identify the herbivore species, and rearing of parasitoids in the laboratory to identify them.
- **Publication reference:** Kopelke, J. P., Nyman, T., Cazelles, K., Gravel, D., Vissault, S., & Roslin, T. (2017). Food-web structure of willow-galling sawflies and their natural enemies across Europe. *Ecology*, *98*(6), 1730-1730.

3-14.Trophic interactions between terrestrial vertebrates across Europe (unpublished). (Alpine, Anatolian, Arctic, Atlantic, Black Sea, Boreal, Continental, Mediterranean, Pannonian, Steppic)

- **Study area:** Europe from Portugal in the west to the Ural Mountains in the east and from Iceland in the north to the Mediterranean Sea in the south. Divided into 10 biogeographical regions: Alpine, Anatolian, Arctic, Atlantic, Black Sea, Boreal, Continental, Mediterranean, Pannonian, Steppic.
- **Interaction types:** Trophic interactions.
- **Type of system:** All terrestrial habitats and biogeographical regions in Europe
- **Number and extent of sites:** Maps of the European bioregions were divided in 10x10 km cells. The number of cells varied among bioregions and were always of the same size.
- **Number of networks:** 1 trophic network per aggregation of cells from 1 to the maximum number of cells per bioregion
- **Type of networks:** Unipartite
- **Taxonomic resolution of the nodes:** All terrestrial vertebrates were resolved to the species level
- **Total number of species and links at the regional scale:** 1140 species and 69724 links at the European level, without dividing by biogeographical regions.
- **Sampling procedure (of species and interactions):** Species distribution maps were obtained from expert knowledge and models of habitat cover (as explained in Maiorano et al. 2013) and interactions were collected from literature records (including atlas, books and research articles) and expert knowledge.
- **Publication reference:** Maiorano, L., Montemaggiori, A., Ficetola, G.F., O'connor, L. and Thuiller, W., (2020). TETRA-EU 1.0: A species-level trophic metaweb of European tetrapods. *Global Ecology and Biogeography*, *29*(9), pp.1452-1457

15. Trophic interactions between terrestrial vertebrates in the Pyrenees. (Pyrenees)

- **Study area:** southeastern slopes of the Pyrenees (Iberian Peninsula side), from the highest creeks in the centre of the mountain range to the Mediterranean Sea in the east, covering a region of 900000 ha with elevations between 255 and 3140 m.a.s.l.
- **Interaction types:** Trophic interactions.
- **Type of system:** All terrestrial habitats.
- **Number and extent of sites:** 92 cells of 10x10 km.
- **Number of networks:** 1 trophic network per aggregation of cells from 1 to the maximum number of cells (i.e. 92 food webs).
- **Type of networks:** Unipartite
- **Taxonomic resolution of the nodes:** All terrestrial vertebrates were resolved to the species level.
- **Total number of species and links at the regional scale:** 212 species and 846 interactions.
- **Sampling procedure (of species and interactions): Species presence/absence was extracted** from public databases and extensive bibliography search. Interactions were inferred based on species co-occurrence in space and habitat.
- **Publication reference:** Lurgi, M., López, B. C., & Montoya, J. M. (2012). Novel communities from climate change. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, *367*(1605), 2913-2922.

Supplementary Table 1. Power function fit for the relationship of each network property analysed with area size for each dataset. P-value significance is shown by: \degree < 0.1, *<0.05, ** < 0.01, *** < 0.001. We used nonlinear least squares (NLS) with the 'nls' function in R. The scaling functions described in Table S4 were fitted to each dataset. In the *Model* column the best ranked model based on AIC comparison is shown. For all models selected $R^2 > 0.95$. A) Regional spatial domain. B) Biogeographical spatial domain.

Dataset	Property	Param.	Estimate	Std. Error	t-value	Model
Gottin HP	species	Z	0.615	0.0200	30.134***	Extended Power model 1
Gottin HP	species	$\mathbf d$	0.027	0.0101	2.4174**	Extended Power model 1
Chaco	species	Z	0.505	0.0089	51.29***	Extended Power model 1
Chaco	species	$\mathbf d$	0.118	0.0059	16.546***	Extended Power model 1
Garraf PP	species	Z	0.750	0.009	72.259***	Extended Power model 1
Garraf PP	species	d	0.044	0.0023	15.701***	Extended Power model 1
Garraf PP2	species	Z	0.451	0.0045	97.316***	Extended Power model 1
Garraf PP2	species	$\mathbf d$	0.094	0.0023	36.640***	Extended Power model 1
Bristol	species	Z	0.242	0.006	40.059***	Extended Power model 1
Bristol	species	d	0.143	0.004	29.369***	Extended Power model 1
Montseny	species	Z	0.595	0.009	68.559***	Extended Power model 1
Montseny	species	$\mathbf d$	0.050	0.0034	18.303***	Extended Power model 1
Soil 1	species	Z	0.324	0.009	33.927***	Extended Power model 1
Soil 1	species	$\mathbf d$	0.071	0.007	9.487***	Extended Power model 1
Soil ₂	species	Z	0.362	0.0065	57.112***	Extended Power model 1
Soil ₂	species	$\mathbf d$	0.091	0.0060	15.440***	Extended Power model 1
Soil 3	species	Z	0.365	0.0038	90.792***	Extended Power model 1
Soil 3	species	d	0.095	0.0027	31.425***	Extended Power model 1
Soil 4	species	$\mathbf{Z}% ^{T}=\mathbf{Z}^{T}\times\mathbf{Z}^{T}$	0.375	0.005	67.439***	Extended Power model 1
Soil 4	species	$\mathbf d$	0.098	0.0037	23.282***	Extended Power model 1
Soil 5	species	Z	0.455	0.005	84.377***	Extended Power model 1
Soil 5	species	$\mathbf d$	0.114	0.0042	34.242***	Extended Power model 1
Soil 6	species	Z	0.472	0.005	84.865***	Extended Power model 1
Soil 6	species	$\mathbf d$	0.160	0.0028	53.707***	Extended Power model 1
Soil 7	species	Z	0.403	0.0113	36.68***	Extended Power model 1
Soil 7	species	d	0.096	0.0055	17.615***	Extended Power model 1
Gottin PP	species	$\mathbf{Z}% ^{T}=\mathbf{Z}^{T}\times\mathbf{Z}^{T}$	0.644	0.005	54.980***	Extended Power model 1
Gottin PP	species	$\mathbf d$	0.074	0.002	$16.703***$	Extended Power model 1
Olot	species	z	0.580	0.018	29.652***	Extended Power model 1
Olot	species	$\mathbf d$	0.129	0.0091	12.192***	Extended Power model 1
Quercus	species	$\mathbf{Z}% _{0}=\mathbf{Z}_{0}$	0.607	0.011	51.196***	Extended Power model 1

A) REGIONAL SPATIAL DOMAIN

B) BIOGEOGRAPHICAL SPATIAL DOMAIN

Supplementary Table 2. Power function fit for the links-species relationship for each dataset. P-value significance is shown by: \degree < 0.1, \degree < 0.05, \degree * < 0.01, *** < 0.001. We used nonlinear least squares (NLS) with the 'nls' function in R. A) Regional spatial domain. B) Biogeographical spatial domain.

A) REGIONAL SPATIAL DOMAIN

B) BIOGEOGRAPHICAL SPATIAL DOMAIN

Supplementary Table 3. Coefficient of variation (cv) of each parameter of the best ranked power function across datasets within each spatial domain, regional and biogeographical, to characterize the change of each network property with area. The extended power 1 is the best ranked function across datasets and, therefore, shown in the table. For those cases where there were a significant number of datasets fitting better a power law, the coefficient of variation across those datasets of the z-estimate of the power law is also shown. Datasets from the biogeographical domain show larger coefficient of variation than datasets from the regional domain for all parameters describing the changes with area for all network properties. Exceptions are the d-estimates for Links/species and indegree, which show a larger cv for the regional than for the biogeographical domain, indicating that the concave shape is more consistent across datasets at the biogeographical domain. See supplementary table 4 for the description of each function.

Supplementary Figure 4. The degree distribution of each ecological network at each area of the aggregation procedure was fitted to four different functions that have been identified as typical of the shapes observed in degree distributions in ecological networks: power law, truncated power law, lognormal and exponential. The cumulative probabilities $Pc(k)$, for $\geq k$, where $P(k)$ is the probability a species has *k* prey in the network, and is given by $P(k) \sim k^{\gamma} e^{-K/\gamma}$ where $e^{-K/\gamma}$ introduces a cut-off at some characteristic scale γ . Although for most datasets the best fitted function did not change as area increases, indicating that the basic structure is preserved, the parameters of the fitted functions did change with area. **A) Changes with area of the power function exponent for regional datasets.** The exponent γ of the power function $(P(k) \sim k^{\gamma})$ that best described the degree distribution of datasets at regional scales, decreased with area, indicating that as area increases the difference between the most specialist (i.e. smallest number of interacting partners) species in the network and the most generalist (i.e. largest number of interacting partners) decreases. Therefore, it indicates a general increase of the number of interactions. **B) Changes in exponential function parameter with area.** The exponent γ of the power function ($P(k) \sim e^{-K/\gamma}$) that best described the degree distribution of datasets at the regional domain, increased with area, indicating a general increase in the number of interactions each species has. **C) Changes in the parameters of the truncated power law function with area.** The truncated power function $(P(k) \sim k^{\gamma} e^{-K/\gamma})$ was the function that best described network degree distributions at the biogeographical domain. While the parameter controlling the power law regime did not consistently change with area, the second parameter **(D)** that determines the cut-off after which there is the exponential decay of the tail of the degree distribution, increased with area. This indicates that the characteristic scale of the network changes with area, and thus, as area increases the number of interactions before the cutoff increases.

A) Changes with area of the power function exponent for regional datasets.

B) Changes in exponential function parameter with area.

C) Changes in the parameter γ of the truncated power law function with area.

D) Changes in the parameter k/γ of the truncated power law function with area.

Supplementary Table 4. Set of functions used to test Network-Area relationships using the *sar* package in R**.**

Supplementary Figure 5. Null model comparison. For each dataset we show the spatial scaling of species, links, links/species, indegree and consumer:resource ratio for the original data (blue), null model 1 (red) and null model 2 (green) (see Methods for a description of each null model). The scaling of the number of links with the number of species is also shown. We provide the slope of the links-species relationship to be able to compare with the constant connectance hypothesis (slope=2; the number of links in a web increases approximately as the square of the number of trophic species: $L \approx S^2$) and the link–species scaling law (slope=1; the number of links per species in a web is constant and scale invariant at roughly two: $L \approx 2S$). The slope was calculated performing a linear model fit, which can slightly differ from the values obtained when performing a power law fit to the data when the data does not behave as a perfect power law. Notice that many of the instances of null model 1, show a relationship between the number of links and the number of species with a slope close to 2. The reason for this is that since in null model 1 the number of links is not fix, when randomly picking a given number of species, at small spatial scales the number of links associated to the selected species is much lower than in the original networks. As a consequence of this low connectivity at small spatial scales in the random networks in comparison with the original ones, the number of links increases faster when increasing the number of species to reach the total number of links in each metaweb. The total number of links has to be reached because when all species are sampled at the largest spatial scale, all their links are also necessarily sampled. **A) Null model comparison for the regional spatial domain.** Notice that for the Soil networks we show the comparison only for one of them due to space constraints. All soil datasets showed the same patterns than the one illustrated below. **B) Null model comparison for the biogeographical spatial domain.**

A) Regional spatial domain

Supplementary Table 5. Proportion of values that fell within the 95% confidence interval of the original data for each null model for regional datasets. The 95% confidence interval of the original data was calculated for each network property at each spatial extent. Then we calculated the proportion of values of each null model that fell within this confidence interval. **A) Null model 1 for regional datasets. B) Null model 2 for regional datasets.** Notice that for null model 1 almost all values of species richness (proportion close to 1) were within the confidence interval since the number of species was explicitly set to be the same as in the original data. The proportion of number of links, links per species, indegree and consumer:resource ratio was much more variable across datasets and smaller. Similarly, for null model 2, the proportion of values of species, links and links of species that fell within the confidence interval was close to 1, while for indegree and consumer:resource ratio was much smaller (specially for bipartite networks).

A) Null model 1 for regional domain

B) Null model 2 for regional domain

Supplementary Table 6. Proportion of values that fell within the 95% confidence interval of the original data for each null model for biogeographical datasets. The 95% confidence interval of the original data was calculated for each network property at each spatial extent. Then we calculated the proportion of values of each null model that fell within this confidence interval. **A) Null model 1 for biogeographical datasets. B) Null model 2 for biogeographical datasets.** Notice that for null model 1 almost all values of species richness (proportion close to 1) were within the confidence interval since the number of species was explicitly set to be the same as in the original data. The proportion of number of links, links per species, indegree and consumer:resource ratio was much more variable across datasets and smaller. Similarly, for null model 2, the proportion of values of species, links and links of species that fell within the confidence interval was close to 1, while for indegree and consumer:resource ratio was much smaller (specially for bipartite networks).

A) Null model 1 for biogeographical domain

B) Null model 2 for biogeographical domain

Supplementary Figure 6. Null model comparison of the spatial scaling of degree distributions. The top-ranked model describing the degree distribution of each ecological network across the area range using the null model 1 and the null model 2. Area values were rescaled between 0 and 1. In **A** and **B**, we show the comparison for the regional datasets of null models 1 and 2, respectively. In **C** and **D**, we show the comparison for the biogeographical datasets of null models 1 and 2, respectively. For regional datasets, the spatial scaling of degree distributions of the networks built with null model 1 resembled the patterns observed in the original networks, suggesting that important structural patterns such as the degree distribution might be inhereted from the metaweb. In contrast, networks built with null model 2 showed very different scaling patterns for network degree distributions. The degree distributions of many of the datasets were best represented by an exponential function, which corresponds with the random distribution of links used in null model 2. Soil food webs are not presented in the plot below for null model 2 because none of the models tested fitted their degree distributions. For biogeographical datasets we did not observe such big differences between the patterns observe for null model 1 and null model 2. Most differences were observed with the empirically sampled network galpar that showed similar patterns as the ones described for the regional networks.

B) Regional Domain Null Model 2

Supplementary Figure 7. Spatial scaling of species, links, links/species and indegree for all datasets where networks were build based on empirical sampling of species and interactions. This corresponds to all regional networks plus the biogeographical networks 'Salgal' and 'Galpar'(Kopelke et al. Ecology 2017). We do this analysis to test the potential effect of the data type on the patterns observed given that while for the regional datasets, all networks were built from empirical sampling of both species and the interactions, most datasets in the biogeographical category were based on inferred interactions using different methodologies. For all datasets analysed here (including the two biogeographical datasets) we used the random aggregation of spatial units. For each dataset, each point represents the mean value of the analysed network property across the total amount of replicates in the aggregation procedure, for a given area. All network properties have been re-scaled for all datasets to start at 0. We observe that when analysing empirically-sampled datasets alone, even those expanding large spatial extents show similar scaling patterns. However, obtaining empirically sampled data of ecological interactions for domains encompassing full continents is truly challenging.

Supplementary Figure 8. Spatial scaling of species, links, links/species and indegree for biogeographical networks using the random aggregation of spatial units.

Another potential driver of the differences observed across spatial domains could be the aggregation procedure used in each case. While the spatial units of the regional datasets were aggregated randomly, for the biogeographical datasets we employed an aggregation method based on neighbouring cells (see Methods). Due to the large spatial extent covered by these datasets, an aggregation procedure where each aggregated sampling unit is randomly selected in space will generate a much faster increase of network properties with area due to the large heterogeneity encapsulated in the spatial units. For each dataset, each point represents the mean value of the analysed network property across the total amount of replicates in the aggregation procedure, for a given area. All network properties have been re-scaled for all datasets to start at 0. Notice that with the random aggregation procedure the spatial scaling of network properties do not follow a function of the power law family (see Supplementary Table 5).

Supplementary Table 7. Fit of the best functions for the relationship of species with area size for each dataset of the biogeographical category when using random aggregation of spatial units. We only illustrate the relationship between species and area due to space constraints, but the rest of the network properties analysed behave similarly. We used nonlinear least squares (NLS) with the 'nls' function in R. The scaling functions described in Table S4 were fitted to each dataset. In the *Model* column the best ranked model based on AIC comparison is shown. For all models selected $R^2 > 0.95$.

