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1 Ecological network complexity scales with area

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57 **Larger geographical areas contain more species –an observation raised to a law in ecology.**
58 **Less explored is whether biodiversity changes are accompanied by a modification of**
59 **interaction networks. We use data from 32 spatial interaction networks from different**
60 **ecosystems to analyse how network structure changes with area. We find that basic**
61 **community structure descriptors (number of species, links, and links per species) increase**
62 **with area following a power-law. Yet, the distribution of links per species varies little with**
63 **area, indicating that the fundamental organization of interactions within networks is**
64 **conserved. Our null model analyses suggest that the spatial scaling of network structure is**
65 **determined by factors beyond species richness and the number of links. We demonstrate**
66 **that biodiversity–area relationships can be extended from species counts to higher levels of**
67 **network complexity. Therefore, the consequences of anthropogenic habitat destruction**
68 **may extend from species loss to wider simplification of natural communities.**

69

70 **INTRODUCTION**

71 **Biotic interactions, the missing link**

72 Research on the spatial scaling of biodiversity has historically focused on the increase of species
73 richness with area¹⁻³ and on other components of biodiversity, such as functional or
74 phylogenetic diversity⁴⁻⁶. The Species Area Relationship (SAR) is essential to estimate species
75 richness in a region and species loss following habitat destruction and range contraction⁷⁻⁹.
76 Ecological communities are, however, more than disconnected collections of species. Instead,
77 they can be represented as networks, with species as nodes and interactions among species as
78 links¹⁰. Ecological interactions are fundamental to predict ecosystem responses to environmental
79 changes¹¹⁻¹³ and to sustain important ecosystem functions¹⁴⁻¹⁶. Understanding how the structure
80 of interaction networks changes with area is, thus, crucial to fully characterize the spatial scaling
81 of biodiversity and to predict ecosystem responses to human activities.

82 The influence of spatial processes on the organization of interaction networks has long
83 interested ecologists¹⁷⁻¹⁹. However, research on the spatial scaling of network structure has been

84 scarce^{20–22}. This scaling concerns two hierarchical levels: the number of building blocks within
85 communities (species and their interactions) and the relationships between them. The scaling of
86 the number of links (i.e., biotic interactions) with area has been previously predicted²⁰ by
87 unifying the SAR with the well-established scaling of the number of links with species
88 richness^{23–26}. Similarly, recent theoretical research has shown that a number of network–area
89 relationships (NARs) can emerge from different spatial mechanisms and assembly processes,
90 such as different SARs across trophic levels or dispersal limitation²¹. Yet, empirically
91 documenting the specific shape of these relationships and assessing their potential universality
92 across biomes, interaction types, and spatial domains remains a major challenge.

93 The power function of the form $S \sim cA^z$ has been found to describe the increase in
94 species richness with area A across all ecosystem types^{1,27}, with parameter z varying
95 substantially with the spatial extent studied^{27–29}. Whether other aspects of network complexity
96 can be captured by the same functional form, and how the parameters of such scaling vary with
97 network properties and spatial extent, are questions of fundamental importance for
98 characterizing the effects of area loss on biodiversity. Similarly, as many aspects of network
99 structure can change with species diversity and network connectance^{30–33} (i.e., the proportion of
100 realised interactions among all potential ones), it is important to determine whether the spatial
101 scaling of network structure is a trivial consequence of the increase of species richness with
102 area, or whether such scaling of network properties follow rules beyond those applying to
103 species richness.

104 **A unique dataset across ecosystems and biomes**

105 We compiled 32 datasets from different ecosystems across the globe describing
106 interaction networks (including both mutualistic and antagonistic interactions) within two
107 spatial domains: regional and biogeographical. The regional domain represents communities for
108 which sampling was conducted locally in a replicated fashion within narrow spatial extents (i.e.,
109 maximum spatial extent of ca. 1000 km²). The biogeographical spatial domain includes datasets
110 for which the sampling units span much broader areas, encompassing multiple biomes (see

111 Methods and Supplementary Text 1). Thus, biogeographical data comprise communities
112 exposed to larger environmental heterogeneity, stronger dispersal barriers and historical
113 contingencies, which combine to produce diversity patterns at large spatial scales. Hence, we
114 expected *a priori* the scaling relationships for the biogeographical domain to be steeper than
115 those for the regional domain, as within the biogeographical domain, species assemblages can
116 be evolutionary less related and exhibit greater turnover of species and links. Each dataset
117 contained interaction data, using different methodologies to document pairwise interactions. To
118 characterise changes in network properties with changes in area, we sequentially aggregated the
119 sampling units available, scoring the structure of the network at each step of the aggregation
120 procedure (see Methods).

121 RESULTS & DISCUSSION

122 **Links or species: which one is gained faster?**

123 We found that network complexity increased with area at all levels: at the level of the number of
124 building blocks (species and links) and at the level of their combinations (links per species;
125 Figure 1; Table 1 and Supplementary Table 1). For all datasets, the relationships followed a
126 power-law function, regardless of the spatial extent of observation or interaction type. Within
127 both the regional and biogeographical domain, we found that an extended power function best
128 describes the scaling of network complexity with area (see Methods and Supplementary Table
129 1). This function has the form $N = cA^{(zA^{-d})}$, where N is a given network property, A is area,
130 and c , z and d are fitted parameters, where z represents the slope of a given NAR in log-log
131 space (i.e., the scaling exponent) and d controls the strength of the asymptotic flattening.

132 We found systematic differences in the shape of the scaling relationships between the
133 regional and biogeographical domains. All measures of network complexity followed a linear-
134 concave increase with area size in the regional domain (i.e. $z \gg d > 0$) while in the
135 biogeographical domain, the increase was convex for most datasets ($z > 0 > d$) (but see
136 Supplementary Figure 7 and Supplementary Figure 8). The biogeographic domain also showed

137 larger variability across datasets than the regional domain, suggesting lower predictability at
138 larger spatial extents (Supplementary Table 3).

139 The number of links increased faster with area than the number of species, within both
140 the regional and biogeographical domains. Importantly, whether links increase faster than
141 species with area will depend on how the number of links scales with species richness^{20,21}.
142 Previous empirical studies^{23–26} have used a power function to relate the increase of the number
143 of links with species richness, and found the value of the scaling exponents to lie between 1 and
144 $2^{25,26}$ – coining the expressions of the “link-species scaling law”³⁴ versus “constant connectance
145 hypothesis”²⁴, respectively. Consistent with previous work, we found the increase in the number
146 of links with an increase in species richness to follow a power law in all data sets (Figure 2,
147 Supplementary Table 2). The exponents were larger for the biogeographical (mean \pm SD: $z =$
148 1.78 ± 0.20) than for the regional domain ($z = 1.60 \pm 0.20$). For both spatial domains, the
149 scaling exponents of the links-per-species relationship were thus clustered between 1.5 and 2,
150 but with substantial variability in specific values (Figure 2, Supplementary Table 2). The high
151 variation observed suggests that the species richness of a community may carry little
152 information on how the number of links will change with area. Instead, the scaling of the
153 number of links with species richness may need to be established on a network-specific basis²⁰.

154 **The unpredictability of vertical diversity**

155 Within a network, the links can be organized in multiple ways. In our dataset, the mean number
156 of resources used by a consumer (i.e. mean indegree: $\text{Links}/\text{Species}_{\text{consumer}}$) increased with area.
157 The general shape of the relationship was similar to that of the other complexity measures
158 analysed, i.e. linear-concave in the regional domain and convex in the biogeographical domain
159 (Figure 3, Supplementary Table 1). Still, compared to the relationships observed for other
160 network properties, we observed greater variability in indegree-area relationships within spatial
161 domains (Supplementary Table 3). This variability is partially driven by the variability in
162 changes in consumer to resource ratios with area observed across datasets (Supplementary Table
163 1). Although previous studies have shown a consistent increase of the slope of SARs with

164 trophic level^{35,36}, we did not observe any consistent increase nor decrease of the
165 consumer:resource richness ratio with area at any of the spatial domains (Supplementary Table
166 1). These findings suggest that the spatial scaling of vertical diversity properties, such as the
167 proportion of species per trophic level, might be system-specific.

168 **The scale-invariance of degree distributions**

169 Beyond the network properties considered above, other network properties were more consistent
170 across scales. The degree distribution of ecological networks is typically highly skewed, with
171 many specialist species and few generalists^{37,38}. This skewness may influence the stability and
172 robustness of communities³⁸ and it is tightly linked to widely studied network properties, such
173 as nestedness^{39,40}, (i.e. the degree to which specialist species interact with subsets of the species
174 interacting with generalists). Previous theoretical work has suggested that the skewness of
175 ecological networks is preserved across spatial scales²¹, an expectation borne out in our data.
176 Despite variability in the degree distribution across datasets, the same function provided a good
177 fit to the degree distribution of most ecological networks across the full range of areas (see
178 Methods and Figure 3). Although we observed variation in the parameters of the functions
179 (Supplementary Figure 4), the consistency in the fundamental shape suggests that community
180 robustness to species loss (independently of whether it is high or low) may be maintained across
181 spatial scales.

182 **Disentangling the effect of species richness**

183 Given the influence of species richness and network connectance on many aspects of network
184 structure³⁰⁻³³, we aimed to investigate whether network structure changes with area beyond
185 those changes associated to the increase in species richness and links with area. To do so, we
186 generated random networks with two different null models, as reflecting the case where the
187 spatial scaling of network structure emanates from the spatial scaling of species richness alone
188 (with no change in links per species), or the spatial scaling of both species richness and links,
189 respectively. In both models, we started from the metaweb (i.e. the overall network pooled
190 across all original networks within each specific study), then randomly drew the same number

191 of species as observed in the original, local networks. In null model 1, local random networks
192 were drawn as random subsets of the metaweb, picked to have the same species richness as the
193 observed local networks. In other words, after randomly selecting a given number of species
194 from the metaweb, we only kept interactions among this subset of species, thereby determining
195 the number of links of the network generated. Thus, this procedure mimics a scenario where
196 random local networks have the same number of species as the observed local networks, but the
197 number of links and the associated network properties may differ. In null model 2, we preserved
198 both species richness and the number of interactions observed in the original networks, but
199 distributed the links randomly among the species (see Methods). Accordingly, null model 2
200 mimics a scenario where a change in area causes a potential change in indegree and network
201 degree distribution, while not affecting either the number of species or links. For each of the
202 100 randomizations under each scenario, we then scored each of the complexity metrics defined
203 above: species, links, links per species, indegree and network degree distribution.

204 The observed spatial scaling of network structure in the original networks differed
205 significantly from the results generated by the null models. The number of links in empirical
206 networks increased more slowly with an increase in the number of species than expected from a
207 random sample of species from the metaweb (i.e. null model 1) (Supplementary Figure 5). This
208 slower increase is driven by the fact that local original networks show greater complexity (i.e.
209 more links per species) than random networks. This result suggests that the scaling of the
210 number of links is shaped by factors beyond the species richness of a community, such as
211 evolutionary constraints, phenological matching or competition. In contrast, other structural
212 properties, such as mean indegree and degree distributions, are consistent with the pattern
213 derived from null model 1 (Supplementary Figure 5 and Supplementary Figure 6;
214 Supplementary Table 5 and Supplementary Table 6). The latter consistency indicates that these
215 particular network properties might be inherited from the metaweb, and that the particular co-
216 occurrence structure of species in the empirical data is not meaningfully impacting the degree
217 distribution. This interpretation is supported by patterns observed under null model 2. When

218 links are reshuffled randomly amongst selected species from the metaweb, the pattern is
219 substantially different from the observed one: here, both the mean indegree and network degree
220 distributions of the randomized networks strongly deviate from that of their original
221 counterparts (Supplementary Figure 5 and Supplementary Figure 6; Supplementary Table 5 and
222 Supplementary Table 6). Similarly, the observed spatial scaling of the consumer:resource ratio
223 was poorly predicted by both null models.

224 Overall, our null model analyses suggest that the spatial scaling of network structure is
225 determined by factors beyond species richness and the number of links. With a change in area,
226 we see changes in important features of ecological networks – such as vertical diversity,
227 consumer specialisation, and degree distribution – well beyond those expected if changes were
228 driven by the number of species and/or links alone.

229 **The fragility of biotic interactions**

230 In conclusion, our analyses of multiple interaction networks from different biomes,
231 interaction types, and spatial domains allowed us to explore the generality in the spatial scaling
232 of several structural properties of ecological networks. Our results demonstrate how previously-
233 established biodiversity–area relationships can be extended from species counts^{2,3,27} to higher
234 levels of network complexity. The increase in the number of interactions in which each species
235 is involved when area increases indicates that trophic interactions might be more vulnerable to
236 habitat loss than species richness^{41,42}. Therefore, the consequences of anthropogenic habitat
237 destruction may extend from species loss to wider simplification of natural communities^{43–45},
238 with further consequences for the functioning of ecosystems^{14–16,46,47}. The systematic scaling of
239 network complexity with area suggests that trophic interactions will be lost with habitat
240 destruction in a predictable manner, and describing the factors shaping this sequence allows us
241 to better anticipate the effects for ecosystem functioning. Importantly, the scaling of the number
242 of interactions with species richness proved variable across datasets, and our null model
243 analysis indicated that other complexity metrics cannot be predicted from species richness

244 alone. Both of these patterns suggest that we need network-specific knowledge on the
245 relationship between links and species to accurately predict the effects of habitat loss on
246 network complexity. To estimate the spatial scaling of the number of links, a general
247 understanding of the species-area relationship may still suffice, if it is supplemented by
248 informed assumptions regarding the scaling exponent of the links-species relationship. For such
249 assumptions, our current results will form a useful point of departure, given their foundation in a
250 wide set of scales and biomes.

251 Future studies should put effort towards unravelling the potential ecological
252 mechanisms affecting the slopes of NARs, as well as disentangling the importance of the
253 methodological aspects (Supplementary Figure 7 and Supplementary Figure 8; Supplementary
254 Table 7), as has been widely done for SARs²⁷. Explicitly investigating the effect of habitat
255 heterogeneity, for instance, would help elucidate the effect of area, not only on network size and
256 the number of links, but also on its modular structure. Such insight is urgently needed, given
257 that heterogeneous landscapes are likely to promote the emergence of compartments within
258 networks^{48,49}. Similarly, it is important to investigate how our observations could inform
259 predictions about the effects of habitat loss caused, for instance, by link extinction debt or
260 changes in trophic regulation^{41,42}. Yet, it is also fundamental to understand how our predictions
261 of the effects of habitat loss on network structure would resemble those obtained by direct
262 experiments of habitat destruction. Gaining a deeper understanding of the mechanisms behind
263 NARs will allow us to not only anticipate the potential consequences of habitat loss, but to also
264 provide management recommendations with a solid foundation in the structure and functioning
265 of natural ecosystems.

266 **METHODS**

267 To measure network-area relationships (NARs) for ecological communities from different
268 biomes across the world, we used 32 empirical datasets comprising species recorded in different
269 localities, and with different types of interactions. This is the most comprehensive synthesis of
270 spatial interaction network datasets to date. Depending on the study, local observations span

271 either a regional or biogeographical spatial extent. Our analysis allowed us to identify
272 universalities in the ways that network properties change with area, for datasets comprising
273 different interaction types. To evaluate whether there are universalities in the ways that
274 networks of ecological interactions scale across space, we quantified the exponents of the
275 relationships between all network properties analysed with area when fitted to a power function.
276 The spatial scaling of network degree distributions was assessed by fitting four different
277 distributions at each spatial domain and comparing the best fit across the entire range of areas.
278 Additionally, we used two different null models to disentangle the effects of the spatial scaling
279 of species richness on the patterns observed in other complexity metrics.

280

281 ***Data classification***

282 32 datasets comprising species distributions and their interactions were obtained from different
283 sources and classified into two categories according to the geographical extent covered: regional
284 or biogeographical spatial domains. The main features of the type of data considered in each
285 category, including sampling method, location, and interaction types, are briefly described
286 below. Additional details about each dataset can be found in Supplementary Text 1.

287

288 *Regional spatial domain.* Datasets in this category are distinguished from biogeographical
289 networks by their geographical extent and sampling methods. Regional-domain data were
290 collected with locally replicated samples over relatively narrow spatial extents up to ca. 1000
291 km². Sample units are generally the same size or a series of localities of roughly equal size. A
292 total of 19 datasets were considered in the regional domain, covering different ecosystems and
293 geographical locations across the globe. The datasets are: networks describing plant-pollinator
294 interactions and host-parasitoid interactions from Mediterranean scrublands located in Garraf (3
295 datasets^{50,51}), and forests located in the Natural Parks of Montseny (1 dataset⁵²) and Olot (1
296 dataset⁵³) in Catalonia, Spain; host-parasite interactions networks describing insect herbivores
297 (gallers and leaf miners) of the Pedunculate Oak (*Quercus robur*) and their parasites in a
298 temperate forest in Finland (1 dataset⁵⁴); plant-pollinator interactions from a temperate forest in

299 Argentinian Patagonia (1 dataset⁵⁵); soil food webs from agroecosystems across The
300 Netherlands (7 datasets⁵⁶); terrestrial food webs within small islands of a temperate saltmarsh
301 mudflat in south-eastern England (1 dataset⁵⁷); intertidal food webs from the Northeastern
302 Pacific in Alaska, USA (1 dataset⁵⁸); networks of plant-pollinator interactions and host-
303 parasitoid interactions in fragmented calcareous grasslands in central Germany (2 datasets⁵⁹);
304 and networks of plant-leafminer-parasitoid interactions from forest fragments embedded in an
305 agricultural matrix landscape in central Argentina (1 dataset⁶⁰).

306

307 *Biogeographical spatial domain.* Datasets from this category span broad (i.e. biogeographical)
308 spatial extents. There are two types of biogeographical datasets: can be comprised of either (1)
309 datasets where local communities are built based on the information of the presence of all
310 species found in each location and where the interactions between species have been inferred
311 from literature review and expert knowledge; and (2) datasets where local communities are built
312 based on direct observations of ecological interactions at each locality. The datasets of type (1)
313 comprise: the European terrestrial vertebrate trophic network (food web, ⁶¹) divided among 10
314 biogeographical regions that characterise each region according to its climatic conditions. Local
315 communities for this dataset are defined at the 10km × 10km grid level (10 datasets); and the
316 terrestrial vertebrate food web of the Catalan Pyrenees (1 dataset;¹²), where local communities
317 are also defined at the 10km × 10km grid level. The datasets of type (2) comprise networks of
318 plant-herbivore interactions and herbivore-parasitoid interaction sampled from plants of the
319 genus *Salix* and spanning a large latitudinal gradient from Italy to northern Norway (2
320 datasets;⁶²).

321

322 ***Building network-area relationships***

323 To analyse the spatial scaling of network structure we built NARs for each dataset described
324 above. The procedure to generate NARs was slightly different between spatial domains.

325

326 *Regional spatial domain.* The spatial extent was rescaled for each dataset. The smallest spatial
327 scale considered was a single sampling unit. The spatial scaling of network structure was
328 defined by sequentially aggregating each of the sampling units available until all replicated
329 samples were considered. The aggregated sampling units are not contiguous, given that the
330 specific location of each of them was not considered. We analysed network structure at each
331 step of the aggregation procedure. Given that the order in which sampling units (i.e. local
332 communities) are aggregated might generate a bias in the aggregation procedure, we replicated
333 the procedure 100 times for each dataset where the aggregation order was randomly generated
334 without replacement.

335

336 *Biogeographical spatial domain.* The fundamental difference between the two spatial domains
337 considered is that biogeographical data span large spatial extents, thus comprising communities
338 exposed to large environmental gradients. This environmental heterogeneity suggests potential
339 differences in scaling patterns, when compared to communities sampled regionally, which cover
340 smaller geographical extents. Due to the large spatial extent covered by these datasets, an
341 aggregation procedure where each aggregated sampling unit is randomly selected in space,
342 independently of its location, would generate a fast accumulation of species and links at small
343 areas due to the large heterogeneity among the sampling units (Supplementary Figure 8 and
344 Supplementary Table 7), generating a fast accumulation of species and links at small areas. For
345 this reason, we employ an aggregation method based on neighbouring cells, while still
346 preserving the statistical power of randomising across replicated aggregation instances (here, we
347 refer the reader to Supplementary Figure 8 and Supplementary Table 7 for results based on the
348 random aggregation of sites). Two types of data comprise this category: those for which species
349 presences and their interactions were recorded in the field from single georeferenced locations
350 across the latitudinal gradient⁶²; and those where species presences were extracted from species
351 distributions maps and interactions were inferred based on the joint condition of species co-
352 occurrence in space and an indication that the two species interact, as extracted from the
353 literature⁶¹. The latter datasets, therefore, include all potential interactions between species,

354 which are not necessarily realised locally. Local sampling units of these latter datasets were
355 defined as the 10×10 km cells on a gridded map. The spatial scaling of network structure is thus
356 simulated by merging adjacent cells of the map in an increasing manner. Starting from a
357 randomly chosen cell, subsequent communities occupying larger areas were defined as
358 collections of neighbouring cells forming increasingly larger clusters of cells, chosen in counter-
359 clockwise fashion from the starting cell (i.e., spiral fashion). Thus, the sampling units that are
360 aggregated are contiguous. We measured network properties at each step of the aggregation
361 procedure. We repeated the aggregation procedure 100 times. For datasets with georeferenced
362 locations, the spatial scaling of network structure was defined by sequentially aggregating the
363 closest communities (in terms of Euclidean distance) to the starting point.

364

365 *Network properties*

366 We analysed the spatial scaling of network complexity at both spatial scales measuring the
367 number of species (S), the total number of links (i.e. biotic interactions; L) present in the
368 network and the number of links per species (L/S). We also quantified the relationship between
369 species richness and the total number of links in the network (i.e. links-species scaling).
370 Specialisation was measured at the network level by computing the mean in-degree (mean
371 number of resources utilized by a consumer; L/S_c) of the community (also known as generality
372 or diet breadth in food webs).

373

374 To further assess how the structure of ecological networks scales across space in different
375 ecosystems, we examined their degree distribution. The degree distribution $P(k)$ of a network is
376 defined as the probability of finding a species that has k links to resources in the network.
377 Degree distributions provide a notion of how links are structured across the network, and their
378 shape has been related to different aspects of community stability^{46,63–65}. In particular, scale-free
379 degree distributions are considered the hallmark of network organisation; conferring stability
380 properties to ecological communities. We fitted four different functions that have been
381 identified as typical of the shapes observed in degree distributions in ecological networks:

382 power law, truncated power law, lognormal and exponential^{63,66}. After fitting these distributions
383 to the network of interactions built for each spatial scale analysed, for each dataset, the most
384 parsimonious one as measured by Akaike Information Criterion (AIC) was recorded as the best
385 representation of the data. We did that for each replicate of each dataset, selecting the
386 distribution that was best ranked in most of the replicates. Looking at whether the top-ranked
387 distribution (i.e., the lowest AIC) changes with area provides insights into the scale invariance
388 of this network property. Additionally, we looked at the changes of the parameters involved in
389 each function with area (Supplementary Figure 4).

390

391 *Network-Area relationships fitting*

392 After constructing NARs based on the 100 replicates for each dataset, we analysed the scaling
393 relationships by fitting a suite of functions that have traditionally been used to quantify species-
394 area relationships^{67,68} (see Supplementary Table 4 for the full set of functions tested). These
395 scaling functions incorporate in different ways the network property as the response variable
396 and area as the predictor variable, using a characteristic exponent, or a variation of it, to define
397 the relationship of network properties to area size. For example, the power law ($N = cA^z$),
398 relates N (a network property), to area (A) using a constant c and a scaling exponent (z).
399 Similarity in the fitted parameters obtained for different datasets was then used to evaluate
400 universalities in NARs. Scaling functions in Supplementary Table 4 were fitted to each dataset
401 (after network properties were calculated at each spatial extent) using the *sar* package in R⁶⁸.
402 We used R^2 and p -values to assess goodness of fit. Comparison across models and selection of
403 the best supported model was done with AIC. Amongst all fitted functions, we focused on the
404 top five models that were best supported and selected (if possible) the best ranked model from
405 the power family to facilitate comparisons among datasets. We note that the functions were
406 fitted to the original data in arithmetic space and that the re-scaling of the properties to start at 0
407 was performed for visualisation purposes alone.

408

409 *Null models*

410 To understand the contribution of species richness and the number of links for the spatial
411 scaling of the associated network properties analysed we used two null models. For null model
412 1, we checked for each dataset the number of species present in each spatial unit and we
413 randomly picked the same number of species from the corresponding metaweb. We then built
414 the network for those species taking from the metaweb all the interactions present between the
415 selected species. Thus, the resulting assemblages can differ from the original networks in the
416 number of links between species and, in turn, in the associated network properties analysed. In
417 contrast, for null model 2, we checked that the number of species is present in each spatial unit
418 but also the number of links present and randomly distributed those links between the selected
419 species. While networks built with null model 1 can potentially preserve part of the structure
420 from each metaweb given that the selected species preserve the links they have in the metaweb,
421 networks built with null model 2 can be considered random networks given that there is no
422 inherited structure from the metaweb. Thus, null model 1 allows us to determine the
423 contribution of the identity of the species (with their respective links) to the observed patterns,
424 while null model 2, allows us to further test whether there is any contribution of area into
425 network structure beyond species richness and the number of links. For both null models, we
426 generated networks of different sizes by adding the number of species of the subsequent spatial
427 units of each dataset. At each step of species addition, we calculated all network metrics. We
428 replicated the procedure 100 times for each dataset. We evaluate the resulting network-area
429 relationships (where area is the number of spatial units from which we extracted the number of
430 species) by fitting a power function, as we did for the original networks. We finally compared
431 the spatial scaling of network properties with those obtained in the original networks
432 (Supplementary Figure 5 and Supplementary Figure 6; Supplementary Table 5 and
433 Supplementary Table 6).

434 **Code availability.** Custom code used to perform the analyses are available online here:
435 <https://doi.org/10.5061/dryad.zcrjdfndg>, here: [https://github.com/nuriagaliana/Ecological-](https://github.com/nuriagaliana/Ecological-network-complexity-scales-with-area)
436 [network-complexity-scales-with-area](https://github.com/nuriagaliana/Ecological-network-complexity-scales-with-area) or here: <https://github.com/mlurgi/global-network-area>.

437 **Data availability.** All datasets analysed during the current study are available online here:
438 <https://doi.org/10.5061/dryad.zcrjdfndg>, here: [https://github.com/nuriagaliana/Ecological-](https://github.com/nuriagaliana/Ecological-network-complexity-scales-with-area)
439 [network-complexity-scales-with-area](https://github.com/nuriagaliana/Ecological-network-complexity-scales-with-area) or here: <https://github.com/mlurgi/global-network-area>.

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455

456 **Author contributions**

457 NG, JMM and ML designed research with contributions from all co-authors. NG and ML
458 conducted research and analysed the data. JB, LC, BCL, CE, IG, CHC, FJ, DM, CM, SOC, SR,
459 AR, ISD, AT, DV, SW, TR and WT contributed the data. JMM, VAB, KC, MJF, SL, KM, AM,
460 DG, TR, SV and WT supported research. NG and JMM wrote the manuscript with substantial
461 contributions from DG, TR and WT, and feedback from all co-authors.

462 **Competing interests**

463 The authors declare no competing interests.

464 **Additional information**

465 Supplementary information is available for this paper.

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467 (galiana.nuria@gmail.com)

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473 **Table 1.** Parameter estimates for the fit of the extended power model ($N = cA^{(zA^{-d})}$) to the
 474 network properties analysed. Mean and standard deviation of d and z are shown for each
 475 network property analysed in both spatial domains. The model fit was performed on the original
 476 data in arithmetic space and not on the rescaled properties.

Network property	Parameter	Spatial Domain	
		Regional	Biogeographical
Species	d	0.08 ± 0.03	-0.38 ± 0.78
	z	0.48 ± 0.12	0.05 ± 0.41
Links	d	0.07 ± 0.03	-0.19 ± 0.13
	z	0.72 ± 0.10	0.41 ± 0.63
Links/Species	d	0.05 ± 0.11	-0.31 ± 0.57
	z	0.26 ± 0.10	0.08 ± 0.11
Indegree	d	0.04 ± 0.12	-0.27 ± 0.22
	z	0.31 ± 0.13	0.07 ± 0.19

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494 **Figures**

495 **Fig 1. Spatial scaling of network complexity.** The relationship of species (a,d), links (b,e), and
496 links/species (c,f) with area for regional (top) versus biogeographical (bottom) networks. For
497 each dataset, each point represents the mean value of the analysed network property across the
498 total amount of replicates in the aggregation procedure, for a given area. For all datasets, all
499 network properties have been re-scaled to start at 0 for visualisation purposes. In the
500 biogeographical domain, three datasets show a linear-concave increase of the number of species,
501 network links and links per species with area, similar to those observed in the regional domain;
502 these differences may be explained by differences in sampling methods among datasets (see
503 Methods and Discussion; Supplementary Text 1).

504

505 **Fig 2. Scaling of the number of links with species richness.** For networks spanning both
506 regional (a) and biogeographical (b) spatial domains, the number of links scales with species
507 following a power law (Supplementary Table 2). Each point represents the mean values across
508 all replicates in the aggregation procedure. Note that for visualisation purposes, all x - and y -
509 values in all datasets have been re-scaled to start at 0. To allow convenient comparison with the
510 constant connectance hypothesis and the link–species scaling law, the slope of each log-log
511 relationship is provided in Supplementary Table 2. Note that for constant connectance, the slope
512 equals 2, as the number of links in a web increases approximately as the square of the number of
513 trophic species: $L \approx S^2$. For the link–species scaling law, the slope equals 1, as the number of
514 links per species in a web is constant and scale invariant at roughly two: $L \approx 2S$.

515

516 **Fig 3. Spatial scaling of mean indegree and network degree distribution.** The mean number
517 of resources per consumer (i.e., mean indegree) increases with area within both regional (left)
518 and biogeographical (right) spatial domains (a-b). Each point represents the mean value across
519 every replicate in the aggregation procedure at a given area. Note that for visualisation purposes,
520 all x - and y -values in all datasets have been re-scaled to start at 0. The shape of the network

521 degree distributions is consistent across area at both regional and biogeographical domains. In
522 (c-d) two datasets are shown as illustration: *Garraf-PP* and *Galpar*, respectively (see
523 Supplementary Text 1). The cumulative probabilities of finding a species in the network that
524 has k links to resources in the network, are normalized by the mean number of links per species
525 in the network. One replicate for a subset of areas is shown for each dataset to facilitate
526 visualization. Each colour represents network degree distribution for a given area. From dark
527 blue, representing the smallest area (i.e. 1 spatial unit), to yellow, representing the largest area
528 for each dataset (40 spatial units for *Garraf-PP* and 373 spatial units for *Galpar*). Notice that
529 the starting point of each distribution changes with area, indicating that at smaller spatial scales,
530 the most specialized species of the network have more interacting partners than at larger spatial
531 scales. Yet, the shape of the degree distribution is preserved. The top-ranked model describing
532 the degree distribution of each ecological network across the area range (e-f). Although the
533 degree distribution of most ecological networks was characterised by the same function along
534 the range of areas, the specific shape of each function changed with area (see Supplementary
535 Figure 4). Area values were re-scaled between 0 and 1.

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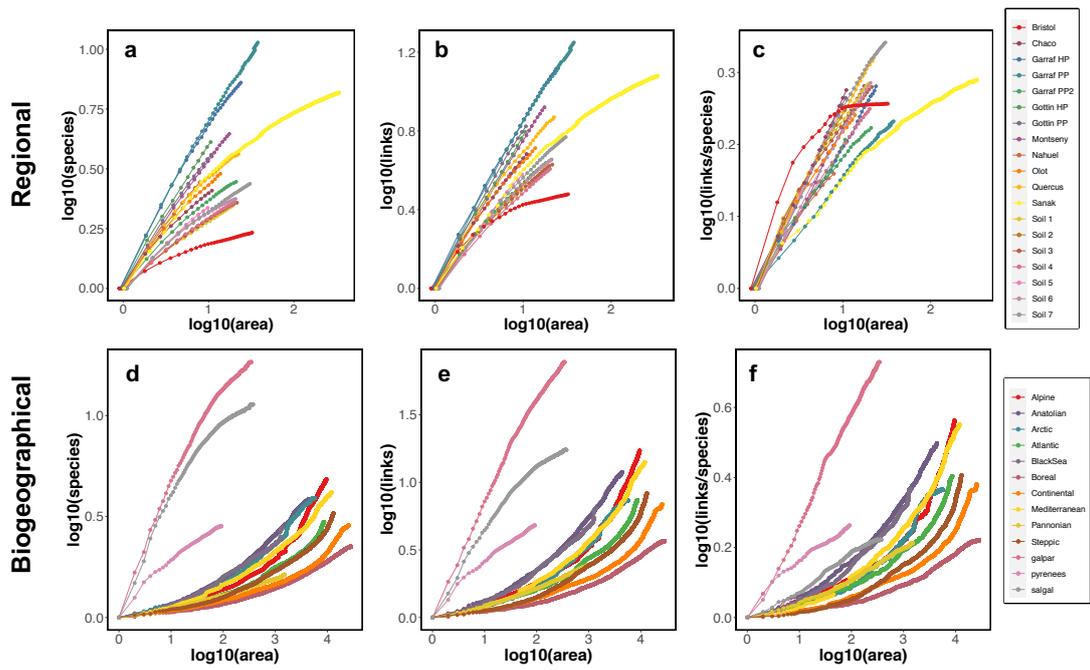
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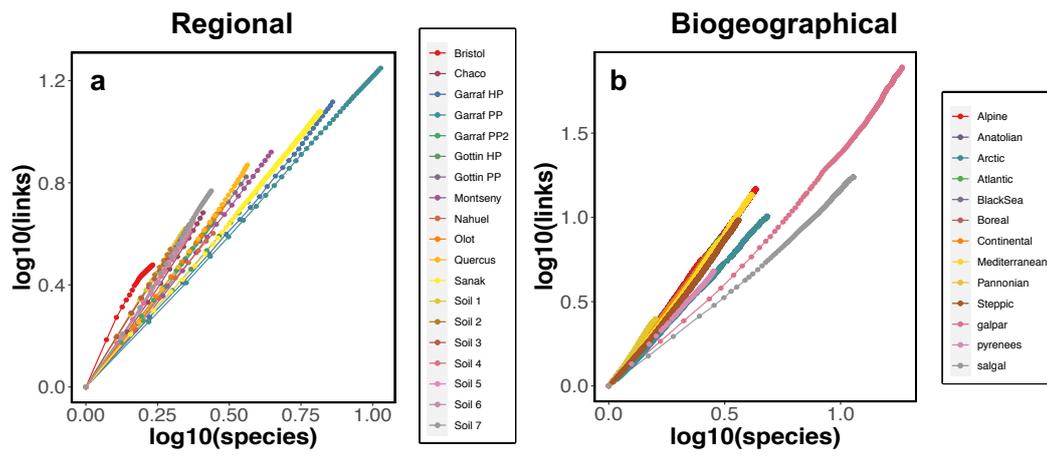
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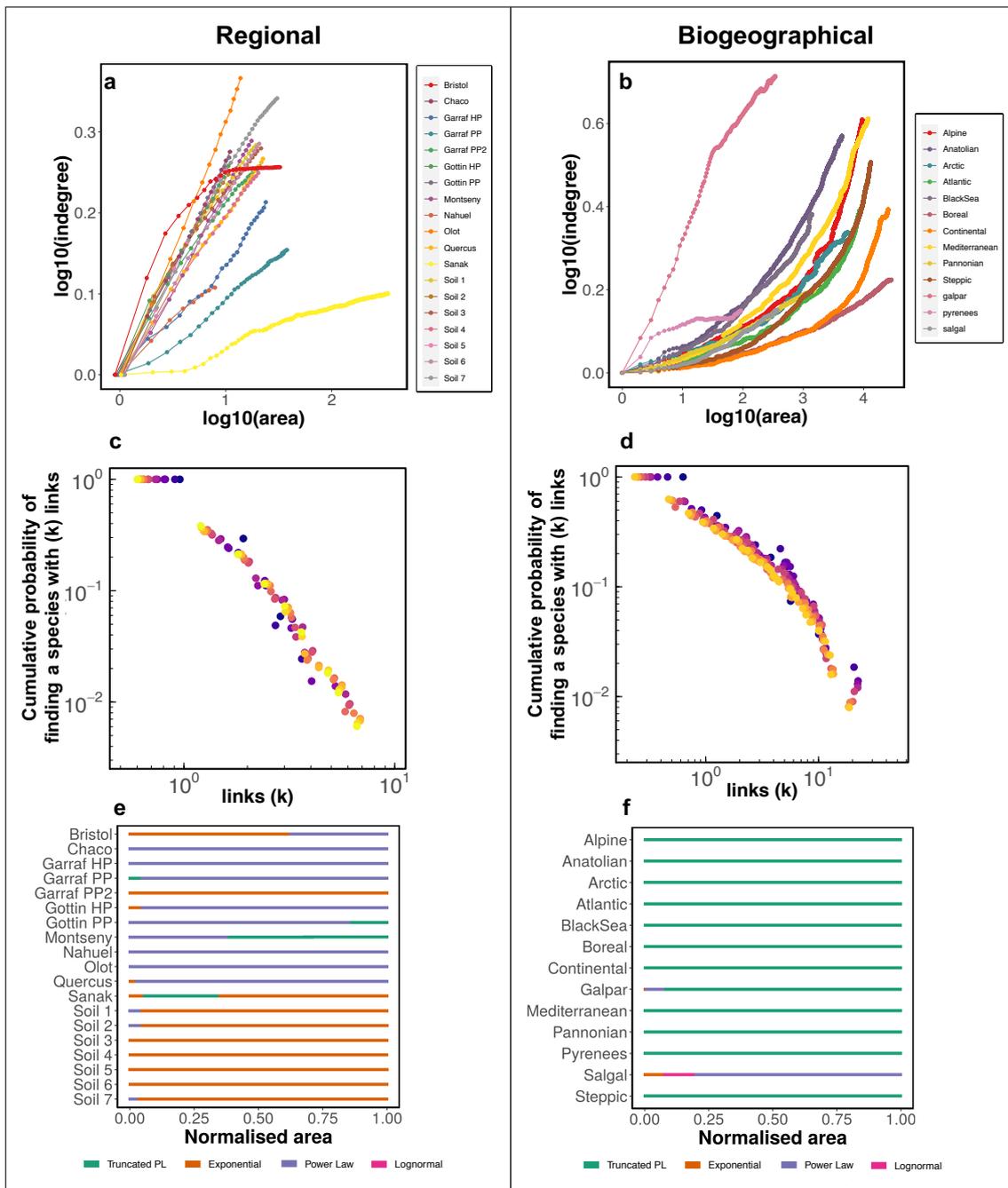
Figure 1

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Figure 2



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Figure 3