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2 Spatial analyses of multi-trophic terrestrial vertebrate assemblages in Europe

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4 **RUNNING TITTLE**

5 Distribution of multi-trophic food webs

6

7 Abstract

Aim While much has been said on the spatial distribution of taxonomic and phylogenetic diversity of vertebrates, how this diversity interacts in food webs and how these interactions change across space is largely unknown. Here, we analyzed the spatial distribution of tetrapod food webs and asked whether the variation in local food web structure is driven by random processes or by natural and anthropogenic factors.

13 **Location** Europe.

14 **Time period** Present.

15 **Major taxa studied** Tetrapods.

16 Methods We combined an expert-based food web (1140 species and 70,601 links) of all 17 European tetrapods with their respective spatial distributions. We mapped seventeen different 18 food web metrics representing complexity, chain length, vertical diversity and diet strategy 19 across Europe and tested whether their distribution reflects the spatial structure of species 20 richness using a null model of food web structure. Then, to avoid multi-collinearity issues, we 21 defined composite descriptors of food web structure that we then related to a set of 22 environmental layers summarizing both natural and anthropogenic influences, and tested their 23 relative importance in explaining the spatial distribution of European terrestrial vertebrate food 24 webs.

25 **Results** From the seventeen metrics, seven showed a non-random spatial distribution across

Europe and could be summarized along two major axes of variation in food web structure. The first was related to species richness, mean trophic level and proportion of intermediate species, while the second was related to connectance and proximity of species within the web. Both descriptors varied with latitudinal gradients. Best descriptors of food web structure were mean annual temperature and seasonality (positively correlated with the first axis), and human footprint (positively correlated with the second one).

Main conclusions We provide the first comprehensive spatial description of vertebrate food web structure across Europe, and demonstrate the importance of climate and anthropogenic pressure in shaping the spatial structure of European tetrapod food webs.

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36 KEY WORDS: biodiversity, environmental gradients, food web comparison, metaweb, network

37 properties, null model, tetrapod communities

38 INTRODUCTION

39 Documenting large-scale biodiversity distribution and understanding what drives variation 40 between or within different regions of the world has long fascinated naturalists (Wallace, 1876). 41 The recent and ever-increasing rise of large-scale distribution databases (e.g. IUCN, BirdLife, 42 Map Of Life) has led to new comprehensive analyses of biodiversity distribution. Thanks to 43 available data on species traits and phylogenetic relatedness, global and regional distributions 44 of species, traits and phylogenetic diversity are now well documented for terrestrial vertebrates 45 (Jetz & Fine, 2012; Jetz *et al.*, 2012; Mazel *et al.*, 2014, 2017).

46 Such measurements of biodiversity (taxonomic, functional and phylogenetic diversity) focus on a group of species co-occurring in a certain area or region, which are subsequently compared 47 48 with measurements of other areas to identify localities with higher or lower biodiversity (e.g. 49 hotspots vs. coldspots, Mazel et al. 2014). However, species assemblages are not just the mere sum of species co-occurring in an area, they share a myriad of biotic interactions (e.g. predation, 50 51 competition, facilitation, etc.) that originate a variety of ecological networks through space. 52 While past biogeographic studies have investigated how species or trait diversity vary in space 53 and the underlying role of environment (e.g. Davies et al., 2011; Safi et al., 2011; Mazel et al., 54 2017), we know little about the spatial distribution of ecological networks (Pellissier et al. 2017). 55

Food webs are representations of communities' trophic interactions, where each node in the network represents a species and each edge is a directional feeding interaction from a prey to a predator. Food web ecology has focused on the trophic relationships between species within discrete communities with the goal of inferring the underlying processes acting upon them, such as the relation between species diversity and food web structure, community assembly processes, and even robustness of those communities to species extinctions (Montoya *et al.*, 2006). However, since the pioneering work of Kitching (2000) on latitudinal gradients of

aquatic food-web structure, food web ecology has shifted from finding food web structural
generalities across isolated communities to searching for large-scale spatial distribution of
ecological networks, such as latitudinal gradients, and relations with climate and resource
availability (Post, 2002; Kortsch *et al.*, 2015; Wood *et al.*, 2015; Montoya & Galiana, 2017;
Pellissier *et al.*, 2017; Poisot *et al.*, 2017; Roslin *et al.*, 2017).

68 Large-scale spatial distribution of food web structure may be driven by multiple factors. First, 69 food web structure follows both species richness and compositional gradients (Riede et al., 70 2010; Baiser et al., 2012) and any process acting upon these features of biodiversity, such 71 environmental sorting of species, will cause food webs to be spatially structured (Pellissier et 72 al., 2017). Second, food web topology may reflect community adaptations to environmental 73 stability. The latitude-niche breadth hypothesis for instance postulates that species have more 74 specialized diets in the tropics and become more generalist towards the poles, as higher environmental stability and amount of energy in the tropics allow for greater species packing 75 76 (MacArthur, 1955; Schleuning et al., 2012). Yet, this hypothesis does not seem to be verified 77 across different systems (Cirtwill et al., 2015) and lacks testing across large spatial scales. 78 Third, resource availability in conjunction with disturbances and environmental variability may 79 also affect food web topology. Low resource availability for primary consumers limits species 80 richness and food chain length, while disturbances and ecosystem size drive food chain length 81 at intermediate levels of resource availability (Kaunzinger & Morin, 1998; Post, 2002). Again, 82 such observations are not ubiquitous (Zanden & Fetzer, 2007), and this last hypothesis has yet 83 to be tested across large environmental gradients and for complex (i.e. speciose) food webs.

Here, motivated by these hypotheses we built the first comprehensive food web of European terrestrial vertebrates. For this, we used a combination of expert knowledge and literature, and mapped the food web structure of all vertebrate assemblages naturally occurring in Europe, west Russia and Turkey, using a uniform spatial grid at 10 km resolution. Since the above88 mentioned hypotheses focus on different facets of food web topology we analyzed a large set 89 of food web descriptors such as complexity metrics (species richness, connectance, number of 90 trophic interactions), vertical diversity metrics (proportion of basal, intermediate and top 91 predator species), feeding strategy metrics (generality, vulnerability and omnivory), and trophic 92 level metrics. We compare local observations of food web metrics to a null model in order to 93 reveal significant associations with environmental variables.

Most network metrics cannot be dissociated from each other because they covary with either the number of species or connectance (Vermaat *et al.*, 2009; Riede *et al.*, 2010; Baiser *et al.*, 2012; Poisot & Gravel, 2014). Hence, we decomposed the food web structure into two composite descriptors (Pellissier *et al.*, 2017) and investigated how the environment, landscape, and anthropogenic pressure influenced their spatial distribution.

99 We expected annual temperature and precipitation to be good predictors of food web spatial 100 structure because they are major drivers of species sorting and community assembly over large 101 spatial scales (Currie, 1991; Vázquez & Stevens, 2004; Riede et al., 2010; Ledger et al., 2012). 102 Likewise, ighly productive sites should provide more resources for consumers, therefore 103 supporting higher trophic levels (Wright, 1983; Post, 2002). Thus, we expected higher trophic 104 levels in areas with high productivity. We also anticipated habitat fragmentation and human 105 disturbance to shape European food webs. High levels of fragmentation may reduce the strength 106 of interactions between species or even prevent species from interacting, ultimately leading to 107 networks with lower link density (Hagen et al., 2012).

108

109 MATERIALS AND METHODS

110 Study area and species distributions

111 The study area included Europe (excluding Macaronesia region and Iceland), and western 112 regions of Turkey and Russia (hereafter referred to as 'Europe'). We extracted species ranges

113 for terrestrial vertebrates (tetrapods) naturally occurring within the study area from Maiorano 114 et al., (2013). In total, our analyses focused on 510 bird, 288 mammal, 239 reptile and 103 115 amphibian species (see Appendix S1 Table S1.1 in Supporting Information for full species list). 116 Species range data followed a regular grid of 300 m resolution (WGS84), where cells took 117 values of zero for unsuitable habitat, one for secondary habitat and two for primary habitat 118 (Maiorano et al., 2013). We treated secondary and primary habitat equally as "suitable habitat". 119 All species range maps were up-scaled to a 10x10 km equal-size area grid (ETRS89; total of 120 78,873 cells). We considered species potentially present in a 10x10 km cell (hereafter referred 121 as local assemblage) when they had least one 300 m suitable habitat cell within it. In 122 supplementary material S3 we showed that the proportion of suitable habitat needed for a 123 species to be present in each cell did not affected the spatial distribution of species richness nor 124 connectance, hence not affected the spatial distribution of local food web structure (see below).

125

126 European tetrapod metaweb and local food web structure

127 A trophic metaweb compiles all predator-prey interactions between species of a given regional species pool (Pascual & Dunne, 2006). Here, we designed the most complete metaweb of 128 129 European terrestrial vertebrates from expert knowledge, published information and field guides 130 (see supplementary material for reference list). As in previous studies (e.g. Lurgi et al., 2012), 131 all vertebrates species whose diet did not include another species of the metaweb (such as 132 herbivores, insectivores, piscivores and detritivores) were defined as basal species. Then, we 133 searched for trophic interactions between species that fed upon other vertebrates (and 134 omnivores) from an exhaustive literature review. We defined a trophic interaction as predation 135 on any life stage of a species (e.g. egg and larval when applicable, juvenile or adult). Trophic 136 interactions between a predator and a prey were identified from published accounts of their observation, morphological similarities between potential prey and literature-referenced prey 137

and, in the absence of this information, the diet of the predator's sister species. Twelve general
diet categories were added to the metaweb, which included detritus, coprophagous, mushrooms,
mosses and lichens, algae, fruits, grains, other plant parts, invertebrates, fish, domestic animals
and carrion.

The metaweb comprised 70,601 trophic interactions distributed across 1140 terrestrial vertebrate species (60% of basal species, from which X % were herbivores and X % of nonherbivore basal species, 33% of intermediate species and <1% of top predator species) and a connectance of 0.05. On average, species had 62 interactions (including prey and predator interactions) and were 2 interactions away from each other.

We defined local food webs by intersecting the metaweb with local community composition (Gravel et al. 2018). In the few cases where a given species was present in a cell, but had no available prey, or did not share a common habitat type with any of its prey, the species was considered absent in that particular location (i.e. assuming a false positive in the distribution data; Gravel *et al.*, 2011). We assumed that basal resources are widely distributed across the landscape and therefore that basal species always have a resource.

153 For each local food web, we calculated seventeen food web properties pertaining to four 154 groups: complexity, strategy, vertical diversity and trophic level. Complexity metrics included 155 species richness, connectance, clustering coefficient, characteristic path length and link density 156 (average distance between species and average number of interactions per species, 157 respectively). Strategy metrics refer to dietary niche properties of species, and included 158 generality (mean number of prey) and vulnerability (mean number of predators), their 159 respective standard deviations, proportion of omnivore species and average trophic similarity 160 between species. Vertical diversity metrics quantify the proportion of species along three major 161 trophic levels, basal, intermediate and top level. Note that we defined basal species as non-162 autotroph species without terrestrial vertebrate prey. Trophic level metrics refer to vertical

trophic position of species within a food web, and included the mean trophic level and the maximum trophic level. See Table 1 for the list of metrics and their definitions. Food web metrics were calculated using the 'igraph' and 'cheddar' *R* packages (Csardi & Nepusz, 2006; Hudson *et al.*, 2013) in *R* v. 3.4.1 (R REF).

167

168 Climatic, energetic and habitat variables

169 We extracted four climatic variables from the WorldClim database (Hijmans et al., 2005) at 170 30° resolution: annual mean temperature, temperature seasonality (standard deviation of 171 monthly mean temperature), total annual precipitation and coefficient of variation of 172 precipitation. We chose these variables since they correlate with vertebrates ranges (Boucher-173 Lalonde et al., 2014). We approximated the amount of resources available to the primary 174 consumers in each cell with estimates of net primary productivity (grams of carbon per year at 175 0.25 decimal degrees spatial resolution; Imhoff et al., 2004). We also represented the 176 anthropogenic influence on natural landscapes using the human footprint index from the Last 177 of the Wild database v2 (1 km spatial resolution; WCS & CIESIN, 2005). We resampled all 178 climatic variables, primary productivity and human footprint data by averaging at each 10x10 179 km cell. We also measured habitat diversity and heterogeneity using, respectively, the Shannon-180 Weiner and evenness indices applied to the GlobCover V2.2 habitat classification at 300 m cell 181 resolution. See Appendix S2 in Supporting Information for more information about the spatial 182 distribution of the climatic, energetic and habitat variables.

183

184 Statistical analyses

Our analyses consisted of three sequential steps. 1) We checked if the spatial distribution of each local metric is different from random using a null model, and selected the metrics that differed from null expectations for subsequent analyses. 2) We reduced the complexity of the retained metrics applying a principal components analysis (PCA) and selecting the first two axes of variation. 3) We related these two axes of variation to climate, resource availability, habitat diversity and human disturbance using generalized additive models (GAMs).

191

192 *Is the spatial distribution of food web properties random?*

193 Food web structure may vary with species richness, independently of any other constrains 194 acting upon it (e.g. environment). We thus built a null model to test whether European local 195 food webs and their associated properties could result from a draw from the European species 196 pool, irrespective of their interactions. The null hypothesis is that species are randomly 197 distributed in space, independently of the local environment and of their position in the 198 metaweb. The null model consisted of randomly drawing species from the metaweb for each 199 cell and then extracting the correspondent local food webs. We applied three constraints to the 200 null model, 1) species richness is the same as observed, 2) with respect of the proportion of 201 squamates, birds, mammals and amphibians, 3) non-basal species needed at least one vertebrate 202 prey (excluding diet categories) to be included in the food web (Gravel et al., 2011). We 203 randomly drew and kept food webs that met all three conditions, until we had 999 food webs 204 for each value of each cell (from 10 to 305 species). We then re-calculated the 17 food web 205 metrics to obtain a distribution of metrics under the null hypothesis (Table 1). For each cell, we 206 compared the observed food web metrics to the corresponding null distribution and computed 207 the associated *p-value*. We adjusted *p-values* for multiple comparisons using a false discovery 208 rate method based on Benjamini & Hochberg, (1995), present in the function p.adjust in the 209 'stats' R package. We retained food web metrics that had 90% of rejection rate, i.e. 90% of all 210 local food web metrics were significantly different from ones of random assemblages. 211 Considering that we computed one test per cell (total of 78,873 cells), a food web metric should 212 be significantly different from random in approximately 71,000 cells in order to be kept in our

analysis.

214

215 *How to reduce the dimensionality in local food web properties?*

216 Many food web metrics are correlated (Vermaat et al., 2009) either because of their 217 mathematical formulation or because of combinatory constraints (Poisot & Gravel, 2014). We 218 applied a PCA on the eight retained variables over the 78,873 cells of Europe (Table 1) to 219 analyze the most insightful axes of variations between these metrics. This allowed not only 220 understanding how food web metrics co-vary with each other, but also summarizing food web 221 structure of European assemblages (as a whole) into a set of meaningful axes. We emphasize 222 that the correlation structure among metrics we analyzed is not only driven by the fundamental 223 constraints linking metrics referred above, but also driven by the effect of spatial variation in 224 food web composition. From the PCA, we kept only the axes that explained each at least 20% 225 of the total variance, hereafter referred as food web structural composite descriptors. This 226 analysis was performed in R using the 'ade4' package (Dray & Dufour, 2007).

227

228 How to statistically relate food web structural descriptors to environmental predictors?

We related positions on the PCA axes to spatial drivers (climate, energetic and habitat variables) using GAMs. GAMs are more flexible than generalized linear models, which are more appropriate given we had no *a priori* expectations regarding the shape of the relationships between response and predictor variables. To avoid fitting overly complex relationships, we constrained the GAMs with a maximum smoothing degree of 3 (i.e. polynomial of degree 2, maximum). All models were fitted using the function *gam* present in the 'mgcv' *R* package (Wood, 2017).

Note that both the environmental variables and food web topological metrics inevitably showsome level of spatial autocorrelation. To account for spatial dependency unexplained by the

238 spatial drivers, we built an autocovariate variable for each of the composite descriptors to 239 estimate how much the response variable for any site reflects the values of the neighboring sites 240 (Dorman et al. 2007; function autocov dist in 'spdep' R package). However, since this 241 autocovariate was unconditional to environmental variation (i.e. the response variable could 242 show a spatial autocorrelation because the environment is itself autocorrelated), we modelled 243 each autocovariate variable (for each structural composite descriptor) to the set of 244 environmental variables using a bootstrap aggregating model (random forest function in 245 'randomForest' R package; Liaw et al., 2002). We then extracted the residuals of the model and 246 used them as spatial variables independent of the spatial predictors in the GAMs. Hereafter, these variables will be referred as spatial residuals variables. 247

248 We used the permutation accuracy importance method (Strobl et al., 2007, 2009) to estimate 249 the importance of each predictor variable on the spatial distribution of local food web metrics. 250 The predictor in test is randomized so that its original association to the response variable is 251 broken. Then, the randomized variable (through means of permutations) and the remaining 252 unchanged predictors are used to predict the response. A variable importance score is then 253 measured as the Pearson correlation coefficient (ρ) between the original prediction and the 254 prediction after permutation of the selected predictor (Strobl et al., 2009). The lower the 255 correlation, the more important the variable is. This whole procedure was repeated 1000 times. 256 To facilitate the interpretation of results, we reported the average $1 - \rho$. Values close to 1 257 reflected high importance, values close to 0, no importance.

In supplementary material S6 we show that using individual food web metrics or the composite descriptors from the PCA yields equivalent results and relationships with the predictors. Hence, we opted to PCA axes as they summarize the main dimensions of food web structure.

263 **RESULTS**

264 Local food web structure

265 Most of the seventeen food web structural metrics showed a strong spatial structure (Figure 1 266 for a selection of six metrics; see Appendix S3 Fig. S3.2 for all other metrics, and Table 1 for 267 descriptive statistics). Assemblages in northern latitudes (United Kingdom, Denmark and 268 Scandinavian Peninsula) and in mountain ranges (such as Alps and Carpathians) had fewer 269 species, with shorter food chains and higher proportion of basal species than in the rest of 270 Europe. Species in these locations had larger diet breadths (i.e. higher generality) on average. 271 Food webs in central and eastern Europe were more speciose and with longer food chains. 272 Within these food webs, species were more evenly distributed between basal and intermediate 273 species, with top predator species always representing less than 5 % of the community. In 274 southern Europe, along the Mediterranean basin, food webs were the most species rich and had 275 the highest linkage densities and clustering coefficients. In this region, food chains lengths were 276 as high as for continental food webs, while connectance in the Anatolian region (Turkey) and 277 southeast of Spain, was as high as in near arctic assemblages. In other words, assemblages 278 across the Mediterranean basin were the most species rich and highly interacting.

279

280 Deviation of local food web structure from random assembly

Deviations of local food webs from the null expectation varied between the different metrics and across the species richness gradient (Table 1; see Appendix 4 Fig. S4.3 in Supporting Information). We observed that only seven food web metrics differed at least 90% of the times from what could be expected from random draws from the metaweb (link density, connectance, proportion of intermediate and omnivore species, mean trophic level, characteristic path length and cluster coefficient). However, at low levels of species richness, most of these metrics do not differ from a random assembly (see Fig. S4.3). The remainder food web properties consistently fell within the random intervals irrespective of species richness (e.g. vulnerability, generality, mean and maximum trophic level; Table 1). In other words, the spatial distribution of these metrics could be explained purely by their correlation with the distribution of species richness and its spatial drivers.

292

293 Composite descriptors of the local realized food webs

294 Two main axes of variation, explaining approximately 76.6% of the total variance, 295 summarized the co-variation of six food web properties (link density, connectance, proportion 296 of intermediate and omnivore species and characteristic path length; Table 2; Fig. 2). The first axis, hereafter called the richness composite descriptor, explained 49.2% of structural variation 297 298 and was negatively related with species richness, link density (average number of interactions), 299 proportion of intermediate and omnivore species and mean trophic level (Table 2; Fig. 2). This 300 result indicates that food webs with more species have more links per species, a higher 301 proportion of intermediate species (i.e. proportion of species having both prey and predators in 302 local food webs) and more species at higher trophic levels.

The second descriptor, hereafter named the *connectance* composite descriptor, explained 27.5% of the total variance and was mainly related to food web complexity, through connectance, clustering coefficient and characteristic path length (Table 2; Fig. 2). Along this descriptor, connectance and clustering coefficient were both negatively correlated with characteristic path length, suggesting that food webs with lower connectance were less clustered and had proportionally longer paths between species.

309

310 Environment drivers of local food web descriptors

311 Environmental drivers explained a significant proportion of the variance of the two composite

descriptors (74.3% of *richness*, and 42.5% for *connectance*; Table 3). The *richness* composite

313 descriptor had a strong, linear and negative relationship with temperature variables (mean 314 annual temperature and temperature seasonality; Fig. 3a), with sites with high temperatures and 315 seasonality supporting richer assemblages, with more intermediate species, higher link densities 316 and trophic levels. Net primary productivity, had a weaker importance relatively to temperature 317 variables, but had a negative correlation with the *richness* composite descriptor. We observed 318 an increase in species richness and link density up to intermediate productivity from lower to 319 intermediate productive areas; however, the contribution of net primary productivity to food 320 web structure was close to zero in intermediate to high productivity areas (Fig. 3a). Human 321 footprint had the smallest effect on the richness composite descriptor, which seemed to saturate 322 above intermediate levels of human footprint.

Conversely, the variation in the *connectance* composite descriptor was most affected by mean annual temperature and human footprint (Table 3). Food webs had higher connectance and more closely interacting species at higher annual average temperatures, and the showing a clear positive effect of human foot print up to intermediate values, after which the effect stabilizes (Fig. 3b). Finally, total annual precipitation correlated positively with the *connectance* composite descriptor at low to intermediate precipitation, but negatively at larger precipitation levels (Fig. 3b).

330

331 Spatial residuals variables were only relevant for the *connectance* composite descriptor,
332 indicating that other spatial variables not considered here can be affecting the spatial
333 distribution of food web structure.

334

335 **DISCUSSION**

Large-scale variation of food web structure is still largely unknown in terrestrial systems.Thanks to the compilation of a large dataset comprising pairwise trophic interactions between

European terrestrial vertebrates, their geographical distributions and habitat preferences, weextracted local food webs and successfully explored how they vary across Europe.

340 The latitudinal gradient of diversity is one of the most conspicuous patterns of biogeography. 341 We not only re-visit this relationship for European terrestrial vertebrates (Fig. 1), but also show 342 that it influences food web spatial structure. Most food web metrics, particularly those related 343 to feeding strategies and vertical diversity metrics, did not differ from what would be expected 344 under random assemblages of species, indicating that species richness was the key driver of 345 their variation, especially at species-poor locations. However, species richness failed to explain 346 the spatial distribution of other important features of food web structure, such as mean trophic 347 level, link density and connectance. This reveals that even at large spatial scales and resolutions, 348 the fingerprint of species interactions is visible on biodiversity distribution, but cannot be 349 summarized by species richness alone.

The description of ecological networks with reduced dimensions can provide understanding 350 351 on how they are structured within a community, from a functional (Eklöf et al., 2013) or 352 structural perspective (Baiser et al., 2012). The reduction analysis of food web metrics revealed 353 two major axes of structural variation, one mainly related to species richness and the other to 354 connectance. We expected species richness and connectance to behave independently from each 355 other and form the two major axes of variation in food web structure (Martinez, 1994; Riede et 356 al., 2010; Dunne et al., 2013). Indeed, Vermaat et al. (2009) showed a similar correlation 357 structure among food web metrics for 14 empirical food webs, and a similar decomposition was 358 also observed by Baiser et al. (2012) for North American aquatic food webs. On the other hand, 359 the constant connectance hypothesis (Martinez 1992) poses that the proportion of realized 360 interactions within a food web (i.e. connectance) is independent of species richness if link 361 density increases proportionally with the number of species. Our analyses confirmed these two 362 major dimensions for on European terrestrial vertebrate food webs .

Climatic gradients, namely temperature and precipitation, have long been observed as drivers 363 364 of biodiversity at both local and global scales (Evans et al., 2005). Climate can affect food web 365 structure in several ways. First, it acts as a filter on species assembly (Keddy, 1992), which may 366 affect the functional composition of communities and therefore food web structure (Lurgi et 367 al., 2012; Blanchard, 2015). Second, climate variability may directly affect food web structure. 368 A more stable climate may allow for longer food web chains and narrower diet niches (Menge 369 & Sutherland, 1987; Vázquez & Stevens, 2004; Cirtwill et al., 2015),. Interannual temperature 370 variability has also been shown negatively correlated with modularity (Welti & Joern, 2015). 371 Our results show that European variation in food web structure, summarized by two composite 372 descriptors, is mostly related to annual average temperature and its seasonality. While 373 environmental constancy, particularly in climate conditions, is believed to lead to more speciose 374 communities, we find the opposite here, where climate variability was positively associated 375 with species-rich and longer food webs. There could be several reasons for our observations. 376 On the one hand, our measure of climate variability was calculated between 1970 and 2000, 377 which is likely not representative of the past climatic history to which European terrestrial 378 vertebrates were exposed to. Environmental constancy at larger temporal scales may be a more 379 important driver of species richness and food web complexity than seasonal variability. For 380 instance, Dalsgaard et al., (2013) found a link between historical climate change (across the last 381 21,000 years) and present day pollinator network structure at the global scale. On the other 382 hand, the observed gradient in temperature seasonality coincides with important processes that 383 shaped vertebrate distribution across Europe. Baquero & Tellería (2001) suggest that the 384 decreasing mammalian richness from East-central Europe outwards is related to a decrease in 385 available land area (peninsular effect on species distributions), but also to environmental 386 harshness to the north, loss of suitable habitats and population bottlenecks during glacial periods 387 to the west, and human pressure since Neolithic times to the south - regions that coincide with

388 lower temperature seasonality and lower water availability (Hawkins et al., 2003). This is not 389 to be confounded with endemicity, which is higher in southern regions of Europe (Baquero & 390 Tellería, 2001). Mouchet et al. (2015) have also noted that species richness across terrestrial 391 vertebrates was more driven by land-use covariates than climate covariates toward south and 392 southwestern Europe. Hence, although human footprint did not stand out as an important driver 393 in our models, the combination of long-term and present human intervention and ancient 394 climatic fluctuations, which coincide with the temperature seasonality gradient, could be 395 driving the observed relationship between species richness, trophic food chain length and 396 seasonality.

397

398 Productivity is often hypothesized to drive the latitudinal gradient of species richness, as 399 higher amounts of energy available to primary consumers should support more diverse 400 communities (Hurlbert & Haskell, 2003). Although the overall effect of productivity was 401 weaker than climate, we found an influence on the richness composite descriptor at limiting 402 productivity levels (from low to intermediate primary productivity). Unproductive locations 403 were associated with species-poor networks that had lower trophic levels and lower link density 404 (both via the richness composite descriptor and by mean trophic level model, as shown in 405 supplementary material). Previous empirical studies have shown similar relationships, with 406 food web structure in terms of trophic level, omnivory, and proportion of top predators co-407 varying positively with primary productivity (Vermaat et al., 2009). Further, our results agree 408 with the theoretical expectation that higher resource availability and lower trophic levels should 409 propagate up the food web, promoting rich species assemblages with longer trophic chains and 410 supporting species at higher trophic level, and that this relationship should be stronger in the 411 least productive environments (Jenkins et al., 1992; Post, 2002).

412 Human presence may lead to changes in land-use, habitat fragmentation and pollution, which

413 in turn can negatively affect biodiversity (Barnosky et al., 2011; Cardinale et al., 2012) and 414 food web structure (Evans et al., 2013). Accordingly, human footprint was among the most 415 important predictors of vertebrate food web structure. It was strongly related to the connectance 416 composite descriptor, with a negative relationship to the proportion of realized links and species 417 proximity in the web (Fig. 3b; Table 3). However, in this case we cannot assume this to be a 418 cause-effect relationship, because the effect of human footprint was only noticeable below 419 intermediate levels, and because there is a strong spatial coincidence between human footprint 420 and climate. Climatic conditions and resource availability may affect the spatial distribution of 421 human density and species diversity alike, which would explain why the two composite 422 descriptors correlate positively with human population densities (Araújo, 2003). Indeed, despite 423 the weak importance of human footprint on the richness composite descriptor (Table 3), we 424 observed a positive relationship at low to intermediate levels of human disturbance (Fig. 3a). Also, even though species richness and connectance metrics were nearly orthogonal in our 425 426 ordination space (Fig. 2), they were negatively correlated at low to intermediate values of 427 richness. The highest connectance was found in northeastern Europe, where both human 428 presence and species richness were lowest (Fig. 1; see also Appendix 3 Table 3.2). In these 429 areas, vertebrate assemblages were mostly composed by lower trophic level species and 430 comprised a few highly generalist predators, leading to highly dense and realized foods webs. 431 Hence, the negative relationship between the *connectance* composite descriptor and human 432 footprint is more likely arising from low values of species richness.

The importance of the spatial residuals variable on the *connectance* composite descriptor model suggested the presence of other important spatial variables. Since we used species distributions to design European vertebrate assemblages, biogeographical processes, such as barriers to species dispersal, island sizes, presence of peninsulas or even other biotic factors, could lead to spatial similarities and/or dissimilarities in food web structure not explained solely by climate and primary productivity, but rather through compositional turnover (Kortsch *et al.*,
2018). Further work is needed to include such processes under a spatial analysis framework of
food web structural turnover (Poisot *et al.*, 2012).

441 Here, we focused on terrestrial vertebrates and so, by definition our local food webs were 442 incomplete. To address this issue, we included nodes of general diet categories, such as 443 invertebrates, plants and fish, to represent absent trophic information from the non-vertebrate 444 components of the food webs. More than 70% of our species had their diet composed (entirely 445 or partly) of diet categories, thus we are likely missing a large part of food web complexity and 446 structure associated with the non-vertebrate portion of our food webs. In addition, given that 447 diet categories represented more than one trophic level (primary producers, but also consumers 448 like fish and invertebrates), our analysis overestimated the proportion of basal species, 449 particularly of non-herbivore basal species. Yet, the generality of the hypotheses explored here 450 should still be applicable. The positive effect of resource availability should reverberate from 451 lower to higher trophic levels (Post, 2002), thus being reflected on purely vertebrate webs which 452 are composed of species at generally high trophic levels. Moreover, resource availability has 453 been shown to positively impact taxonomic diversity across the taxa represented in our food 454 webs, and at similar scales (Waide et al., 1999). Therefore, we are confident that the patterns 455 we observe reflect the structuring effects of the environment and resource availability on 456 European terrestrial food webs.

Two limitations to our design are the even contribution of each prey to a predator's diet and the fact that trophic interactions were constant in space (i.e. if two species interacted in the metaweb, they always interacted across their intercepted geographical range). The former implied that we did not account for biomass or energetic requirements (in contrast, weighted food webs interactions may be defined by biomass relationships) and as consequence we may have inflated omnivory and connectance. The latter implied that adaptability in species' diets 463 and behaviors was not taken into account (e.g. predator diet shift due to presence of competitors 464 or prey behavioral changes in function of predator presence; Preisser et al., 2009; Van Dijk et 465 al., 2008; Poisot et al., 2012) and as a consequence our webs may have an inflated number of 466 trophic interactions. Further, environmental conditions may also influence the realization of 467 interactions, which would affect the spatial distribution of food web structure. In addition, 468 trophic interactions in our metaweb were defined based not only on empirical studies, but also 469 on a potential array of prey for each predator species, which may lead to inflated generality and 470 vulnerability. More work is necessary to quantify the level of uncertainty related to how 471 metaweb and local food webs were defined. For instance, this could be done by using highly 472 resolved empirical food webs and quantifying how their topological properties differ, relatively 473 to food webs obtained using the methodology described here.

474 Nevertheless, this pioneer work sheds light into how food webs are structured across
475 continental scales, and serves as an example for future biogeographical food web studies that
476 seek to understand and predict biodiversity patterns.

477

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670 Tables

Table 1. Food web properties, respective mean, standard deviation and null rejection rates across Europe. Rejection rates in bold highlight

Food web property		Definition	Mean (SD)	Rejection rate
Species richnes	S	Number of species	194.8 (40.14)	N/A
Connectance		Proportion of realized links that occur in a web.	0.084 (0.01)	0.99
Link density		Average number of links per species.	17.33 (3.26)	0.99
Clustering coefficient		Probability of linkage of two species, given that both are linked to a third species.	0.28 (0.03)	0.99
Characteristic p	ath length	The mean shortest food chain length between species pairs	1.83 (0.03)	0.99
Vulnerability		Maan and standard deviation of number of modetars non-species	1.01 (0.01)	0
SD of Vulnerability		 Mean and standard deviation of number of predators per species. 	0.71 (0.08)	0
Generality		Man and the last last time from the framework in	2.33 (0.21)	0.86
SD of Generality		- Mean and standard deviation of number of prey per species	2.26 (0.23)	0.85
Maximum tropl	nic similarity	Mean maximum number of links (in- and outward) shared between all pairs of species.	0.75 (0.02)	0.77
Proportion of	non-herbivores	Proportion of species that prey on non-plant diet categories	0.53 (0.03)	0.53
basal species	herbivores	Proportion of species that prey exclusively of plant diet categories	0.04 (0.01)	0.43
Proportion of in	termediate species	Proportion of species with prey and predators.	0.42 (0.03)	0.96
Proportion of to	p predator species	Proportion of species without any predators.	0.01 (0.01)	0
Proportion of omnivores Proportion of species that fee		Proportion of species that feed on more than one trophic level.	0.43 (0.03)	0.96
Mean trophic level		Mean prey average trophic level	2.35 (0.08)	0.96
Maximum trophic level		Maximum prey average trophic level	3.58 (0.14)	0

672 variables (rejection rate > 90%) that were retained in the subsequent analyses.

- Table 2. Correlation between six food web properties and the two major principal components
- 675 axes of the PCA (richness and connectance composite descriptor). In total, both composite
- 676 descriptors explained 76.6% of food web spatial variance (measured by this six variables).

Topological metric	<i>Richness</i> composite descriptor	<i>Connectance</i> composite descriptor	
Species richness	-0.45	0.14	
Connectance	0.13	-0.64	
Link density	-0.44	-0.15	
Characteristic path length	-0.24	0.48	
Cluster coefficient	-0.06	-0.50	
Proportion of intermediate species	-0.40	-0.19	
Proportion of omnivore species	-0.37	-0.1	
Mean trophic level	-0.47	-0.09	

677

Table 3. Variable importance for each structural composite descriptor model based on "permutation accuracy importance" method. In the *richness* composite descriptor model, temperature variables (annual average and seasonality) were the most important variables. Whereas in the *connectance* composite descriptor model, spatial residuals were the most important variable, suggesting that other spatial processes are acting on this composite descriptor, not accounted by the other variables. *Richness* descriptor model explained 68.9% of the variance, while *connectance* composite descriptor model explained 38.0%.

	<i>Richness</i> composite descriptor	<i>Connectance</i> composite descriptor
Spatial residuals	0.11	0.37
Average annual Temp.	0.41	0.35
Temp. seasonality	0.46	0.11
Precipitation	0.00	0.08
Coeff. of var. precip.	0.02	0.03
Shannon index	0.08	0.08
Habitat evenness	0.03	0.00
Primary productivity	0.11	0.11
Human footprint	0.02	0.25

687 **Figure captions**

688

689 Figure 1. Spatial distribution of six metrics of the European tetrapod food webs: species 690 richness, link density, connectance, characteristic path length, proportion of intermediate 691 species and proportion of omnivore species. For a detailed description of these metrics see 692 Table 1. The distribution of the 16 food web metrics is provided in Appendix S3, Figure S3.2 693 in Supporting Information.

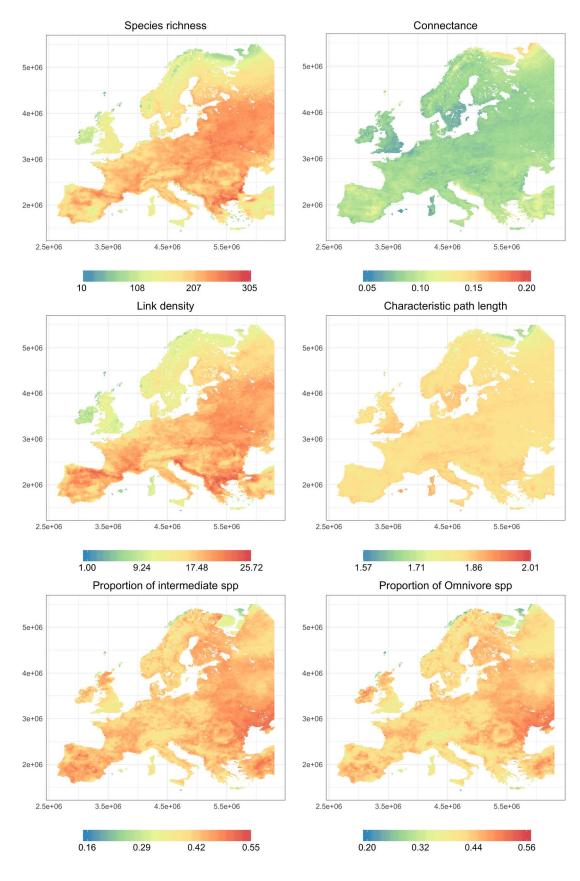
694

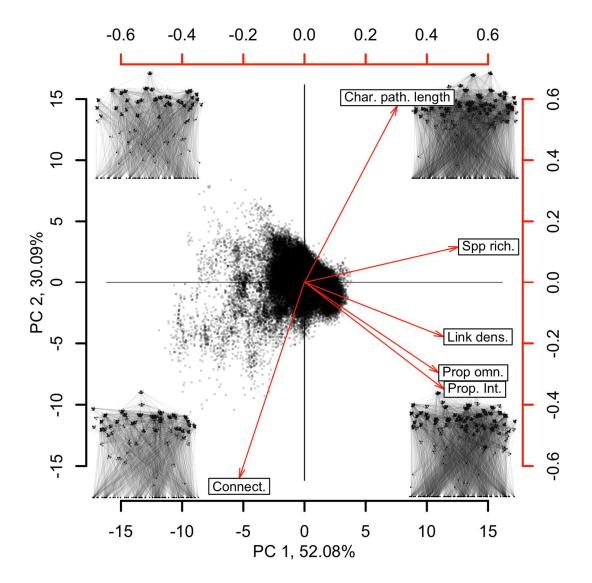
695 Figure 2. Principal components analysis (PCA) of European food web metrics. Red arrows 696 represent the direction and value of correlations between individual topological metrics and 697 each structural food web descriptors. The first component (richness structural composite 698 descriptor) was negatively correlated with species richness (Spp rich.), link density (Link 699 dens.), proportion of intermediate (Prop. int.) and omnivore (Prop. omn.) species and mean 700 trophic level (Mean TL). The second component (connectance composite descriptor) was 701 related highly correlated with connectance (Connect.), characteristic path length (Char. path 702 lenght) and cluster coefficient (Cluster coeff.). The four food webs representing the general 703 typology of food webs in each quadrant, and were drawn from the closest point to the centroid 704 of each quadrant.

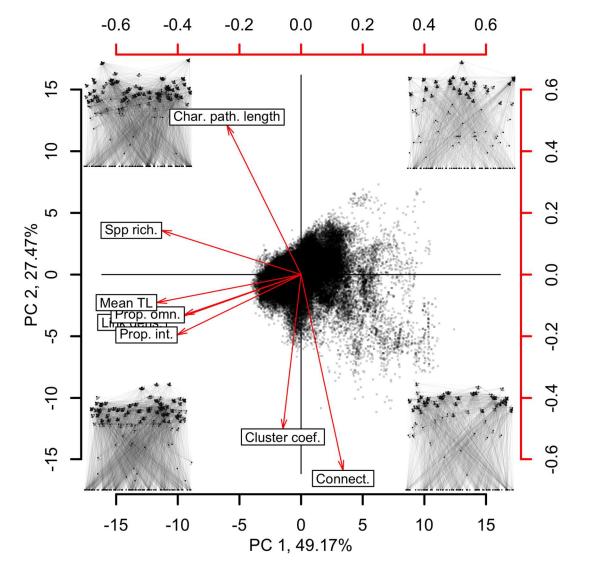
705

706 Figure 3. Partial response plots of (a) Food web richness composite and (b) connectance 707 composite descriptor models of the European food web in function of the climatic and landscape 708 predictors. Lines are the estimated effects of each predictor with the respective 95% confidence 709 intervals shaded in grey. Note that these intervals are very narrow. For single food web metrics 710 see supplementary material S6.

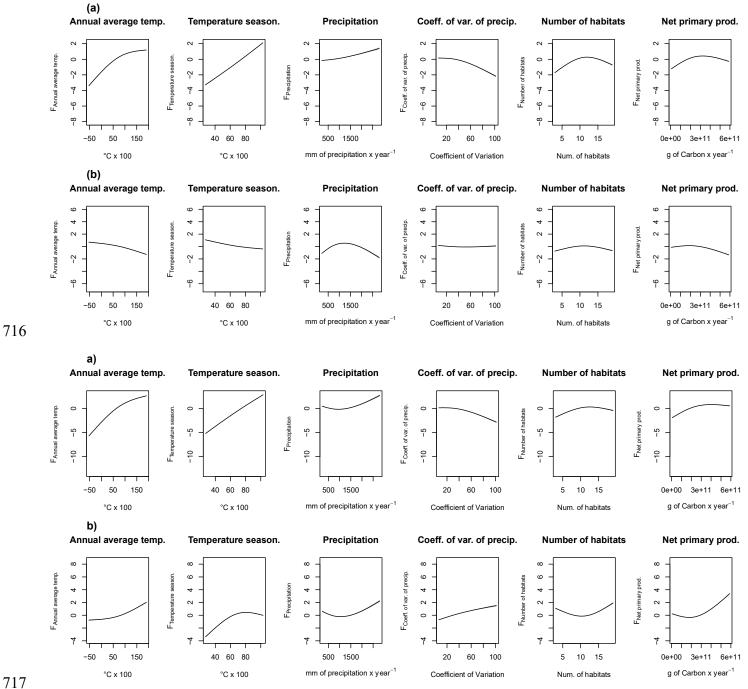
711 Figure 1.











- 718 Supporting information

719 Appendix S1 contains: Table S1.1.: List of the tetrapod species considered in the analysis (in

- 720 XLSX format).
- 721
- 722 Appendix S2 contains: Figure S2.1.: Spatial distribution of climatic variable, primary
- 723 productivity, habitat diversity and human productivity.

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725 Appendix S3: Suitable habitat threshold sensitivity analysis.

- 727 Appendix S4 contains: Table S4.2.: Pairwise spearman correlation between food web metrics;
- 728 Figure S4.2.: Spatial distribution of individual food web metrics.
- 730 Appendix S5 contains: Figure S5.3.: Local food web metrics and null distributions.

- 732 Appendix S6: Relationship between individual food web metrics and landscape, climatic
- 733 descriptors