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Appendix 1

Food web construction

The Biodiversity Data Bank of Catalonia (BDBC, <<http://biodiver.bio.ub.es/biocat/>>), centralises all the information of plant and animal citations in Catalonia. Information is stored spatially explicitly, at 10 × 10 km resolution, and includes the presence of a species and the year the species is observed. No information on population densities is provided in the database. The information in the BDBC was complemented with the database of the Catalan Institute of Ornithology (<www.ornitologia.org/ca/>), and several atlases for mammals, reptiles and amphibians, all at the 10 × 10 km resolution. A database of species distribution was obtained for the 1970–2010 time period. However, in this paper we use only data from 1984 to 2001, due to low quality of some data before 1984 and after 2001.

Construction of the annual food webs

The presence/absence information of species on each 10x10 km cell of the geographical grid was accompanied of species-specific features including the habitats in which each species lives, its average adult body mass, and trophic group (reptiles, amphibians, birds, birds of prey, mammals and carnivore mammals). Body masses were obtained from an exhaustive search in the literature for all species present in the database. Fish, invertebrates, carrion and primary producers were not resolved to the species level, and were not considered in our analyses. Because of this, species that are typical from the second trophic level are referred to throughout the text as basal (e.g. passerine

birds). For each year and cell, an elevation range for each species was assigned according to the maximum and minimum elevations of all habitats (among 33 categories re-classified from the former 244 habitats) suitable for that species present at that cell. Habitats in each cell were obtained from the map of habitats of the Generalitat de Catalunya, which has a resolution of 30 metres. For example, for a given cell C with habitats (A, B, F, G) inside, and a species X able to live in habitats (A, B and E): if X is present in C, then the minimum and maximum elevations for species X in cell C would be the min value between the minimum elevations of habitats A and B in cell C, and the max value between the maximum elevations of habitats A and B in cell C, respectively. Species were also classified depending on the period of the year in which they were present, spring–summer (SS), autumn–winter (AW) and all year (ALL) species.

Trophic interactions were extracted from an exhaustive literature review, describing the whole set of known trophic links among the species in our database. Only interactions at the species level were included. The database included 2676 feeding interactions coming from a variety of empirical studies, including gut content analyses, fecal analyses, direct observations, rest analyses from bird nests or mammal burrows, and pellet analyses. Only in some exceptional cases, expert knowledge assessment was used to verify and/or complete some data.

In summary, co-occurrence of species, and hence realised trophic links, were dependent upon four factors: 1) grid cell, 2) elevation, 3) habitat and 4) season. If a pair of species coincided in these criteria, and the literature reported a trophic relationship among them, then a link was added to the food web between them. One network for each elevation for each year over the period considered was constructed, resulting in a total of nine⁹ food webs (one for each elevation and season).

Appendix 2

Food web and node properties

Food web properties

Connectance (C). The connectance of the network is defined as the fraction of all possible links that are realized (L/S^2) and represents a standard measure of food web complexity (Williams et al. 2002).

Standard deviation of generality and of vulnerability (VulSD). These two properties quantify the variability of species' normalized prey (G_i) and predator (V_i) counts, respectively, and are calculated as follows:

$$G_i = \frac{1}{L/S} \sum_{j=1}^s a_{ij}$$

$$V_i = \frac{1}{L/S} \sum_{j=1}^s a_{ij}$$

where L , S and a_{ij} are defined as above. Normalizing with L/S makes standard deviations comparable across different webs by forcing mean G_i and V_i to equal 1 (Williams and Martinez, 2000).

Mean food chain length (MFCL) is the mean length of the shortest paths from each node to any other node in the network. It reflects the vertical complexity of a food web (Williams and Martinez 2000).

Modularity (M). The modularity of a food web as a given partition of the nodes of the network into modules:

$$M \equiv \sum_{s=1}^{N_M} \left[\frac{l_s}{L} - \left(\frac{d_s}{2L} \right)^2 \right]$$

where N_M is the number of modules, L is the number of links in the network, l_s is the number of links between nodes in module s , and d_s is the sum of the degrees of the nodes in module s . A good partition of a network into modules must comprise many within-module links and as few as possible between-module links. This attribute quantifies the modular structure of the network, which is widely believed that plays a critical role in their functionality (Guimerà and Amaral 2005).

Node properties

Indegree and outdegree. Indegree describes the number of prey species or diet breadth a node has. Outdegree describes the number of predator species a node has.

Node role. The role of a node includes information both about the network topology and the functionality of the node. The role of a node can be determined by its within-module degree and its participation coefficient, which define how the node is positioned in its own module and with respect to other modules. We calculated the role of each node following the methodology described by Guimerà and Amaral (2005) where roles are classified depending on how ‘well connected’ they are within the module as non-hub nodes (nodes with few links; poorly connected) or hub nodes (nodes with many links; well connected). Then they are more finely characterized by defining how the node is positioned with respect to other modules, that is its participation coefficient.

Non-hub nodes can be divided into four different roles: *R1*: ultra-peripheral nodes; that is, nodes with all their links within their module; *R2*: peripheral nodes; that is, nodes with most links within their module; *R3*: nodes with many links to other modules; and *R4*: nodes with links

homogeneously distributed among all modules. On the other hand, **hub nodes** can be divided into three different roles: *R5*: hub nodes with the vast majority of links within their module; *R6*: hubs with many links to most of the other modules; and *R7*: hubs with links homogeneously distributed among all modules.

Appendix C

Statistical analyses

GLM were used to analyse differences in invasion success depending on: 1) the network (response variable: invasion true or false; explanatory variable: season and elevation. 2) invader characteristics (response variable: invasion true or false; explanatory variable: fraction of vulnerability of the invader, fraction of generality of the invader, invader role, \log_{10} (invader body size), invader group. 3) network attributes (response variable: invasion true or false; explanatory variable: S, L/S). GLM were also used to analyse differences in network attributes depending on the season and elevation (response variable: C, S, L, L/S, M, GenSD, VulSD, MFCL; explanatory variable: Season and elevation), and to analyse species lost depending on their characteristics (response variable: lost; explanatory variable: species role, species outdegree, species indegree, \log_{10} (species body size), species longevity, species centrality, species betweenness).

ANCOVAs were used to analyse differences in invasion success depending on network attributes controlling by the number of species (response variable: invasion true or false; explanatory variable: C, L, M, MFCL, GenSD, VulSD). K.S. test were used to analyse differences between network attributes before and after an invasion had succeed (response variable: C, S, L, L/S, M, GenSD, VulSD, MFCL; explanatory variable: invaded or non invaded network).

ANOVAs were used to analyse differences between the effects exerted on network attributes (when an invasion had succeed) depending on the invader characteristics (response variable: C, S, L, L/S, M, GenSD, VulSD, MFCL; explanatory variable: invader role, invader group, fraction of vulnerability of the invader, fraction of generality of the invader). To analyse this difference depending on the invader body size, a GLM was used. χ^2 -tests were used to analyse differences between the effect exerted by the fraction of generality of the invader and the fraction of vulnerability of the invader depending on its group and its role (response variable: fraction of generality of the invader and the fraction vulnerability of the invader; explanatory variable: Invader group and invader role). To analyse this difference depending on the invader body size, a LM was used.

Appendix 4

Recalculation of the interaction strengths

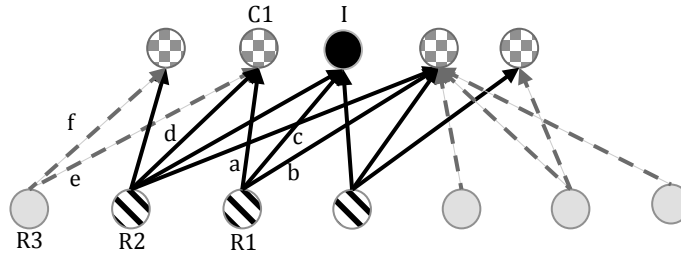


Figure A4.1. Illustration of the recalculation of the interactions strengths between the species in the sub-network given by the invasive and the species it interacts with. In this way extinctions due to invasion are determined. Once the introduced species' links are assessed, a two-steps process is performed in order to recalculate the weights of the interactions in which its partners, and the species related to those, are involved. In the first step the links (black arrows) that relate the invader's prey (square-patterned nodes) with their predators (line-patterned nodes) are recalculated. In the second step, the links (dashed arrows) relating these predators with their other prey (light grey nodes) are recalculated. Finally, if the new sum of interactions strengths is higher for a given prey, or lower for a given predator, than the sum – given by the extinction threshold, $ExtThr$ – (see text) before the invasion, that species goes extinct.

To illustrate the process, we focus on the particular example involving the nodes and links labelled in Fig. 1.b of the manuscript. For the first step described above we take prey R1 from the set of prey of the invasive species. Since this species is suffering from an enlarged predation pressure due to the presence of the introduced species (link 'c'), the interaction strengths against its other predators will be affected, since they will have now to share this resource with the invasive. This is simulated in our experiments by decreasing the weight of the interactions between R1 and its other predators (links 'a' and 'b') by an amount proportional to the weight of the new interaction 'c', and to the number of predators R1 has: two. We are going to label this change ΔW

= $c / 2$. Thus a' (the new value of a) equals $a - \Delta W$; equivalently, $b' = b - \Delta W$.

For the second step in the recalculation process we choose C1 from the set of predators of R1. As before, since C1 is now obtaining less resource from R1, due to competition with I, it will have to increase its predation pressure over its other prey (R2 and R3), in order to compensate for this deficiency. This is done in our model by increasing the weight of these interactions (links 'd' and 'e') by an amount proportional to the decrease on 'a', ΔW introduced above, and the number of prey C1 has aside from R1: again, two. We are going to label this change $\Delta W_2 = \Delta W / 2$. Thus d' (the new value of d) equals $d + \Delta W_2$, and equivalently, $e' = e + \Delta W_2$.

Once all the weights recalculations are performed, we check whether any extinction has occurred following the criteria introduced above. The original sum of the weights of the out-links of prey R1 is the weight of the link 'a' plus the weight of the link 'b' (i.e. original = $a + b$). After the invasion, its sum of weights becomes: current = $a + b + c$. According to the rule introduced above, R1 will go extinct if: current $>$ original + Δ , where $\Delta = (\text{original}) * \text{ExtThr}$. Similarly C1, for example, will go extinct if $a' + d' + e' < (a + d + e) - (a + d + e) * \text{ExtThr}$. Note that this time current (= $a' + d' + e'$) has to be *smaller* than original (= $a + d + e$) *less* Δ (= original * ExtThr) in order for extinction to occur. *Smaller* because we are looking at consumers instead of resources, and *less* because the ability of C1 to gain resource is effectively decreasing, and so Δ is now a proxy for the amount that their resource is allowed to decrease before it goes extinct.

To complete our example we assign values to the links analysed in the example and perform the calculations described. Thus, in our case, a possible example could be, $a = 1.1$, $b = 1.4$, $c = 2$, $d = 0.2$, $e = 0.1$, $f = 0.3$, and $\text{ExtThr} = 0.5$. Hence, applying the calculations we obtain: $\Delta W = 1$, and therefore, $a' = 0.1$, $b' = 0.4$. Similarly, $\Delta W_2 = 0.5$, which makes $d' = 0.7$ and $e' = 0.6$. When checking for extinctions we observe that R1 disappears because original = 2.5 and current = 4.5, which renders true our relationship current $>$ original + Δ ($4.5 > 3.75$). In the same way we find that R3 also goes extinct, since original = 0.4 and current = 0.9, making current larger than

original + Δ (0.2), again. It is interesting to note that in spite of having to share resources with I now, C1 does not go extinct, because current (1.4) is not smaller than original (1.4) minus Δ (0.7), and hence it has not lost as many resources as we are allowing it to lose in order to persist. This process is done for each prey and each predator.

References

- Guimerà, R. and Amaral, L. N. 2005. Cartography of complex networks: modules and universal roles. – *J. Stat. Mech. (Online)*. 2005, nihpa35573.
- Williams, R. J. and Martinez, N. D. 2000. Simple rules yield complex food webs. – *Nature* 404:180–183.
- Williams, R. J. et al. 2002. Two degrees of separation in complex food webs. – *Proc. Natl Acad. Sci. USA* 99: 12913–12916.