Supplement 1

Methodology

The following figures and Tables S1 & S2 (tables in Supplement 2) summarise the data we used to build the network of trophic (predator-prey) interactions for the Marine Protected Area Namuncurá - Burdwood Bank (MPA N-BB) ecosystem. Table S1 is the complete list of trophic interactions and references that confirm each of them. Table S2 is the species list with details on trophic species cases (aggregated taxa).

Food web construction

With the gathered trophic data, we constructed a matrix of pairwise interactions; a value of 1 or 0 was assigned to each element a_ij of the matrix depending on whether the predator j preyed or not on the prey i. Then we transformed such a matrix into an oriented graph with L trophic interactions between S nodes or species (Figure 1).

Matrix of pairwise interactions

i species

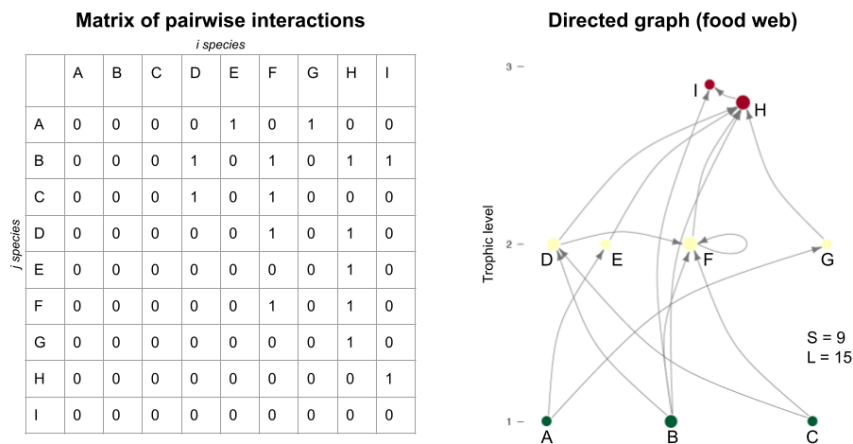|	A	B	C	D	E	F	G	H	I
A	0	0	0	0	1	0	1	0	0
B	0	0	0	1	0	1	0	1	1
C	0	0	0	1	0	1	0	0	0
D	0	0	0	0	0	1	0	1	0
E	0	0	0	0	0	0	0	1	0
F	0	0	0	0	0	1	0	1	0
G	0	0	0	0	0	0	0	1	0
H	0	0	0	0	0	0	0	0	1
I	0	0	0	0	0	0	0	0	0

Directed graph (food web)

S = 9
L = 15

Fig. S1. Matrix of pairwise interactions and the oriented graph (food web) derived from it. Number of species S = 9, number of interactions (L) = 15.

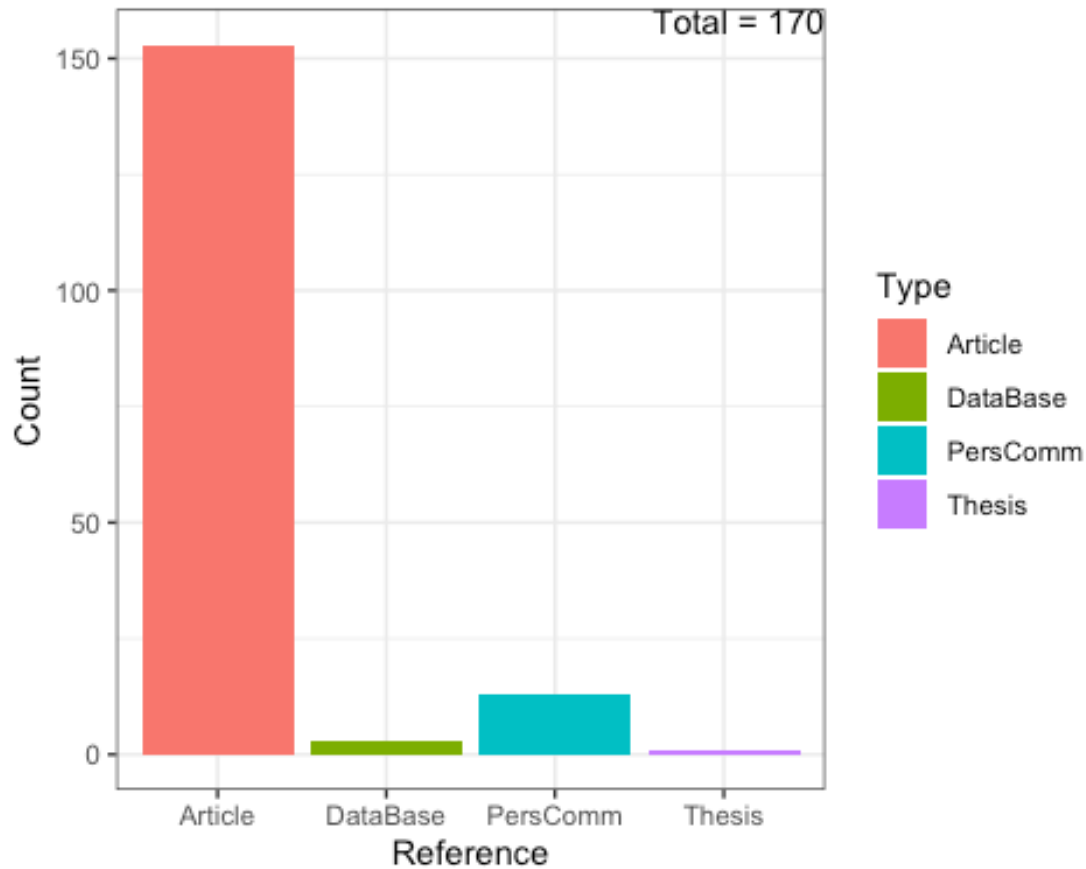Fig. S2 resumes the type and number of references reviewed.

Fig. S2. Summary of references used to build the network of trophic (predator-prey) interactions for the MPA N-BB ecosystem.

Network analysis

Betweenness

It is the frequency with which a node is on the shortest path between any other pair of nodes (Freeman, 1978). A node will have high betweenness when it appears on many shortest paths between other pairs of nodes. It is calculated as:

$$BC_i = \sum \frac{g_{vij}}{g_{vj}}$$

being $v \neq j, v \neq i, j \neq i$, where BC_i is the betweenness for species i; g_{vj} is the number of shortest paths between nodes v and j; and g_{vij} is the number of shortest paths which pass through node i.

Closeness

It is the number of steps required to reach every other node from a given node in the network (Freeman, 1978). It is calculated as the inverse of distances (number of interactions) to all other nodes in the network:

$$C_i = \frac{1}{\sum d_{ij}}$$

being $i \neq j$, where d_{ji} is the distance between node j and i.

Trophic similarity

It measures the trophic overlap based on shared and unique resources (prey) and consumers (predators) of a species. It is calculated as:

$$TS_i = \frac{c}{(a + b + c)}$$

where a is the number of prey and predators unique to one node, b is number of prey and predators unique to the other node and c is the number of prey and predators common to both nodes. Where two nodes have exactly the same set of prey and predators, $TS = 1$; where two nodes have no prey or predators in common, $TS = 0$.

Topological roles

Beforehand, we need to calculate modularity. Modularity was calculated as the difference between realized and expected within-modules interactions, divided by the total number of interactions. We used a stochastic algorithm called "simulated annealing" (Guimerà and Nunes Amaral, 2005), that assumes that the nodes of the same module have more links than one would expect in a random network. The modules are obtained from dividing all the nodes in the network to maximize modularity. In this way, the modularity index is defined as:

$$M = \sum_s \left(\frac{I_s}{L} - \left(\frac{d_s}{2L}\right)^2 \right)$$

where s is the number of modules or compartments, I_s is the number of links between species in the modules, d_s is the sum of degrees for all species in module s and L is the total number of links.

Species topological roles were calculated using the method of functional cartography (Guimerà and Nunes Amaral, 2005). Roles are determined according to two parameters:

a) the standardized within-module degree (dz), a z-score that reflects how well a species is connected to other species inside the module, relative to other species within its own module:

where k_{is} is the number of links of species i within its own module s, and ks are the average and standard deviation of k_{is} over all species in s, respectively.

b) the participation coefficient PC, estimates the links distribution of species i among modules:

where k_i is the total number of links of species i and k_{is} is the number of links of species i to species in module s. To determine the role of each species, the $dz - PC$ parameters space was divided into four regions (Kortsch et al., 2015), with two threshold values: dz = 2.5 and PC = 0.625. Thus, the species were classified as follows:

- Module hub ($dz \geq 2.5$, PC < 0.625): The species has a relatively high number of links, but at least 60% within its own module.

- Module specialist (dz < 2.5, PC < 0.625): The species has relatively few links and most within its own module.

- Module connector (dz < 2.5, $PC \geq 0.625$): The species has relatively few links and most between modules.

- Network connector ($dz \geq 2.5$, $PC \geq 0.625$): The species has a high connectivity between and within the modules.

Trophic level

Trophic levels (TL) of species were calculated using the shortweighted TL formula of Williams and Martinez (2004). Shortweighted trophic level is defined as the average of the shortest TL and prey-averaged TL. Shortest TL of a consumer in a food web is equal to 1 + the shortest chain length from this consumer to any basal species (Williams and Martinez, 2004). Prey averaged TL is equal to 1 + the mean TL of all consumer's trophic resources, calculated as:

$$TL_j = 1 + \sum_{i=1}^{S} l_{ij} \frac{TL_i}{n_j}$$

where TL_j is the trophic level of species j; S is the number of species in the food web; l_{ij} is the connection matrix with S rows and S columns, in which for column j and row i, l_{ij} = 1 if species j consumes species i and l_{ij} = 0 if not; and n_j is the number of prey species in the diet of species j. For basal species TL = 1 given that they have no prey.

Results

Table S3 (in Supplement 2) presents an exhaustive list of the species-level properties for the food web of the MPA Namuncurá - Burdwood Bank I ecosystem.

Fig. S3 shows the species' topological roles in the food web graph. Species, represented by circles, are coloured by role: network connector (dark purple), module connector (light pink), module hub (light green), and module specialist (dark green). Network connector = 1 species; module connector = 41 species; module hub = 10 species; and module specialist = 328 species.
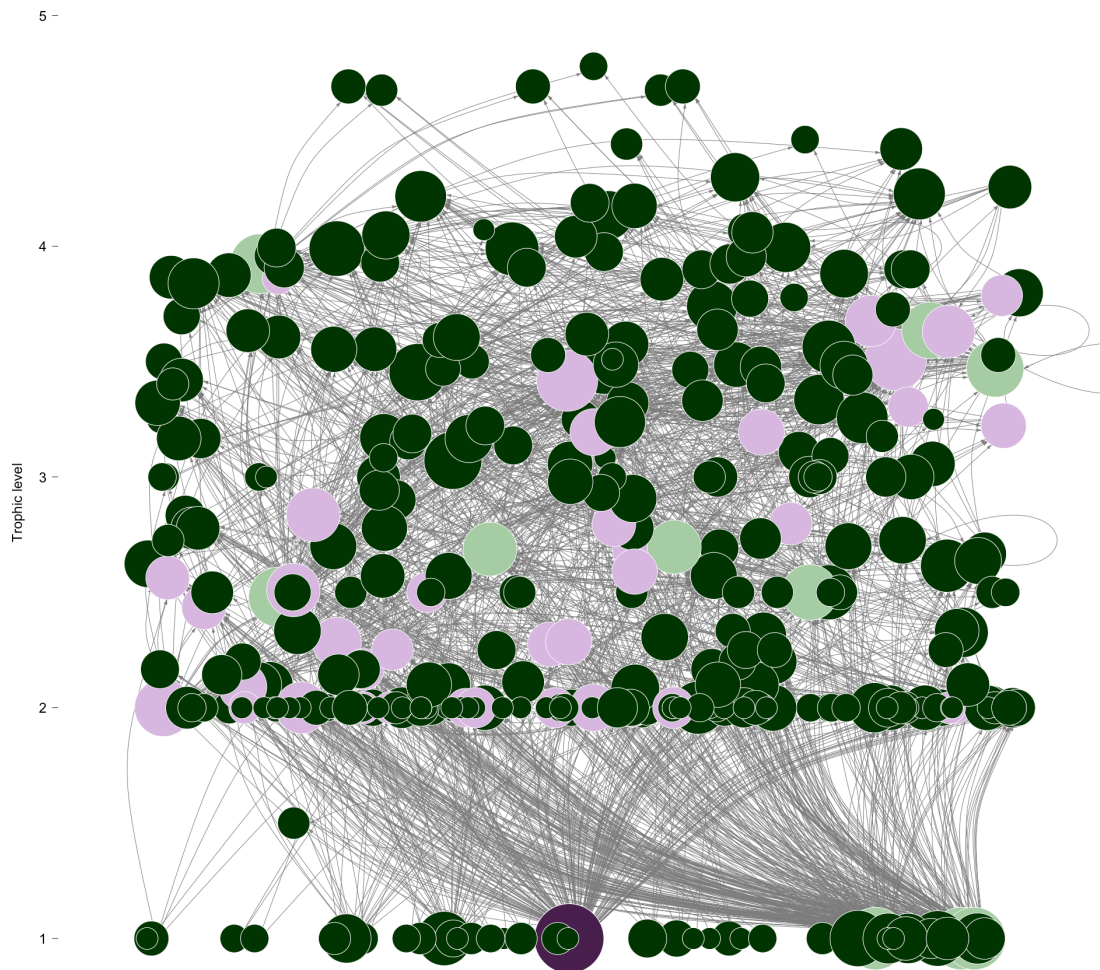
Fig. S3. Graph of the food web showing species coloured by topological role: network connector (dark purple), module connector (light pink), module hub (light green), and module specialist (dark green). Circle diameter is relative to the number of interactions.

References

Guimerà, R., Nunes Amaral, L.A., 2005. Functional cartography of complex metabolic networks. Nature 433, 895–900. https://doi.org/10.1038/nature03288

Kortsch, S., Primicerio, R., Fossheim, M., Dolgov, A.V., Aschan, M., 2015. Climate change alters the structure of arctic marine food webs due to poleward shifts of boreal generalists. Proceedings of the Royal Society B: Biological Sciences 282, 20151546. https://doi.org/10.1098/rspb.2015.1546

Williams, R.J., Martinez, N.D., 2004. Limits to Trophic Levels and Omnivory in Complex Food Webs: Theory and Data. The American Naturalist 163, 458–468. https://doi.org/10.1086/381964