The role of marine mammals in the Barents Sea food web

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Abstract: 200 words

Marine mammals are important players in the Barents Sea ecosystem but their food web role is poorly known. We identify food web-related characteristics within and between phylogenetic groups for 19 marine mammals. As a group, they are directly connected to the most central species in the Barents Sea (i.e. cod and haddock) and consume over half of the available species. Pinnipeds are the most homogenous phylogenetic group with high omnivory and many prey species. Mysticetes are split between well-connected species with high omnivory like the humpback whale, and peripheral specialists like the blue whale. Some species are consistently clustered together based on food web-derived indices, suggesting redundancy in topological role forming two groups. One is dominated by Arctic seals and the other by baleen whales. Marine mammals generally contribute to network modularity as their trophic links are mostly within their module. However, Atlantic species such as grey seals act as module connectors decreasing modularity which might negatively affect ecosystem robustness with perturbation effects spreading further and quicker in the food web. In the Arctic reaches of the Barents Sea, climate warming is likely to bring about extensive changes in food web structure and robustness through a redistribution of species.

Key words: Food webs - Barents Sea - Marine mammals – Network – Topological role

Introduction:

Marine mammals are top predators that influence food webs through direct predation indirect cascading effects and risk-mediated effects (Frank *et al.*, 2005; Frid *et al.*, 2007a; Heithaus *et al.*, 2008; Baum and Worm, 2009; Roman *et al.*, 2014; Hammerschlag *et al.*, 2019). Although marine mammals are generally thought to be important players in many marine ecosystems due to their abundance, large body size and high trophic status (Bowen, 1997; Estes *et al.*, 2009), their food web structural role as a group and per species is rarely assessed. A few studies have considered bottom-up or top-down forcing and include a complete food chain (Springer *et al.*, 2003; Bundy and Fanning, 2005; Trites *et al.*, 2006). Yet, the focus has been on a single species or a few species in relation to their main prey abundance and distribution (Mackinson *et al.*, 2006; Bluhm and Gradinger, 2008; Skern-Mauritzen *et al.*, 2011; Durant *et al.*, 2014) or their habitat use (Moore, 2008). Marine mammals are a diverse phylogenetic group with a variety of diet and habitat requirements, but they may also display some degree of resource overlap in certain regions (Spitz *et al.*, 2006; Bogstad *et al.*, 2015; Haug *et al.*, 2017). However, the ecological role of marine mammals from a food web perspective and their degree of dietary overlap have not been investigated, nor the similarities and differences between species. These knowledge gaps challenge conservation and management practices while drastic changes are occurring in most marine ecosystems especially at high latitudes (Dalpadado *et al.*, 2014; Laidre and Regehr, 2017). The role of top predators in an ecosystem can rarely be assessed empirically, except in cases of extirpation or sharp decline in a species' abundance (Frid *et al.*, 2007a; Heithaus *et al.*, 2008), and is thus usually evaluated by modelling approaches (Lindstrøm *et al.*, 2009; Morissette *et al.*, 2012; Heymans *et al.*, 2014). Food web topology can help to assess the ecological role of species within an ecosystem (Jordán *et al.*, 2006) without the extensive and detailed data requirements of a fully parametrized ecosystem model.

Food web analyses are useful tools to address ecological role in ecosystems based on a species' links to prey and predators and on its position in the ecological network (Luczovich *et al.*, 2003; Dunne, 2009; Jordán, 2009; Lai *et al.*, 2012). Food webs provide a description of species interactions, ecosystem structure and functioning (Dunne *et al.*, 2002a; Ings *et al.*, 2008; Olivier and Planque, 2017) and determine how perturbations propagate and energy flows from basal to top species (Rooney *et al.*, 2006). Trophic interactions are considered to be one of the main regulators of ecosystem dynamics (Link, 2002; Allesina and Pascual, 2008), and the food web structure can help evaluate ecosystem vulnerability. At a smaller scale, species are not connected randomly in a food web, but are generally found in highly organised substructures (Dunne *et al.*, 2002a). These configurations are tightly linked to a food web's robustness to perturbations (Dunne and Williams, 2004). The role of species in maintaining ecosystem functioning depends, at least partly, on their direct links to the other species and on their topological position (Dunne *et al.*, 2002a; Jordán *et al.*, 2006; Jordán, 2009). For example, central and functionally unique species, which strongly affect food web structure, might propagate the ecological effects of perturbations through trophic cascades, whereas species that are more peripheral may be less influential on the network characteristics and dynamics. Identification of key players and understanding of the role of species, or groups of species, is therefore of paramount importance for conservation measures (Jordán, 2009; Worm and Paine, 2016).

Here we use a topological network approach to assess the ecological role of marine mammals in a highly resolved food web topology from the Barents Sea (Planque *et al.*, 2014). Our objectives were to 1) describe the topological position of marine mammals through food web-related properties, 2) to assess their topological similarities and 3) to characterize differences both within and between phylogenetic groups from a food web perspective.

Material and methods:

Study area

The Barents Sea is a shallow shelf sea (400 m of maximum depth) that is part of the Arctic continental shelf. Its limits are defined by the shelf break bordering the Norwegian Sea on the West, the archipelago of Novaya Zemlya in the East, the Arctic shelf edge in the North and the Norwegian and Russian continental coastlines in the South (Oziel *et al.*, 2017). It is a transition zone from warm and saline Atlantic water to cold and fresh Arctic water. In the last decades substantial oceanographic changes have occurred in this region with a dramatic increase of atmospheric and water temperatures and a higher inflow of Atlantic water (Dalpadado *et al.*, 2012, 2014; Eriksen *et al.*, 2017). This in turns is causing changes in the ecosystem by affecting the distributional range of species and their trophic links (Fossheim *et al.*, 2015; Kortsch *et al.*, 2015; Frainer *et al.*, 2017; Johannesen *et al.*, 2017). The Barents Sea is highly productive, supporting a large biomass from phytoplankton to marine mammals and seabirds (Dalpadado *et al.*, 2014) as well as an intense fishery activity taking place all year-round (ICES, 2014). The Barents Sea includes one of the world's largest fishery area targeting marine mammals, fish, crustaceans and molluscs (Misund *et al.*, 2016). The most important target species include northeast Atlantic cod *(Gadus morhua)*, capelin *(Mallotus villosus)*, haddock *(Melanogrammus aeglefinus)* and Greenland halibut *(Reinhardtius hippoglossoides)*(Gjøsæter, 2009).

Food web data

A food web consists of species and their trophic relationships (Odum, 1983). Network theory provides a mathematical framework that allows to represent these systems as the nodes and links of an ecological network (Pimm *et al.*, 1991). To minimize bias due to uneven resolution in food web data (Dunne 2009), species can be grouped into trophospecies (TS), i.e. species sharing prey and predators. We used a highly resolved Barents Sea food web topology compiled by Planque *et al.*, (2014) updating the trophic links between marine mammals and their prey (Tables S1, S2, S3). We also added boreal marine mammal species with potential for poleward expansion, such as the grey seal *(Halichoerus grypus)*, harbour seal *(Phoca vitulina)* and the blue whale *(Balenoptera musculus)*, and Arctic species whose numbers are currently increasing such as the bowhead whale *(Balaena mysticetus)* (Gilg and Born, 2005; Wiig *et al.*, 2010). The trophic links are binary (unweighted), only indicating whether a feeding link between two species exists or not.

Binary food webs provide useful information on the pathways of energy flow, the network structure and the topological role of species. As binary food webs do not include the relative importance of a prey item in a predator’s diet, as is the case for weighted food webs, they ignore a predators’ preferences and foraging efficiencies for its various prey. A limitation of ignoring prey importance is that excessive emphasis may be given to weak feeding links. However, given the difficulty of acquiring quantitatively reliable diet data, a binary food web approach allows to circumvent this problem by stating which species could be eaten by a predator if available. The strength of the approach is that it delivers information on the ecological role and food web position of species. It also provides insights on pathways of energy flow and structural properties of ecological networks that are otherwise not possible to obtain for comprehensive food webs. This approach also provides an overview of a species' dietary plasticity, which is important to consider when changes in prey abundance and distribution occur.

In total, the food web comprised 239 species or TS including detritus and members of the five ecological groups: plankton (52 including 43 zooplankton species and 9 phytoplanton species), benthic invertebrates (81), fish (77), seabirds (9) and marine mammals (19) (Fig. 1a). Diet information for certain species was not available from the Barents Sea; in such cases we included diet information from other ecosystems. We assumed that if a link was documented in an ecosystem other than the Barents Sea, and if the prey and predator are both found in the Barents Sea food web, then the link is also likely to exist in the Barents Sea.

Food web metrics

All numerical and statistical analyses were performed using the software R (R Core Team 2018).

The structure of food webs can be described using a series of metrics (Table 1) calculated on the basis of the number of species, the number of trophic links and their distribution across the network (Lau *et al.*, 2017). These indices are calculated at the network level. Here we calculated 14 standard measures of food web structural properties (See Table 1 for the definitions) : number of species, number of links, links density, connectance, average degree, in-degree out-degree, level of omnivory, average shortest path, average trophic level, proportion of predator, omnivore, cannibal and basal species (Pimm *et al.*, 1991; Christensen and Pauly, 1992; Dunne *et al.*, 2002b; Williams *et al.*, 2002; David *et al.*, 2004; Dunne and Williams, 2004; Bascompte *et al.*, 2005; Thompson *et al.*, 2007; Kones *et al.*, 2009).

To indirectly explore the robustness of the network to the removal of its most connected species, we fitted the cumulative distribution of degrees with three simple models: power law, exponential and truncated distribution (de Santana *et al.* 2013). Networks that follow a power law degree distribution are very vulnerable to the removal of the most connected nodes, whereas networks that follow an exponential degree distribution are less vulnerable (Dunne *et al.*, 2002a; Estrada, 2007; de Santana *et al.*, 2013). This is because in the first case, a small proportion of species form links with the majority of the other species in the network, forming a structural bottleneck. Hence the disappearance of these very connected species would cause the collapse of the network through secondary extinctions (Estrada, 2007). In the second case no such species exist as the number of links are spread more evenly between all the species providing a greater network robustness to species' removal (Estrada, 2007).

Food webs tend to divide into groups of more densely connected species called modules (Clauset *et al.*, 2004; Newman, 2006). Species belonging to the same module have more trophic links with each other compared to the rest of the species and tend to have shorter paths between them. We partitioned the species into food web modules using the walktrap algorithm (Pons and Latapy, 2006), which relies on a random walk. The algorithm assumes that species belonging to the same food web module will be connected by the shortest paths assuming a random walk (Pons and Latapy 2006) because they are more likely to have direct links with each other than with other species in the food web. The algorithm returns module affiliations for each species. We used the R package "igraph" for the above computations (Csardi and Nepusz, 2006).

Species-specific centrality measures and topological role

The importance of a species within a network can be evaluated based on the centrality of its position relative to other species (Wasserman and Faust, 1994). Central species tend to have a greater influence on the network structure than peripheral ones (Jordán *et al.*, 2006; Jordán, 2009; Lai *et al.*, 2012). Each species can be characterized by a series of metrics (Table 1) assessing their centrality and multiple centrality measures are generally recommended because single indices do not offer an exhaustive description of a species' topological position and role (Lai *et al.*, 2012). These species-specific metrics can be either direct (taking into account only the immediate neighbours or direct links) or indirect (taking into account further links in the network) (Table 1).

We first calculated four direct centrality measures: (i) the in-degree (number of prey), (ii) the out-degree (number of predators), (iii) the degree (the total number of prey and predators), and (iv) the level of omnivory. Further, we calculated six indirect centrality measures: (i) eigenvector centrality, which reflects the centrality of a species by taking into account the centrality of its neighbour essentially representing a weighted version of degree centrality (Wasserman and Faust 1994 in Lai et al 2012); (ii) the betweenness centrality. which reflects how often a species lies on the shortest path between a pair of species; (iii) information centrality, which is similar to betweenness centrality but considers all paths between a pair of species (Wasserman and Faust, 1994); (iv) closeness centrality, which measures how many steps away a species is from the others in the network. The greater the closeness centrality of a species the quicker it will affect the other species through both direct and indirect effects. We also used (v) Google's PageRank algorithm (Brin and Page, 1998) as a variant of the eigenvector centrality measure because it takes into account the direction of the feeding links and therefore places more emphasis on the in-degree, i.e. number of prey (Allesina and Pascual, 2009). In addition, the (vi) trophic level (TL) of each species was calculated based on path lengths from the basal species to the species of interest, using either all the shortest paths

(SWTL, based on paths with minimum number of intermediate species), or all the longest paths (LWTL, based on paths with maximum number of intermediate species), weighted by the number of prey species (Thompson *et al.*, 2007). An averaged TL was also calculated for each species based on the average shortest path, essentially representing the weighted average of its food items. All above indices were calculated using the “CINNA” and “igraph” package in R (Csardi and Nepusz, 2006; Ashtiani, 2019).

Whether species interact only within their modules or equally with species in other modules will determine their role in the spreading of perturbations and in energy flow pathways. To assess this we used the method of functional cartography (Guimerà and Nunes Amaral, 2005; Kortsch et al., 2015) which characterizes how each species is positioned in its own module and with respect to species in other modules. Each species was assigned a module membership based on the walktrap algorithm as described above. The within and between module linkage of a species was addressed using two metrics: the z-score or within-module degree and the participation coefficient score (PC) or among-module degree (table 1). The z-score reflects how well a species is connected to species in its own module relative to the other species within its module, measured in terms of standard deviations from the mean. In our case, this represents whether a species has more or less links within its module compared to the module average. The 2.5 threshold proposed by Guimera and Nunes Amaral (2005) is used as reference to identify species with considerable higher within module linkage than average. Accordingly, species with $z > 2.5$ are qualified as module hubs whereas species with $z <2.5$ are non-hubs. Conversely, the PC score indicates how well a species is connected to species belonging to other modules and its values vary continuously between 0 and 1. Guimera and Nunez Amaral (2005) define a species that has at least 60% of its links within its module as peripheral, interacting preferentially with species within its module. This corresponds to $PC = 0.625$. A species with all its links within its own module will have a PC

= 0 whereas for a species with all its links evenly distributed among modules PC will tend towards 1. To determine each species' topological role, the z-PC space is divided into four regions by the threshold values of z=2.5 and PC = 0.625 (Guimerà and Nunes Amaral, 2005; Olesen *et al.*, 2007; Carstensen *et al.*, 2012; Kougioumoutzis *et al.*, 2014; Kortsch *et al.*, 2015; Torre *et al.*, 2019). Species with $z > 2.5$ and $PC < 0.625$ are defined as **module hubs** because they have few links outside of their own module but connect to most of the species within their module. They are important within their module as they maintain its coherence. Species with $z < 2.5$ and $PC < 0.625$ are defined as **network periphera**l because they have few links outside of their module and connect with few species within their module. These species are often specialist species with the lowest number of prey. Species with $z < 2.5$ and $PC > 0.625$ are defined as **module connectors** as their links tend to be evenly distributed among modules. These species are important to network coherence as they connect modules together. Finally species with $z > 2.5$ and $PC > 0.625$ are defined as **network connectors** because they have links with most of the species within their module and the majority of their links with other modules. Hence these species are important both for their own module but also for the entire network coherence.

We used a principal component analysis (PCA) to compare marine mammal species to other functional groups in terms of centrality measures and to assess how homogenous they are as a group. Before analysis, each centrality measure was centred and standardized to limit the effect of differences in variance among variables on the PCA outcome.

Topological redundancy of marine mammals; intra- and inter- functional group comparison

Quantifying structural redundancy in communities is not a straightforward task, but network analysis provides a synthetic framework for assessing similarities in direct and indirect trophic interactions (Clarke and Warwick, 1998; Walker *et al.*, 1999; Jordán, 2009). We consider several metrics encompassing different aspects of similarity at the local scale (direct neighbours) and at the network scale (considering the network positions of each species). We chose four indices of similarity. 1) The trophic overlap quantifies the percentage of diet overlap between two species based on the presence of an item in the diet of a consumer. This measure is not symmetrical as two species usually have different diet breadth and takes into account only a part of a species' direct neighbours (here the prey species). 2) The Jaccard index is a measure of structural equivalence and is defined as the ratio of shared prey and predators over the total number of prey and predators for both species (Lai *et al.*, 2012; Olivier and Planque, 2017). This index considers all the direct neighbours (prey and predators). The index was calculated using a custom written code in R. 3) The regular equivalence index measures the similarity between two species based not only on their direct links (prey and predators) but also considering their position within the food web (Luczovich *et al.*, 2003). Therefore this index allows to partition species into groups that play the same structural roles even if they do not share the same prey or predators. The index of regular equivalence was calculated with the CATREGE algorithm (Borgatti and Everett, 1993) using the sna R package (Butts, 2008). 4) Finally we used the Euclidian distance between pairs of marine mammals species calculated on the basis of the 14 metrics described in the previous paragraph. We assume that the greater the distance between two (or more) species, the more dissimilar they are in terms of functional characteristic (Walker *et al.,* 1999). The trophic overlap and Jaccard indices are linked to the concept of dietary niche overlap and competition (Pianka, 1974) whereas the concepts of regular equivalence and network centrality are linked to the trophic role of two species and their potential functional redundancy regardless of their diet overlap (Luczovich *et al.*, 2003). Obviously two species with complete niche overlap and the same set of predators will also have the same functional role in the food web; however two species with very different sets of prey and predators can have the same topological role (Olivier and Planque, 2017).

For each index of similarity, we performed a hierarchical clustering, computing p-values for each cluster via multiscale bootstrap resampling. High p-values (>0.95) indicate that clusters of species are strongly supported by the data (Shimodaira, 2004). The clustering was performed using the pvclust package in R (Suzuki and Shimodaira, 2006).

Results

Structural properties of the food web

The 239 trophospecies included in the food web were connected through 2464 links yielding a link density of 10.3 links per species. The average number of links was 20.4 per species with an equal average number of prey or predators (10.2 ± 12.6 and 10.2 ±14.3 respectively). At the network scale, 4% of all the potential links (if all species in the food web were linked) were realized (connectance = 4%), and 97% of the species had at least one prey. Basal species consisted mainly of primary producers and detritivores (3% of the species, n=7). Conversely, 93% of the species had at least one predator while 7% did not have any. Fifty-two percent of the species were omnivores, i.e. they were feeding across several TL and 11% were cannibals. The shortest path length between the consumers and each of the seven basal species was on average 2.3 whereas average TL was 3.08. The cumulative degree distribution was best fitted by an exponential distribution ($AIC_{exp} = -650$; $AIC_{power} = -160$; $AIC_{truncated} = 22$) (Fig. 2).

Marine mammals in the food web

As a group, marine mammals consume 134 available TS of the Barents Sea food web, which represents 56% of the available species. Prey of marine mammals belong to 60 different families, including zooplankton, benthos, fish and other marine mammals. This group has the highest number of prey items per species than any other ecological group ($mean_{mammals} = 27.5, \pm 16$; $mean_{plankton} = 4.9 \pm 4.9$; $mean_{benthos} = 4.5 \pm 8.0$; $mean_{fish} = 15.5 \pm 18.1$; $mean_{birds} = 13.1 \pm 10.8$ prey / predator). Metrics calculated for each species of marine mammals are presented in table 2. The number of marine mammals’ prey ranges from four, for the sperm whale (*Physeter microcephalus*), to 52 for the harbour porpoise (*Phocoena phocoena*) and differs between phylogenetic groups (Fig. 2, table2). Odontocetes (toothed whales) show a particular large spread in number of prey items and include species with the lowest and highest number of in-degrees. Mysticetes (baleen whales) and pinnipeds (seals) have both a greater total number of links compared to odontocetes and pinnipeds are more homogenous as a group (Fig. 2, table 2). It is also worth noting that the polar bear *(Ursus maritimus)* is among the species with the lowest total number of trophic links (prey + predators) with only 8 direct links.

The PCA based on the food web characteristics of each species shows that most of the marine mammals share similar characteristics compared to other functional groups (Fig. 3a). The first axis of the PCA indicates that marine mammals are generally associated with longer paths, high TLs between 3.5 and 5.2, large number of prey, small number of predators (range 0-4) and are connected to the maximum number of basal species (n=7). They score low on the second axis that mostly characterizes species by their measures of centrality in the food web. However, marine mammals are connected to the most central species in the network as shown by their globally high eigenvector centrality scores and page rank scores. As a group, marine mammals have food web characteristics based on centrality measures similar to those of seabirds and some predator fish and opposite to plankton and benthic invertebrates (Fig. 3a). This is confirmed by the position of the centroids for each group, showing a proximity between fish, marine mammals and seabirds, while plankton and benthic invertebrates tend to be more similar to each other and located away from the other groups (Fig. 3a).

Although marine mammals as a group show some commonalities, some differences between phylogenetic groups and species are apparent (Table 2, Fig. 3b). Pinnipeds are the most homogenous group associated with the highest level of omnivory and large number of prey which are well connected to the rest of the network as shown by the high average eigen vector values. We note the exception of the walrus *(Odobenus rosmarus)* that has the highest level of omnivory (0.81) of all marine mammals and the lowest number of prey (n=19) of the pinnipeds (range 19-49). Mysticetes, on the other hand are generally less central than the pinnipeds although there is a certain variability in the group. For example, two species, the blue whale and the bowhead whale are specialists with a low TL (range 3.5-3.8) feeding mostly on peripheral planktonic prey (Fig. 1b). The three other baleen whales species feeding on a wider diversity of prey at a higher TL (range 3.8-4.5) are more omnivorous. Odontocetes are the most heterogeneous group including species with few prey and low centrality measures such as the sperm whale, and more central species such as the harbour porpoise, which has centrality measures similar to those of pinnipeds. Species with the highest TL are the polar bear and the killer whale (TL= 5.2) *(Orcinus orca)* feeding also on other species of marine mammals, whereas the species with the lowest TL (TL=3.5) is the bowhead whale feeding mostly on zooplankton.

Marine mammal module affiliation

The walktrap algorithm split the food web into four distinct modules containing 55, 49, 42 and 93 species (Fig. 1a). Module A was dominated by plankton, modules B and C by benthos and module D had a majority of fish (Fig. 1a, Fig. 4). The clustering coefficient measuring the probability that two nodes adjacent to a third are also linked was on average 0.21 in the food web.. Marine mammals were segregated in two distinct modules, A and D, which comprise 5 and 14 marine mammal species, respectively (Fig. 1, 4). Mysticetes segregate in module A dominated by plankton whereas pinnipeds and odontocetes are found in module D dominated by fish (Fig. 4). Two species do not follow this pattern; the white-beaked dolphin *(Lagenorhynchus albirostris)* grouped with the baleen whales (module A) and the minke whale *(Balaenoptera acutorostrata)* grouped with the pinnipeds and the rest of the odontocetes (module D This patterns might be due to the fact that white-beaked dolphins share 73 % of their prey item with marine mammals from module A and minke whales share92% of their prey items with marine mammals from module D.

Marine mammals tend to interact more with species within their modules than in other modules. This is especially true for baleen whales in module A that have 86% of their links within that module (Fig. 4). This is also the case, although to a lesser extent for marine mammal species in module D with 60% of their links within module D (Fig. 4). The above finding agrees with the functional cartography analysis (Fig. 5). The majority of marine mammal species are considered as network peripherals interacting mainly with species within their own modules, although there is a wide spread especially in their among-module connectivity (PC) scores. Some species, such as the blue whale, interact mainly with species within their own module, while others, like the harbour porpoise, interact more with species outside of their module. One species acts as module connector: the grey seal *(Halichoerus grypus)*. It is worth noting that the walrus *(Odobenus rosmarus)* and the bearded seal *(Erignathus barbatus)* metrics are close to those of module connectors.

Diet overlap and topological redundancy

The dietary niche overlap is the highest among baleen whales (mysticetes) followed by seals while the lowest overlap occurs within the odontocetes (Fig. 6a, S1a, Table 3). The same observation is true by considering the Jaccard index, which takes into account only the shared prey and predators for every pair of marine mammal (Fig. 6b, S1b, Table 3). The dietary niche of the fin, bowhead and blue whales are entirely included within the humpback’s niche (mysticetes) whereas minke whale’s diet overlaps the least with other species in its phylogenetic group. Conversely, the blue whale has the largest overlap with the other mysticetes (Fig. 6b, S1b, Table 3).

The diet of pinnipeds is included within the diet of several odontocetes with the exception of the killer whale which consumes pinnipeds. Based on the clustering analysis, some species were consistently grouped together both considering the percentage of diet overlap and the Jaccard index: ringed, harp and hooded seal; white beaked dolphin and beluga whale; and the remaining baleen whales with the exception of the minke whale (Fig. S1a,b and Table 3).

There is a great variability in the regular equivalence and centrality distances both within and across phylogenetic groups (Fig. 6 c, d, Fig. S1c, d, Table 3). The greatest topological similarity occurred between pinniped species but some individual species such as the minke whale also shows great similarities with the seals. Based on these two metrics, species cluster in two main groups: one including the seals, harbour porpoise and the minke whale and the other including the remaining species. The composition of these two groups is relatively similar between the two methods (Fig. S1 c, d, Table 3).

Discussion

Marine mammals are often simply characterized as being top predators, but our results show that these species occupy diverse positions within the food web, and play different ecological roles. Marine mammals range from network peripherals, feeding mainly at one TL within one module and on a few prey items to module connectors, with many prey items belonging to several TLs and modules. Overall, marine mammals occupy high trophic positions, associated with the longest trophic chains, have few predators and the highest average number of prey per species compared the other ecological groups. As a group, they have direct trophic links to over half of the available species in our Barents Sea food web. Hence, they may contribute to the stability of the food web, which is enhanced when species at high TLs feed on multiple prey species (Gross *et al.*, 2009). This aspect is consistent with top predators connecting otherwise separate energy channels (Neutel *et al.*, 2007). Indeed, each marine mammal species is indirectly linked to six or seven of the seven basal species found in the food web. By connecting separate energy channels (for example phytoplankton and detritivore-driven channels), marine mammals may enhance the robustness of the food web to bottom-up perturbations (Neutel *et al.*, 2007; Gross *et al.*, 2009) by allowing the rewiring of energy paths if one chain was to disappear. This would ultimately allow the persistence of upper trophic levels, although some intermediate levels may disappear (Staniczenko *et al.*, 2010). Overall, marine mammals are split between specialist species with few prey items and generalist species with many prey items, and varying levels of omnivory. Species with both high level of omnivory and large number of prey are mostly Atlantic species associated with warmer waters masses and independent of sea ice. These species have the potential to invade Arctic regions undergoing rapid climate-driven change, where they may have a competitive advantage over Arctic top predators which suffer from loss of sea ice and an increased importance of novel, boreal prey species (Fossheim et al., 2015). The structure of Arctic food webs might thus be modified becoming less modular and robust (Kortsch et al., 2015, 2018) and the invasion of boreal species may trigger extinction cascades (Romanuk *et al.*, 2017).

Marine mammals are not among the most central species in the food web, but they feed on some of the most central species in the network (for example Atlantic cod *Gadus morhua*, and calanoid copepods). Thus, changes in marine mammal distribution or abundance may indirectly affect many species in the ecological network through top-down processes. For example, loss or increase of top predators can result in trophic cascades (Frank *et al.*, 2005; Heithaus *et al.*, 2008), which will be particularly pronounced when those predators are generalists with many prey on a single TL. The minke whale and the harbour, harp and hooded seals, target collectively over 50 different prey items mainly within the same TL, with the potential to deplete that TL. Although depleting the whole range of these prey species is unlikely, feeding on a single TL could decrease the overall predation pressure on TLs below. The prey of minke whale, harbour, harp and hooded seals are mainly fish, and include important commercial species such as Atlantic cod, herring *(Clupea harengus),* capelin *(Mallotus villosus)* and Atlantic mackerel *(Scomber scombrus)* (Tjelmeland and Bogstad, 1998).

Fisheries could enhance the risk for trophic cascades by targeting the same fish species as the above-mentioned marine mammal species. Intense fishing has been shown to cause the collapse of fish stocks and to have synergistic effects with natural predation by grey seals off Newfoundland and in the Baltic (Eero *et al.*, 2011; Hammerschlag *et al.*, 2019). In the case of Newfoundland, the collapse of the demersal fish community led to drastic ecosystem changes. The collapse of cod, haddock and hake amongst others led to trophic cascades that caused new fishery regime targeting benthic macroinvertebrates (Frank *et al.*, 2005). In this context, grey seals benefitted from the cod collapse because it released small pelagic fish stocks and benthic invertebrates from the cod's predation and decreased the overall competition. The ability of the grey seal as a generalist predator to switch prey was subsequently linked to an increase of its population (Frank *et al.*, 2005).

Trophic cascades can also happen when "super predators", here marine mammals feeding on other marine mammals, switch prey. In the Barents Sea, the polar bear, the walrus and the killer whale feed partly on other marine mammals. They are known to switch prey by either targeting other marine mammals or by targeting other species at a lower TL; this may change the predation pressure on TLs below and thus initiate trophic cascades (Estes *et al.*, 2009). This has been illustrated in the Aleutian Islands, when killer whales consumed sea otters instead of pinnipeds releasing predation pressure on sea urchins and causing the depletion of the kelp forest due to over grazing by the sea urchins (Springer *et al.*, 2003; Estes *et al.*, 2009;

Ripple *et al.*, 2016; Hammerschlag *et al.*, 2019). Information on killer whales in the Barents Sea in sparse but recent tracking data suggest that they occupy the region all year-round (Dietz R. pers. comm.) although their numbers are likely low. Their lack of sea ice dependency likely gives them a competitive advantage over polar bears and walruses; thus killer whales are likely to become a major predator in the Artic. This is already the case in the Canadian Arctic where they prey on bowhead whales, beluga whales, narwhals and seals (Ferguson *et al.*, 2012; Higdon *et al.*, 2012). They have the potential to alter Arctic food web and have been linked to decline in certain marine mammal populations (Wade *et al.*, 2007). Trophic cascades can also be mediated through risk effect by inducing changes in prey-predator dynamics through behavioural switches. In the Northwest Atlantic, harbour seals underutilise the deep-dwelling pollock *(Pollachius pollachius)* population in order to avoid predation by the Pacific sleeper shark *(Somniosus pacificus)* and prey preferentially on surface herring. When the sharks were removed due to intensive by catch, seals started preying more intensely on Pollock releasing herring from predation and initiating trophic cascades (Frid *et al.*, 2007b). The Barents Sea equivalent of the sleeper shark, the Greenland shark *(Somniosus microcephalus)* has also been suggested as a potential important predator for the Svalbard harbour seal population (Leclerc *et al.*, 2012). However, the ecological role of this shark species remain unclear due to the lack of basic biological knowledge. For example it is unclear whether this species only scavenges or actively hunt seals in this region.

Marine mammals are a phylogenetically diverse group and our results show differences in network positioning both within and between phylogenetic groups. Pinnipeds include the most generalist species feeding on many central species, but there are large interspecific differences within this group. The bearded seal feeds on many fish and benthic invertebrates from a variety of TLs which results in a high level of omnivory. The walrus on the other hand relies on a smaller number of prey species, but shows the highest level of omnivory in the marine mammal group, consuming benthic invertebrates, fish and marine mammals. By feeding on invertebrates buried in the sea floor, these two Arctic species may also contribute to the abiotic environment through oxygenation of the sediment. This highlights their importance in the ecosystem not only through their direct trophic links but as ecosystem engineers (Hacquebord, 2001; Roman *et al.*, 2014). The five remaining species of pinnipeds are very similar topologically, although their food items may differ. It is interesting to note that this group is composed of both ice-associated species (ringed, harp and hooded seals) and boreal species (harbour and grey seals) with very different habitat requirements. Mysticetes and Odontocetes are heterogeneous groups with both specialist species feeding on a low number of similar prey items, such as the blue and sperm whales, and generalist species feeding on many prey items, such as the harbour porpoise. Odontocetes have generally a low level of omnivory, with the exception of the harbour porpoise whereas Mysticetes such as the fin and humpback whales show a level of omnivory close to some pinnipeds.

Marine mammals belong to two of the four modules identified in the Barents Sea food web network and find the majority of their prey items within their own module. Therefore, as a group, marine mammals contribute to the modularity of the food web, but there are large interspecific differences. The first module contains most of the planktivorous baleen whales that find over 80% of their prey species in their own module. An extreme case is the one of the blue whale that feeds only on species within its own module. Therefore, changes affecting large baleen whales abundance, or their foraging strategies will mainly affect species in their own module in a top-down perspective. In addition, baleen whales only utilise a fraction of the available prey in their module and may thereby contribute to the stability of the Barents Sea food web by restricting the propagation of top-down perturbations within a part of their own module (Stouffer and Bascompte, 2011).

Marine mammals in the second module (all the pinnipeds, most of the odontocetes and the minke whale), have more than a third of their prey in the three other modules, which suggests that their contribution to modularity is not as high as that of marine mammals in the first module. Perturbations linked to these marine mammal species may therefore propagate to other modules of the food web, in addition to their own in which the full range of available species is exploited. The grey seal being the only module connector among marine mammals may be especially important in spreading the effects of perturbations across the food web. Although grey seals are not presently abundant in the Barents Sea and are currently restricted to the southern part, they may expand northwards due to climate-warming (Fossheim et al. 2015). Indeed, the population of grey seals on the Norwegian coast and the Kola Peninsula in Russia has been increasing for the past 30 years which may trigger an expansion of their distributional range. Anecdotic records of grey seals in Greenland have been reported where individuals have been observed North up to Disko Bay and suggest that grey seals are occasional visitors to Greenlandic waters (Rosing-Asvid *et al.*, 2010). Harbour and grey seals often haul out in similar areas and there is a permanent harbour seals population on the West coast of Svalbard (Lydersen and Kovacs, 2005; Blanchet *et al.*, 2014). It is therefore not unlikely that grey seals could also colonize the archipelago especially with the current warming and decrease of sea ice in the region. This species could contribute to the borealization of the Arctic region of the Barents Sea in a manner similar to what is already observed in fish communities. Such module connecting generalist species may decrease the modularity of the Arctic food web, as has been shown for Atlantic cod and haddock (Kortsch et al., 2015).

Due to similarities in direct trophic links and the degree of centrality of prey species, some marine mammals consistently grouped together and also showed similarities with seabirds and some predatory fish, indicating some potential redundancy across different functional groups.

Although topological redundancy does not necessarily imply functional redundancy (Chalcraft and Resetarits, 2003), high topological redundancy is linked to higher robustness of a system (Walker *et al.*, 1999), as the loss of some species might be compensated by the presence of others (Staniczenko *et al.*, 2010; Lai *et al.*, 2012). Indeed, simulations have shown that food webs are more robust when they have a high number of “overlap species” that can compensate species loss by rewiring thus avoiding secondary extinctions (Staniczenko *et al.*, 2010).

Similarities in topological position does not automatically imply dietary overlap. The degree of diet overlap between marine mammals species is extremely varied ranging from no overlap at all (polar bear and blue whale) to very high overlap (humpback and fin whales). Several mechanisms might decrease the competitive pressure, for example, the dietary niche breadth and the habitat selectivity of each species. Fin, minke and humpback whales have broader dietary niches than the blue and bowhead whales, which would allow the former species to shift to other prey items. Bowhead whales overlap most in diet with fin whales but choose waters with high sea ice concentration that are avoided by other whales (Wiig *et al.*, 2010; Reeves *et al.*, 2014), thus decreasing the competitive pressure. Additional prey selection mechanisms may also decrease the competitive pressure by each species targeting different sizes of the same prey species as it is the case for some pinnipeds (Wathne *et al.*, 2000; Preez *et al.*, 2017). Potential for dietary competition is high within the pinnipeds with the exception of the walrus. The ringed, harp and hooded seals are very similar topologically (Wathne *et al.*, 2000) and all of them also share a strong affiliation with sea ice. However, harp and hooded seal use areas beyond the borders of the Barents Sea, which offers larger foraging areas whereas the ringed seal largely stays within its boundaries and forages in ice-associated areas (Hamilton *et al.*, 2015; Vacquie-Garcia *et al.*, 2017; Blanchet *et al.*, 2018). Competitive pressure can also decrease if one of the species is able to undertake niche shift due to behavioural plasticity. This has recently been shown for beluga whales and ringed seals in the Svalbard archipelago. These species have high dietary and spatial overlap. However, beluga whales do not use glacier fronts as heavily as in the past and their behaviour is consistent with foraging on Atlantic fish species that are new in the region (Hamilton *et al.*, 2019). Two of the three "super predators", the polar bear and the killer whale have a high dietary overlap with the diet of the polar bear being completely included within the killer whale's. However, they have very different habitat use strategies, the polar bear using solid land or ice platforms for foraging while the killer whale forages mainly at sea. There is a potential for competition at the marginal ice zone where both species might co-occur, but polar bear has access to other terrestrial food sources that are not included in our analyses (Iversen *et al.*, 2013).

For the purpose of this study, we have considered that all the species present in the Barents Sea occupy this environment homogenously. Yet, some species have strict habitat preferences and some of these potentially redundant species may not co-occur spatially. For example, the sperm whale and the narwhal have very similar topological positions and occupy the same module, although their diet does not overlap. They are, however, unlikely to interact because they occupy different regions of the Barents Sea, the narwhal being a strictly Arctic species whereas the sperm whale is found in the southern part of the Barents Sea and along the shelf edge (Christensen *et al.*, 1992). A similar relation is observed between the white-beaked dolphin a pelagic species, and the beluga, a coastal/ice-associated species. These species may thus perform the same role in the ecosystem but in different regions of the Barents Sea, and may therefore not be topologically redundant at the regional level. This shows that the spatial distribution of each species must be considered when exploring potential functional or network redundancy and competition. This is especially true considering the rapid and extensive environmental changes currently occurring in the Barents

Sea (Kovacs *et al.*, 2011) which might bring previously spatially separated species closer together and modify the structure of regional food webs as has been shown for fish communities (Kortsch *et al.*, 2015, 2018; Frainer *et al.*, 2017)

Conclusions:

In the Barents Sea, marine mammals contribute to the modularity of the food web, connect several energy channels, and have direct links to the most central species. Interspecific differences in the food web-related properties of marine mammals suggest a diversity of contributions to the structure of the food web and its robustness to perturbations. Topological similarities suggesting redundancy are apparent between and within some phylogenetic groups. However, the importance of redundancy likely depends on whether these similar species actually overlap spatially or are segregated between Arctic and Atlantic domains. Climate-induced changes in species distributions currently observed in the Barents Sea are likely to affect the structure of regional food webs as species assemblages change.

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Figure 1: (a) Food web of the Barents Sea. Circles represent single species or trophospecies coloured by their ecological group (plankton, benthic invertebrates, fish, seabirds or marine mammals) and the circle size is proportional to the number of direct predator and prey links. The grey circle represent detritus. Each line represents a feeding link between two species. Species are plotted according to their trophic positioning (y axis) and their module affiliation (x axis). (b-c) The coloured barplots represent the number of prey items consumed by marine mammals in module A and D per ecological group. The overlaid black barplots represent the number of preys consumed by these marine mammal species within the module they belong to. The list of marine mammals present in modules A and D is shown in the two side inserts. Abbreviations for each marine mammal's species is available in table S1.

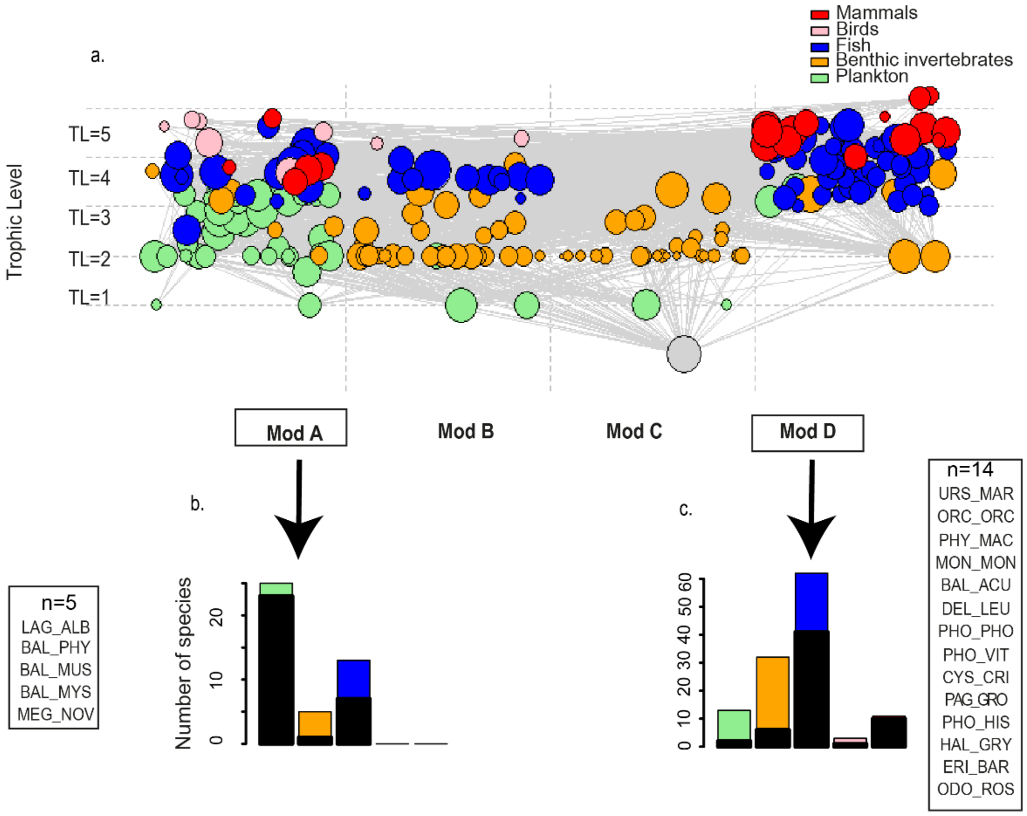


Figure 2: Observed and fitted values of cumulative distribution function of degree (in-degree + out-degree) for each species in the Barents Sea food web. The cumulative distribution function represents the probability of a species having at least a number of degree = x (ranging from 1 to 142). The red curve shows the predictions for the best-fitted model (exponential). Each coloured dot represents a species colour-coded by its ecological groups (plankton, benthic invertebrates, fish, birds, mammals). In addition, marine mammals' species are plotted by phylogenetic groups (mysticetes= ■, pinnipeds=▲, odontocetes=♦, Ursidae=▼) below the red curve. Therefore each marine mammal's species is represented by one black symbol and by one red dot. Note that all the data points are jittered horizontally to improve readability and that the true degree values are located on the red curve.

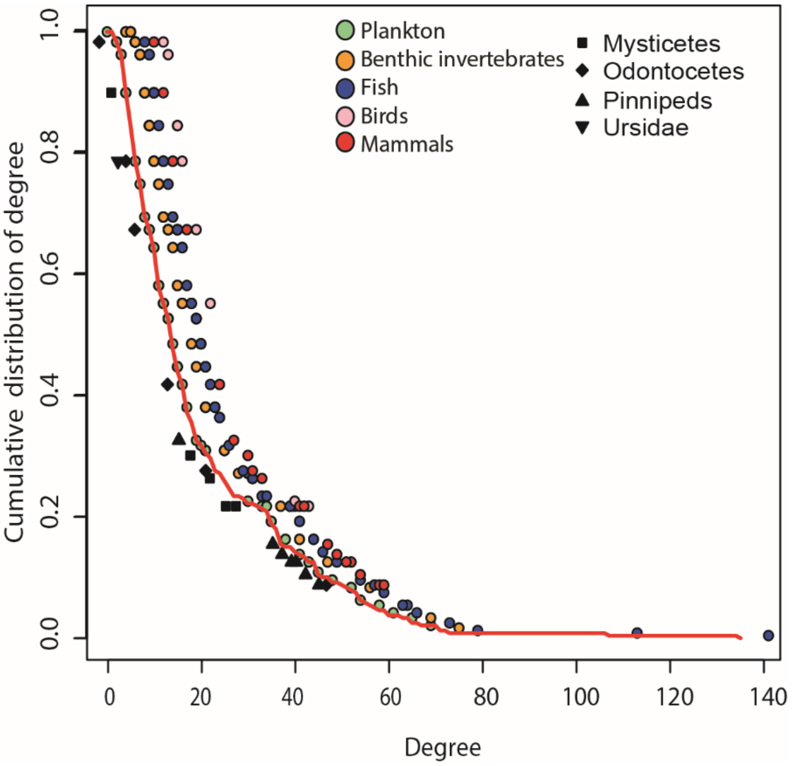
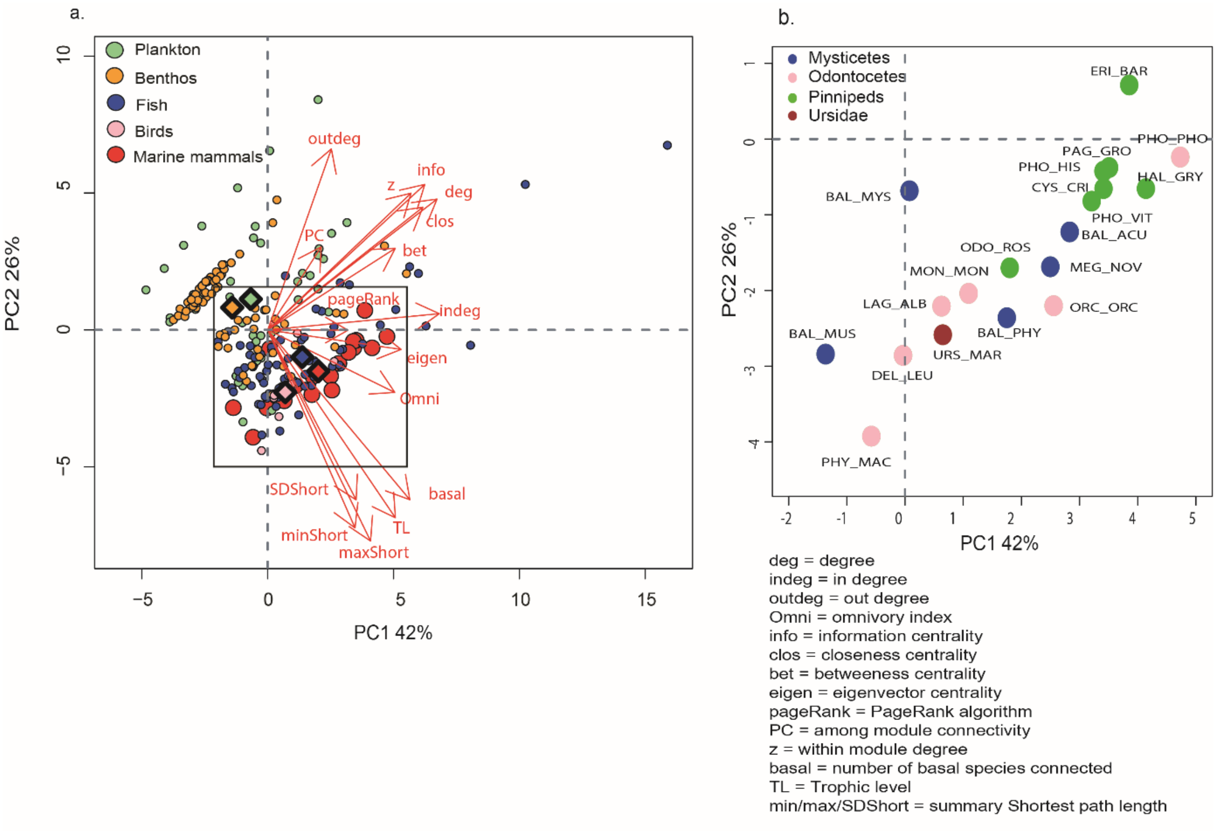


Figure 3: a) Principal component analysis (PCA) of the species or trophospecies present in the Barents Sea food web and characterized by 15 centrality measures. The five ecological groups (plankton, benthic invertebrates, fish, birds and marine mammals)are colour-coded. The 19 marine mammal species are plotted in larger red circles. The diamonds (♦) represent the centroid for each ecological group. b) Separate representation of the PCA space focusing on marine mammal species (located inside the black rectangle in a)). Each species is colour coded according to their phylogenetic group (mysticetes=blue, pinnipeds=green, odontocetes=pink, Ursidae=brown). For the abbreviation of the species' names, see table S1.



deg = degree
indeg = in degree
outdeg = out degree
Omni = omnivory index
info = information centrality
clos = closeness centrality
bet = betweeness centrality
eigen = eigenvector centrality
pageRank = PageRank algorithm
PC = among module connectivity
z = within module degree
basal = number of basal species connected
TL = Trophic level
min/max/SDShort = summary Shortest path length

Figure 4: Module affiliation of marine mammal prey species included in modules A and D. Barplots representing the number of feeding links between marine mammals in module A (n=5) and the species in modules A, B, C and D (a) through d)). The black barplots represent the number of preys consumed by marine mammals inside a module while the coloured barplots represent the composition of the modules essentially showing the proportion of a group consumed by marine mammals within each module. The proportion of realized links between marine mammals and their prey from one module to another is shown on the right side of each individual plot. For example marine mammals in module A have 84% of their feeding links with species present in module A. e) through h) show the same representation for marine mammals present in module D (n=14). Marine mammals present in modules A and D are listed in the two side inserts. Abbreviations for each marine mammal species is available in table S1.

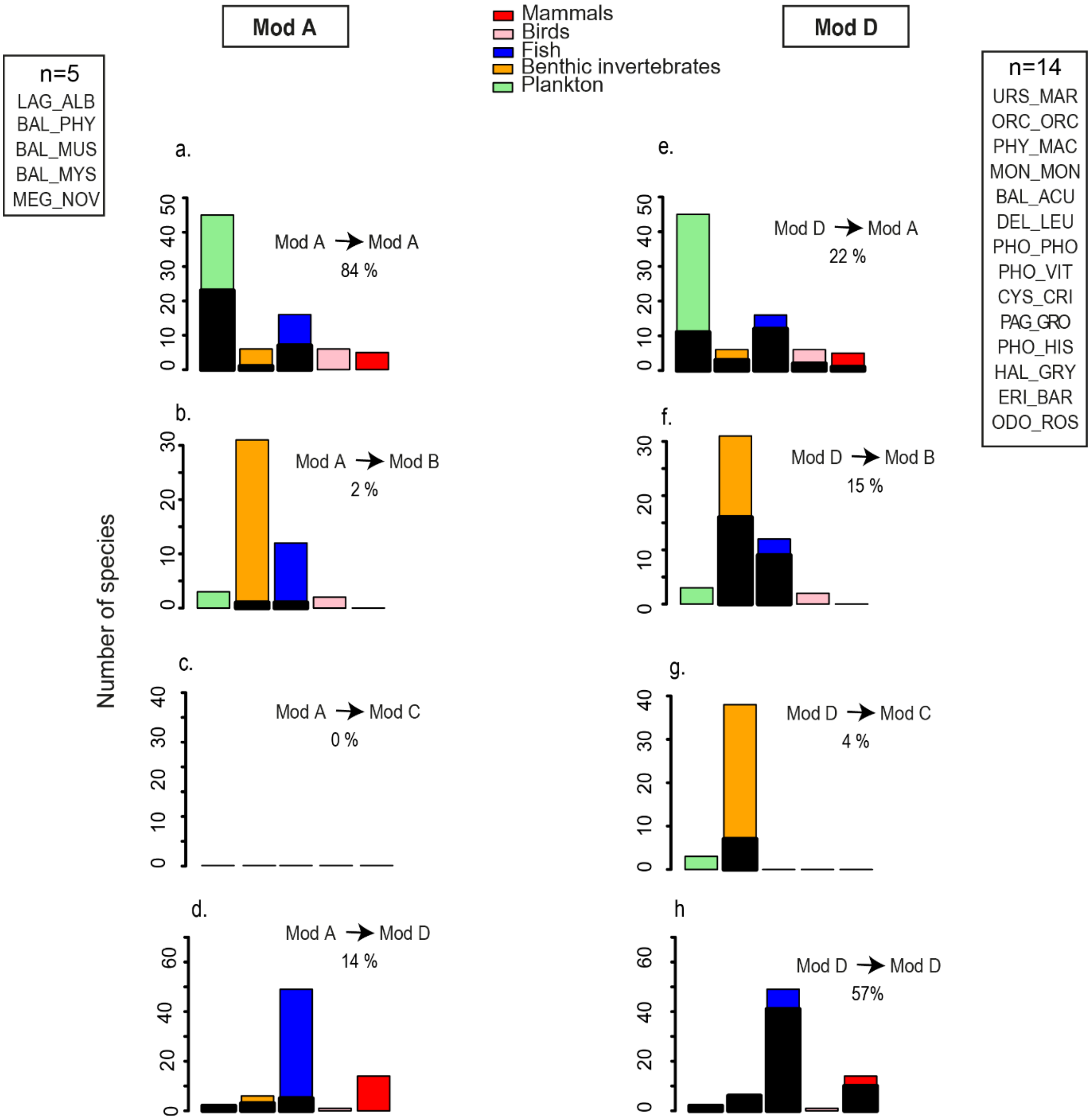


Figure 5: Topological role of marine mammal with respect to modularity. The x axis represents the among module connectivity (PC) and the y-axis represents the within module degree (z). The PC – z space is split in four different regions yielding four functionalities in the network: peripheral, module hub, network connector and module connector. Each species is represented by a square colour-coded by ecological group (green=plankton, orange=benthic invertebrate, blue=fish, pink=birds). Each species of marine mammals is represented by a circle colour-coded by their phylogenetic group (mysticetes = blue, pinnipeds = green, odontocetes =p ink, Ursidae = brown).

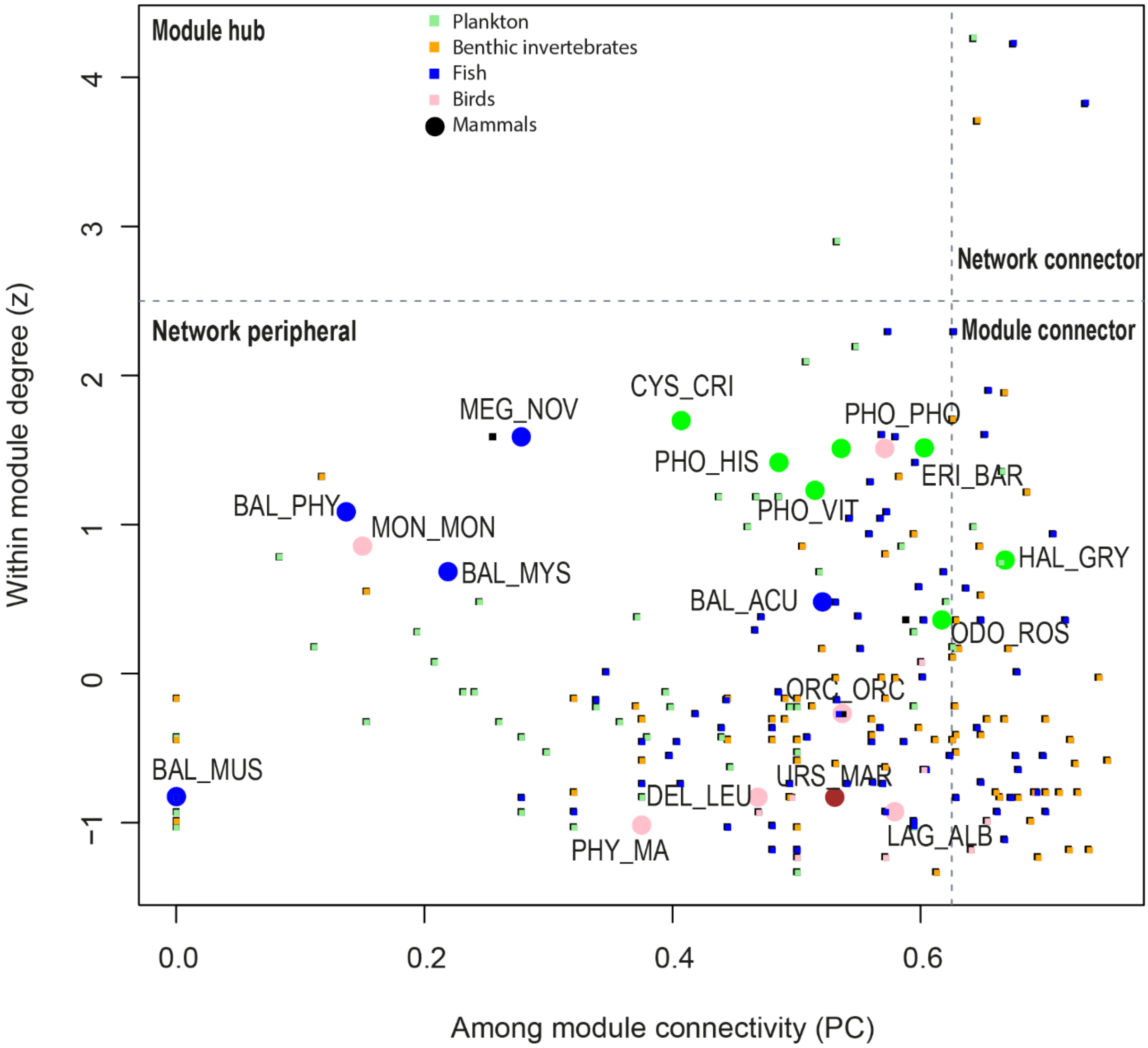
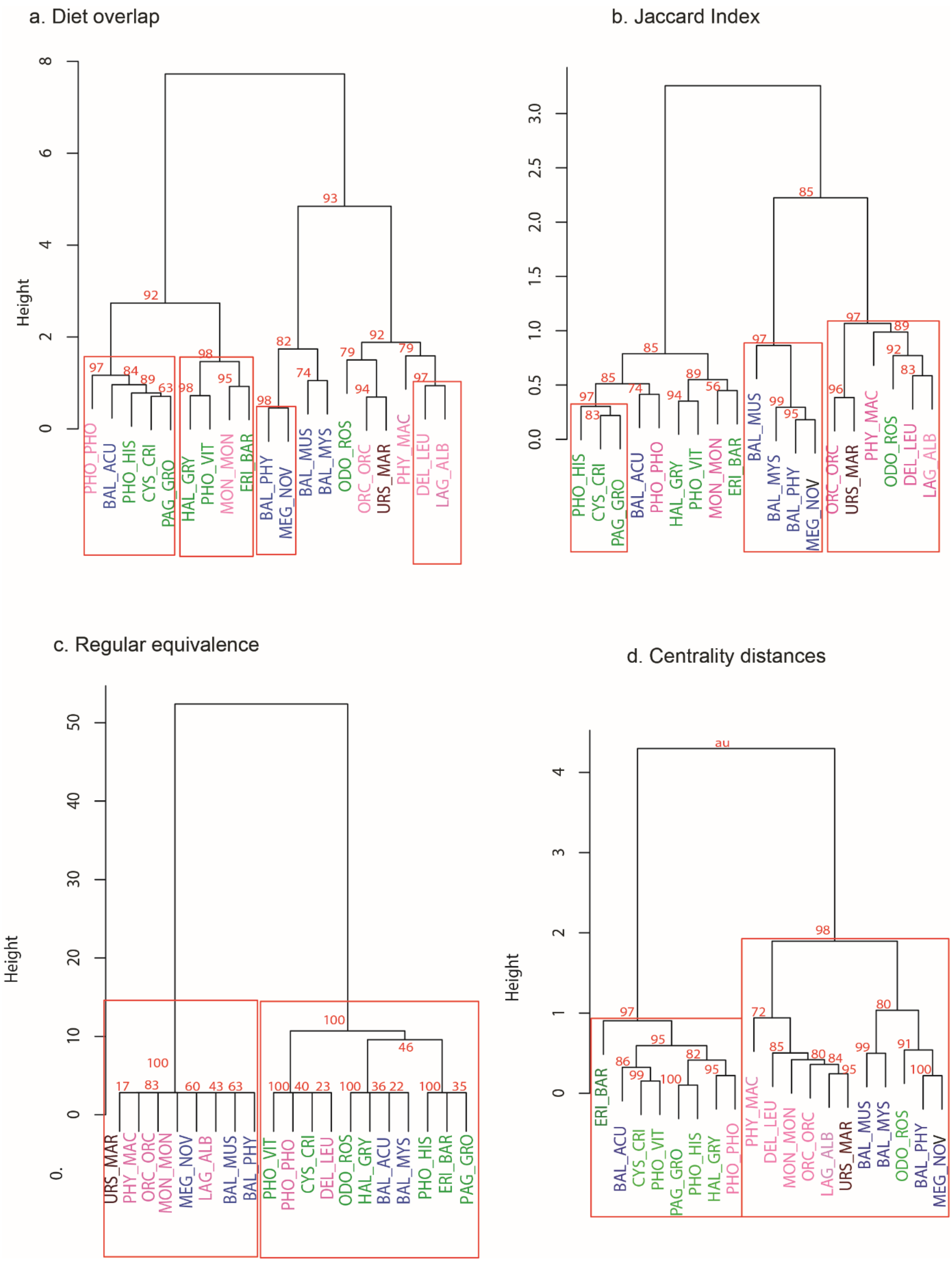


Fig 6: Results of hierarchical clustering of marine mammals species with uncertainty analysis (p-values in red) obtained via multiscale bootstrap resampling for four similarity measures a) diet overlap, b) Jaccard index, c) regular equivalence and d) on the Euclidian distance of the centrality measures. Clusters with a p-value greater than 95% are strongly supported by the data and highlighted by the red rectangles. The species' name abbreviations are color-coded by phylogenetic group (blue= mysticetes, green = pinnipeds, pink=odontocetes, brown= Ursidae).



a. Diet overlap

b. Jaccard Index

c. Regular equivalence

d. Centrality distances

Figure S1: Functional similarity between each pairs of marine mammals based on four similarity measures presented as heatmaps. The first two maps focus local view considering only the direct links while the two last ones take into account the entire network. a) diet overlap between each pairs of marine mammals. The overlap is expressed as a percentage of the diet of species in the column included within the diet of the species in the row. The warmer the colour, the greater the overlap. Note that the matrix is not symmetrical and that the diagonal represents the overlap of the diet of between a species and itself and is therefore 100% . b) Jaccard index defined as the ratio of shared prey and predators over the total of preys and predators of the two species. The warmer the colour, the greater the overlap. Note that the matrix is symmetrical and that the maximum of the index is 0.5 representing the overlap between a species and itself. c) Regular equivalence representing the similarity between pairs of species based on their position inside the food web based on their preys and predators. Note that the matrix is symmetrical and that the maximum of the index is 5 representing the regular equivalence between a species and itself. d) Euclidian distances of network-related centrality metrics between pairs of species. Note that the matrix is symmetrical. The species' name abbreviations are color-coded by phylogenetic groups (blue= mysticetes, green = pinnipeds, pink=odontocetes, brown= Ursidae).

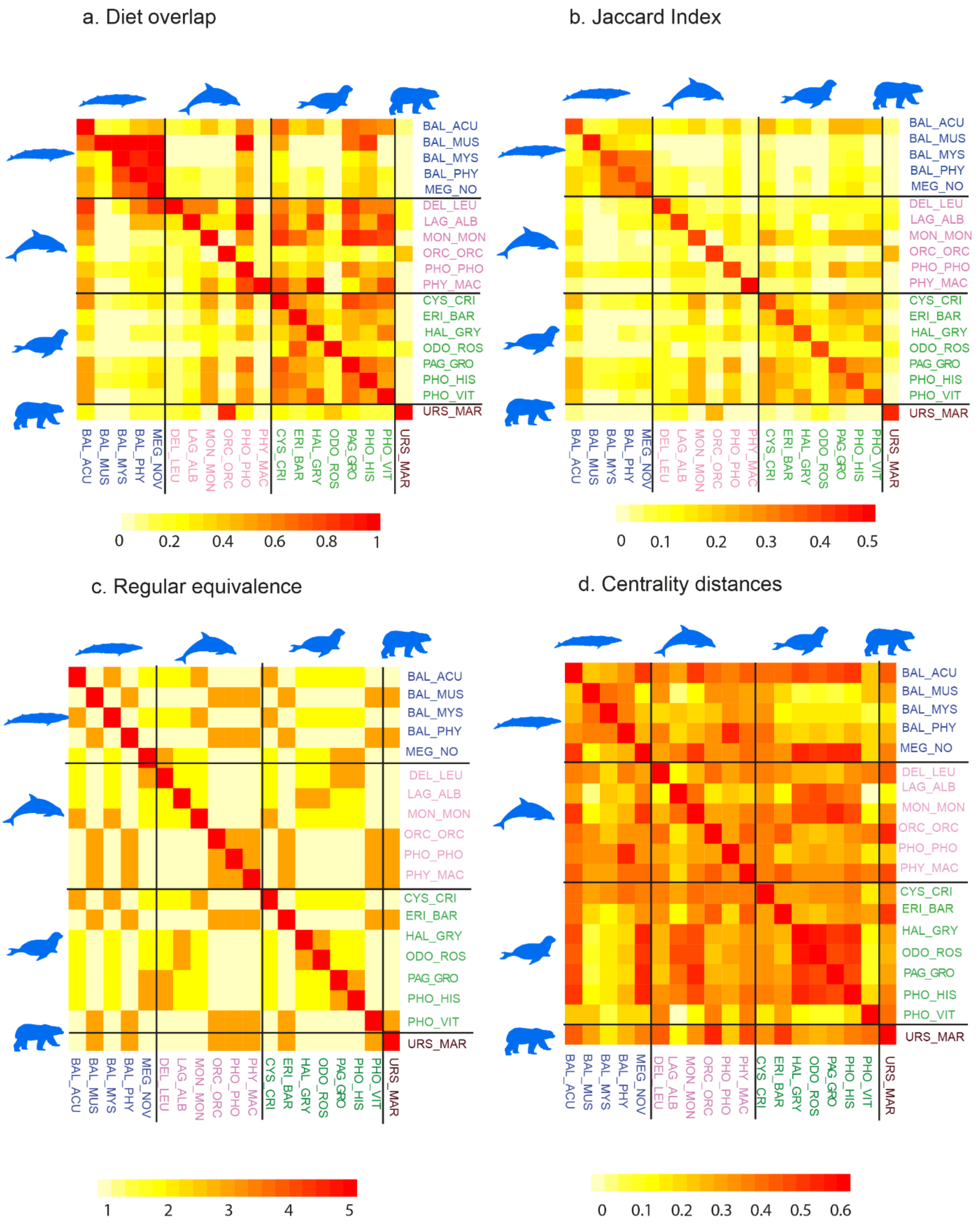


Table 1: Food web-related metrics and their definition.

	Metric	Definition	Reference
Node			
Definitions	Basal species	Species with no prey	Pimm et al., 1991
	Omnivore species	Species feeding at more than one trophic level	Pimm et al., 1991
	Predator species	Species with at least one prey species	Pimm et al., 1991

	Prey species	Species with at least one predator species	Pimm et al., 1991
	Intermediate species	Species with at least one prey and one predator species	Pimm et al., 1991
	Cannibal species	Species feeding on themselves	Pimm et al., 1991; Claessen et al., 2004
Centrality measures			
	In-degree	Number of prey species	Wasserman and Fau Dunne et al. 2002
	Out-degree	Number of predator species	Wasserman and Fau al. 2002
	Degree	Number of prey and predator species	Wasserman and Fau
	Shortest path length	Shortest path length between each species and a basal species	Thompson et al., 200
	Longest path length	Longest path length between each species and a basal species	Thompson et al., 200
	Trophic level based on the shortest paths (SWTL)	Average shortest path lengths weighted by the number of prey species	Williams and Martine
	Trophic level based on the longest paths (LWTL)	Average longest path lengths weighted by the number of prey species	Williams and Martine
	Level of omnivory	Standard deviation of the short weighted trophic levels of each species' prey species	Bascompte et al. 200 al. 2009
	Eigen vector centrality	Degree weighted by the centrality of each of its prey species	Wasserman and Fau
	Betweenness centrality	Number of time a species lies on the shortest path between a pair of species	Wasserman and Fau
	Information centrality	Number of time a species lies on the all the paths between a pair of species	Wasserman and Fau
	Closeness centrality	Average number of steps away from the other species	Wasserman and Fau
	Google's PageRank	Eigen vector measure calculated using a modified version of the Google'PageRank algorithm	Brine and Page 1998 and Pascual 2009
	Among module connectivity (PC)	Number of links between a species and species in other modules normalized by its degree	Guimear and Nunez 2005; Kortsch et al.
	Standardized within module connectivity (z)	The number of links between a species and other species in its module standardized by the average and standard deviation of the number of links in its module	Guimear and Nunez 2005; Kortsch et al.
Network metrics	Number of species	Total number of species or trophospecies in the food web	Dunne et al. 2002
	Number of links	Total number of trophic relationships represented in the food web	Dunne et al. 2002
	Link density	Mean number of trophic relationships per species	Dunne et al. 2002

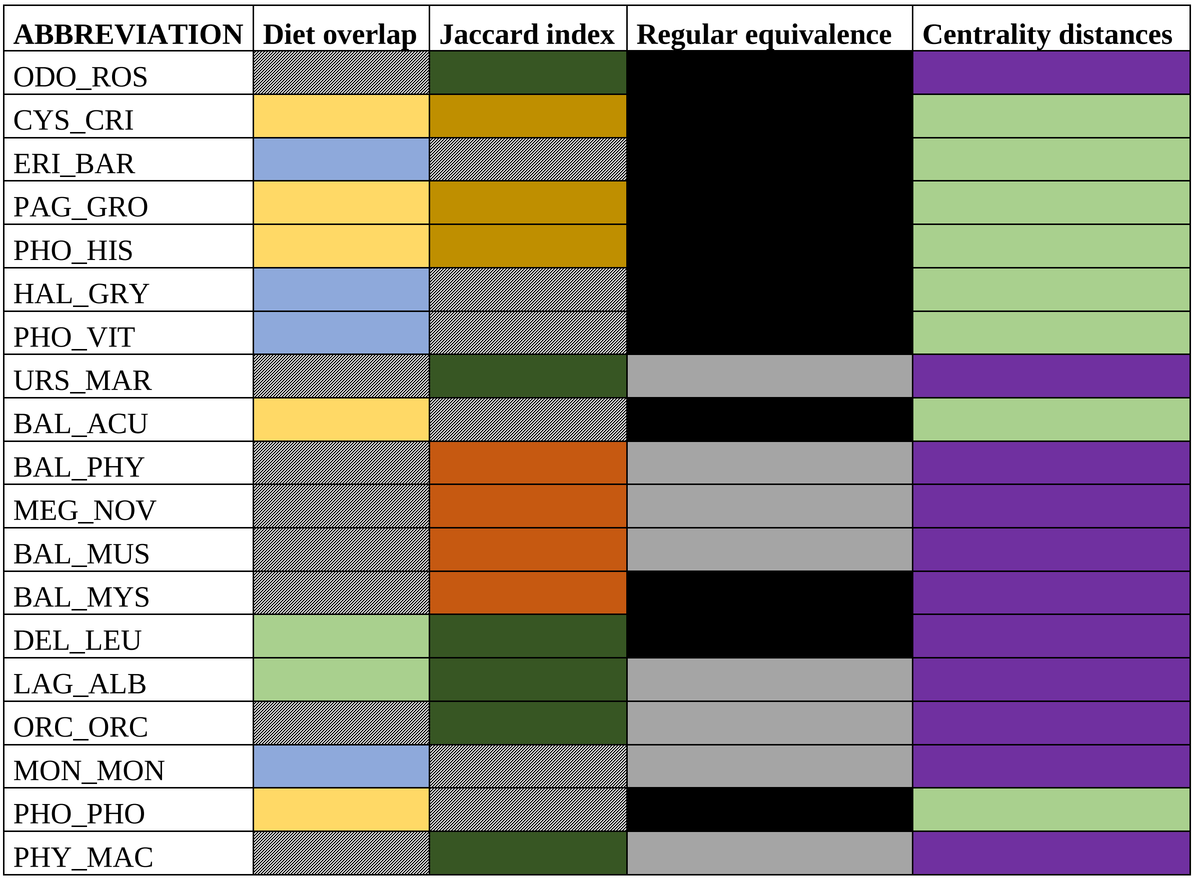
Connectance	Proportion of direct realized links out of the number of possible links	Dunne et al. 2002
Average degree	Average number of trophic relationships per species	Dunne et al. 2002
Average in-degree	Average number of prey links per species	Dunne et al. 2002
Average out-degree	Average number of predation links per species	Dunne et al. 2002
Level of omnivory	Average omnivory level of the species in the food web	Bascompte et al. 200 al. 2009
Average shortest path length	Average shortest food chain connecting each pair of species in the food web	Thompson et al. 200
Average trophic level	Average of all the shortest paths from basal species to each species	Thompson et al. 200
Proportion of predators	Proportion of species with at least one prey species	Dunne et al. 2009
Proportion of omnivores	Proportion of species feeding at more than one trophic level	Petchey et al. 2008
Proportion of cannibals	Proportion of species feeding on themselves	Petchey et al. 2008
Proportion of basal species	Proportion of species with no prey species	Petchey et al. 2008

Table 2: Food web – related metrics calculated for the 19 species of marine mammals present in the Barents Sea food web.

Group	Abbreviation	in-degree	out-degree	degree	eigen	between	closeness	informatio
Mysticetes	BAL_MUS	6	0	6	0,000	0,000	0,384	-0,002
Mysticetes	BAL_MYS	23	1	24	0,000	6,912	0,437	0,000
Mysticetes	BAL_PHY	27	0	27	0,090	0,000	0,446	0,000
Mysticetes	MEG_NOV	36	0	36	0,073	0,000	0,473	0,001
Mysticetes	BAL_ACU	34	1	35	0,360	6,330	0,510	0,001
Mean		***25,2***	***0,4***	***25,6***	***0,105***	***2,648***	***0,450***	***0,000***
Median		***27***	***0***	***27***	***0,073***	***0,000***	***0,446***	***0,000***
Odontocetes	PHY_MAC	4	0	4	0,060	0,000	0,375	-0,002
Odontocetes	DEL_LEU	5	3	8	0,021	2,164	0,433	-0,001
Odontocetes	MON_MON	25	0	25	0,106	0,000	0,437	0,000
Odontocetes	LAG_ALB	11	0	11	0,242	0,000	0,463	0,000
Odontocetes	ORC_ORC	18	0	18	0,663	0,000	0,466	0,000
Odontocetes	PHO_PHO	51	2	53	0,527	22,010	0,538	0,002
Mean		***19***	***0,8***	***19,8***	***0,270***	***4,029***	***0,452***	***0,000***
Median		***14,5***	***0,0***	***14,5***	***0,174***	***0,000***	***0,450***	***0,000***
Pinnipeds	ODO_ROS	19	2	21	0,098	16,768	0,453	0,000
Pinnipeds	PHO_HIS	41	4	45	0,224	73,848	0,516	0,002
Pinnipeds	CYS_CRI	41	2	43	0,329	13,425	0,517	0,001
Pinnipeds	PHO_VIT	38	3	41	0,270	39,018	0,517	0,001
Pinnipeds	PAG_GRO	44	4	48	0,257	74,758	0,517	0,001
Pinnipeds	HAL_GRY	45	1	46	0,381	21,613	0,525	0,002
Pinnipeds	ERI_BAR	49	3	52	0,172	76,061	0,531	0,003

Mean		***39,6***	***2,7***	***42,3***	***0,247***	***45,070***	***0,511***	***0,002***
Median		***41,0***	***3,0***	***45,0***	***0,257***	***39,018***	***0,517***	***0,001***
Ursidae	URS_MAR	8	0	8	0,292	0,000	0,442	-0,001

Table 3: Summary of the results of the hierarchical clustering on four similarity measures. The cells colours indicate which species are grouped together each of the similarity measures. The shaded cells indicate species that were not assigned a group based on the clustering method.



ABBREVIATION	Diet overlap	Jaccard index	Regular equivalence	Centrality distances
ODO_ROS	▨	🟩	⬛	🟪
CYS_CRI	🟨	🟫	⬛	🟩
ERI_BAR	🟦	▨	⬛	🟩
PAG_GRO	🟨	🟫	⬛	🟩
PHO_HIS	🟨	🟫	⬛	🟩
HAL_GRY	🟦	▨	⬛	🟩
PHO_VIT	🟦	▨	⬛	🟩
URS_MAR	▨	🟩	▒	🟪
BAL_ACU	🟨	▨	⬛	🟩
BAL_PHY	▨	🟧	▒	🟪
MEG_NOV	▨	🟧	▒	🟪
BAL_MUS	▨	🟧	▒	🟪
BAL_MYS	▨	🟧	⬛	🟪
DEL_LEU	🟩	🟩	⬛	🟪
LAG_ALB	🟩	🟩	▒	🟪
ORC_ORC	▨	🟩	▒	🟪
MON_MON	🟦	▨	▒	🟪
PHO_PHO	🟨	▨	⬛	🟩
PHY_MAC	▨	🟩	▒	🟪

Table S1: Abbreviations and taxonomy of the 19 species of marine mammals included in the Barents Sea food web

Species	Latin name	Abbreviation	Order	Family
Walrus	*Odobenus rosmarus*	ODO_ROS	Carnivora	Odobenidae
Hooded seal	*Cystophora cristata*	CYS_CRI	Carnivora	Phocidae
Bearded seal	*Erignathus barbatus*	ERI_BAR	Carnivora	Phocidae
Harp seal	*Pagophilus groenlandicus*	PAG_GRO	Carnivora	Phocidae
Ringed seal	*Phoca hispida*	PHO_HIS	Carnivora	Phocidae
Grey seal	*Halichoerus grypus*	HAL_GRY	Carnivora	Phocidae
Harbour seal	*Phoca vitulina*	PHO_VIT	Carnivora	Phocidae
Polar bear	*Ursus maritimus*	URS_MAR	Carnivora	Ursidae
Minke whale	*Balaenoptera acutorostrata*	BAL_ACU	Cetacea	Balaenopterida
Fin whale	*Balaenoptera physalus*	BAL_PHY	Cetacea	Balaenopterida

Humpback whale	*Megaptera novaeangliae*	MEG_NOV	Cetacea	Balaenopterida
Blue whale	*Balenoptera musculus*	BAL_MUS	Cetacea	Balaenopterida
Bowhead whale	*Balaena mysticetus*	BAL_MYS	Cetacea	Balaenopterida
beluga	*Delphinapterus leucas*	DEL_LEU	Cetacea	Delphinidae
White beaked dolphin	*Lagenorhynchus albirostris*	LAG_ALB	Cetacea	Delphinidae
Killer whale	*Orcinus orca*	ORC_ORC	Cetacea	Delphinidae
Narwhal	*Monodon monoceros*	MON_MON	Cetacea	Monodontidae
Harbour porpoise	*Phocoena phocoena*	PHO_PHO	Cetacea	Phocoenidae
Sperm whale	*Physeter macrocephalus*	PHY_MAC	Cetacea	Physeteridae

Table S2: Abbreviations and corresponding species latin names of the 239 species included in the Barents Sea food web. The group correspond to the ecological group (plankton, benthic invertebrate, fish, sea bird, marine mammal).

TROPHOSPECIES	**ABBREVIATION**	**GROUP**
AUTOTHROPH_FLAGELLAT	AUT_FLA	1_Plankton
SAGITTA_SPP	SAG_SPP	1_Plankton
EUPHYSA_FLAMMEA	EUP_FLAM	1_Plankton
SARSIA_SPP	SAR_SPP	1_Plankton
DIMOPHYES_ARCTICA	DIM_ARC	1_Plankton
AGLANTHA_DIGITALE	AGL_DIG	1_Plankton
EUKROHNIA_HAMATA	EUK_HAM	1_Plankton
CYANEA_CAPILLATA	CYA_CAP	1_Plankton
AURELIA_AURITA	AUR_AUR	1_Plankton
ACARTIA_SPP	ACA_SPP	1_Plankton
CALANUS_FINMARCHICUS	CAL_FIN	1_Plankton
CALANUS_GLACIALIS	CAL_GLA	1_Plankton
CALANUS_HYPERBOREUS	CAL_HYP	1_Plankton
MICROCALANUS_SPP	MIC_SPP	1_Plankton
PSEUDOCALANUS_SPP	PSE_SPP	1_Plankton
PAREUCHAETA_GLACIALIS	PAR_GLA	1_Plankton
PAREUCHAETA_NORVEGICA	PAR_NOR	1_Plankton
PAREUCHAETA_SPP	PAR_SPP	1_Plankton
METRIDIA_LONGA	MET_LON	1_Plankton
METRIDIA_LUCENS	MET_LUC	1_Plankton
OITHONA_SIMILIS	OIT_SPI	1_Plankton
OITHONA_SPINIROSTRIS/ATLANTICA	OIT_SIM	1_Plankton
ONCAEA_BOREALIS	ONC_BOR	1_Plankton
APHERUSA_GLACIALIS	APH_GLA	1_Plankton
GAMMARUS_WILKITZKII	GAM_WIL	1_Plankton
ONISIMUS_GLACIALIS	ONI_GLA	1_Plankton
ONISIMUS_NANSENI	ONI_NAN	1_Plankton
THEMISTO_ABYSSORUM	THE_ABY	1_Plankton
THEMISTO_LIBELLULA	THE_LIB	1_Plankton

MEGANYCTIPHANES_NORVEGICA	MEG_NOR	1_Plankton
NEMATOSCELIS_MEGALOPS	NEM_MEG	1_Plankton
THYSANOESSA_INERMIS	THY_INE	1_Plankton
THYSANOESSA_LONGICAUDATA	THY_LON	1_Plankton
THYSANOESSA_RASCHII	THY_RAS	1_Plankton
BEROè_SP	BER_SP	1_Plankton
MERTENSIA_OVUM	MER_OVU	1_Plankton
BOLINOPSIS_INFUNDIBULUM	BOL_INF	1_Plankton
DETRITUS	DET_IND	1_Plankton
HETEROTROPH_FLAGELLAT	HET_FLA	1_Plankton
ICE_ALGAE	ICE_ALG	1_Plankton
MACROALGAE	MAC_IND	1_Plankton
DIATOM	DIATOM	1_Plankton
PROTOZOOPLANKTON	PROZOO	1_Plankton
MIXOTROPH_FLAGELLATES	MIX_FLA	1_Plankton
CLIONE_LIMACINA	CLI_LIM	1_Plankton
LIMACINA_HELICINA	LIM_HEL	1_Plankton
LIMACINA_RETROVERSA	LIM_RET	1_Plankton
PHYTOPLANKTON_INDET	PHY_IND	1_Plankton
BACTERIA_INDET	BAC_IND	1_Plankton
FRITILLARIA_BOREALIS	FRI_BOR	1_Plankton
OIKOPLEURA_DIOICA	OIK_DIO	1_Plankton
OIKOPLEURA_SPP	OIK_SPP	1_Plankton
OIKOPLEURA_VANHOEFFENI	OIK_VAN	1_Plankton
PARAMPHINOME_JEFFREYSII	PAR_JEF	2_Benthos
SPIRORBIDAE_INDET	SPI_IND	2_Benthos
LUMBRINERIS_SP	LUM_SP	2_Benthos
HETEROMASTUS_FILIFORMIS	HET_FIL	2_Benthos
EUCLYMENINAE_INDET	EUC_IND	2_Benthos
LUMBRICLYMENE_MINOR	LUM_MIN	2_Benthos
MALDANE_SARSI	MAL_SAR	2_Benthos
POLYCHAETA	POL_IND	2_Benthos
SCALIBREGMA_INFLATUM	SCA_INF	2_Benthos
POLYNOIDAE_INDET	POLY_IND	2_Benthos
AGLAOPHAMUS_MALMGRENI	AGL_MAL	2_Benthos
GALATHOWENIA_SP	GAL_SP	2_Benthos
MYRIOCHELE_HERRI	MYR_HEE	2_Benthos
CHONE_SP	CHO_SP	2_Benthos
SPIOCHAETOPTERUS_TYPICUS	SPI_TYP	2_Benthos
PRIONOSPIO_CIRRIFERA	PRI_CIR	2_Benthos
SPIOPHANES_KROEYERI	SPI_KRO	2_Benthos
APHELOCHAETA_MARIONI	APH_MAR	2_Benthos
CHAETOZONE_SP	CHA_SP	2_Benthos
CIRRATULIDAE_INDET	CIR_IND	2_Benthos
TEREBELLIDES_STROEMI	TER_STRO	2_Benthos

PYCNOGONIDA_G_SP	PYC_G_SP	2_Benthos
ELECTRA_ARCTICA	ELE_ARC	2_Benthos
BRYOZOA_INDET	BRY_IND	2_Benthos
ASCIDIACEA_G_SP	ASC_G_SP	2_Benthos
ACTINIARIA_G_SP	ACT_G_SP	2_Benthos
NEPHTHEIDAE_SP	NEP_SP	2_Benthos
HYDROZOA_INDET	HYD_IND	2_Benthos
PARALITHODES_CAMTSCHATICUS	PAR_CAM	2_Benthos
RHACHOTROPIS_SP	RHA_SP	2_Benthos
ARRHIS_PHYLLONYX	ARR_PHY	2_Benthos
GAMMARIDAE_INDET	GAM_IND	2_Benthos
PONTOPHILUS_NORVEGICUS	PON_NOR	2_Benthos
SABINEA_SP	SAB_SP	2_Benthos
SCLEROCRANGON_SP	SCL_SP	2_Benthos
CHIONOECETES_OPILIO	CHI_OPI	2_Benthos
HYAS_SP	HYA_SP	2_Benthos
PAGURUS_SP	PAG_SP	2_Benthos
PANDALUS_BOREALIS	PAN_BOR	2_Benthos
NYCTIPHANES_COUCHII	NYC_COU	2_Benthos
ASELLOTA_INDET	ASE_IND	2_Benthos
ERYTHROPS_SP	ERY_SP	2_Benthos
BALANUS_SP	BAL_SP	2_Benthos
OSTRACODA_INDET	OST_IND	2_Benthos
ASTERIAS_RUBENS	AST_RUB	2_Benthos
URASTERIAS_LINCKII	URA_LIN	2_Benthos
PONTASTER_TENUISPINUS	PON_TEN	2_Benthos
CTENODISCUS_CRISPATUS	CTE_CRI	2_Benthos
CROSSASTER_PAPPOSUS	CRO_PAP	2_Benthos
HELIOMETRA_GLACIALIS	HEL_GLA	2_Benthos
STRONGYLOCENTROTUS_SP	STRO_SP	2_Benthos
STICHOPUS_TREMULUS	STI_TRE	2_Benthos
CUCUMARIA_FRONDOSA	CUC_FRO	2_Benthos
MOLPADIA_BOREALIS	MOL_BOR	2_Benthos
GORGONOCEPHALUS_SP	GOR_SP	2_Benthos
OPHIACANTHA_BIDENTATA	OPH_BID	2_Benthos
OPHIOPHOLIS_ACULEATA	OPH_ACU	2_Benthos
OPHIOSCOLEX_GLACIALIS	OPH_GLA	2_Benthos
OPHIOCTEN_SERICEUM	OPH_SER	2_Benthos
OPHIOPLEURA_BOREALIS	OPH_BOR	2_Benthos
OPHIURA_SP	OPH_SP	2_Benthos
FORAMINIFERA	FOR_IND	2_Benthos
BATHYARCA_GLACIALIS	BAT_GLA	2_Benthos
ASTARTE_SP	AST_SP	2_Benthos
MENDICULA_FERRUGINOSA	MEN_FER	2_Benthos
THYASIRA_GOULDI	THY_GOU	2_Benthos

HIATELLA_ARCTICA	HIA_ARC	2_Benthos
MYA_TRUNCATA	MYA_TRU	2_Benthos
YOLDIELLA_SOLIDULA	YOL_SOL	2_Benthos
CHLAMYS_ISLANDICA	CHL_ISL	2_Benthos
SIMILIPECTEN_GREENLANDICUS	SIM_GRE	2_Benthos
MACOMA_SP	MAC_SP	2_Benthos
GONATUS_FABRICII	GON_FAB	2_Benthos
ROSSIA_SP	ROS_SP	2_Benthos
BUCCINUM_SP	BUC_SP	2_Benthos
COLUS_SP	COL_SP	2_Benthos
BENTHOS_LARVAE	BEN_LAR	2_Benthos
GEODIA_SP	GEO_SP	2_Benthos
PORIFERA_G_SP	POR_G_SP	2_Benthos
PHASCOLION_STROMBUS	PHA_STR	2_Benthos
CIONA_INTESTINALIS	CIO_INT	2_Benthos
FISH_LARVAE	FI_LA	3_Fish
ARCTOZENUS_RISSO	ARC_RIS	3_Fish
CLUPEA_HARENGUS	CLU_HAR	3_Fish
ARCTOGADUS_GLACIALIS	ARC_GLA	3_Fish
BOREOGADUS_SAIDA	BOR_SAI	3_Fish
GADICULUS_ARGENTEUS	GAD_ARG	3_Fish
GADUS_MORHUA	GAD_MOR	3_Fish
MELANOGRAMMUS_AEGLEFINUS	MEL_AEG	3_Fish
MERLANGIUS_MERLANGUS	MER_MER	3_Fish
MICROMESISTIUS_POUTASSOU	MIC_POU	3_Fish
POLLACHIUS_POLLACHIUS	POL_POL	3_Fish
POLLACHIUS_VIRENS	POL_VIR	3_Fish
TRISOPTERUS_ESMARKII	TRI_ESM	3_Fish
BROSME_BROSME	BRO_BRO	3_Fish
ENCHELYOPUS_CIMBRIUS	ENC_CIM	3_Fish
GAIDROPSARUS_ARGENTATUS	GAI_ARG	3_Fish
MOLVA_MOLVA	MOL_MOL	3_Fish
MACROURUS_BERGLAX	MAC_BER	3_Fish
GASTEROSTEUS_ACULEATUS	GAS_ACU	3_Fish
BENTHOSEMA_GLACIALE	BEN_GLA	3_Fish
ARGENTINA_SP	ARG_SP	3_Fish
MALLOTUS_VILLOSUS	MAL_VIL	3_Fish
AMMODYTES_SPP	AMM_SPP	3_Fish
ANARHICHAS_DENTICULATUS	ANA_DEN	3_Fish
ANARHICHAS_LUPUS	ANA_LUP	3_Fish
ANARHICHAS_MINOR	ANA_MIN	3_Fish
SCOMBER_SCOMBRUS	SCO_SCO	3_Fish
ANISARCHUS_MEDIUS	ANI_MED	3_Fish
LEPTOCLINUS_MACULATUS	LEP_MAC	3_Fish
LUMPENUS_FABRICII	LUM_FAB	3_Fish

LUMPENUS_LAMPRETAEFORMIS	LUM_LAM	3_Fish
GYMNELUS_SPP	GYM_SPP	3_Fish
LYCENCHELYS_KOLTHOFFI	LYC_KOL	3_Fish
LYCODES_ESMARKII	LYC_ESM	3_Fish
LYCODES_EUDIPLEUROSTICTUS	LYC_EUD	3_Fish
LYCODES_GRACILIS	LYC_GRA	3_Fish
LYCODES_PALLIDUS	LYC_PAL	3_Fish
LYCODES_RETICULATUS	LYC_RET	3_Fish
LYCODES_ROSSI	LYC_ROS	3_Fish
LYCODES_SEMINUDUS	LYC_SEM	3_Fish
GLYPTOCEPHALUS_CYNOGLOSSUS	GLY_CYN	3_Fish
HIPPOGLOSSUS_HIPPOGLOSSUS	HIP_HIP	3_Fish
HIPPOGLOSSOIDES_PLATESSOIDES	HIP_PLA	3_Fish
LIMANDA_LIMANDA	LIM_LIM	3_Fish
MICROSTOMUS_KITT	MIC_KIT	3_Fish
PLEURONECTES_PLATESSA	PLE_PLA	3_Fish
REINHARDTIUS_HIPPOGLOSSOIDES	REI_HIP	3_Fish
AGONUS_CATAPHRACTUS	AGO_CAT	3_Fish
LEPTAGONUS_DECAGONUS	LEP_DEC	3_Fish
ULCINA_OLRIKII	ULC_OLR	3_Fish
ARTEDIELLUS_ATLANTICUS	ART_ATL	3_Fish
GYMNOCANTHUS_TRICUSPIS	GYM_TRI	3_Fish
ICELUS_SPP	ICE_SPP	3_Fish
MYOXOCEPHALUS_SCORPIUS	MYO_SCO	3_Fish
TRIGLOPS_MURRAYI	TRI_MUR	3_Fish
TRIGLOPS_NYBELINI	TRI_NYB	3_Fish
TRIGLOPS_PINGELII	TRI_PIN	3_Fish
CAREPROCTUS_SP	CAR_SPP	3_Fish
CYCLOPTERUS_LUMPUS	CYC_LUM	3_Fish
EUMICROTREMUS_SPINOSUS	EUM_SPI	3_Fish
LIPARIS_FABRICII	LIP_FAB	3_Fish
LIPARIS_GIBBUS	LIP_GIB	3_Fish
LIPARIS_MONTAGUI	LIP_MON	3_Fish
PARALIPARIS_BATHYBIUS	PAR_BAT	3_Fish
COTTUNCULUS_MICROPS	COT_MIC	3_Fish
SEBASTES_MARINUS	SEB_MAR	3_Fish
SEBASTES_MENTELLA	SEB_MEN	3_Fish
SEBASTES_SPP	SEB_SPP	3_Fish
SEBASTES_VIVIPARUS	SEB_VIV	3_Fish
MAUROLICUS_MUELLERI	MAU_MUE	3_Fish
BATHYRAJA_SPINICAUDA	BAT_SPI	3_Fish
AMBLYRAJA_HYPERBOREA	AMB_HYP	3_Fish
AMBLYRAJA_RADIATA	AMB_RAD	3_Fish
RAJELLA_FYLLAE	RAJ_FYL	3_Fish
SOMNIOSUS_MICROCEPHALUS	SOM_MIC	3_Fish

ETMOPTERUS_SPINAX	ETM_SPI	3_Fish
SQUALUS_ACANTHIAS	SQU_ACA	3_Fish
ALLE_ALLE	ALL_ALL	4_Birds
FRATERCULA_ARCTICA	FRA_ARC	4_Birds
URIA_AALGE	URI_AAL	4_Birds
URIA_LOMVIA	URI_LOM	4_Birds
LARUS_ARGENTATUS	LAR_ARG	4_Birds
LARUS_HYPERBOREUS	LAR_HYP	4_Birds
LARUS_MARINUS	LAR_MAR	4_Birds
RISSA_TRIDACTYLA	RIS_TRI	4_Birds
FULMARUS_GLACIALIS	FUL_GLA	4_Birds
ODOBENUS_ROSMARUS	ODO_ROS	5_Mammals
CYSTOPHORA_CRISTATA	CYS_CRI	5_Mammals
ERIGNATHUS_BARBATUS	ERI_BAR	5_Mammals
PAGOPHILUS_GROENLANDICUS	PAG_GRO	5_Mammals
PHOCA_HISPIDA	PHO_HIS	5_Mammals
HALICHOERUS_GRYPUS	HAL_GRY	5_Mammals
PHOCA_VITULINA	PHO_VIT	5_Mammals
URSUS_MARITIMUS	URS_MAR	5_Mammals
BALAENOPTERA_ACUTOROSTRATA	BAL_ACU	5_Mammals
BALAENOPTERA_PHYSALUS	BAL_PHY	5_Mammals
MEGAPTERA_NOVAEANGLIAE	MEG_NOV	5_Mammals
BALENOPTERA_MUSCULUS	BAL_MUS	5_Mammals
BALAENA_MYSTICETUS	BAL_MYS	5_Mammals
DELPHINAPTERUS_LEUCAS	DEL_LEU	5_Mammals
LAGENORHYNCHUS_ALBIROSTRIS	LAG_ALB	5_Mammals
ORCINUS_ORCA	ORC_ORC	5_Mammals
MONODON_MONOCEROS	MON_MON	5_Mammals
PHOCOENA_PHOCOENA	PHO_PHO	5_Mammals
PHYSETER_MACROCEPHALUS	PHY_MAC	5_Mammals

Table S3: Marine mammals prey links as used in the food web; one indicates a trophic link between a consumer (column) and a prey (row). A zero indicates no trophic link. In the columns, the marine mammal species' name abbreviations are color-coded by phylogenetic group (green = pinnipeds, brown= Ursidae, blue= mysticetes, pink=odontocetes).

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
ACA_SPP	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
ACT_G_SP	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
AGL_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
DIG																			
AGL_MAL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AGO_CAT	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
ALL_ALL	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
AMB_HYP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AMB_RAD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AMM_SPP	1	0	0	1	1	0	0	1	1	1	0	0	0	1	1	1	1	0	0
ANA_DEN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANA_LUP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
ANA_MIN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANI_MED	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
APH_GLA	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
APH_MAR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARC_GLA	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0
ARC_RIS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARG_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
ARR_PHY	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
ART_ATL	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
ASC_G_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ASE_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AST_RUB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AST_SP	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0
AUR_AUR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AUT_FLA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BAC_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BAL_ACU	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
BAL_MUS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BAL_MYS	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
BAL_PHY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BAL_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BAT_GLA	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
BAT_SPI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BEN_GLA	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
BEN_LAR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BER_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BOL_INF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BOR_SAI	1	0	0	0	1	1	1	0	1	1	1	1	0	1	1	1	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
BRO_BRO	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
BRY_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BUC_SP	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
CAL_FIN	1	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
CAL_GLA	1	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
CAL_HYP	1	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
CAR_SPP	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CHA_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CHI_OPI	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	1	0	0
CHL_ISL	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
CHO_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CIO_INT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CIR_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CLI_LIM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CLU_HAR	1	0	0	1	1	1	0	1	1	1	0	0	1	1	0	1	1	0	1
COL_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
COT_MIC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CRO_PAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTE_CRI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CUC_	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
FRO																			
CYA_CAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CYC_LUM	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	1	0	1	0
CYS_CRI	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
DEL_LEU	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
DET_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DIATOM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DIM_ARC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ELE_ARC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENC_CIM	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
ERI_BAR	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
ERY_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ETM_SPI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EUC_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EUK_HAM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EUM_SPI	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
EUP_FLAM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FI_LA	1	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0
FOR_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FRA_ARC	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
FRI_BOR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FUL_GLA	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
GAD_ARG	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
GAD_MOR	1	0	0	0	1	0	1	1	1	0	0	0	1	1	1	1	0	0	1
GAI_ARG	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
GAL_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GAM_IND	0	0	1	0	1	0	0	0	0	1	0	0	0	1	1	1	0	0	0
GAM_WIL	0	0	1	0	1	0	1	0	0	1	0	0	0	1	1	1	0	0	0
GAS_ACU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GEO_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GLY_CYN	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	1	0	0
GON_FAB	0	0	0	1	1	0	1	1	1	0	1	0	0	1	1	1	1	1	0
GOR_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GYM_SPP	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
GYM_TRI	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	0	0
HAL_GRY	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HEL_GLA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HET_FIL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HET_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
FLA																			
HIA_ARC	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HIP_HIP	0	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	0	0	0
HIP_PLA	0	0	0	0	1	0	1	1	1	0	0	0	0	1	0	1	1	0	0
HYA_SP	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	1	0	0
HYD_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ICE_ALG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ICE_SPP	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	0	0
LAG_ALB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LAR_ARG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LAR_HYP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LAR_MAR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LEP_DEC	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
LEP_MAC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
LIM_HEL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIM_LIM	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
LIM_RET	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP_FAB	0	0	0	0	1	0	1	0	0	0	1	1	0	1	1	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
LIP_GIB	0	0	0	0	1	0	1	0	0	0	1	1	0	1	1	0	0	0	0
LIP_MON	0	0	0	0	1	0	1	0	0	0	1	1	0	1	1	1	0	0	0
LUM_FAB	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0
LUM_LAM	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1	1	0	0	0
LUM_MIN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LUM_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LYC_ESM	1	0	0	0	1	0	0	0	0	0	1	0	0	1	1	1	1	0	0
LYC_EUD	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	1	1	0	0
LYC_GRA	0	0	0	0	1	0	1	0	0	0	1	0	0	1	1	1	1	0	0
LYC_KOL	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
LYC_PAL	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	1	1	0	0
LYC_RET	1	0	0	0	1	0	1	0	0	0	1	0	0	1	1	1	1	0	0
LYC_ROS	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	1	1	0	0
LYC_SEM	1	0	0	0	1	0	1	0	0	0	1	0	0	1	1	1	1	0	0
MAC_BER	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MAC_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MAC_SP	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
MAL_SAR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MAL_	1	0	0	1	1	1	0	1	1	1	1	0	0	1	1	1	1	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
VIL																			
MAU_MUE	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
MEG_NOR	1	1	1	1	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0
MEG_NOV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MEL_AEG	1	0	0	0	1	0	0	1	1	0	0	0	0	0	0	1	1	0	0
MEN_FER	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
MER_MER	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0
MER_OVU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MET_LON	0	0	1	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
MET_LUC	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
MIC_KIT	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
MIC_POU	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
MIC_SPP	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
MIX_FLA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL_BOR	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
MOL_MOL	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
MON_MON	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MYA_TRU	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
MYO_SCO	1	0	0	0	1	0	1	1	0	0	1	1	0	1	1	0	1	0	0
MYR_HEE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NEM_MEG	0	1	1	1	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0
NEP_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NYC_COU	0	1	1	1	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0
ODO_ROS	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
OIK_DIO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OIK_SPP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OIK_VAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OIT_SIM	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
OIT_SPI	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
ONC_BOR	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
ONI_GLA	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
ONI_NAN	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
OPH_ACU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OPH_BID	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OPH_BOR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OPH_GLA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
OPH_SER	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OPH_SP	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
ORC_ORC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
OST_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PAG_GRO	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1
PAG_SP	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	1	0	0
PAN_BOR	0	0	0	0	0	1	1	1	0	0	1	0	0	1	1	1	1	0	0
PAR_BAT	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
PAR_CAM	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
PAR_GLA	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
PAR_JEF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PAR_NOR	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
PAR_SPP	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
PHA_STR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PHO_HIS	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1
PHO_PHO	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
PHO_VIT	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
PHY_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
PHY_MAC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PLE_PLA	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	1	0	0
POL_IND	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
POL_POL	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
POL_VIR	1	0	0	0	1	0	0	1	0	1	0	0	1	0	0	1	1	1	0
POLY_IND	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
PON_NOR	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
PON_TEN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
POR_G_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PRI_CIR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROZOO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PSE_SPP	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
PYC_G_SP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RAJ_FYL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REI_HIP	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0
RHA_SP	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
RIS_TRI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROS_SP	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1	0	0
SAB_SP	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1	0	1	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
SAG_SPP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SAR_SPP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SCA_INF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SCL_SP	0	0	0	0	0	0	1	1	0	0	0	1	0	1	1	0	1	0	0
SCO_SCO	1	0	0	1	0	0	0	1	1	1	0	0	1	0	0	1	1	0	0
SEB_MAR	0	0	0	0	1	0	0	0	0	0	1	0	0	0	1	1	1	0	0
SEB_MEN	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0
SEB_SPP	1	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	1	1	0
SEB_VIV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SIM_GRE	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
SOM_MIC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SPI_IND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SPI_KRO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SPI_TYP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SQU_ACA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
STI_TRE	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
STRO_SP	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
TER_STRO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
THE_	1	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0

	BAL_ACU	**BAL_MUS**	**BAL_MYS**	**BAL_PHY**	**CYS_CRI**	**DEL_LEU**	**ERI_BAR**	**HAL_GRY**	**LAG_ALB**	**MEG_NOV**	**MON_MON**	**ODO_ROS**	**ORC_ORC**	**PAG_GRO**	**PHO_HIS**	**PHO_PHO**	**PHO_VIT**	**PHY_MAC**	**URS_MAR**
ABY																			
THE_LIB	1	0	0	0	1	0	0	0	0	1	0	0	0	1	1	0	0	0	0
THY_GOU	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
THY_INE	1	1	1	1	1	0	0	0	0	1	0	0	0	1	1	1	0	0	0
THY_LON	1	1	1	1	1	0	0	0	0	1	0	0	0	1	1	1	0	0	0
THY_RAS	1	1	1	1	1	0	0	0	0	1	0	0	0	1	0	1	0	0	0
TRI_ESM	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	1	1	0	0
TRI_MUR	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	0	0
TRI_NYB	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	0	0
TRI_PIN	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	0	0
ULC_OLR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
URA_LIN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
URI_AAL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
URI_LOM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
URS_MAR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
YOL_SOL	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0