

Ecography

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Supplementary material

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Appendix 1: Barents Sea, maps and environmental data

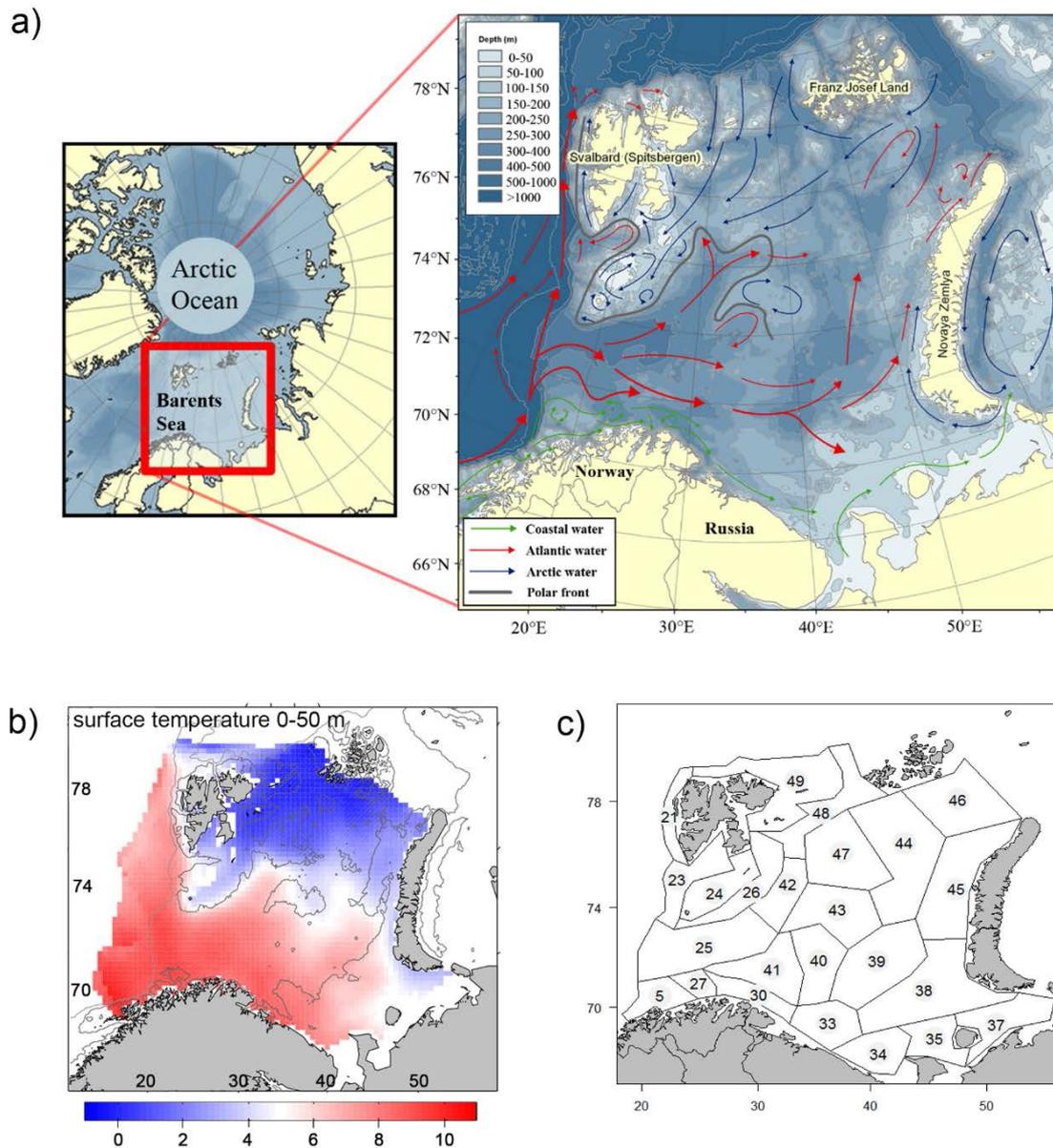


Figure 1. a) Map of the Barents Sea showing the dominant ocean currents (courtesy of Svein Østerhus, University of Bergen). The Atlantic and Arctic water masses carried with the currents are indicated with red and blue arrows, see legend in the bottom-left corner. The bathymetry is indicated with blue gradients, see legend in the top-left corner. b) Map of the Barents Sea showing upper layer temperatures (0–50m; in °C) for the period 2004–2007 (August/September). The region where the Atlantic (red) and Arctic (blue) water masses meet is named the polar front. c) For the purpose of this study, the Barents Sea was divided into 25 sub-regions or polygons. The polygons are defined as geographical units in a numerical end-to-end ecosystem model, the Atlantis model, currently under development and implementation for the Barents Sea (Fulton et al., 2011; Hansen et al., 2016). The polygons were defined according to habitat characteristics such as oceanography, climatic conditions and bottom structure, and result in internally, relatively homogenous sub-regions with respect to the environment.

Environmental data

The temperature and salinity data from 2004 to 2007 were obtained from Conductivity-Temperature-Depth profiles observed annually in August and September by the Institute of Marine Research and Knipovich Polar Research Institute of Marine Fisheries and Oceanography in joint Norwegian-Russian ecosystem surveys designed to cover the entire Barents Sea (e.g., Olsen et al. 2011). Following an approach of Lind et al. (2016), the temperature and salinity data were interpolated each year separately on horizontal fields covering the entire Barents Sea using the Data- Interpolating Variational Analysis (DIVA) (Troupin et al., 2012). The method uses specifically designed finite element grids that restrict information from flowing across bathymetric contours, and accompanying error fields were applied to remove extrapolated areas from the gridded fields (Lind et al. 2016). The interpolation was performed on 51 vertical z-levels from surface to 250 m depth (i.e. every fifth meter) and on a terrain-following near-bottom level made from the deepest measurement in each observed profile as long as this was maximum 15 m from the corresponding echo depth. The horizontal fields were re-gridded onto a 25x25 km area-conserving grid. Temporal-mean horizontal fields were calculated for each vertical level and averaged over each polygon, giving a temporal-spatial-mean vertical profile of temperature and salinity for each polygon (Fig. SI 2a,c). The accompanying standard deviations of temperature and salinity were also calculated to capture the water column variability of these environmental variables (Fig. SI 2b,d and SI 3b). Temporal-mean fields of temperature and salinity in 0–50 m depth, referred to here as ‘upper layer fields’, were also calculated (Fig. 1f in main text).

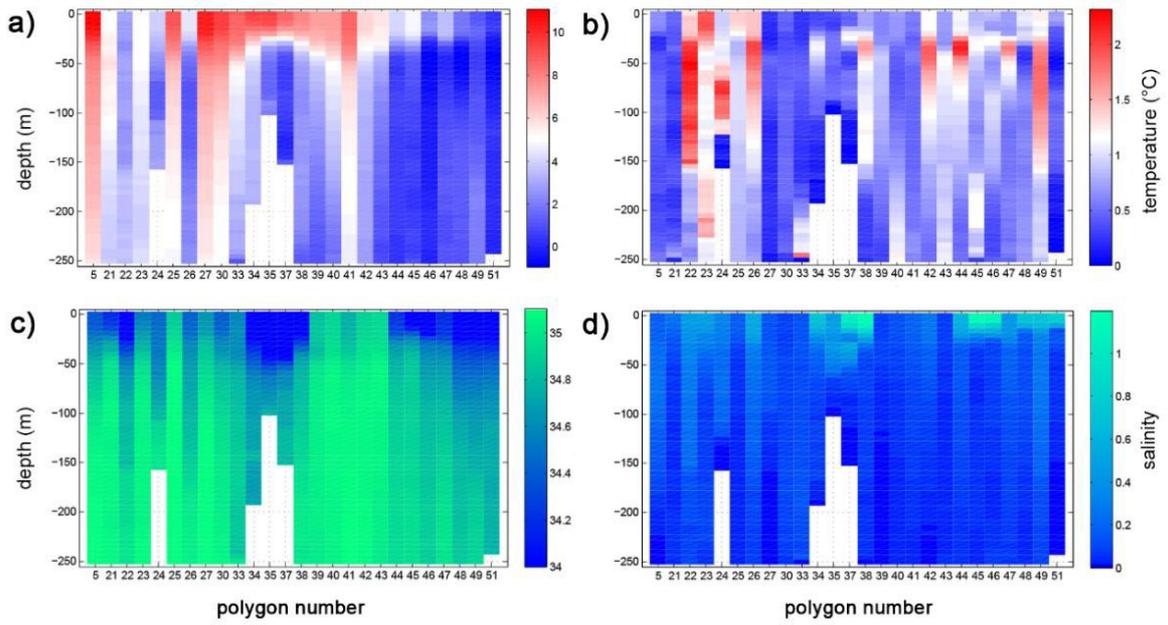


Figure 2. Temporal-mean (2004-2007) vertical profiles of temperature and salinity, averaged horizontally over each polygon, showing a) mean temperature ($^{\circ}\text{C}$); b) standard deviation of temperature ($^{\circ}\text{C}$); c) mean salinity (psu) and d) standard deviation of salinity (psu).

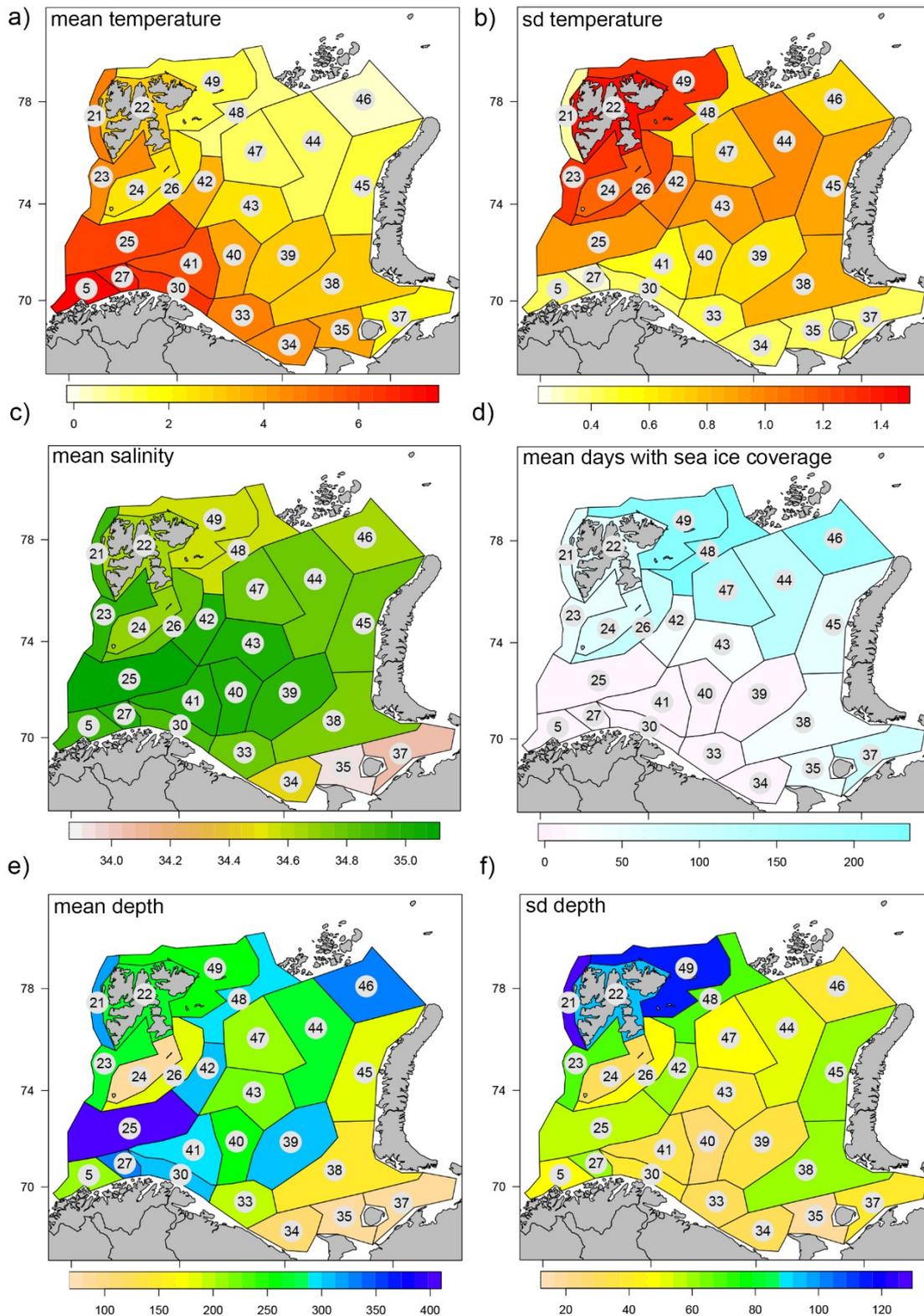


Figure 3. Spatial variation of the environmental variables used in the redundancy analysis: a) mean water column temperature; b) standard deviation of water column temperature; c) mean water column salinity (not included in the RDA); d) mean number of days with sea ice concentration > 15 % (not included in the RDA); e) mean bottom depth; and f) standard deviation of bottom depth.

References

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Appendix 2: The ecosystem survey and the Barents Sea food-web metaweb

Ecosystem survey data

Since 2004, the joint Russian–Norwegian Barents Sea Ecosystem Survey has sampled taxa from the entire water column and sea floor (except for benthic infauna) in a joint effort to map the whole ecosystem (Olsen et al., 2011). The survey takes place in August/September each year, since 2004, when sea ice is at its minimum. The species distribution data used to construct the regional (polygon) food webs are therefore representative for the late summer period of the year (i.e. a period of intensive feeding for most marine organisms). Each year approximately 300–700 stations (hydrographic stations, pelagic and demersal trawls, hydrobiological stations) are sampled throughout the Barents Sea (App. 2, Fig. 1). Multiple sampling methodologies are deployed to gather information on epibenthos, plankton, fish, sea birds and marine mammals. The species distribution data at station level is most resolved for epibenthos and fish. Sea birds and marine mammals are observed along transects and were located to the polygons for the use of assembling food webs in this study.

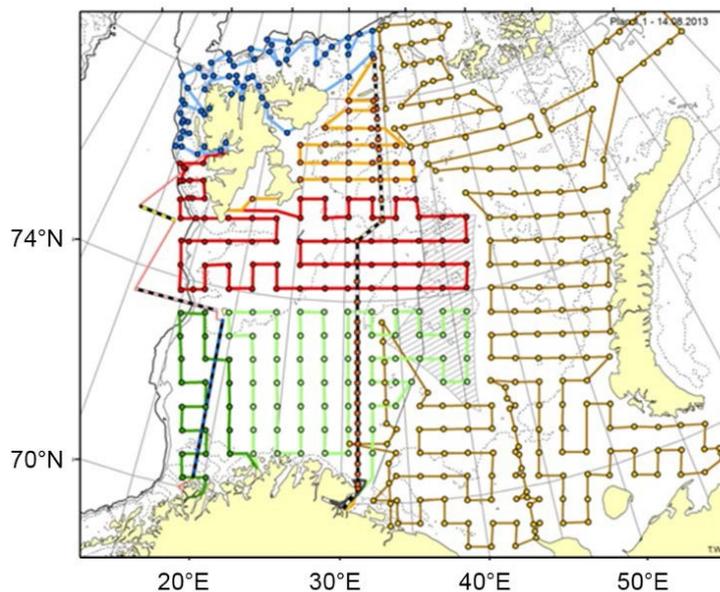


Figure 1. Map with stations and transects from the joint Russian-Norwegian Barents Sea Ecosystem survey. The lines indicate the sampling transects and the dots the sampling stations (> 400 stations). Figure printed with permission from the Institute of Marine Research, Norway. The sampling takes place every year, since 2004 in August/September.

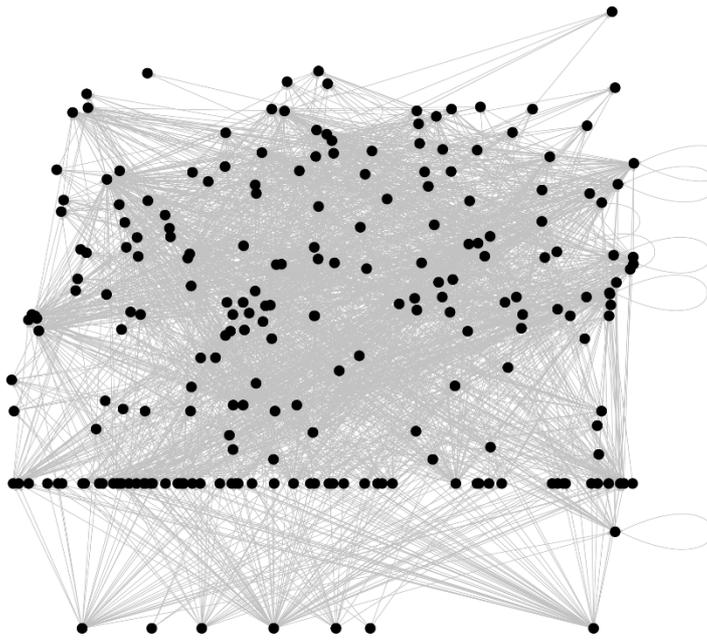


Figure 2. Illustration of the Barents Sea metaweb. The Barents Sea food web metaweb represents the most common taxa from the seafloor to the surface across the entire Barents Sea, comprising 233 trophospecies and 2218 feeding links. The Barents Sea metaweb and species distribution information from the ecosystem survey were used to subsample the 25 polygon food webs. The subsampling procedure is described in the main text in figure 2.

The food-web metaweb

The food-web metaweb represents the most common taxa from the seafloor to the surface for the whole Barents Sea, comprising 233 trophospecies and 2218 feeding links (App. 2, Fig. 2). The food web includes detritus and bacteria, 8 basal taxa (e.g. phytoplankton), 43 zooplankton, 79 benthic, and 77 fish, as well as 9 sea birds and 15 marine mammals. Taxa from the metaweb and their corresponding feeding links were used to compile the 25 regional food webs combined with the species distribution information from the ecosystem survey. A detailed description of the criteria used to compile the metaweb can be found and downloaded from the *Ecological Archives* website (Planque et al., 2014). Please use the updated data files from August 2015 using this link: <http://www.esapubs.org/archive/ecol/E095/124/metadata.php>.

The 25 regional food webs

To study how food webs vary along environmental gradients in the Barents Sea, we constructed 25 sub-food webs by choosing subsets of taxa and their corresponding feeding links specific to predefined sub regions (polygons). Information on occurrence of taxa within the defined polygons (25 sub-regions) was obtained from the data sampled by the joint Russian–Norwegian

ecosystem survey (App. 2, Fig. 1) (Olsen et al., 2011). The 25 food webs are representative for the early years (2004–2007) of the ecosystem survey. This period was chosen to capture a snapshot of species distributions and food-web structure before the documented community-wide shift in fish distributions as a response to warming in the Barents Sea (Fossheim et al., 2015). Fish and epibenthos data were obtained on station level, and occurrence of marine mammals, sea birds and zooplankton were assigned to polygons based on transect recordings from the ecosystem survey. Benthic infauna (owing to poor information on occurrence) and all aggregated basal groups were marked present in all the sub-regions, with the exception of sea-ice algae, which are only present in the arctic polygons. Much of the discussion revolved around the role of fish in creating observed food-web structures. First of all, because the fish data are the most resolved in terms of the number of sampling stations and taxonomic resolution, and, secondly, because fish species play an important structuring role as connectors between the primary and secondary producers and the top predators in the marine food web. The food webs in this paper are some of the best taxonomically and spatially resolved marine food webs existing, and unlike most comparative food-web studies, the degree of aggregation of the trophospecies between areas is the same. This implies that the observed variation in food-web structure between the 25 food webs cannot be attributed to differences in the classification and aggregation of trophospecies, but should be attributed to differences in species composition and region-specific trophic link configuration.

References

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Appendix 3: Null model computation procedure and output

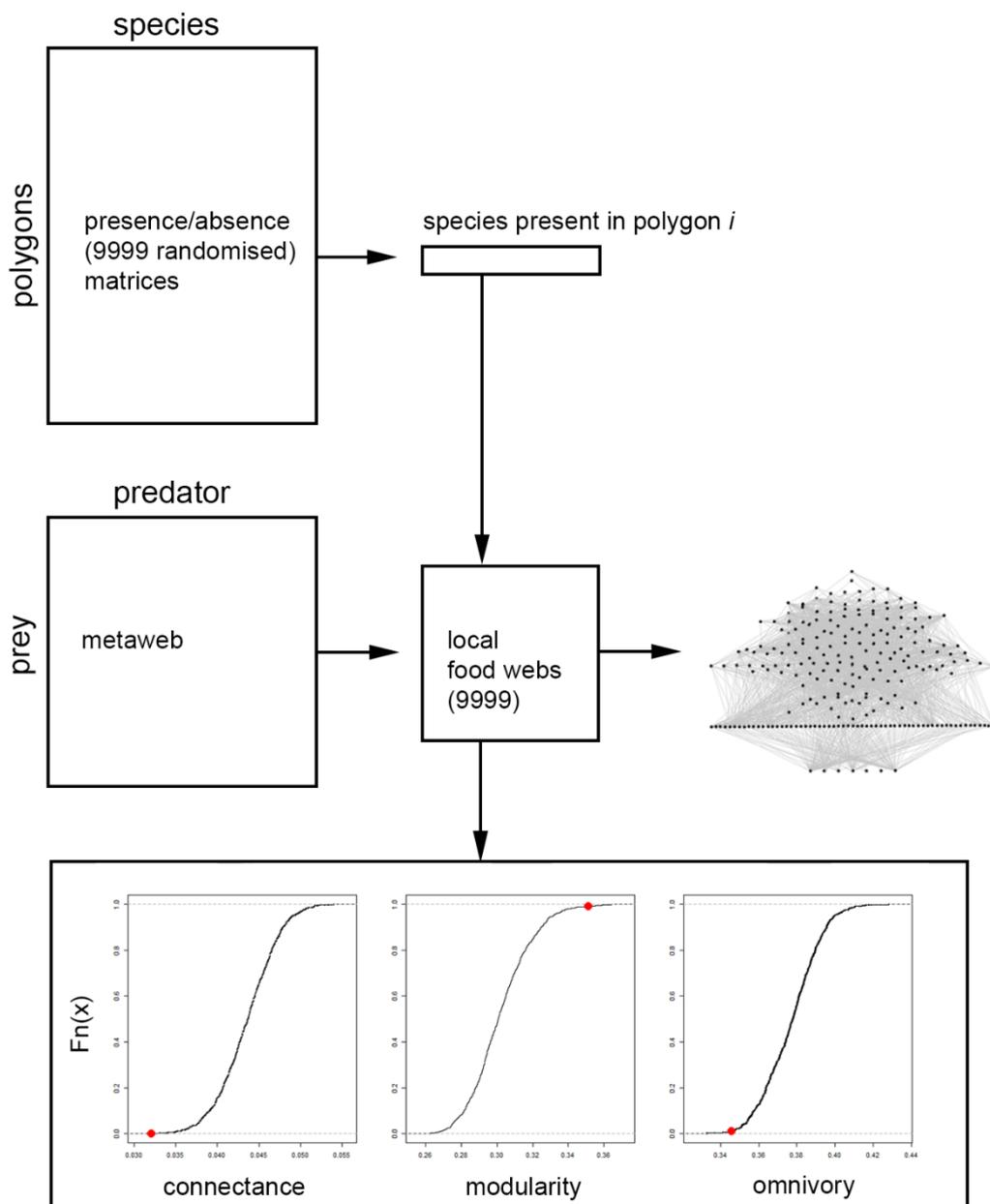


Figure 1. Diagram of the steps used to estimate how much the empirical food-web structure is deviating from a null model (i.e. random) expectation. 9999 food-web simulations were performed on the polygon-by-species matrix using a swap algorithm. These randomized polygon-by-species matrices were used together with the Barents Sea metaweb to subsample 9999 local food webs for each polygon. The empirical food-web values were then compared to the null-model distributions. Empirical values were considered to deviate strongly from the randomized food webs if the empirical value was outside the 0.05 to 0.95 quantile range of the null distribution.

Null model output

Table 1. Results of the null model analyses performed with the curveball swap algorithm. The p-value describes the probability of obtaining a food-web structure equal to or more extreme than the empirical structure, under the null model. If the empirical values were outside the 0.05 to 0.95 quantiles of the null distribution, they were considered to deviate strongly from the randomized food webs. Empirical values below or equal to 0.05 and values above or equal to 0.95 are indicated with black and bold numbers.

	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW	FW
no.	L	LD	C	Clust	Comp	LOmni	Can	Omni	PredP	PreyP	mSWTL	Bas	Int	Top	VulSD	GenSD	mPath
5	0,74	0,77	0,80	0,93	0,11	0,49	0,64	0,63	0,80	0,21	1,00	0,83	0,19	0,81	0,25	0,26	0,65
21	0,29	0,29	0,28	0,37	0,19	0,74	0,95	0,28	0,30	0,66	0,88	0,08	0,72	0,23	0,23	0,70	0,38
22	0,90	0,90	0,90	0,97	0,16	0,59	0,44	0,97	0,54	0,50	0,94	0,95	0,35	0,51	0,29	0,29	0,74
23	0,75	0,75	0,75	0,87	0,22	0,63	0,79	0,49	0,85	0,15	0,98	0,16	0,27	0,83	0,69	0,46	0,49
24	0,74	0,73	0,73	0,49	0,78	0,75	0,23	0,92	0,61	0,39	0,62	0,76	0,25	0,62	0,16	0,31	0,83
25	0,88	0,88	0,88	0,93	0,26	0,83	0,99	0,66	0,82	0,18	0,95	0,0001	0,27	0,78	0,30	0,44	0,80
26	0,85	0,85	0,85	0,67	0,19	0,96	0,30	0,99	0,33	0,67	0,70	0,58	0,75	0,38	0,50	0,34	0,71
27	0,95	0,95	0,95	0,98	0,05	0,79	0,97	0,67	0,49	0,48	0,99	0,0001	0,58	0,51	0,09	0,43	0,85
30	0,87	0,87	0,87	0,87	0,44	0,96	0,83	0,77	0,52	0,50	0,68	0,0001	0,70	0,49	0,10	0,81	0,74
33	0,99	0,99	0,99	0,97	0,01	0,44	0,95	0,91	0,46	0,54	0,52	0,25	0,52	0,39	0,03	0,59	0,58
34	0,94	0,94	0,94	0,72	0,23	0,05	0,80	0,57	0,35	0,65	0,85	0,81	0,65	0,42	0,00	0,63	0,41
35	0,99	0,99	0,99	0,71	0,06	0,66	0,68	0,32	0,01	0,99	0,36	0,89	0,98	0,01	0,00	0,78	0,41
37	0,58	0,61	0,65	0,20	0,37	0,63	0,18	0,08	0,08	0,94	0,21	0,47	0,96	0,06	0,03	0,86	0,29
38	0,84	0,87	0,89	0,48	0,03	0,17	0,78	0,11	0,08	0,94	0,03	0,74	0,92	0,07	0,14	0,71	0,14
39	0,65	0,65	0,65	0,80	0,53	0,24	0,94	0,77	0,80	0,22	0,38	0,0001	0,28	0,73	0,68	0,13	0,44
40	0,59	0,59	0,59	0,77	0,48	0,95	0,81	0,96	0,75	0,23	0,79	0,0001	0,37	0,70	0,65	0,57	0,62
41	0,71	0,71	0,71	0,92	0,27	0,93	0,82	0,69	0,74	0,25	0,90	0,0001	0,38	0,74	0,42	0,50	0,80
42	0,86	0,86	0,86	0,75	0,43	0,86	0,51	0,99	0,48	0,52	0,55	0,26	0,62	0,47	0,47	0,50	0,18
43	0,48	0,48	0,48	0,37	0,76	0,43	0,53	0,59	0,61	0,39	0,18	0,0001	0,50	0,61	0,82	0,65	0,24
44	0,00	0,0001	0,0002	0,00	1,00	0,27	0,00	0,01	0,97	0,03	0,01	0,76	0,03	0,97	1,00	0,01	0,39
45	0,00	0,0001	0,0001	0,00	1,00	0,02	0,00	0,01	0,95	0,05	0,01	0,97	0,04	0,95	1,00	0,02	0,20
46	0,00	0,0022	0,0022	0,00	0,99	0,24	0,00	0,02	0,90	0,10	0,02	0,79	0,06	0,91	1,00	0,02	0,08
47	0,29	0,29	0,29	0,65	0,76	0,33	0,36	0,22	0,34	0,66	0,20	0,96	0,41	0,52	0,77	0,15	0,49
48	0,16	0,16	0,16	0,69	0,46	0,01	0,08	0,15	0,84	0,16	0,13	0,95	0,08	0,87	0,95	0,12	0,09
49	0,71	0,71	0,71	0,75	0,15	0,08	0,42	0,70	0,06	0,94	0,60	0,95	0,91	0,11	0,31	0,69	0,06

Appendix 4: Hierarchical clustering of food webs

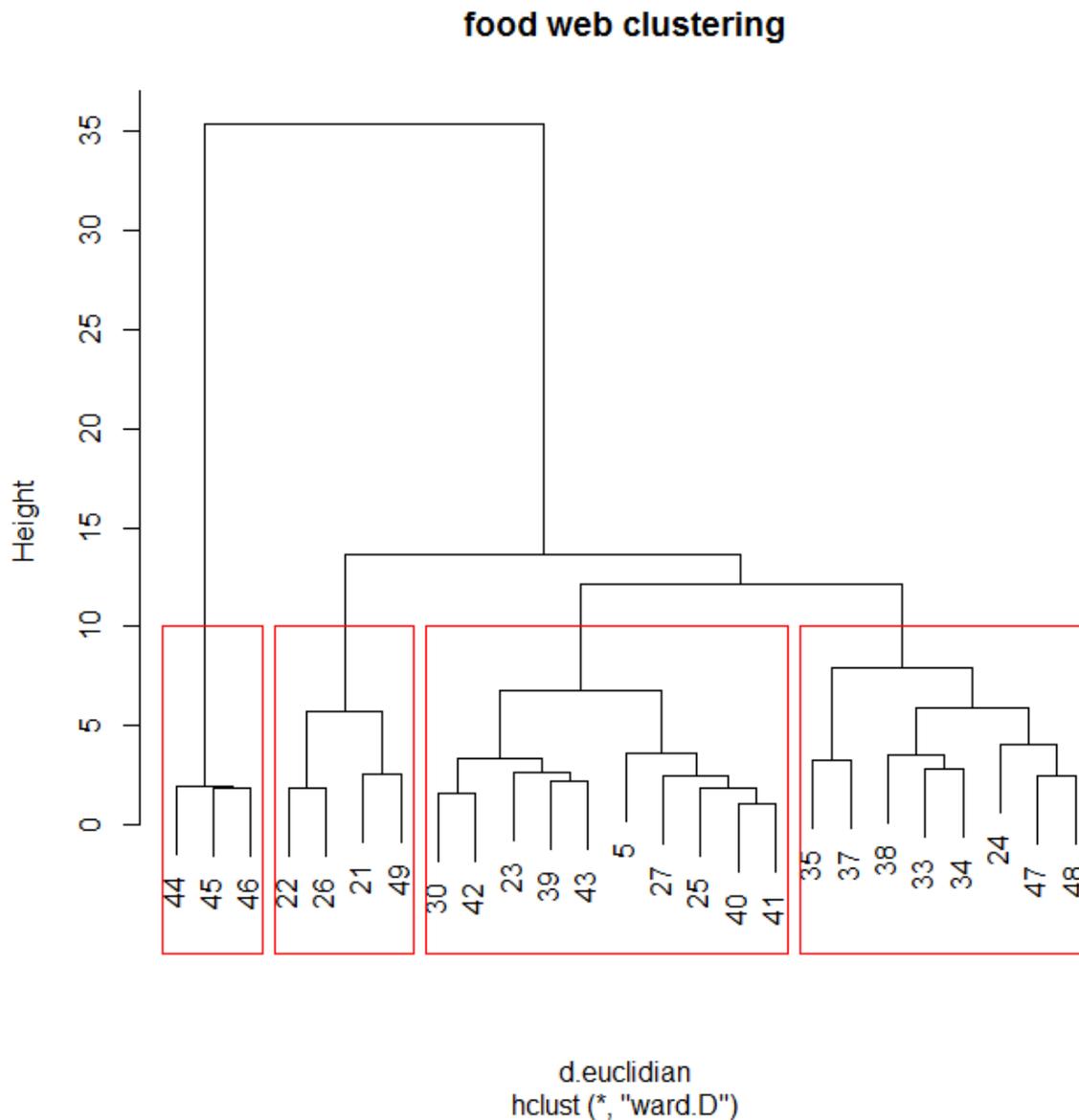


Figure 1. Cluster dendrogram of Barents Sea food webs based on Euclidean distance and ward clustering. Ward linkage emphasizes sharp differences between, and strong homogeneity within, clusters. The cut level of the dendrogram is chosen based on the configuration of distances between food webs. See figure S2 for a cut based on bootstrapping.

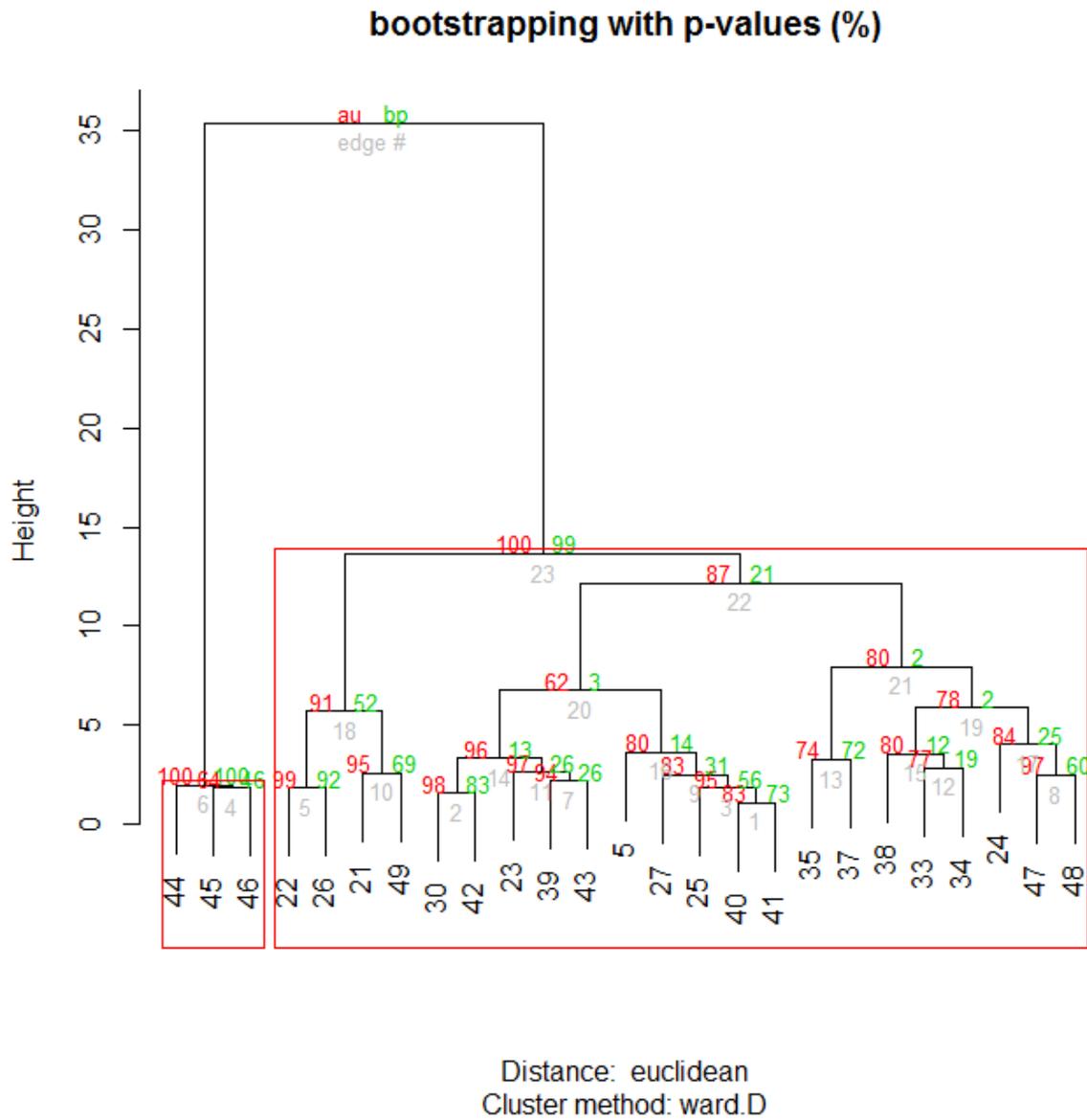


Figure 2. Cluster dendrogram of Barents Sea food webs with uncertainty analysis (p-values). Two types of p-values are given: the red values are the AU (approximately unbiased) p-values and the green are the computed by normal bootstrap probability (BP). The AU is a better approximation to unbiased p-values than BP. Clusters with AU p-values larger than 95 % (highlighted with the red rectangles) are strongly supported by the data. In our spatial food-web data, the main separation that is highly supported by the data identifies two clusters, the Arctic polygons (44, 45, and 46), and all the remaining ones.

Appendix 5: Summary of RDA and permutation test

Table 1. Summary table of the RDA analysis

Analysis	Total Inertia (variance)	Inertia constrained axis	Inertia unconstrained axis	Eigenvalues	
				RDA 1	RDA 2
RDA	1.00	0.47	0.53	0.26	0.10

Table 2. Permutation test of significance for the individual terms included in the RDA (Number of permutations, 999). The terms included in the RDA were mean temperature (mean.temp), standard deviation of temperature (SD.temp), mean depth (mean.depth) and standard deviation of depth (SD.depth).

	Df	Variance	F	Pr(>F)
mean.temp	1	3.5306	7.3737	0.001 ***
SD.temp	1	1.7014	3.5534	0.017 *
mean.depth	1	1.3460	2.8112	0.047 *
SD.depth	1	1.8461	3.8556	0.017 *
Residual	20	9.5760		
Significance codes: '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '' 1				

Appendix 6: Relationship between turnover in species composition and interaction

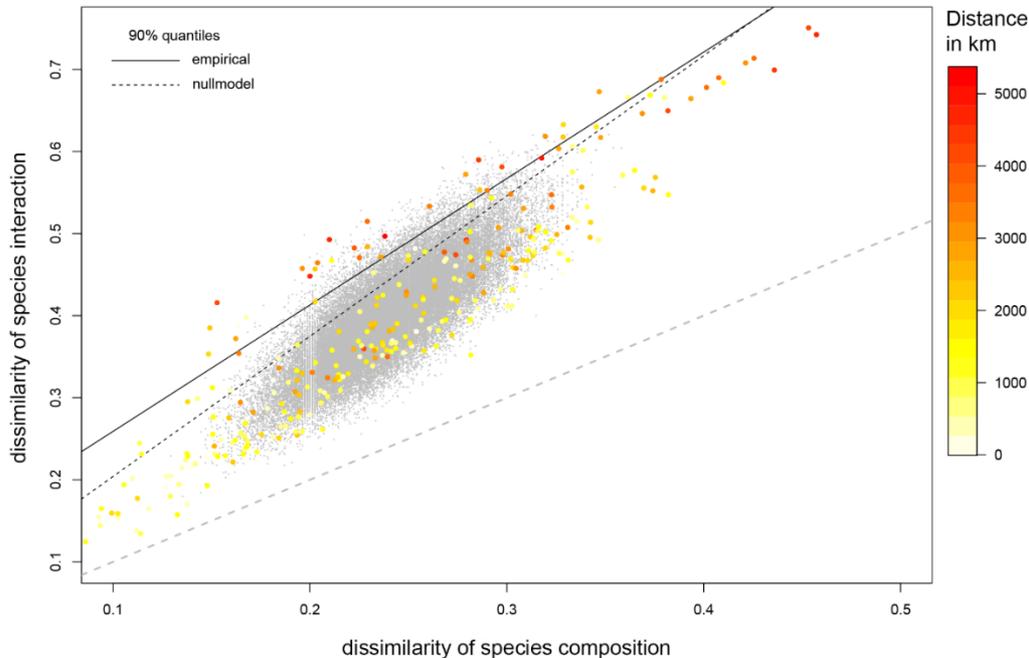


Figure 1. Relationship between interaction turnover and turnover in species composition for all possible pair-wise comparisons (300) among the 25 food webs (colored circles). The small grey dots are pairwise dissimilarities among 200 null model randomizations of the 25 food webs of the Barents Sea. The yellow to red colors of the circles indicate the geographic distance in kilometers between the pairs of empirical food webs. The gradient bar to the right of the figure provides a legend of the geographic distances. The dashed grey line indicates the 1:1 relationship. The two upper lines are the 90% quantiles of the empirical (solid line) and the randomized (dashed line) food webs.

Figure 1 shows how interaction turnover increases with turnover in species composition for the empirical food webs, as well as for randomized null model food webs. For both empirical and null model food webs, the relationship had a steeper slope than a 1:1 relationship. However, for a given compositional difference, the empirical food webs display relatively higher spread reaching higher values of interaction structure, as shown by the higher intercept of the 90% quantile regression trend line of the empirical food webs compared to the random webs. These higher interaction turnover values were typically associated with pairs of food webs located far from each other. This is an important finding stressing how food webs found in different environments display larger structural differences than expected from a random spatial swapping of species that does not allow for environmental filtering. Further, the empirical food webs displayed a greater range of differences in species composition (with lower and higher values) than the null model

webs.

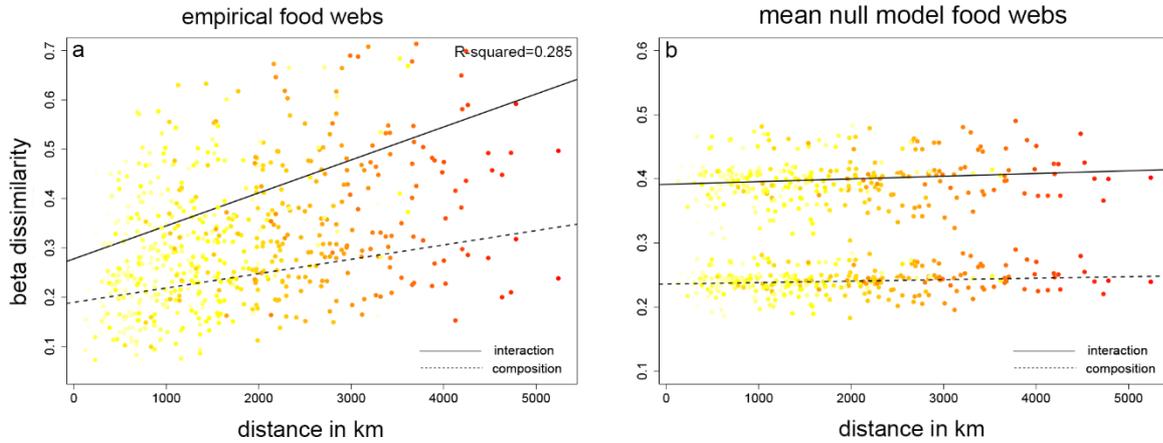


Figure 2. a) Dissimilarity in interaction (solid line) and composition (dashed line) as a function of geographic distance (km) for the 25 empirical food webs. b) Dissimilarity in mean interaction (solid line) and mean composition (dashed line) as a function of geographic distance (km) for 200 null model realizations of the 25 food webs. The color of the dots in panel a & b correspond to the geographic distances as illustrated in the gradient bar in fig 1 app. 6. The interaction dissimilarity increased significantly with geographic distances which accounted for 28.5% of the variation in interaction turnover.

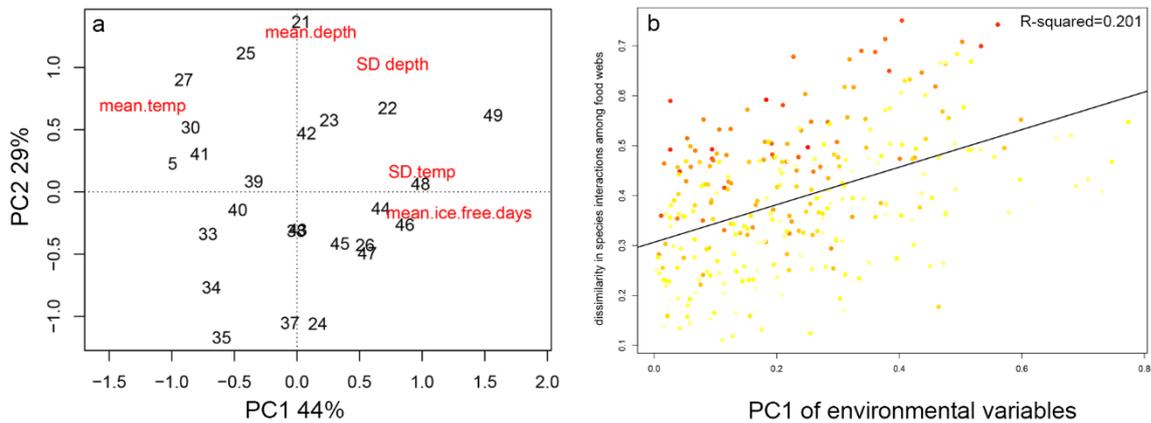


Figure 3. a) PCA of environmental variables; b) dissimilarity in species interactions as a function of the PC1 axis of the environmental variables. The color of the dots in panel b correspond to the geographic distances as illustrated in the gradient bar in fig 1 app. 6. The interaction dissimilarity increased significantly with increasing distance along the environmental gradient (PC1) which accounted for 20.1 % of the variation in interaction turnover.