

A diversity of food webs in the Barents Sea

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Summary

A food web topology describes the diversity of species and their trophic interactions, i.e. who eats whom. Structural analysis of food web topologies provides insight into ecosystem function and health. It appears simple, at first sight, to list all species and their trophic interactions. However, the large number of species at low trophic levels (e.g. unicellular organisms) and the unfeasibility of monitoring all trophic interactions in the ocean makes it impossible to construct complete food web topologies. In practice, food web topologies are simplified by aggregating species into groups termed tropho-species. It is not clear though, how much simplified food webs retain the structural properties of more detailed networks. Using the most comprehensive Barents Sea food web to date, we investigate the performance of methods to construct simplified versions using three approaches: taxonomic, structural and regular clustering. We then evaluate how topological properties (e.g. connectance) vary with the level of network simplification. Results show that comparability of food webs requires that food webs be constructed and simplified with a specific common methodology.

Introduction

The Barents Sea is a biologically productive region under the influence of winter convection and inflows from Atlantic and Arctic waters. Primary production is channelled up towards higher trophic through trophic interactions. These interactions can be investigated using food web topologies, which depict the diversity of species and of their trophic links. Although it may appear simple to construct such network of 'who eats whom', building a complete food web topology is impossible in practice. The great number of taxonomic species at low trophic levels generally imposes aggregation of species into groups termed trophospecies, while for high trophic levels, individuals from the same species may be divided into distinct stages (e.g. larvae to adults) that have different diet preferences and predators. Such situations result in asymmetrical representations of species within food webs (Jordán, 2003), with likely impacts on the interpretation of food webs structural properties. In the Barents Sea, it is unclear how much the incompleteness and asymmetry of topological representations may impact interpretation of food web structure and dynamics. In the present work, we apply objective aggregation methods to the most comprehensive food web topology of the Barents Sea (Planque *et al.*, 2014) and assess how food web structural properties vary with aggregation level.

Materials and Methods

We use an updated version of the topology presented in Planque *et al.* (2014) which comprises 233 taxa and over 2190 links. In addition, we compare this topology to two others for the same area, proposed by Bodini *et al.* (2009) and Dømmasnes *et al.* (2002). Specific food web metrics (e.g. connectance) are used to evaluate the effect of aggregation on food web structural properties. In the present work, we investigate three different approaches to food web simplification: 1) *phylogenetic aggregation*, in which species are grouped based on their phylogeny (i.e. two species phylogenetically close are more similar); 2) *structural equivalence*, in which two species are considered close when they share a similar set of prey and predators; 3) *regular equivalence*, in which similarity is defined on the basis of species position in the food webs. After grouping, the links between newly formed tropho-species are re-calculated following different linkage criteria. The five linkage criteria used are based on the proportion of trophic links between all pairs of trophospecies before grouping: >0%, 25%, 50%, 75% and 100%. Food web properties are then reassessed by calculating food web metrics for each simplified food web.

Results and Discussion

Structural equivalence allows for continuous aggregation (i.e. a single species can be included into a group at each aggregation step). Food web metrics revealed sensitive to both aggregation and linkage criteria. For example, measures of connectance as a function of aggregation level display large variations between distinct linkage criteria (Fig. 1). For the Barents Sea food web, our results demonstrate that when using structural equivalence and linkage criteria in the range 25-50%, original connectance is preserved when the food web is simplified down to ~100 species.

Structural properties of food webs with lower resolution (i.e. less species) were significantly different (e.g. Planque and Bodini food webs connectance were five times lower than Dommasnes food web connectance). Those results demonstrate that *ad hoc* choices made during the construction of food webs can greatly affect interpretation of food web structures. Our results show that previous conclusions based on earlier food webs of the Barents Sea may be artefact of low-resolution food webs or of the procedures used to construct them.

We identify that both taxonomic and structural equivalence using permissive linkage criterion allow a good trade-off between sensitivity to aggregation and sensitivity to linkage criteria. Procedures for building and aggregating food webs should be standardised and systematically documented. The sensitivity of food web analyses to topological constructions should also be evaluated.

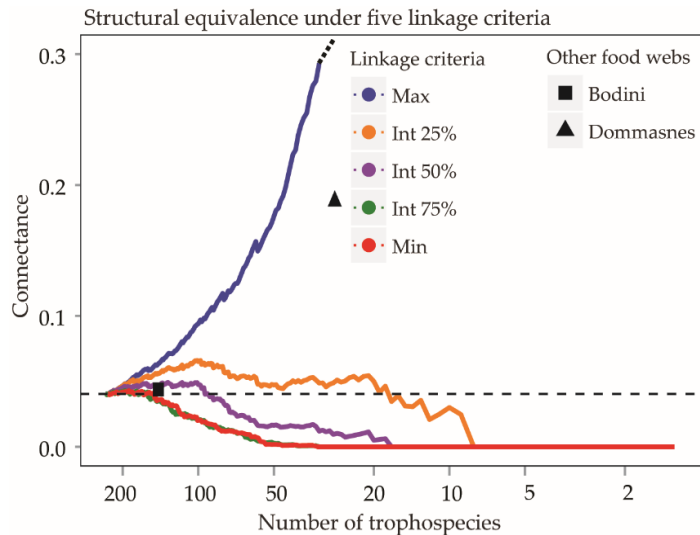


Figure. 1 Connectance computed for each aggregated food webs under structural equivalence for five linkage criteria (individual colours). The black dashed line indicates that the curve goes beyond the y-scale.

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