Ecological Insights: Analyzing the Barents Sea Food Web Using Social Network Analysis

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Abstract

The study focuses on exploring the Barents Sea food-web meta-web, a larger network comprising multiple food webs within an ecological community. The research utilizes a social network analysis (SNA) approach to uncover insights into the interconnections and trophic dynamics of species in this unique marine ecosystem. The study aims to identify key trophospecies, understand their significance across trophic groups, detect communities within the food web, and apply centrality measures to gain insights for conservation and management strategies. The data analysis and visualization are performed using Gephi software and R programming. The findings reveal the importance of GAD_MOR trophospecies from the Zooplankton group in shaping the food web dynamics. However, this species is absent in higher trophic groups due to trophic transfer efficiency and selective feeding behavior. The study also identifies three distinct communities within the food web, indicating interconnectedness and species interactions. Moreover, the application of centrality measures provides insights into the structural and functional roles of species, assisting in conservation and management strategies. The results highlight the complex nature of the Barents Sea ecosystem and emphasize the significance of interdependencies for effective ecological preservation and sustainable management.

Keywords: Barents Sea, food web, SNA, key species, stability

1. Introduction

A food-web meta-web represents a broader network that consists of multiple food webs within a large ecological community. It serves as a framework to study the interconnections and trophic dynamics of the species on a larger scale [1]. Trophospecies represents a term used to describe a variety of taxa within the food web, ranging from species-level resolution to broader taxonomic groups. It also provides insights into energy flow, species interactions, and biodiversity patterns. Therefore, this study is useful to examine the collective structure and functioning of the Barents Sea ecosystem by integrating its food-web meta-web.

The Barents Sea, a thriving marine ecosystem nestled in the Arctic region, has captured the attention of scientists around the globe due to its exceptional biodiversity and intricate trophospecies interactions. Many researchers have been increasingly drawn to this unique environment and seeking to unravel the dynamics of its food-web meta-web [2]. With the employment of a social network analysis (SNA) approach, this study aims to unveil insights of the Barents Sea food-web meta-web data as well as gaining a comprehensive understanding of its ecological structure and the trophospecies groups.

Hence, this research aspires to answer the research questions stated below:

i. What is the significance of the key trophospecies in the Barents Sea food web, and how does it vary across different trophic groups?

ii. How does the interaction among trophospecies within the Barents Sea food web contribute to the stability of the ecosystem?

iii. What insights can be gained from applying the centrality measures in the context of conservation and management strategies of the Barents Sea ecosystem?

These research questions converge on the main objective of this study: to unveil the insights concealed within the Barents Sea food-web meta-web. The social network analysis approach provides a powerful toolset to study interconnected systems, where nodes represent trophospecies and edges represent their ecological relationships, hence achieving the objective of the study [3]. The social analysis network was generated using Gephi software (version 0.10.1) and R programming. Gephi and R Programming were chosen for their robust capabilities and flexibility. Gephi's intuitive interface helps visualize complex networks, while R's extensive libraries allow for detailed statistical and graph analysis and customization, enabling a comprehensive understanding of food web dynamics.

The remainder of the study is structured as follows; Section 2 presents a comprehensive literature review on the analyses carried out in the Barents Sea food and network analyses conducted on a marine food web. Subsequently, Section 3 outlines the dataset and methodology utilized in this study. This will be followed by a comprehensive discussion of the experimental results using Gephi and R programming softwares in Section 4. Finally, Section 5 concludes the study, summarizing its key findings and implications of the Barents Sea food-web meta-web.

2. Related Works

2.1 Related Studies on the Barents Sea

The first study examines the components and structure of the food web in the Barents Sea, with a specific focus on how energy moves through the ecosystem. The amount of primary production in the Barents Sea varies greatly and is influenced by changes and fluctuations in the climate. The pelagic region is mainly dominated by small phytoplankton cells that are connected to an efficient microbial loop, which in turn interacts with the grazing food web. In ice-covered waters, planktonic algae play a significant role in primary production, while there is a strong connection between the pelagic and benthic regions, especially in the marginal ice zone. The deep-water communities and benthos are responsible for channeling a substantial 80% of the harvestable production. Keystone organisms such as Calanus finmarchicus and C. glacialis copepods, as well as capelin and herring, support a diverse range of higher trophic level organisms and contribute significantly to the fishery. However, higher trophic levels, including cod, seals, whales, and seabirds, compete for a relatively small portion of the harvestable energy. The exploitation of resources among these competitors is influenced by factors like climate variability, differences in recruitment, availability of resources, and management strategies, all of which depend on the efficient transfer of energy from primary production to lipid-rich pelagic fishes and zooplankton [4].

In the second review of the related studies on the Barents Sea, researchers investigated how the warming of the Barents Sea affects the spatial shifts of functional groups. They achieved this by developing and applying a dynamic, spatial food web model called Ecospace. This model incorporated the habitat requirements of different species and their ecological interactions to simulate the potential effects of climate change. To evaluate the accuracy of the model, the predicted distribution of biomass for functional groups was compared to field-surveyed data from both relatively cold and warm years. The Ecospace model considered the habitat foraging capacities of 74 out of a total of 108 functional groups, taking into account environmental factors such as water temperature and bottom depth. Two scenarios were created to represent a cold year in 2004 and a warm year in 2013, with variations in bottom temperature, surface temperature, and ice coverage. By comparing the modeled and observed spatial distributions in both warm and cold years, using metrics like centre of gravity, inertia, and spatial overlap, the researchers found that the model provided a satisfactory representation of past functional group distributions. The results indicated that both the modeled and observed distributions exhibited poleward shifts. The average centre of gravity position shifted by 41 km and 68 km, respectively, for the 35 functional groups with the least sampling uncertainty. Furthermore, the model predicted a community-wide shift towards the northeast at an average rate of 4.4 km per year and 67 km per degree Celsius between 2004 and 2013. Overall, the Ecospace model successfully represented past species distributions in the Barents Sea and demonstrated its potential for predicting how temperature-driven changes could affect spatial distributions. This predictive capability holds promise for assessing the impact of climate change on the distributions of species and functional groups in future scenarios [6].

The next study focuses on the monitoring of radioactive contamination levels in fish stocks whereby holds significant importance for both Norwegian fisheries and their consumers, as well as the fish export industry. This study specifically focuses on the bioaccumulation of caesium-137 (137Cs) within the marine food webs of the Barents and Norwegian Seas. The researchers sought to understand the extent to which this radioactive element accumulates in various organisms throughout the food chain. The study findings reveal that the overall levels of 137Cs in the examined organisms were generally low, with concentrations below 1 Bq kg−1 wet weight. However, despite these low levels, a notable pattern of bioaccumulation was observed. The concentration of 137Cs was found to be approximately ten times higher in the top predator of the food web, the harbour porpoise (Phocoena phocoena), compared to the lower-level organism, the amphipod Themisto sp.

To further quantify the bioaccumulation process, the researchers calculated Concentration Factors (CF), which represent the ratio of 137Cs levels in organisms to seawater. The CF values varied among the different organisms studied. For instance, a mixture of krill and amphipods exhibited a CF of 10±3, indicating a moderate concentration of 137Cs. In contrast, harbour porpoises demonstrated a significantly higher CF of 165±5, indicating a substantial concentration of 137Cs in these top-level predators. This suggests that as 137Cs moves up the food chain, it becomes increasingly concentrated in higher-level organisms. These findings highlight the potential risks associated with radioactive contamination in marine ecosystems. It emphasizes the importance of ongoing monitoring and management of radioactive substances in fish stocks. By understanding the bioaccumulation patterns and concentration factors, stakeholders can make informed decisions regarding seafood safety and ensure the well-being of both consumers and the fish export industry. Continuous vigilance in monitoring radioactive contamination levels is crucial to safeguarding the marine environment and maintaining the sustainability of fisheries in the Barents and Norwegian Seas [7].

2.2 Related Studies on Marine Food Web Analysis

The first study involved the development of two mass-balanced network models representing different time periods in the Hooghly Matla estuarine system: a less exploited phase from 1985-1990 and a highly exploited phase from 1998-2003. These models aimed to quantitatively compare the biological interactions and relationships among ecologically important groups within the system. A total of 20 functional groups, including shrimps, squids, crabs, mackerel, small pelagics, demersal fishes, benthic feeders, predator fishes, and trash fish, were identified and their biomass values estimated based on catch production and bottom trawling surveys. The models revealed a high Ecotrophic Efficiency (>0.5) for most groups occupying higher trophic levels, indicating effective energy transfer within the system. The model outputs provided valuable insights into the interactions among different components, particularly in terms of energy flow. It was observed that many fish populations were heavily exploited, leading to changes in the overall trophic structure primarily driven by top-down effects. System statistics and network flow indices derived from the model outputs indicated that the estuary was undergoing degradation and experiencing stress, resulting in a certain degree of instability.

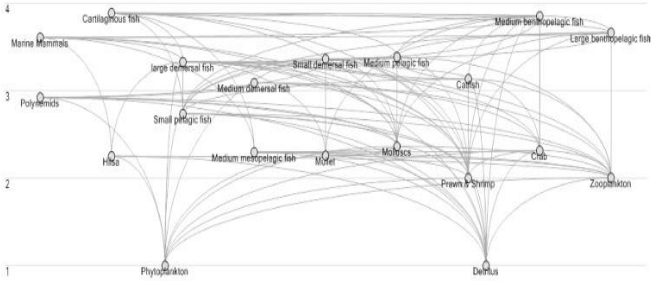

Figure 1: Flow Diagram of the HMES Where the Nodes Represent the Components, Curved Lines Show Food Web Connectivity and Horizontal Straight Lines Represent the Trophic Levels

By modeling the trophic structure of the Hooghly Matla estuarine system and adjacent mangroves for two distinct time periods, this study enabled the quantification of biomass, matter exchanges, and energy flows between different components during those periods. The species in this ecosystem were found to be distributed across seven trophic levels, with trophic level 3 playing a significant role in energy transfer through prey-predator interactions. Intense competition was observed among groups at trophic level 3. However, due to the depletion of lower trophic levels caused by fishing activities, it is anticipated that the landings of these fish will decrease in the near future, potentially affecting the entire food web of the estuarine system [8].

The second study addresses the anticipated ecological changes in the Norwegian and Barents Seas caused by climate change, emphasizing the need to comprehend the historical factors and trophic interactions that have influenced the dynamics of this marine ecosystem. To explore these dynamics, the researchers employed a historical food web model called Ecopath with Ecosim (EwE), which was calibrated using data spanning from 1950 to 2014. The model was then utilized to simulate ecosystem responses under various temperature scenarios until 2100, considering factors such as fishing, trophic interactions, primary production anomalies, and ocean temperature.

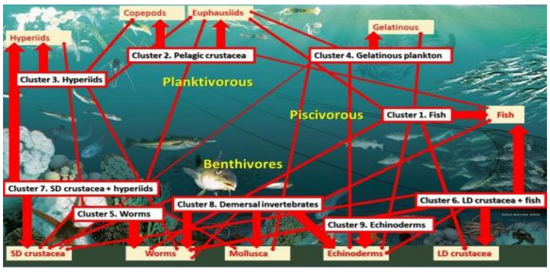

Figure 2. Conceptual model for the Barents Sea Trophic Structure and Interactions

The results of the simulations revealed that pelagic species like mackerel and blue whiting shown in Figure 2 were projected to experience an increase in biomass as ocean temperatures rise. On the other hand, boreal species such as redfish, prawns, and capelin were expected to witness a decrease in biomass. The warmest scenarios predicted a decline in the biomass of cod due to reduced availability of preferred prey and increased predation pressure from pelagic species on juvenile cod. By providing a comprehensive understanding of the NorBar ecosystem from 1950 to 2014, this model serves as a valuable reference point and offers insights into the potential response of the ecosystem to changing ocean temperatures. These quantitative advancements are essential for promoting sustainable development in rapidly evolving marine environments. [9].

The third study introduces a novel add-on package developed using the versatile R software. This package offers a range of powerful features designed to enhance the analysis of food webs. It provides functionalities such as life-cycle loop analysis, flexible food web plotting, and statistical analysis, enabling researchers to delve into the intricate dynamics of ecological networks. One of the notable advantages of this package is its ability to generate vertical models of food web plots based on trophic ranks identified from the food web matrix. By organizing the food web in a vertical format, it allows for a clearer visualization and understanding of the hierarchical structure and energy flow within the ecosystem.

In their future work, the researchers have planned to incorporate more advanced analyses into the package. One such analysis is the assessment of food web stability using the Routh-Hurwitz criteria, a mathematical tool commonly used to examine the stability of dynamic systems. By integrating this criterion, researchers will gain insights into the potential resilience and robustness of food webs under different conditions. Additionally, the team aims to include other statistical measures that can provide valuable information about various properties of food web structures, enabling a more comprehensive analysis of ecological interactions. To demonstrate the effectiveness of the package, the researchers applied it to specific case studies. Firstly, they examined the life-cycle graph of V. americana, a species of interest, which resulted in the identification of ten directed loop matrices and a non-decomposable matrix, aligning with previous findings. They further presented five representative loops along with associated elasticity analysis, which shed light on the sensitivity of the ecosystem to changes in specific trophic interactions.

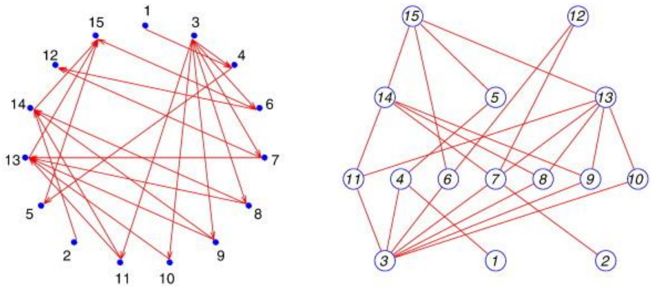

Figure 3 (a). Two ways of graphic plotting for the Knysna estuary food web; circular plotting and vertical plotting

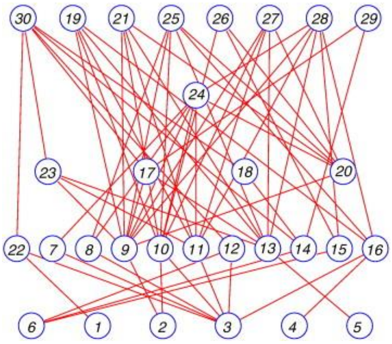

Figure 3 (b). Food web of an Elm-Maple Forest from Illinois

Furthermore, the package was employed to analyze and visually depict two real food webs from the Knysna estuary and an Elm-Maple Forest. Through the graphical representation, the researchers emphasized the crucial role of basal species and pathways in maintaining the stability of these food webs. This analysis highlighted the significance of understanding the fundamental building blocks of food webs and their contributions to overall ecosystem resilience. Overall, the development of this package offers a valuable tool for researchers studying food webs, providing them with enhanced capabilities to explore complex ecological relationships, assess stability, and gain insights into the functioning of ecosystems in a changing world [10].

The final literature review conducted was based on Food webs, which depict the complex interactions among species in an ecosystem, have traditionally focused on understanding the relationships between organisms without considering specific taxonomic details. While there is abundant empirical data on present-day food webs, there remains a significant knowledge gap regarding the role of different hominin species in extinct ecosystems documented in the fossil record. The literature review highlights several gaps in the current understanding of marine and paleo food webs. While previous studies have modeled trophic interactions and energy flows in ecosystems like the Hooghly Matla estuarine system and the Barents Sea, they often lack the integration of advanced analytical tools to reveal the interactions between the species. Additionally, there is a need for more detailed simulations and stability assessments under various environmental scenarios, which are crucial for predicting future ecological changes. The review also points out the limited focus on the role of specific species, such as Homo species in Pleistocene ecosystems, and their influence on trophic dynamics. This study aims to address this gap by examining Early and Middle Pleistocene paleo-communities in Western Eurasia and employing social network analytics, with a focus on understanding changes in interactions among large mammals during this time period and the influence of Homo species on these changes. To accomplish this, the researchers constructed 27 paleo food webs using archaeological and paleontological data from European assemblages, specifically considering large mammals, including various Homo species. The analysis proceeded in two stages. First, the researchers calculated and compared the main structural features of the networks across different geographical areas, time periods, and cases with and without Homo species. Second, they assessed the significance of Homo species within their respective food webs by calculating different measures of structural centrality.

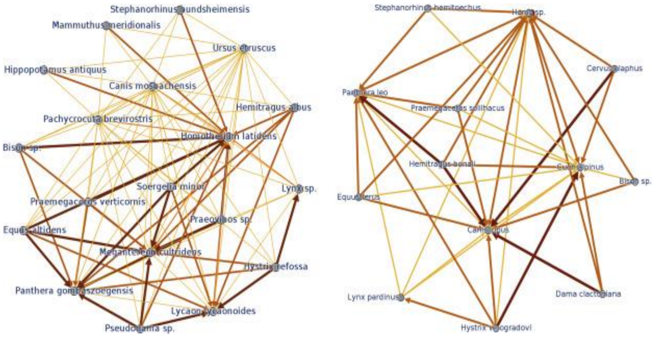

Figure 4. Two Examples of Paleo Food-Web Visualization Corresponding to Venta Micena (left) and Atapuerca Galeria GIIa (right).

The findings of the study reveal that the Pleistocene food webs shared fundamental characteristics with modern food webs, although certain parameters exhibited notable differences. Additionally, comparing the networks across different time periods highlighted a distinct change associated with the Mid-Pleistocene Revolution. Importantly, the study emphasizes the pivotal trophic position of hominins within the food webs, as they served as central species that played a critical role in energy flow. In conclusion, this study enhances our understanding of Pleistocene ecosystem dynamics and the role of Homo species within ancient food webs. By analyzing the structure and interactions of these networks, researchers gain valuable insights into ecological relationships and energy flow patterns during this significant period in Earth's history [11].

3. Dataset and Methodology

3.1 Dataset

The dataset of Barents Sea food-web meta-web used in this study was obtained from an online resource, specifically from the article titled *Social network analysis as a tool for marine spatial planning: Impacts of decommissioning on connectivity in the North Sea* published in the journal "Journal of Applied Ecology" [12]. The dataset consists of four worksheets, each providing crucial information about the species within the Barents Sea ecosystem. The tables below provide a glimpse; first five columns, including the column header of each worksheet in the dataset.

Table 1. Species Name

TROPHOSPECIES	ABBREVIATION	GROUP
ACARTIA_SPP	ACA_SPP	2_Zooplankton
ACTINIARIA_G_SP	ACT_G_SP	3_Benthos
AGLANTHA_DIGITALE	AGL_DIG	2_Zooplankton
AGLAOPHAMUS_MALMGRENI	AGL_MAL	3_Benthos

The first worksheet provides a list of species included in the food web analysis, along with their full names, abbreviations, and trophospecies groups as shown in the table above.

Table 2. Subregion by Species Matrix

POLY_NO	DET_IND	AUT_FLA	BAC_IND
5	1	1	1
21	1	1	1
22	1	1	1
23	1	1	1

Table 2 represents the second worksheet; a subregion-by-species matrix that captures the presence or absence of the trophospecies within each polygon. The polygons represent the distinct subregions exist within the Barents Sea ecosystem. The matrix is structured with trophospecies listed as columns and polygon numbers as rows. The purpose of this matrix is to provide information on the distribution of species across different subregions within the Barents Sea.

Table 3. Pairwise List

	PREDATOR	**PREY**
1	ACA_SPP	ACA_SPP
2	ACA_SPP	AUT_FLA
3	ACA_SPP	DIATOM
4	ACA_SPP	HET_FLA

The table in the third worksheet contains a pairwise list of interactions between trophospecies within the Barents Sea food web. This list provides information about predator-prey relationships within the ecosystem.

Table 4. Barents Sea Meta-Web Adjacency Matrix

	DET_IND	AUT_FLA	BAC_IND	DIATOM	HET_FLA
DET_IND	0	0	0	0	0
AUT_FLA	0	0	0	0	1
BAC_IND	0	0	0	0	1
DIATOM	0	0	0	0	0

The fourth worksheet, specifically, was utilized in this study to analyze the food-web meta-web. T Worksheet 4, the Barents Sea Food-Web Meta-Web, is the primary focus of analysis in this study. It represents a binary adjacency food web matrix that captures the trophic interactions within the Barents Sea ecosystem. Each row and column in the matrix corresponds to a specific trophospecies within the Barents Sea food web. The elements in the matrix are binary values, where 1 indicates a trophic interaction and 0 indicates no trophic interaction. If a trophospecies in the column (predator) consumes the trophospecies in the corresponding row (prey), the matrix element is assigned a value of 1. Conversely, if no trophic interaction occurs between the trophospecies in the column and row, the matrix element is assigned a value of 0.

3.2 Software Used

The methodology utilized were Gephi software (version 0.10.1) and R programming for data analysis and visualization. Gephi, a powerful network analysis and visualization tool, was utilized to generate and analyze the Barents Sea food-web meta-web network. By utilizing Gephi, we were able to answer the first two research questions regarding Barents Sea food-web meta-web which are exploring and manipulating network data, allowing for the identification of key players, community detection, and visual representation of network structures.

Furthermore, R programming was employed to complement the third research question which is to determine the optimal representation of blab la bla. The igraph package in R programming software is widely used to answer the aforementioned research question. Thus, by leveraging the flexibility and power of R programming, we were able to conduct in-depth analyses on the Barents Sea food-web meta-web data, uncovering further insights and patterns. Hence, the utilization of By Gephi and R programming softwares contribute to the growing field of network analysis in ecology and showcases the power of these tools in unraveling the dynamics of food-web meta-webs. The findings from this research have implications for ecological research, conservation efforts, and sustainable management practices in the Barents Sea region and beyond.

3.3 Data Preparation

The data preparation for the analysis was performed using Gephi, a network analysis software. The dataset consisted of trophospecies within the Barents Sea food web, where the target and source variables represented the species involved in predator-prey relationships. Additionally, each trophospecies was assigned to a specific group indicating its trophic level.

Upon examining the data, it was observed that there were a total of 223 nodes, representing the individual trophospecies, and 2220 edges, indicating the connections between them. To ensure the accuracy of the data and the correct representation of trophic groups in Gephi, a simple graph was generated, allowing for a visual verification. The size of the nodes were adjusted, providing a clear visual representation of the trophospecies and their relationships. The in-degree measure was utilized to analyze the connectivity and centrality of the trophospecies within the food web. The initial dataset was transformed into a network representation using Gephi, allowing for further analysis and exploration of the interactions among trophospecies in the Barents Sea food web.

4.Results

A. RQ1: What is the significance of the key trophospecies in the Barents Sea food web, and how does it vary across different trophic groups?

Visual representation of the trophospecies in the Barents Sea ecosystem was done by employing the degree measure. The text method approach has been utilized to rank the trophospecies based on their degree. This methodology provides informative information to explore the variations in the trophic structure and interdependencies of the main key trophospecies between different groups.

The social network analysis carried out in Gephi has revealed interesting insights of the Barents Sea food-web meta-web data. The *GAD_MOR* trophospecies is seen to be the key player within the network by employing the ranking method using the in-degree measure. The text of the trophospecies are enabled to visually represent enabling a clearer understanding of the centrality and importance of *GAD_MOR* within the Barents Sea food-web meta-web data. This results have been cross-checked in Data Laboratory, confirming that *GAD_MOR* trophospecies appeared the most in column ID.

The in-degree method is chosen as the suitable method to describe the food web because it provides valuable information about the trophic interactions and interdependencies within the network. Species with a higher in-degree value are more connected and receive more interactions from other species, indicating their importance in the flow of energy and resources through the ecosystem. By ranking the trophospecies based on their in-degree, the key trophospecies can be identified that play a significant role in shaping the dynamics of the food web [13].

Notably, *GAD MOR* trophospecies belongs to the Zooplankton group, a critical component of the Barents Sea ecosystem. The Zooplankton group typically occupies the lowest position in the food web hierarchy [14]. It serves as a vital source of sustenance for numerous other species in a marine ecosystem. This observation highlights the pivotal role played by *GAD_MOR* in shaping the dynamics of the ecosystem, underscoring the significance of its preservation and management for the stability of the Barents Sea ecosystem.

Moreover, an in-depth analysis was conducted to further explore the role and significance of key player which is the *GAD_MOR* trophospecies in the Barents Sea food web. This investigation serves the purpose to determine whether the *GAD_MOR* trophospecies identified in the overall food web maintains the same importance when filtering is performed based on their respective groups. The following figures depict a comparative analysis between each trophic group and the ecosystem overview to conduct a more in-depth analysis of the *GAD_MOR* trophospecies. The trophic groups that are compared to are Zooplankton, Benthos, Fish, Basal, Mammals, Birds and Seabirds groups. This is shown in Figure 5(a) to Figure 5(g).

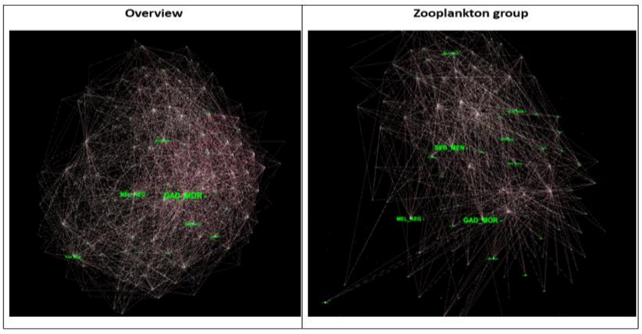

Figure 5(a). Comparison between the Overview of Barents Sea Ecosystem and the Zooplankton Group

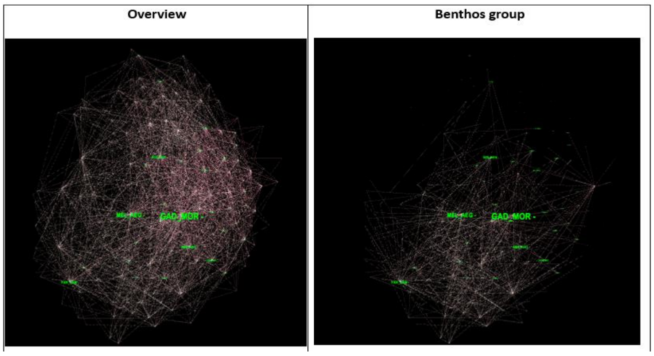
Overview
Benthos group

Figure 5(b). Comparison between the Overview of Barents Sea ecosystem and the Benthos group

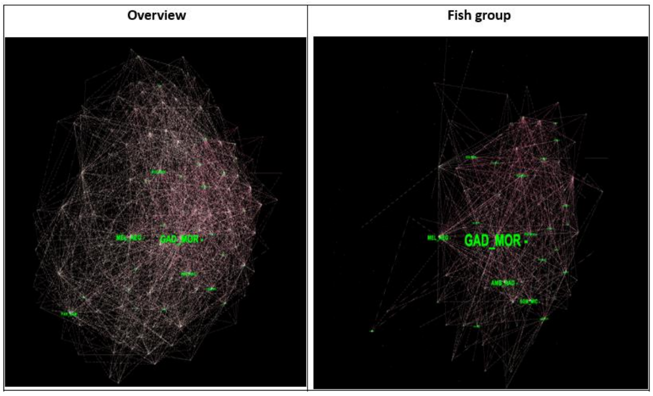
Overview
Fish group

Figure 5(c). Comparison between the Overview of Barents Sea ecosystem and the Benthos group

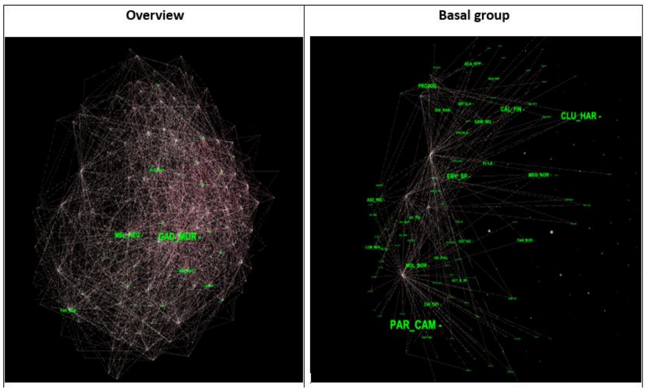
Overview
Basal group

Figure 5(d). Comparison between the Overview of Barents Sea ecosystem and the Basal group.

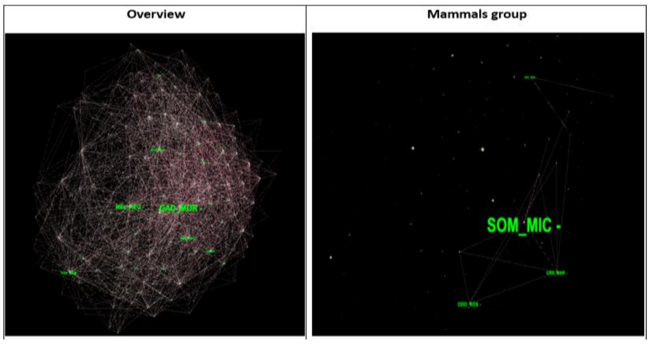

Figure 5(e). Comparison between the Overview of Barents Sea ecosystem and the Mammals group

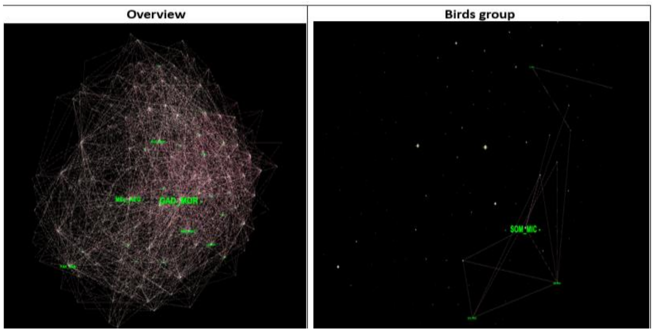

Figure 5(f). Comparison between the Overview of Barents Sea ecosystem and the Birds group

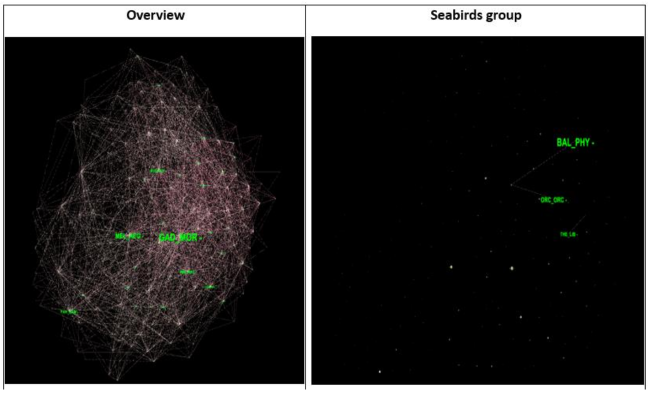

Figure 5(g). Comparison between the Overview of Barents Sea ecosystem and the Seabirds group

While *GAD_MOR* trophospecies emerged as one of the largest players in the food web based on overall connectivity, it was observed that this species does not play a significant role when the filtering feature is performed in Gephi based on their respective groups. This can be seen, in the Basal group Figure 3(d), Mammals group Figure 3(e), birds group Figure 3(f) and Seabirds group Figure 3(g). This proves that the *GAD_MOR* trophospecies coming from Zooplankton group the lowest trophic group in the ecosystem was found to be absent in the higher food level web group.

The absence of species from lower trophic levels in higher trophic level interactions can be attributed to several factors. One primary reason is the transfer of energy and biomass through the food chain. As energy moves from lower trophic levels to higher trophic levels, there is typically a loss of energy due to metabolic processes and inefficiencies in energy transfer. This phenomenon is known as trophic transfer efficiency [15]. This means that less energy is available to support species at higher trophic levels, limiting their interactions with lower trophic level species. Additionally, species at higher trophic levels often have specific dietary preferences, which may exclude lower trophic level species from their diet. Understanding these dynamics is crucial for comprehending the structure and function of food webs in ecosystems.

Species at lower trophic levels such as Zooplankton play a crucial role in converting solar energy into biomass through photosynthesis. They form the foundation of the food web by providing energy-rich organic matter. However, as energy is transferred up the food chain, there is a decrease in available energy, limiting the number of species that can be supported at higher trophic levels [16]. This explains why *GAD_MOR* trophospecies is absent in high level trophic group.

Additionally, the structure of the food web is influenced by feeding preferences and adaptations of organisms. Predators at higher trophic levels often exhibit specific dietary preferences and feeding strategies that favor certain prey species over others. This selective feeding behavior can lead to the exclusion or limited interactions with species at lower trophic levels that do not fit within their preferred diet. One of the reasons why Zooplankton species are not apparent in higher group levels.

RQ2*:* How does the interaction among trophospecies within the Barents Sea food web contribute to the stability of the ecosystem?

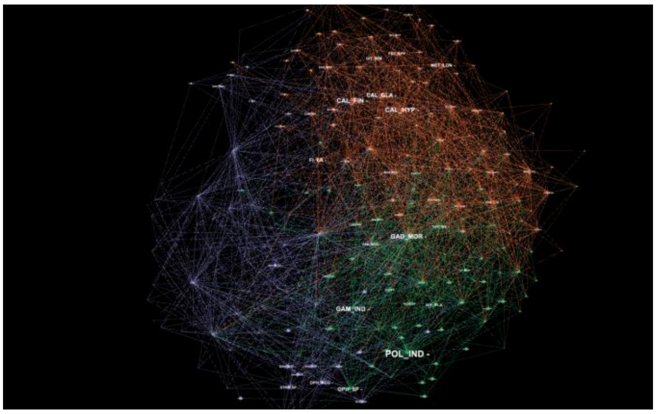

Figure 6. Community Detection of Barents Sea Food-Web Meta-Web using Gephi

The detection of three distinct communities based on Gephi's modularity measure in the Barents Sea food web indicates the presence of interconnected species groups within the ecosystem (see Figure 6). The fact that most groups can be found in multiple clusters underscores the interdependence and interactions among species in forming a cohesive food web. This observation is particularly relevant in the context of the Barents Sea, a complex and diverse marine ecosystem.

The Barents Sea is renowned for its rich biodiversity, encompassing various trophic levels and species interactions. Within this ecosystem, species rely on one another for survival and energy transfer. For example, primary producers such as Zooplankton and the Benthos group form the foundation of the food web by converting sunlight into organic matter through photosynthesis. Zooplankton, including the GAD_MOR trophospecies, then feed on the primary producers, transferring energy up the trophic levels.

The interconnectivity of species within the Barents Sea food web is crucial for the functioning and stability of the ecosystem. Each species occupies a specific niche and contributes to the overall energy flow and nutrient cycling. By forming communities or clusters, species within these groups are more likely to have direct or indirect interactions, facilitating the transfer of energy and resources [17].

Additionally, the presence of species in multiple clusters suggests that certain species play multiple roles or have diverse ecological interactions within the food web. This versatility can be attributed to factors such as diet flexibility, omnivory, or a wide range of ecological adaptations. These species act as linkages between different trophic levels and contribute to the resilience and stability of the food web [18].

Furthermore, the occurrence of species in multiple clusters indicates that species interactions are not isolated or restricted to specific groups. This finding supports the idea that a functional food web requires connectivity and interactions among species across different trophic levels and communities. Isolation or limited interactions within specific clusters could disrupt the flow of energy and destabilize the ecosystem [19].

In summary, the presence of three communities in the Barents Sea food web, with overlapping species across clusters, reinforces the understanding that a functioning food web relies on interconnectedness and species interactions. This observation aligns with the complex nature of the Barents Sea ecosystem, where various species rely on each other for energy transfer, nutrient cycling, and overall ecosystem functioning. Understanding these interdependencies is crucial for effective management and conservation strategies in the Barents Sea and other similar marine ecosystems.

RQ3: What insights can be gained from applying the centrality measures in the context of conservation and management strategies of the Barents Sea ecosystem?

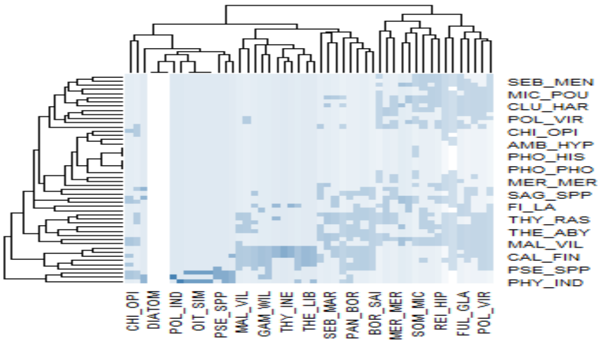

Figure 7 (a). Heatmap of trophospecies based on highest degree centrality measure

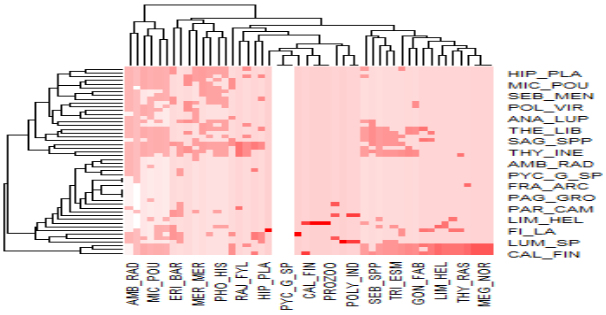

Figure 7 (b). Heatmap of trophospecies based on highest betweeness centrality measure

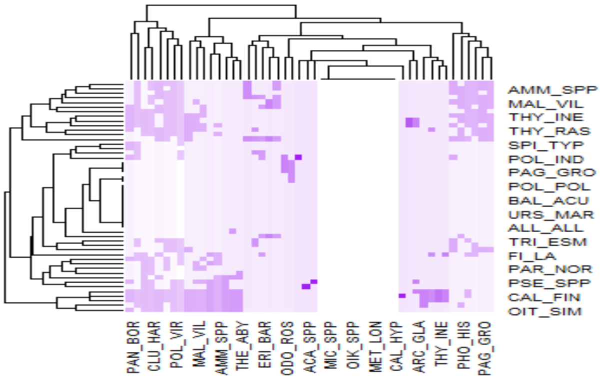

Figure 7 (c). Heatmap of trophospecies based on highest closeness centrality measure

The generation of a heatmap based on centrality measures in R programming provides a powerful tool for analyzing and understanding the dynamics of a food web, particularly in the context of conservation management. By focusing on the top nodes with the highest centrality values, researchers can identify the most influential species and their relative importance within the network. The heatmap visually represents these key players, allowing for easy comparisons and highlighting their centrality values in terms of degree, closeness, or betweenness centrality. This analysis provides valuable insights into the structural characteristics and functional roles of these species, including their connectivity, efficiency, and bridging capabilities. See Figure 7(a) to Figure 7(c).

The color-coded heatmap enhances the interpretation of centrality values by using darker colors for higher values and lighter colors for lower values. This color differentiation aids in the identification of species with the highest centrality and their significance within the food web. Such information is crucial for conservation and management strategies, as it helps prioritize species for protection, restoration, or targeted interventions. It is important to note that the selection of the top nodes is subjective and can be customized based on research objectives, data characteristics, and network properties to ensure a comprehensive understanding of the food web dynamics.

When interpreting the heatmap, the absence of colors for certain species indicates their lower centrality values compared to more central species. However, this does not diminish the importance of these species in the ecosystem. Each species plays a unique role, and factors such as limited direct relationships, shorter paths to other nodes, or reduced bridging capabilities contribute to their lower centrality values. It is essential to consider the broader ecological context and the specific roles of these species to fully grasp their contributions to the stability and functioning of the food web.

Degree centrality, as represented in the heatmap, quantifies the number of connections a species has within the food web. It helps identify species that have a high number of interactions and are potentially important for energy transfer and species interactions. These species act as keystones in maintaining the stability of the ecosystem [20]. Closeness centrality, on the other hand, measures how quickly information or resources can flow through a species. A heatmap of closeness centrality highlights species that play central roles in information or resource transfer, indicating their efficiency and ecological importance [21]. Lastly, betweenness centrality measures the extent to which a species acts as a bridge between other species. A heatmap of betweenness centrality identifies species that connect different trophic levels or communities, playing a critical role in maintaining the stability and functioning of the ecosystem [22].

Applying heatmaps of centrality measures to marine food webs provides valuable insights into species interactions, energy flow, and bridging capabilities across trophic levels. By identifying key species with high centrality values, conservation efforts can prioritize the protection of these important players, ensuring the resilience and stability of marine ecosystems [23]. Degree centrality, closeness centrality, and betweenness centrality measures offer meaningful information for understanding ecological dynamics, and their integration into conservation planning and decision-making processes can contribute to the effective preservation and sustainable management of marine environments [24].

In conclusion, centrality measures, visualized through heatmaps, offer a powerful tool for understanding the importance and roles of species within food webs. By assessing centrality values, researchers can identify key species, evaluate ecological connectivity, and understand their contributions to energy transfer and ecosystem stability. Integrating these measures into conservation and management strategies helps prioritize species for protection, inform restoration efforts, and promote the long-term sustainability of marine environments.

5. Conclusions

This research brings hope for understanding and conserving the Barents Sea ecosystem. Through a comprehensive analysis of trophospecies and the application of various centrality measures, valuable insights into the dynamics and interconnections of the food web are gained. This understanding is crucial for developing effective strategies for conservation and management.

An important finding of this research is the identification of key trophospecies, specifically the *GAD_MOR* trophospecies from the Zooplankton group, as a crucial player in the food web. Recognizing the significance of preserving and managing this species highlights its role in maintaining the stability of the Barents Sea ecosystem. By prioritizing the protection and sustainable management of *GAD_MOR* and other influential species, conservation efforts can be directed towards ensuring their survival, fostering hope for the preservation of these species and the overall ecological balance of the Barents Sea.

Additionally, the analysis of community detection and the presence of interconnected species groups within the Barents Sea food web inspire hope for the resilience and functioning of the ecosystem. The identification of distinct communities and the presence of overlapping species among clusters emphasize the interdependence and interactions among species in forming a cohesive food web. This understanding is crucial for designing conservation strategies that consider the holistic nature of the ecosystem and promote its stability.

The use of centrality measures, visualized through heatmaps, offers hope for improved conservation and management practices. By identifying species with high centrality values, conservation efforts can prioritize the protection and restoration of these influential species. Integrating centrality measures into conservation planning and decision-making processes enhances the effectiveness of preservation and management efforts, ultimately contributing to the long-term sustainability of marine environments.

As a result, this research instils hope by providing valuable insights into the trophic structure, interdependencies, and roles of species within the Barents Sea ecosystem. Deepening our understanding of these complex ecological dynamics enables the development of targeted and effective conservation and management strategies. This research fosters optimism for preserving biodiversity, maintaining the stability of the food web, and ensuring the long-term health of the Barents Sea ecosystem.

The findings of this study align with previous research by confirming the critical role of key trophospecies, such as the GAD_MOR from the Zooplankton group, in maintaining ecosystem stability. However, this study contrasts with earlier works by employing advanced social network analytics, which provided deeper insights into species interdependencies and ecosystem dynamics. The identification of distinct communities and overlapping species groups underscores the interconnectedness highlighted in prior studies, but with more statistical analysis. Additionally, the use of social network analysis measures to prioritize conservation efforts offers a novel approach that enhances traditional methods. Overall, this research builds on and extends previous studies, offering a more comprehensive and nuanced understanding of the Barents Sea ecosystem.

6. Limitation of Study and Future Work

This study has several limitations, including data quality and completeness, which can affect the reliability of the social network analysis. The Gephi and R programming models rely on assumptions that the analysis is based on historical data, potentially overlooking recent changes or future variations in the ecosystem. The focus on key trophospecies might miss the roles of less prominent species that also impact ecosystem stability. The findings are specific to the Barents Sea and may not be directly applicable to other ecosystems, which may need to be analysed further. Future work should enhance data collection with up-to-date observations and refine models to better simulate ecological interactions. Expanding the study to include other marine ecosystems can help validate the findings. Integrating climate change scenarios will assess long-term impacts on the food web. Combining social network analysis with other ecological tools will provide a holistic understanding of ecosystem dynamics. These steps will inform more effective conservation strategies.

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