Assessing the Drivers of Form and Function at a Continental Scale Using Trait-Based Food Web Models

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BACKGROUND

Food web ecology has largely been governed by theory over the last several decades, with few studies utilizing empirical data to assess food web dynamics. Where experimental approaches have been used, these have often occurred across very limited spatial scales, such as a single river or river reach. The National Science Foundation's National Ecological Observatory Network (NEON) is a large database with extensive information on algae, macroinvertebrate, and fish assemblages from the locations seen in Figure 1. In order to create heuristic food web models from these data, we developed a trait mining pipeline to find and predict interactions among organisms.

Figure 1. Field sites from the National Ecological Observatory Network (NEON) are fully instrumented and provide detailed biotic and abiotic data that can be used for food web modeling.

METHODS

Text Mining for Traits

In order to mine traits for this project, we used Boolean search terms in Google Scholar for a specific family and genus. We searched through the first twenty articles that were retrieved by the search for mentions of trophic interactions and functional feeding groups regarding the target genus. The search was deemed successful if three pieces of information were found within the twenty articles.

Trait-Based Food Web Models

Food webs are important for determining the overall health of an ecosystem and the strength of its trophic connections. Visualizing the interactions in an ecosystem can help ecologists analyze its properties and better focus conservation efforts. Figure 2 shows the pipeline for generating heuristic food webs using text mining and existing databases.

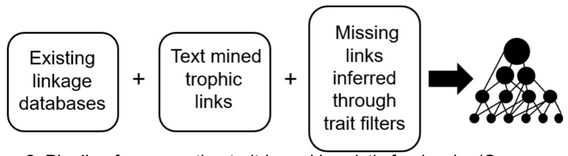

Figure 2. Pipeline for generating trait-based heuristic food webs (Compson et al. 2018).

RESULTS

Food Web Properties

This project resulted in an organized list of trophic interactions to supplement the NEON database. This database will be used to create a pipeline for generating heuristic food webs and to extract metrics that give information on ecosystem stability (Figure 6, Figure 3). The NEON database can also be used to assess the drivers of food web structure and ecosystem functions, which is an ongoing goal of this research.

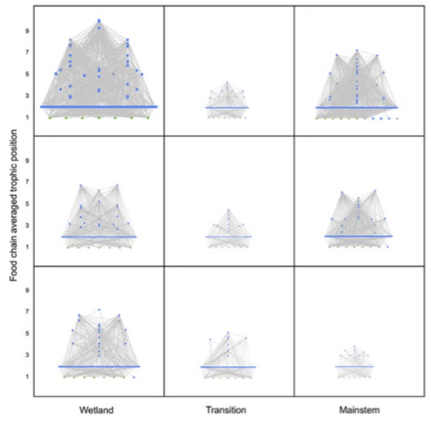

Figure 3. Metawebs of the Grand Lake Meadows (Compson et al. 2019).

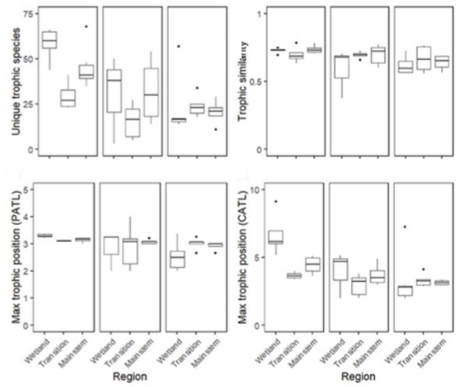

Figure 4. Heuristic food web metrics vary across sites of the Grand Lake Meadows (Compson et al. 2019).

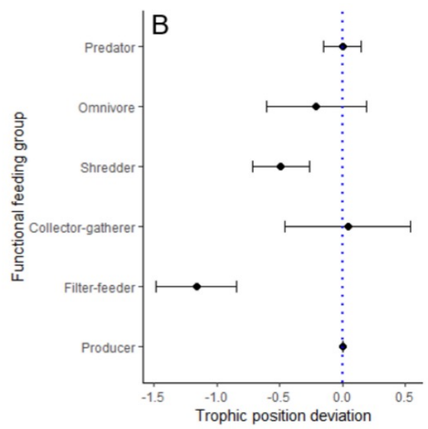

Figure 5. Deviation in trophic position of key functional feeding groups (Compson et al. 2019).

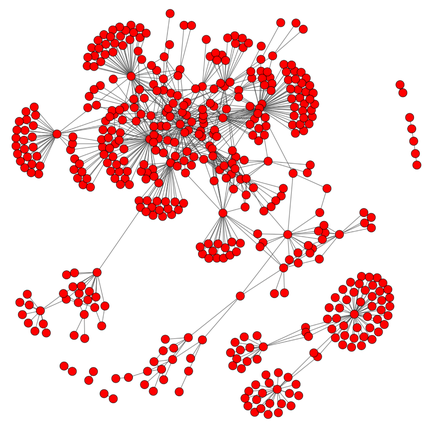

Figure 6. Ecological interaction network of trophic interactions
In the GLOBI database.

CENTRALITY METRICS

Extracting centrality metrics from graphical food webs allows for deeper analysis of the most influential genera within the ecosystem. The metrics also act as predictors for measured ecosystem functions (Figure 4). Two types of centrality metrics that we focused on are eigenvector centrality and betweenness centrality. Eigenvector centrality returns scores based on the nodes with the highest scoring connections, and betweenness centrality measures the connectedness of each interaction in the graph.

Highest Eigenvector Centrality	Highest Betweenness Centrality
Micropterus	Conchapelopia + Larsia
Procladius	Lampetra + Salmo
Polypedilum	Ichthyomyzon + Micropterus
Larsia	Thymallus + Oncorhynchus
Sialis	Oncorhynchus + Ichthyomyzon
Ablabesmyia	Hydropsyche + Conchapelopia

DISCUSSION

Given the extent of human-induced environmental change we are experiencing in the Anthropocene, ecologists and land managers are in dire need of tools to rapidly assess ecosystem structure. Food webs, which are models depicting how organisms are trophically structured in an ecosystem, are powerful tools for visualizing community data and their metrics have been shown demonstrate aspects of ecosystem health and functioning (Figure 5).

Our research produced an organized list of the trophic interactions among NEON taxa not included in existing trophic linkage databases. Together, these data will be used to create a pipeline for generating heuristic food webs and to extract metrics to determine their potential as predictors of measured ecosystem functions currently measured by NEON (e.g., primary production, respiration). Using these existing NEON data, future work will also assess the drivers of food web structure and ecosystem functions.

A broader implication of this work will be the development of a pipeline to rapidly construct heuristic food webs from existing biodiversity data, including information rich genomic datasets generated from DNA metabarcoding. These food web models promise to provide new, taxa-free bioindicators (sensu Makiola et al. 2020) which are urgently needed by land managers for assessing ecosystem status in a changing world.

References provided upon request.