Characterization and Keystone Species Identification from Food Webs using Graph Metrics

Andre Sharp[1], Ashlyn Woodward[1], Sarvesh Sathish[2], Medha Gollapudi[2]
Zacchaeus Compson[3]

University of North Texas [1]Department of Computer Science & Engineering,
[2]Texas Academy of Math & Science,
University of North Texas [3]Department of Biological Sciences

Abstract

Food webs are powerful tools for the visualization of complex community interactions and the assessment of the structural properties of these dynamic systems. Many of the properties of food webs are indicative of ecosystem functions, such as trophic position or connectance, and can illuminate the health and function of an ecosystem. Using data from the National Science Foundation's National Ecological Observatory Network (NEON) and the Global Biotic Interactions (GLOBI) database, we created heuristic food webs to model species and their interactions within certain environments. Through the application of community detection graph algorithms, we plotted the webs using Python's igraph and network-x packages in order to measure centrality metrics of the graphs. As a result of these webs, we were able to create a method which identifies keystone species within an environment, that in turn can help ecologists focus their conservation methods in a more constructive fashion.

Background

The environment can be analyzed using food webs displayed as graphs to evaluate environmental stability, understand the influence of each genus, and analyze the interactions between organisms.
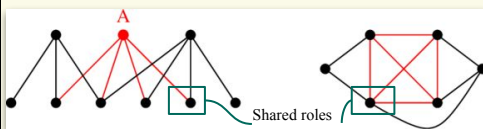
Centrality metrics can be used to investigate the redundancy theorem (shown in the figure above), which states that organisms share roles in food webs so significant population changes are prevented from disrupting the web.

Community Detection
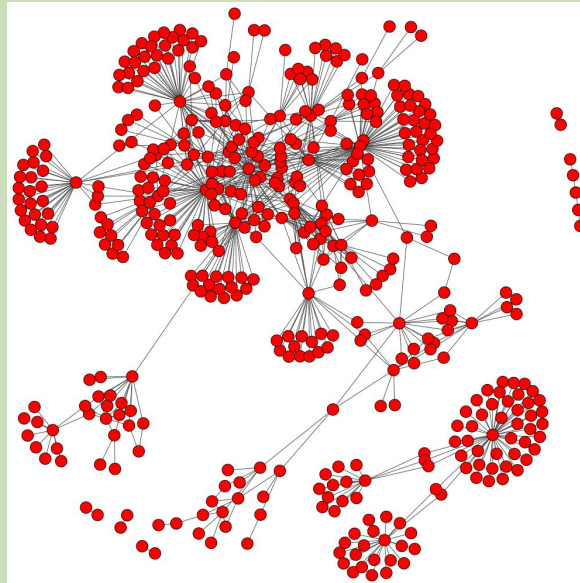
Food web of 'eats' interactions in aquatic environment

Taxa with highest eigenvector centrality (descending order):

Micropterus, Procladius, Polypedilum, Larsia, Sialis, Ablabesmyia
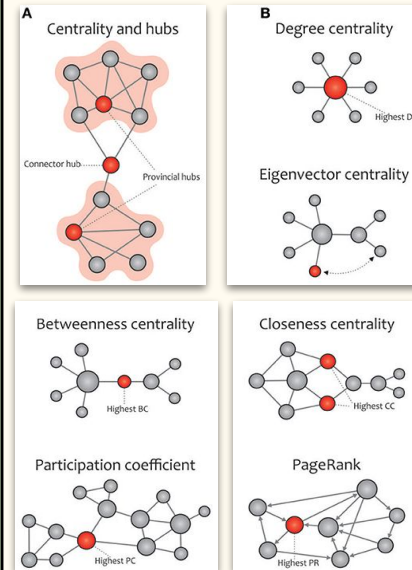

Interactions with highest Betweenness Centrality (descending order):

(Conchapelopia, Larsia),
(Lampetra, Salmo),
(Ichthyomyzon, Micropterus),
(Thymallus, Oncorhynchus),
(Oncorhynchus, Ichthyomyzon),
(Hydropsyche, Conchapelopia)

Centrality Metrics

References

M. E. J Newman 'Networks: An Introduction', page 224 Oxford University Press 2011.

Clauset, A., Newman, M. E., & Moore, C. "Finding community structure in very large networks." Physical Review E 70(6), 2004.

Evaluation of Notable Taxa and Centrality Metrics

Eigenvector centrality was investigated for each taxa because it provides a quantitative measure of how influential each genus is to the overall network. Genera that were found to have the highest eigenvector centrality tended to be insects belonging to the bloodworm family with the exception of Micropterus (black bass) and Sialis (eastern bluebird). These particular taxa are insects with two select predators which can indicate a more influential and robust relationships when compared with abundance data.

Betweenness centrality was investigated for each interaction to quantify its potential influence to the oval network based off shortest path. Interestingly enough Lamprey predator relationships exhibited the highest betweenness centrality. This can be most likely be explained by its many interactions with various participants in both a predatory relationship but a parasitic relationship as well.

Conclusion

By modeling the environment as a graph, graph algorithms can be used to:

- Predict the effects of introducing a new species to the environment
- Predict the impact of extinct or endangered organisms on the environment
- Evaluate environmental stability
- Quantify the influence of environmental organisms