MATLAB library to analyze bipartite ecological networks developed in the Wietz lab at Georgia Tech from 2012-2016 (Phage-Bacteria-Nets project)

Website: https://www.bco-dmo.org/dataset/560466
Version: 16 June 2015
Version Date: 2015-06-16

Project
» Understanding the Effects of Complex Phage-Bacteria Infection Networks on Marine Ecosystems (Phage-Bacteria-Nets)

Contributors	Affiliation	Role
Weitz, Joshua	Georgia Institute of Technology (GA Tech)	Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

- Dataset Description
- Data Files
- Parameters
- Deployments
- Project Information
- Funding

Dataset Description

A MATLAB library to analyze bipartite ecological networks. The main goal of BiMat is to facilitate the analysis of nestedness and modularity of bipartite ecological networks. For more information, instructions, and examples, see the BiMat Start Guide (PDF)

[table of contents | back to top]

Data Files

File
BiMat.csv (Comma Separated Values (.csv), 296 bytes) MD5:dc1be518d04f25fd6667a3f72b27ee63 Primary data file for dataset ID 560466

[table of contents | back to top]

Parameters

Parameter	Description	Units
description	Brief description of the link.	dimensionless
link	Link to external resource.	dimensionless

[table of contents | back to top]

Deployments

lab_Weitz

Website	https://www.bco-dmo.org/deployment/560523
Platform	Georgia_Tech
Start Date	2012-08-01
End Date	2016-07-01

[table of contents | back to top]

Project Information

Understanding the Effects of Complex Phage-Bacteria Infection Networks on Marine Ecosystems (Phage-Bacteria-Nets)

Website: http://ecotheory.biology.gatech.edu

Coverage: Theory and modeling project; lab-based, Georgia Tech

Description from NSF award abstract:
Bacteria and their viruses (phages) make up two of the most abundant and genetically diverse groups of organisms in the oceans. The extent of this diversity has become increasingly apparent with the advent of environmental sequencing. However, the ongoing discovery of new taxonomic diversity has, thus far, out-paced gains in quantifying the function of and interactions among phages and bacteria. Improved quantitative understanding of how diverse groups of phages exploit bacterial hosts will improve predictions of microbial population dynamics, ecosystem functioning, and the large-scale dynamics of global biogeochemical cycles. This project will develop a theoretical framework for characterizing the effect of complex phage-bacteria interactions on marine ecosystem structure and function. The theoretical framework is grounded in the analysis of cross-infection assays of bacteriophages with their bacterial hosts, termed phage-bacteria infection networks (PBINs). Recent discoveries concerning the structure of PBINs will be combined with a novel eco-evolutionary dynamics modeling framework in the service of the following aims:

Aim 1. Develop theoretical methods to analyze PBINs that include quantitative infection data to characterize complex patterns of cross-infection found in marine ecosystems.

Aim 2. Establish eco-evolutionary multi-strain models that incorporate complex PBIN data to evaluate hypotheses regarding how cross-infection within PBINs affects community stability.

Aim 3. Utilize the multi-strain model to predict how PBINs influence: (i) the ratio of viral to bacterial population abundances; and (ii) the flux of carbon and nutrients at the ecosystem level.

The theory developed in this project will improve characterizations of phage- bacteria interactions in marine ecosystems and establish a framework to link phage-bacteria interactions with ecosystem function. First, the project will generalize preliminary findings of multi-scale structure within empirical PBINs by developing novel network theories that can be applied to quantitative infection data. Properties of marine PBINs will be analyzed to assess whether they are hierarchically organized, organized into modules, and/or possess multi-scale structure. The statistical structure of PBINs will be integrated with multi-scale coevolutionary models. These co-evolutionary models will be utilized to evaluate hypotheses regarding how cross-infection structure affects community stability. Finally, these coevolutionary models will be used to consider carbon and nutrient regeneration via viral lysis of bacterial hosts. PBIN structure will be varied to establish a link between cross-infection and key indices of ecosystem structure and function, with specific applications to Roseobacter and Synechococcus hosts. Analytical methods and large-scale simulations will be utilized to achieve these goals, closely linked to empirical datasets.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1233760

[table of contents | back to top]