

NPHZ-V ecosystem model developed in the Wietz lab at Georgia Tech from 2012-2016 (Phage-Bacteria-Nets project)

Website: <https://www.bco-dmo.org/dataset/560513>

Version: 17 June 2015

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Project

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

Contributors	Affiliation	Role
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Dataset Description

NPHZ-V ecosystem model; described in:

Weitz, J.S., Stock, C.A., Wilhelm, S.W., Bourouiba, L., Coleman, M.L., Buchan, A., Follows, M.J., et al. 2015. A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. The ISME Journal, 9, 1352-1364. doi:[10.1038/ismej.2014.220](https://doi.org/10.1038/ismej.2014.220) ([PDF of Paper + Supplementary Info](#))

In Weitz et al. (2015), the authors "propose a step toward integration of viruses into global ecosystem models: a dynamic multitrophic model of a surface ocean microbial ecosystem. The model includes the interactions among organic and inorganic nutrients, phytoplankton (both cyanobacteria and eukaryotic autotrophs), heterotrophic bacteria, zooplankton and viruses" - termed a "NPHZ-V model".

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Data Files

File
NPHZ-V.csv (Comma Separated Values (.csv), 471 bytes) MD5:99b74f38dcf267f80daef70874eda213
Primary data file for dataset ID 560513

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Parameters

Parameter	Description	Units
description	Brief description of the links.	dimensionless
file	Link to data file.	dimensionless
external_link	Link to external resource.	dimensionless

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Deployments

lab_Weitz

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

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Project Information

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

Website: <http://ecothery.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.

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Funding

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

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