Virus and Microbial Cell Abundances from Marine Samples; study completed at Georgia Tech by J. Weitz

Website: https://www.bco-dmo.org/dataset/661836
Data Type: Other Field Results
Version: 18 October 2016
Version Date: 2016-10-18

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

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Dataset Description

Virus and microbial cell abundances from 25 marine surveys.

Data is also available via: http://weitzgroup.github.io/Virus_Microbe_Abundance/

Data are freely available Open source via Creative Commons Attribution 4.0 International License, see: http://creativecommons.org/licenses/by/4.0/legalcode

The original publication is:
C.H. Wigington et al. 2016. Re-examination of the relationship between marine virus and microbial cell abundances Nature Microbiology 1:15024. doi:10.1038/nmicrobiol.2015.24

Methods & Sampling

Marine virus abundance data were aggregated from 25 studies. A total of 5,671 data points were aggregated. The data collection dates ranged from 1996 to 2012. Data were primarily collected from coastal waters in the northern hemisphere, predominately during the summer months, with the notable exceptions of long-term coastal monthly monitoring sites, that is, the studies USC MO, BATS and MOVE.

See the original publication for more information:
C.H. Wigington et al. 2016. Re-examination of the relationship between marine virus and microbial cell abundances Nature Microbiology 1:15024. doi:10.1038/nmicrobiol.2015.24

Data Processing Description

Analyses of the data were performed using R version 3.1.1. Scripts and original data are provided at

https://github.com/WeitzGroup/Virus_Microbe_Abundance

BCO-DMO Processing:
- modified parameter names to conform with BCO-DMO naming conventions;
- formatted dates to mm/dd/yyyy;
- replaced spaces with underscores.

Data Files

File
Marine_VMR.csv (Comma Separated Values (.csv), 318.32 KB) MD5:bccf80eef7a424b7d9447928e67ec1a3 Primary data file for dataset ID 661836

Parameters

Parameter	Description	Units
obs	Observation identifier	unitless
date	Date of observation in mm/dd/yyyy format	unitless
study	Name of the study which made the abundance estimates	unitless
lon	Longitude of the sample	decimal degrees
lat	Latitude of the sample	decimal degrees
depth	Depth of the sample	meters
bacteria	Bacterial abundance	counts per milliliter (counts/mL)
virus	Viral abundance	counts per milliliter (counts/mL)

Deployments

lab_Weitz

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

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.

Funding

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