# Environmental data for SPOT virus sampling in Southern California during 2014 (Bacterial, Archaeal, and Protistan Biodiversity project)

**Website**: https://www.bco-dmo.org/dataset/550666
**Version**: 2015-01-29

**Project**
» Pattern and Process in Marine Bacterial, Archaeal, and Protistan Biodiversity, and Effects of Human Impacts (Bacterial, Archaeal, and Protistan Biodiversity)
» Marine viral dynamics and incorporation into microbial association networks (Marine Viral Dynamics)
» MO: Assembly of Marine Microbial Communities (Mar. Microbial Communities)

**Program**
» Dimensions of Biodiversity (Dimensions of Biodiversity)

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|---|---|---|
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## Table of Contents


- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Parameters
- Instruments
- Deployments
- Project Information
- Program Information
- Funding


## Dataset Description

These data pertain to the water samples for which the SPOT virus samples were collected. They include physical data plus nutrient concentrations, bacterial and viral abundances.

### Methods & Sampling

Water samples were collected on monthly trips to the SPOT station in the San Pedro Basin beginning in 2000 and continuing through and past 2014.

Cruise logs are available at: http://dornsife.usc.edu/spot/document-access/

### Data Processing Description

Detailed information on the **methodology** (pdf), including:
Satellite measurements
Assigning Taxonomic Identities to ARISA peaks
Environmental parameter variability

Seasonal variability of microbial community structure
Mantel test approach
Interannual variability of microbial community structure
Alpha diversity:
Variability between depths
Relation to season
Relation to community similarity between depths
Relation to community change
Environmental parameters and community structure: Mantel tests
Temporal dynamics of microbial taxa over time
Transformations
Taxonomic Groups
OTUs

**Relevent References:**

Beman JM, Steele JA, Fuhrman JA. (2011). Co-occurrence patterns for abundant marine archaeal and bacterial lineages in the deep chlorophyll maximum of coastal California. ISME J 5: 1077-1085.

* Cram JA, Chow C-ET, Sachdeva R, et al. (2014) Seasonal and interannual variability of the marine bacterioplankton community throughout the water column over ten years. The ISME Journal. doi: 10.1038/ismej.2014.153.

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Fuhrman J, Azam F (1982) Thymidine incorporation as a measure of heterotrophic bacterioplankton production in marine surface waters - evaluation and field results. marine biology 66:109-120.

Kirchman D, K'nees E, Hodson R (1985) Leucine incorporation and its potential as a measure of protein synthesis by bacteria in natural aquatic systems. Appl Environ Microbiol 49:599-607.

Morel A, Gentili B (2009) A simple band ratio technique to quantify the colored dissolved and detrital organic material from ocean color remotely sensed data. Remote Sensing of Environment 113:998-1011. doi: 10.1016/j.rse.2009.01.008

Noble RT, Fuhrman JA. (1998). Use of SYBR Green I for rapid epifluorescence counts of marine viruses and bacteria. Aquat. Microb. Ecol 14: 113-118.

Parsons TR (1984) A manual of chemical and biological methods for seawater analysis, 1st ed. Pergamon Press, Oxford [Oxfordshire]; New York

Patel A, Noble RT, Steele JA, Schwalbach MS, Hewson I, Fuhrman JA. (2007). Virus and prokaryote enumeration from planktonic aquatic environments by
epifluorescence microscopy with SYBR Green I. Nat Protoc 2: 269-276.

Stramski D, Reynolds RA, Babin M, et al. (2008) Relationships between the surface concentration of particulate organic carbon and optical properties in the eastern South Pacific and eastern Atlantic Oceans. Biogeosciences 5:171-201.

**BCO-DMO Processing:**

- added conventional header with dataset name, PI name, version date
- renamed parameters to BCO-DMO standard or more descriptive terms
- replaced na with nd
- reformated data from m/d/yyyy to yyyy-mm-dd
- reduced number of digits for most parameters

[ table of contents | back to top ]

## Data Files

| File |
| --- |
| **SPOT_virus_environ.csv** (Comma Separated Values (.csv), 7.27 KB)<br>MD5:c56531a7805d82da409531b5f18dfbe2<br>Primary data file for dataset ID 550666 |

[ table of contents | back to top ]

## Parameters

| Parameter | Description | Units |
| --- | --- | --- |
| cruise_id | cruise identification | unitless |
| platform | vessel name | unitless |
| date | date of cruise | yyyy-mm-dd |
| time_start | cruise start time | HH:MM |
| time_end | cruise end time | HH:MM |
| lat | station latitude; north is positive | decimal degrees |
| lon | station longitude; east is positive | decimal degrees |
| day_len | length of day; geosphere package in R; daylength(date; 33.55) | hours |
| day_len_change_per_month | day length change per month: geosphere package in R; daylength(date; 33.55) | hours |
| SSHD_sat | Sea Surface Height Deviation - Aviso: 0.25 degrees; global; science quality; monthly average | meters |
| MEI | Multivariate ENSO Index | standard departure |
| temp | temperature | degrees Celsius |
| sal | salinity | practical salinity units |
| NO2 | nitrite concentration | microMoles |

| | | |
|---|---|---|
| NO2_NO3 | nitrate concentration | microMoles |
| PO4 | phosphate concentration | microMoles |
| pstar_P_N | [Phosphate]- [Nitrate + Nitrite]/16 | microMoles |
| chl_a_sat | chlorophyll-a satellite monthly | mg/m^3 |
| chl_a | chlorophyll-a by Niskin measurements | mg/m^3 |
| prim_prod | primary productivity satellite monthly average | mg_C/m^2/day |
| cmax_depth | depth of chlorophyll maximum | meters |
| leu_uptake | bacterial Productivity (Leucine) | cells/ml/day |
| thy_uptake | bacterial Productivity (Thymidine) | cells/ml/day |
| turnover_leu | [bacteria]/bacterial productivity (Leucine) | days |
| turnover_thy | [bacteria]/bacterial productivity (Thymedine) | days |
| bact_abun | bacterial abundance | cells/ml |
| viral_abund | viral abundance | VLP/ml |
| virus_bact_ratio | virus to bacteriaratio | unitless |
| ISO_DateTime_Local_start | local time formatted as ISO 8601:2004(E) standard | YYYY-MM-DDTHH:MM:SS.xx |
| yrday_local | Sequential day of the year with decimal. | decimal number |

[ table of contents | back to top ]

## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | CTD Sea-Bird |
| **Generic Instrument Name** | CTD Sea-Bird |
| **Generic Instrument Description** | A Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics. This instrument designation is used when specific make and model are not known or when a more specific term is not available in the BCO-DMO vocabulary. Refer to the dataset-specific metadata for more information about the specific CTD used. More information from: http://www.seabird.com/ |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Fluorescence Microscope |
| **Generic Instrument Description** | Instruments that generate enlarged images of samples using the phenomena of fluorescence and phosphorescence instead of, or in addition to, reflection and absorption of visible light. Includes conventional and inverted instruments. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Niskin bottle |
| **Generic Instrument Name** | Niskin bottle |
| **Generic Instrument Description** | A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc. |

[ table of contents | back to top ]

## Deployments

**lab_Fuhrman_2014**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/535519 |
| **Platform** | USC |
| **Start Date** | 2014-10-17 |
| **End Date** | 2014-10-17 |
| **Description** | Microbial diversity laboratory studies.  Monthlly cruises to collect water samples in Los Angeles, California area. |

[ table of contents | back to top ]

## Project Information

**Pattern and Process in Marine Bacterial, Archaeal, and Protistan Biodiversity, and Effects of Human Impacts (Bacterial, Archaeal, and Protistan Biodiversity)**

**Website**: http://dornsife.usc.edu/labs/usc-microbial-observatory/

**Coverage**: San Pedro Ocean Time Series; approx. 33N, 118W

*Description from NSF award abstract:*
Bacteria, Archaea, and Protists dominate global elemental cycling and are immensely diverse genetically, taxonomically, and functionally. Yet the extent of marine microbial diversity, its patterns, and relationships among genetic, taxonomic, and functional diversity are very poorly characterized, even though the ocean covers 70% of the planet's surface. Among the least well known variables is the effect of human impacts on native marine microbial systems, although it is recognized that impacted systems are more prone to events like harmful algal blooms. Knowledge of these relationships and impacts are necessary to anticipate the responses of biota to global changes and feedback mechanisms that may alter the extents, rates, and even pathways of such changes. This project will expand upon an existing NSF-funded 10+-year monthly ocean time series (Microbial Observatory) that has focused on a single site midway between Los Angeles and Santa Catalina Island, to also include quarterly sampling adjacent to the impacted LA Harbor region to the barely-impacted Catalina coast. USC already runs facilities in LA Harbor and Catalina, with daily boats between (no cost). Measurements include (1) Genetic diversity: high throughput DNA sequences of "housekeeping" and functional genes. (2) Taxonomic diversity: high throughput tag sequences of small subunit ribosomal RNA genes, flow cytometry, automated image analysis (3) Functional Diversity: (a) Functional measurements (carbon fixation and respiration rates, microbial growth and grazing rates, cell size, morphology, and biomass variations), (b) distribution and expression of particular target functional genes involved with processes central to the cycles of carbon, nitrogen, and sulfur, (c) exploratory metatranscriptomics to explore functionalities that were not anticipated. (4) Integrating these: Multivariate statistical and network approaches including newly developed techniques (e.g. Bayesian networks to examine cause-effect relationships), and high speed computational approaches to assess the relationships among the genetic, taxonomic, and functional aspects of biodiversity observed. The PIs will also examine the collected data for signatures and specific effects (on organism identity and functions) associated with human impacted harbor site vs. the relatively pristine one.

The PIs will use network and time series analysis, along with other statistical tools to integrate "classical" microbial and oceanographic rate process measurements, flow cytometric and microscopic characterizations of communities, along with targeted as well as untargeted metagenomics and metatranscriptomics to relate genetic and taxonomic diversity with specific functions (at organismal, food web, and system levels). For example, they should be able to determine how different variants of particular taxa (e.g. at resolution levels ranging from what might be considered near the subspecies to genus levels) would differ in their association with particular measured functions, functional genes, or particular other taxa - or they might see how particular clusters of related organisms behave similarly or differently in their associations. This project offers an unprecedented and potentially transformative opportunity to combine and integrate measurements of genetic, taxonomic, and functional diversity along with direct measurements of system function in a well studied marine system that includes a gradient from one of the world's busiest harbors to a largely pristine ocean habitat. Far beyond just describing the distributions of organisms and functions (itself a necessary first step), they will specifically link spatial and temporal variations in a variety of functions with variations in genetic and taxonomic community composition.

**Marine viral dynamics and incorporation into microbial association networks (Marine Viral Dynamics)**

**Website**: http://dornsife.usc.edu/labs/fuhrmanlab/research/

**Coverage**: Southern California between Los Angeles and Santa Catalina Island; Approx. 33.5N, 118.5 W

*Description from NSF award abstract:*
Marine microbes are tremendously abundant and are major players and driving forces in global biogeochemical cycles of carbon, nitrogen, phosphorus, and iron. We learned over the past two decades that viruses are pervasive elements in marine systems, with significant ecological, biogeochemical, genetic, and evolutionary

effects on cellular marine organisms, but we have remarkably little information about the dynamics of marine viral community structure and how it relates to the community structure of their hosts (largely bacteria and phytoplankton). Such information is critical for developing proper conceptual and practical models of the roles of viruses and how these change over time and space. The goals of this project are:
(1) primarily, to characterize a significant subset of the natural virus community and its dynamics, along with bacterial host communities, as they change over daily to monthly time scales at the USC well-studied marine Microbial Observatory site (midway between Los Angeles and Santa Catalina Island), testing hypotheses regarding repeating patterns, host range effects, and taxa-time relationships, and
(2) secondarily, to incorporate these viruses into microbial association networks by statistically connecting particular types of viruses to specific potential hosts.

Approaches for this study include:
(a) nested daily, weekly, and monthly collection of bacteria and viruses for nucleic acid samples,
(b) amplification of conserved genes, as proxy phylogenetic markers, from a few moderately-well-characterized broad viral groups previously readily found in seawater (i.e. the T4-like myoviruses, T7-like podoviruses), as well as bacterial rRNA genes,
(c) extensive sequencing, after screening by community fingerprinting, from the mixed amplified products,
(d) binning of the sequences or fingerprint fragments into operational taxonomic units (OTUs) at different levels of resolution,
(e) evaluation of the results with statistical approaches to examine temporal patterns, relationships (including time-lagged ones) with other viral OTUs, bacteria, protists (monthly only), and environmental parameters,
(f) incorporating the viral OTUs mathematically into microbial association networks.

Data on environmental parameters, bacteria, and protists are already being collected monthly for an existing Microbial Observatory, so the viral work is complementary to this project, providing a major value-added component. Similarly, this project will add selected daily and weekly microbial data to the Microbial Observatory. Data from the literature and from the PI's preliminary results show they have the technology and capability to meet the first goal, and to our knowledge this would be the first such data set of its scope and kind. The investigators have already published in 2006 that the bacterial communities at the 5m depth of this site show a predictable repeating annual cycle in bacterial community composition, so the expectation of a predictable repeating viral community is not unreasonable. They also have some preliminary data showing some repeated viral occurrences. The second goal requires that there are indeed significant statistical relationships between the viruses and other measured parameters, which the PI anticipates to be the case, but of course cannot predict; if they cannot be demonstrated, this result itself would be informative and would constrain the possible modes of microbial/viral interactions.

**MO: Assembly of Marine Microbial Communities (Mar. Microbial Communities)**

**Coverage**: San Pedro Channel and Basin off southern California coast

Abstract:

The USC Microbial Observatory was established in 2000. The research focus of this observatory is an investigation of the microbial diversity and microbial community composition at a study site in the San Pedro Channel and Basin off the coast of southern California. The Channel area encompasses a diversity of coastal ocean habitats. The near-coast region borders one of the most highly urbanized areas of the country (greater Los Angeles) while open ocean waters impinge on the Channel Island archipelago that extends to within 30 km of the mainland. The San Pedro Basin is a deep-water environment (approximately 890 m) that exhibits very low oxygen concentration. The overarching objective of this project is the derivation of fundamental understanding of how microbial communities in the ocean are organized spatially (with depth) and temporally (at scales of months-to-years), and how environmental and biological factors shape this organization. The basic premise of the research is that "guilds" or "consortia" of microbial species exist that constitute functional subunits within the huge diversity of taxa that comprise planktonic microbial communities. The microbial species forming these guilds are functionally interdependent, and act as ecological units that replace one another in time and space as environmental conditions change. The program consists of monthly sampling at four depths in order to document the abundance, biomass and species composition of all planktonic microorganisms at the mid-channel sampling station. A variety of microscopical and molecular biological approaches are employed to examine archaeal, bacterial and microeukaryote (microalgal, protozoan, micrometazoan) diversity. The observatory is unique in that it entails an assessment of the complete spectrum

of microorganisms (from viruses to the largest protists) in the water column. Genetic fingerprinting of the total microbial community is the primary tool for revealing the trophic roles and relationships among microbial taxa (predation, mutualism, commensalism, parasitism/infection), and to generate hypotheses on the interdependences among these species. Experimental studies involve manipulative food web experiments to test hypotheses concerning the relationships and interactions among the various microbial species. The data support extensive statistical analyses to identify relationships between microbial taxa, and with environmental parameters.

This research program strives to develop a fundamental understanding of the factors controlling the structure of microbial communities in aquatic ecosystems. Therefore, the results have far-reaching consequences for predicting biogeochemical processes mediated by microbial activities in nature. The project also incorporates a strong educational component aimed at reaching students ranging from elementary school children to graduate students. The information resulting from the research is incorporated into undergraduate and graduate courses taught by the principal investigators, and both types of students participate actively in the research. In addition, the principal investigators and graduate students supported by this project participate directly in an ongoing teacher education program (Centers for Ocean Science Education Excellence; COSEE-West) that reaches middle and high school students, many of whom are Hispanic, African-American or other ethnic minorities and most of whom are economically disadvantaged. This education/outreach goal is accomplished through an existing teacher enhancement and student enrichment program that incorporates the research from this microbial observatory into a learning experience that enhances student awareness of environmental science, microbiology and the natural world. The observatory principal investigators work is featured and publicly available on the internet as a part of the USC Microbial Observatory Website at http://www.usc.edu/microbialobservatory)

[ table of contents | back to top ]

## Program Information

**Dimensions of Biodiversity (Dimensions of Biodiversity)**

**Website**: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

**Coverage**: global

(adapted from the NSF Synopsis of Program)
Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

[ table of contents | back to top ]

## Funding

| Funding Source | Award |
| --- | --- |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1136818 |
| NSF Division of Molecular and Cellular Biosciences (NSF MCB) | MCB-0703159 |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1031743 |


[ table of contents | back to top ]