

Daily RBRconcerto data from surface waters off of the Santa Monica Pier, California from April 16-25th, 2018 as part of the San Pedro Ocean Time-series (SPOT)

Website: <https://www.bco-dmo.org/dataset/746395>

Data Type: Other Field Results

Version: 1

Version Date: 2018-09-18

Project

» [Protistan, prokaryotic, and viral processes at the San Pedro Ocean Time-series](#) (SPOT)

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Abstract

Daily casts with a RBRconcerto instrument were conducted at the Santa Monica Pier, California from April 16-25th, 2018 as part of the San Pedro Ocean Time-series (SPOT) project. Casts were conducted in surface waters (1-2 m depth) and measured conductivity, temperature, pressure, dissolved oxygen saturation, chlorophyll a, and salinity.

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Coverage

Spatial Extent: Lat:34.007653 Lon:-118.500153

Temporal Extent: 2018-04-16 - 2018-04-25

Methods & Sampling

Sampling and analytical procedures:

We used the RBRconcerto during the daily sampling period April 16-25th 2018 in surface waters off of the Santa Monica Pier, California. The RBRConcerto was lowered into the water for 10 minutes between 1 to 2 meters depth during which we sampled nearby sea water for downstream RNA extractions and 18S rRNA gene tag sequence processing.

Data Processing Description

RBRconcerto data was processed, trimmed and compiled with the OCE package in R (version 0.9-23). We trimmed the downcast and upcast parts of the data, resulting in consistent scans from 1000 to 2999 for each day.

BCO-DMO Data Manager Processing Notes (after communication with data submitter):

- * added a conventional header with dataset name, PI name, version date
- * modified parameter names to conform with BCO-DMO naming conventions
- * blank values in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system.
- * added lat/lon values (in decimal degrees) to the dataset from the single deployment location provided in the metadata for this dataset.
- * Added ISO_DateTime_UTC column from local time values
- * pressure column rounded to two decimal places.

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Data Files

File
CTD.csv (Comma Separated Values (.csv), 2.83 MB) MD5:fa85361cf7f948ae20653467fdb486f0 Primary data file for dataset ID 746395

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Related Publications

Kelley, D. & Richards, K. (2018). oce: Analysis of Oceanographic Data. R package version 0.9-23.

<https://CRAN.R-project.org/package=oce>

Methods

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Parameters

Parameter	Description	Units
Date	Date (local,UTC-7) in format m/d/yyyy	unitless
Time	Time (local,UTC-7) in format HH:MM:SS	unitless
conductivity	Conductivity	milli-Siemens per centimeter (mS/cm)
temperature	Water temperature	degrees Celsius (C)
pressure	Pressure	decibars (dbar)
dissolvedosaturation	Dissolved oxygen saturation	percent (%)
chlorophylla	Chlorophyll a	micrograms per liter (µg/l)
salinity	Salinity	Practical Salinity Units (PSU)
scan	Scan (RBRconcerto measurement number)	unitless
lat	Latitude	decimal degrees
lon	Longitude	decimal degrees
ISO_DateTime_UTC	Timestamp (UTC) in standard ISO 8601:2004(E) format YYYY-mm-ddTHH:MM:SSZ	unitless

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Instruments

Dataset-specific Instrument Name	RBR concerto DO FI CTD
Generic Instrument Name	CTD Richard Brancker Research
Dataset-specific Description	The RBRconcerto instrument (Conductivity, Temperature, Pressure (Depth), Dissolved Oxygen, Fluorescence), calibrated in 2018 by RBR.
Generic Instrument Description	The RBR Conductivity, Temperature and Depth instrument: http://www.rbr-global.com/products/ct-and-ctd-loggers/rbrconcerto-ctd

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Deployments

SPOT_SMP

Website	https://www.bco-dmo.org/deployment/746419
Platform	shoreside Santa Monica Pier
Start Date	2018-01-01
End Date	2019-12-31

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Project Information

Protistan, prokaryotic, and viral processes at the San Pedro Ocean Time-series (SPOT)

Coverage: San Pedro Channel off the coast of Los Angeles

Planktonic marine microbial communities consist of a diverse collection of bacteria, archaea, viruses, protists (phytoplankton and protozoa) and small animals (metazoan). Collectively, these species are responsible for virtually all marine pelagic primary production where they form the basis of food webs and carry out a large fraction of respiratory processes. Microbial interactions include the traditional role of predation, but recent research recognizes the importance of parasitism, symbiosis and viral infection. Characterizing the response of pelagic microbial communities and processes to environmental influences is fundamental to understanding and modeling carbon flow and energy utilization in the ocean, but very few studies have attempted to study all of these assemblages in the same study. This project is comprised of long-term (monthly) and short-term (daily) sampling at the San Pedro Ocean Time-series (SPOT) site. Analysis of the resulting datasets investigates co-occurrence patterns of microbial taxa (e.g. protist-virus and protist-prokaryote interactions, both positive and negative) indicating which species consistently co-occur and potentially interact, followed by examination gene expression to help define the underlying mechanisms. This study augments 20 years of baseline studies of microbial abundance, diversity, rates at the site, and will enable detection of low-frequency changes in composition and potential ecological interactions among microbes, and their responses to changing environmental forcing factors. These responses have important consequences for higher trophic levels and ocean-atmosphere feedbacks. The broader impacts of this project include training graduate and undergraduate students, providing local high school student with summer lab experiences, and PI presentations at local K-12 schools, museums, aquaria and informal learning centers in the region. Additionally, the PIs advise at the local, county and state level regarding coastal marine water quality.

This research project is unique in that it is a holistic study (including all microbes from viruses to small metazoa) of microbial species diversity and ecological activities, carried out at the SPOT site off the coast of southern California. In studying all microbes simultaneously, this work aims to identify important ecological interactions among microbial species, and identify the basis(es) for those interactions. This research involves (1) extensive analyses of prokaryote (archaeal and bacterial) and eukaryote (protistan and micro-metazoan) diversity via the sequencing of marker genes, (2) studies of whole-community gene expression by eukaryotes and prokaryotes in order to identify key functional characteristics of microorganismal groups and the detection of active viral infections, and (3) metagenomic analysis of viruses and bacteria to aid interpretation of transcriptomic analyses using genome-encoded information. The project includes exploratory metatranscriptomic analysis of poorly-understood aphotic and hypoxic-zone protists, to examine their stratification, functions and hypothesized prokaryotic symbioses.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1737409

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