Autonomous Underwater Vehicle Monterey Bay Time Series - CTD from AUV Makai on 2016-02-03

Website: https://www.bco-dmo.org/dataset/644012
Data Type: Cruise Results
Version: 1
Version Date: 2023-08-15

Project
» Center for Microbial Oceanography: Research and Education (C-MORE)

Contributors	Affiliation	Role
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Abstract
Autonomous Underwater Vehicle (AUV) Monterey Bay Time Series from Feb 2016. This data set includes CTD and fluorometer data from the Makai AUV, as context for ecogenomic sampling using an onboard Environmental Sample Processor (ESP).

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Coverage

Spatial Extent: **N**:36.8338 **E**:-121.828 **S**:36.7837 **W**:-121.888
Temporal Extent: 2016-02-03

Methods & Sampling

MBARI AUVs

Data Processing Description

Original sensor data were bin averaged to 2-second resolution.

BCO-DMO Processing Description

The date and time columns in the submitted file were combined to create an ISO datetime column named ISO_DateTime_UTC and of format YYYY-MM-DDThh:mm:ssZ

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Data Files

File
AUV Monteray Bay CTD filename: 644012_v1_auv_monteray_bay_ctd.csv (Comma Separated Values (.csv), 2.80 MB) MD5:5885af1113684d9f2a739c4ae15de9a6 Primary data file for dataset ID 644012, version 1

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Parameters

Parameter	Description	Units
ISO_DateTime_UTC	Date and time (UTC) formatted to ISO 8601 standard	unitless
lat	latitude (north is positive)	decimal degrees
lon	longitude (east is positive)	decimal degrees
depth	depth sample	meters
temp	Temperature from CTD	degrees Celsius
sal	Salinity from CTD	dimensionless
chl_a_fluor	chlorophyll-a fluorometric method	micrograms/liter

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Instruments

Dataset-specific Instrument Name	Makai AUV
Generic Instrument Name	Autonomous Underwater Vehicle
Generic Instrument Description	An Autonomous Underwater Vehicle (AUV) is a free-roving platform operating in the water column with propulsion but no human operator on board (e.g. Autosub, Gavia).

Dataset-specific Instrument Name	Environmental Sample Processor
Generic Instrument Name	Environmental Sample Processor
Generic Instrument Description	The MBARI Environmental Sample Processor—the ESP—provides on-site (in situ) collection and analysis of water samples from the subsurface ocean. The instrument is an electromechanical/fluidic system designed to collect discrete water samples, concentrate microorganisms or particles, and automate application of molecular probes and qPCR which identify microorganisms and their gene products. The ESP also archives samples so that further analyses may be done after the instrument is recovered. Environmental Sample Processor See references below for methodology used on the ESP: Greenfield, D.I., R. Marin III, S. Jensen, E. Massion, B. Roman, J. Feldman, C. Scholin (2006). Application of the Environmental Sample Processor (ESP) methodology for quantifying Pseudo-nitzschia australis using ribosomal RNA-targeted probes in sandwich and fluorescent in situ hybridization. Limnology and Oceanography: Methods 4: 426-435. Greenfield, D., R. Marin III, G.J. Doucette, C. Mikulski, S. Jensen, B. Roman, N. Alvarado, and C.A. Scholin (2008). Field applications of the second-generation Environmental Sample Processor (ESP) for remote detection of harmful algae: 2006-2007. Limnology and Oceanography: Methods 6: 667-679. Marin III, R., and C. Scholin (2010). Sandwich Hybridization. In: Microscopic and molecular methods for quantitative phytoplankton analysis (Chapter 12), edited by B. Karlson, C. Cusack, and E. Bresnan, E.. IOC Manuals and Guides, no. 55. (IOC/2010/MG/55) Paris, UNESCO. 110 pp. Ottesen, E.A., R. Marin III, C.M. Preston, C.R. Young, J.P. Ryan, C.A. Scholin, and E.F. DeLong (2011). Metatranscriptomic analysis of autonomously collected and preserved marine bacterioplankton. The ISME Journal, 5: 1881-1895, doi: 10.1038/ismej.2011.70. Ottesen, E.A., C.R. Young, J.M. Eppley, J.P. Ryan, F.P. Chavez, C.A. Scholin, and E.F. DeLong (2013). Pattern and synchrony of gene expression among sympatric marine microbial populations. Proceedings of the National Academy of Sciences, 110: E488-E497, doi: 10.1073/pnas.1222099110. Ottesen, E.A., C.M. Young, S.M. Gifford, J.M. Eppley, R. Marin III, S.C. Schuster, C.A. Scholin, and E.F. DeLong (2014). Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. Science, 345: 207-212, 10.1126/science.1252476. Preston, C.M., A. Harris, J.P. Ryan, B. Roman, R. Marin III, S. Jensen, C. Everlove, J. Birch, J.M. Dzenitis, D. Pargett, M. Adachi, K. Turk, J.P. Zehr, and C.A. Scholin (2011). Underwater application of quantitative PCR on an ocean mooring. PLoS ONE, 6:e22522, doi: 10.1371/journal.pone.0022522. Robidart, J.C., C.M. Preston, R.W. Paerl, K.A. Turk, A.C. Mosier, C.A. Francis, C.A. Scholin, and J.P. Zehr (2011). Seasonal Synechococcus and Thaumarchaeal population dynamics examined with high resolution with remote in situ instrumentation. The ISME Journal, 6: 513-523, doi: 10.1038/ismej.2011.127. Robidart, J., M.J. Church, J.P. Ryan, F. Ascani, S.T. Wilson, D. Bombar, R. Marin III, K.J. Richards, D.M. Karl, C.A. Scholin, and J.P Zehr (2014). Ecogenomic sensor reveals controls on N2-fixing microorganisms in the North Pacific Ocean. The ISME Journal, 8: 1175-1185, 10.1038/ismej.2013.244. Saito, M.A., V.V. Bulygin, D.M. Moran, C. Taylor, and C. Scholin (2011). Examination of microbial proteome preservation techniques applicable to autonomous environmental sample collection. Frontiers in Aquatic Microbiology, 2: doi: 10.3389/fmicb.2011.00215. Scholin, C.. (2010). What are “ecogenomic sensors?” A review and thoughts for the future. Ocean Science 6: 51-60. Ussler III, W., C.M. Preston, P. Tavormina, D. Pargett, S. Jensen, B. Roman, R. Marin III, S.R. Shah, P.R. Girguis, J.M. Birch, V.J. Orphan, and C. Scholin (2013). Autonomous application of quantitative PCR in the deep sea: In situ surveys of aerobic methanotrophs using the deep-sea Environmental Sample Processor. Environmental Science and Technology, 47: 9339–9346, doi: 10.1021/es4023199. Varaljay, V.A, J. Robidart, C.M. Preston, S.M. Gifford, B. Durham, A.S. Burns, J.P. Ryan, R. Marin III, R.P. Kiene, J.P Zehr, C.A. Scholin, M. Moran. 2015. Single-taxon field measurements of bacterial gene regulation controlling DMSP fate. ISME Journal, doi:10.1038/ismej.2015.23|

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Deployments

AUV_Makai_Monterey_Bay_Time_Series

Website	https://www.bco-dmo.org/deployment/643801
Platform	AUV Makai
Start Date	2015-07-22
End Date	2099-01-01
Description	http://www.mbari.org/at-sea/vehicles/autonomous-underwater-vehicles/

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Project Information

Center for Microbial Oceanography: Research and Education (C-MORE)

Website: http://cmore.soest.hawaii.edu/

Coverage: North Pacific Subtropical Gyre (large region around 22 45 N, 158 W)

Project summary

The **Center for Microbial Oceanography: Research and Education** (C-MORE) is a recently established (August 2006; NSF award: EF-0424599) NSF-sponsored Science and Technology Center designed to facilitate a more comprehensive understanding of the diverse assemblages of microorganisms in the sea, ranging from the genetic basis of marine microbial biogeochemistry including the metabolic regulation and environmental controls of gene expression, to the processes that underpin the fluxes of carbon, related bioelements and energy in the marine environment. Stated holistically, C-MORE's primary mission is: *Linking Genomes to Biomes*.

We believe that the time is right to address several major, long-standing questions in microbial oceanography. Recent advances in the application of molecular techniques have provided an unprecedented view of the structure, diversity and possible function of sea microbes. By combining these and other novel approaches with more well-established techniques in microbiology, oceanography and ecology, it may be possible to develop a meaningful predictive understanding of the ocean with respect to energy transduction, carbon sequestration, bioelement cycling and the probable response of marine ecosystems to global environmental variability and climate change. The strength of C-MORE resides in the synergy created by bringing together experts who traditionally have not worked together and this, in turn, will facilitate the creation and dissemination of new knowledge on the role of marine microbes in global habitability.

The new Center will design and conduct novel research, broker partnerships, increase diversity of human resources, implement education and outreach programs, and utilize comprehensive information about microbial life in the sea. The Center will bring together teams of scientists, educators and community members who otherwise do not have an opportunity to communicate, collaborate or design creative solutions to long-term ecosystem scale problems. The Center's research will be organized around four interconnected themes:

- (Theme I) microbial biodiversity,
- (Theme II) metabolism and C-N-P-energy flow,
- (Theme III) remote and continuous sensing and links to climate variability, and
- (Theme IV) ecosystem modeling, simulation and prediction.

Each theme will have a leader to help coordinate the research programs and to facilitate interactions among the other related themes. The education programs will focus on pre-college curriculum enhancements, in service teacher training and formal undergraduate/graduate and post-doctoral programs to prepare the next generation of microbial oceanographers. The Center will establish and maintain creative outreach programs to help diffuse the new knowledge gained into society at large including policymakers. The Center's activities will be dispersed among five partner institutions:

- Massachusetts Institute of Technology,
- Woods Hole Oceanographic Institution,

- Monterey Bay Aquarium Research Institute,
- University of California at Santa Cruz and
- Oregon State University

and will be coordinated at the University of Hawaii at Manoa.

Related Files:

Strategic plan (PDF file)

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Funding

Funding Source	Award
NSF Division of Biological Infrastructure (NSF DBI)	DBI-0424599
David and Lucile Packard Foundation (Packard)	unknown AUV_MontereyBay Packard

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