

Prochlorococcus, Synechococcus, and picoeukaryotic phytoplankton yearly standard deviation from mean global abundance estimated for four CMIP5 climate scenarios using an ensemble of five circulation models

Website: <https://www.bco-dmo.org/dataset/793776>

Data Type: model results

Version: 2

Version Date: 2021-03-09

Project

» [Convergence: RAISE: Linking the adaptive dynamics of plankton with emergent global ocean biogeochemistry](#) (Ocean Stoichiometry)

Contributors	Affiliation	Role
Martiny, Adam	University of California-Irvine (UC Irvine)	Principal Investigator
Flombaum, Pedro	Universidad de Buenos Aires	Co-Principal Investigator, Contact
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

Prochlorococcus, Synechococcus and picoeukaryotic phytoplankton yearly standard deviation from mean global abundance estimated for four CMIP5 climate scenarios using an ensemble of five circulation models from 1900 to 2100.

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Coverage

Spatial Extent: N:89.5 E:180 S:-89.5 W:-180

Temporal Extent: 1901 - 2100

Dataset Description

Prochlorococcus, *Synechococcus* and picoeukaryotic phytoplankton yearly standard deviation from mean global abundance estimated for four CMIP5 climate scenarios using an ensemble of five circulation models from 1900 to 2100.

Methods & Sampling

We estimated *Prochlorococcus*, *Synechococcus* and picoeukaryotic phytoplankton global cell abundance (cell) using quantitative niche models (Flombaum et al 2013, 2020). Inputs for the niche models were temperature and nitrate from Earth System Models, and light from Ocean Color (oceancolor.gsfc.nasa.gov) which identical

across simulations. We estimated *Prochlorococcus* and *Synechococcus* using two methodologies, parametric niche model, and artificial neural networks (ANN). For picoeukaryotic phytoplankton we used only the ANN. The parametric model used only temperature and photosynthetic active radiation as inputs, and the ANN also included nitrate concentration. Standard deviation values were estimated for the parametric model from a 10.000 iteration bootstrap on a yearly basis, and for the ANN as 100 iterations for each unique geographic and depth location.

Data columns containing standard deviation from the mean global cell abundance are labeled after lineage, niche model, scenario, and Earth System Model.

Units: cells.

Lineages: Prochlorococcus, Synechococcus, and picoeukaryotic phytoplankton.

Niche model: Parametric; ANN.

Scenarios: Historic, RCP2.6, RCP4.5, RCP8.5.

Earth System Models: GFDL-ESM2G, HadGEM2-ES, IPSL-CM5A-MR, MPI-ESM-LR, NorESM1-ME (Taylor et al 2012).

Data Processing Description

BCO-DMO Processing:

- renamed columns to conform with BCO-DMO naming conventions;
- replaced NaN with nd ("no data");
- 2021-03-09: replaced v1 of dataset with v2.

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Data Files

File
pro_syn_peuk_CC_global_abund_std.csv (Comma Separated Values (.csv), 88.73 KB) MD5:989d1681bfd1cc0b9acc8b1d9c7a5e4e
Primary data file for dataset ID 793776

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Related Publications

Flombaum, P., Gallegos, J. L., Gordillo, R. A., Rincon, J., Zabala, L. L., Jiao, N., ... Martiny, A. C. (2013). Present and future global distributions of the marine Cyanobacteria *Prochlorococcus* and *Synechococcus*. *Proceedings of the National Academy of Sciences*, 110(24), 9824–9829. doi:[10.1073/pnas.1307701110](https://doi.org/10.1073/pnas.1307701110)

Related Research

Flombaum, P., Wang, W.-L., Primeau, F. W., & Martiny, A. C. (2020). Global picophytoplankton niche partitioning predicts overall positive response to ocean warming. *Nature Geoscience*, 13(2), 116–120.

doi:[10.1038/s41561-019-0524-2](https://doi.org/10.1038/s41561-019-0524-2)

Related Research

Taylor, K. E., Stouffer, R. J., & Meehl, G. A. (2012). An Overview of CMIP5 and the Experiment Design. *Bulletin of the American Meteorological Society*, 93(4), 485–498. doi:10.1175/bams-d-11-00094.1

<https://doi.org/10.1175/BAMS-D-11-00094.1>

Related Research

Visintini, N., Martiny, A. C., & Flombaum, P. (2021). *Prochlorococcus*, *Synechococcus*, and picoeukaryotic phytoplankton abundances in the global ocean. *Limnology and Oceanography Letters*, 6(4), 207–215.

doi:[10.1002/lol2.10188](https://doi.org/10.1002/lol2.10188)

Results

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Parameters

Parameter	Description	Units
Years_for_Historic_scenario	Four-digit year; format: YYYY	unitless
Years_for_scenarios_RCP2_6_RCP4_5_RCP8_5	Four-digit year; format: YYYY	unitless
Prochlorococcus_Parametric_for_HISTORIC_scenario_GFDL_ESM2G_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Prochlorococcus Parametric Historic GFDL-ESM2G	Cells
Prochlorococcus_Parametric_for_HISTORIC_scenario_HadGEM2_ES_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Prochlorococcus Parametric Historic HadGEM2-ES	Cells
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Prochlorococcus_Parametric_for_HISTORIC_scenario_NorESM1_ME_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Prochlorococcus Parametric Historic NorESM1-ME	Cells
Prochlorococcus_Parametric_for_RCP2_6_scenario_GFDL_ESM2G_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Prochlorococcus Parametric RCP2.6 GFDL-ESM2G	Cells
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Prochlorococcus_Parametric_for_RCP8_5_scenario_NorESM1_ME_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Prochlorococcus Parametric RCP8.5 NorESM1-ME	Cells
Synechococcus_Parametric_for_HISTORIC_scenario_GFDL_ESM2G_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus Parametric Historic GFDL-ESM2G	Cells
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Synechococcus_ANN_for_RCP4_5_scenario_IPSL_CM5A_MR_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP4.5 IPSL-CM5A-MR	Cells
Synechococcus_ANN_for_RCP4_5_scenario_MPI_ESM_LR_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP4.5 MPI-ESM-LR	Cells

Synechococcus_ANN_for_RCP4_5_scenario_NorESM1_ME_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP4.5 NorESM1-ME	Cells
Synechococcus_ANN_for_RCP8_5_scenario_GFDL_ESM2G_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP8.5 GFDL-ESM2G	Cells
Synechococcus_ANN_for_RCP8_5_scenario_HadGEM2_ES_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP8.5 HadGEM2-ES	Cells
Synechococcus_ANN_for_RCP8_5_scenario_IPSL_CM5A_MR_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP8.5 IPSL-CM5A-MR	Cells
Synechococcus_ANN_for_RCP8_5_scenario_MPI_ESM_LR_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP8.5 MPI-ESM-LR	Cells

Synechococcus_ANN_for_RCP8_5_scenario_NorESM1_ME_Model	Standard deviation from the mean global cell abundance; labeled after lineage, niche model, scenario, and Earth System Model: Synechococcus ANN RCP8.5 NorESM1-ME	Cells
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Project Information

Convergence: RAISE: Linking the adaptive dynamics of plankton with emergent global ocean biogeochemistry (Ocean Stoichiometry)

NSF Award Abstract:

Due to their sheer abundance and high activity, microorganisms have the potential to greatly influence how ecosystems are affected by changes in their environment. However, descriptions of microbial physiology and diversity are local and highly complex and thus rarely considered in Earth System Models. Thus, the researchers focus on a convergence research framework that can qualitatively and quantitatively integrate eco-evolutionary changes in microorganisms with global biogeochemistry. Here, the investigators will develop an approach that integrates the knowledge and tools of biologists, mathematicians, engineers, and geoscientists to understand the link between the ocean nutrient and carbon cycles. The integration of data and knowledge from diverse fields will provide a robust, biologically rich, and computationally efficient prediction for the variation in plankton resource requirements and the biogeochemical implications, addressing a fundamental challenge in ocean science. In addition, the project can serve as a road map for many other research groups facing a similar lack of convergence between biology and geoscience.

Traditionally, the cellular elemental ratios of Carbon, Nitrogen, and Phosphorus (C:N:P) of marine communities have been considered static at Redfield proportions but recent studies have demonstrated strong latitudinal variation. Such regional variation may have large - but poorly constrained - implications for marine biodiversity, biogeochemical functioning, and atmospheric carbon dioxide levels. As such, variations in ocean community C:N:P may represent an important biological feedback. Here, the investigators propose a convergence research framework integrating cellular and ecological processes controlling microbial resource allocations with an Earth System model. The approach combines culture experiments and omics measurements to provide a molecular understanding of cellular resource allocations. Using a mathematical framework of increasing complexity describing communicating, moving demes, the team will quantify the extent to which local mixing, environmental heterogeneity and evolution lead to systematic deviations in plankton resource allocations and C:N:P. Optimization tools from engineering science will be used to facilitate the quantitative integration of models and observations across a range of scales and complexity levels. Finally, global ocean modeling will enable understanding of how plankton resource use impacts Earth System processes. By integrating data and knowledge across fields, scales and complexity, the investigators will develop a robust link between variation in plankton C:N:P and global biogeochemical cycles.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1848576

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