Cell abundances for taxonomic groups from manually corrected live Imaging FlowCytobot (IFCB) analysis of water samples collected from surface and chlorophyll maximum depths during R/V Pt. Sur cruise PS 18-09 in the western Gulf of Mexico, Sept-Oct 2017

Website: https://www.bco-dmo.org/dataset/840060
Data Type: Cruise Results
Version: 1
Version Date: 2021-02-08

Project
» RAPID: Hurricane Impact on Phytoplankton Community Dynamics and Metabolic Response (HRR)

Contributors	Affiliation	Role
Campbell, Lisa	Texas A&M University (TAMU)	Principal Investigator
Henrichs, Darren W.	Texas A&M University (TAMU)	Co-Principal Investigator
Fiorendino, James	Texas A&M University (TAMU)	Contact
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Cell abundance data for taxonomic groups at seven stations from live Imaging FlowCytobot (IFCB) analysis of water samples collected from surface and chlorophyll maximum depths during R/V Pt. Sur PS 18-09, western Gulf of Mexico, Sept-Oct 2017. These data were inspected visually and manually corrected.

Table of Contents

Coverage

Spatial Extent: **N**:29.0649 **E**:-94.9 **S**:27.2286 **W**:-97.268
Temporal Extent: 2017-09-23 - 2017-10-01

Methods & Sampling

On each of 2 cruise legs 01 and 03, samples were collected at 7 stations (S01, S06, S11, S16, S21, SS and GI) from 2 depths [surface and chlorophyll maximum depth when possible; see HRR-bottle data]) by CTD-rosette. At each station, triplicate 5-ml samples pre-filtered through 150 µm Nitex were analyzed immediately with an onboard Imaging FlowCytobot. All image data can be viewed on the TOAST dashboard: https://toast.tamu.edu/timeline?dataset=HRR_cruise.

Image analysis and feature extraction were performed using software developed by Sosik and colleagues

which is available on github (https://github.com/hsosik/ifcb-analysis/). The automated classification approach of Sosik & Olson (2007), as modified and described by Anglès et al. (2019), was employed and the automated classification results were then inspected visually and **manually** corrected into a total of 102 categories that included 35 categories of diatoms, 30 categories of dinoflagellates, 10 categories of ciliates, 10 categories of flagellates, and 17 'others', which included filamentous cyanobacteria, freshwater chlorophytes, coccolithophorids, and small cells that could not be identified taxonomically from images (refer to Fiorendino et al. 2021. for more details).

For comparison with the Texas Observatory for Algal Succession Time series (TOAST), IFCB images were also classified automatically into one of 112 classes utilizing a custom convolutional neural network (**CNN**) trained on a curated set of images (Henrichs et al. 2021.). See related dataset.

Biomass for each image was estimated using the algorithm developed by Moberg & Sosik (2012) to calculate cellular volume from the extracted image features and then convert to total carbon per image (Menden-Deuer & Lessard 2000) and summed for each class. See related dataset.

Sampling locations:

Sample ID	Station	Leg	Location Lat ^{o}N/Long ^{o}W
L1_S01	S01	1	27.2286 -97.2686
L3_S01	S01	3	
L1_S06	S06	1	27.8358 -96.9874
L3_S06	S06	3	
L1_S11	S11	1	28.2614 -96.4129
L3_S11	S11	3	
L1_S16	S16	1	28.5366 -95.8656
L3_S16	S16	3	
L1_S21	S21	1	28.7644 -95.2978
L3_S21	S21	3	
L1_SS	SS	1	28.9600 -95.0946
L3_SS	SS	3	
L1_GI	GI	1	29.0649 -94.9000
L3_GI	GI	3	

Data Processing Description

- BCO-DMO Processing Notes:
- data submitted in Excel file "manual_count_ifcb.xlsx" sheet "Cell abundance" extracted to csv
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- rounded values to 2 decimal places

[table of contents | back to top]

Data Files

File
IFCB_manual_count.csv (Comma Separated Values (.csv), 13.36 KB) MD5:587f5889ed9994c9aa68ae10335cc514 Primary data file for dataset ID 840060

[table of contents | back to top]

Related Publications

Anglès, S., Jordi, A., Henrichs, D. W., & Campbell, L. (2019). Influence of coastal upwelling and river discharge on the phytoplankton community composition in the northwestern Gulf of Mexico. Progress in Oceanography, 173, 26–36. doi:10.1016/j.pocean.2019.02.001
Results

Fiorendino, J. M., Gaonkar, C. C., Henrichs, D. W., & Campbell, L. (2021). Drivers of microplankton community assemblage following tropical cyclones. Journal of Plankton Research, 45(1), 205–220. https://doi.org/10.1093/plankt/fbab073
Results

Henrichs, D. W., Anglès, S., Gaonkar, C. C., & Campbell, L. (2021). Application of a convolutional neural network to improve automated early warning of harmful algal blooms. Environmental science and pollution research international, 28(22), 28544–28555. https://doi.org/10.1007/s11356-021-12471-2
Results

Menden-Deuer, S., & Lessard, E. J. (2000). Carbon to volume relationships for dinoflagellates, diatoms, and other protist plankton. Limnology and Oceanography, 45(3), 569–579. doi:10.4319/lo.2000.45.3.0569
Methods

Moberg, E. A., & Sosik, H. M. (2012). Distance maps to estimate cell volume from two-dimensional plankton images. Limnology and Oceanography: Methods, 10(4), 278–288. doi:10.4319/lom.2012.10.278
Methods

Olson, R. J., & Sosik, H. M. (2007). A submersible imaging-in-flow instrument to analyze nano-and microplankton: Imaging FlowCytobot. Limnology and Oceanography: Methods, 5(6), 195–203. doi:10.4319/lom.2007.5.195
Methods

Sosik, H. M., & Olson, R. J. (2007). Automated taxonomic classification of phytoplankton sampled with imaging-in-flow cytometry. Limnology and Oceanography: Methods, 5(6), 204–216. doi:10.4319/lom.2007.5.204
Methods

[table of contents | back to top]

Related Datasets

IsRelatedTo

Campbell, L., Henrichs, D. W. (2021) **Biomass of taxonomic groups from manually corrected live**

Imaging FlowCytobot (IFCB) analysis of water samples collected from surface and chlorophyll maximum depths during R/V Pt. Sur cruise PS 18-09 in the western Gulf of Mexico, Sept-Oct 2017. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-08 doi:10.26008/1912/bco-dmo.840147.1 [view at BCO-DMO]

Campbell, L., Henrichs, D. W. (2021) **Cell abundances of taxonomic groups determined using a custom convolutional neural network from live Imaging FlowCytobot (IFCB) at seven stations sampled during R/V Pt. Sur cruise PS 18-09 in the western Gulf of Mexico, Sept-Oct 2017.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-08 doi:10.26008/1912/bco-dmo.840201.1 [view at BCO-DMO]

[table of contents | back to top]

Parameters

Parameter	Description	Units
Major_Category	5 major groups of microplankton	unitless
Class	Taxonomic names of the species or genus (if known) or group identified	unitless
L1GI_1	Cell abundance of class at Leg 1 station GI; replicate 1	cells/milliliter
L1GI_2	Cell abundance of class at Leg 1 station GI; replicate 2	cells/milliliter
L1GI_3	Cell abundance of class at Leg 1 station GI; replicate 3	cells/milliliter
L1SS_1	Cell abundance of class at Leg 1 station SS; replicate 1	cells/milliliter
L1SS_2	Cell abundance of class at Leg 1 station SS; replicate 2	cells/milliliter
L1SS_3	Cell abundance of class at Leg 1 station SS; replicate 3	cells/milliliter
L1S21_1	Cell abundance of class at Leg 1 station S21; replicate 1	cells/milliliter
L1S21_2	Cell abundance of class at Leg 1 station S21; replicate 2	cells/milliliter
L1S21_3	Cell abundance of class at Leg 1 station S21; replicate 3	cells/milliliter
L1S16_1	Cell abundance of class at Leg 1 station S16; replicate 1	cells/milliliter
L1S16_2	Cell abundance of class at Leg 1 station S16; replicate 2	cells/milliliter
L1S16_3	Cell abundance of class at Leg 1 station S16; replicate 3	cells/milliliter
L1S11_1	Cell abundance of class at Leg 1 station S11; replicate 1	cells/milliliter
L1S11_2	Cell abundance of class at Leg 1 station S11; replicate 2	cells/milliliter
L1S11_3	Cell abundance of class at Leg 1 station S11; replicate 3	cells/milliliter
L1S06_1	Cell abundance of class at Leg 1 station S06; replicate 1	cells/milliliter
L1S06_2	Cell abundance of class at Leg 1 station S06; replicate 2	cells/milliliter
L1S06_3	Cell abundance of class at Leg 1 station S06; replicate 3	cells/milliliter
L1S01_1	Cell abundance of class at Leg 1 station S01; replicate 1	cells/milliliter
L1S01_2	Cell abundance of class at Leg 1 station S01; replicate 2	cells/milliliter
L1S01_3	Cell abundance of class at Leg 1 station S01; replicate 3	cells/milliliter
L3GI_1	Cell abundance of class at Leg 3 station GI; replicate 1	cells/milliliter
L3GI_2	Cell abundance of class at Leg 3 station GI; replicate 2	cells/milliliter
L3GI_3	Cell abundance of class at Leg 3 station GI; replicate 3	cells/milliliter
L3SS_1	Cell abundance of class at Leg 3 station SS; replicate 1	cells/milliliter
L3SS_2	Cell abundance of class at Leg 3 station SS; replicate 2	cells/milliliter
L3SS_3	Cell abundance of class at Leg 3 station SS; replicate 3	cells/milliliter
L3S21_1	Cell abundance of class at Leg 3 station S21; replicate 1	cells/milliliter

L3S21_2	Cell abundance of class at Leg 3 station S21; replicate 2	cells/milliliter
L3S21_3	Cell abundance of class at Leg 3 station S21; replicate 3	cells/milliliter
L3S16_1	Cell abundance of class at Leg 3 station S16; replicate 1	cells/milliliter
L3S16_2	Cell abundance of class at Leg 3 station S16; replicate 2	cells/milliliter
L3S16_3	Cell abundance of class at Leg 3 station S16; replicate 3	cells/milliliter
L3S11_1	Cell abundance of class at Leg 3 station S11; replicate 1	cells/milliliter
L3S11_2	Cell abundance of class at Leg 3 station S11; replicate 2	cells/milliliter
L3S11_3	Cell abundance of class at Leg 3 station S11; replicate 3	cells/milliliter
L3S06_1	Cell abundance of class at Leg 3 station S06; replicate 1	cells/milliliter
L3S06_2	Cell abundance of class at Leg 3 station S06; replicate 2	cells/milliliter
L3S06_3	Cell abundance of class at Leg 3 station S06; replicate 3	cells/milliliter
L3S01	Cell abundance of class at Leg 3 station S01	cells/milliliter

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Image FlowCytobot (McLane Research Laboratories, Inc.)
Generic Instrument Name	Imaging FlowCytobot
Generic Instrument Description	The Imaging FlowCytobot (IFCB) is an in-situ automated submersible imaging flow cytometer that generates images of particles in-flow taken from the aquatic environment. https://mclanelabs.com/imaging-flowcytobot/

Dataset-specific Instrument Name	
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Used to collect samples
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

PS1809

Website	https://www.bco-dmo.org/deployment/784313
Platform	R/V Point Sur
Start Date	2017-09-22
End Date	2017-10-03
Description	HRR study with three legs. Chief Scientists: Steve DiMarco (Leg 1); Kristen Thyng (Leg 2); Lisa Campbell (Leg 3). R2R Cruise Page: https://www.rvdata.us/search/cruise/PS1809

[table of contents | back to top]

Project Information

RAPID: Hurricane Impact on Phytoplankton Community Dynamics and Metabolic Response (HRR)

Coverage: Texas coast

NSF Award Abstract:
Hurricane Harvey is the strongest hurricane to hit the Texas coast in decades and the resulting tidal surges, flooding and terrestrial runoff have had a severe impact on the coastal ocean. The effects on the phytoplankton, the first link in the food chain, may be unprecedented. To determine how the phytoplankton community will respond to such drastic changes in salinity, nutrient inputs, and potential toxins, immediate and continuous sampling is the only way to fully capture the effects and to identify when conditions return to "normal". An automated, continuous phytoplankton imaging instrument that is deployed on the Texas coast records images of the phytoplankton and permits calculation of the abundance of different species. Together with molecular information on the genes that have been "turned on", or expressed, outcomes of this project will help determine the responses of individual types of phytoplankton. Extreme storms are expected to increase in frequency with future climate change, so the responses identified now will be valuable in predicting how such events will affect these primary producers, which in turn support most of the food webs in marine ecosystems, in the future.

High temporal resolution observations from the Imaging FlowCytobot (IFCB) have revealed that hurricanes in the Gulf of Mexico cause drastic changes in the phytoplankton community structure. The objectives of this RAPID project are: 1) to characterize the dynamics of the phytoplankton species in relation to the environmental variables along the Texas coast; 2) to assess the short and long-term changes in the phytoplankton community; and 3) to identify the strategies of the phytoplankton community for resource acquisition. To accomplish these objectives, this project will utilize IFCB time series to follow phytoplankton community structure during the recovery period from Hurricane Harvey. In addition, two RAPID response cruises (in late September and early October) to sample at 5 sites along a transect from Galveston to Port Aransas, TX. At each station, CTD profiles and water samples from surface and the chlorophyll maximum will be collected for nutrients, carbonate chemistry, and RNA sequencing for metatranscriptomic analysis. Metatranscriptomics can provide an indication of the metabolic strategies employed and functional relationships within the plankton community in response to changes in the environment. The advantage of a metatranscriptomic approach is that the entire molecular response to the environment is captured. So, while the response of phytoplankton to increased nutrient inputs from floodwater runoff is targeted, the responses to other environmental stresses (toxics, hypoxia, acidification) are also captured. Analyses of this time series using multivariate statistical techniques, such as principal component analysis (PCA), and network analysis, a powerful technique for identifying potential interactions among taxa, will provide insights on the environmental factors and metabolic responses structuring the community during the aftermath of the hurricane.

Related data from the The Texas Observatory for Algal Succession Time-Series (TOAST) can be found at the following: https://toast.tamu.edu/timeline?dataset=HRR_Cruise

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1760620

[table of contents | back to top]