**NOAA-CalCOFI Ocean Genomics (NCOG): Six years and counting**

Robert H. Lampe\(^1,2\), Chase C. James\(^1,2\), Lisa Zeigler Allen\(^1,2\), Ariel J. Rabines\(^1,2\), Ralf Goericke\(^1\), Kelly D. Goodwin\(^3\), Andrew E. Allen\(^1,2\)

\(^1\)Scripps Institution of Oceanography, UCSD \hspace{5mm} \(^2\)J. Craig Venter Institute \hspace{5mm} \(^3\)Atlantic Oceanographic and Meteorological Laboratory, NOAA

The NOAA-CalCOFI Ocean Genomics (NCOG) project has been collecting DNA and RNA on all CalCOFI cruises since 2014.

**Methods**

Seawater collection at 4 depths:
- 10m (DNA+RNA)
- Chl max (DNA+RNA)
- 170m (RNA)
- 515m (RNA)

Semi-automated nucleic acid extraction and library preparation


**Science Highlight**

James et al. (in prep) Ecological response of the pelagic ocean microbiome to cross shelf variation in physical forcing in a coastal upwelling biome

For different microbial taxonomic groups, cross-shore gradients in community structure and diversity are most common. In nearly all examined groups, nitracline depth and chlorophyll a are the strongest predictors of community structure and diversity.

**Science Highlight**

Zeigler Allen et al. (in prep) Regional structuring of the pelagic ocean microbiome in the Southern California Current Ecosystem

Total diatom:*Prochlorococcus* mRNA is strongly correlated with net primary productivity (NPP) and the predicted f-ratio. Therefore, this mRNA ratio correlates with expected patterns of nutrient utilization with *Prochlorococcus* and diatoms dominating at stations more favorable for regenerated or new production, respectively.

**Interested in using genomics data? Get in touch.**

aallen@ucsd.edu

sioweb.ucsd.edu/labs/aallen/

**Open protocols!**

protocols.io

protocols.io/workspaces/ae-allen-lab

GitHub

github.com/AllenLab