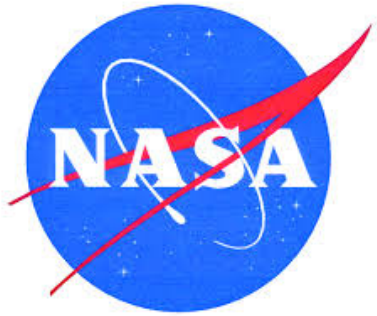


BOEM
Bureau of Ocean Energy Management

MARINE BIODIVERSITY OBSERVATION NETWORK

SANTA BARBARA CHANNEL

Marine Science Institute
University of California Santa Barbara

Who we are

Principal/Associate Investigators

Marine Science Institute
Robert Miller, Andrew Rassweiler, Daniel Reed, Milton Love

Ecology Evolution and Marine Biology
Craig Carlson, Deborah Iglesias-Rodriguez, Doug McCauley

Geography
David Siegel, Phaedon Kyriakidis

Electrical and Computer Engineering
BS Manjunath

USGS
Kevin Lafferty

UCSD - SIO
John Hildebrand

NOAA – NMFS SWFSC
Andrew Thompson

Who we are

Partners

Plumes and Blooms

Channel Islands National Marine Sanctuary

Southern California Coastal Water Research Project

Santa Barbara Coastal Long Term Ecological Research Program

Southern California Coastal Ocean Observing System (SCCOOS)

Channel Islands National Park

Gray Whales Count

CalCOFI

MARINE BIODIVERSITY OBSERVATION NETWORK
SANTA BARBARA CHANNEL

Goals:

1. Integrate biodiversity data to enable inferences about regional biodiversity

2. Develop advanced methods using imagery and genomics for monitoring biodiversity

3. Implement a tradeoff framework that optimizes allocation of sampling effort

PISCO
Since 1999, frequency varies
23 sites, random transects
Variable taxonomic resolution

NPS KFM
Since 1991, biannual
38 sites, islands fixed/random
Variable taxonomic resolution

SBC LTER
Since 2000, annual
11 reefs, mainland conc.
High taxonomic resolution

USGS SNI
Since 1980, semiannual
5 transects, San Nicolas Is.
Variable taxonomic resolution

Primary Data
4 projects,
16 time series

Data cleaning

Filter records

Harmonize design
- Areas, depth ranges
- Frequency
- Fixed vs random

Harmonize taxonomy
- Std codes (WoRMS)
- Resolve ranks
- Life stage
- Closed/open spp list

Quality Control

Cleaned Data
3 time series

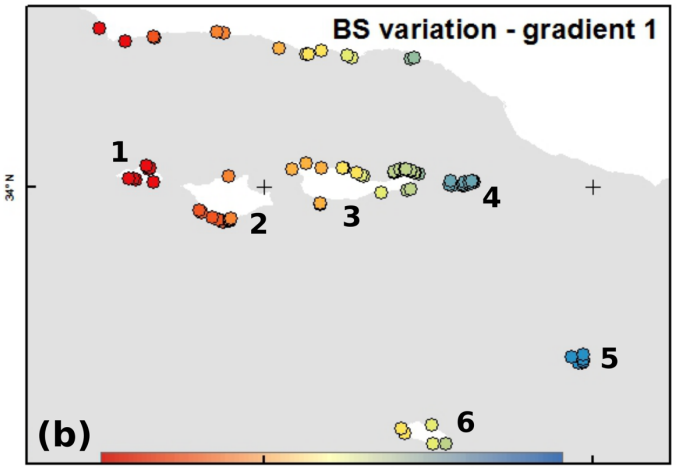
SBC MBON Analysis
- Species distribution
- Community structure
- Environmental drivers
- Species spatial and temporal change

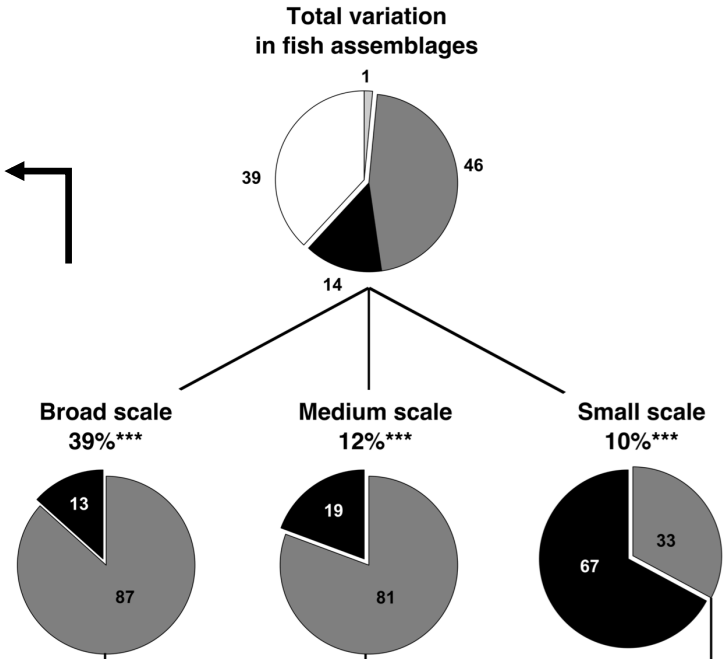
MBON Products

Secondary Data
Biodiversity indices

Uncovering the complex and multiscale drivers of kelp forest communities

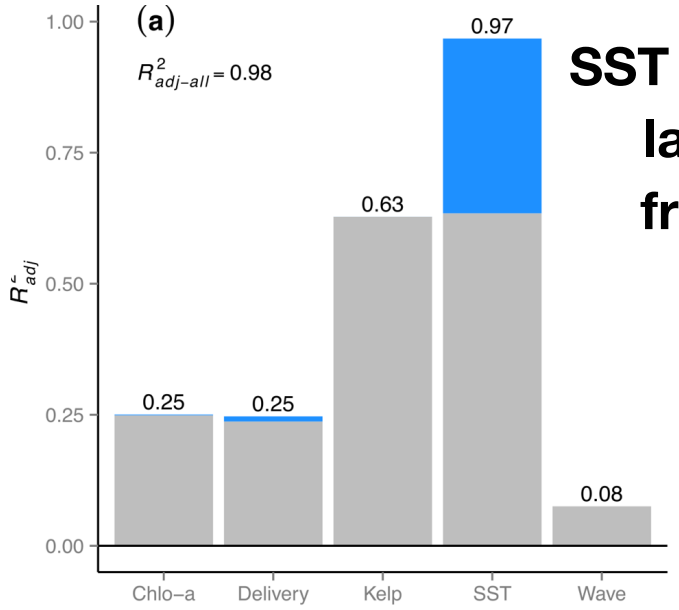
What are the most important scales of variation?





Thomas Lamy

What environmental factor(s) underlie each spatial scale?



SST explains largest fraction

Lamy et al., in review, *Oecologia*

Species Archetype Modelling (SAM) for ecological forecasting

Modelling species response to environmental gradients and reducing dimensionality

Rhiannon Rognstad

DATA MATRICES

Species

Survey

Environment

Survey

GLMs

$E(Y|1) = g^{-1}(\beta|0 + X|1\,\beta|1 + \ldots + X|p\,\beta|p)$

$E(Y|2) = g^{-1}(\beta|0 + X|1\,\beta|1 + \ldots + X|p\,\beta|p)$

$E(Y|3) = g^{-1}(\beta|0 + X|1\,\beta|1 + \ldots + X|p\,\beta|p)$

$E(Y|N) = g^{-1}(\beta|0 + X|1\,\beta|1 + \ldots + X|p\,\beta|p)$

CLUSTERING/FITTING

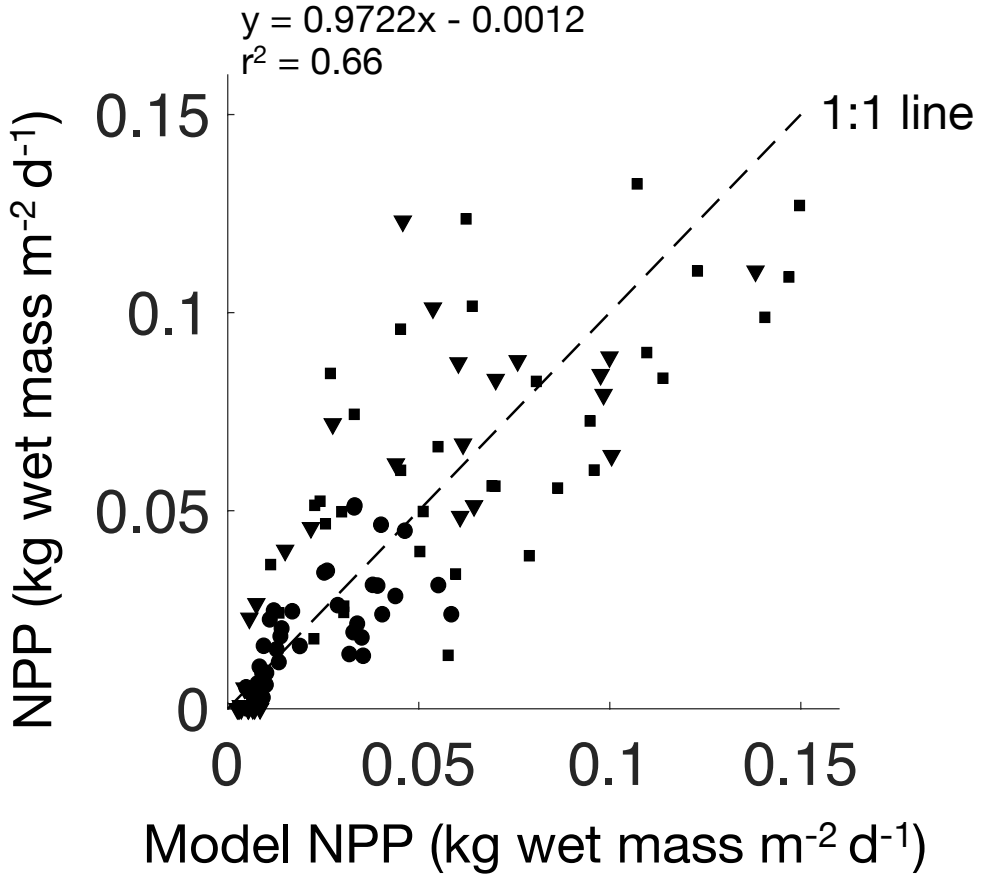
OUTPUT

Species	Arch	Prob
A	1	0.02
A	2	0.97
A	3	0.01
…		
N	3	0.95

	Envt1	Envt2	Envt3
Arch1	-0.9	0.5	-0.3
Arch2	0.5	0.9	0.2
Arch3	0.5	-0.2	0

SAM method: Dunstan et al. 2011, 2013

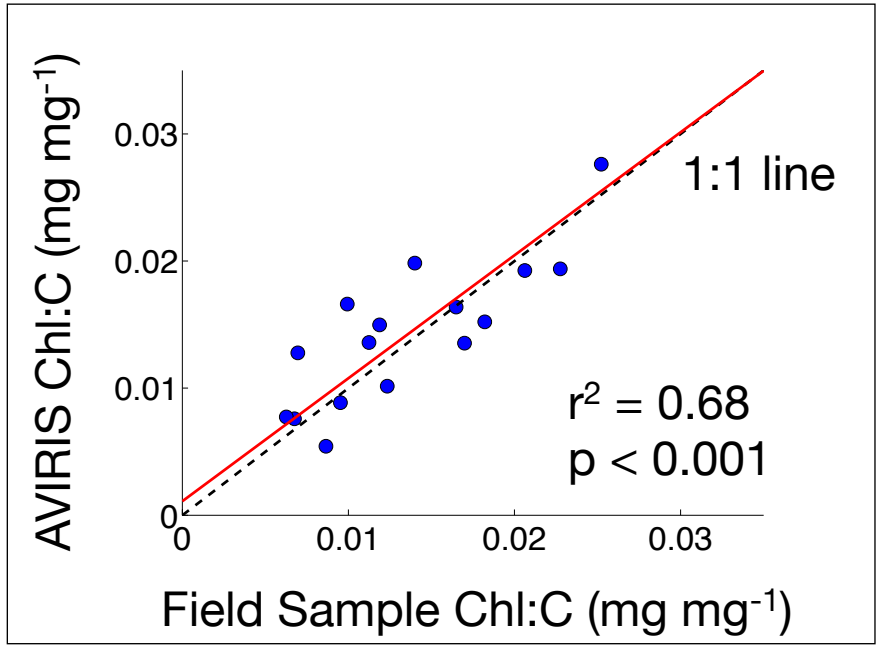
Landsat Kelp Forest Canopy Biomass & NPP



Cavanaugh et al 2010, 2011, 2013, Bell et al. 2015 J Biogeography, Bell et al. L&O in review

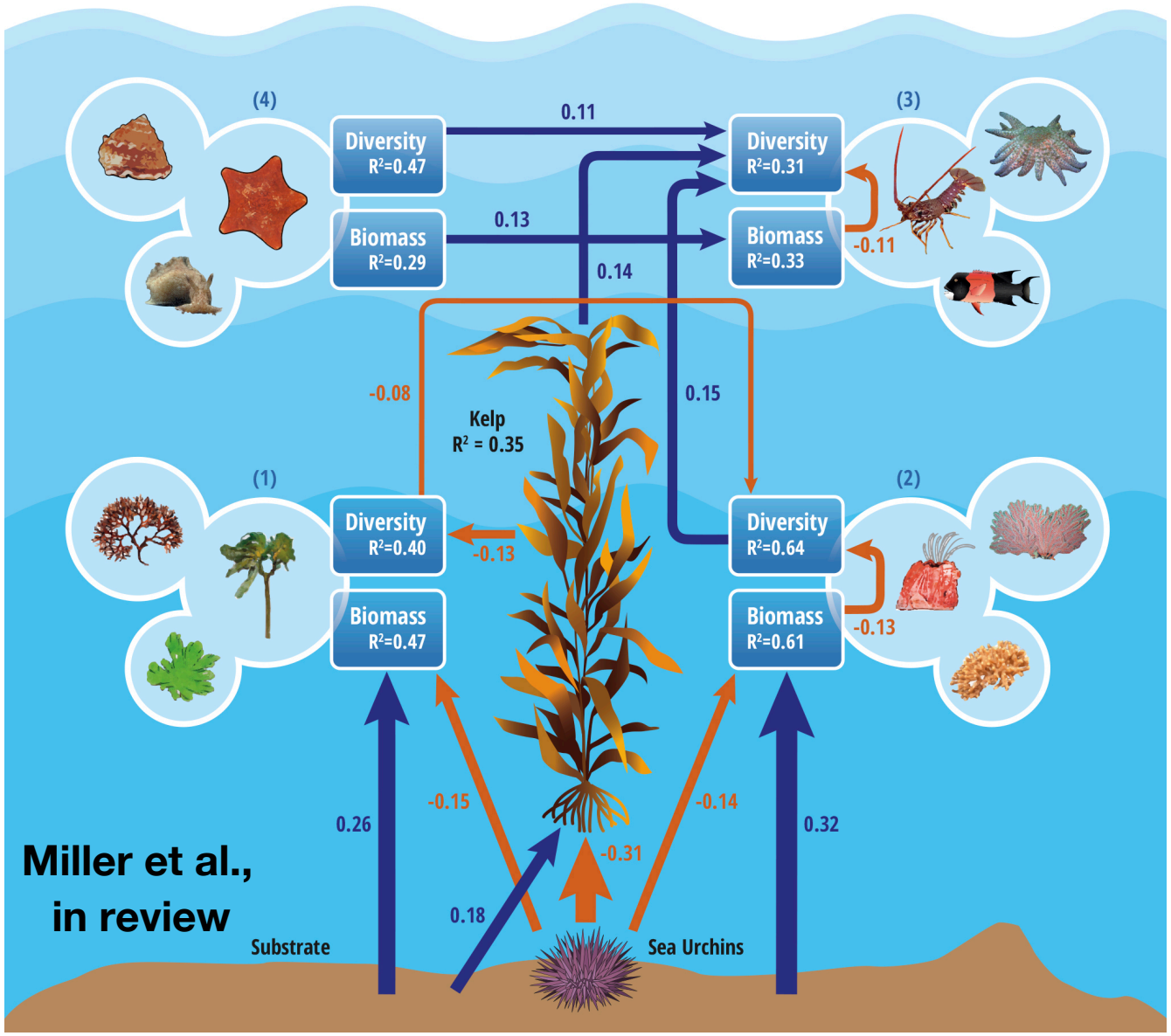
Hyperspectral aerial flights conducted 3x year^{-1} in 2013 – 2015 using the AVIRIS sensor as part of the HyspIRI preparatory campaign

Chl:C estimated from hyperspectral images closely resembles Chl:C measured in the laboratory



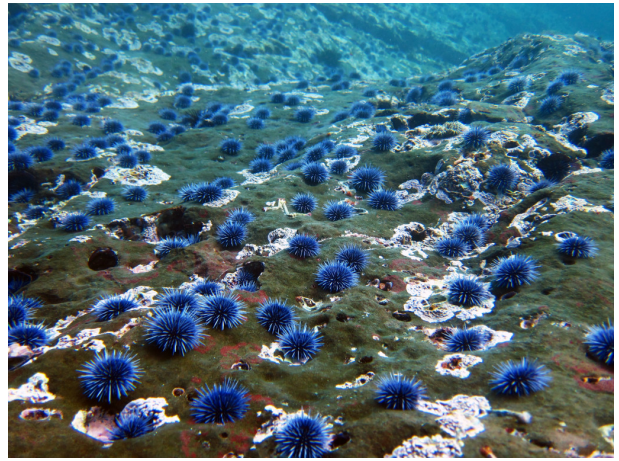
Bell et al. 2015 Remote Sensing Env. and Bell et al. *in prep*

Giant kelp is a foundation species that positively affects reef biodiversity directly and indirectly

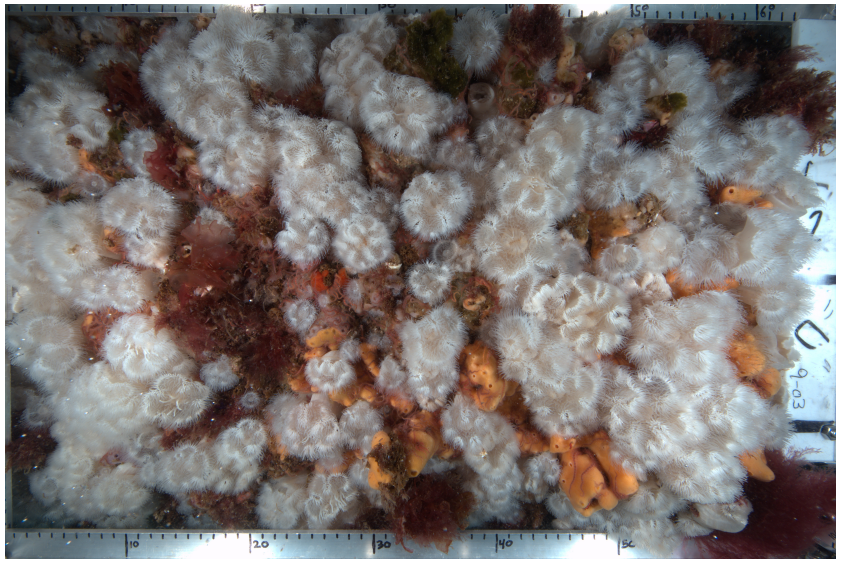


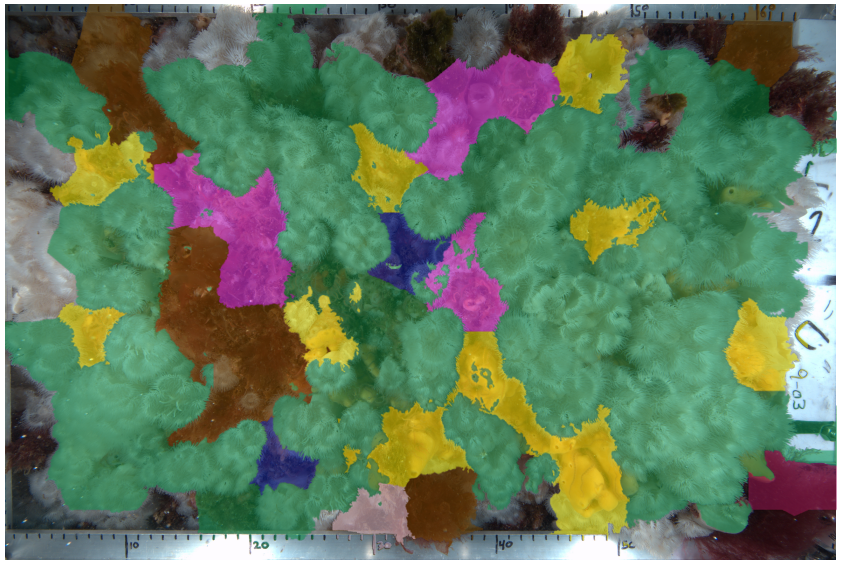
Kelp forest

Urchin barren



Deep learning for image analysis





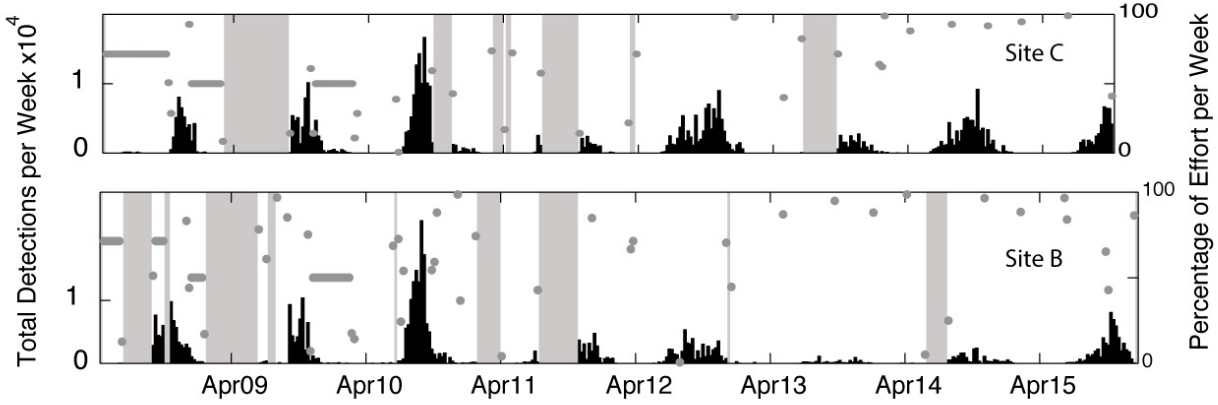
- Scalable deployment of CNN models
- Hierarchical models
  - Taxonomic: Genus -> Species
  - Ontological: Substrate -> Exact object

BisQue

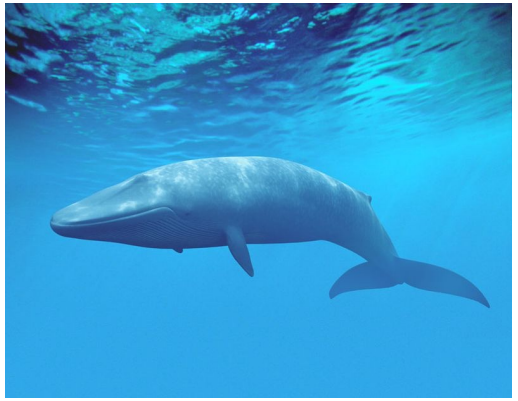
Acoustic Detection of Marine Mammals

Warm anomaly in 2013-2015 caused baleen whales to move into SBC

Hildebrand et al. *in prep*



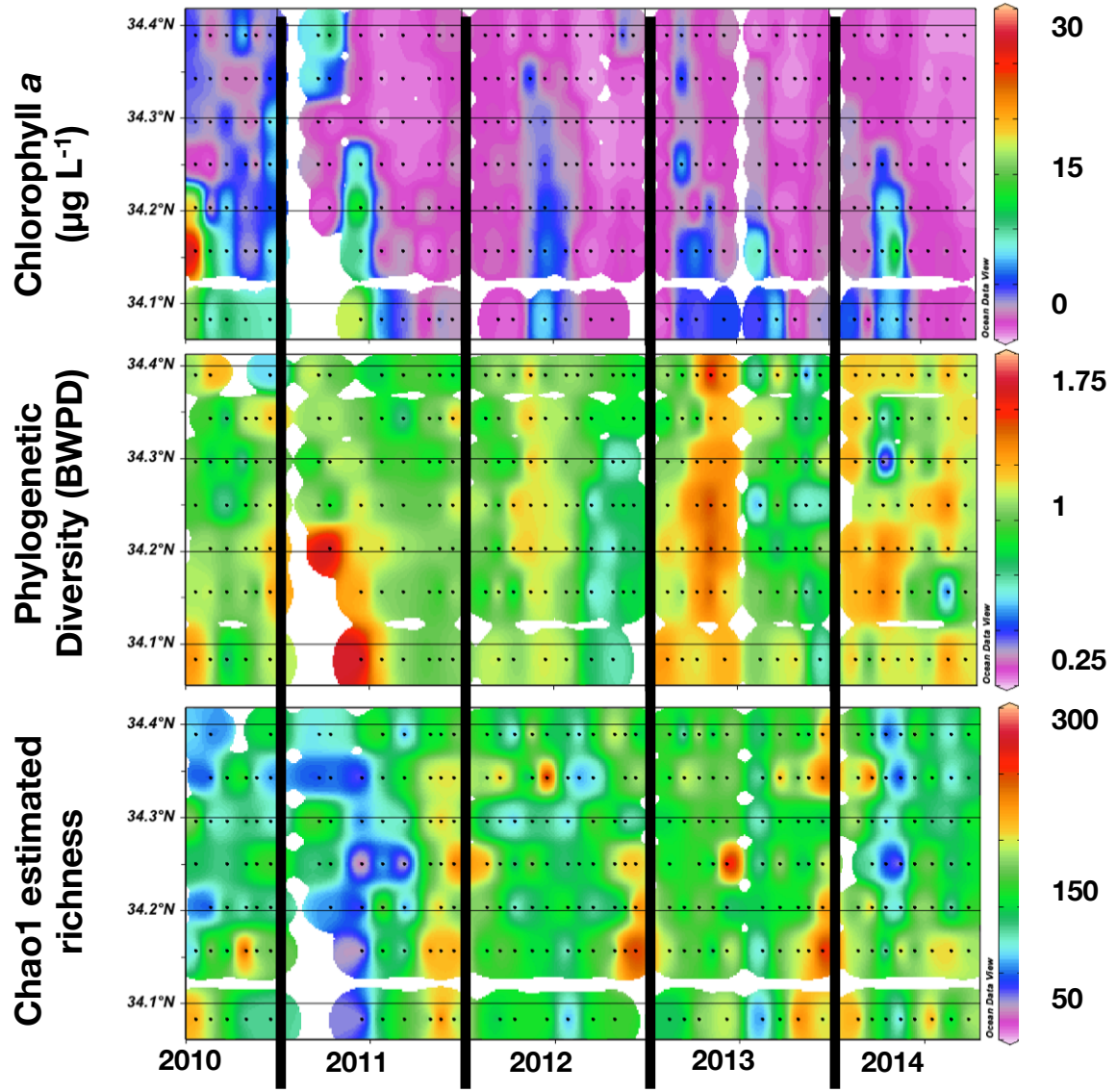
Blue Whale



Fin Whale

Prokaryote diversity and richness show distinct temporal patterns in the surface SBC

South → North, or islands → mainland

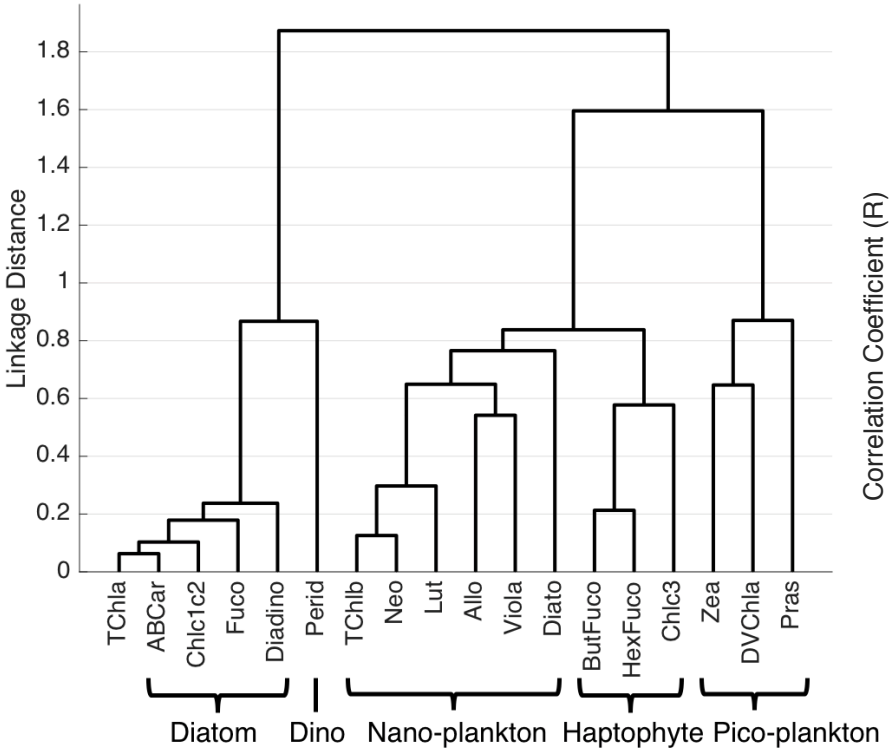


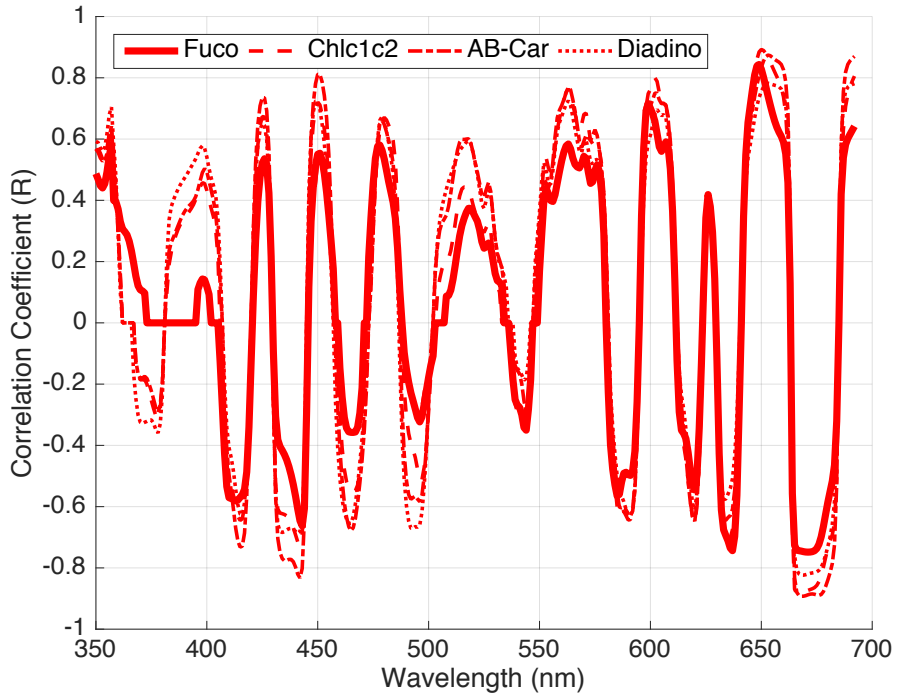
- Time-series from 2010 –2014
- Bacteria and archaea from 16S rRNA gene (V4 region)
- 578 samples from 43 cruises sequenced

Wear et al. *in prep*

Modeling Phytoplankton Pigment "Communities"

- Derivative analysis of phytoplankton absorption spectra isolates absorption features with robust relationships to phytoplankton pigments and communities
- Pigment communities (defined with cluster, EOF analyses) can be modeled using relationships with spectral absorption signatures



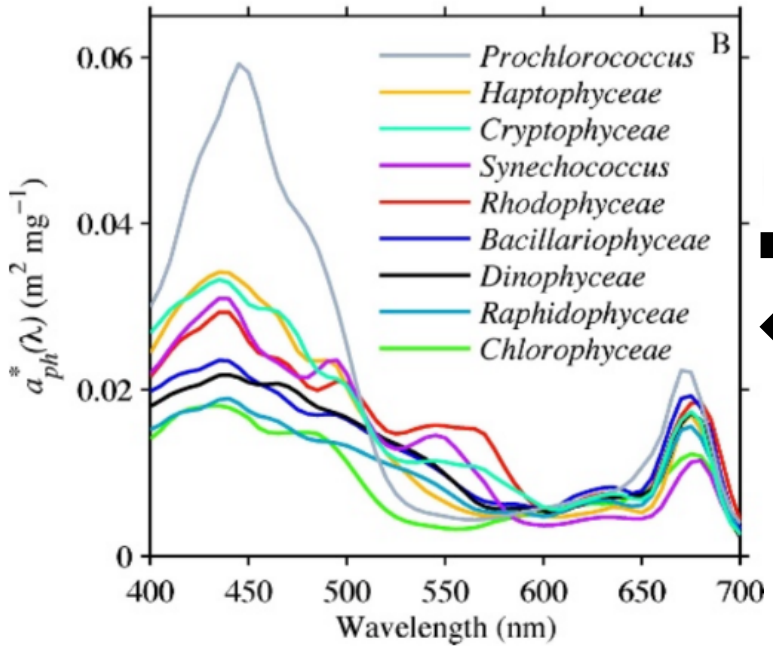


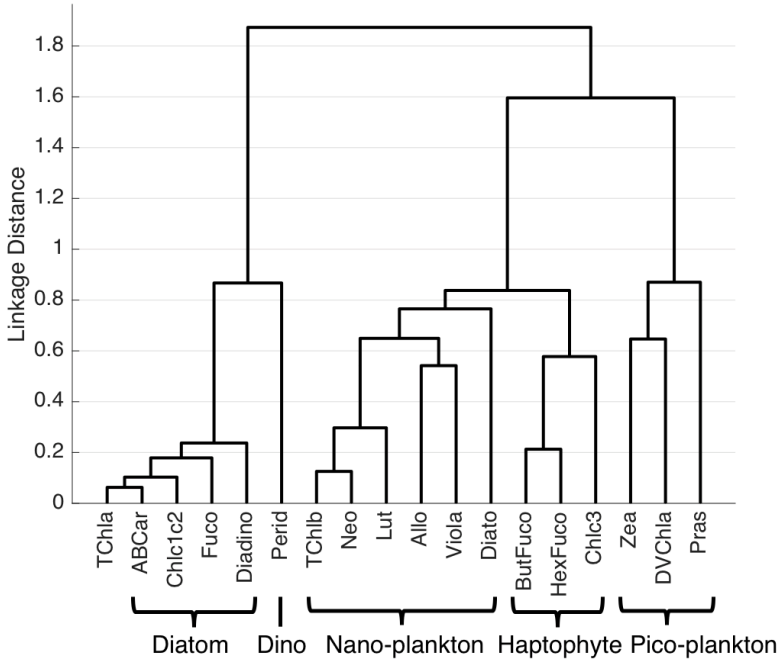
Model Retrievals	R^2
TChlb (green algae)	0.815
HexFuco (haptophytes)	0.733
Fuco (diatoms)	0.856
Perid (dinoflagellates)	0.887
Pigment EOF Mode 1 (Early upwelling mixed bloom)	0.884
Pigment EOF Mode 2 (Diatoms vs. mixed nano-/pico-)	0.852
Pigment EOF Mode 3 (Pico-plankton vs. haptophytes)	0.454
Pigment EOF Mode 4 (Dinoflagellates vs. mixed diatoms/haptophytes)	0.809

*Catlett and Siegel, *in prep.*

Next Steps

- Apply model to hyperspectral remote sensing reflectance observations from AVIRIS and Plumes and Blooms archive
- Incorporate Next-Gen Sequencing observations for validation of phytoplankton community composition retrievals from remote sensing algorithms





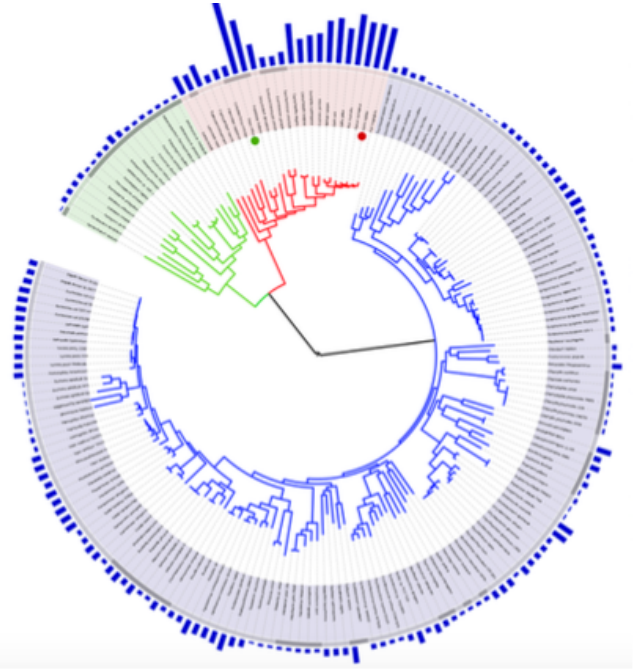
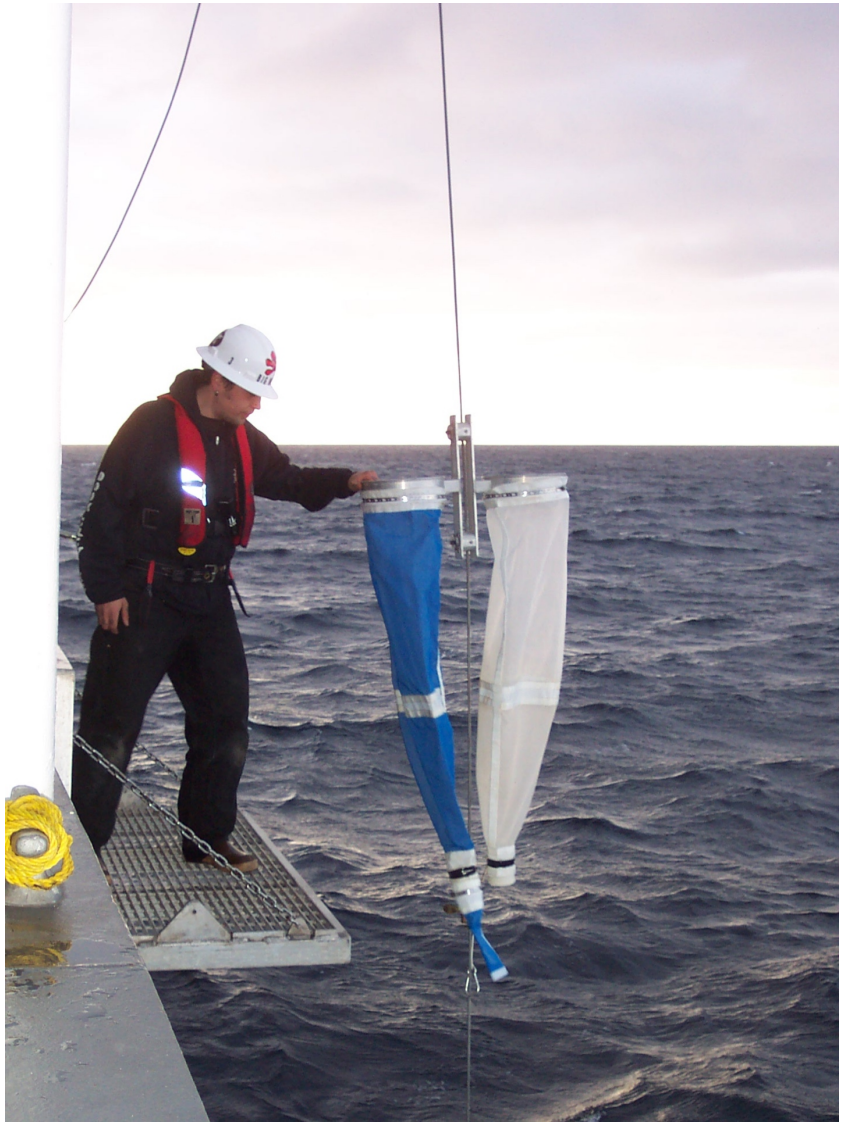


*Figure adapted from Dierssen et al. 2006 (left), Catlett and Siegel *in prep*. (center), and Ciccarelli et al. 2006 (right)

Metabarcoding to identify pelagic ichthyoplankton



Dovi Kacev

- ***Collected 74 samples from three coastal cruises***
- ***Morphologically ID all fish***
- ***Confirmed ID with Sanger sequencing***
- ***In process of bulk tissue sequencing***
- ***Working with Sanctuaries MBON team***