

From fixed functional types to flexible models of microbial community structure in the oceans

Michael Raghib, Stephanie Dutkiewicz,
Michael J. Follows and Simon A. Levin

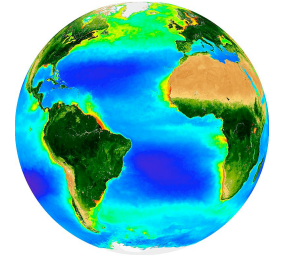


National Science Foundation
WHERE DISCOVERIES BEGIN

GORDON AND BETTY
MOORE
FOUNDATION

Creating positive outcomes for future generations

Outline



Classical NPZD models of microbial aquatic communities

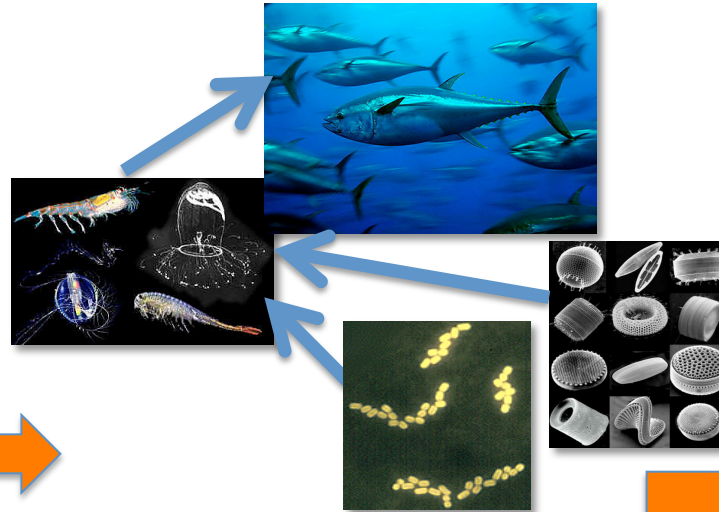
`Emergent' Functional Types, a new modeling approach.

Current directions and project objectives.

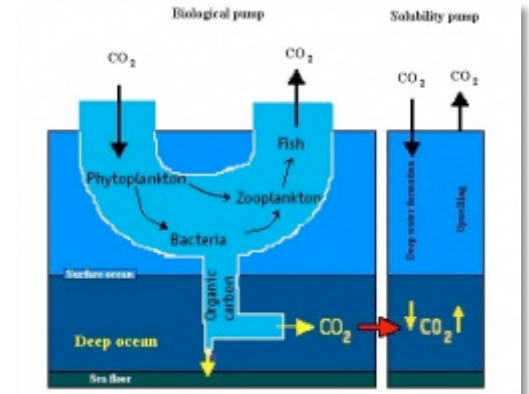
Ocean Ecosystems

Community composition and interactions

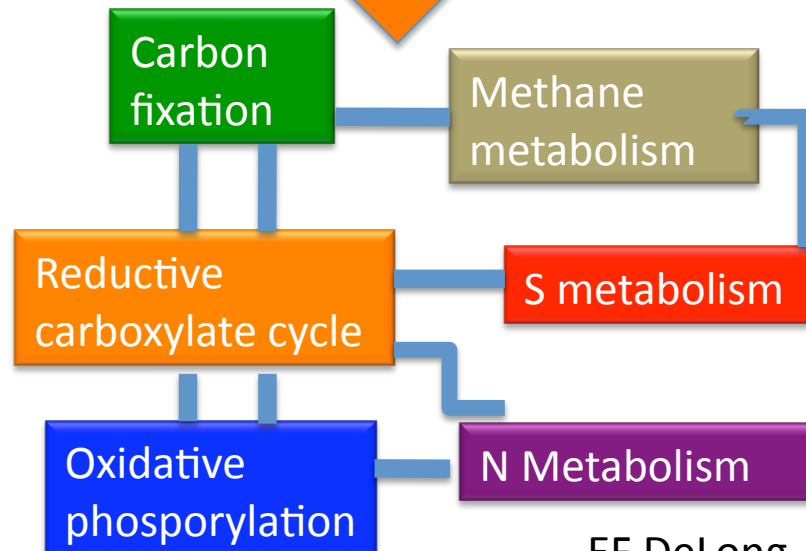
Microbial
Community DNA



Ecosystem functions



Community
Metabolism



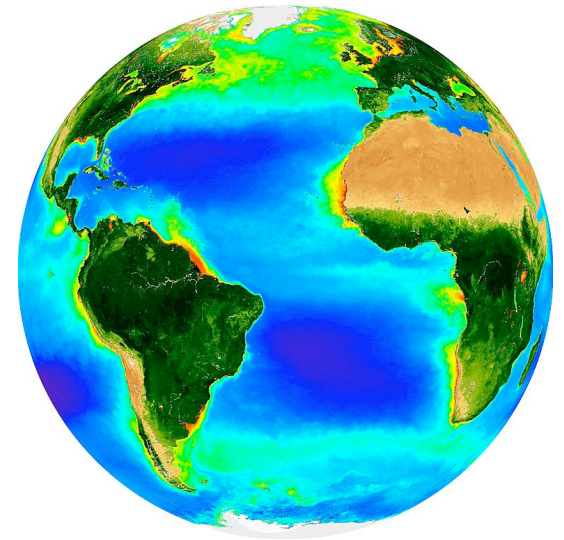
EF DeLong, *Nature* **459**, 200 (2009)

Patterns of interest

Community composition and biomass distribution along environmental gradients

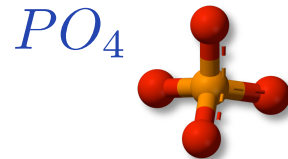
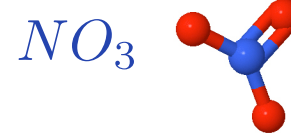
Sheldon size spectra.

Redfield Ratios C:N:P.



Chl a satellite image from SeaWiFS (Boreal winter)
<http://oceancolor.gsfc.nasa.gov/SeaWiFS/>

NPZD Models

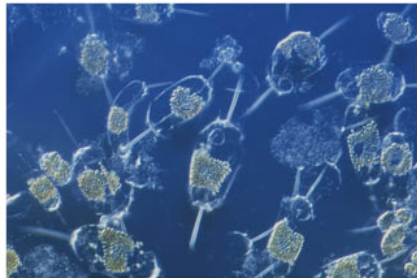


LIGHT

Nutrients

Uptake

Phytoplankton

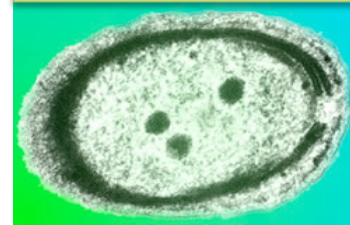


mortality

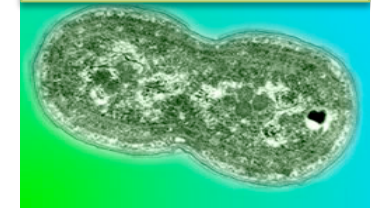
Diatoms



Prochlorococcus



Synechococcus



Coccolitophores



Remineralization

Grazing

Zooplankton

mortality

Small-copepodites



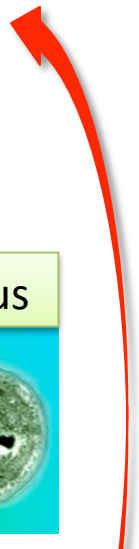
Medium -copepods



Large -krill

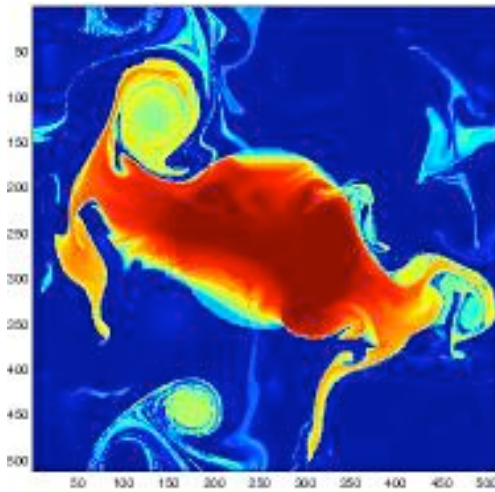


**Detritus
other microbes**

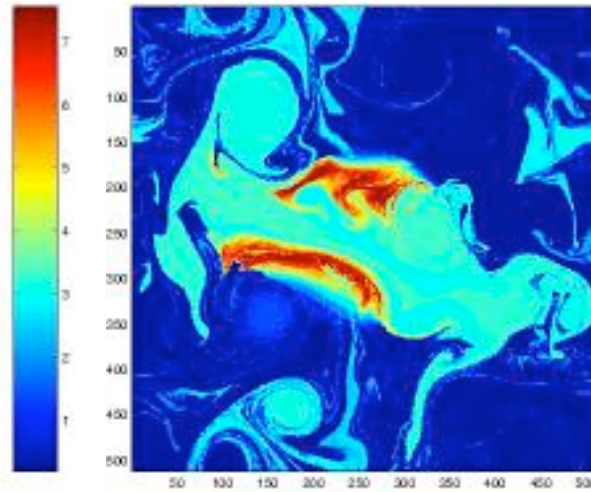


NPZ coupled with CFD

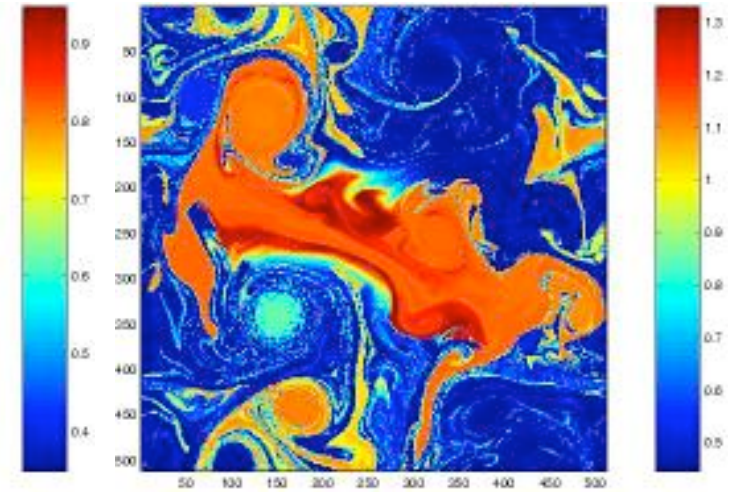
Nutrient field



Phytoplankton



Zooplankton



Pasquero, Bracco, Provenzale, *Shallow Flows*, (2004)

Issues with classical NPZD models

Who decides what constitutes a functional type?

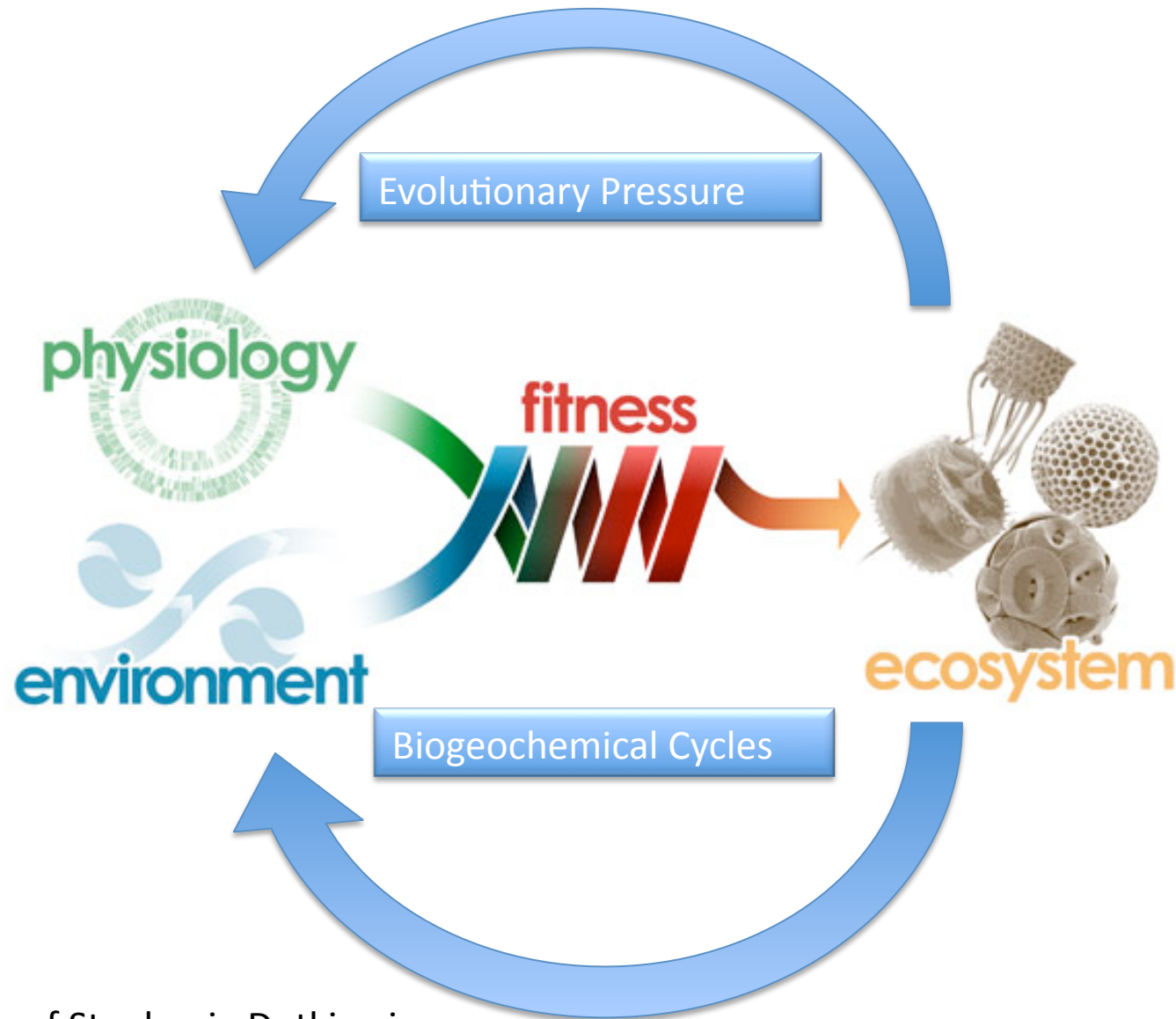
How can one deal with the problem of the diversity that we don't know about, particularly when it is related to variations in metabolism?

What determines the functional forms that control the rates in NPZD models?

What about macroscopic patterns that we yet don't know about (e.g. metagenomics/ new cultivation methods), can theory predict them?

Tracer transport modeling of plankton, many of these organisms actively aggregate.

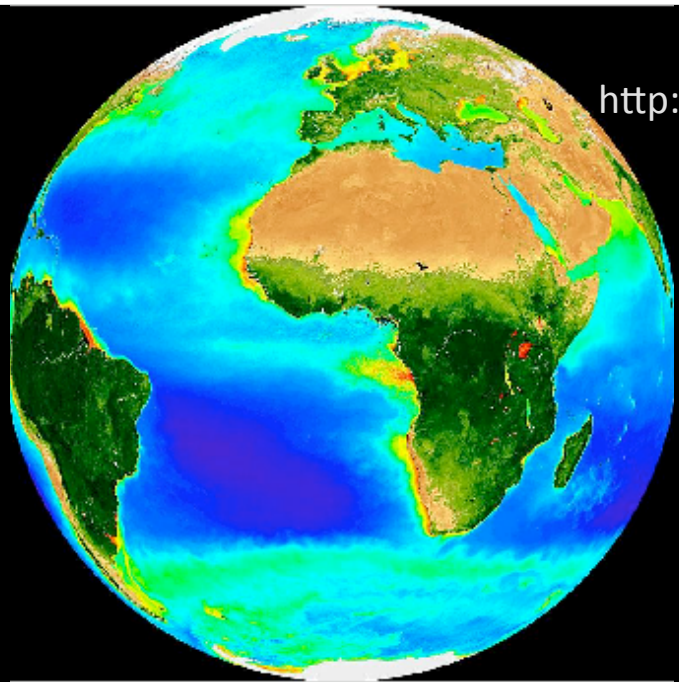
‘Everything is everywhere but the environment selects’
L. Baas-Becking



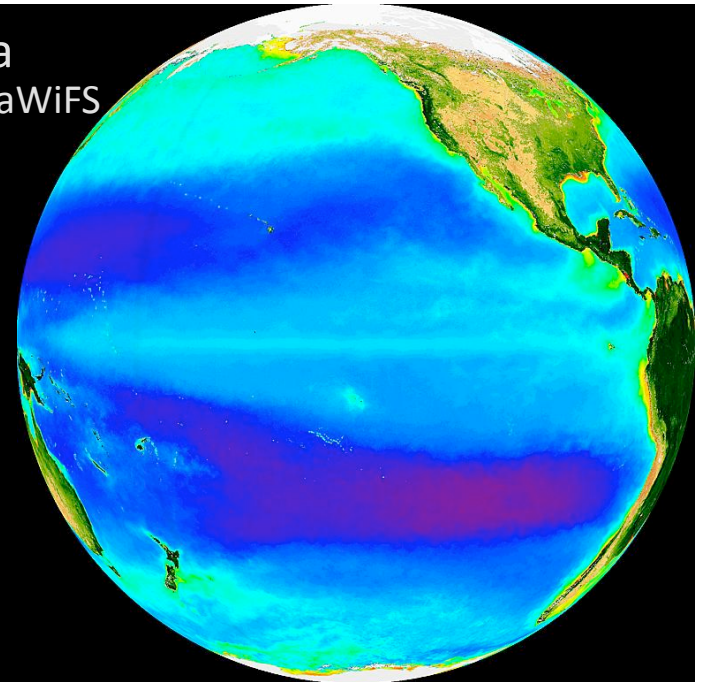
Slide courtesy of Stephanie Dutkiewicz

Towards a Trait-Based Ecology, the MIT-DARWIN Model

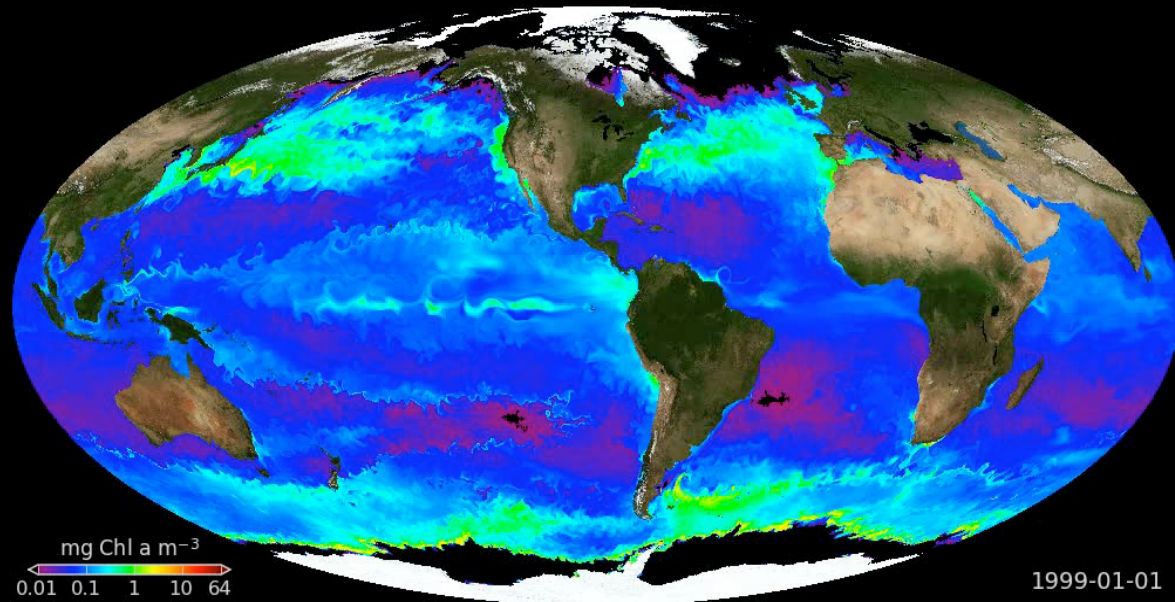
$$\begin{aligned}
 \frac{\partial N_i}{\partial t} &= \underbrace{-\nabla \cdot (\mathbf{u} N_i) + \nabla \cdot (K \nabla N_i)}_{\text{u and K from ECCO2 GCM}} - \underbrace{\sum_j \mu_j P_j}_{\text{Phyto growth}} \underbrace{R_{ij}}_{\text{Remineralization \& other sources}} + S_{N_i} \\
 \frac{\partial P_j}{\partial t} &= -\nabla \cdot (\mathbf{u} P_j) + \nabla \cdot (K \nabla P_j) + \underbrace{\mu_j P_j}_{\text{Growth}} - \underbrace{m_j^P P_j}_{\text{Mortality}} - \underbrace{\sum_k g_{jk} \frac{P_j Z_{k,i=1}}{P_j + k_j^P}}_{\text{Grazing}} - \underbrace{\frac{w_j^P \partial P_j}{\partial z}}_{\text{Sinking}} \\
 \frac{\partial Z_{ki}}{\partial t} &= -\nabla \cdot (\mathbf{u} Z_{ki}) + \nabla \cdot (K \nabla Z_{ki}) - \underbrace{m_k^Z Z_{ki}}_{\text{Remineralization}} + \underbrace{\sum_k g_{jk} \frac{P_j R_{ij}}{P_j + k_j^P}}_{\text{Sinking}} \\
 \frac{\partial PO_i}{\partial t} &= -\nabla \cdot (\mathbf{u} PO_i) + \nabla \cdot (K \nabla PO_i) - \underbrace{r_{PO_i} PO_i}_{\text{Remineralization}} - \underbrace{w_{POM} \frac{\partial PO_i}{\partial z}}_{\text{Sinking}} + S_{PO_i} \\
 \frac{\partial DO_i}{\partial t} &= -\nabla \cdot (\mathbf{u} DO_i) + \nabla \cdot (K \nabla DO_i) - r_{DO} DO_i + S_{DO_i}
 \end{aligned}$$



Chl a from SeaWiFS data
<http://oceancolor.gsfc.nasa.gov/SeaWiFS>

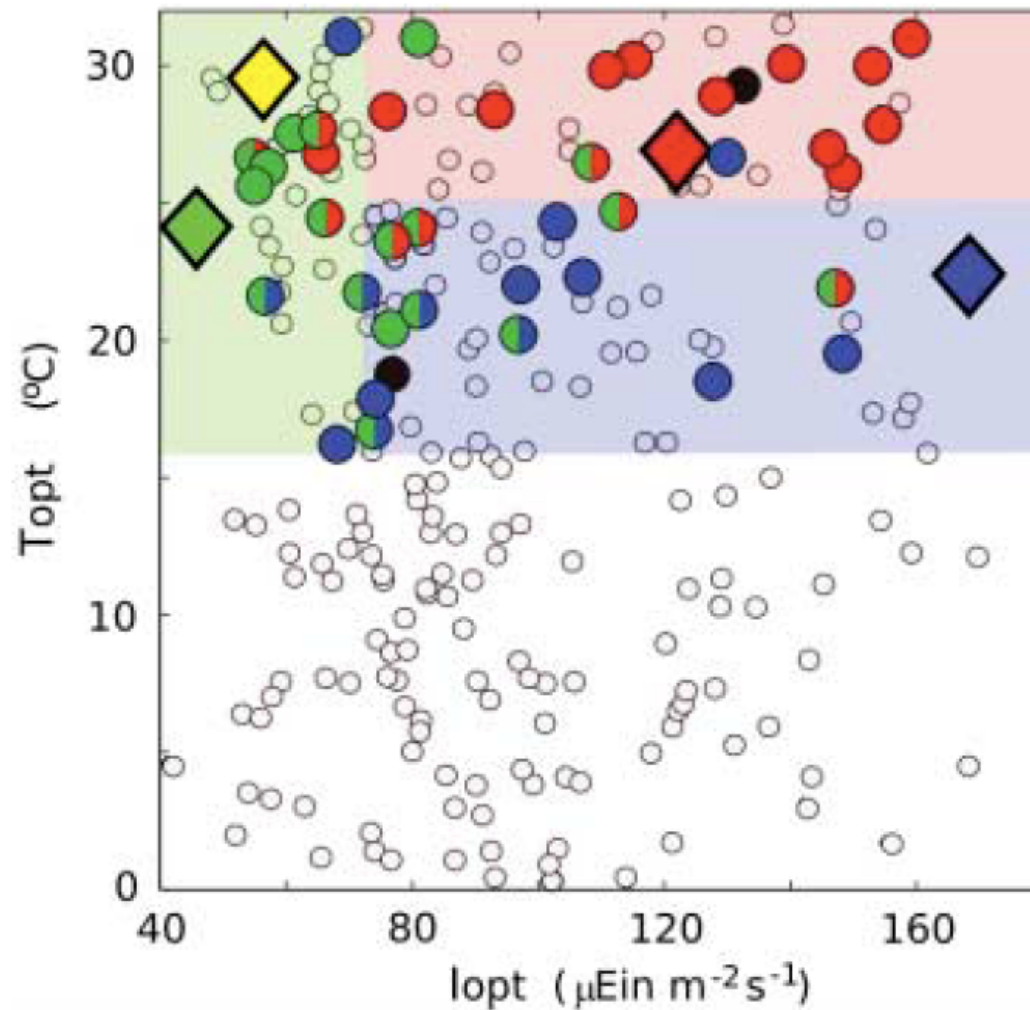


Chl a from the coupled ECCO2-Darwin Model



Images courtesy of Stephanie Dutkiewicz , Oliver Jahn, Chris Hill and Mick Follows

DARWIN output



Winning *prochlorococcus* ecotypes in the DARWIN simulation (circles) vs observed *prochlorococcus* (diamonds) along the AMT-13 Transect.

MJ Follows *et al*, *Science* **315**, 1843 (2007)

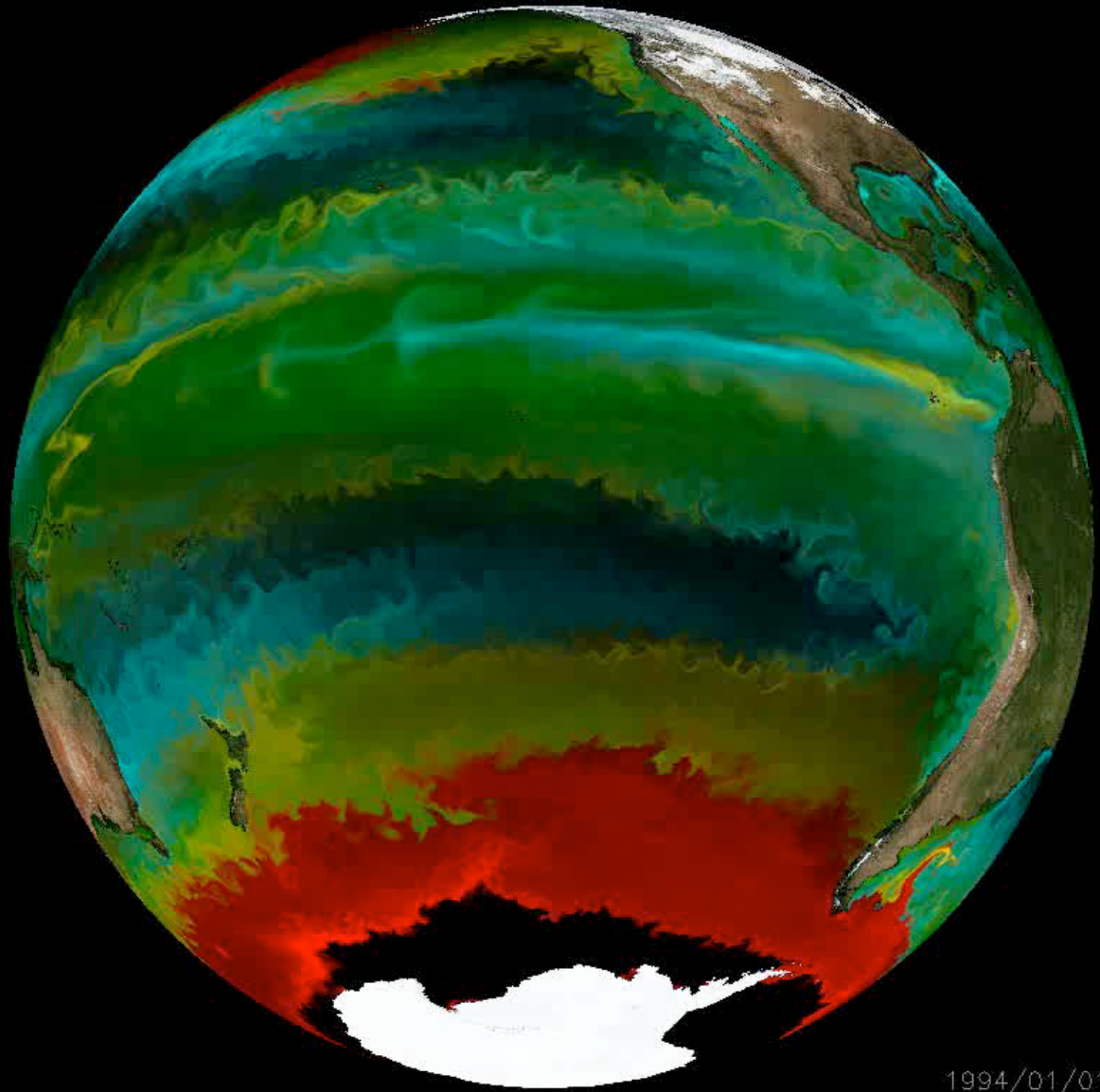
Most abundant types

Prochlorococcus

Synechococcus

Diatoms

Large eukaryote



1994/01/01

Images courtesy of Stephanie Dutkiewicz , Oliver Jahn, Chris Hill and Mick Follows

Project goals-> A *trait*-based representation of the community

Derive nutrient uptake functional form from an individual-based model.

Identify trade-off surface linking maximum growth rates with half saturation constants for N and P.

Derive Droop model from an individual based- model.

Use these functional forms to generate flexible stoichiometries.

Establish the role of viruses, is an additional pool needed?

Develop coarse-grained versions of the successful detailed models amenable to analysis.

