

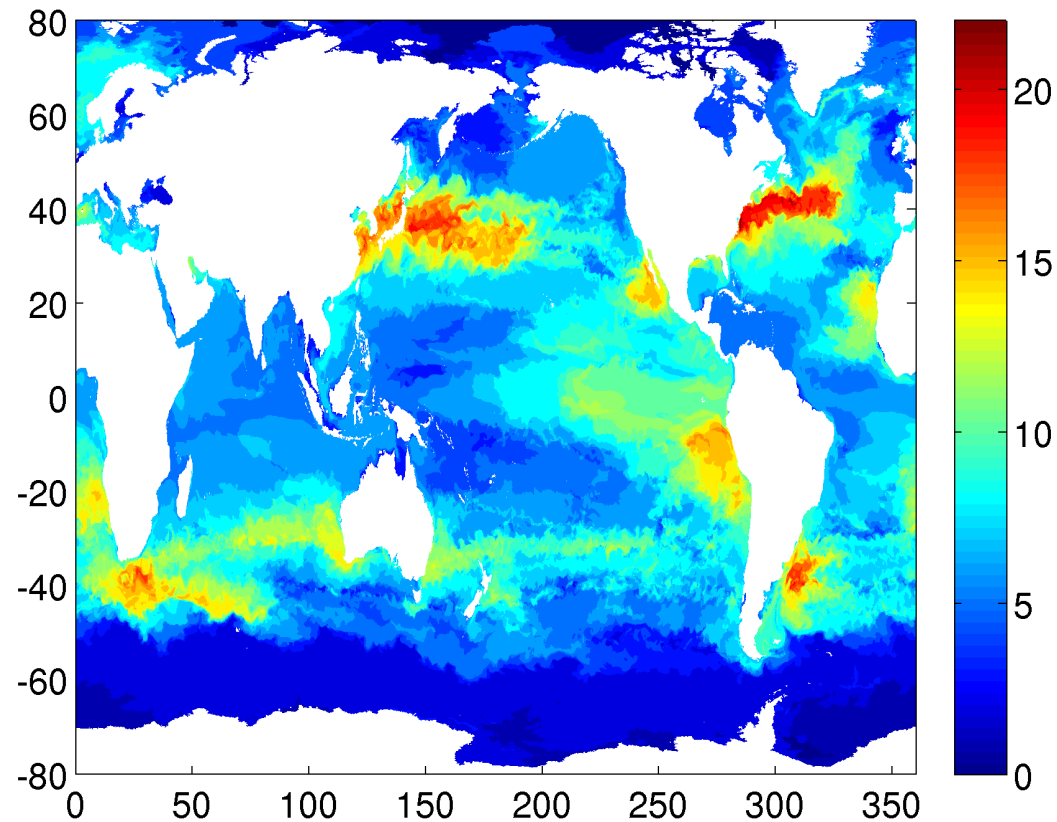
Physical transport, biogeography and diversity of phytoplankton

Sophie Clayton (UW)

Stephanie Dutkiewicz, Oliver Jahn, Mick Follows (MIT)

Andrew Barton (Duke), Jason Bragg (ANU)

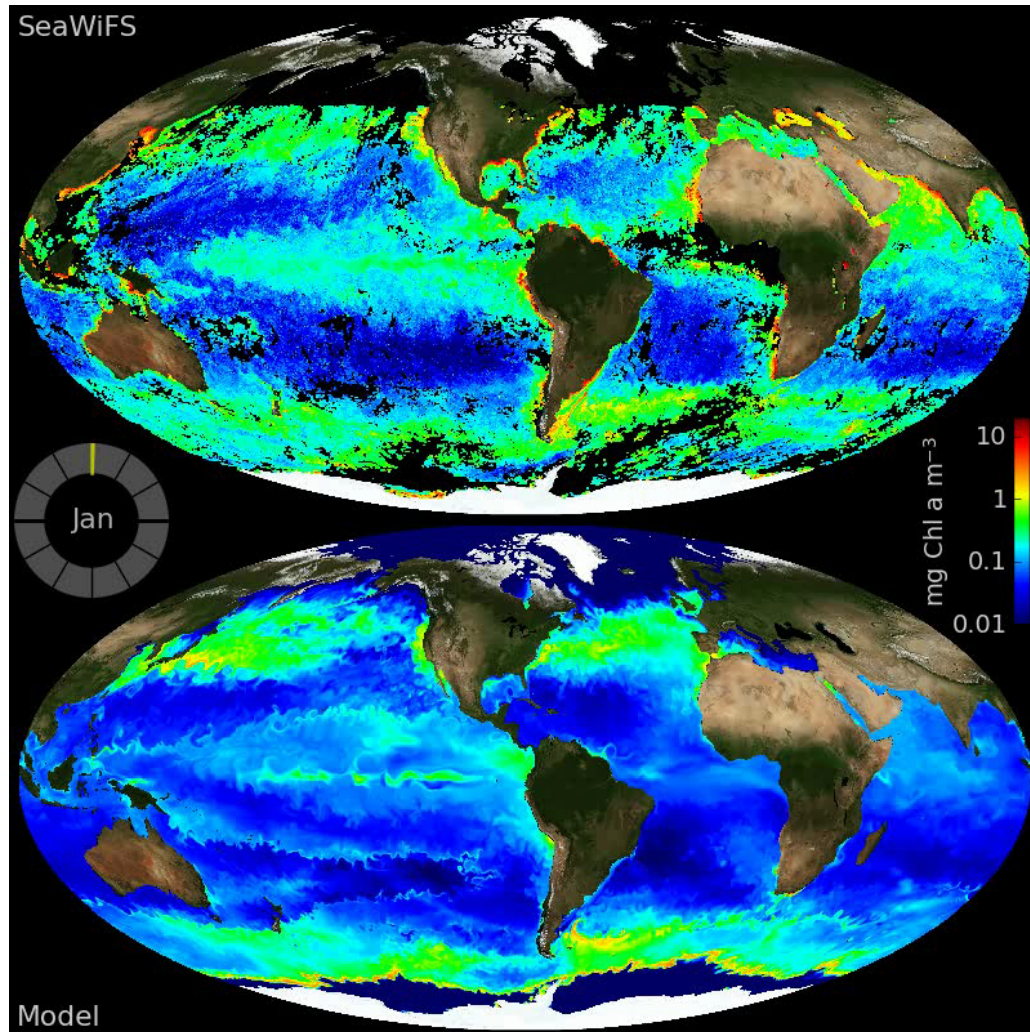
Ocean model:
“species richness”



Clayton et al,
L&O:F&E (2013)

Chl a from remote sensing and simulation

SeaWiFS Chl



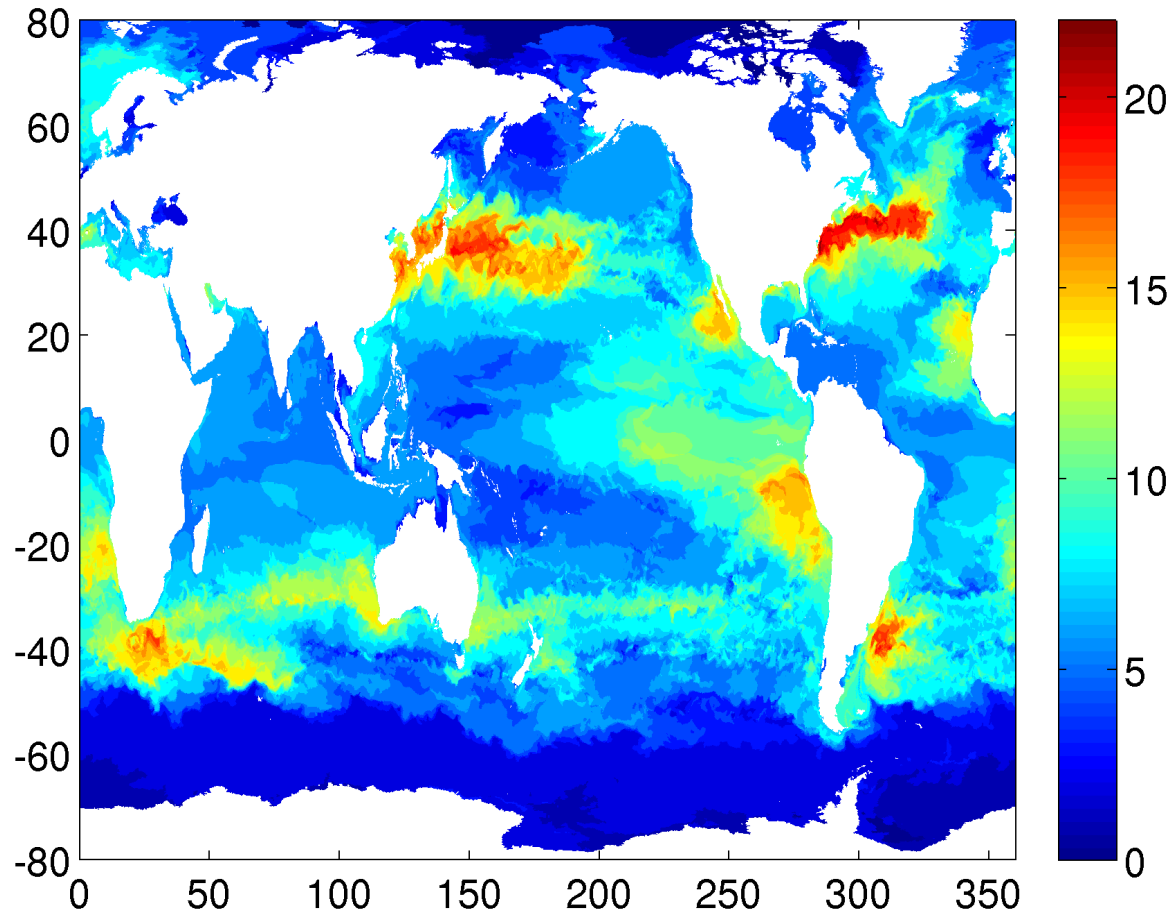
Simulation

Contributions from numerous phytoplankton types



Follows et al,
(2007)

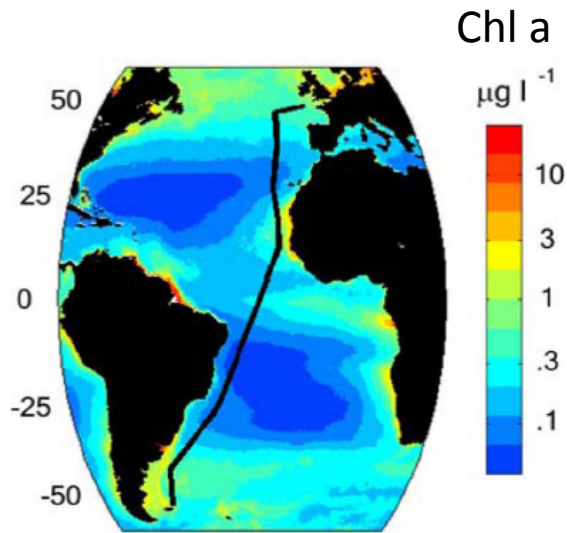
Model's richness: α diversity



α

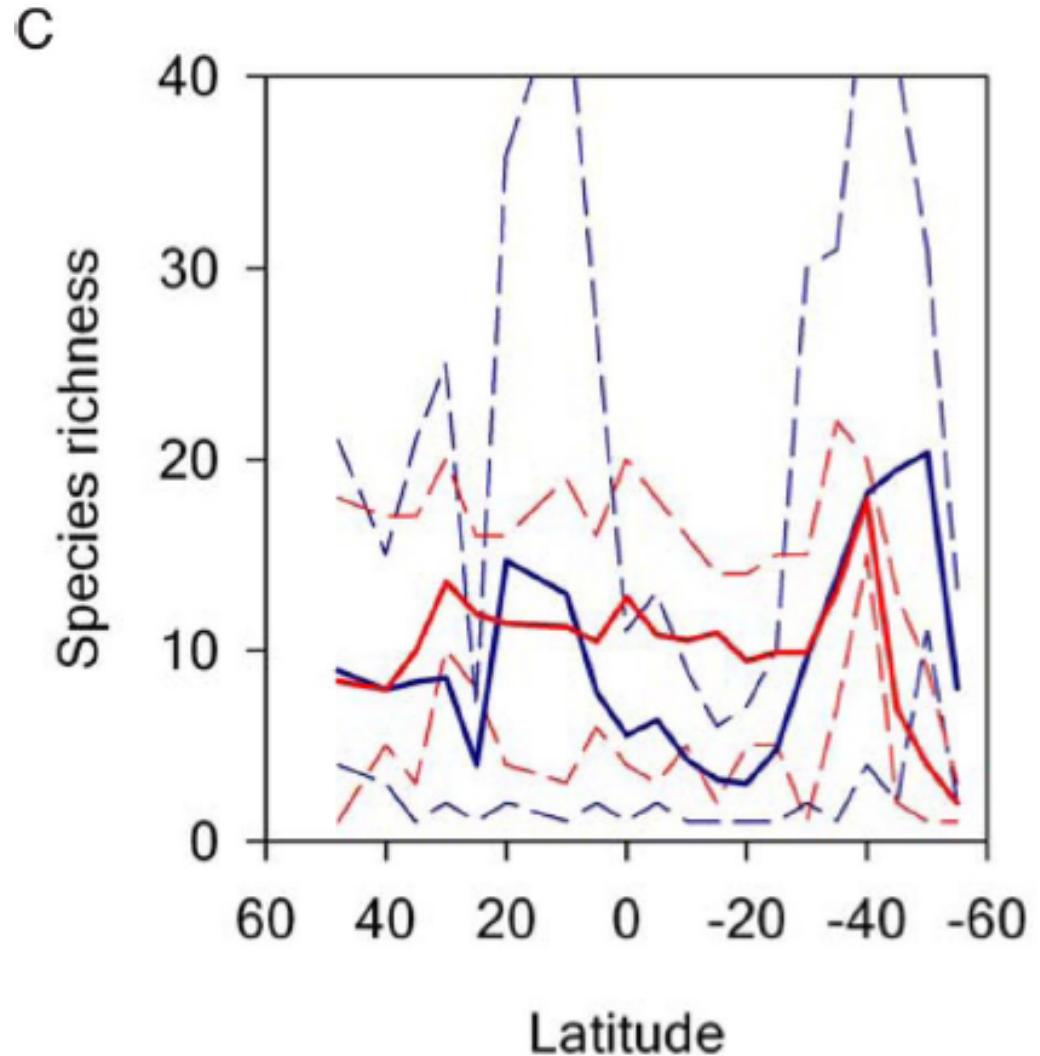
Number of co-occurring phytoplankton types above threshold biomass
(Clayton et al, 2013; Barton et al, 2010)

Are the hotspots real? AMT data

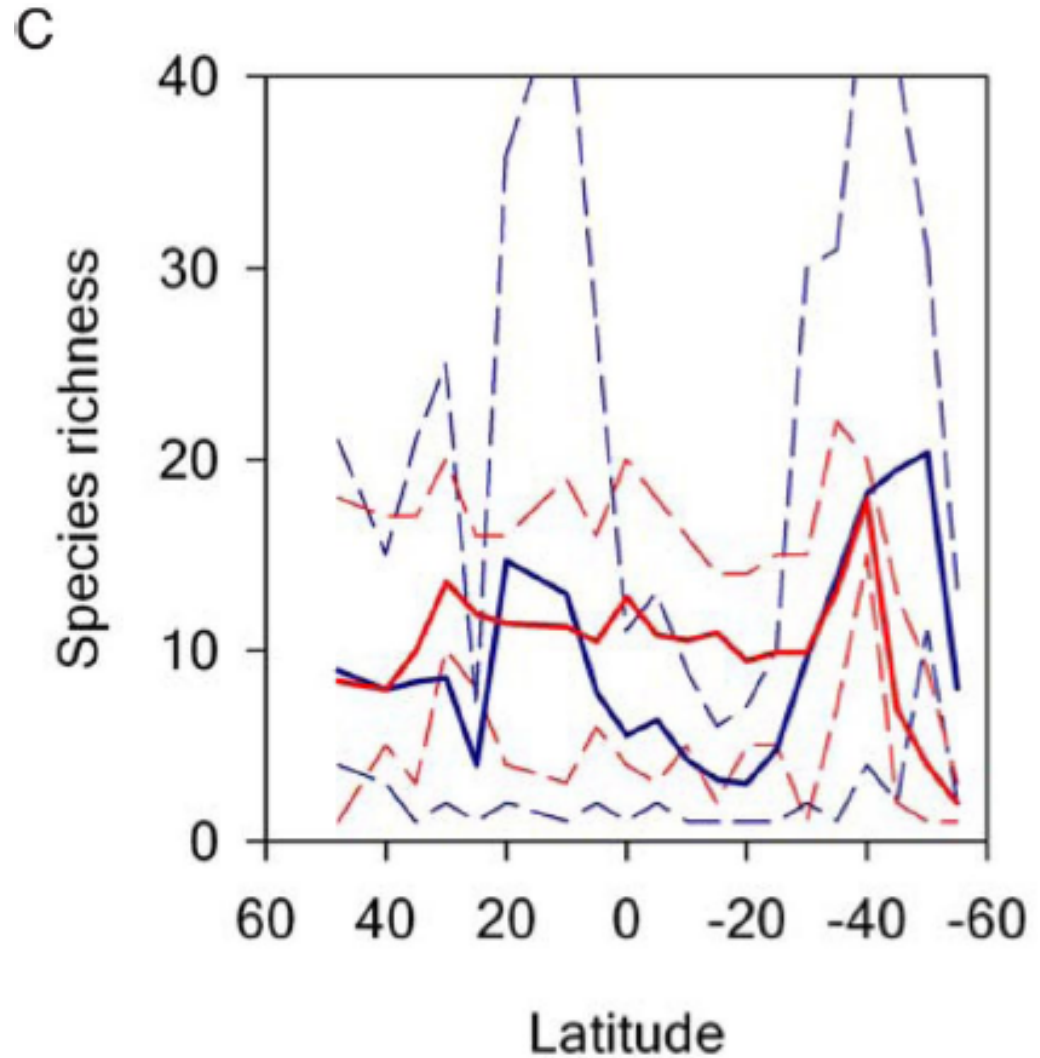
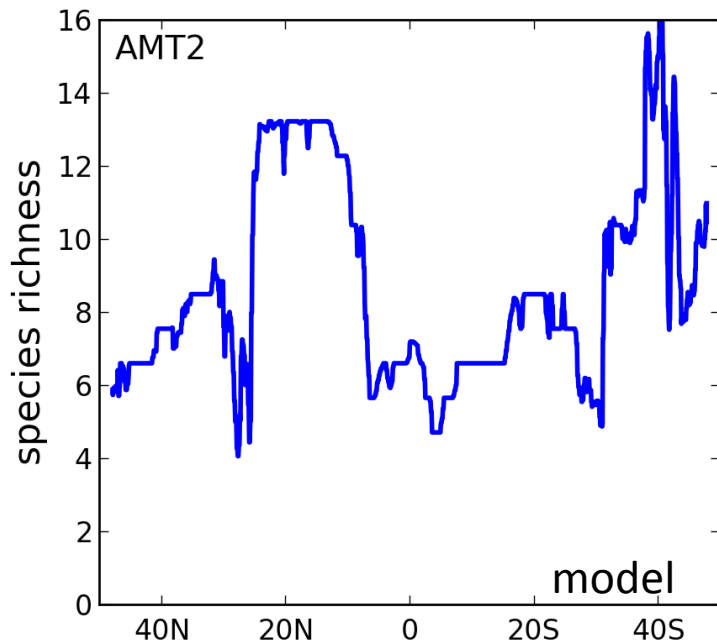
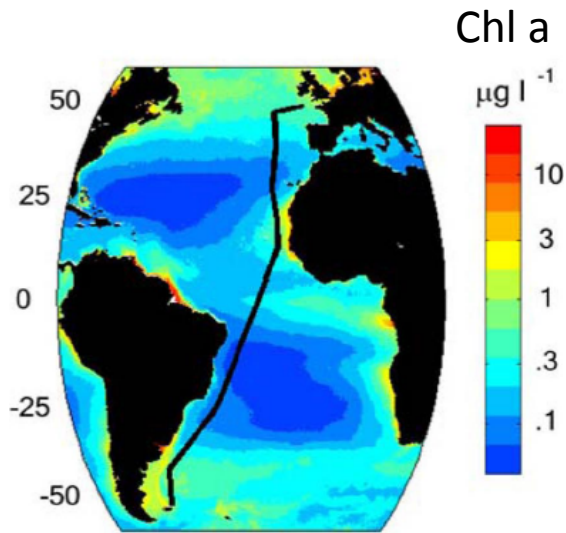


Blue – diatoms

Red – coccolithophores

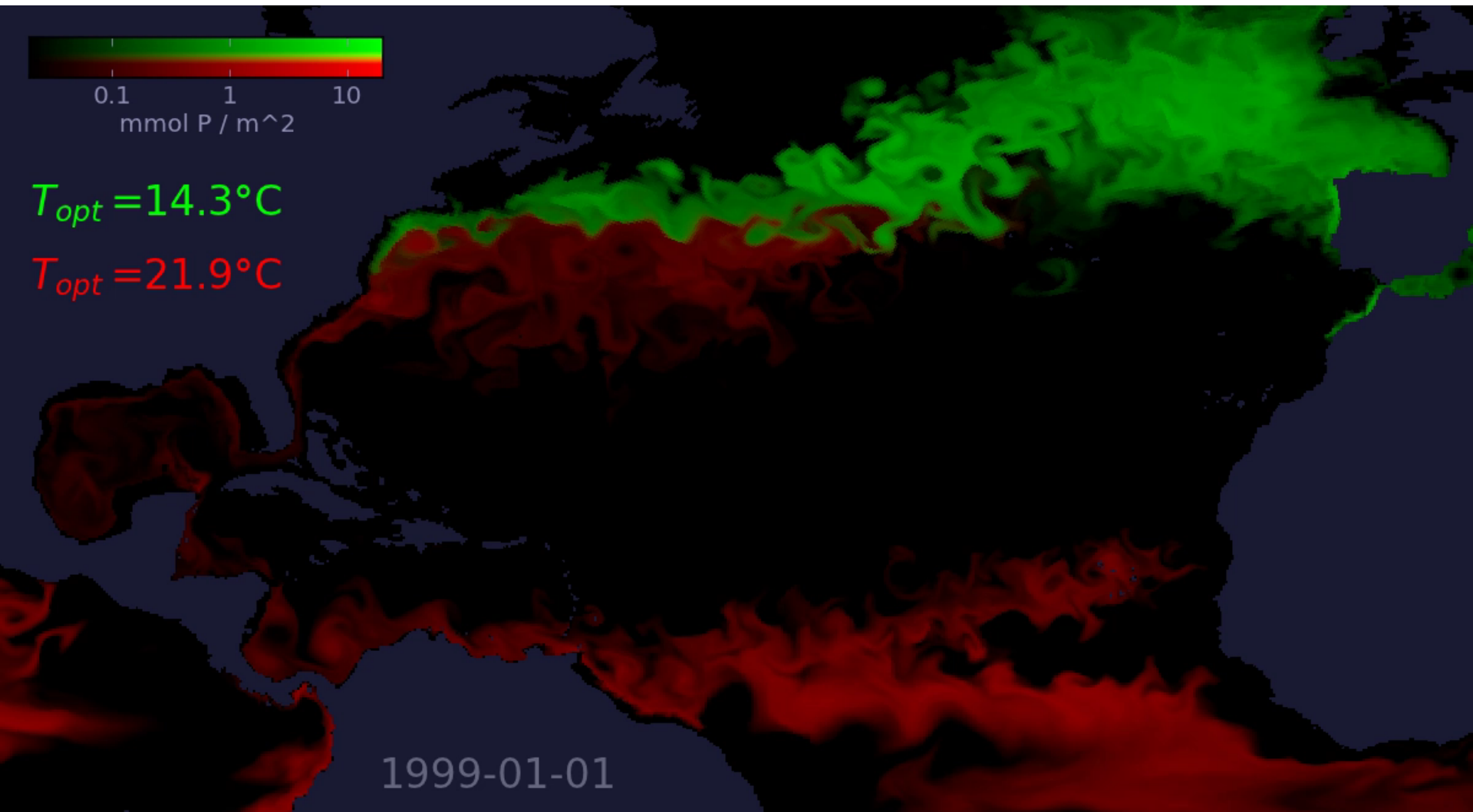


Are the hotspots real? AMT data

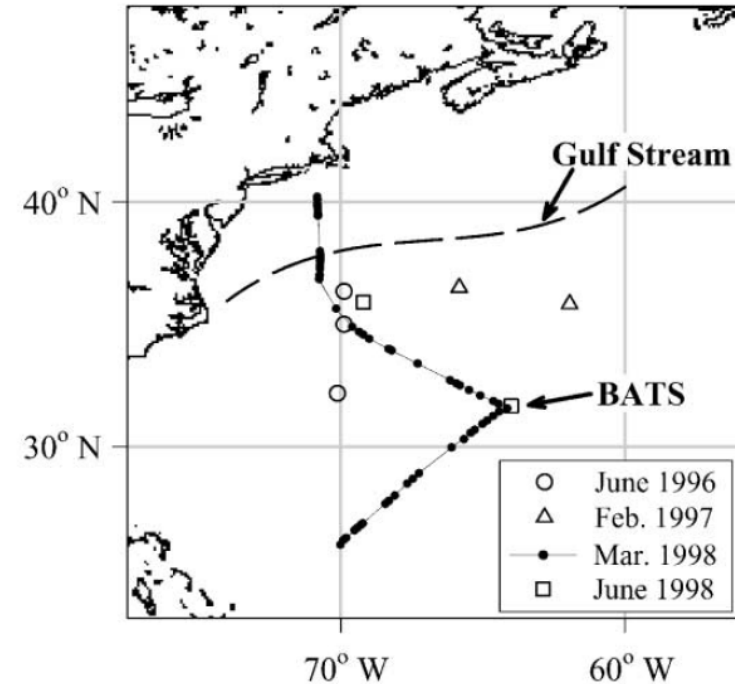
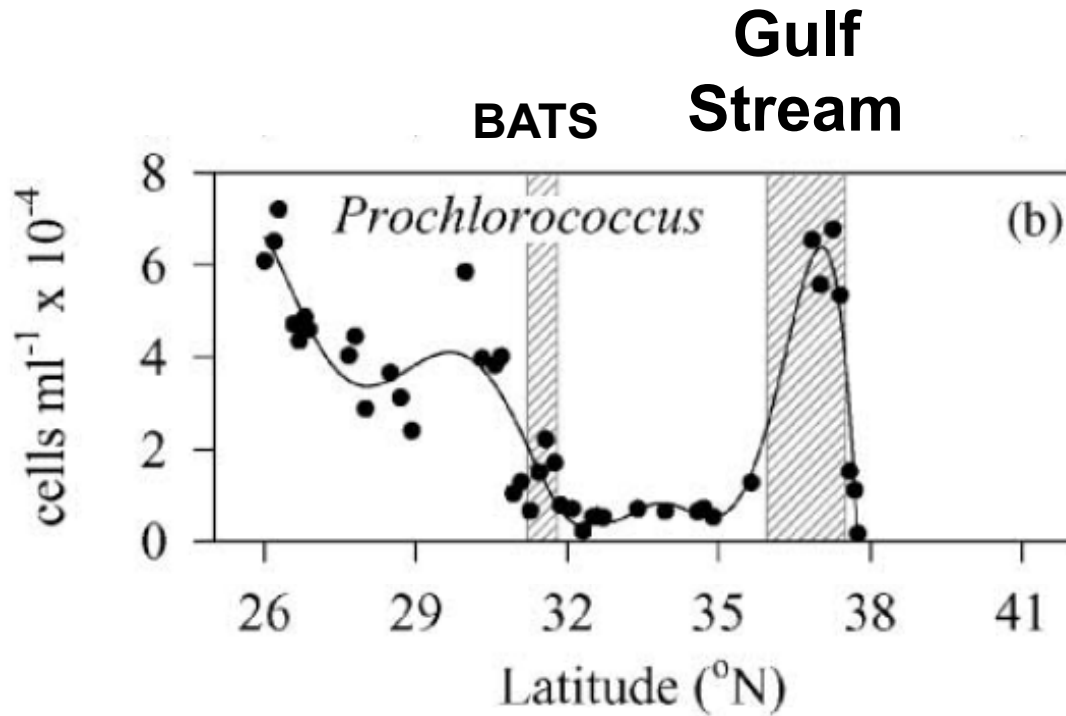


Cermeño et al (2009)

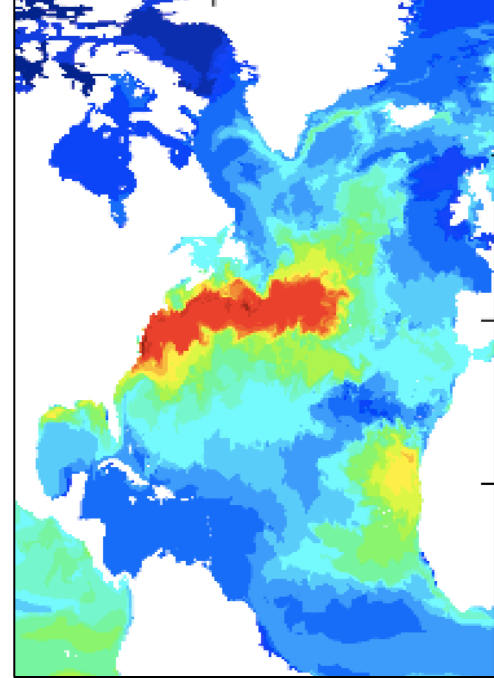
Does the confluence of biomes cause hotspots?



Cavendar-Bares et al DSR (2001): Gulf Stream transport of *Prochlorococcus*

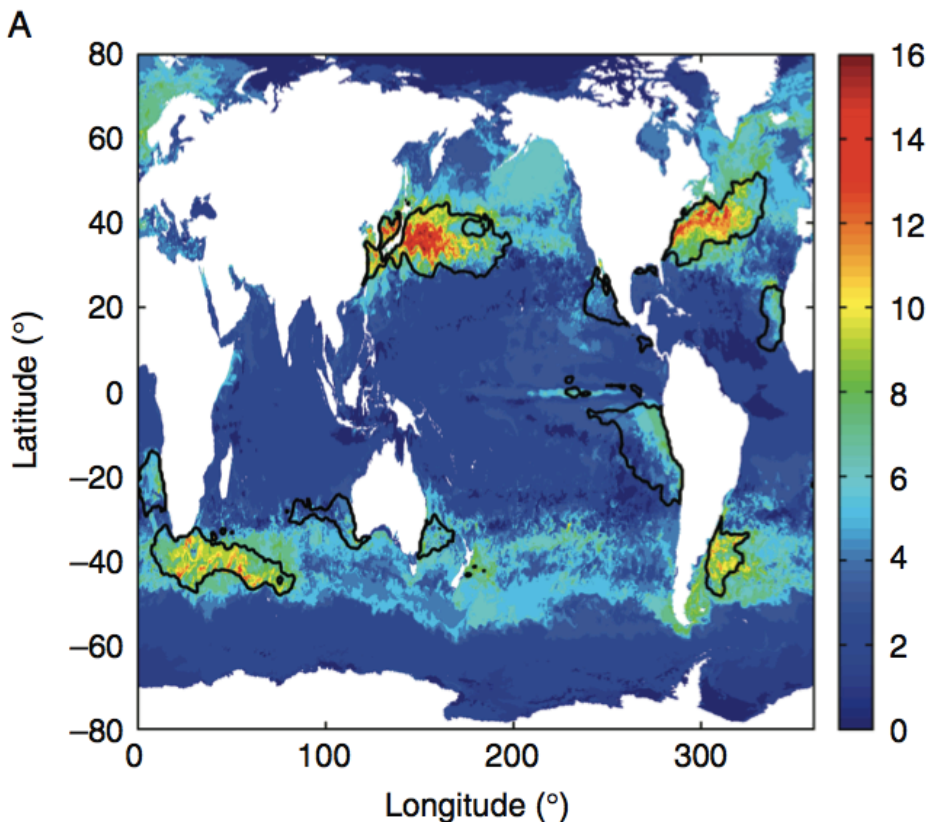


Does immigration cause hotspots? Test in model...



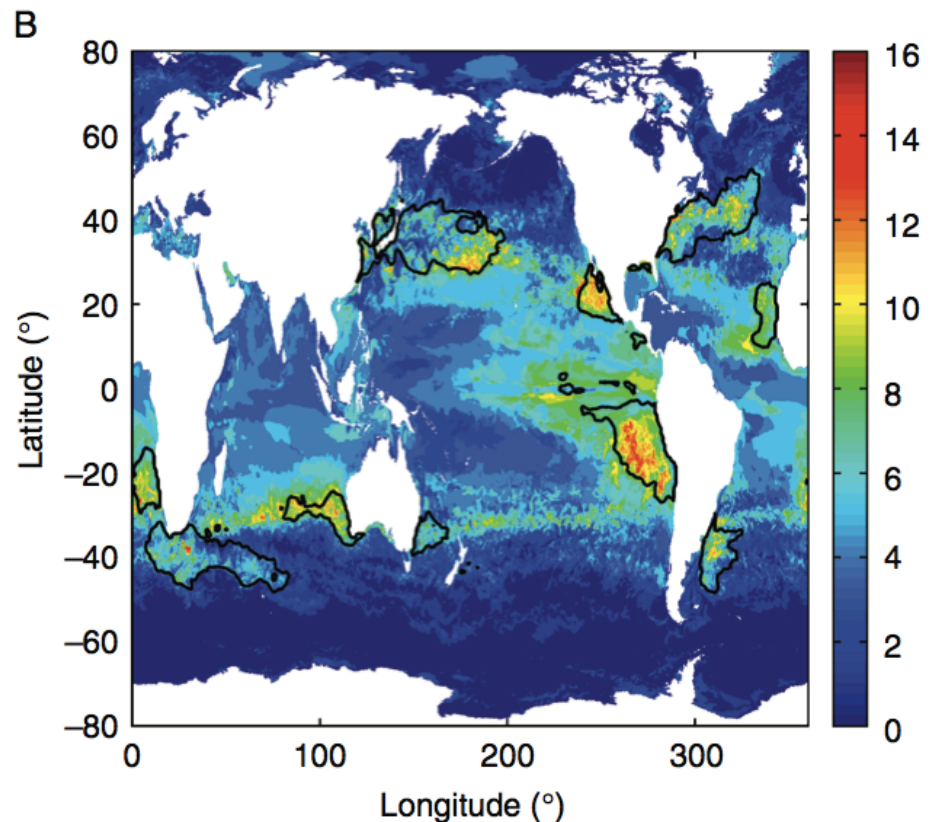
$$\frac{\partial B_i}{\partial t} = \underbrace{\mu_{net,i}(B_i, T, R, I, Z)}_{\text{net biological source}} - \underbrace{\underline{u} \cdot \nabla B_i}_{\text{physical transport}}$$

0	+	-	locally adapted
0	-	+	immigrant



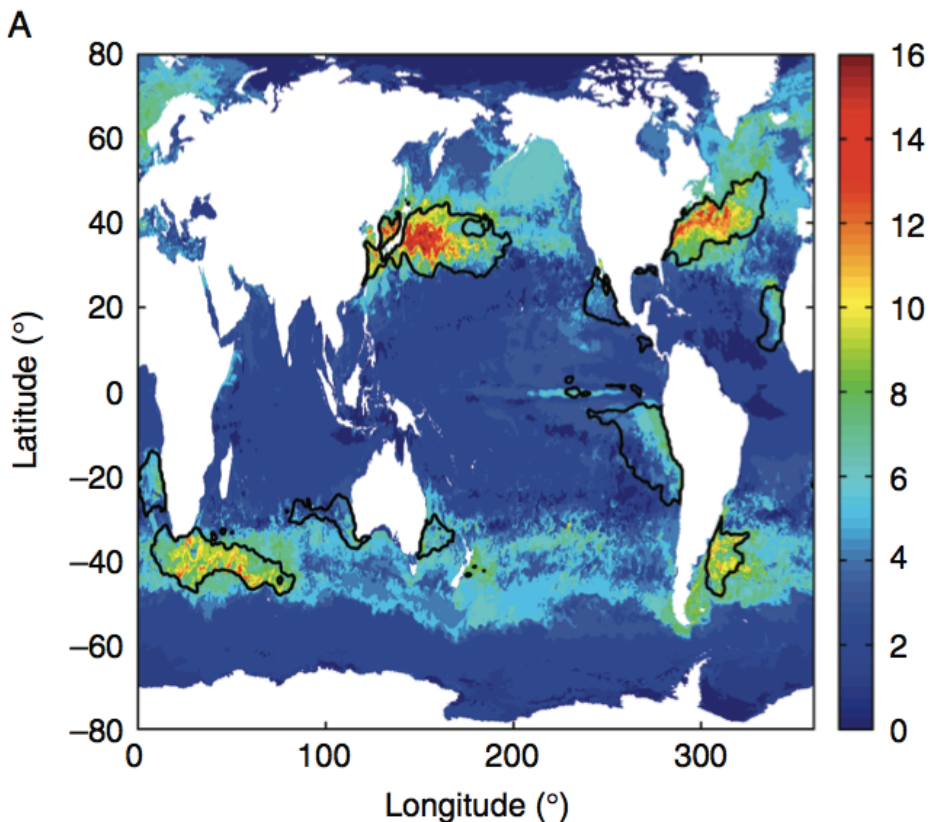
α_{LA} : Σ Locally Adapted

Sources of diversity



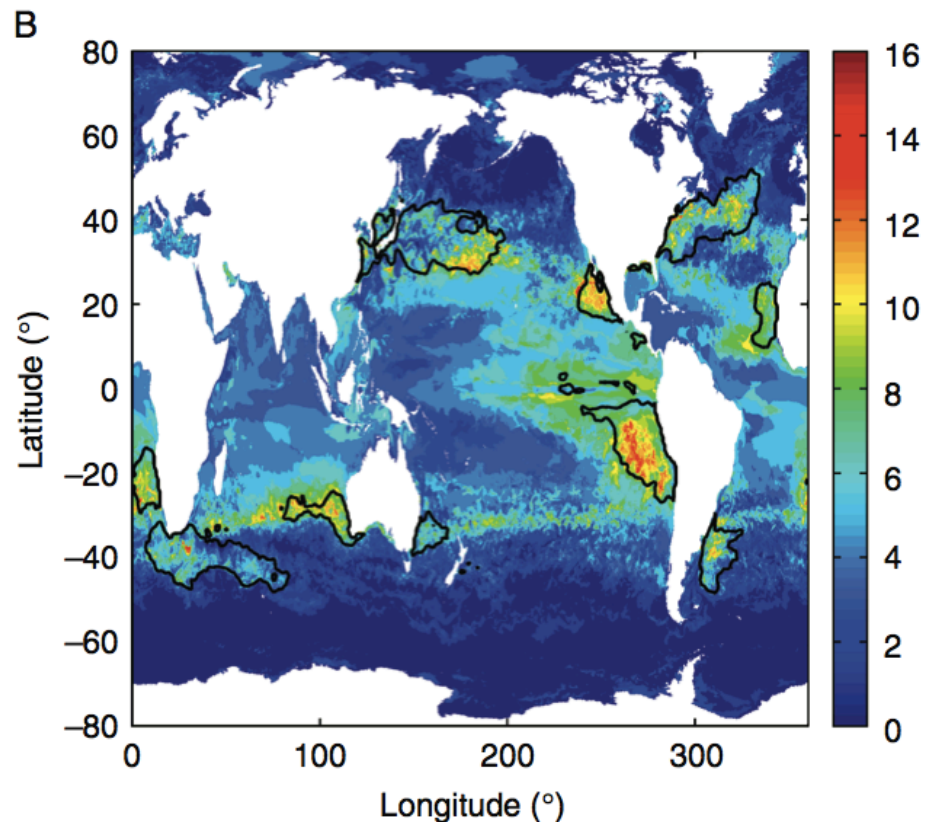
α_I : Σ Immigrants

Sinks of diversity



α_{LA} : Σ Locally Adapted

Sources of diversity



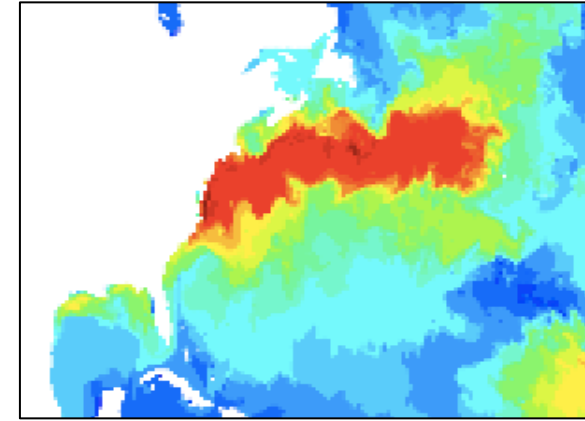
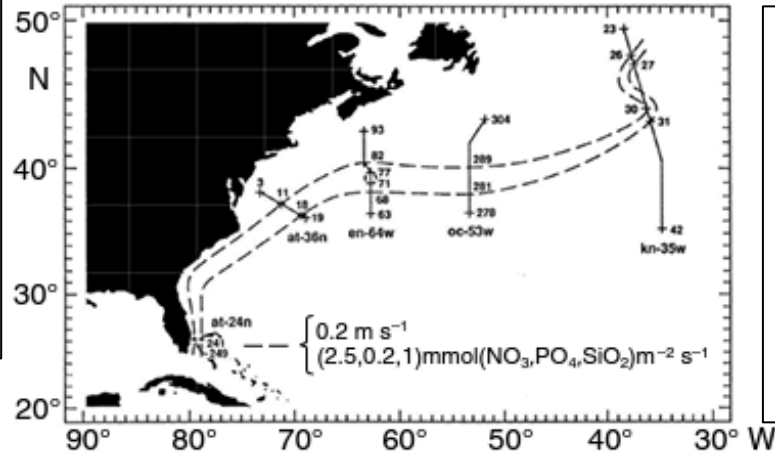
α_i : Σ Immigrants

Sinks of diversity

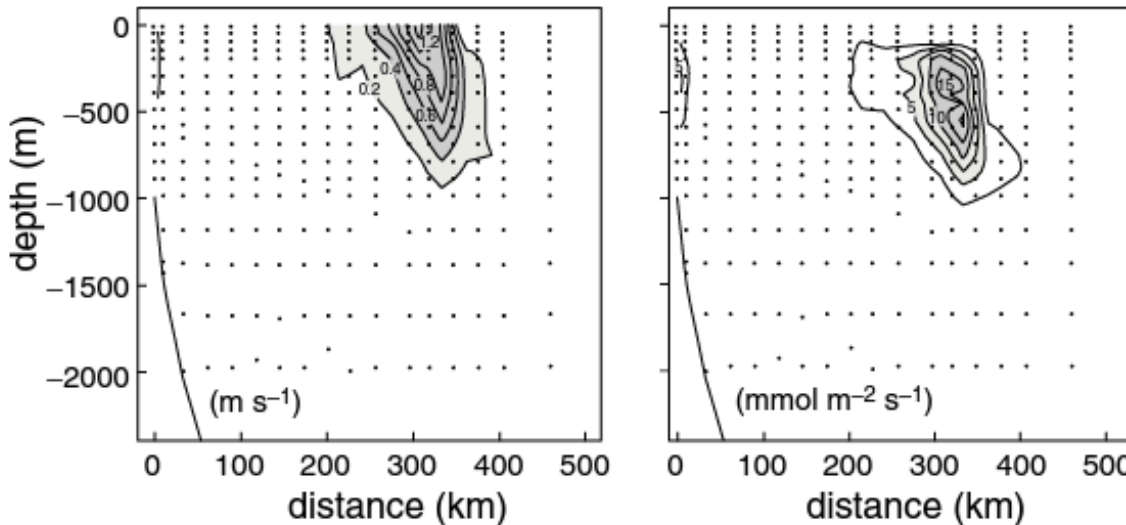
WBC hotspots are sources, not sinks, of diversity: WHY?

“Nutrient streams” fertilize confluence region...

(a) ‘nutrient stream’ in the North Atlantic



(b) vertical sections of velocity and nitrate flux at 36°N

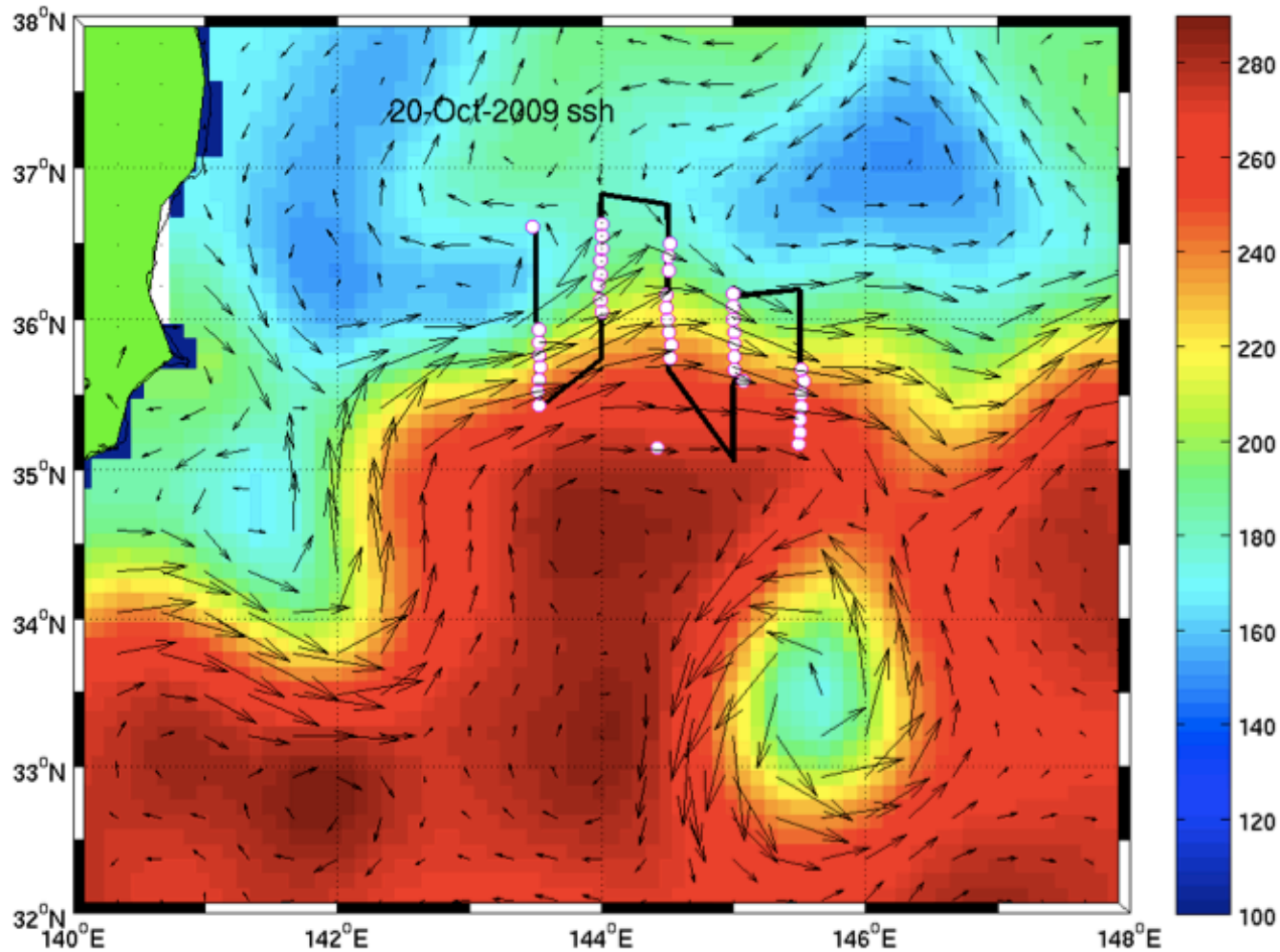


Lateral confluence of populations AND vertical confluence of resources drives “locally adapted” hotspots

Anecdotal support:

Ostreococcus clades at the Kuroshio Front:

Sophie Clayton (UW), Alex Worden (MBARI), Yun-Chi Lin (MBARI), Takeyoshi

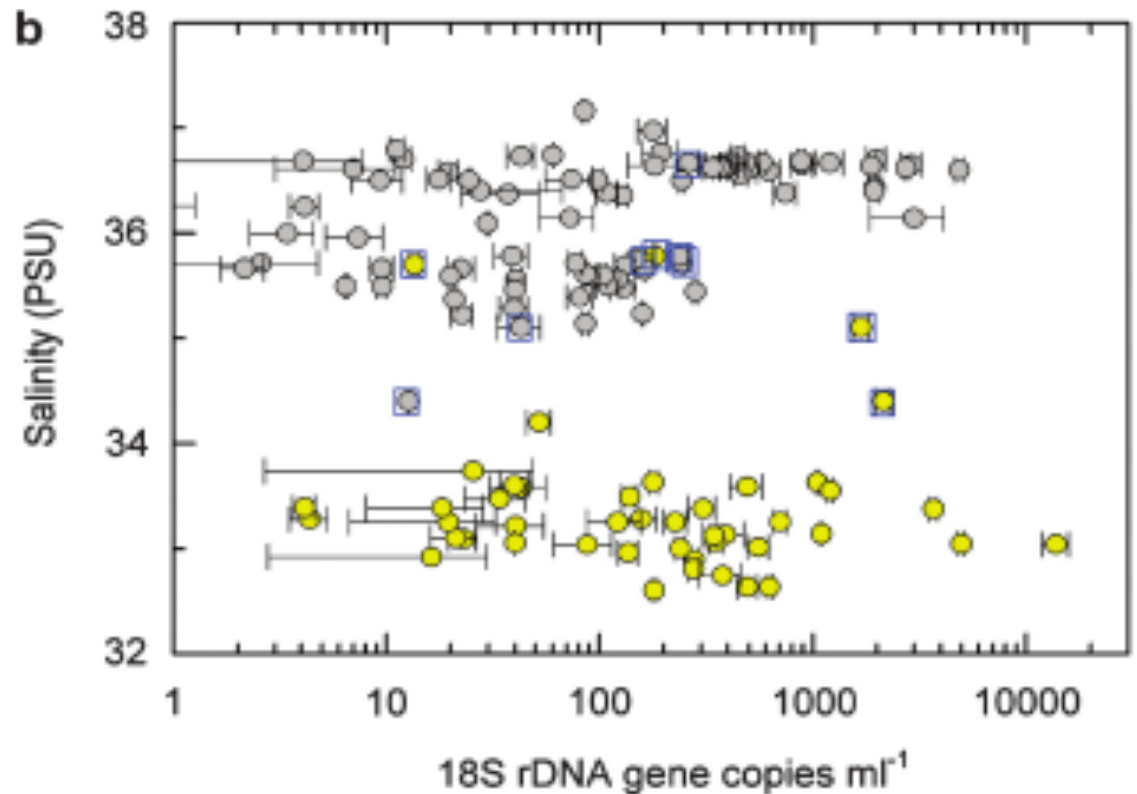
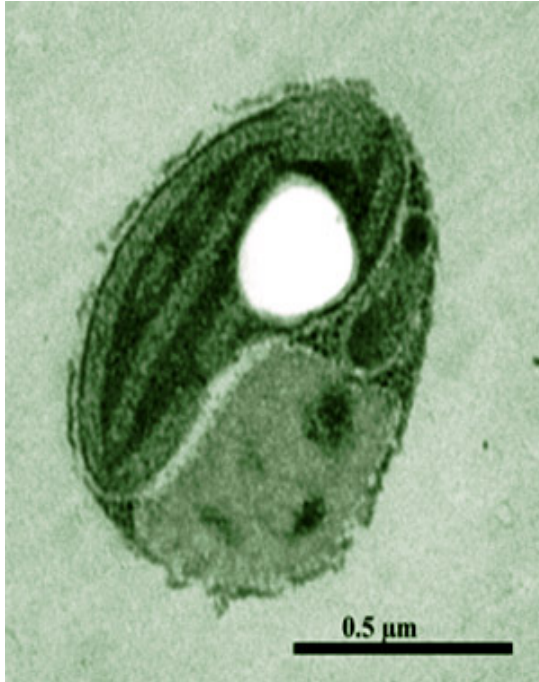


- Kuroshio Front
- October 2009
- Stations ~10km
- Hydrography & mixing rates
- Sophie: Inorganic & organic nutrients, HPLC pigments, flow cytometry, microscopy, genetic analysis

Sea surface height and geostrophic flow

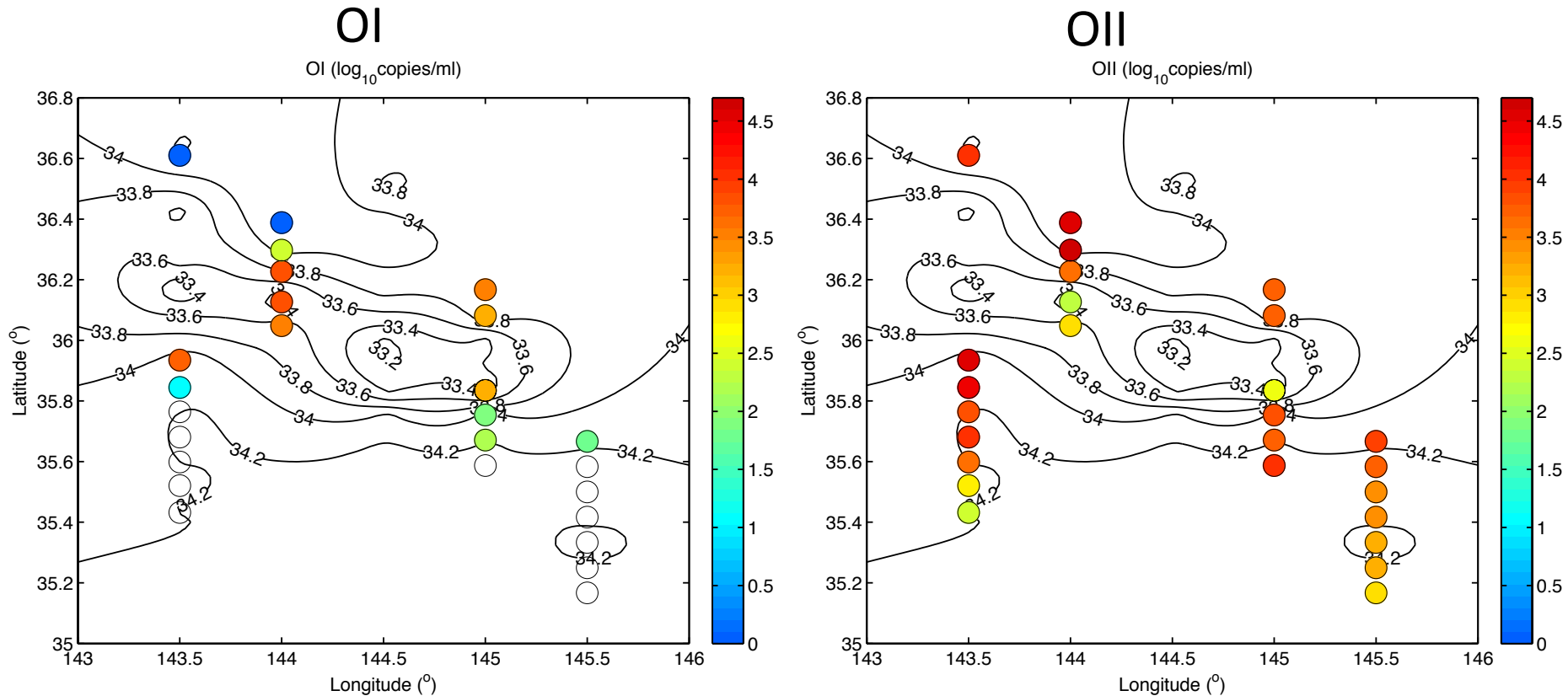
Clayton et al (2014; in prep)

Ostreococcus



- Abundant oceanic picoeukaryote
- Two physiologically distinct clades, identified genetically
 - OI – coastal (yellow)
 - OII – oceanic (grey)
- Typically do not co-occur (Demir-Hilton et al, 2011)

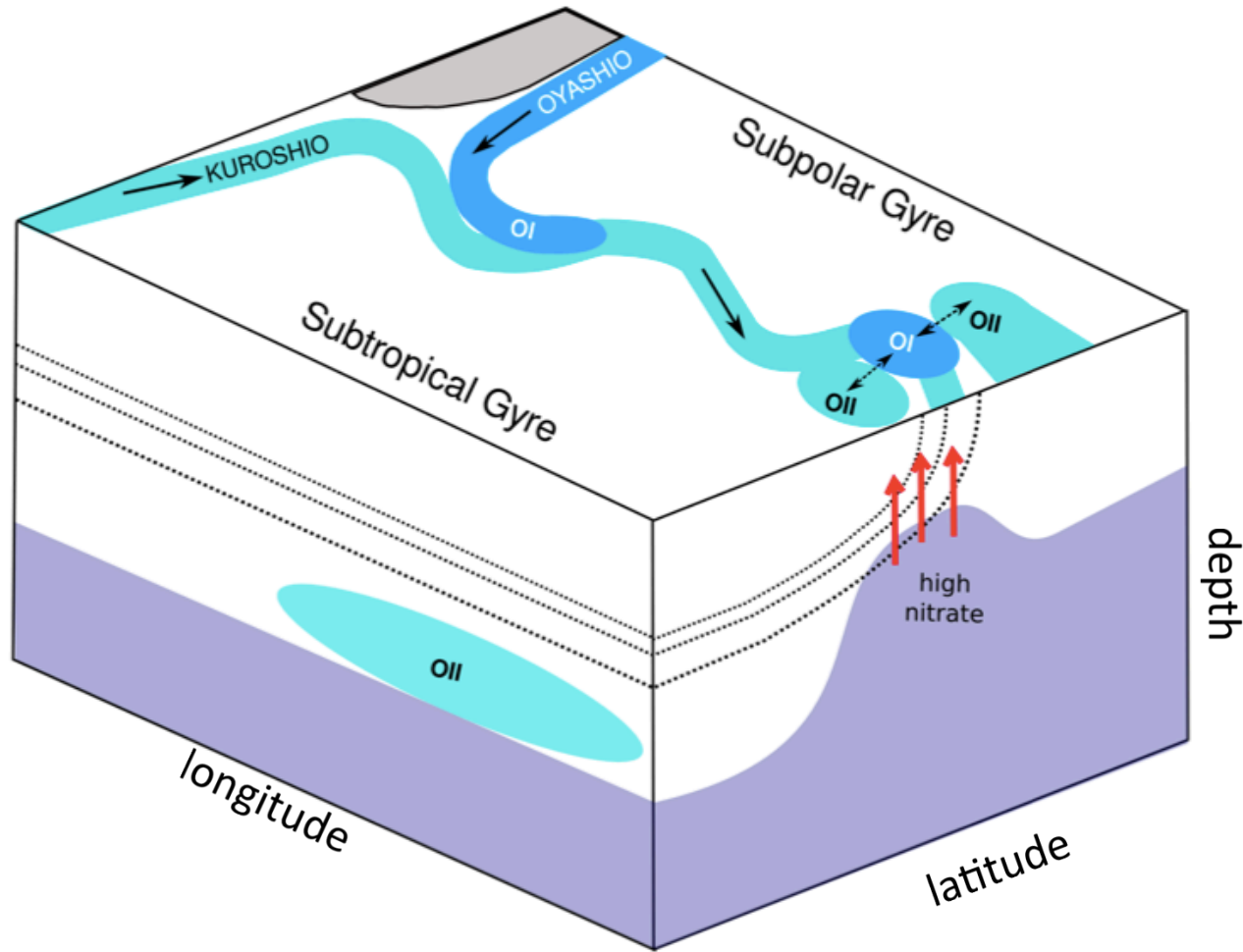
Ostreococcus clades at the Kuroshio Front



Color scale: *Ostreococcus* abundance (\log_{10} copies ml⁻¹)

Contours: salinity (psu)

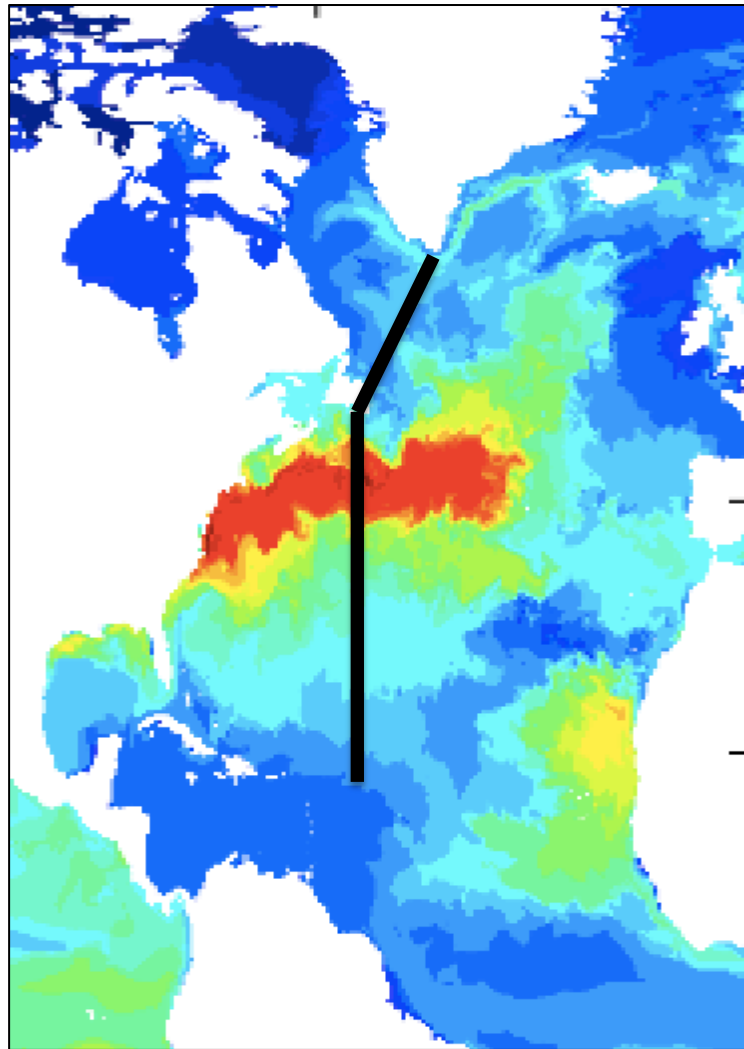
Ostreococcus clades at the Kuroshio Front



Clayton et al
(2014, in prep)

- Genetically identified clades co-occur at the front
- Both at/close to highest observed abundance $>10^4$ copies ml⁻¹
- Confluence of genotypes and resources?

Looking forward: Efficiently test for hypothesized gradients using molecular tools?

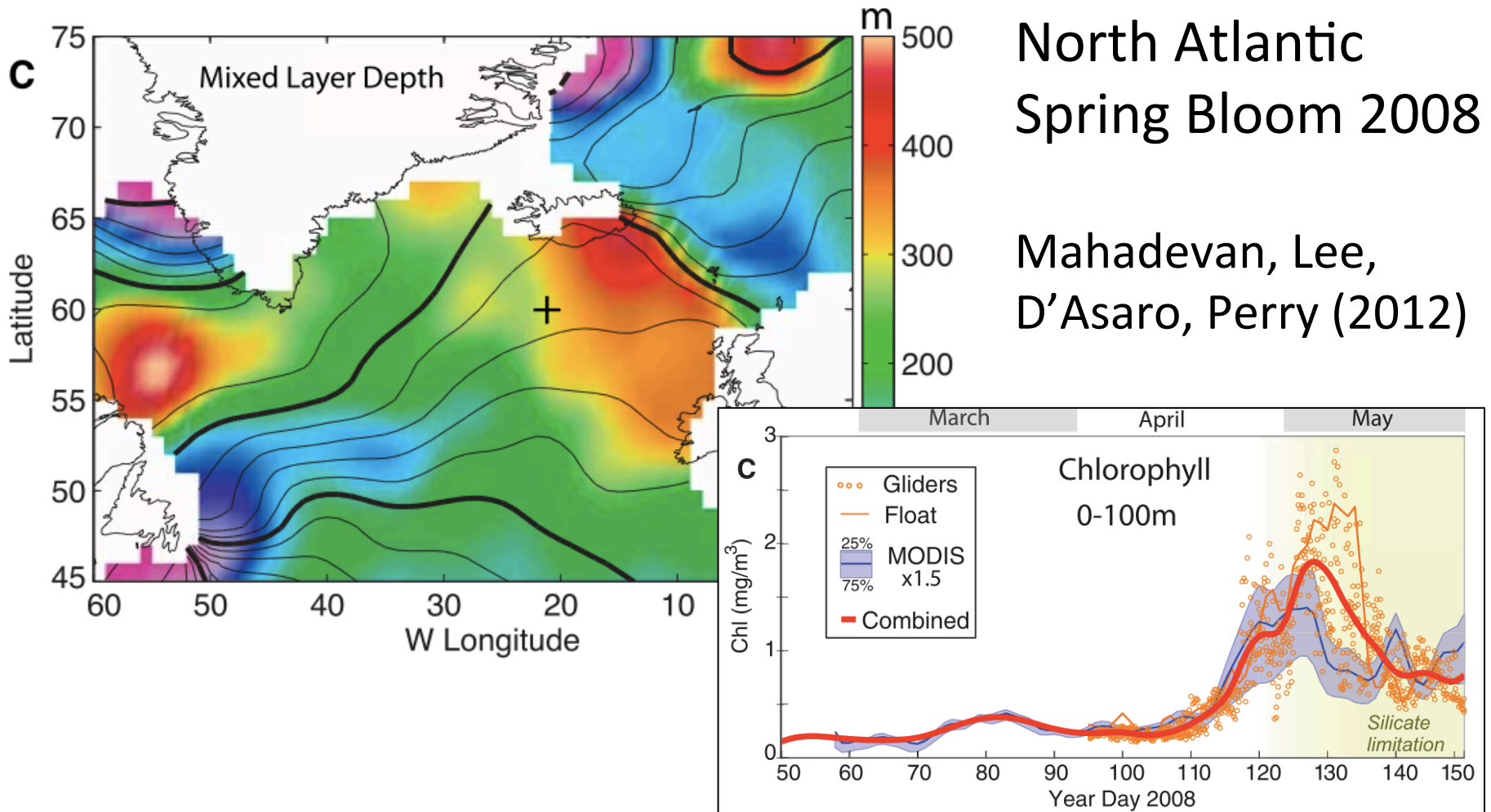


Predicted α -diversity

- Are there “hotspots”?
- Can we identify contributions from remote sources using genetic tags?
- Can we identify who is “happy” and who is not with molecular tools?

North Atlantic Spring Bloom 2008

Mahadevan, Lee,
D'Asaro, Perry (2012)



Example question:

Massive bloom and export of diatoms:

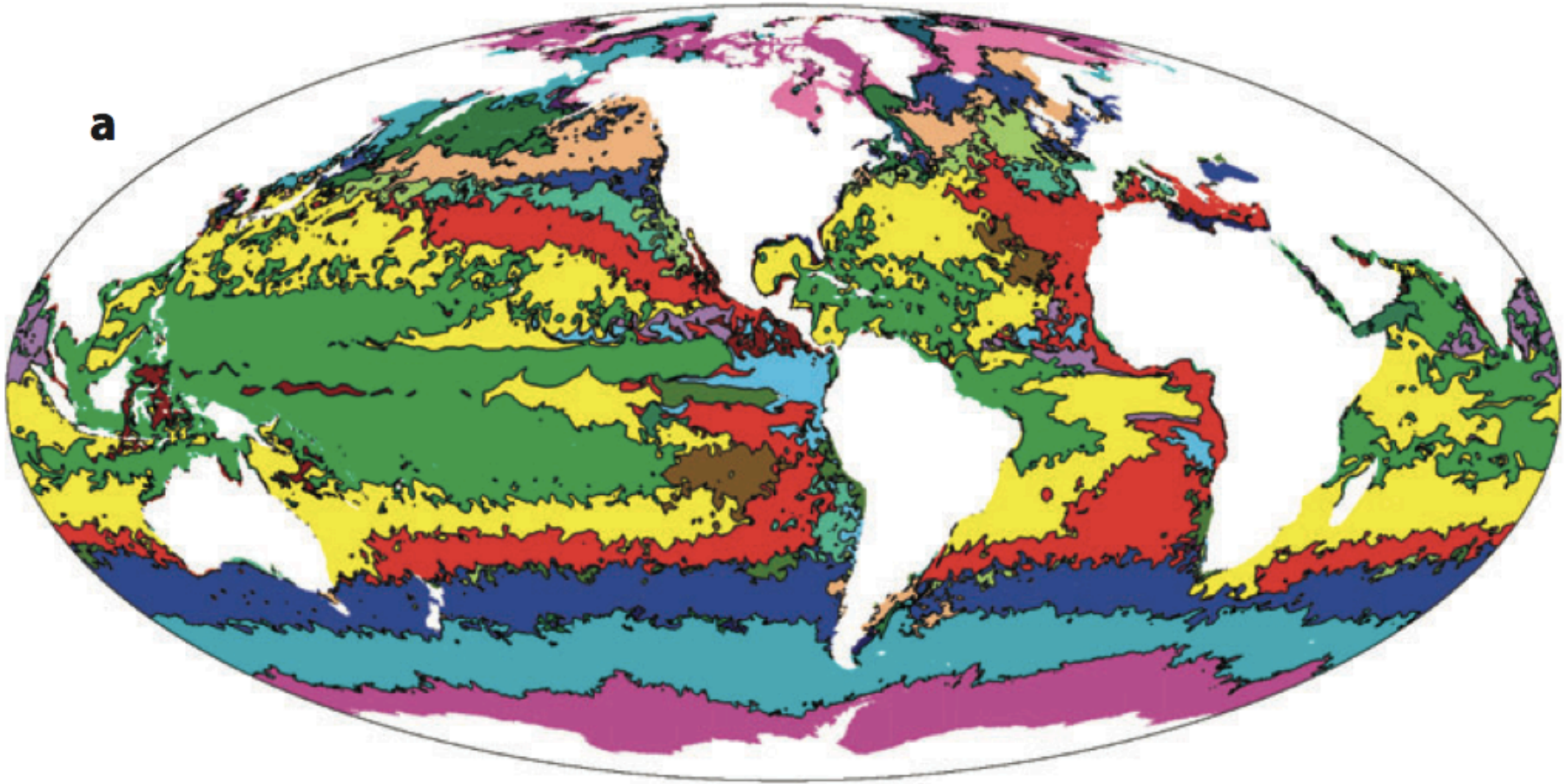
- Where does seed population come from?

Key Points

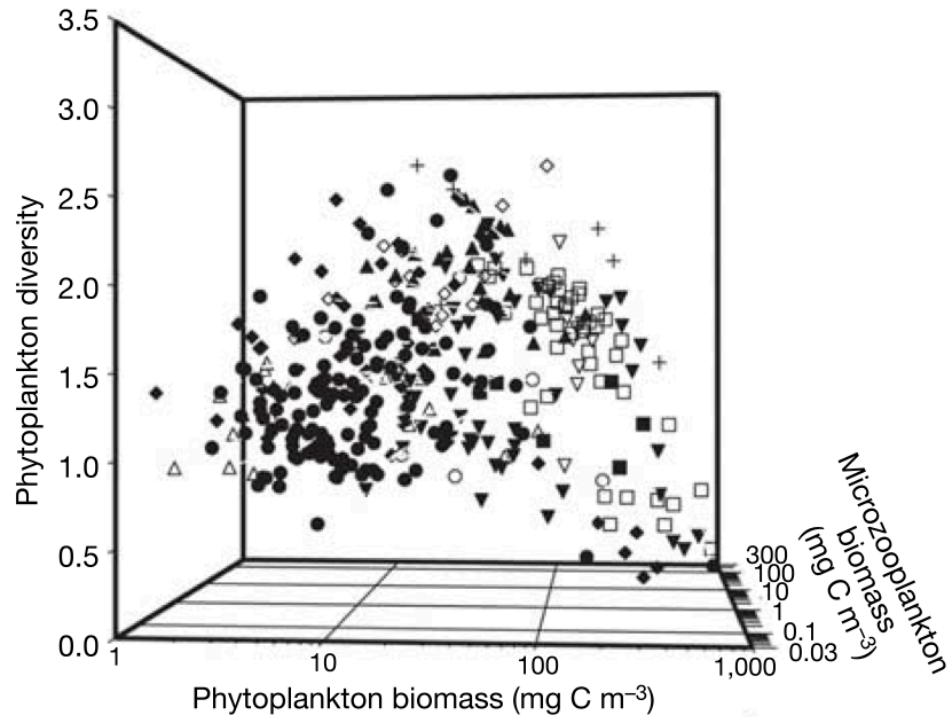
- Biogeography of individual “species”/ecotypes and patterns of biodiversity reflect a balance between biological processes and physical transport
- Testable hypotheses emerging from models and sparse observations
- Molecular tools provide an efficient means with which to address hypotheses, in combination with understanding of physical transport

Extras...

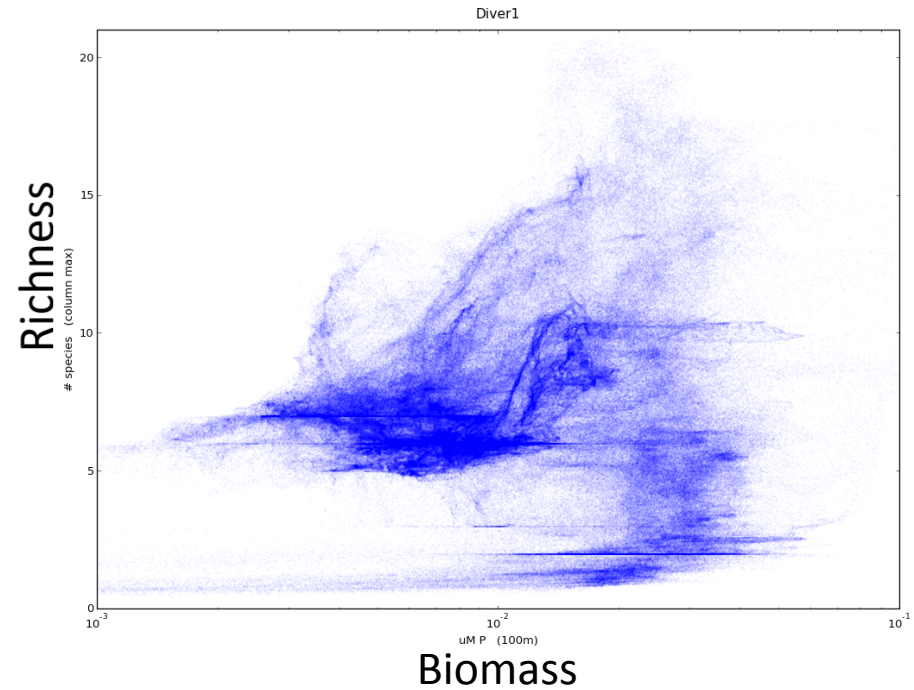
“Biomes” of global model



Is it plausible? Diversity vs biomass



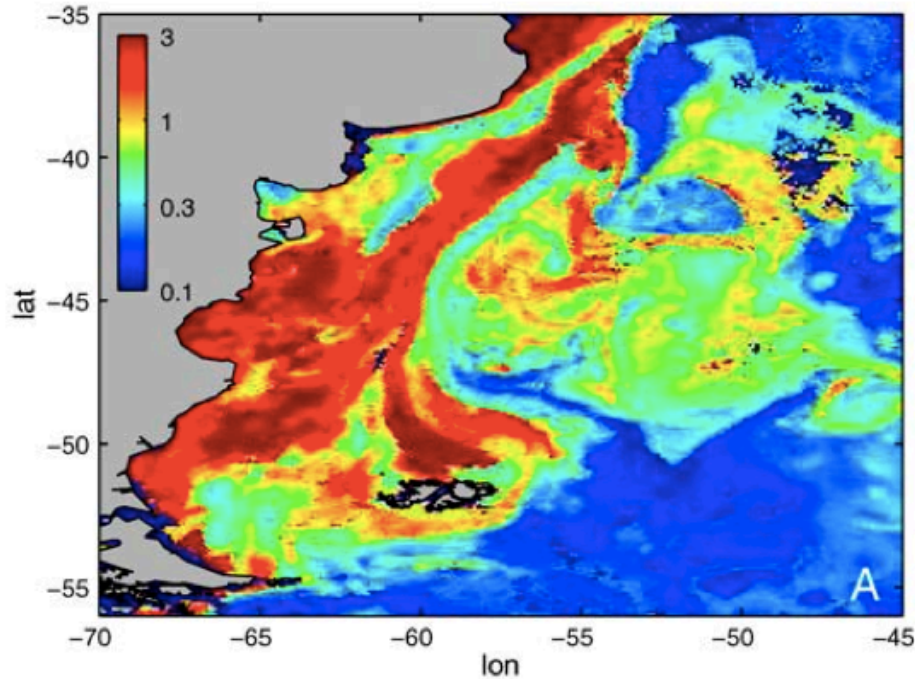
Data compilation:
Irigoien et al (2004)



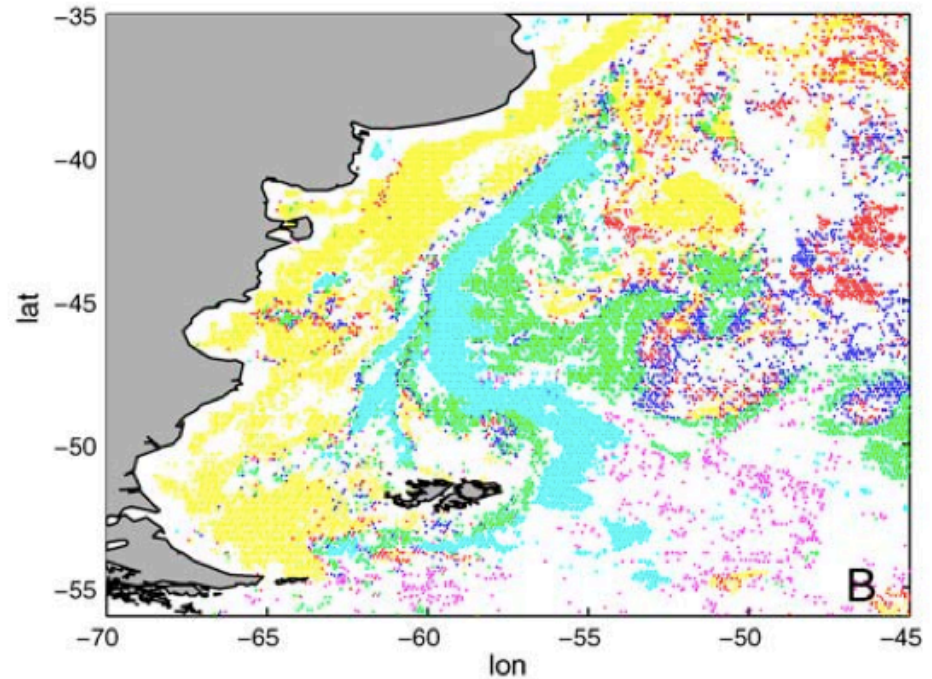
Model

Lateral transport and confluence of biomes

- D'Ovideo et al (2010) – view from space, PHYSAT

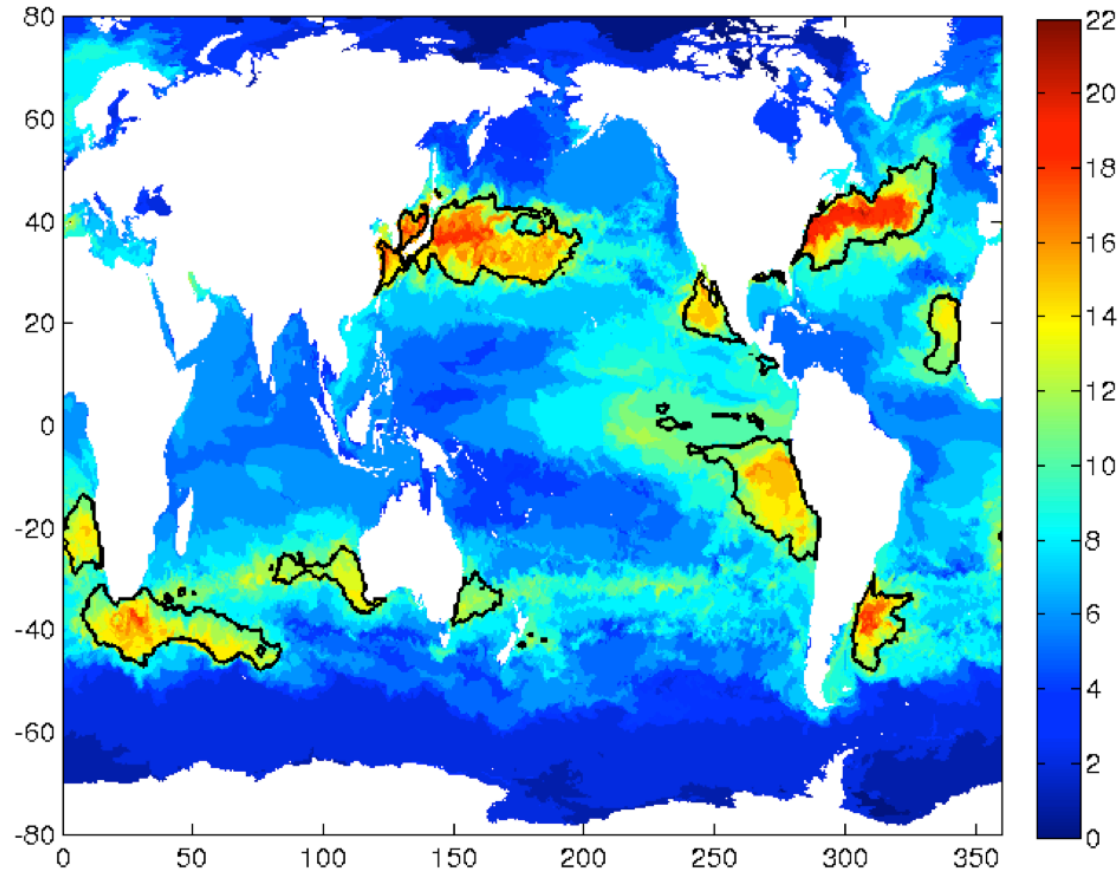


Chlorophyll a



dominant functional group

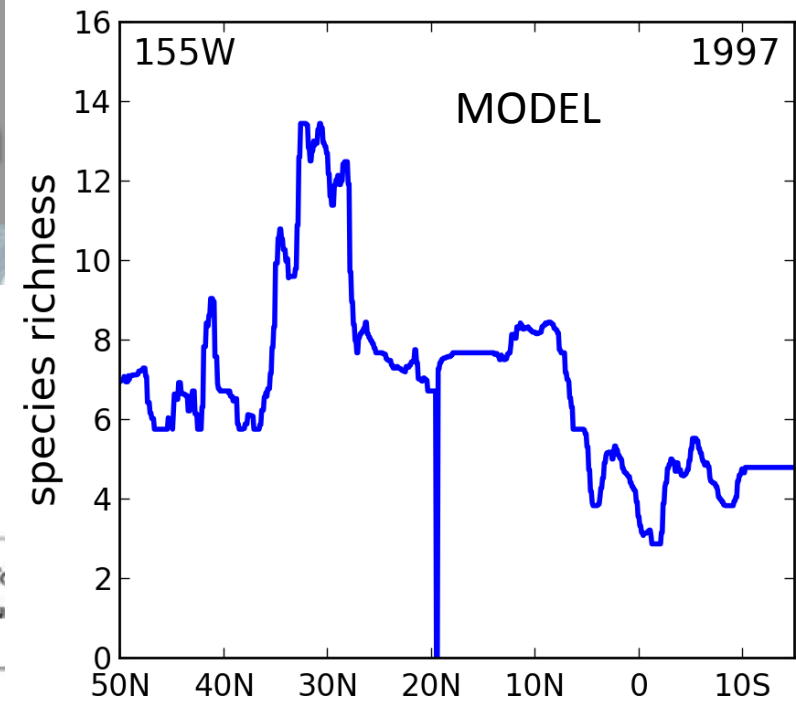
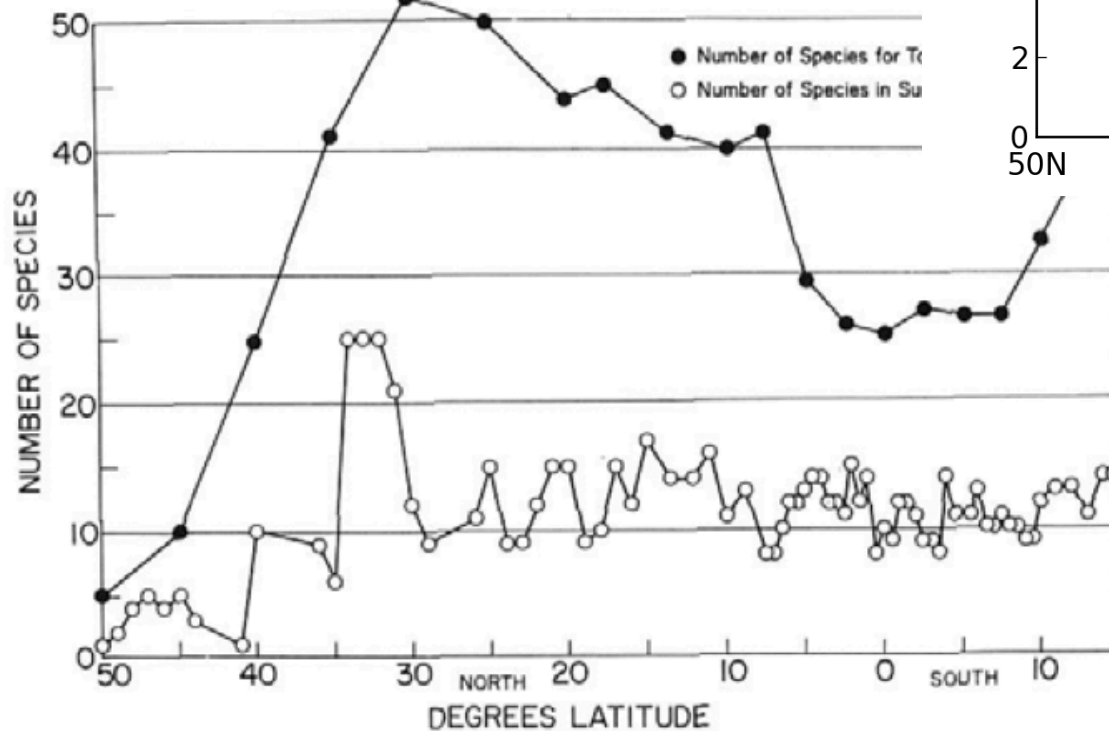
Hotspots of α diversity



α

Number of co-occurring phytoplankton types above threshold biomass
(Clayton et al, 2013; Barton et al, 2010)

Honjo and Okada (1974) Coccolithophore diversity in Pacific



Ecological model: Simplified prognostic equations

$$\frac{\partial B_i}{\partial t} = \mu_{oi} \frac{R}{R + K_{Ri}} B_i - G_{ij}(B_i, Z_j) - \underline{u} \cdot \nabla B_i \quad \text{Phyto}$$

Local rate of
change of
biomass

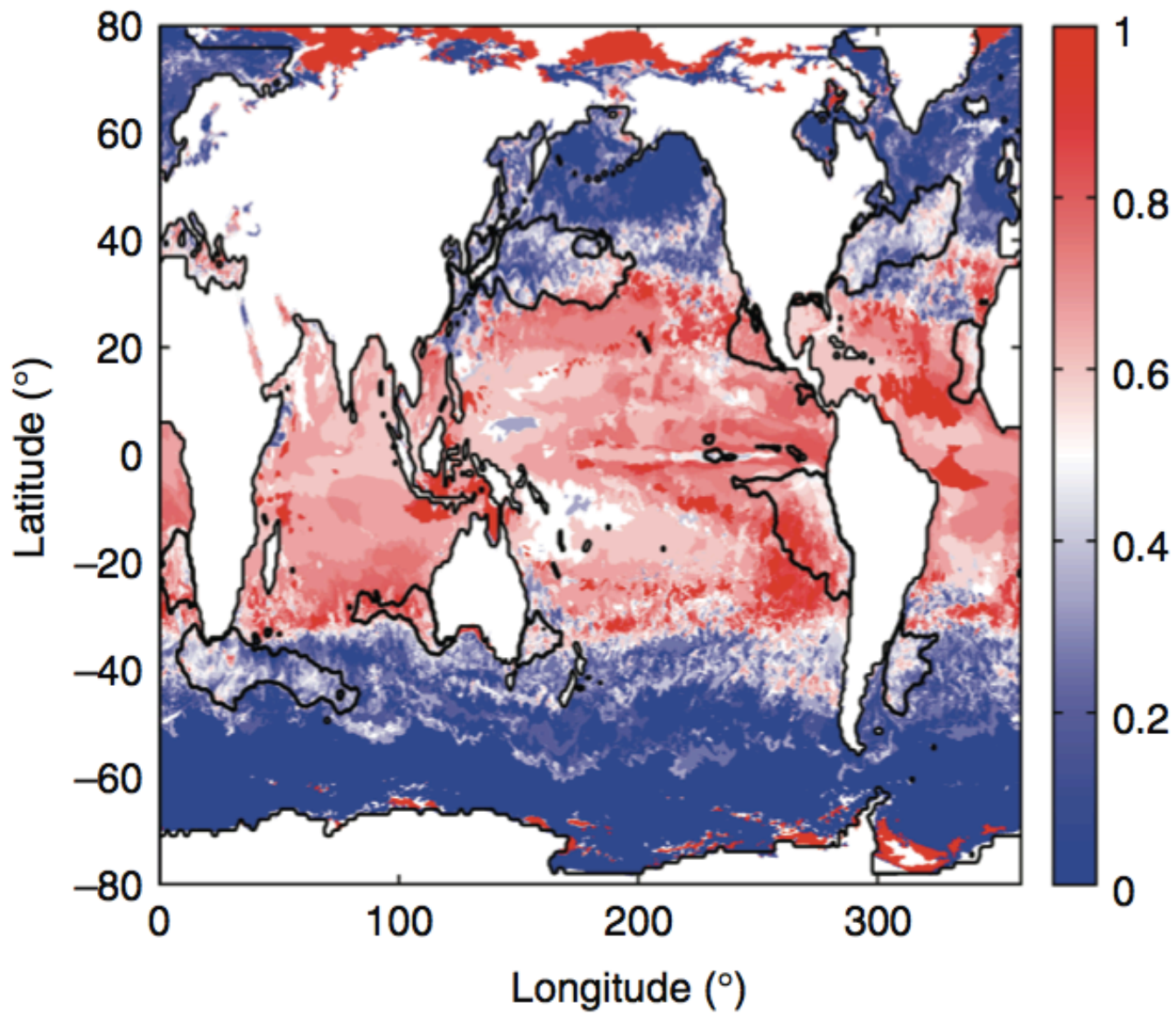
Resource
limited growth

Grazing

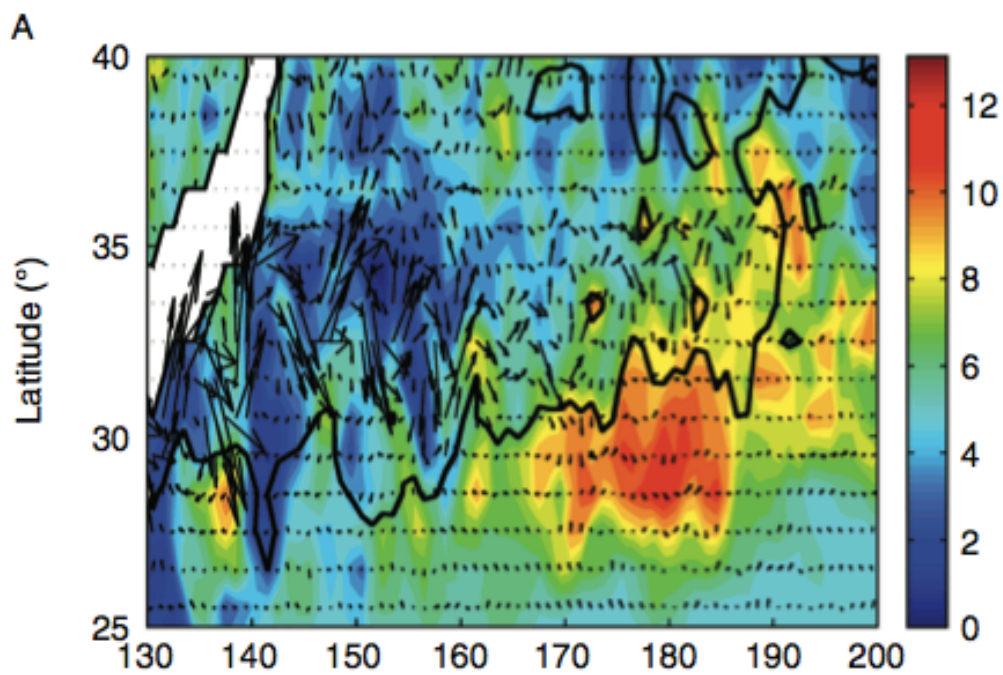
Physical
transport

$$\frac{\partial R}{\partial t} = - \sum_i \mu_{oi} \frac{R}{R + K_{Ri}} B_i + S_R - \underline{u} \cdot \nabla R \quad \text{Resource}$$

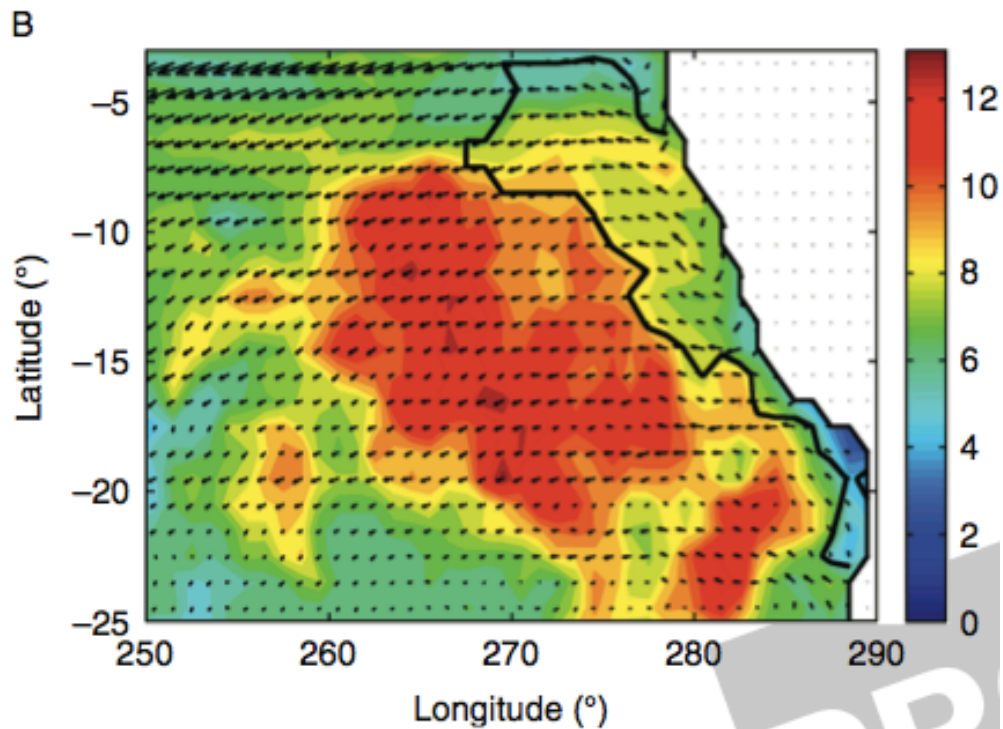
+ grazers, detritus etc...



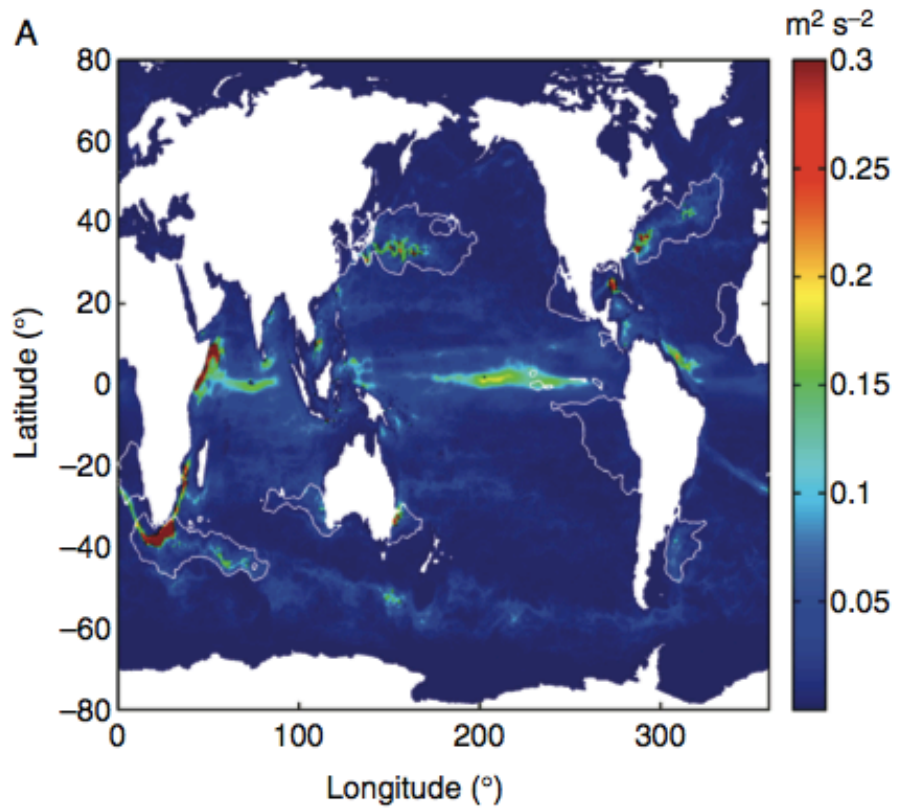
$$\alpha_1 / \alpha$$



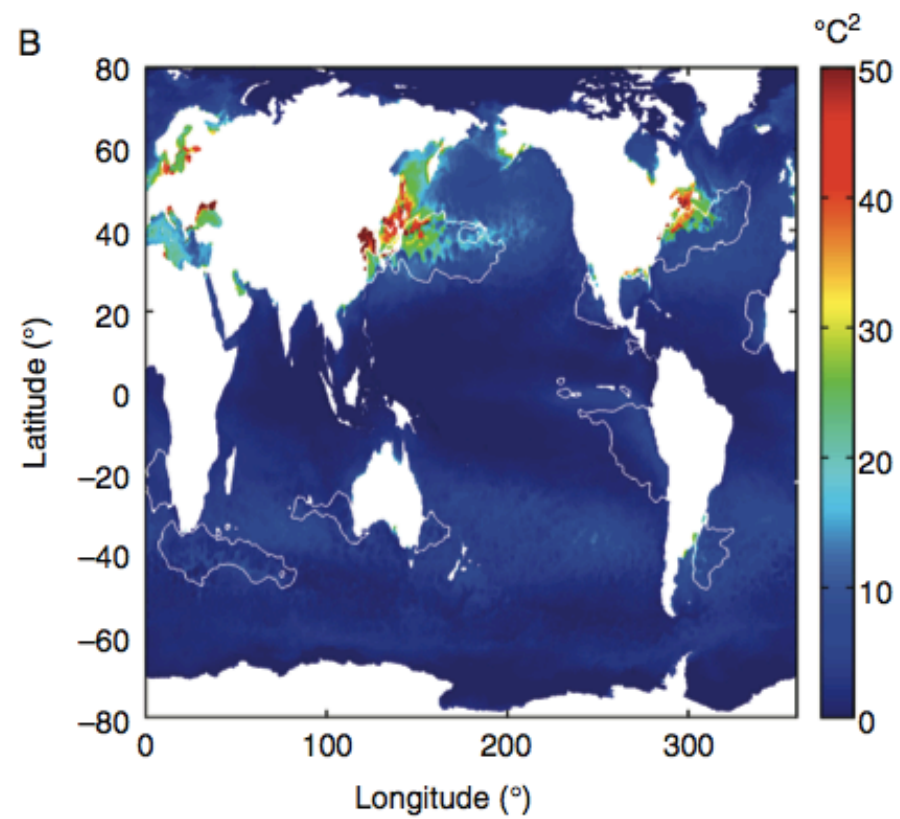
Kuroshio Extension
 α_1



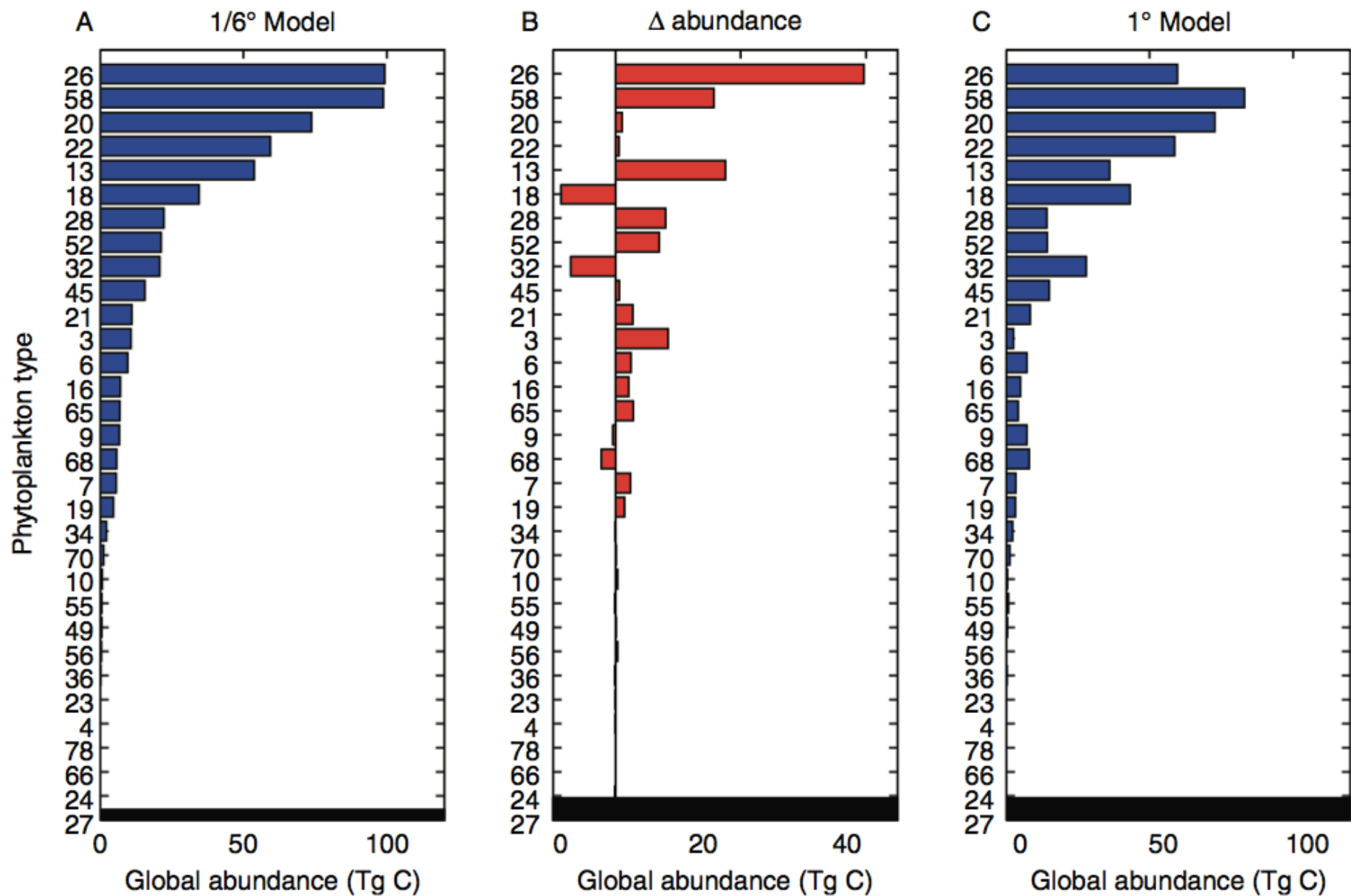
Peruvian upwelling
 α_1

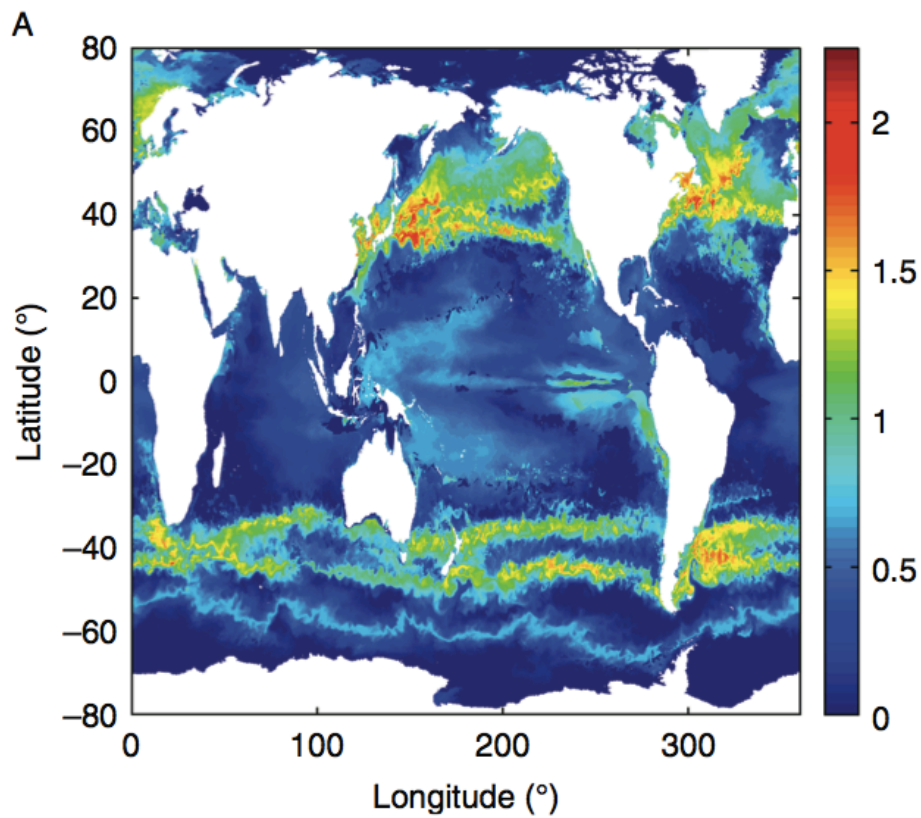


Eddy Kinetic Energy

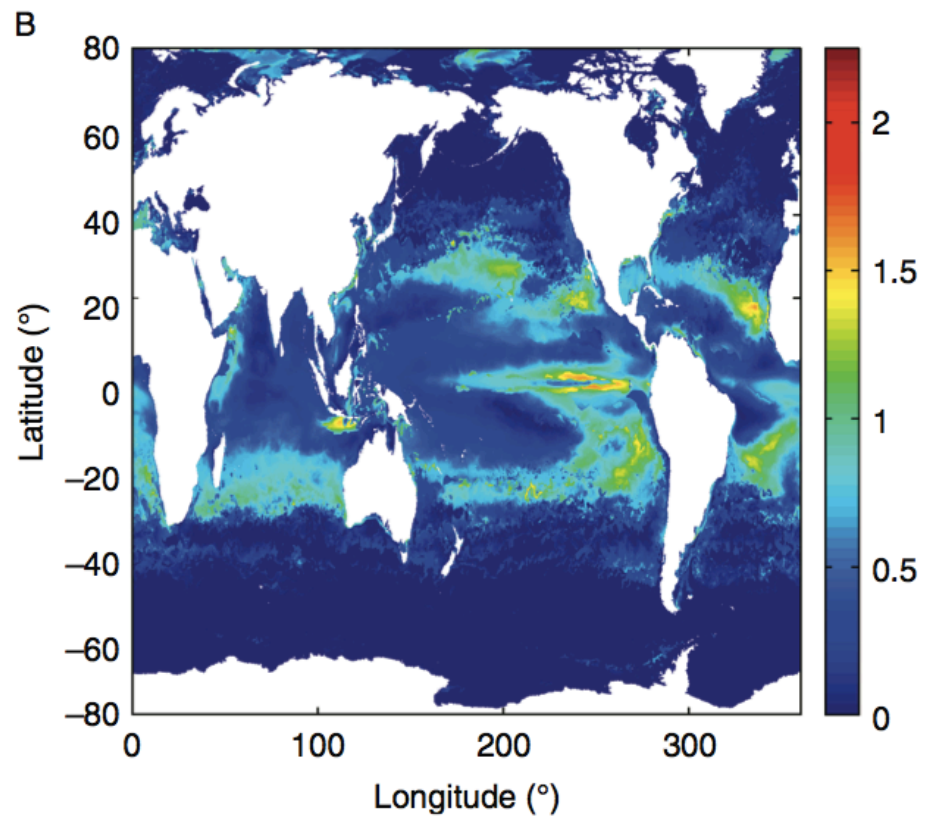


Variance of SST



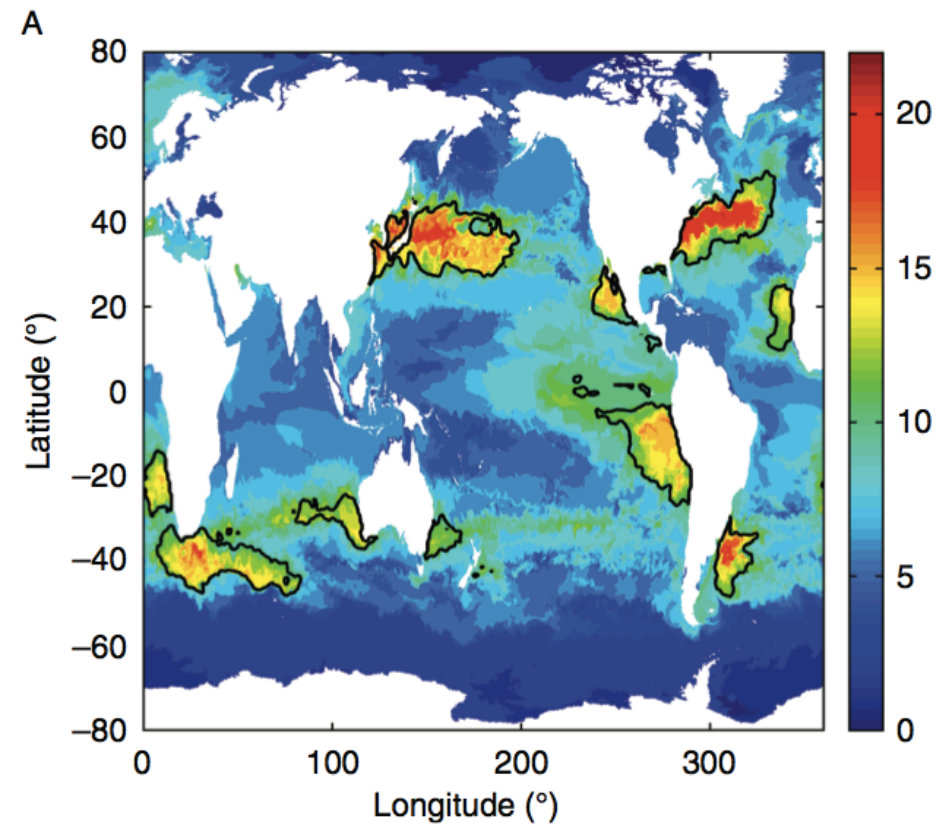


Locally Adapted

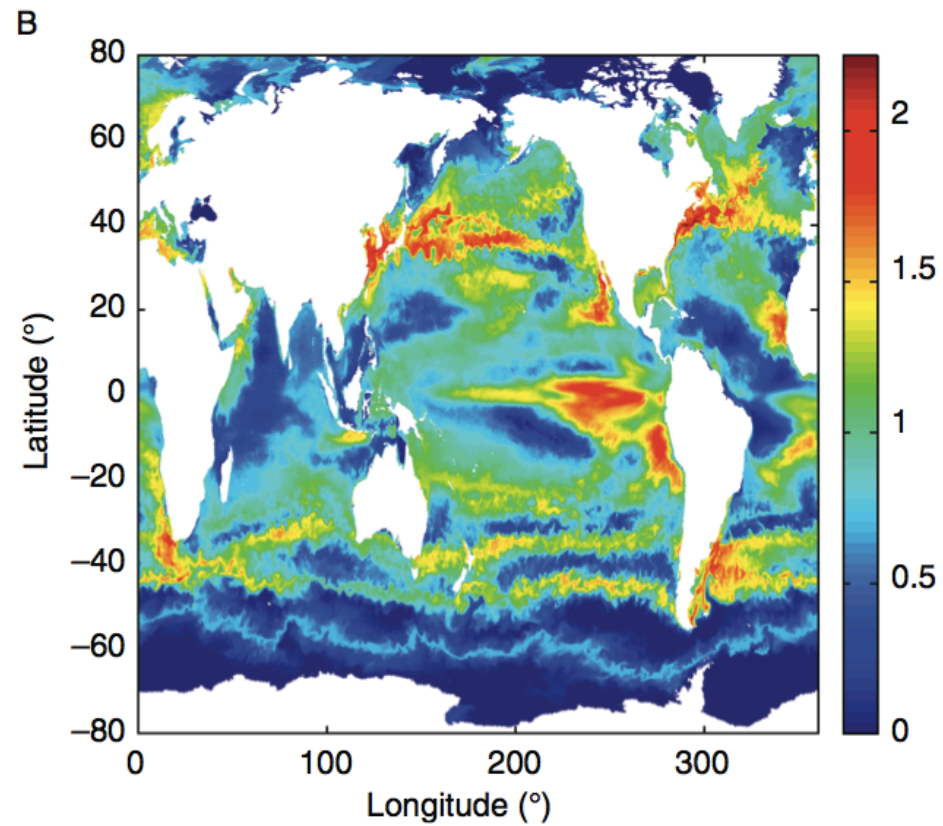


Immigrants

Shannon-Weaver (high-res)



α diversity



Shannon-Weaver index

Alex Worden,
Yun-Chi Lin

Ostreococcus
Clades I and II are
the key players in
the local pico-
eukaryote
population (i.e. in
Kuroshio data set)

