

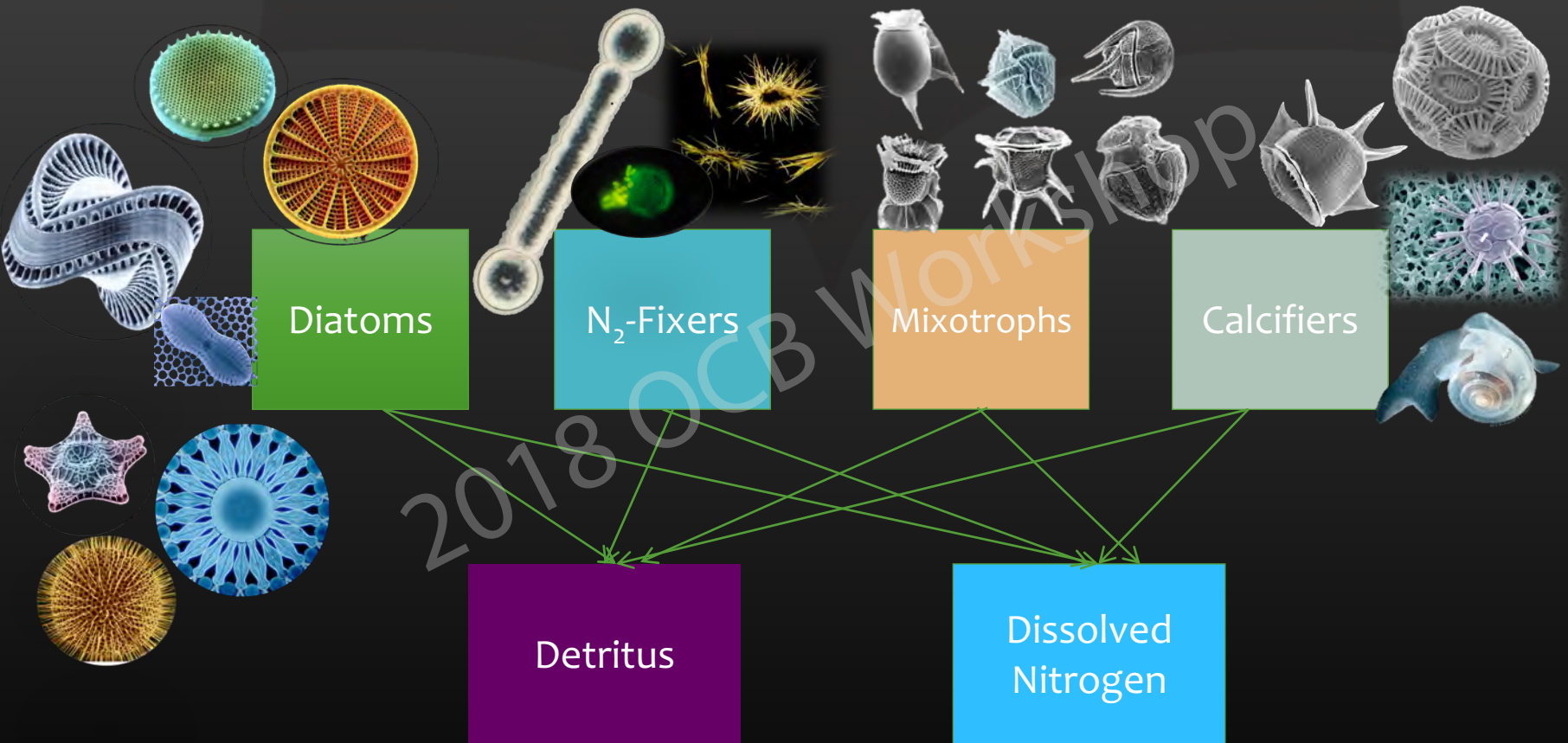
**Who you are?  
or  
What you do?**

Evolution of metabolic function shapes ocean biogeochemistry in a gene based model

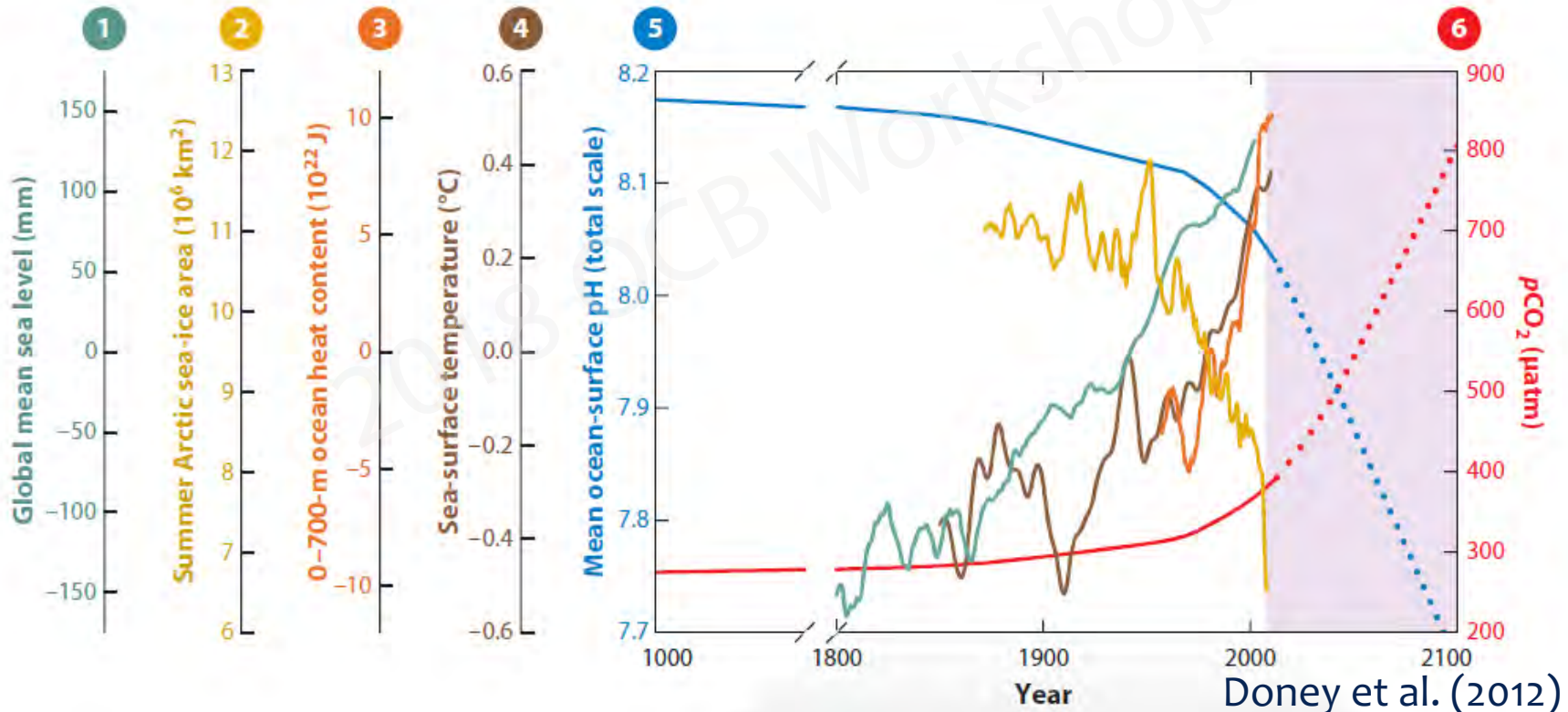
**Victoria Coles**

University of Maryland Center for Environmental Science, Horn Point Laboratory

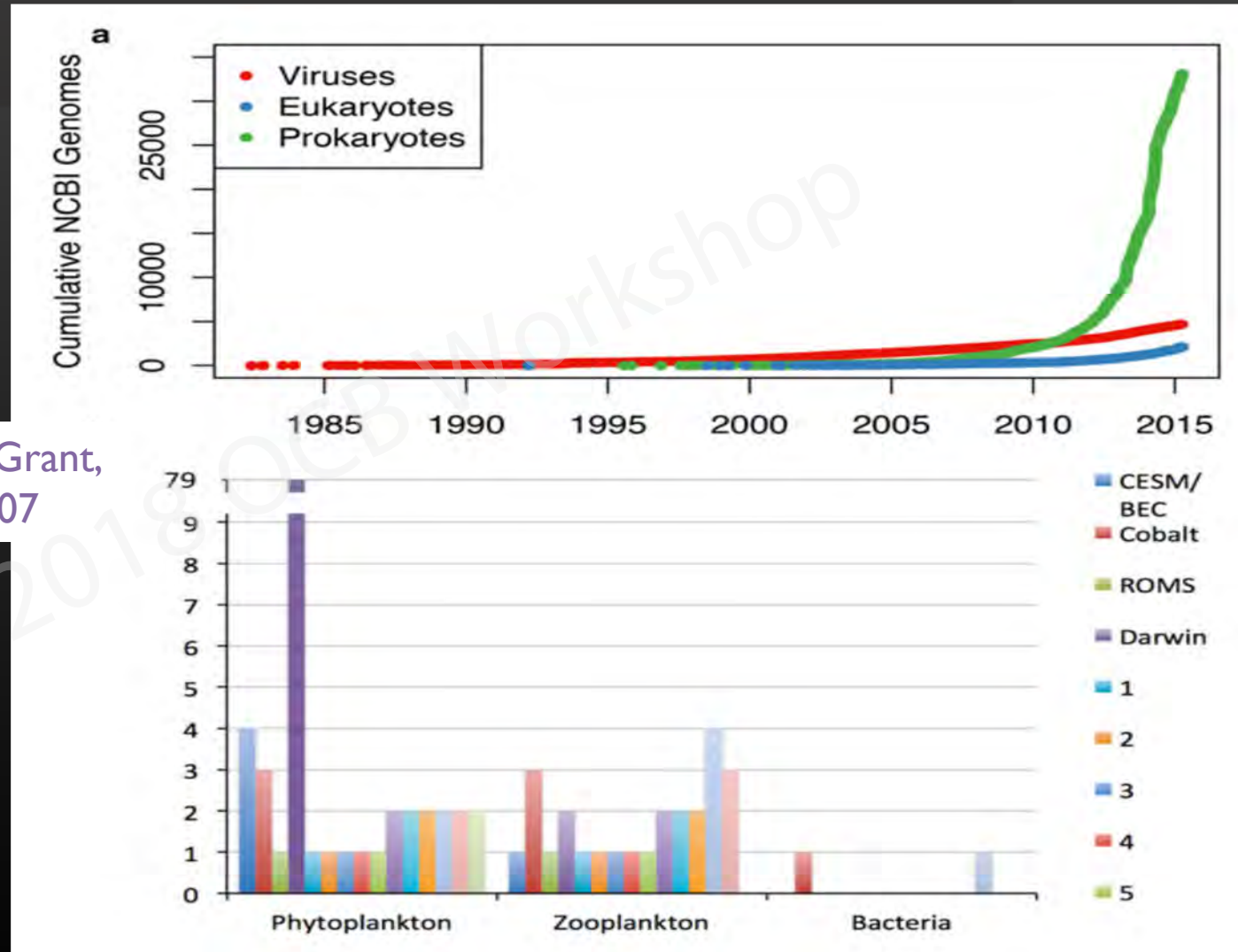
# Some key limitations of (many) functional group models for representing evolutionary processes



# Will the taxa in each functional group respond similarly to changes in pH, temp, nutrient ratios and concentrations?



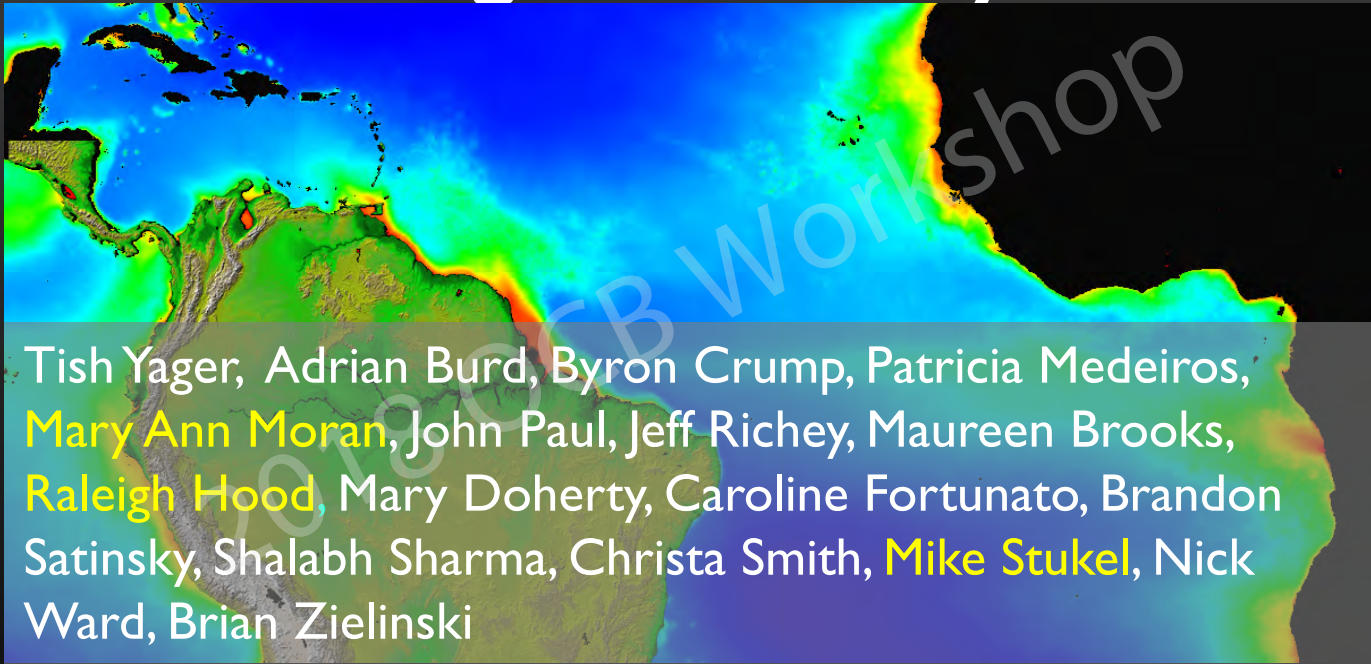
# Mismatch between observational “omics” and models



Follows, Dutkiewicz, Grant,  
Chisholm, Science 2007

Coles and Hood, 2015

Self-organizing communities of microbes - with randomly assembled genomes from a shared pool of metabolic functions - will establish realistic ocean biogeochemistry



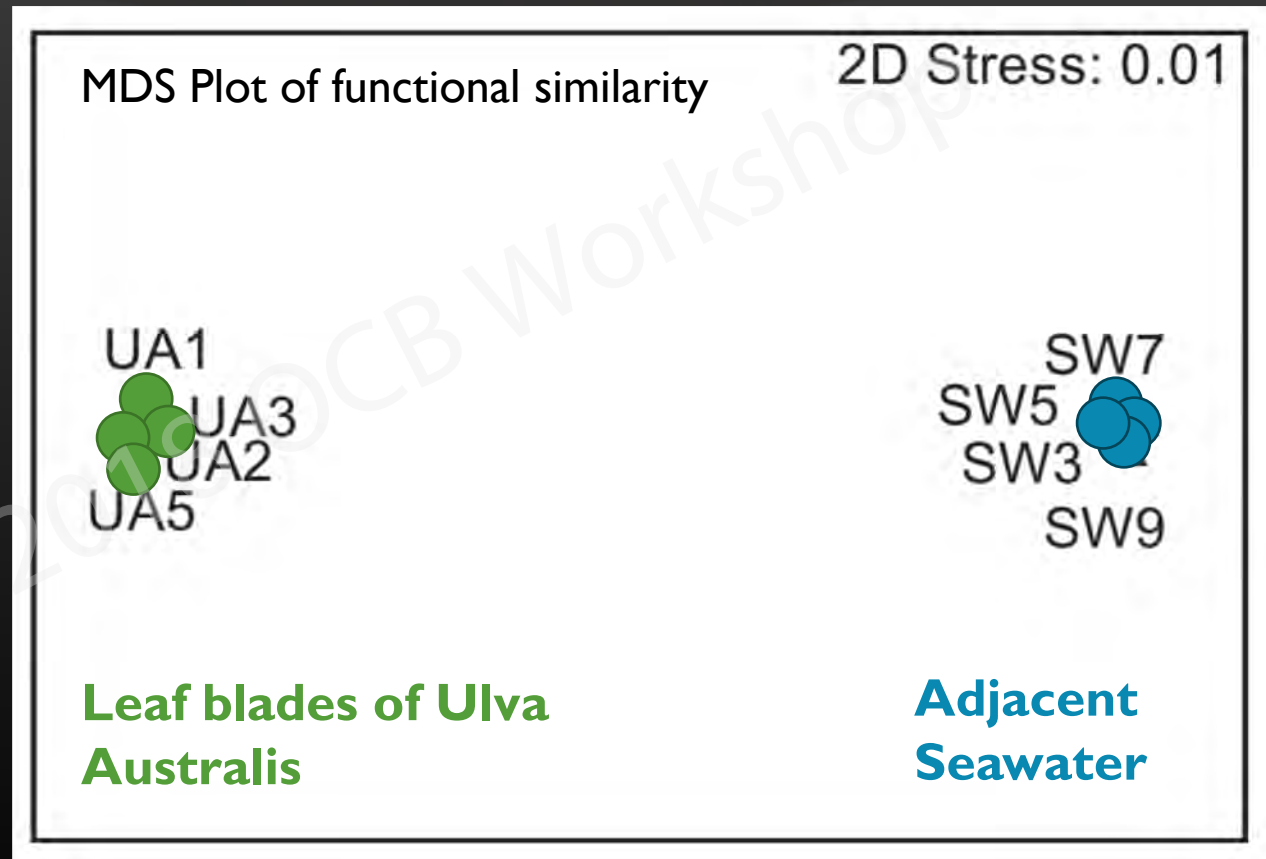
Tish Yager, Adrian Burd, Byron Crump, Patricia Medeiros, Mary Ann Moran, John Paul, Jeff Richey, Maureen Brooks, Raleigh Hood, Mary Doherty, Caroline Fortunato, Brandon Satinsky, Shalabh Sharma, Christa Smith, Mike Stukel, Nick Ward, Brian Zielinski

Gordon and Betty

**MOORE**  
FOUNDATION



# Adjacent surfaces are colonized by different microbial species with similar metabolic function

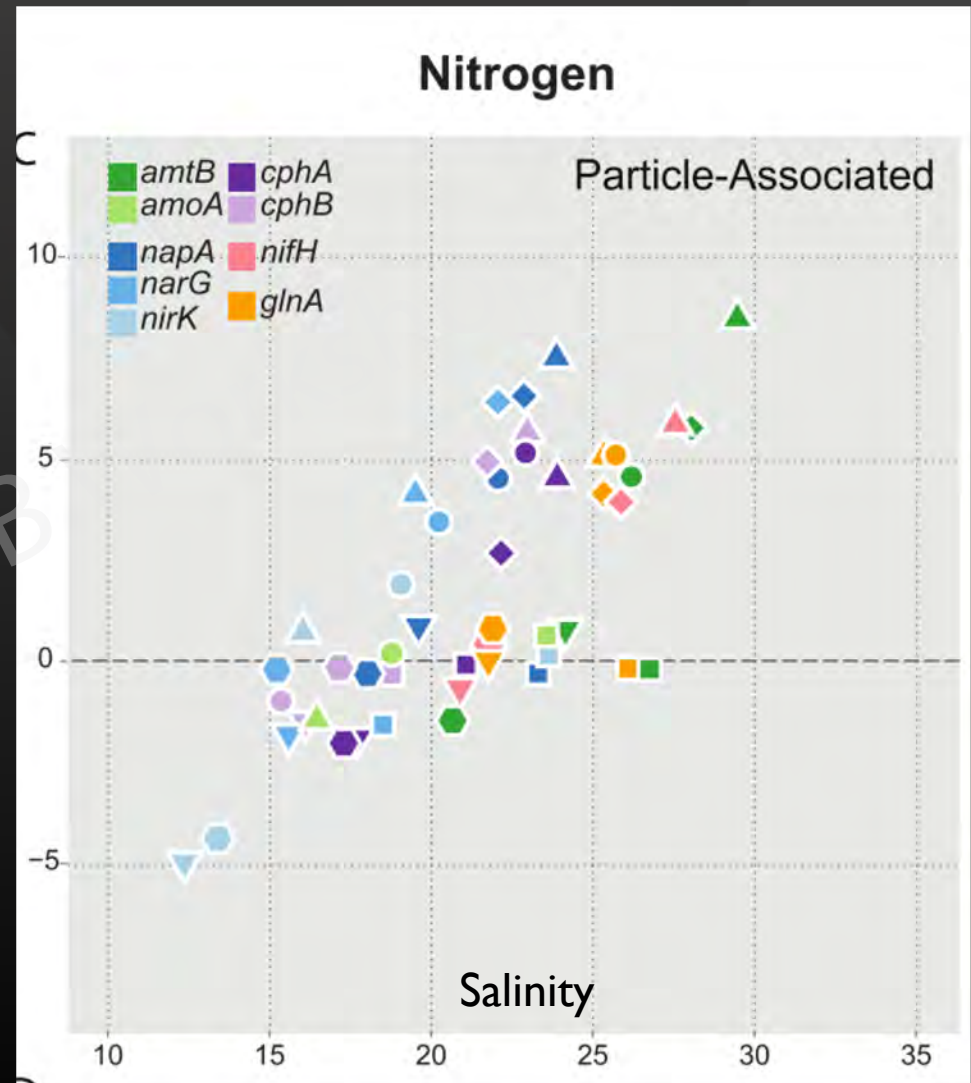


# 2018 OCB Workshop

Animator: Rainier Hood

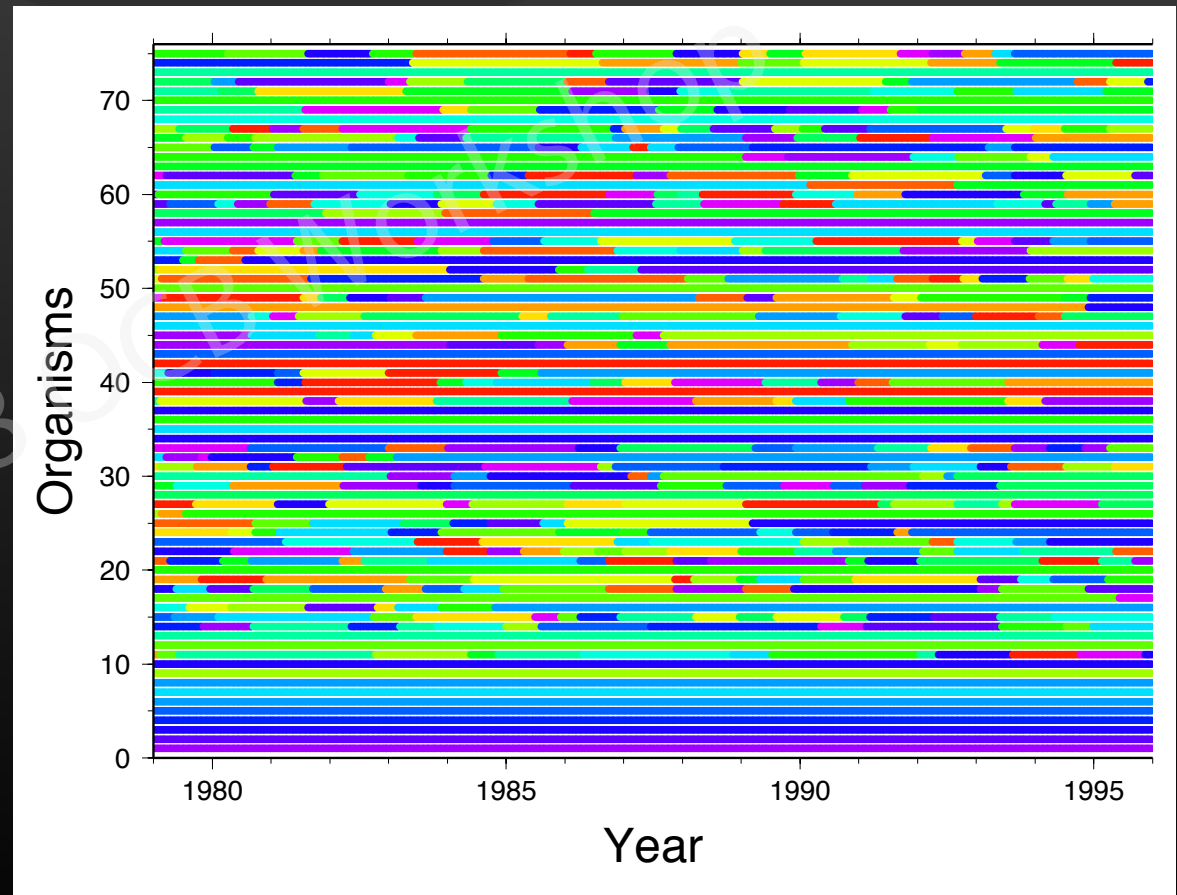
# A library of “genes” coding for functions relevant to nitrogen cycling

Normalized  
expression  
ratio

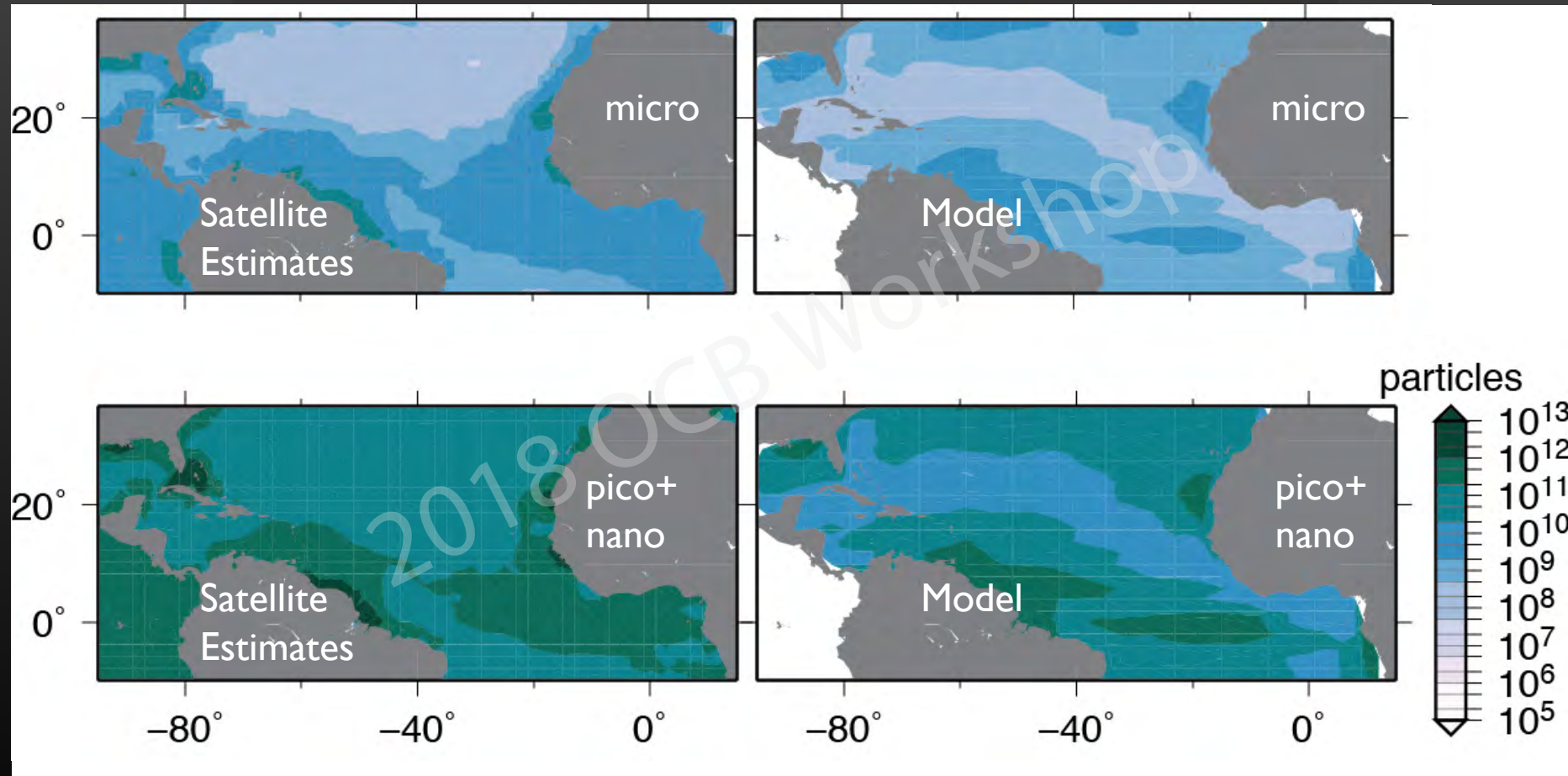




**Broad gene potential is maintained by ongoing insertion of new organisms to replace those that never become successful.**

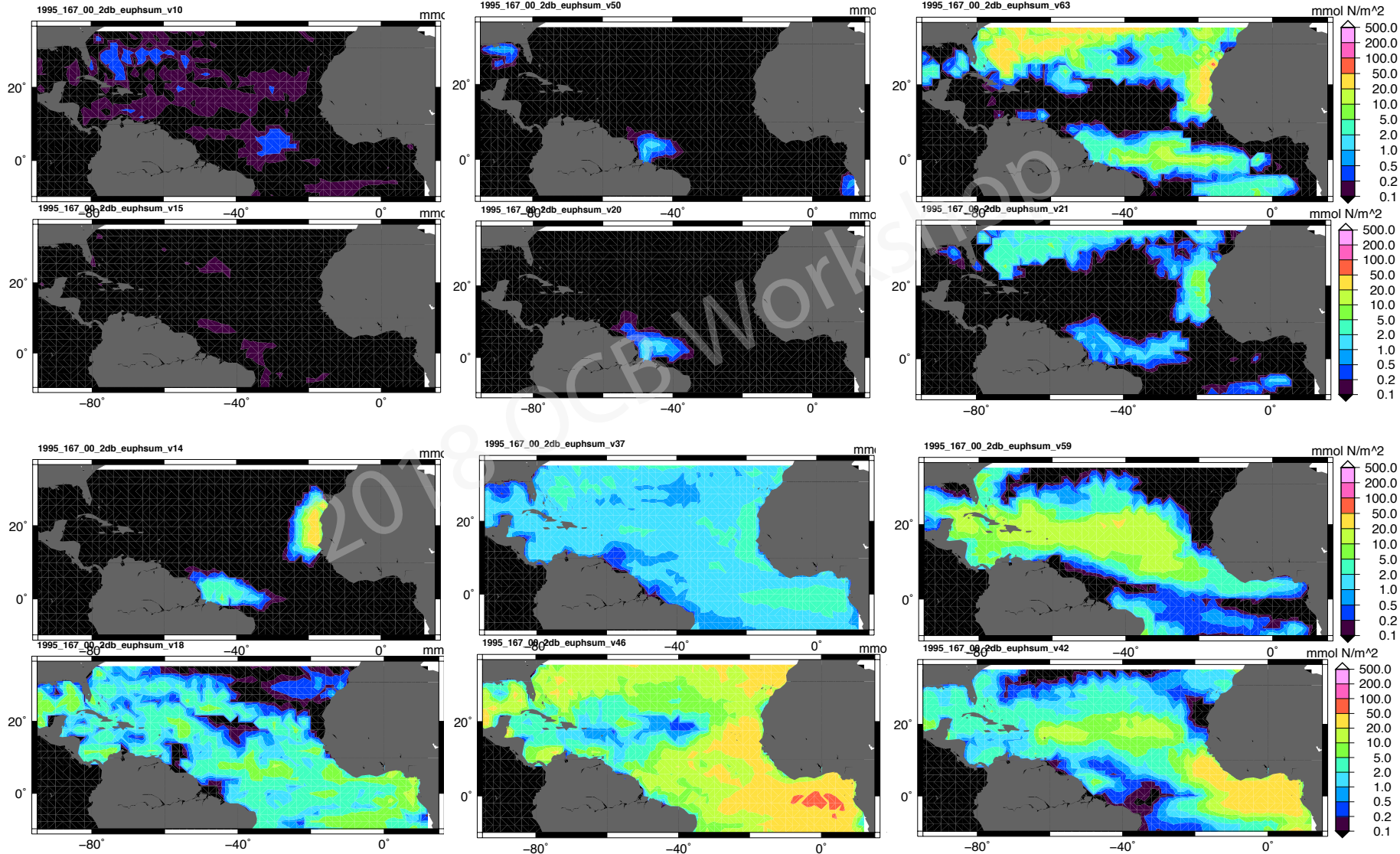


# The emergent model community develops realistic size structure patterns – a key requirement for evaluating export



Satellite fields from Kostadinov et al, 2010

# The emergent community occupies diverse spatial niches

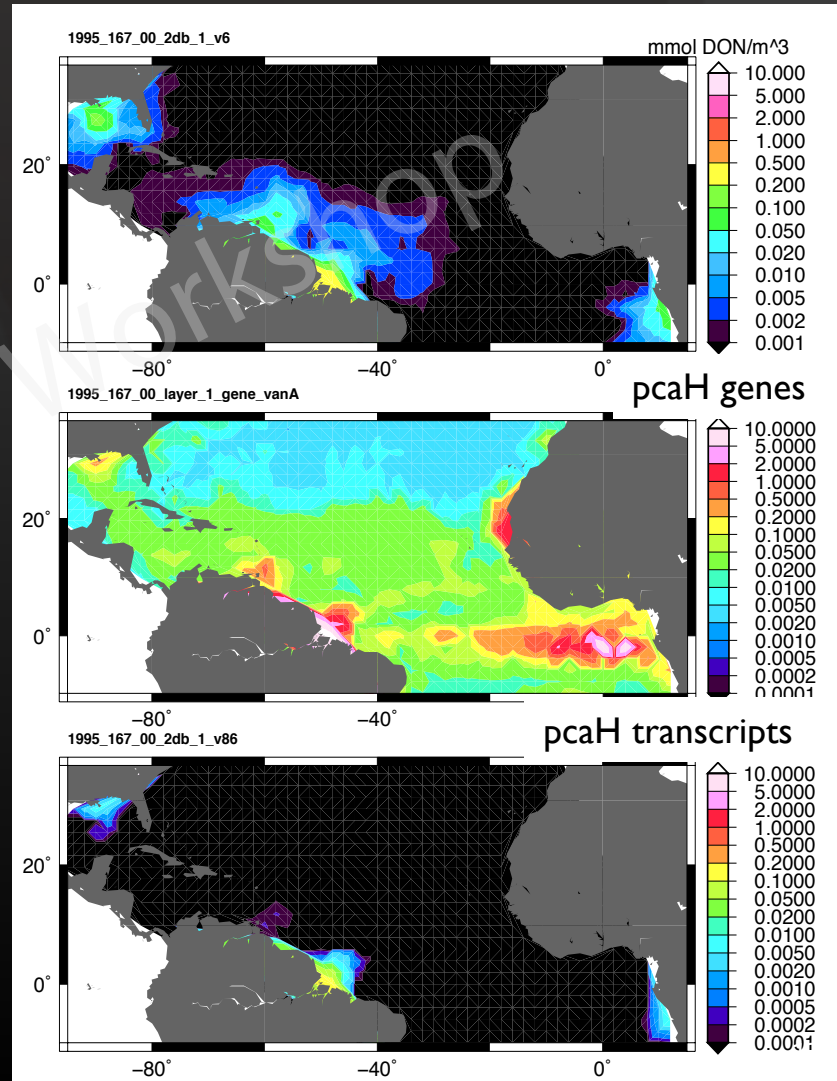


# Emergent patterns in metagenomes and metatranscriptomes can be mapped in relation to substrates

Terrestrial DOM (e.g. lignins)

Metagenomes for aromatic compound metabolism *pcaH* (community potential)

Metatranscripts of *pcaH* (community activity)



# Emergent metagenomic patterns can be compared with observations and cost-benefit choices reviewed.

Terrestrial DOM (e.g. lignins)

pcaH genes

Metagenomes for aromatic compound metabolism *pcaH* (community potential)

pcaH transcripts

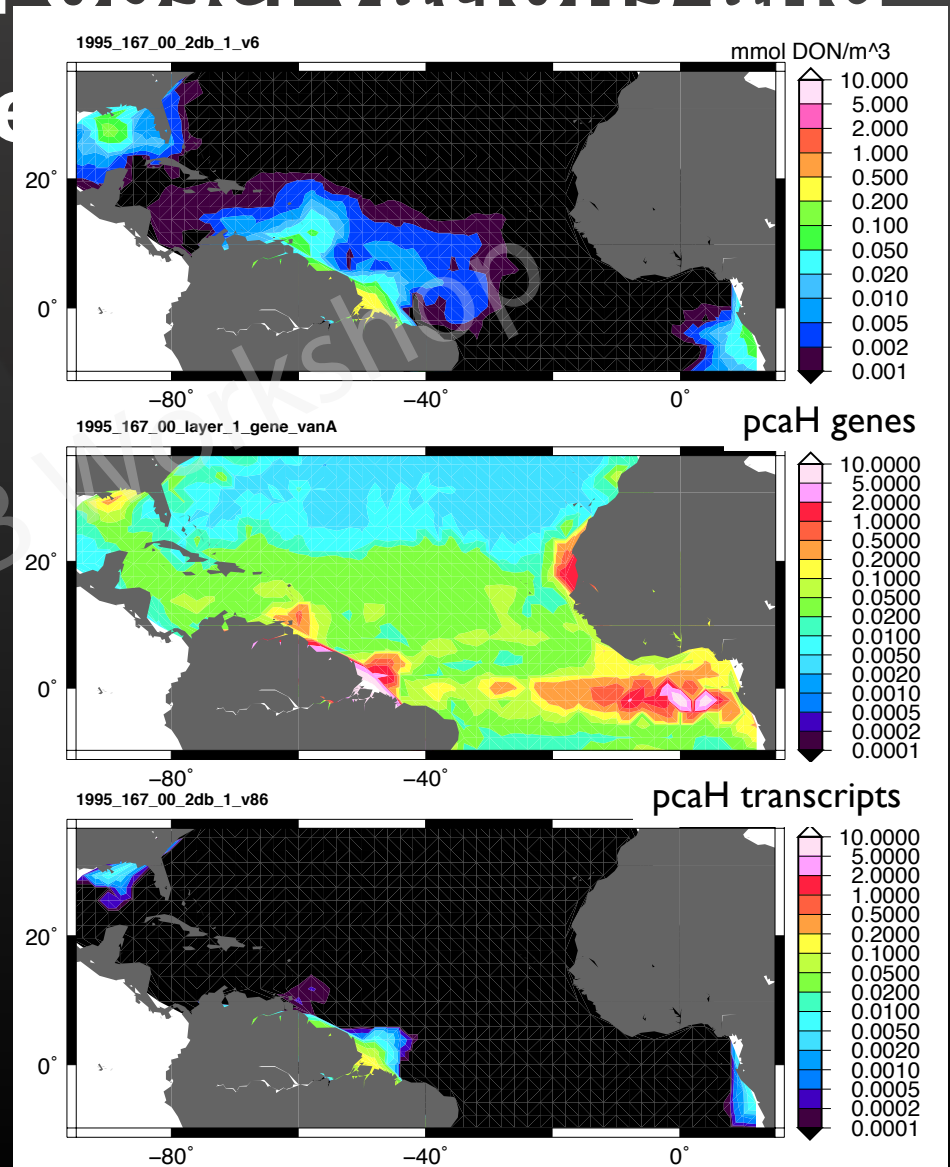
Metatranscripts of *pcaH* (community activity)

# Emergent metagenomic patterns can be compared with observations and cost-benefit choices

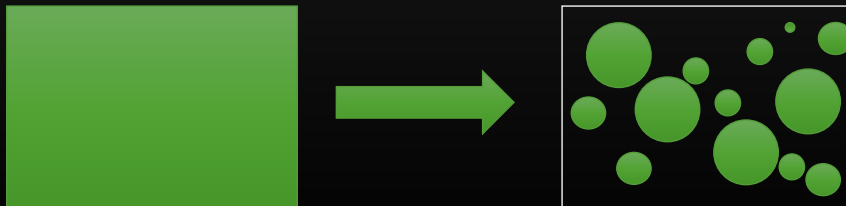
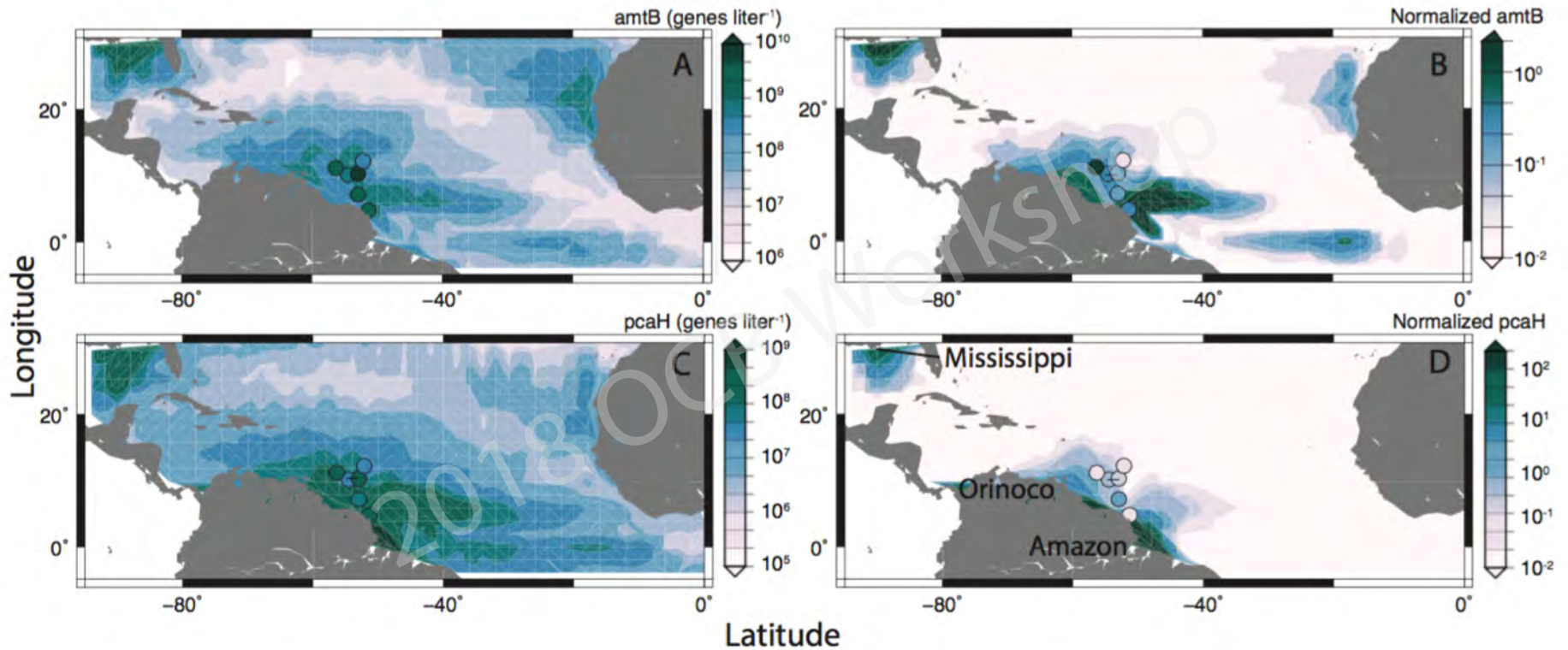
Terrestrial DOM (e.g. lignins)

Metagenomes for aromatic compound metabolism *pcaH* (community potential)

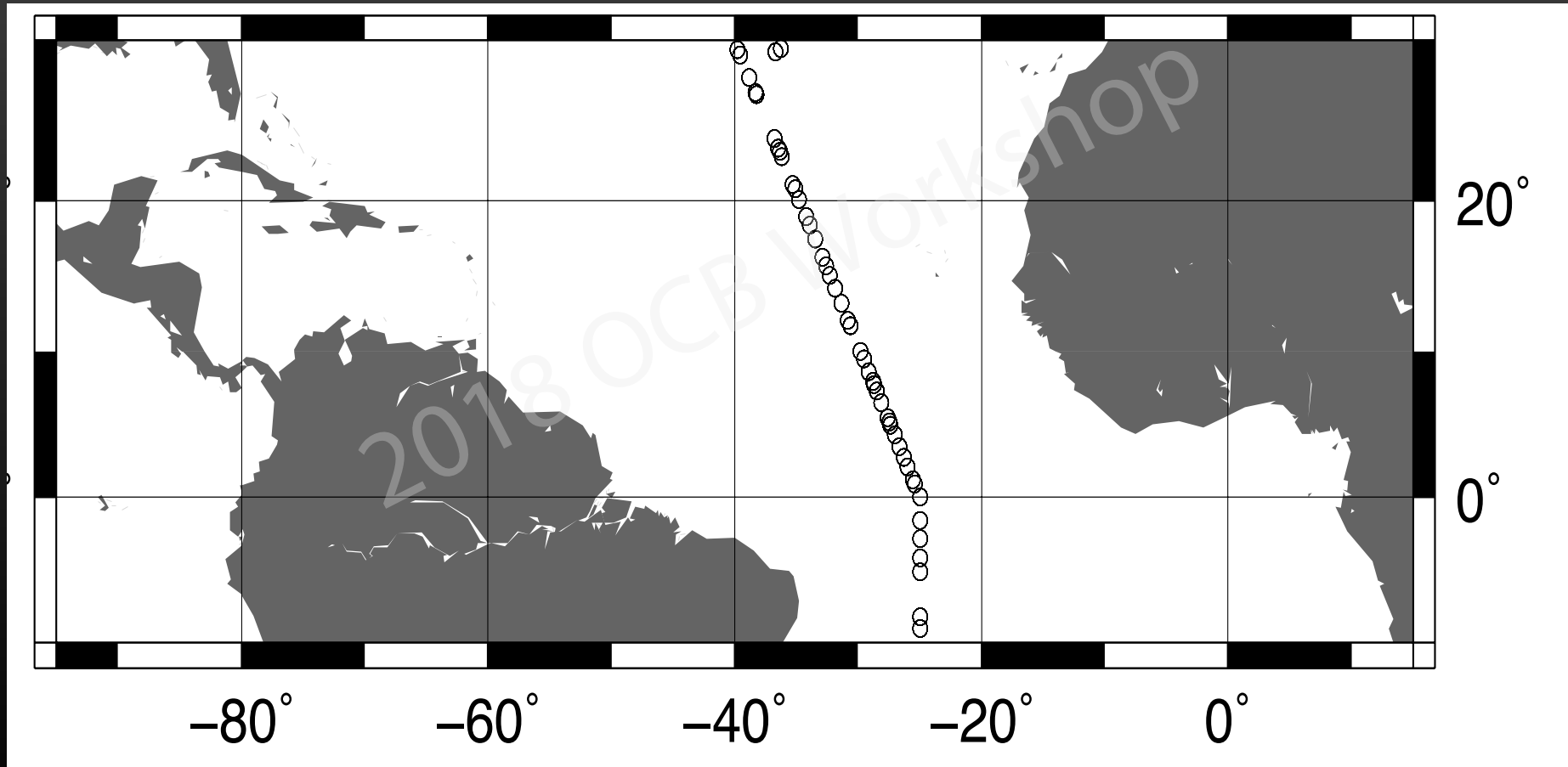
Metatranscripts of *pcaH* (community activity)



# Direct comparison of model with omics observations are reasonable



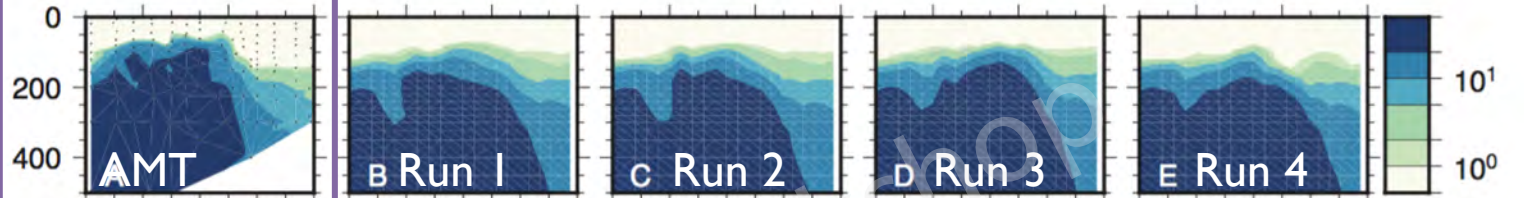
All conversion of DON, PON and  $\text{NH}_4$  to  $\text{NO}_3$  occurs through the emergent community and the genetic potential of each organism



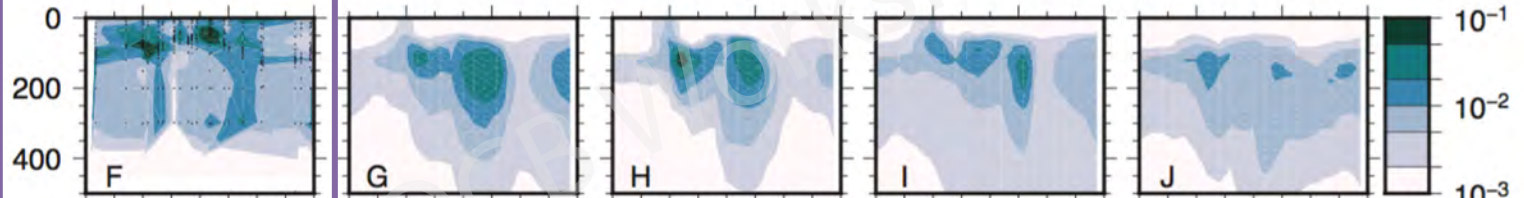


# Model simulations with different organisms but common gene functions show similar biogeochemical gradients

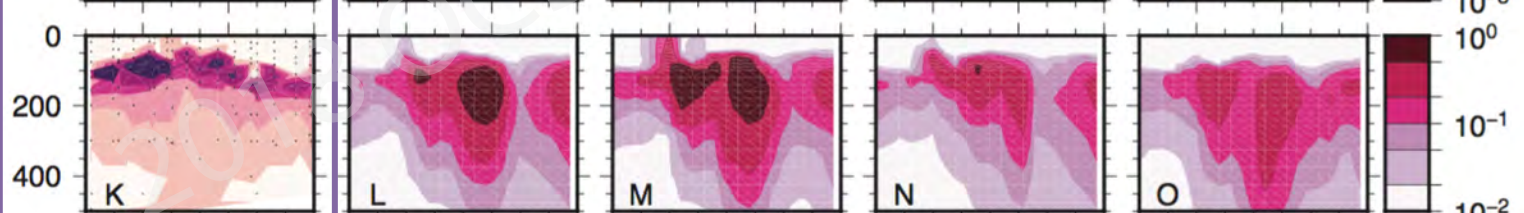
Nitrate



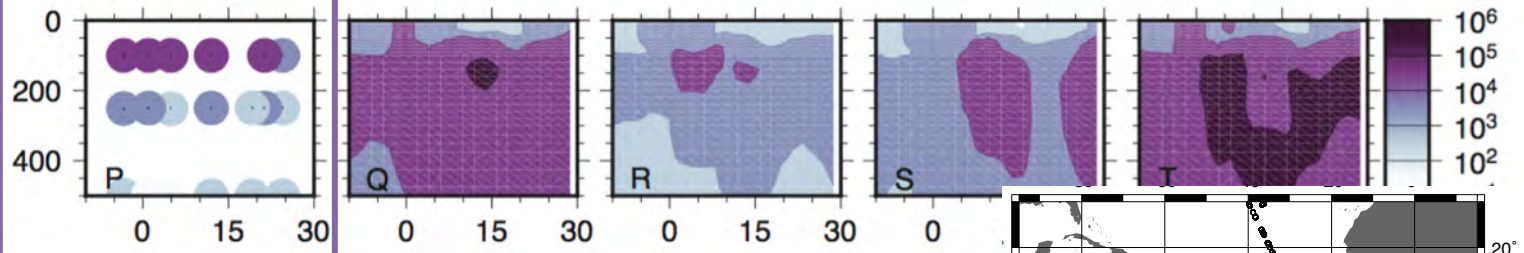
Ammonium



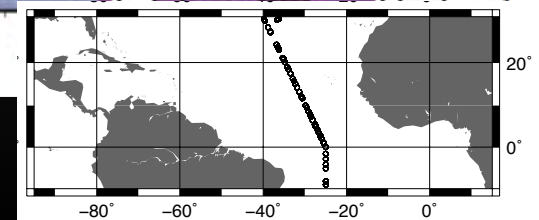
Nitrite /  
amoA  
transcripts



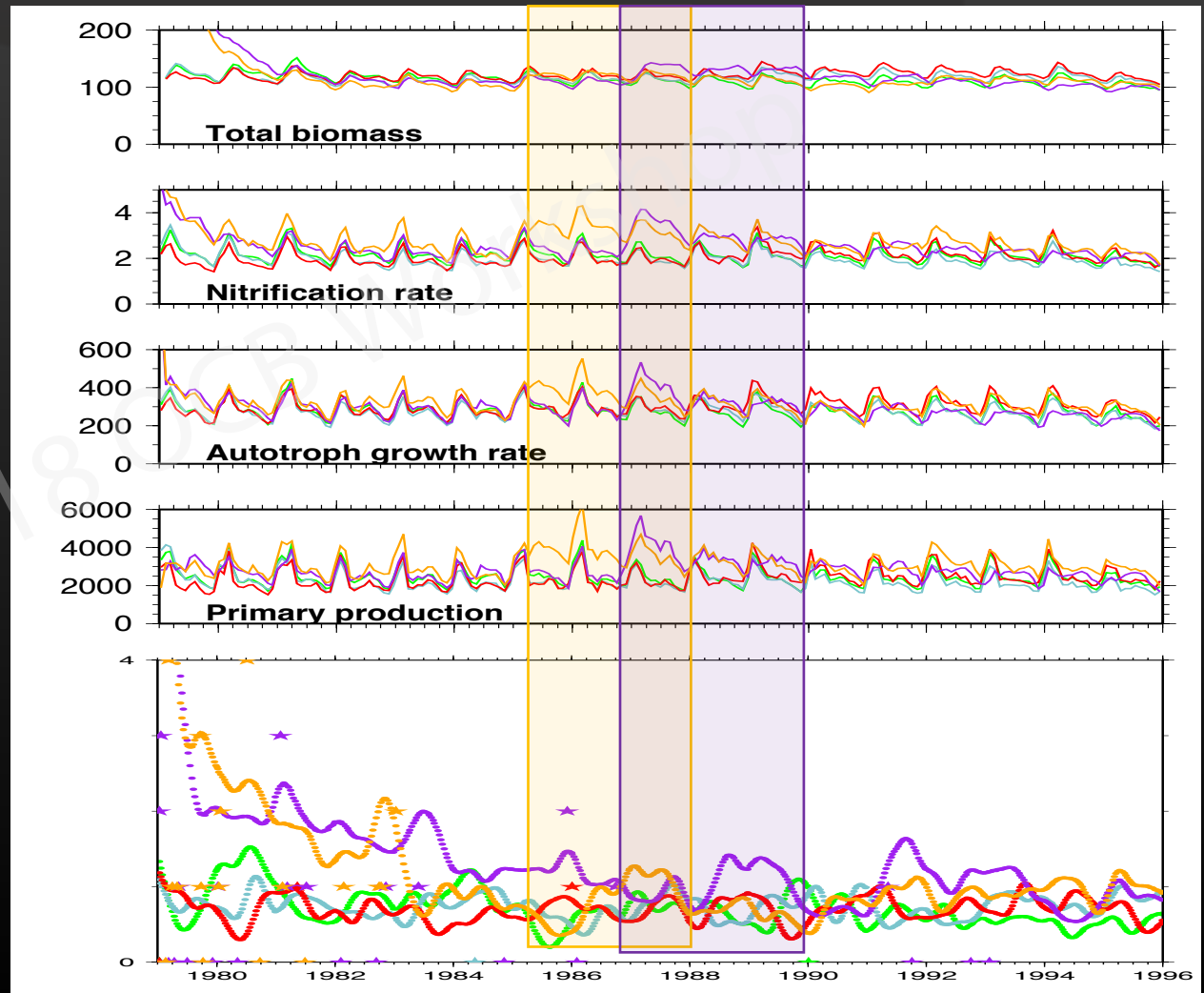
amoA Gene  
copy #



Gene counts from Agogué et al 2008, Nutrients from the Atlantic Meridional Transect Program



# Species introductions (evolution) can strongly reshape the model properties over the short term

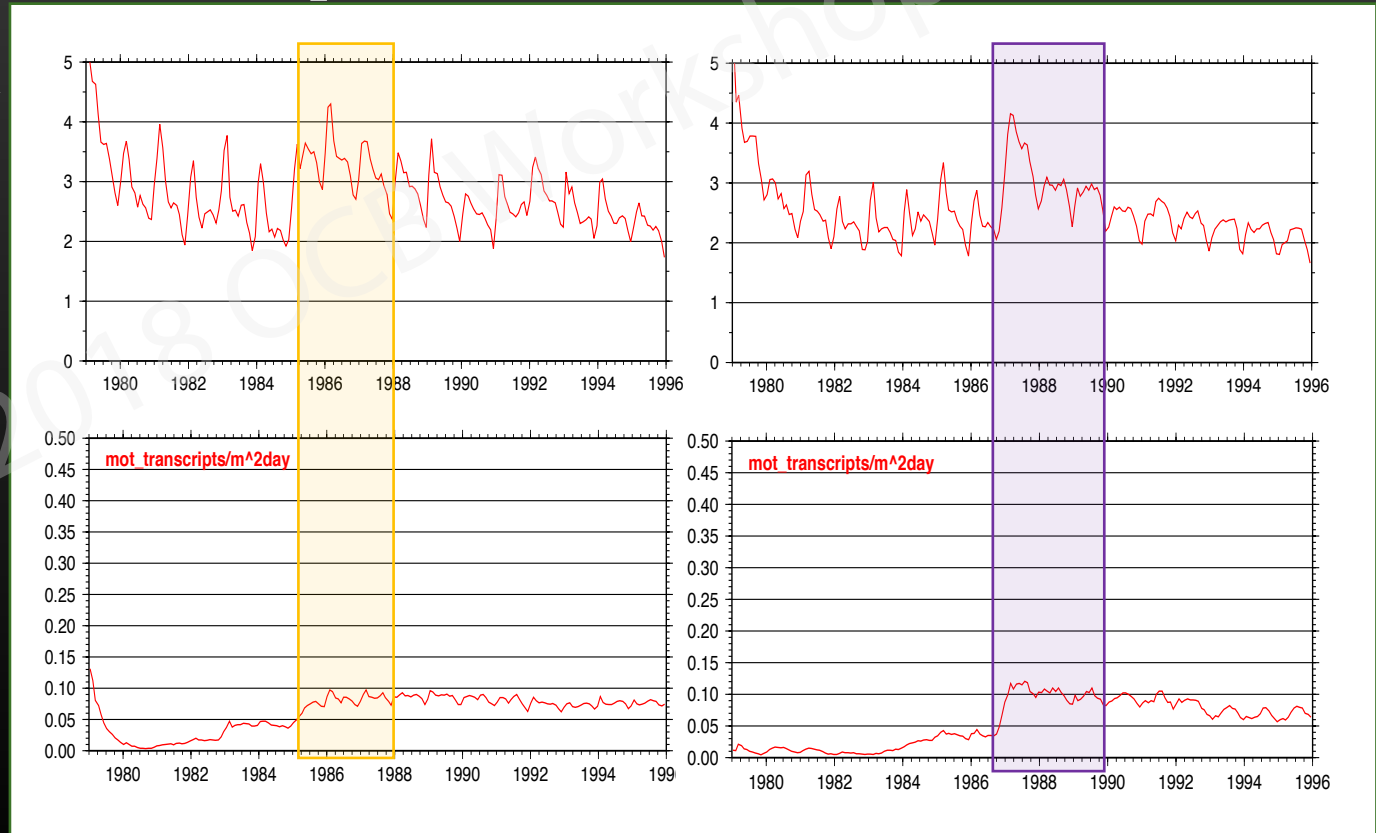


New species  
introduction rate

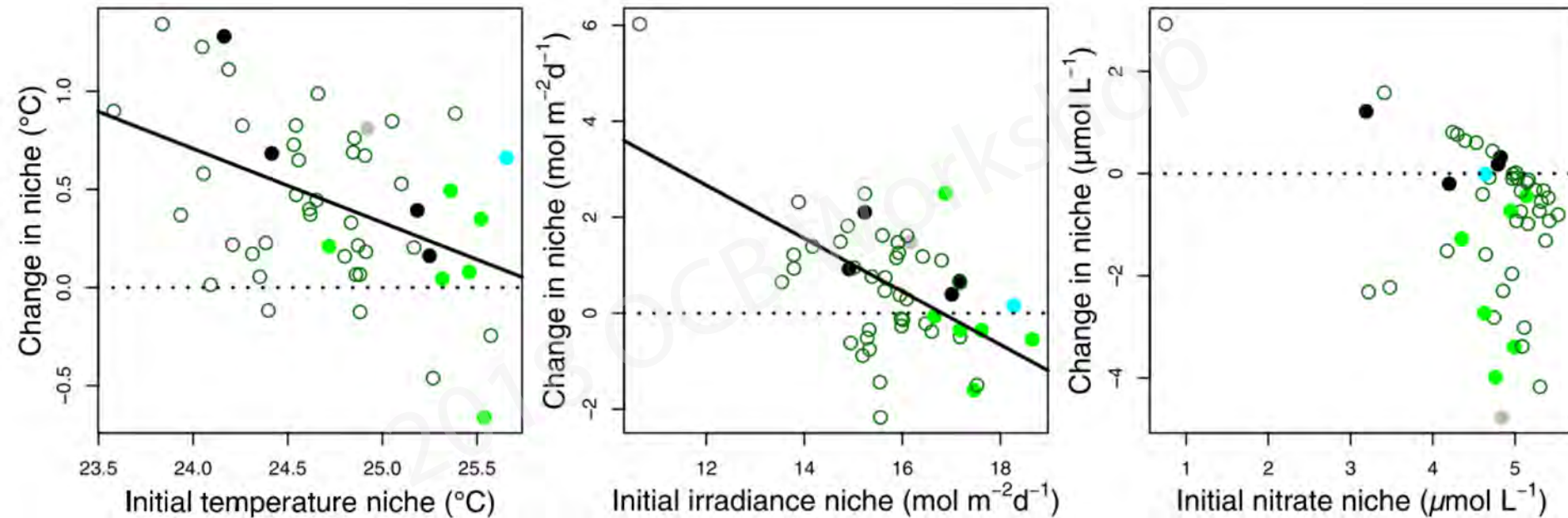
# Changes in organism's ability to nitrify at low ammonium concentrations appears to be a key model sensitivity

Basin averaged amoA transcript concentration

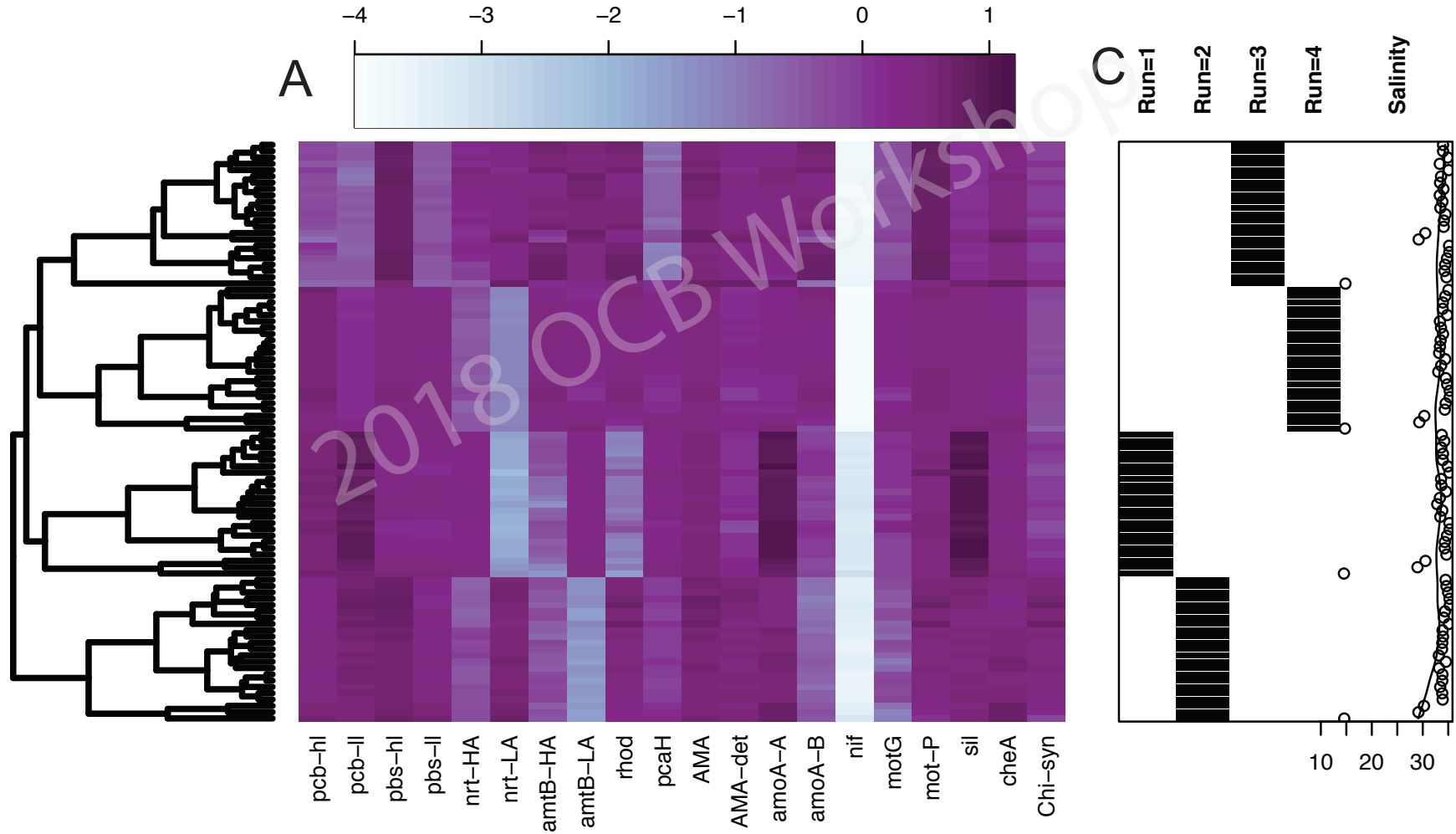
Basin averaged transcript concentration



# Species environmental niche is more flexible for temp. and light than for nitrate



# Model simulations with different organisms have dissimilar metagenomes

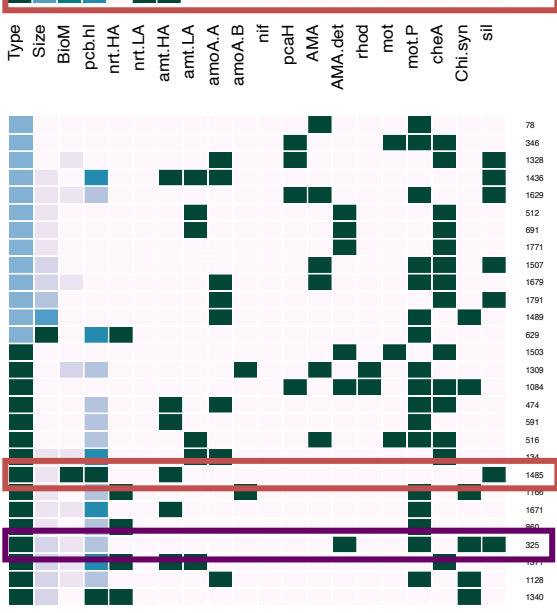
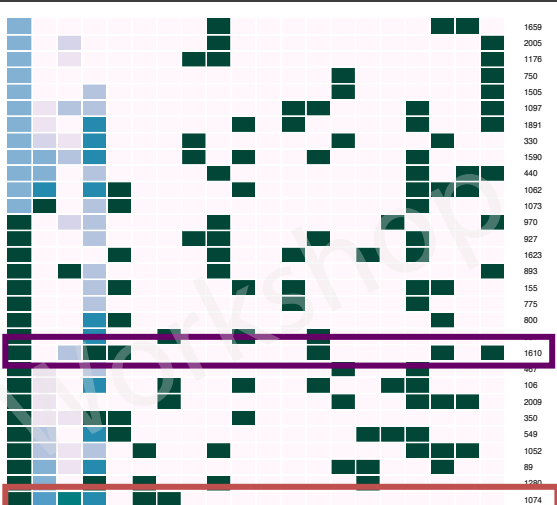
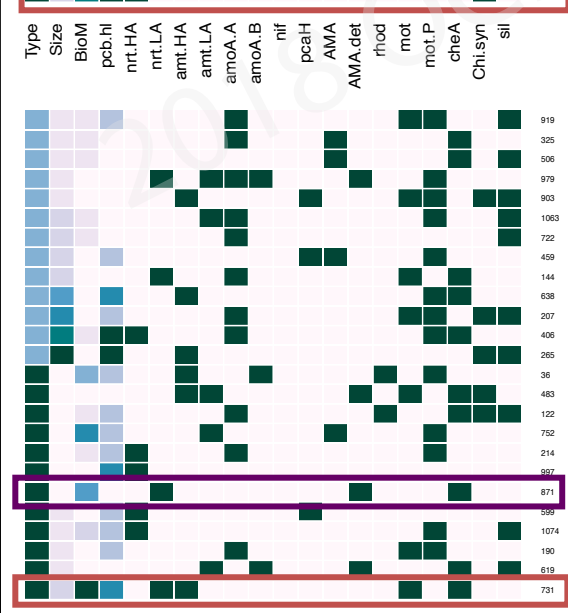
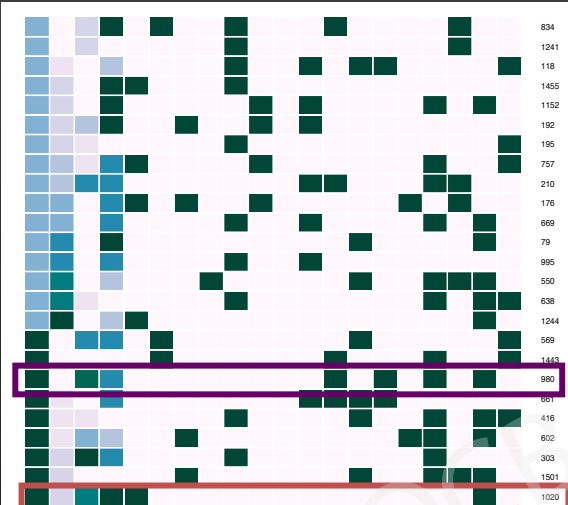


# Model communities differ, but share prochlorococcus and SAR analogs

Run 1

SAR

Prochlorococcus analog



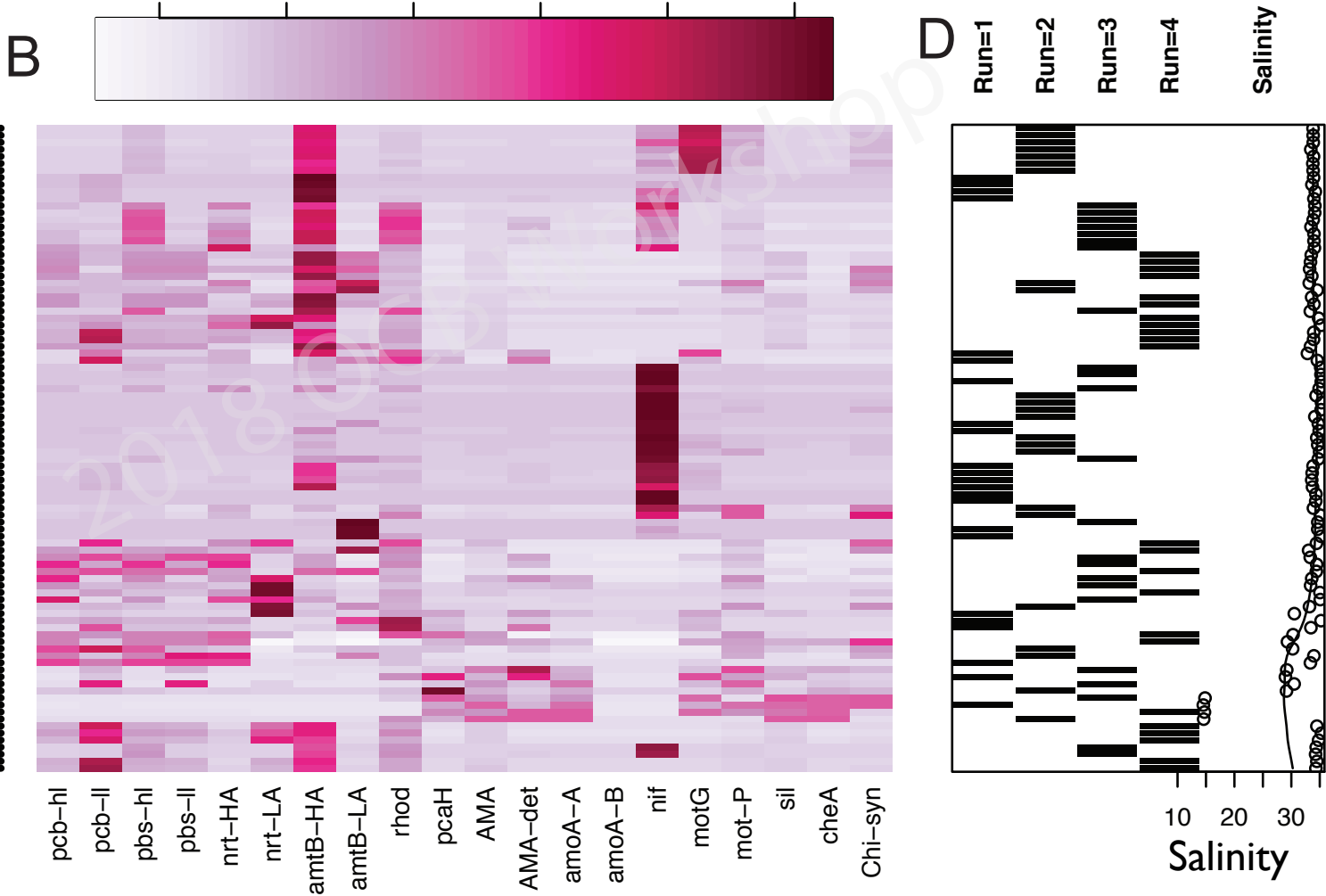
Run 3

Organism #

Run 4

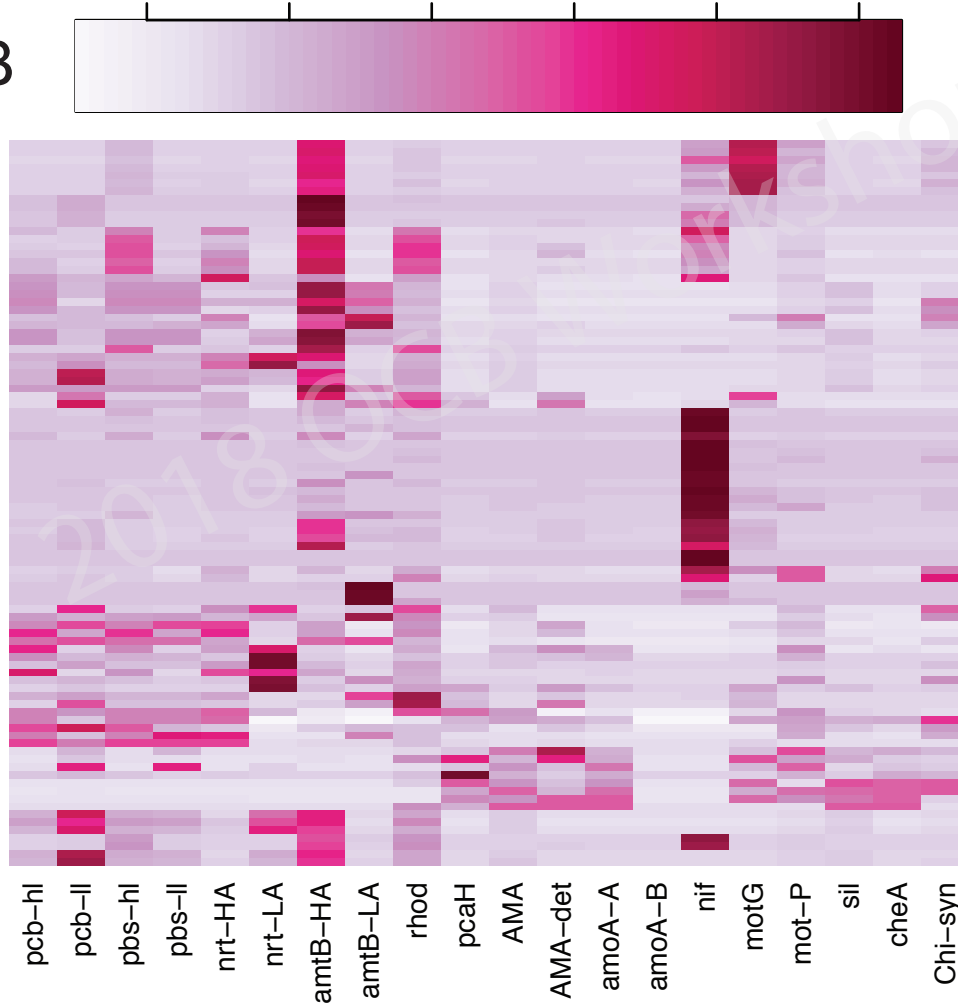
Organism #

# The metatranscriptomes – reflecting realized function – are similar across runs in similar physical environments

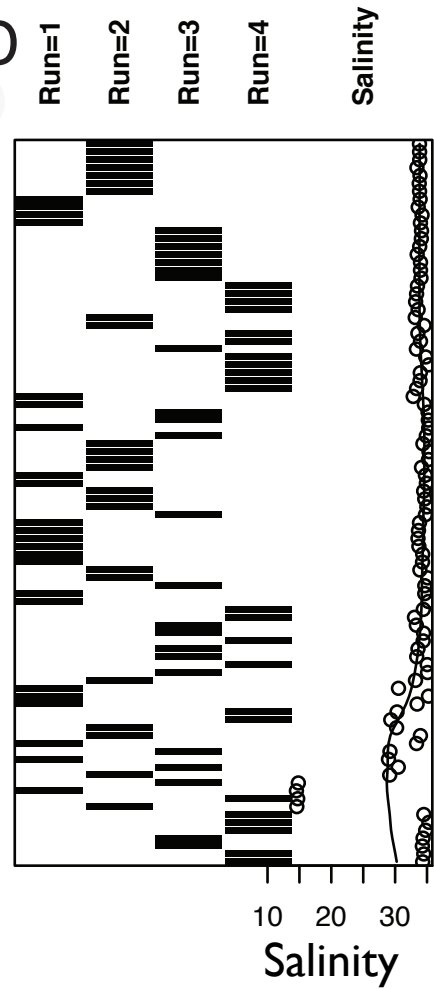


# Its not who you are underneath but what you do that defines you

B

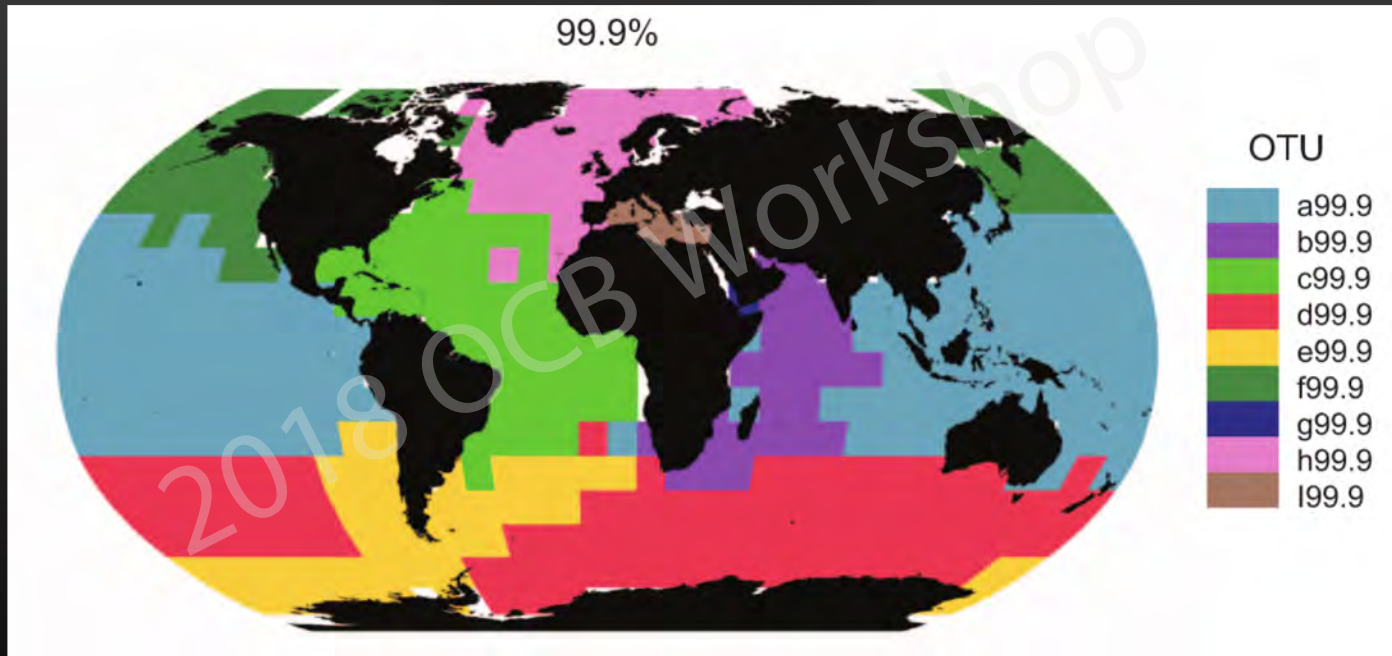


D



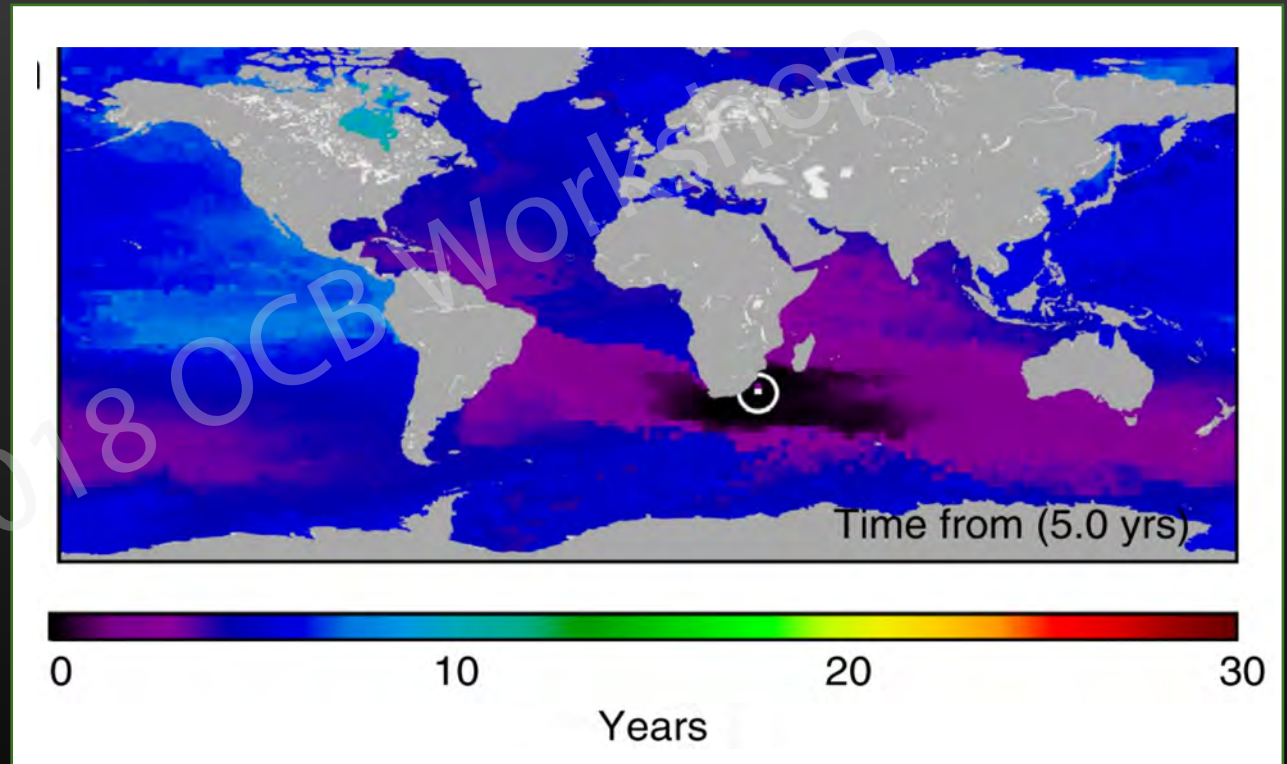


# Neutral evolution is fast enough to generate biogeographic provinces in marine microbes



Hellweger et al. Science 2014

**Dispersion timescales are too short to generate distinct biogeographic provinces in abundant marine microbes**



Jonsson and Watson Nat. Comm 2015

In the model:  
evolution of key metabolic functions sets  
basin biogeochemical gradients

Thus, the evolution of specific lineages  
could potentially be non-deterministic.

Many different trees of life could produce  
the present day ocean

# Discussion questions

- If experimental evolution experiments are not terribly realistic, what are they good for in the first place?
- How many traits are enough traits? How much effort should we put into phenotypic characterisations?
- Is it correct to assume that today's organisms are in their optimum environment / strongly locally adapted to their environment/ at a peak of the fitness landscape in their current environment?
- How often are interspecies interactions other than competition and exploitation important for ocean ecosystem functioning, and does evolution tend to preserve or disrupt them?
- When can we ignore contemporary evolution?
- Do we need to pay attention to evolution if it isn't changing populations in ways that we care or that we can measure?
- What kinds of long term observations need to be put into place to measure evolutionary change?
- Can evolution reshape carbon export (over decadal timescales) or does physics reign supreme?