Community network models to reveal marine plankton systems ecology and evolution

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Journée ADÉM – Lille

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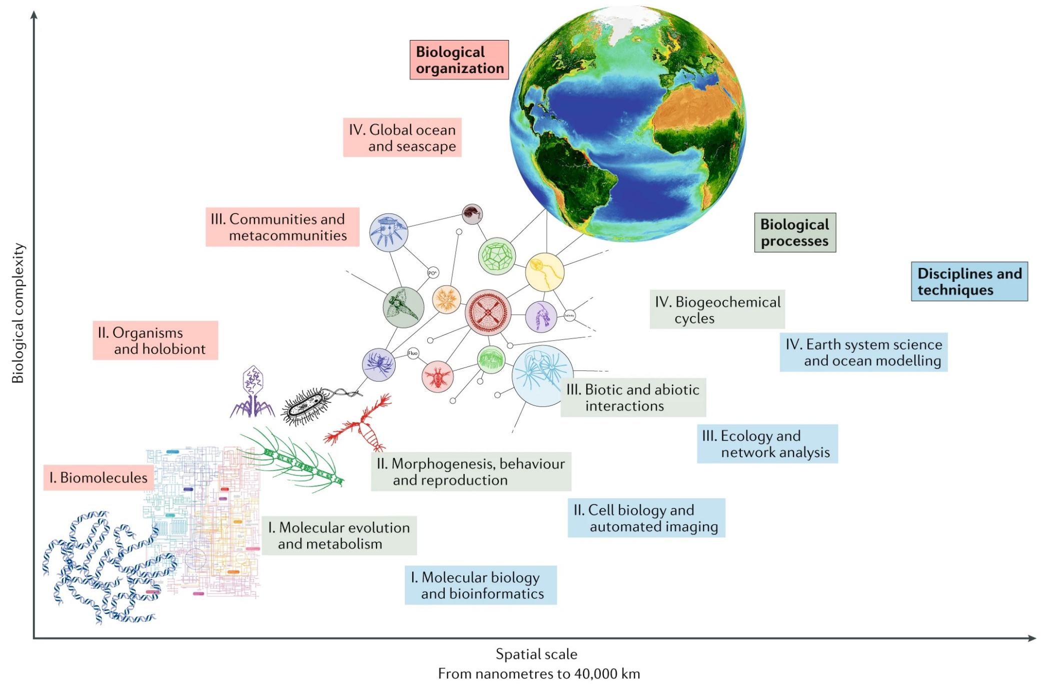
Marine plankton Systems Ecology

- Microbial activities and interactions balance Earth's ecosystems (e.g., primary production, nutrients cycling, nitrogen fixation)
- Marine plankton at the base of the food chain
- Biotic interactions influence diversity and evolution, biogeography and biogeochemistry
- Anthropogenic climate change impacts marine plankton diversity and ecology

➢ An integrated holistic study of biotic and abiotic components of ecosystems and their interactions

➢ Focus on how they are impacted by human activities

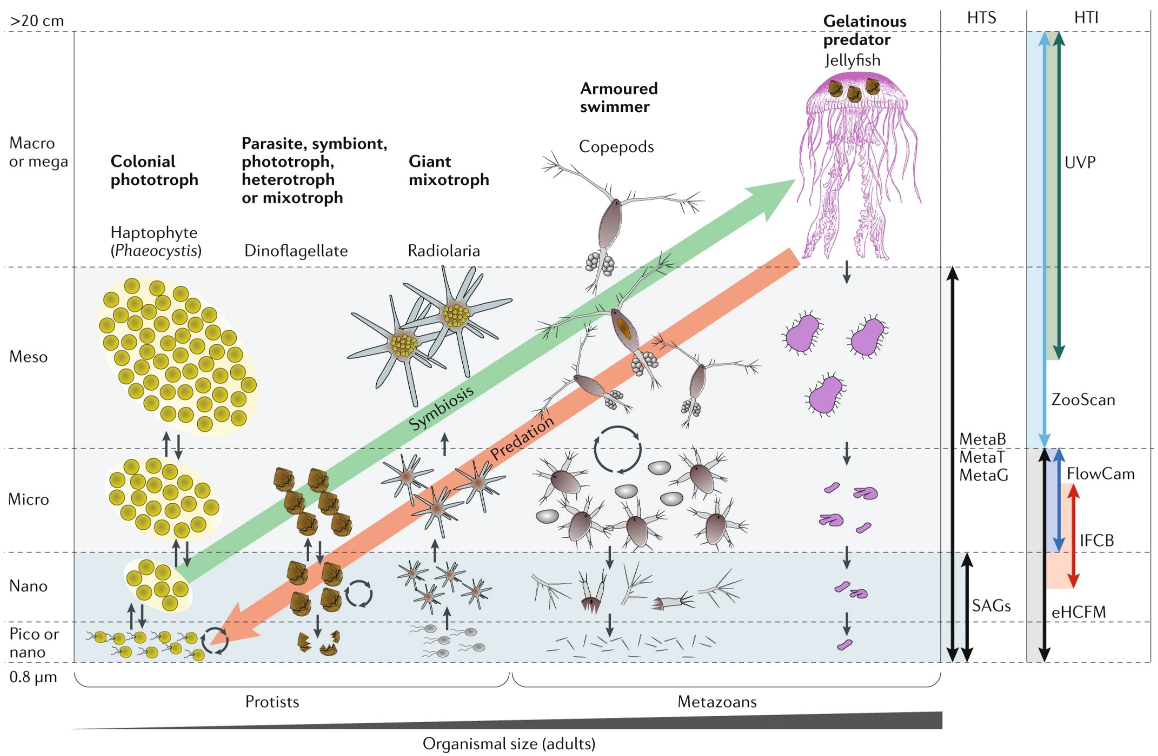
➢ Plankton biome as a fantastic model for integrated holistic study of ecological systems

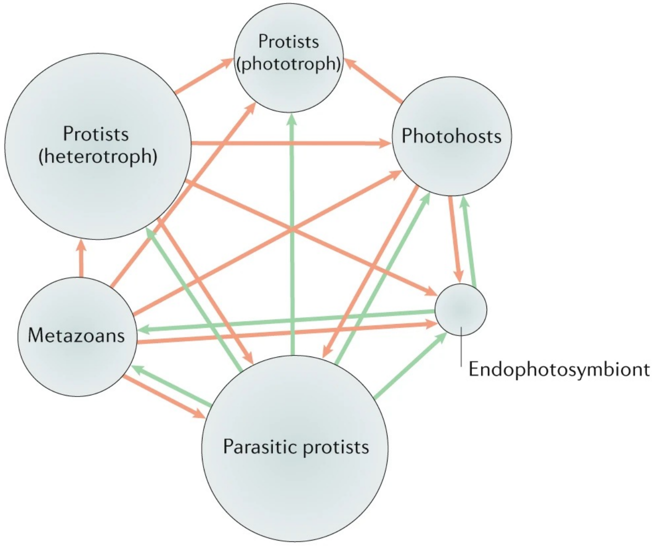


Marine plankton Systems Ecology

Main questions:

- Who lives where, and interacts with whom?
- How can we establish a biogeography of plankton interactions ?
- How diversity and interactions are shaping plankton ecology and evolution ?
- How plankton diversity and interactions will be affected by anthropogenic climate change ?

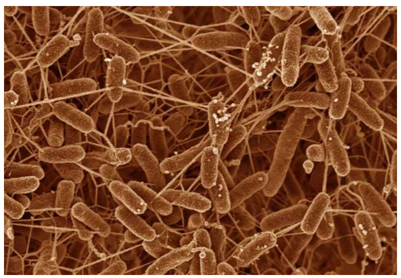




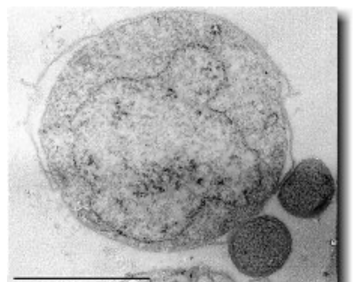
Why inferring microbial ecological associations?

Microbial activities in the wild

- Carry globally relevant processes (primary production, nutrients cycling, etc…)
- Rarely in isolation but often in consortium

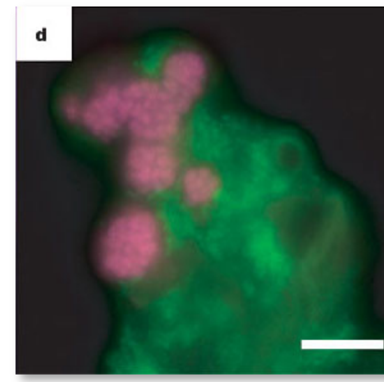


Electrically conductive nanowires in Shewanella oneidensis. Photo byR. Bencheikh and B. Arey



N. equitans attached to the outer membrane of Ignicoccus

Phototrophic consortia, Pelochromatium aggregatum (Overmann et al. 2002)



Anaerobic Oxidation of Methane: AOM consortia, (Raghoebarsing et al. 2006)

Challenges:

- ○ Microbial environmental preferences and biogeography are poorly characterized
- ○ How can we best assess microbial ecological interactions *in situ*?
- ○ How plankton ecological associations are structured across the global ocean?
- ○ How environmental changes will affect these community structures?

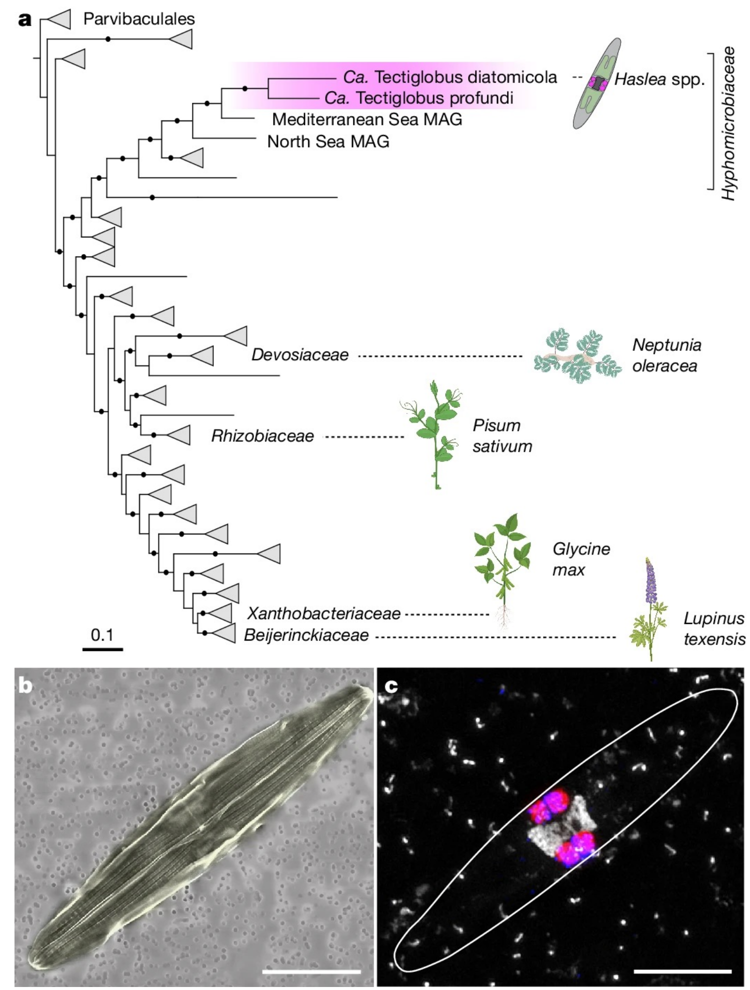
A novel key symbiosis in the global ocean

Article | Open access | Published: 09 May 2024

Rhizobia–diatom symbiosis fixes missing nitrogen in the ocean

Bernhard Tschitschko, Mertcan Esti, Miriam Philippi, Abiel T. Kidane, Sten Littmann, Katharina Kitzinger, Daan R. Speth, Shengjie Li, Alexandra Kraberg, Daniela Tienken, Hannah K. Marchant, Boran Kartal, Jana Milucka, Wiebke Mohr & Marcel M. M. Kuypers

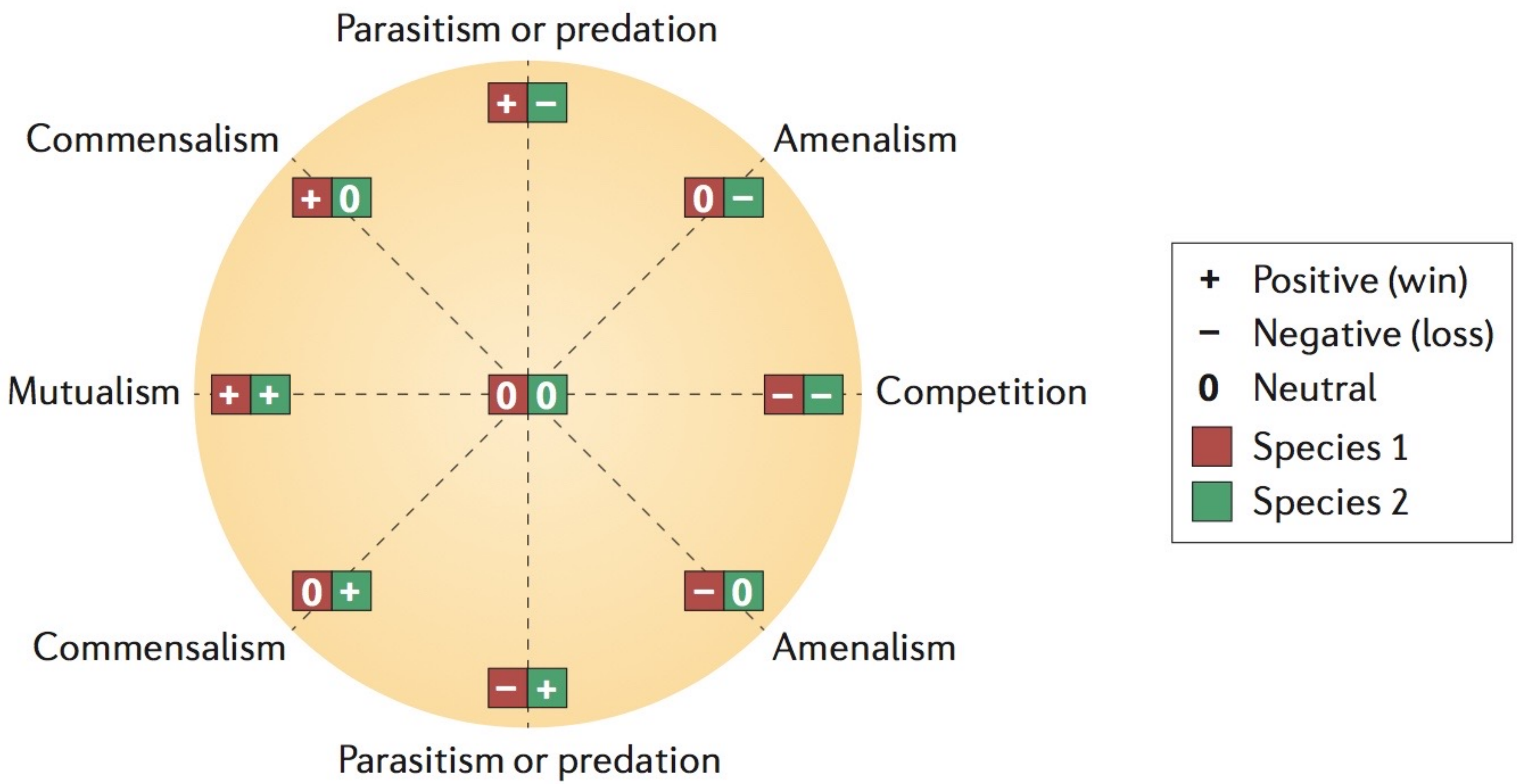
Nature **630**, 899–904 (2024) | Cite this article



An N2-fixing rhizobial diatom endophyte

- A non-cyanobacterial N2-fixing symbiont, ‘Candidatus Tectiglobus diatomicola’, providing its diatom host with fixed nitrogen in return for photosynthetic carbon
- Rhizobia–diatom symbioses can contribute as much fixed nitrogen as cyanobacterial N2 fixers in the tropical North Atlantic (and beyond)

The diversity of ecological associations



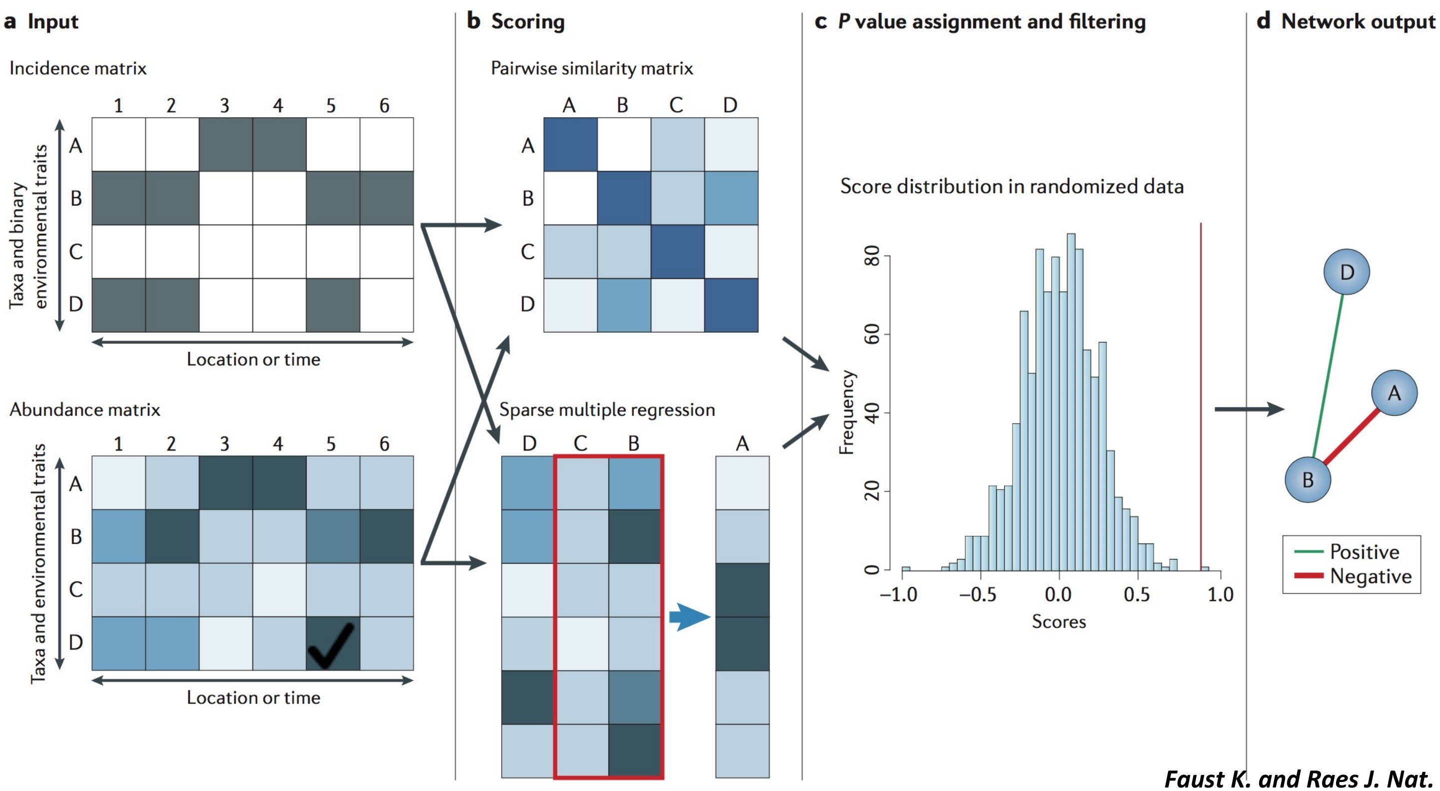
Faust K. and Raes J. Nat. Rev. Microbiol. 2012

How to detect microbial associations?

- Environmental sequencing data give access to microbial abundance across a large number of samples:

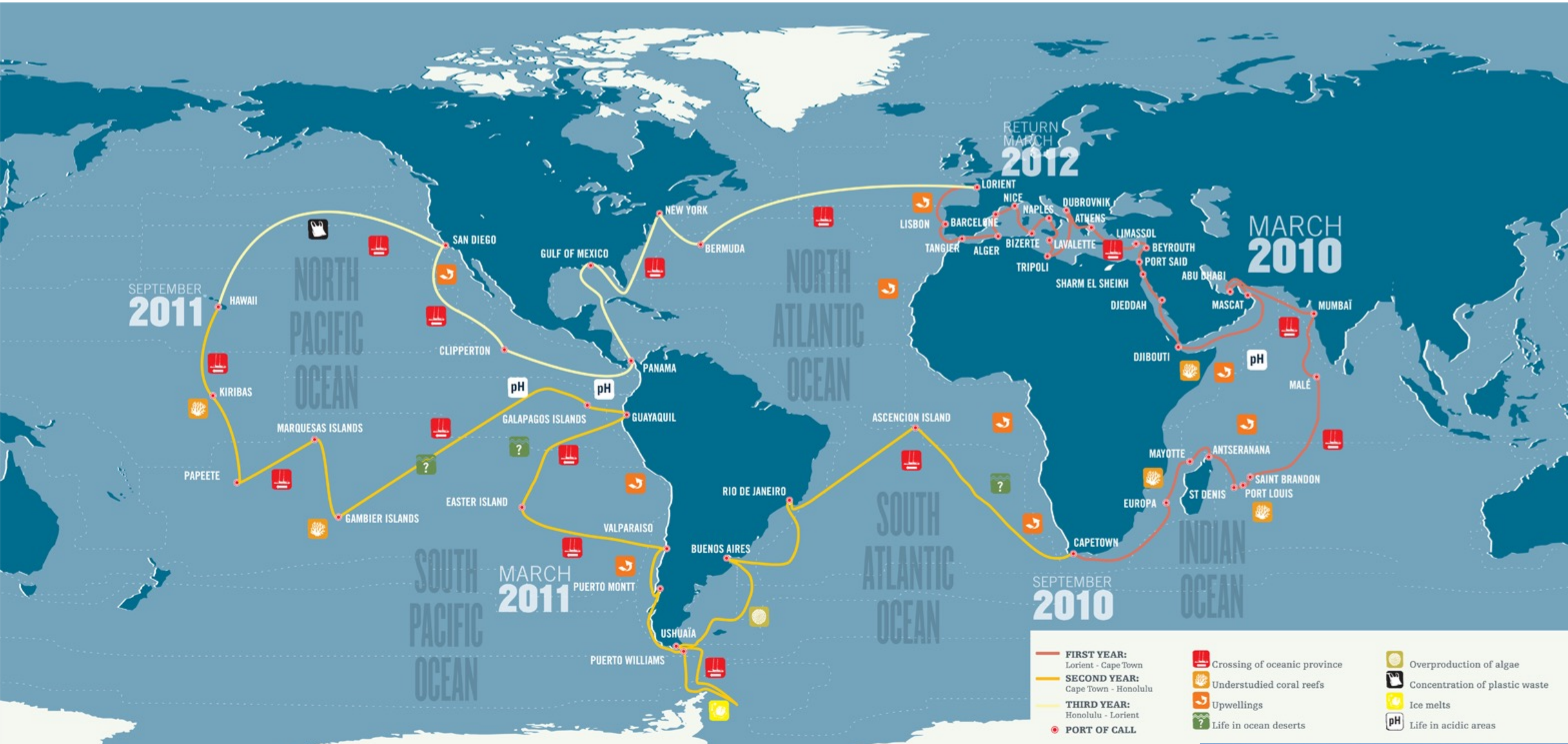
➢ • **Co-presence** (co-occurrence of 2 species across samples) interpreted as niche overlap, mutualism or commensalism.

➢ • **Mutual exclusion** (avoidance of 2 species across samples) interpreted as distinct niche preference, competition or amensalism.



Faust K. and Raes J. Nat. Rev. Microbiol. 2012

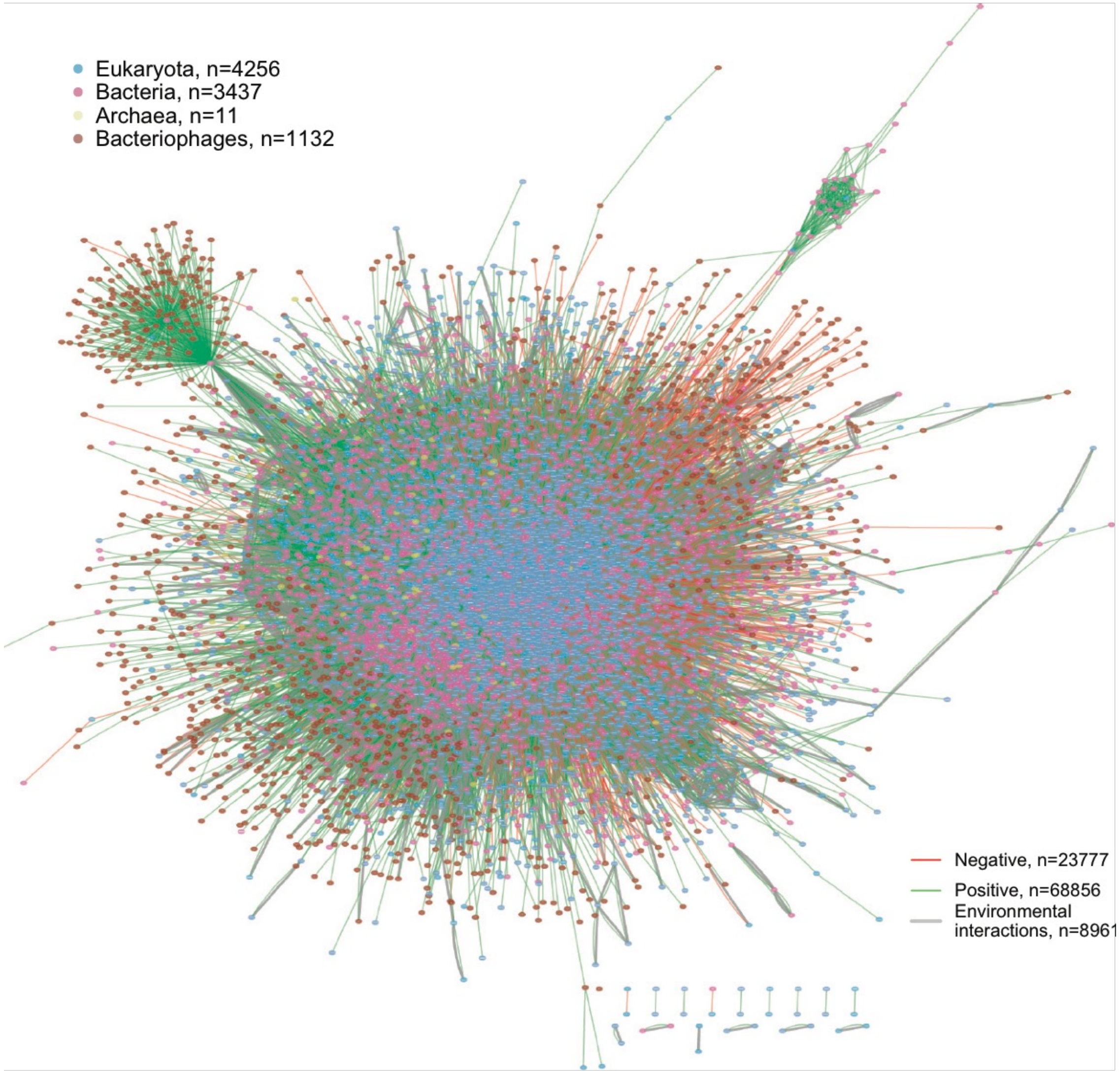
Tara Oceans circumnavigation (2009-2013)



TARA OCEANS

> 40,000 samples (210 stations) for morphological, genetic and environmental analyses across the entire size-spectrum of marine plankton communities using standardized protocol.

A global ocean plankton "*interactome*"

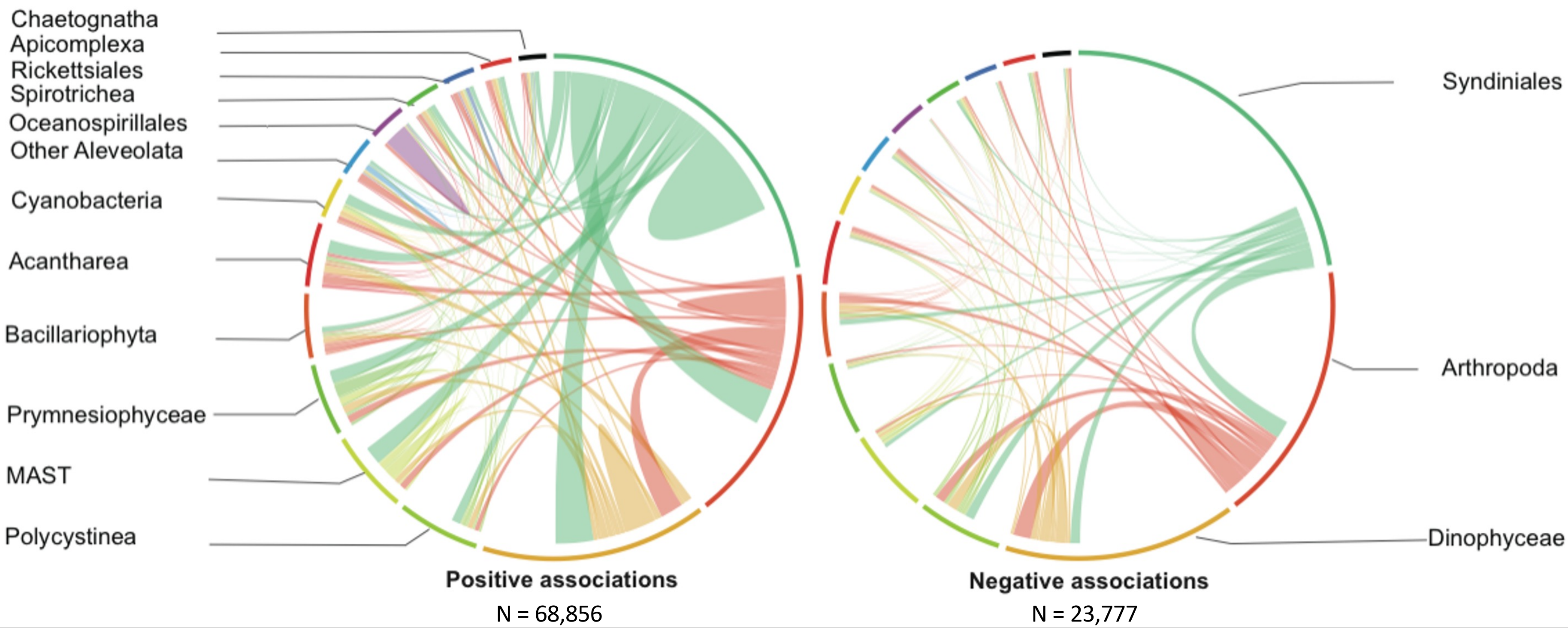


- 127,995 associations
- 92,633 taxon-taxon
- 35,362 taxon-env

- Predicted « Biotic interactions » appear more important than « abiotic interactions »
- Specific associations across plankton functional types and phylogenetic groups
- Large fraction of parasitic interactions

Lima-Mendez et al. Science (2015)

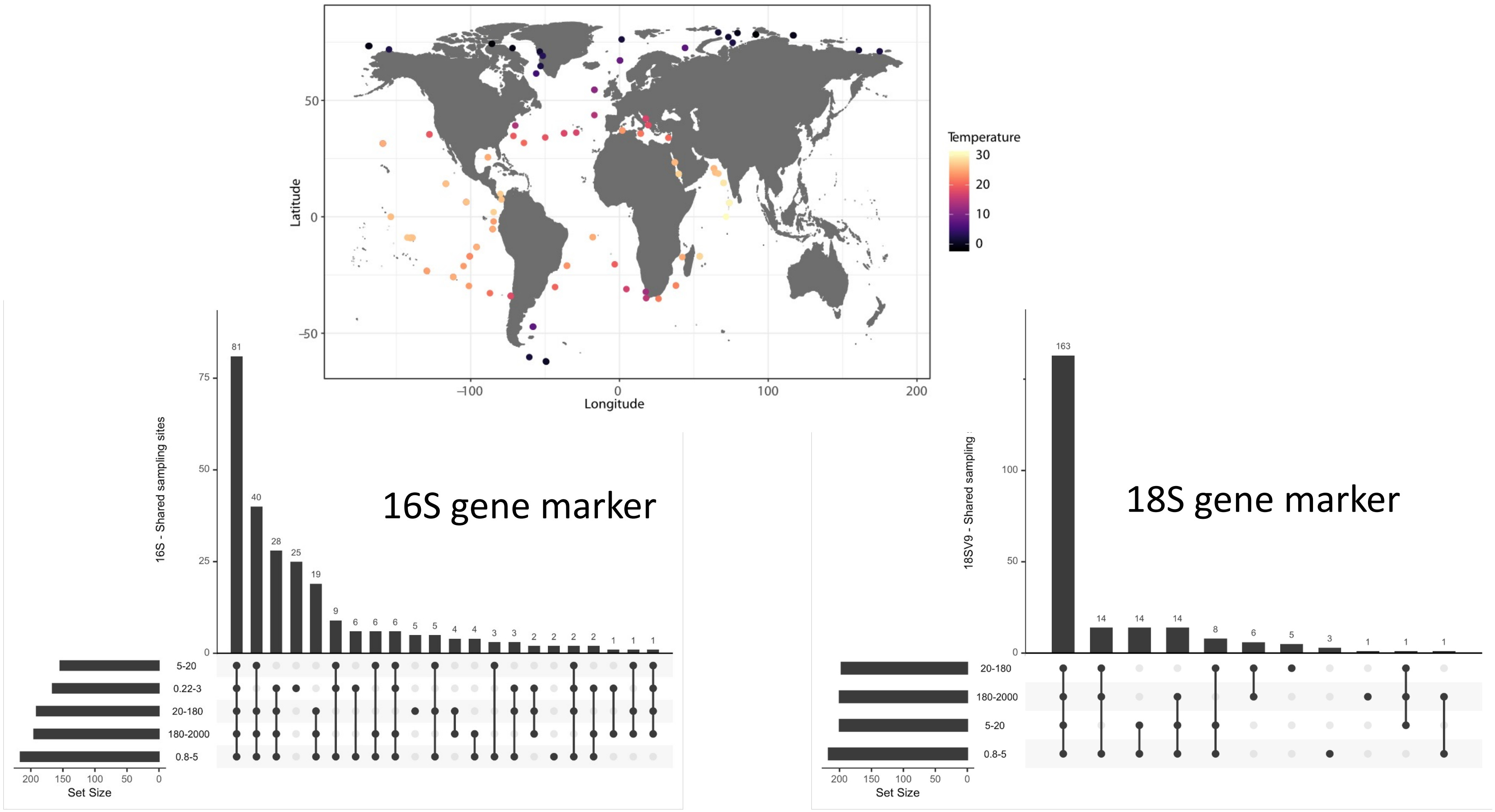
Most predicted associations are positive



« Cooperation » appears more prevalent than « competition »

Lima-Mendez et al. Science (2015)

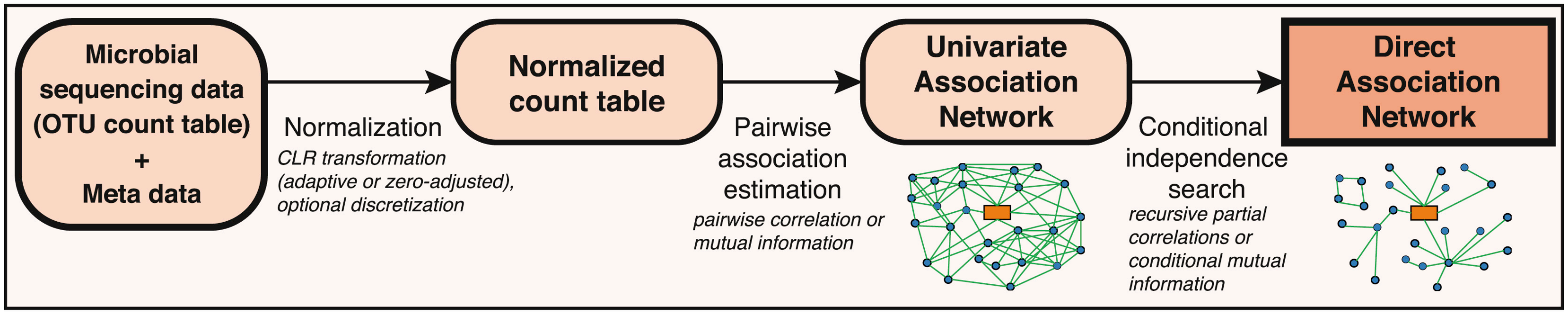
Leveraging *Tara* Oceans global samplings



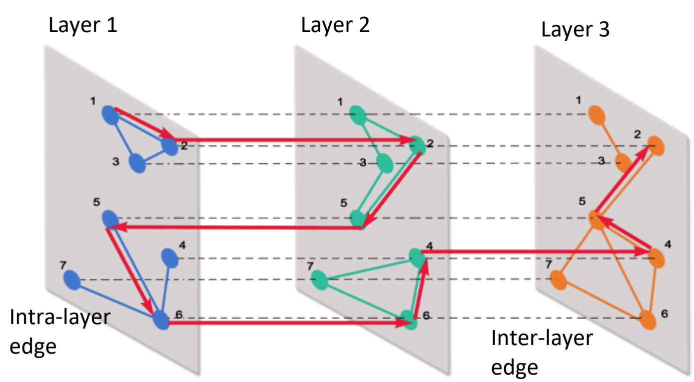
- ✓ Cross-domains (Prok. & Euk.) sequencing data (16S & 18S) across size fractions
- ✓ Global pole-to-pole sampling along the latitudinal axis (extensive temperature gradient)

Inferring “direct” plankton associations

FlashWeave workflow



Tackmann et al. Cell Systems 2019.



Integration of 5 ”layers” of <u>organismal size fractions:</u>

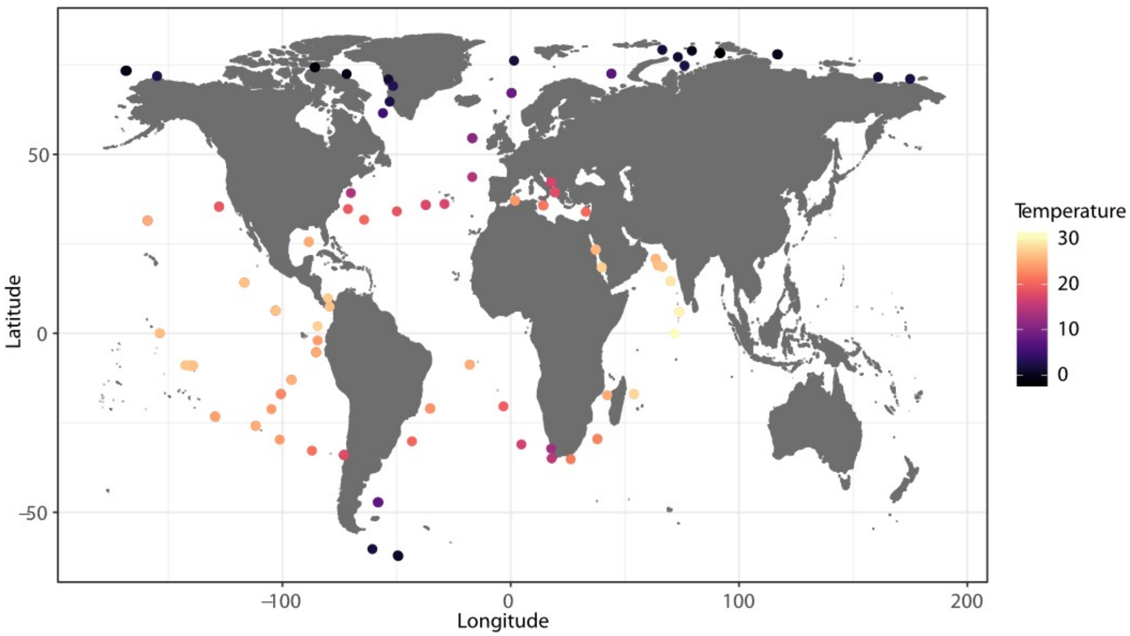
- 0.2 to 3 μm
- 0.8 to 5 μm
- 5 to 20 μm
- 20 to 180 μm
- 180 to 2000 μm

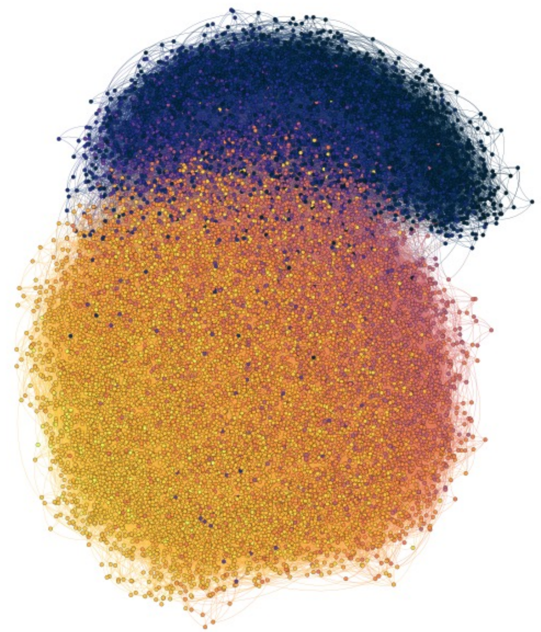
✓ Detection of indirect associations via conditional and iterative independence search

✓ Removal of indirect (purely correlational) associations reported by univariate methods

✓ Graph of predicted direct plankton interactions within and across size fractions

An augmented global ocean plankton *"interactome"*



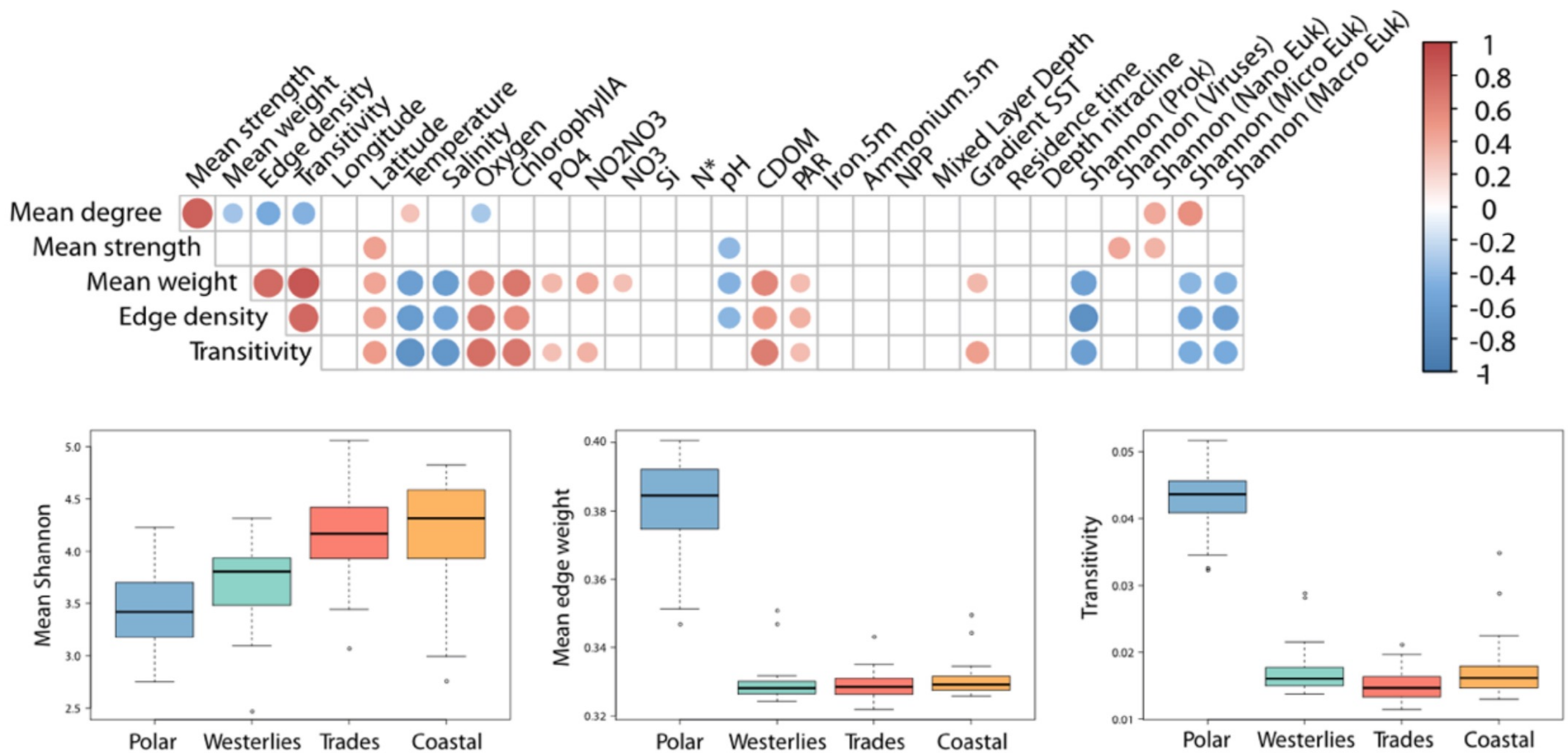


- ✓ Extended by including Arctic polar samples
- ✓ Direct interactions predicted via constraints-based (iterative) probabilistic learning

- ✓ Cross-domains (Prok. & Euk.) predicted interactions from pole-to-pole
- ✓ Strong latitudinal structuration of predicted interactions (along temperature gradient)

Chaffron et al. Science Advances (2021)

Abiotic factors shape plankton interactome structure

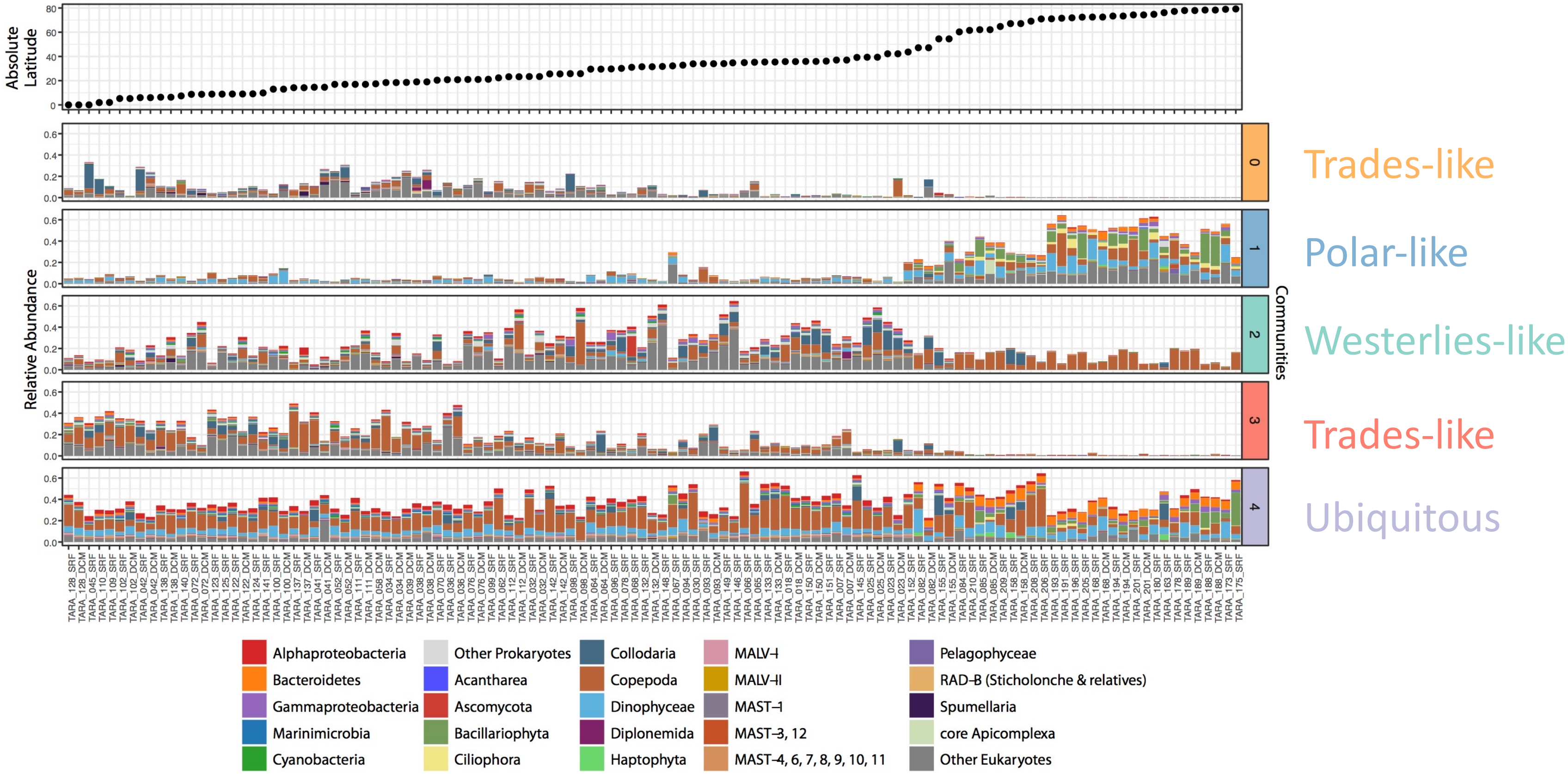


✓ Higher association strength (link weights) and connectivity (transitivity) at the poles

✓ Plankton interactome topology is significantly associated to diversity, temperature, salinity, light (PAR), nutrient concentrations and pH

Chaffron et al. Science Advances (2021)

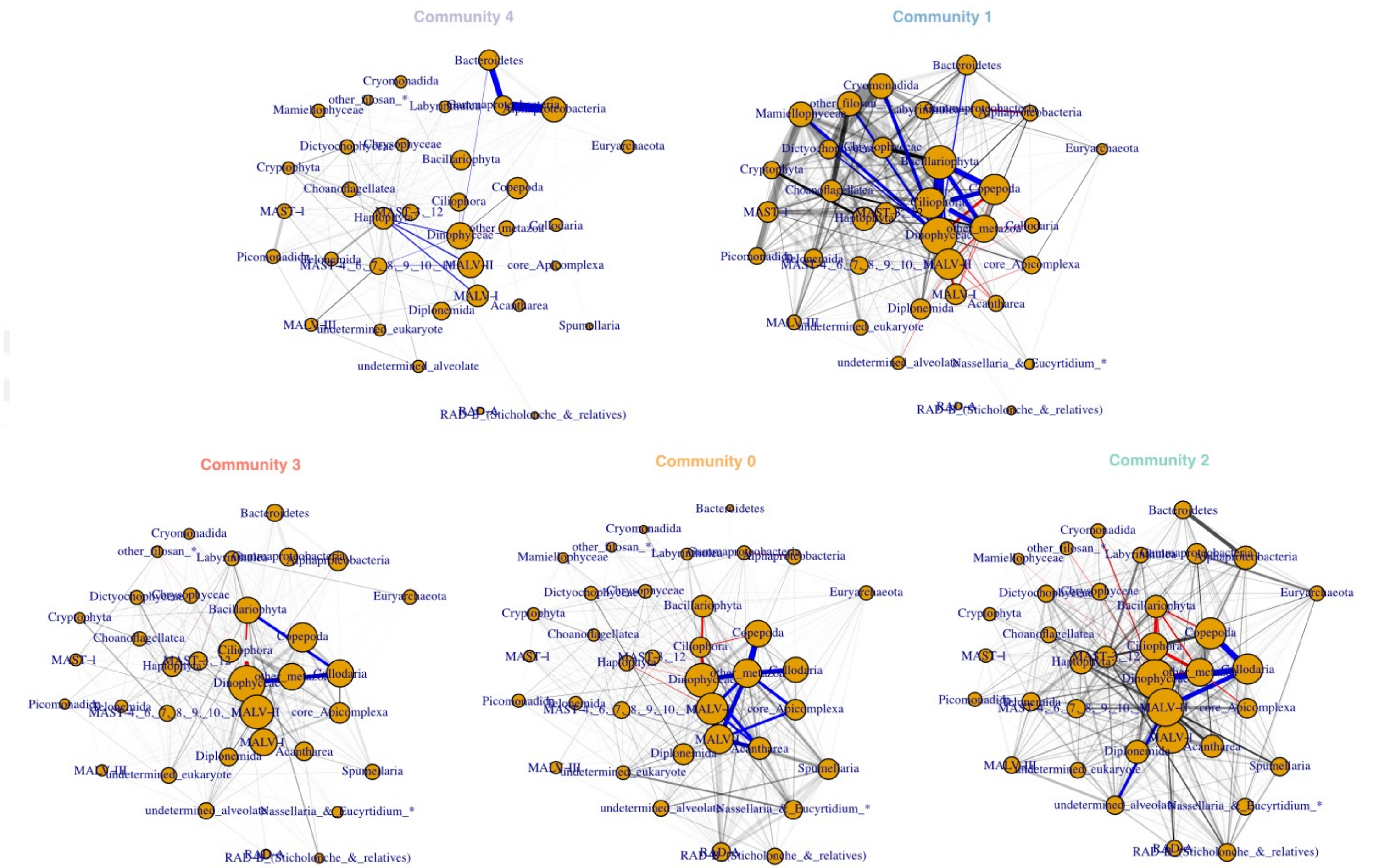
Biome-specific communities emerge from the plankton interactome



- ✓ Eigenvector-based spectral clustering algorithm for community detection
- ✓ Four biome-specific communities emerge from the interactome
- ✓ One “ubiquitous” community spans the entire latitudinal gradient

Chaffron et al. Science Advances (2021)

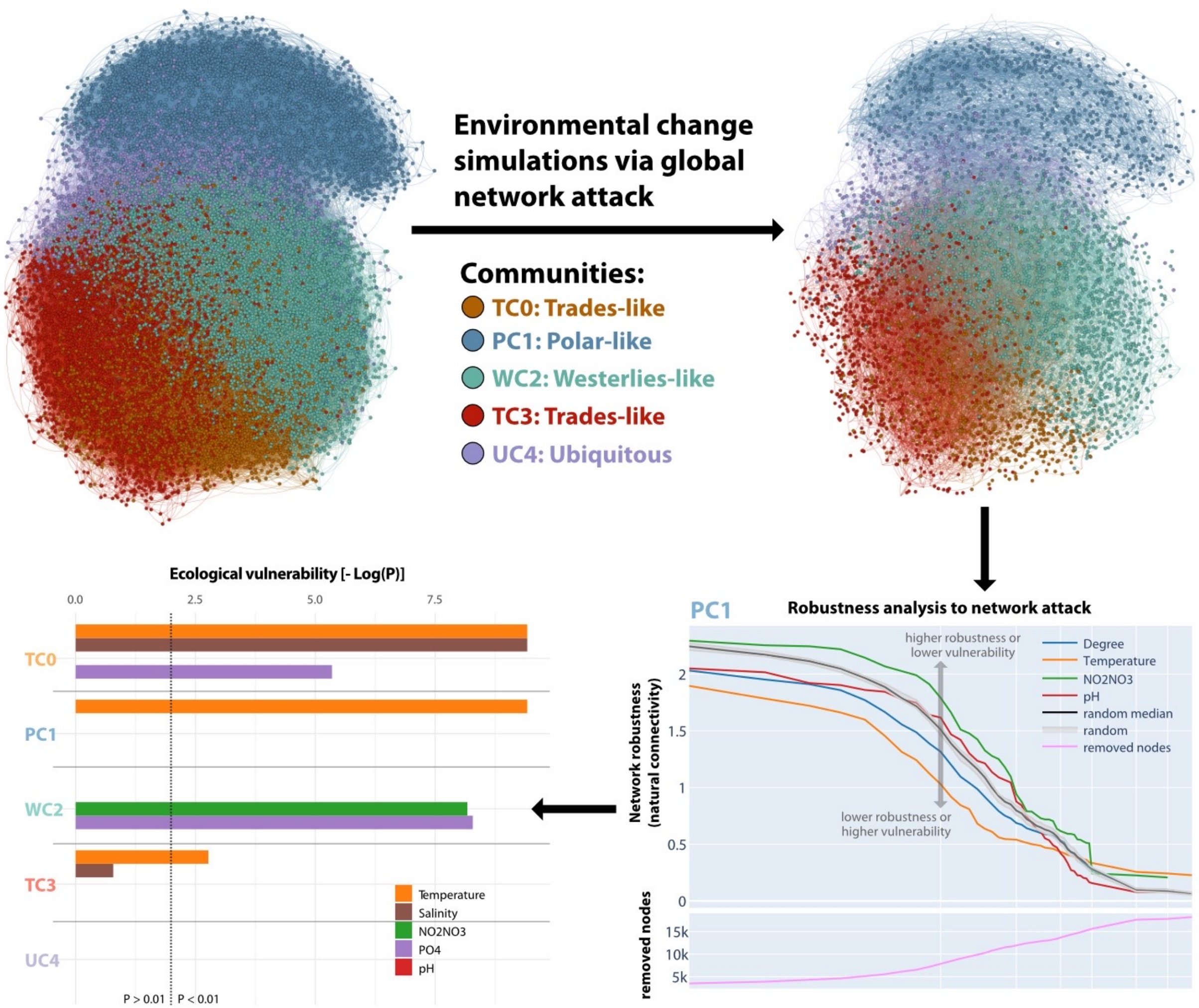
Biome-specific communities emerge from the plankton interactome



- ✓ These communities display very distinct (local) interactomes
- ✓ Specific associations are enriched in each community

Chaffron et al. Science Advances (2021)

Distinct vulnerabilities of plankton communities to environmental change

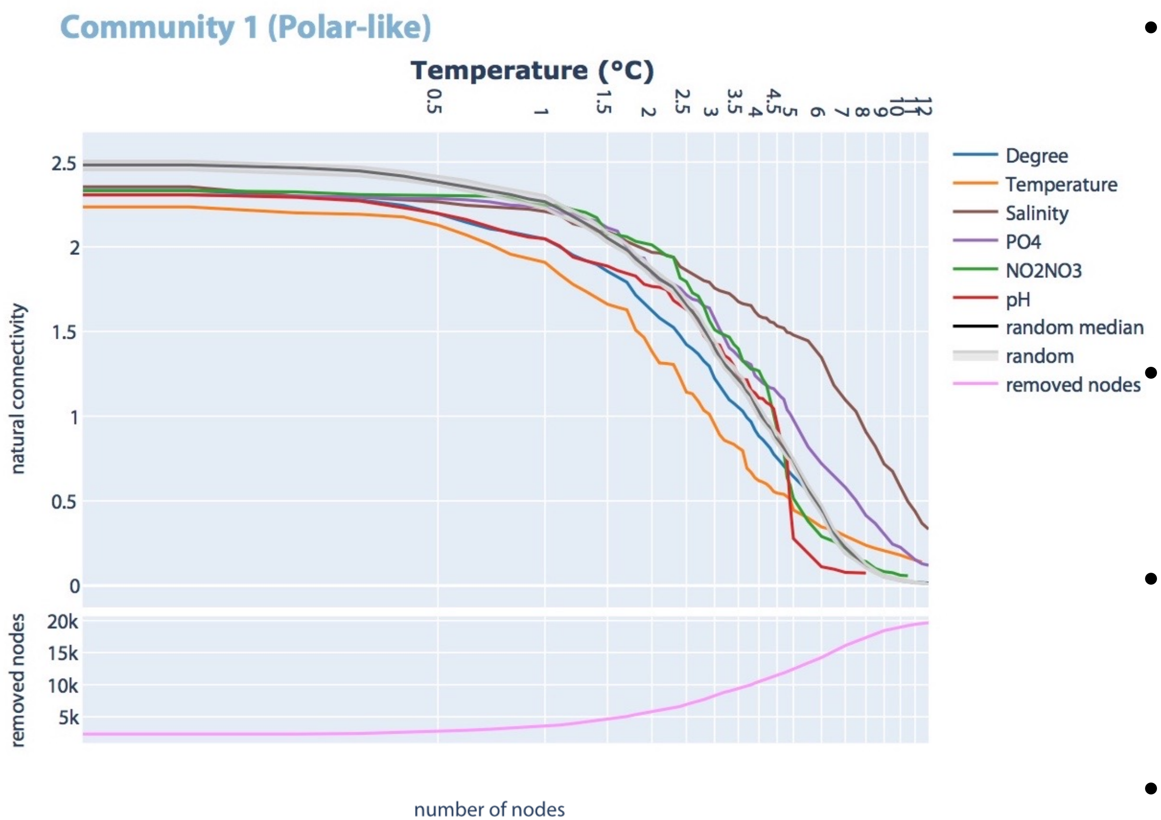


Network robustness analysis:

- **Natural connectivity:** redundancy of alternative paths in a network based on evaluating the weighted number of closed walks.
- **Randic's index:** A degree-based topological index measuring the process of connecting various parts of a network.

Chaffron et al. Science Advances (2021)

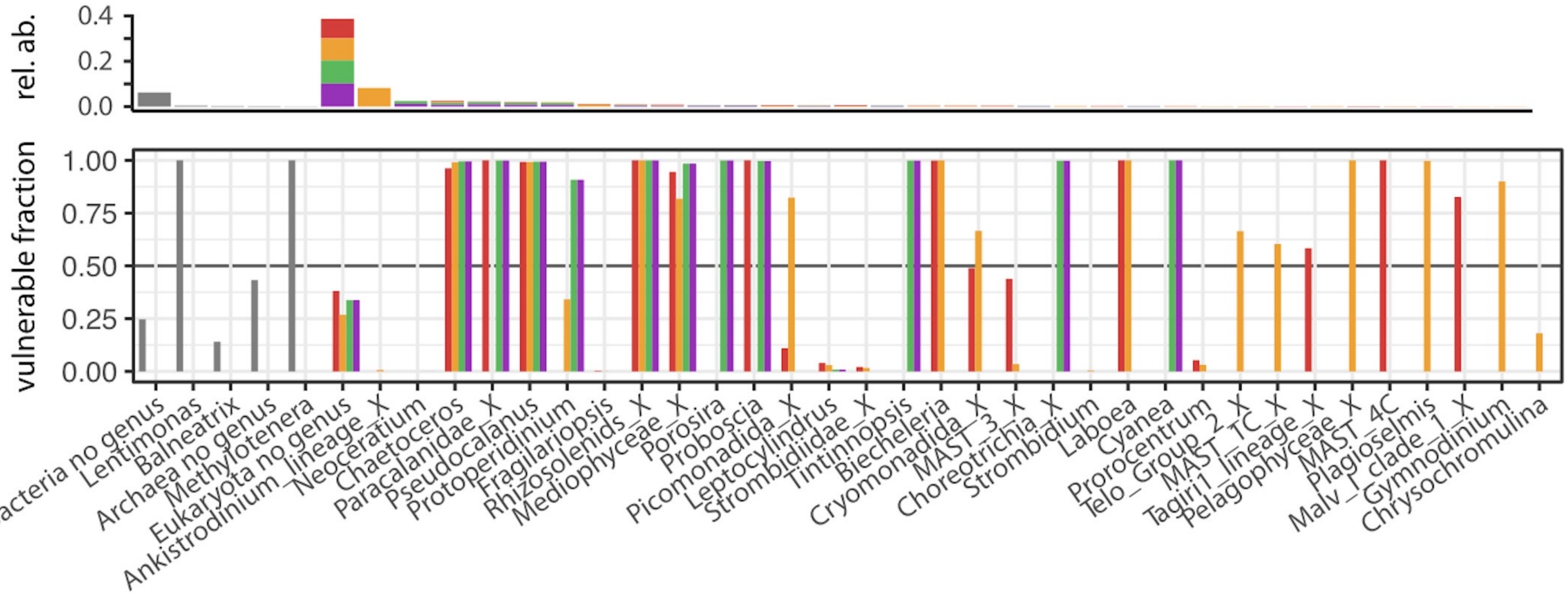
Community-specific vulnerabilities of the *interactome*



- Graph-based perturbations reveal *interactome* **global robustness**
- **Trades vulnerability** to temperature and salinity
- **Westerlies vulnerability** to nutrients conc. changes
- **Polar vulnerability** to temperature changes

Chaffron et al. Science Advances (2021)

Polar lineages potentially most impacted by temperature change

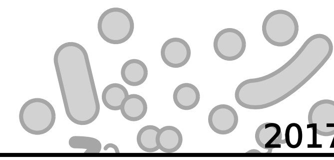


- ✓ *Lentimonas* and *Methylotenera*, and several uncharacterized OTUs
- ✓ Several abundant diatom genera: *Chaetoceros*, *Porosira* and *Proboscia*
- ✓ Copepods genera: *Pseudocalanus* and genera from the family Paracalanidae
- ✓ **Potential species indicators of polar ecosystem change in response to ocean warming**

Chaffron et al. Science Advances (2021)

Environmental genomes are flowing

…e-Assembled Genomes (MAGs)



2014

nature biotechnology

Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes

H Bjørn Nielsen…
Shinichi Sunaga…
Eric Pelletier[10–…
Jean-Michel Batt…
Fouad Boumezb…
Torben Hansen[13…
Pierre Léonard[3,…
Oluf Pedersen[13…
Sebastian Tims[2…
Thomas Sicherit…

2017

Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life

nature microbiology

Donovan H. Parks…
Paul N. Evans, Phi…

2017

SCIENTIFIC DATA

Data Descriptor: The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans

Benjamin J. Tully[1], …

2017

Nitrogen-fixing populations of Planctomycetes and Proteobacteria are abundant in surface ocean metagenomes

nature microbiology

Tom O. Delmont[1*], Christopher Quince…
Michael S. Rappé[4], Sandra L. MacLellan[5…

2018

Metabolic Diversity within the Globally Abundant Marine Group II *Euryarchaea* Drives Ecological Patterns

CSH Cold Spring Harbor Laboratory

bioRxiv THE PREPRINT SERVER FOR BIOLOGY

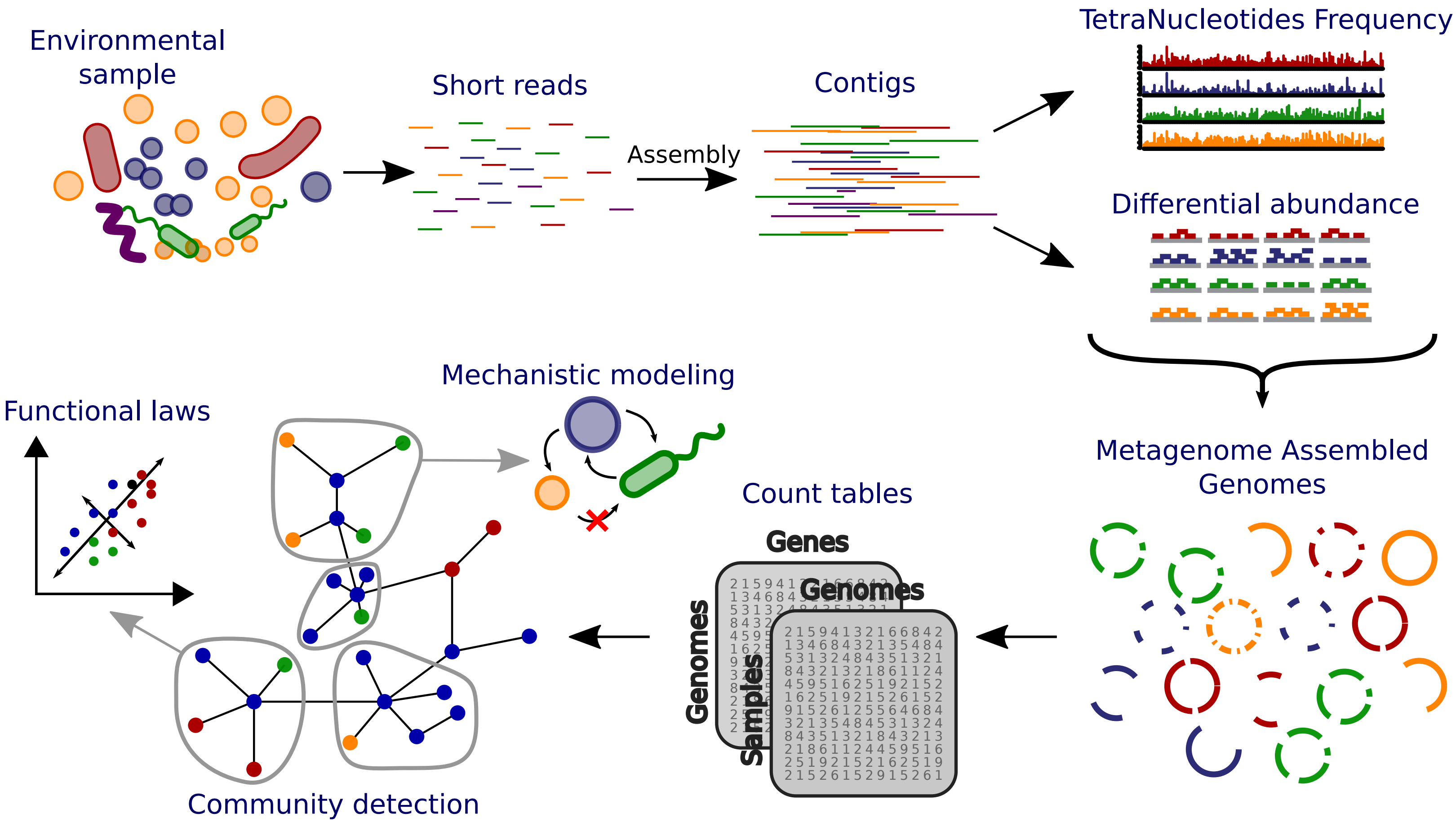
Benjamin J Tully

- Experimentally cha…
- Amplification
- Incomplete genomes

Can we predict and explain plankton community associations in the ocean?

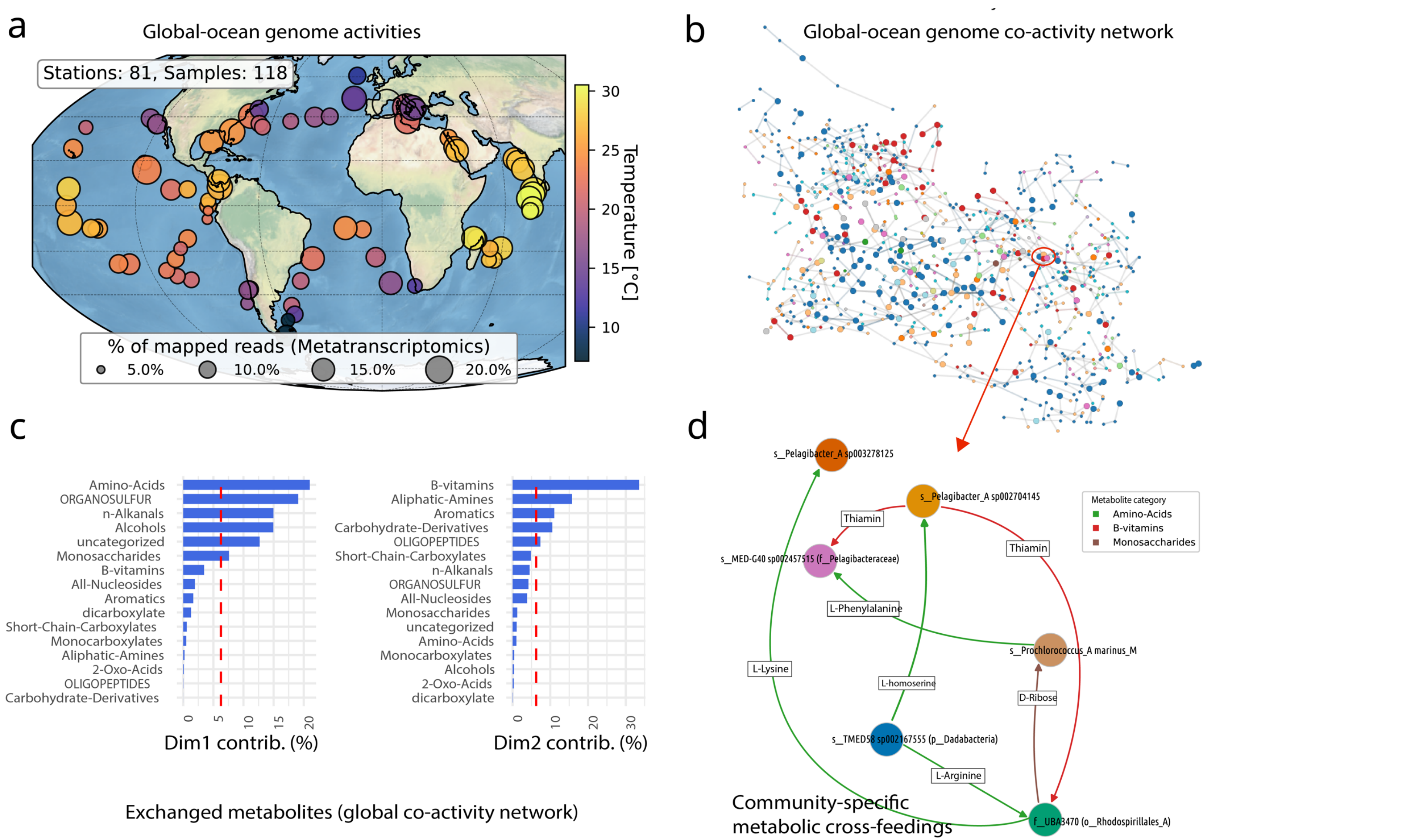
Marinna Gaudin

Nils Giordano



Genome-scale community modelling of epipelagic bacterioplankton communities

✓ Framework integrating ecosystem-scale meta-omics information through ecological and metabolic modelling for a mechanistic understanding of microbial interactions



Giordano, Gaudin et al. Nature Comm. 2024

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