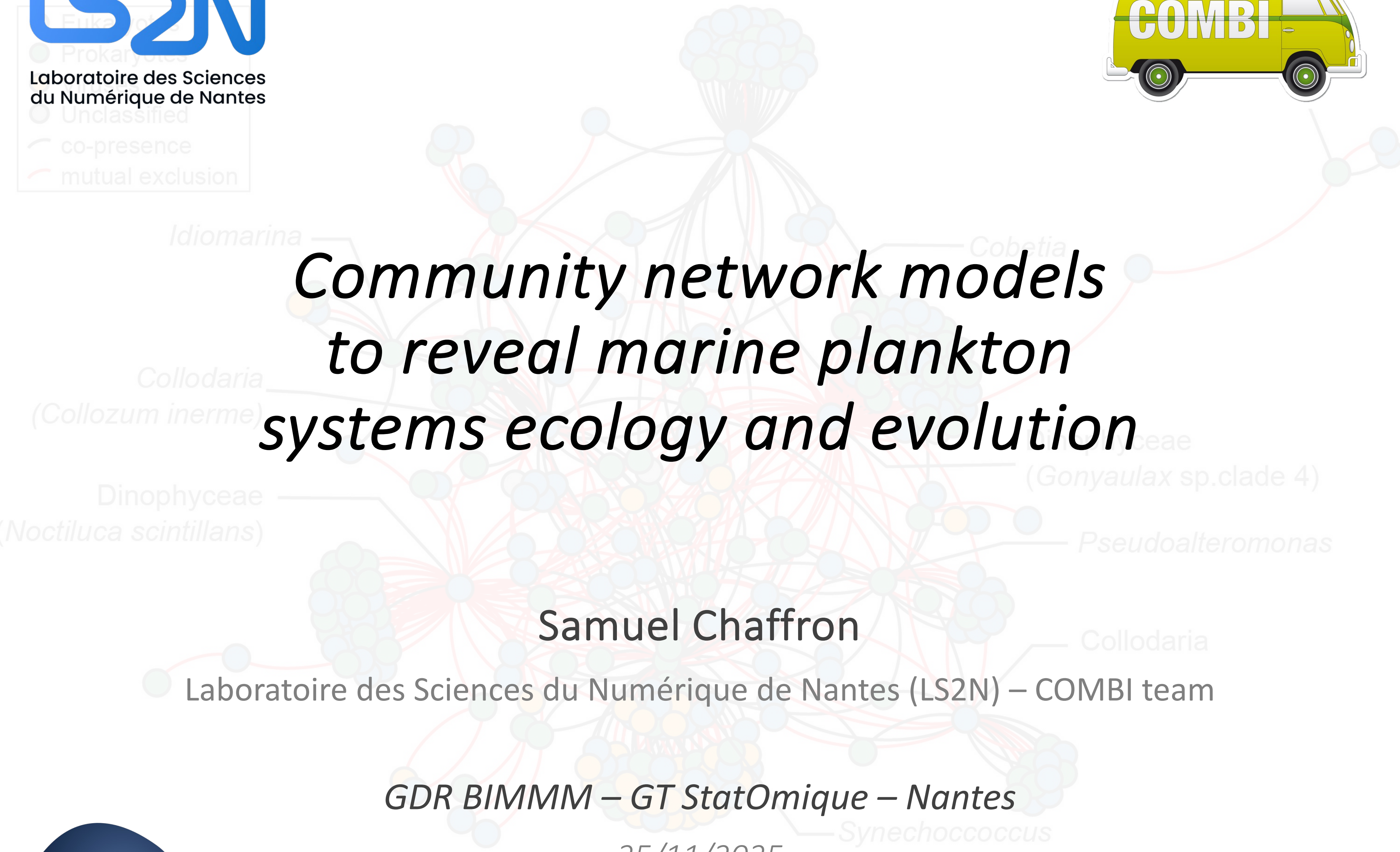


Community network models to reveal marine plankton systems ecology and evolution

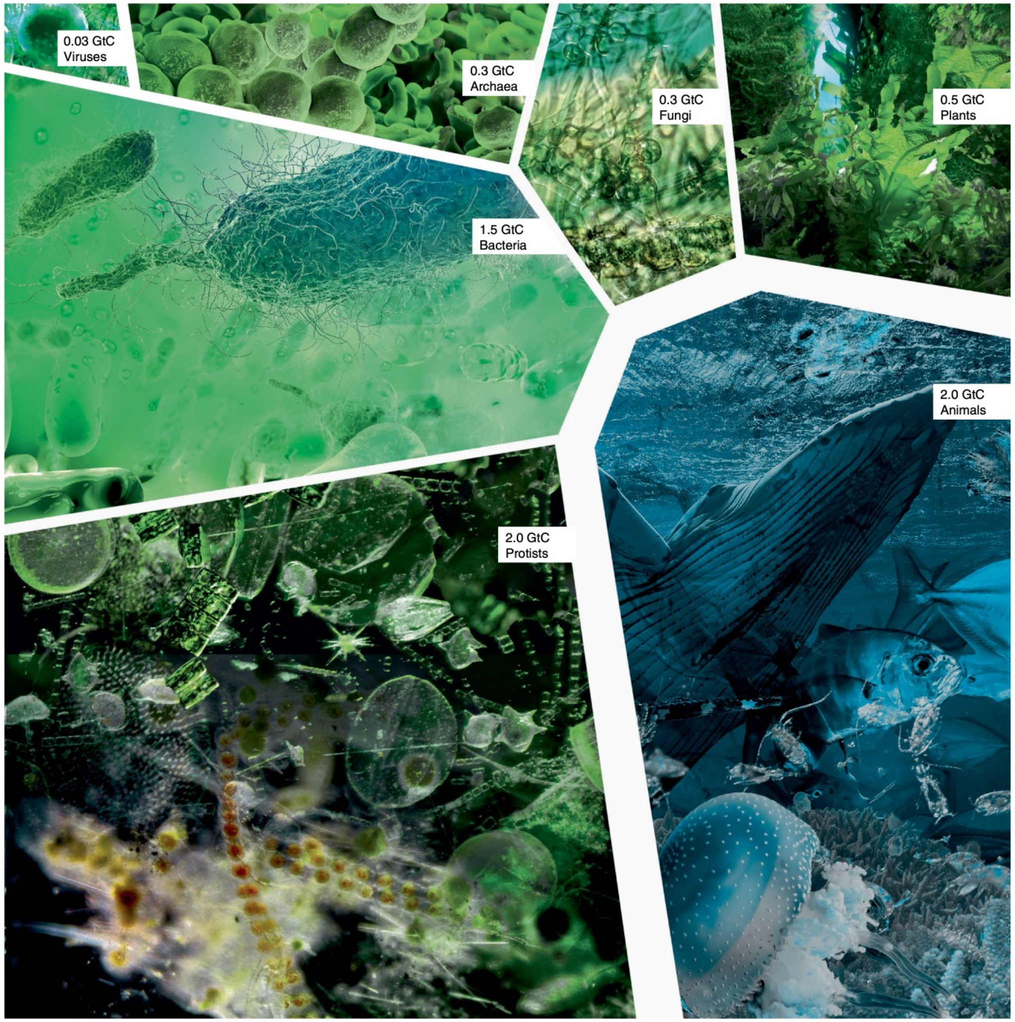
Samuel Chaffron

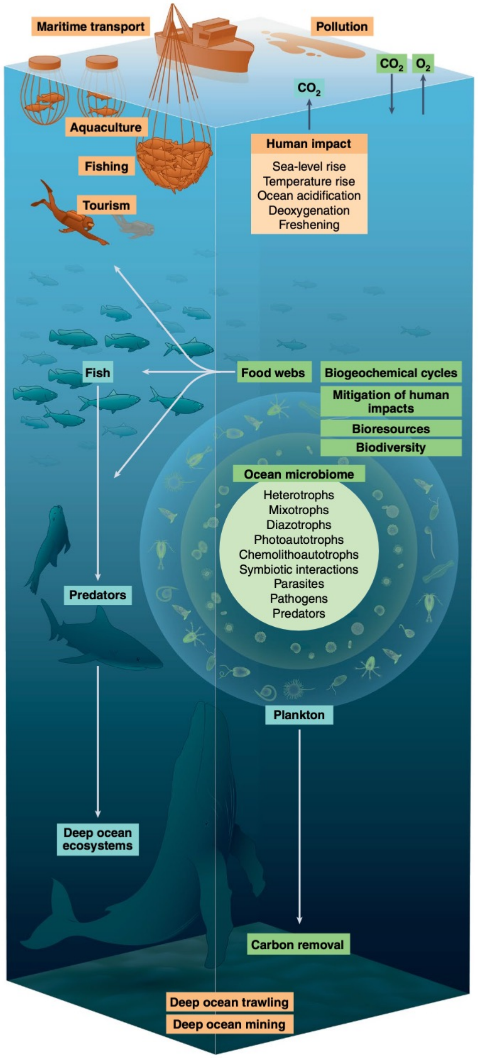
Laboratoire des Sciences du Numérique de Nantes (LS2N) – COMBI team

GDR BIMMM – GT StatOmique – Nantes

25/11/2025

The central role of the Ocean microbiome

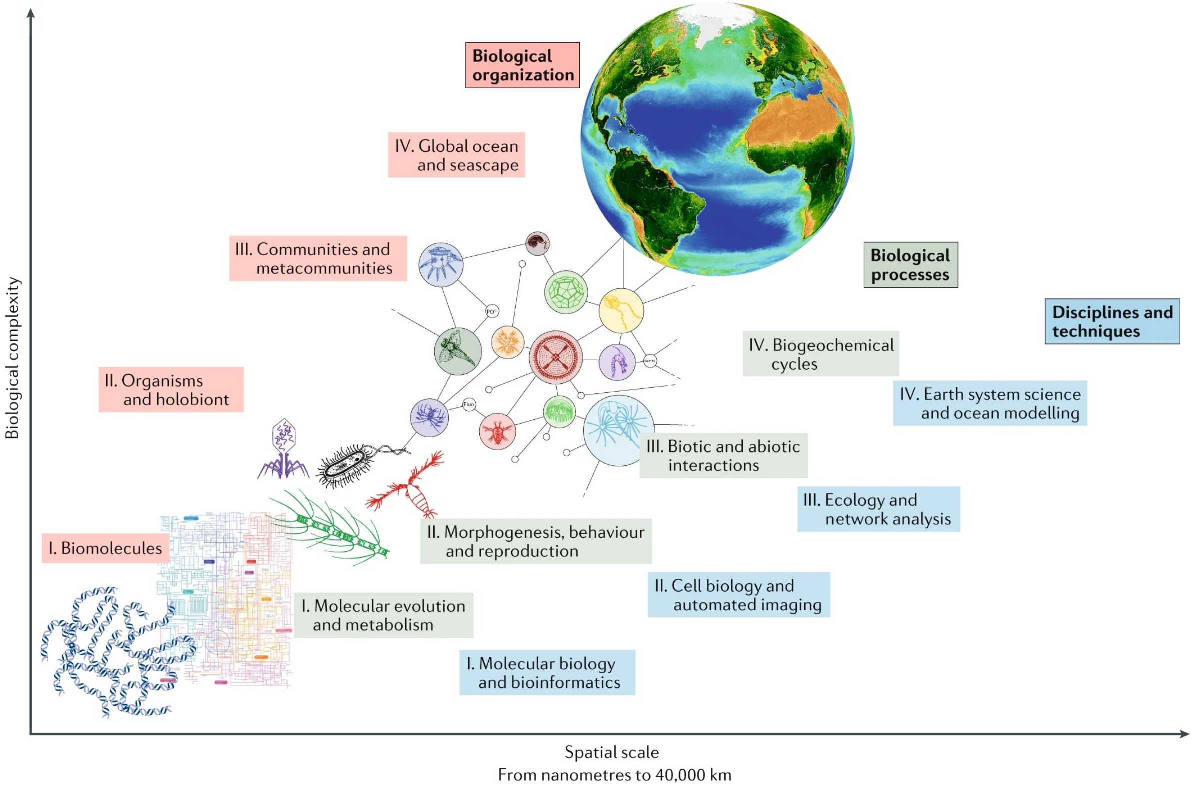




- By far the largest fraction of the estimated total biomass in the ocean (~4.4 GtC)
- Central and essential role of the Ocean microbiome in ecology and planetary health

Marine plankton Ecosystems Microbiology

- Microbial activities (and interactions) balance Earth's ecosystems
- Fix large quantities of CO_2 via primary production (photosynthesis)
- Regulate nutrients and elemental cycles (N, P, S)
- Marine plankton at the base of the food chain, supporting ocean food webs

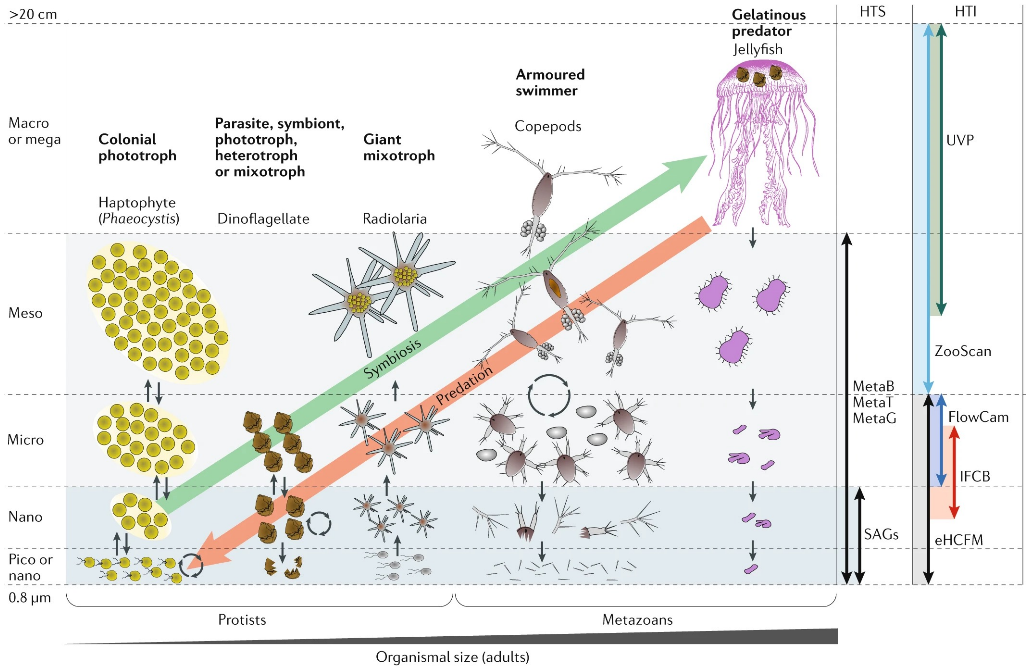


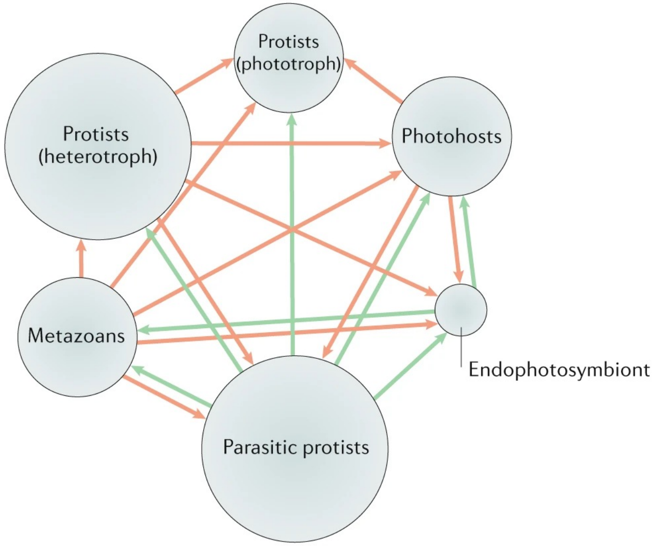
Marine plankton Ecosystems Microbiology

- Biotic interactions influence the diversity, evolution, biogeography, and biogeochemistry of the ocean microbiome
- Anthropogenic climate change impacts marine plankton diversity and interactions

Main questions:

- ○ Who lives where, interacts with whom, and how?
- ○ How interactions are shaping community assembly, ecology and evolution?
- ○ How plankton diversity and interactions will be affected by climate change?

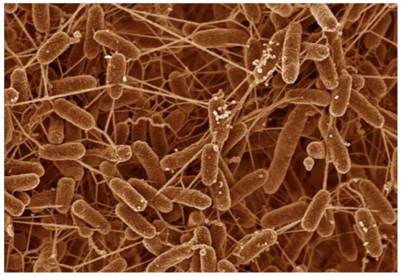




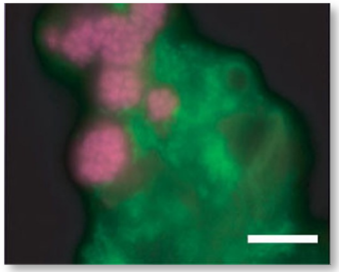
Why studying plankton interactions/symbioses?

Microbial plankton interactions in the wild:

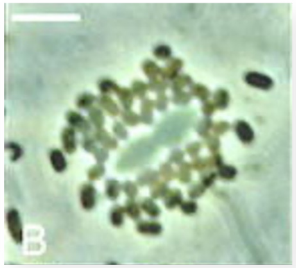
- Carry globally relevant processes (primary production, nutrients cycling)
- **Rarely in isolation but often (always?) in consortium!**



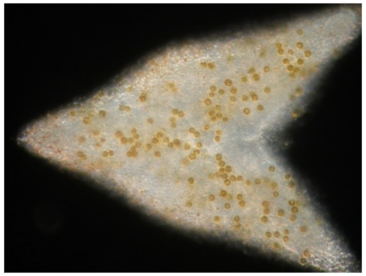
Electrically conductive nanowires in Shewanella oneidensis. Photo byR. Bencheikh and B. Arey



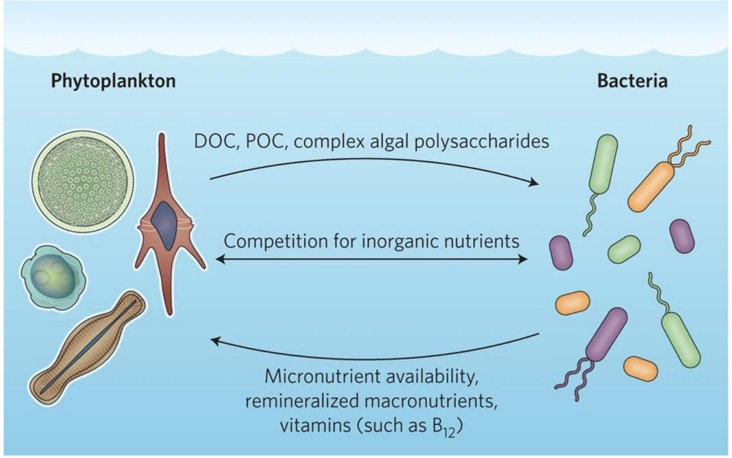
Anaerobic Oxidation of Methane: AOM consortia, (Raghoebarsing et al. 2006)



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



Photosymbiosis: Acantharia with Phaeocystis microalgaes



- ➢ Range of dynamic (spatiotemporal) interactions from **reciprocal exchange of resources** required for growth (e.g., nutrients and vitamins) to **competition** for limiting inorganic nutrients
- ➢ Only a **minority of these interactions are actually known**, most to be discovered!

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

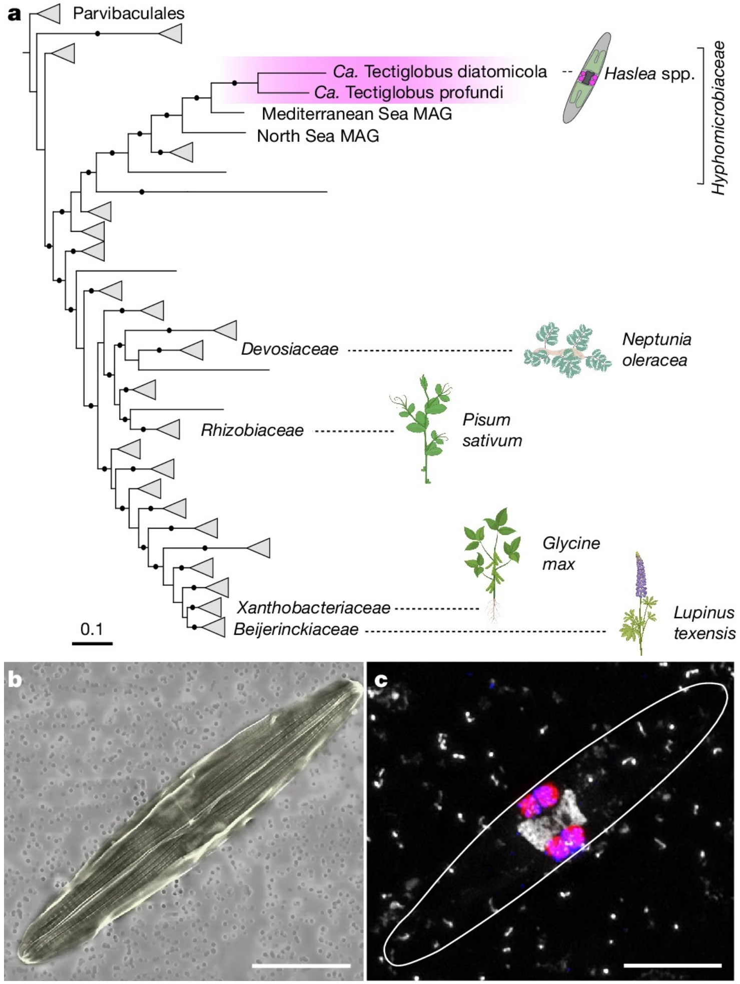
Nature **630**, 899–904 (2024) | Cite this article

15k Accesses | **6** Citations | **296** Altmetric | Metrics

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)

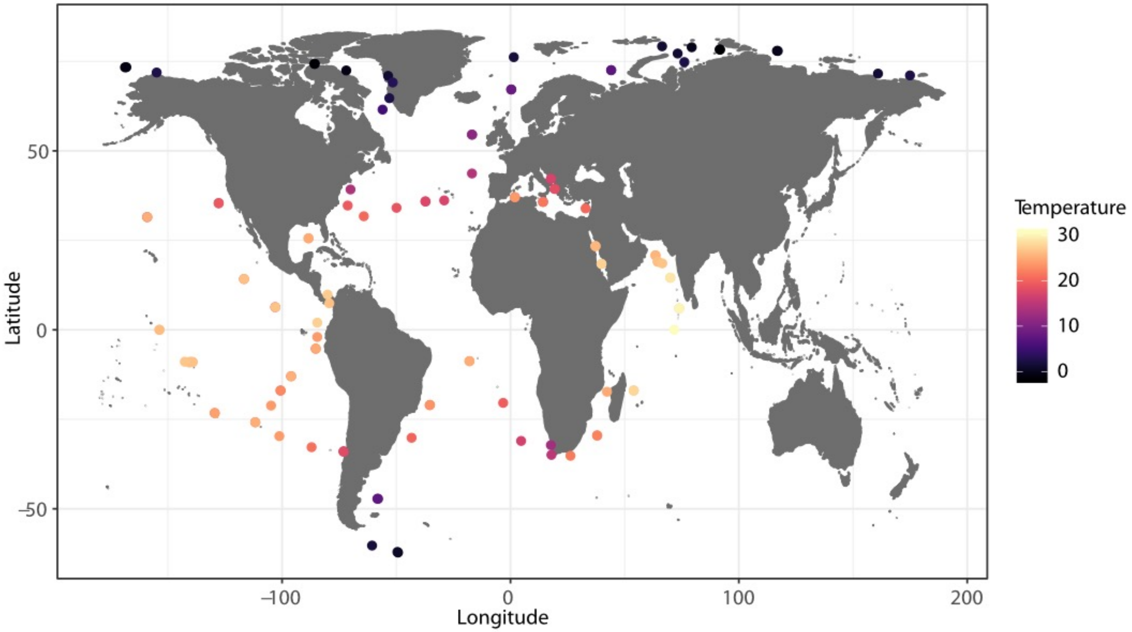


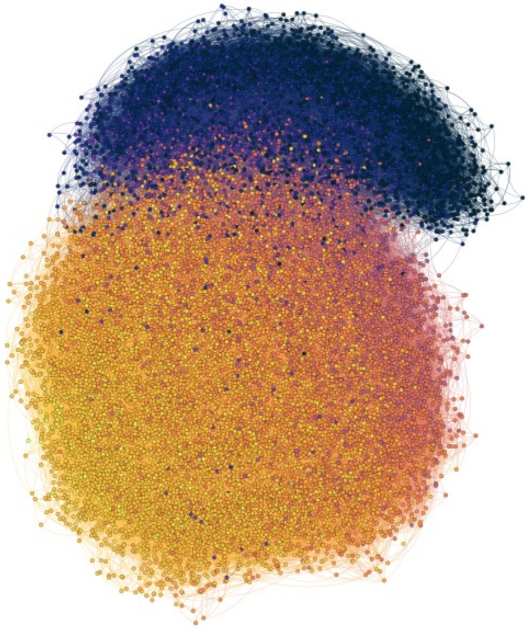
Tara Oceans circumnavigation (2009-2013)

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 co-occurrence network





✓ Including samples from pole-to-pole (Arctic to Southern Ocean)

✓ Direct interactions predicted via constraints-based (iterative) probabilistic learning

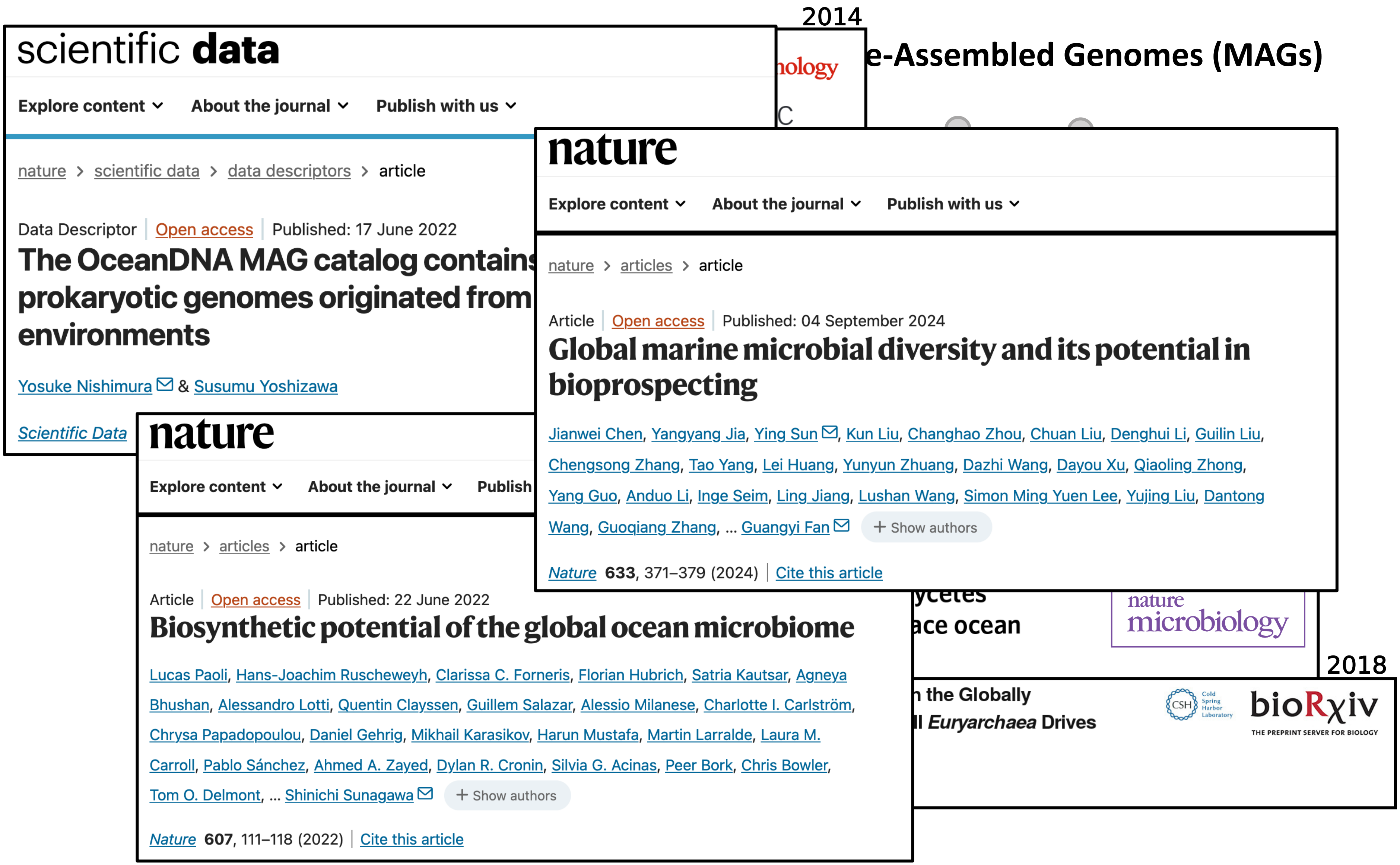
✓ Cross-domains (Prok. & Euk.) predicted interactions from pole-to-pole

✓ Strong latitudinal/temperature-driven structuration of predicted associations

✓ Four biome-specific communities emerging with distinct predicted responses to environmental changes

Chaffron et al. Science Advances (2021)

Environmental genomes are flowing



scientific **data**

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Data Descriptor | Open access | Published: 17 June 2022

The OceanDNA MAG catalog contains
prokaryotic genomes originated from
environments

Yosuke Nishimura & Susumu Yoshizawa

Scientific Data

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nature

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Article | Open access | Published: 04 September 2024

Global marine microbial diversity and its potential in bioprospecting

Jianwei Chen, Yangyang Jia, Ying Sun, Kun Liu, Changhao Zhou, Chuan Liu, Denghui Li, Guilin Liu, Chengsong Zhang, Tao Yang, Lei Huang, Yunyun Zhuang, Dazhi Wang, Dayou Xu, Qiaoling Zhong, Yang Guo, Anduo Li, Inge Seim, Ling Jiang, Lushan Wang, Simon Ming Yuen Lee, Yujing Liu, Dantong Wang, Guoqiang Zhang, … Guangyi Fan + Show authors

Nature **633**, 371–379 (2024) | Cite this article

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Article | Open access | Published: 22 June 2022

Biosynthetic potential of the global ocean microbiome

Lucas Paoli, Hans-Joachim Ruscheweyh, Clarissa C. Forneris, Florian Hubrich, Satria Kautsar, Agneya Bhushan, Alessandro Lotti, Quentin Clayssen, Guillem Salazar, Alessio Milanese, Charlotte I. Carlström, Chrysa Papadopoulou, Daniel Gehrig, Mikhail Karasikov, Harun Mustafa, Martin Larralde, Laura M. Carroll, Pablo Sánchez, Ahmed A. Zayed, Dylan R. Cronin, Silvia G. Acinas, Peer Bork, Chris Bowler, Tom O. Delmont, … Shinichi Sunagawa + Show authors

Nature **607**, 111–118 (2022) | Cite this article

2014

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e-Assembled Genomes (MAGs)

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ace ocean

nature microbiology

2018

n the Globally

ll *Euryarchaea* Drives

Cold Spring Harbor Laboratory

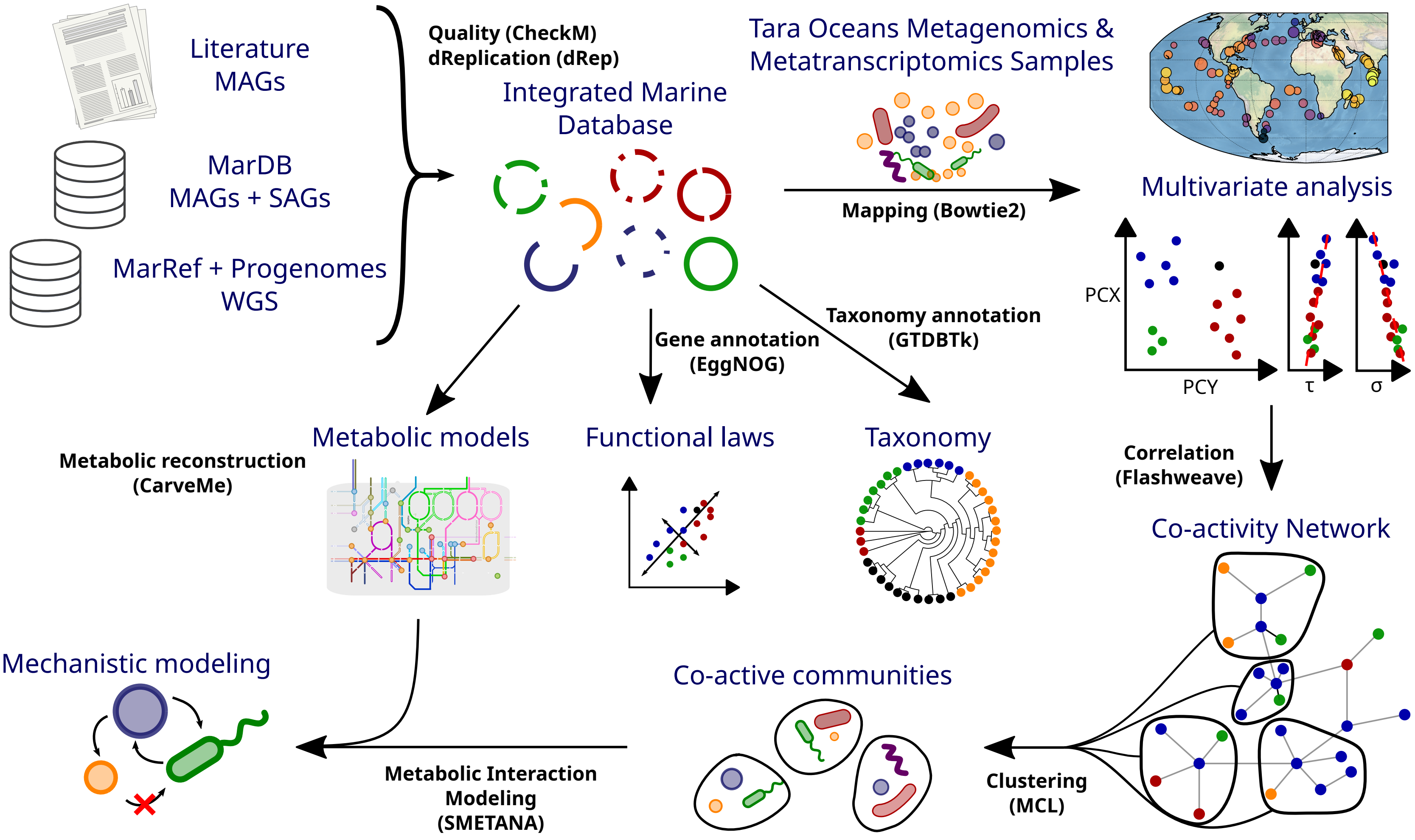
bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

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

Marinna Gaudin

Nils Giordano



Literature
MAGs

MarDB
MAGs + SAGs

MarRef + Progenomes
WGS

Quality (CheckM)
dReplication (dRep)

Integrated Marine
Database

Tara Oceans Metagenomics &
Metatranscriptomics Samples

Mapping (Bowtie2)

Multivariate analysis

Gene annotation
(EggNOG)

Taxonomy annotation
(GTDBTk)

Metabolic reconstruction
(CarveMe)

Metabolic models

Functional laws

Taxonomy

Correlation
(Flashweave)

Co-activity Network

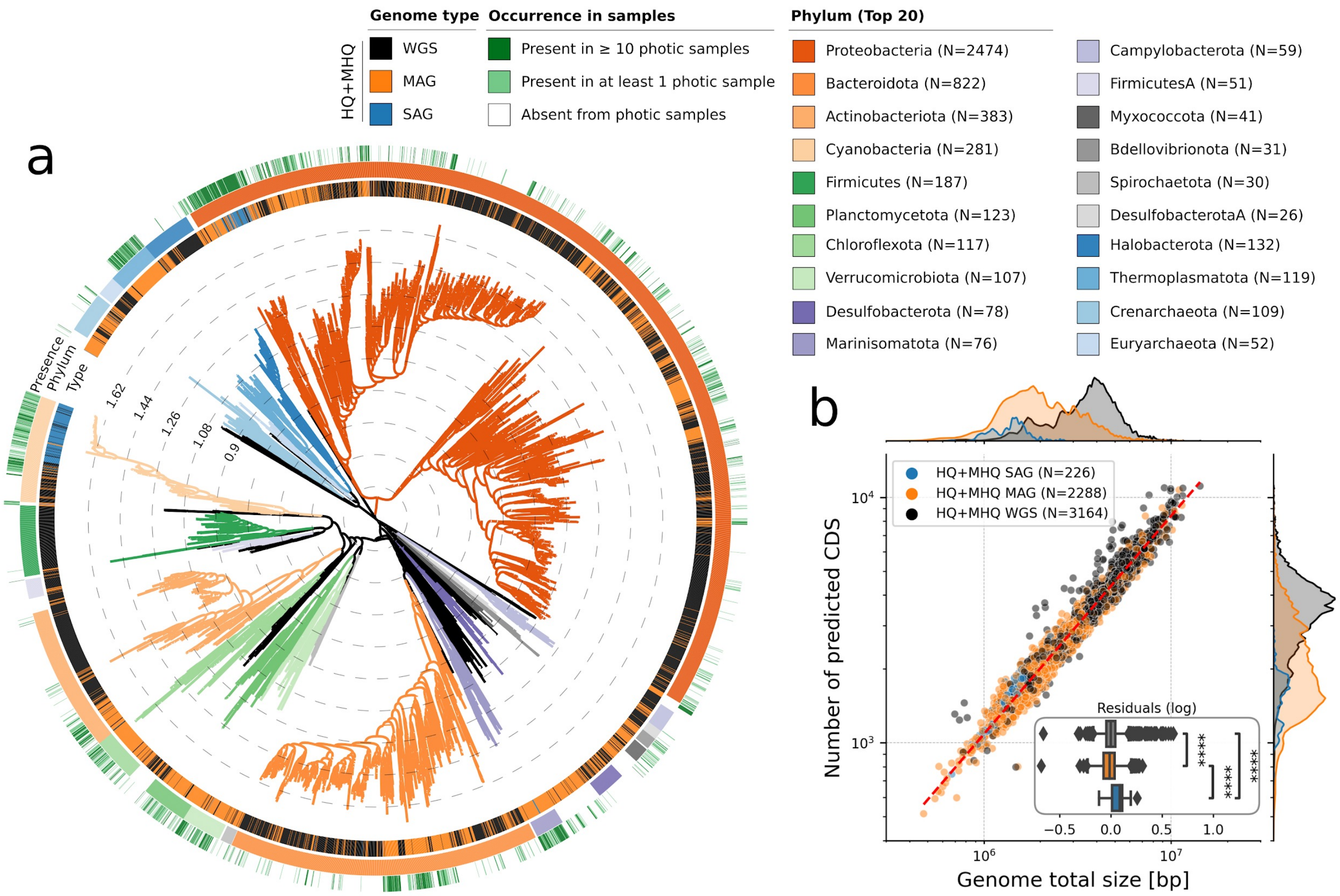
Mechanistic modeling

Co-active communities

Metabolic Interaction
Modeling
(SMETANA)

Clustering
(MCL)

A database of marine bacterial and archaeal genomes



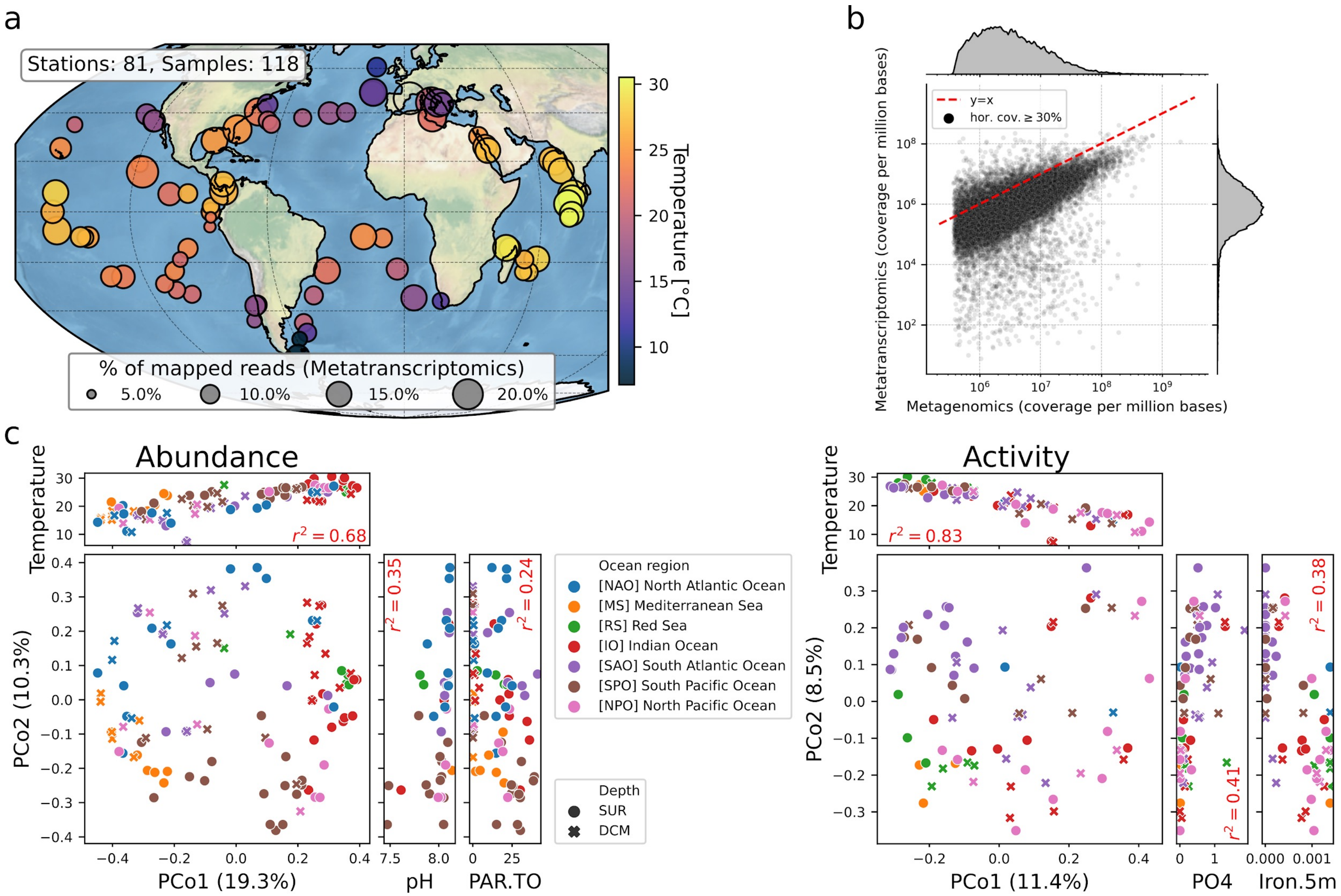
$$n_c = \lambda_c \, g^{\alpha_c}$$

The number of genes n_c in a category increases as a power-law in the total number of genes g

- ✓ Genome scaling law conserved for HQ+MHQ genomes (WGS, MAGs, SAGs)
- ✓ Environmental genomes (MAGs) are significantly smaller in size compared to isolates (WGS)

Giordano, Gaudin et al. Nature Comm. 2024

Global ocean genome abundance and activity profiling

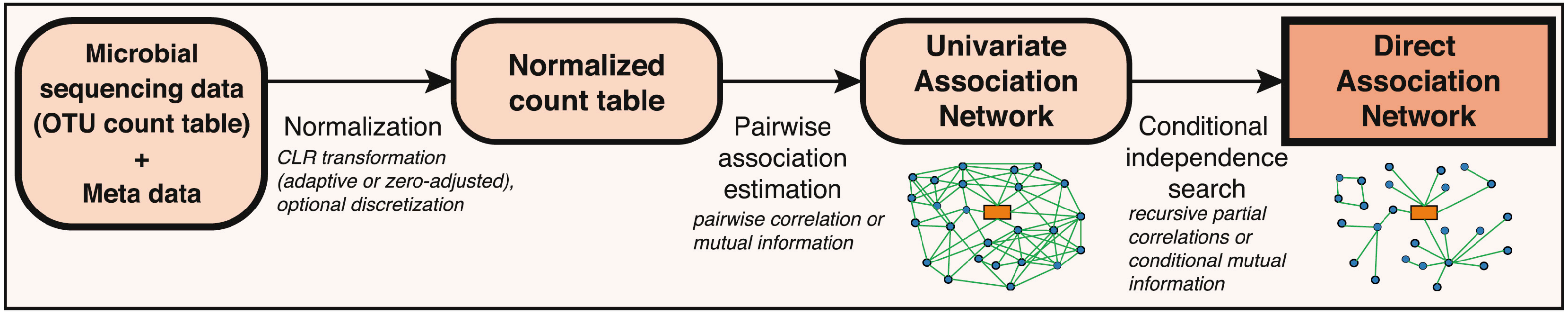


✓ Environmental genomes community abundance and activity are mainly driven by temperature, pH, PAR, PO4 and Iron levels

Giordano, Gaudin et al. Nature Comm. 2024

Inferring direct associations between genomes

FlashWeave workflow



Microbial sequencing data (OTU count table) + Meta data

Normalization

CLR transformation (adaptive or zero-adjusted), optional discretization

Normalized count table

Pairwise association estimation

pairwise correlation or mutual information

Univariate Association Network

Conditional independence search

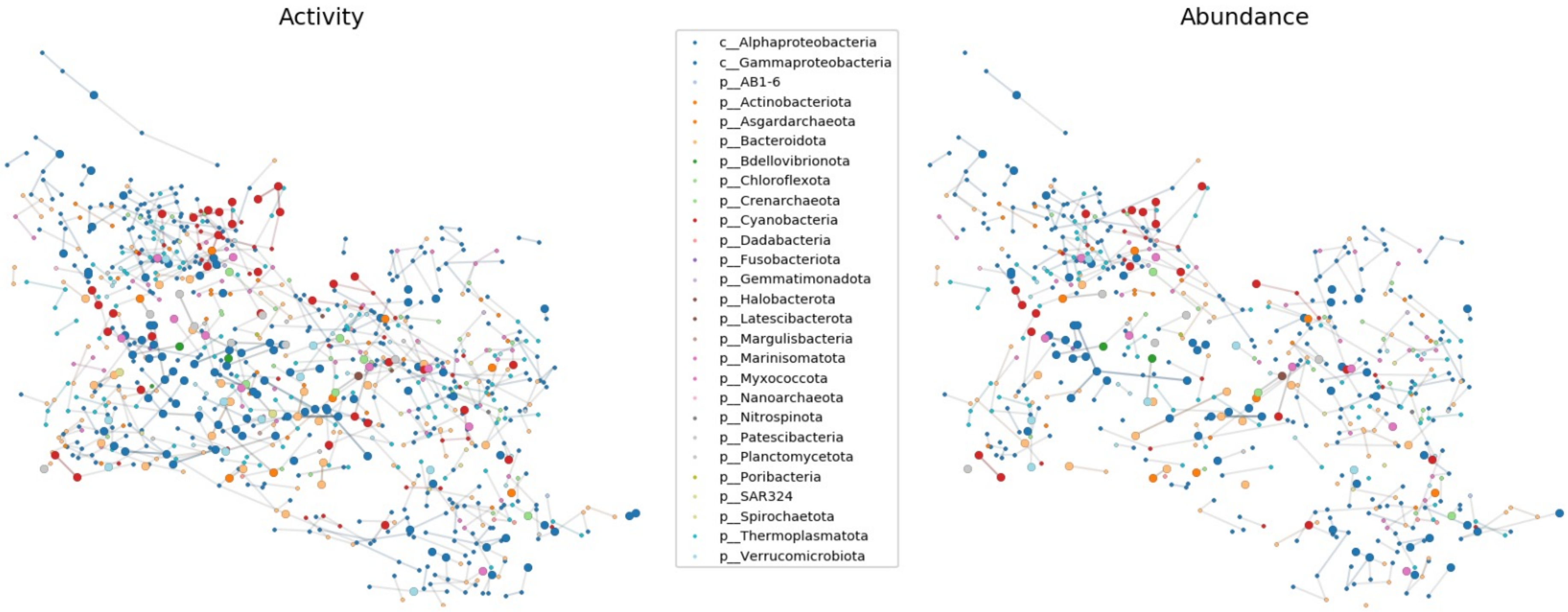
recursive partial correlations or conditional mutual information

Direct Association Network

- ✓ Inference of a global univariate association graph using pairwise correlations
- ✓ Detection of indirect associations via iterative conditional independence search
- ✓ Removal of indirect (purely correlational) associations reported by univariate methods
- ✓ Graph of predicted "direct associations" among co-abundant and co-active genomes

Tackmann et al. Cell Systems 2019

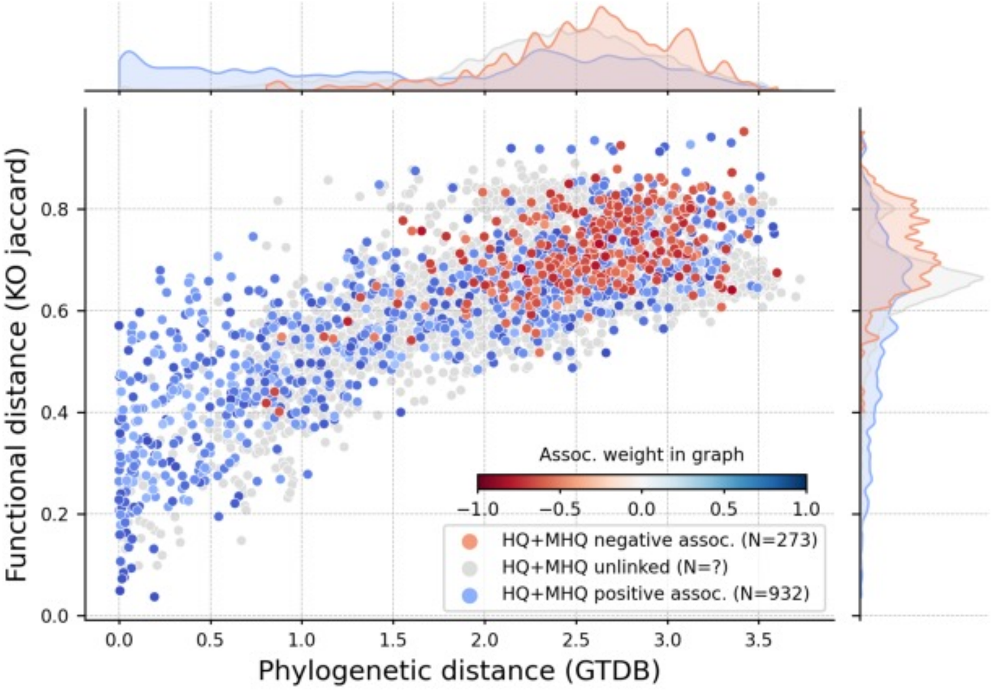
Genome-resolved co-abundance and co-activity networks

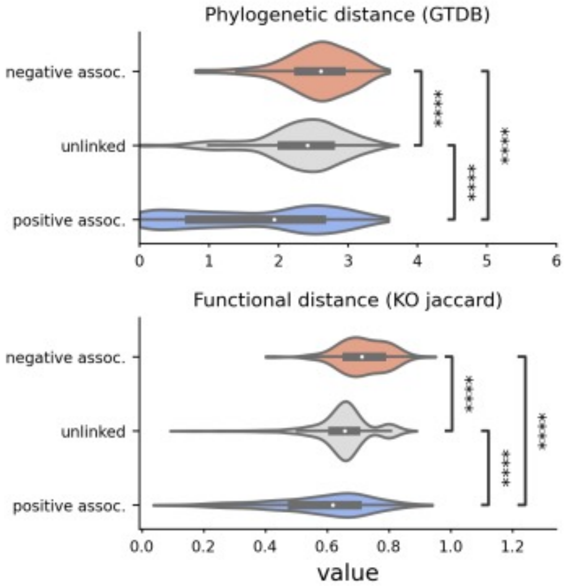


- ✓ Preferential co-activities are detected between environmental genomes in the euphotic zone at global scale
- ✓ Significant number of inter-lineage associations across large phylogenetic distances

Giordano, Gaudin et al. Nature Comm. 2024

Predicted inter-lineage associations across large phylogenetic distances

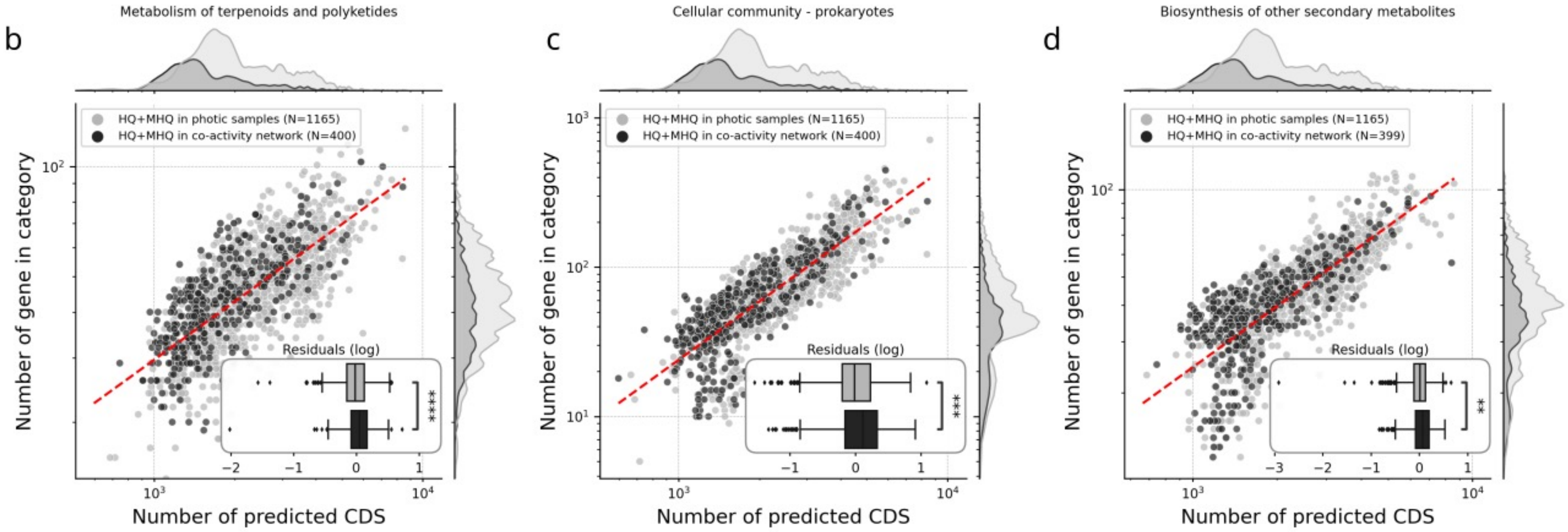




- ✓ Co-active environmental genomes phylogenetically and functionally closer than expected at random
- ✓ Community detection algorithm (MCL) identified several co-active communities of environmental genomes

Giordano, Gaudin et al. Nature Comm. 2024

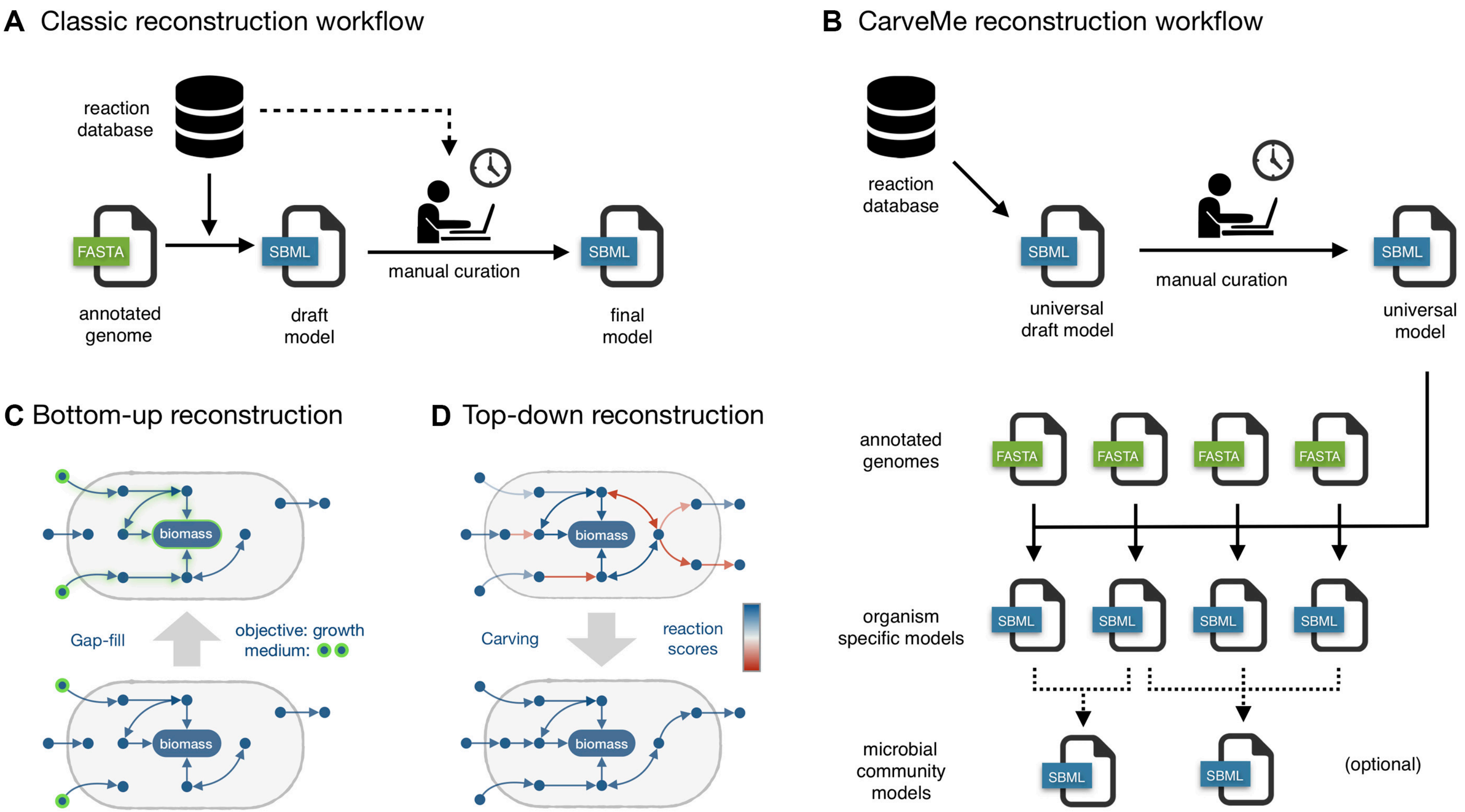
Biotic factors / functional traits shaping bacterioplankton communities



- ✓ Genomic scaling laws enabled the functional comparison of genomes/MAGs
- ✓ Co-active genomes encoded a higher metabolic potential for:
  - Terpenoids / polyketides and other secondary metabolites biosynthesis
  - Quorum sensing and biofilm formation (cellular community)

Giordano, Gaudin et al. Nature Comm. 2024

Automated reconstruction of genome-scale metabolic models for microbial species



A Classic reconstruction workflow

B CarveMe reconstruction workflow

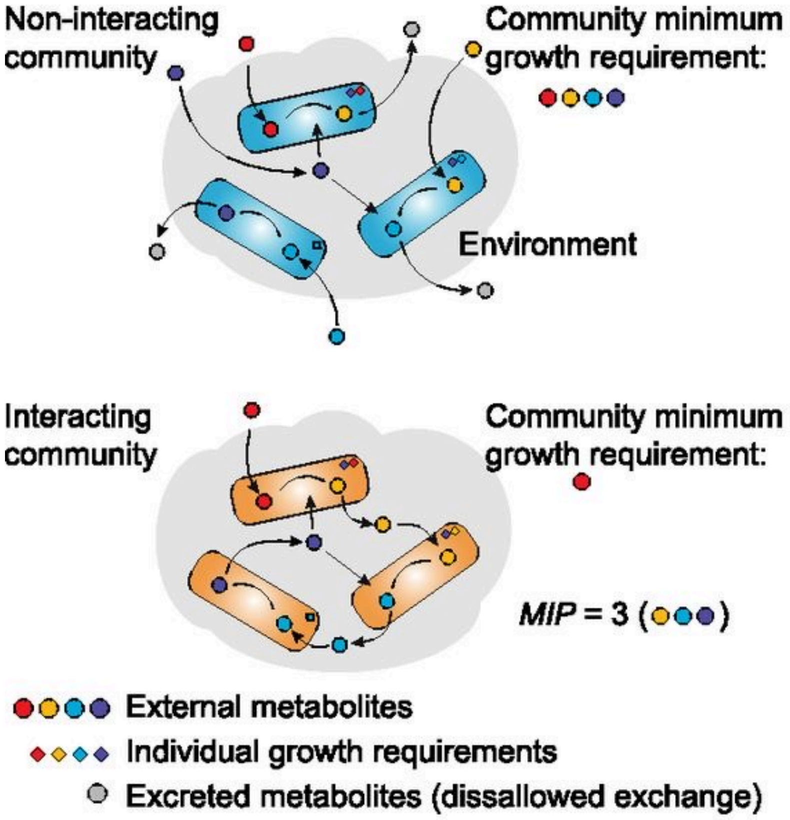
C Bottom-up reconstruction

D Top-down reconstruction

Machado et al. NAR (2018)

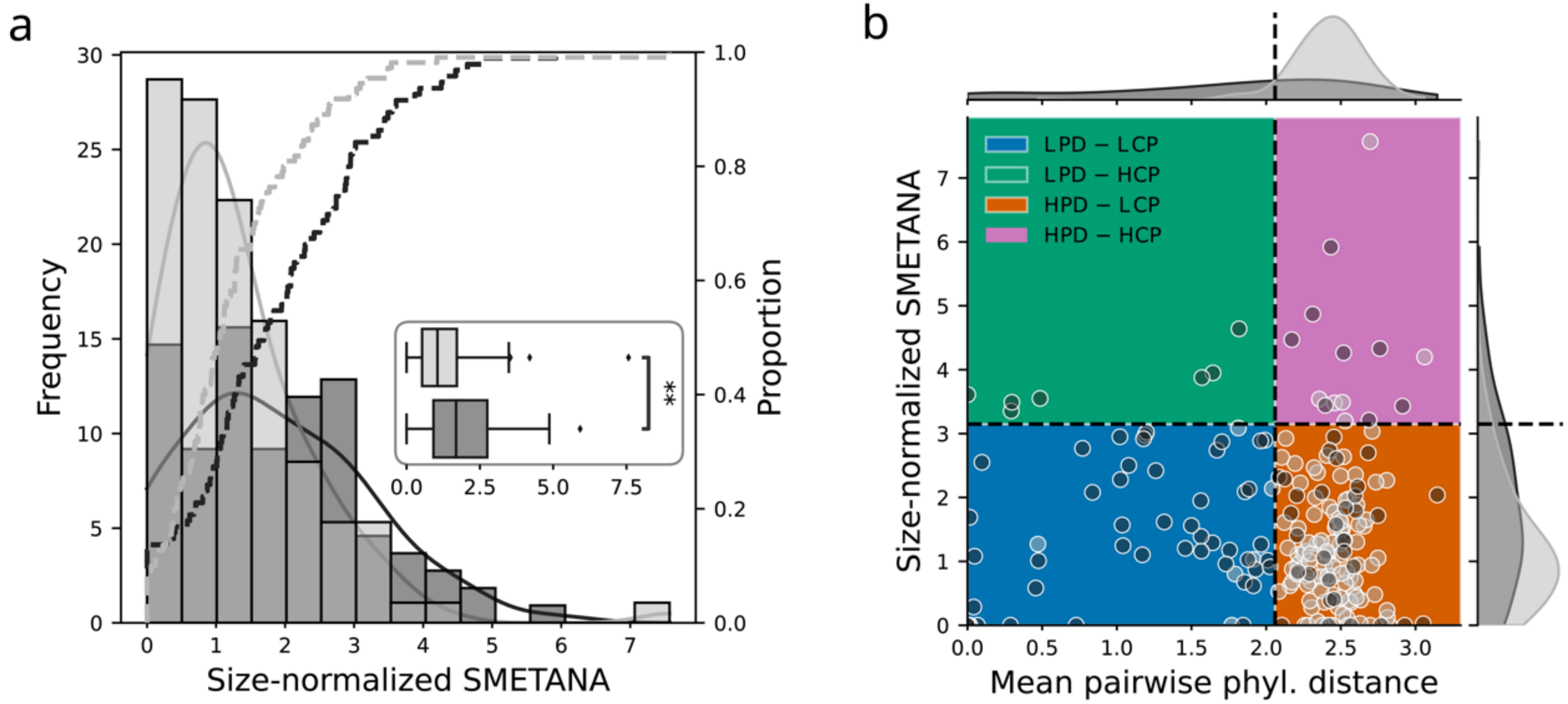
Metabolic modelling of co-active genome communities

- Multi-species flux-balance model to predict competition/interactions scores for a community (MIP)
- Flux simulations in a minimal medium to identify metabolic exchanges essential for the survival of the community
- SMETANA score = growth dependency for a pair of species as the product of 3 interspecies dependencies scores: (i) species coupling score (SCS), (ii) metabolite uptake score (MUS), and (iii) metabolite production score (MPS)



Zelezniak et al. PNAS (2015)

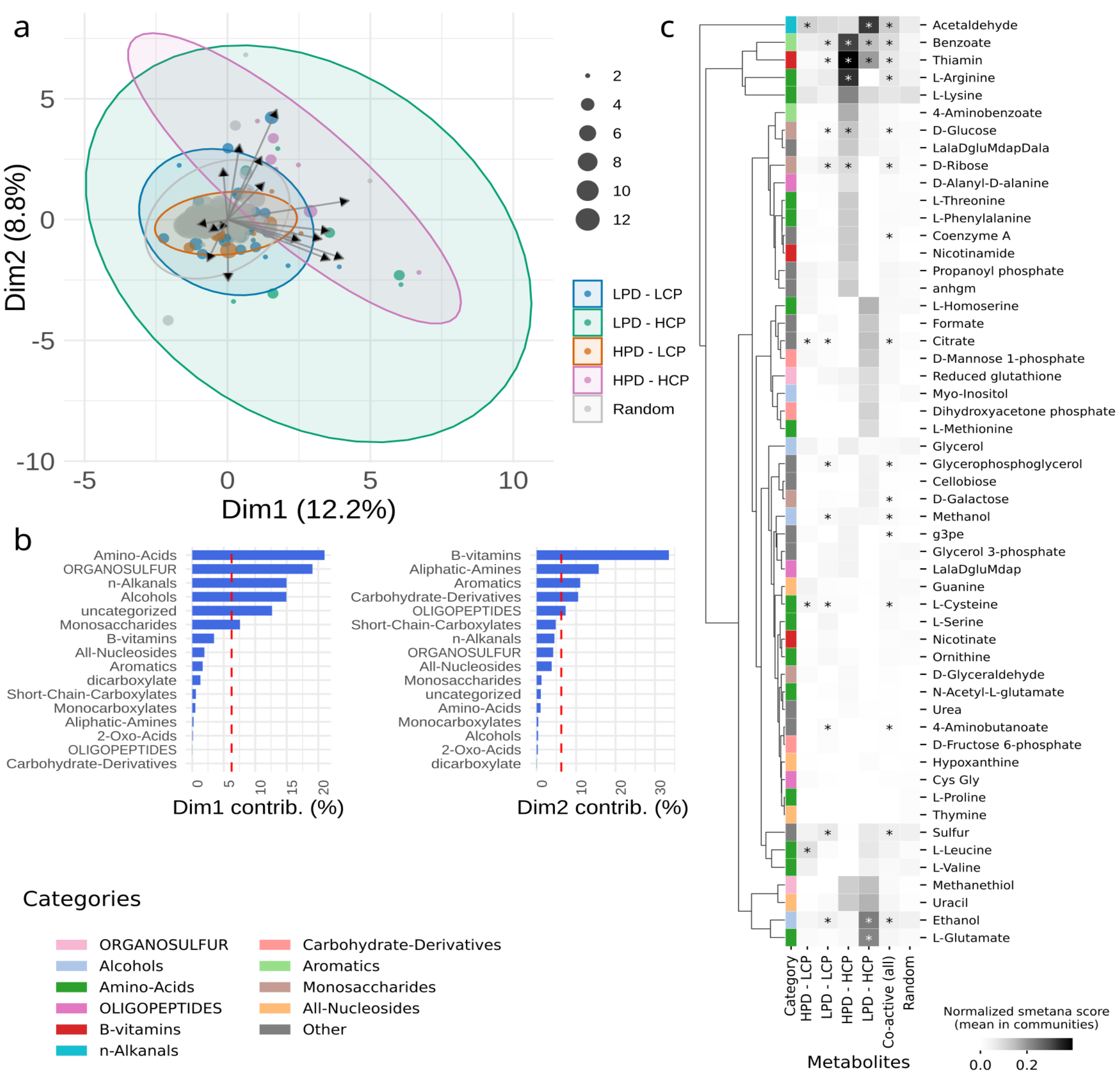
Higher metabolic interaction potential predicted within co-active communities



- ➢ Community metabolic modeling (FBA-based) to infer potential interaction mechanisms (metabolites cross-feeding) within communities
- ➢ Co-active genome communities display a higher potential for metabolic interaction
- ➢ Four community types defined by phylogenetic distance and interaction potential

Giordano, Gaudin et al. Nature Comm. 2024

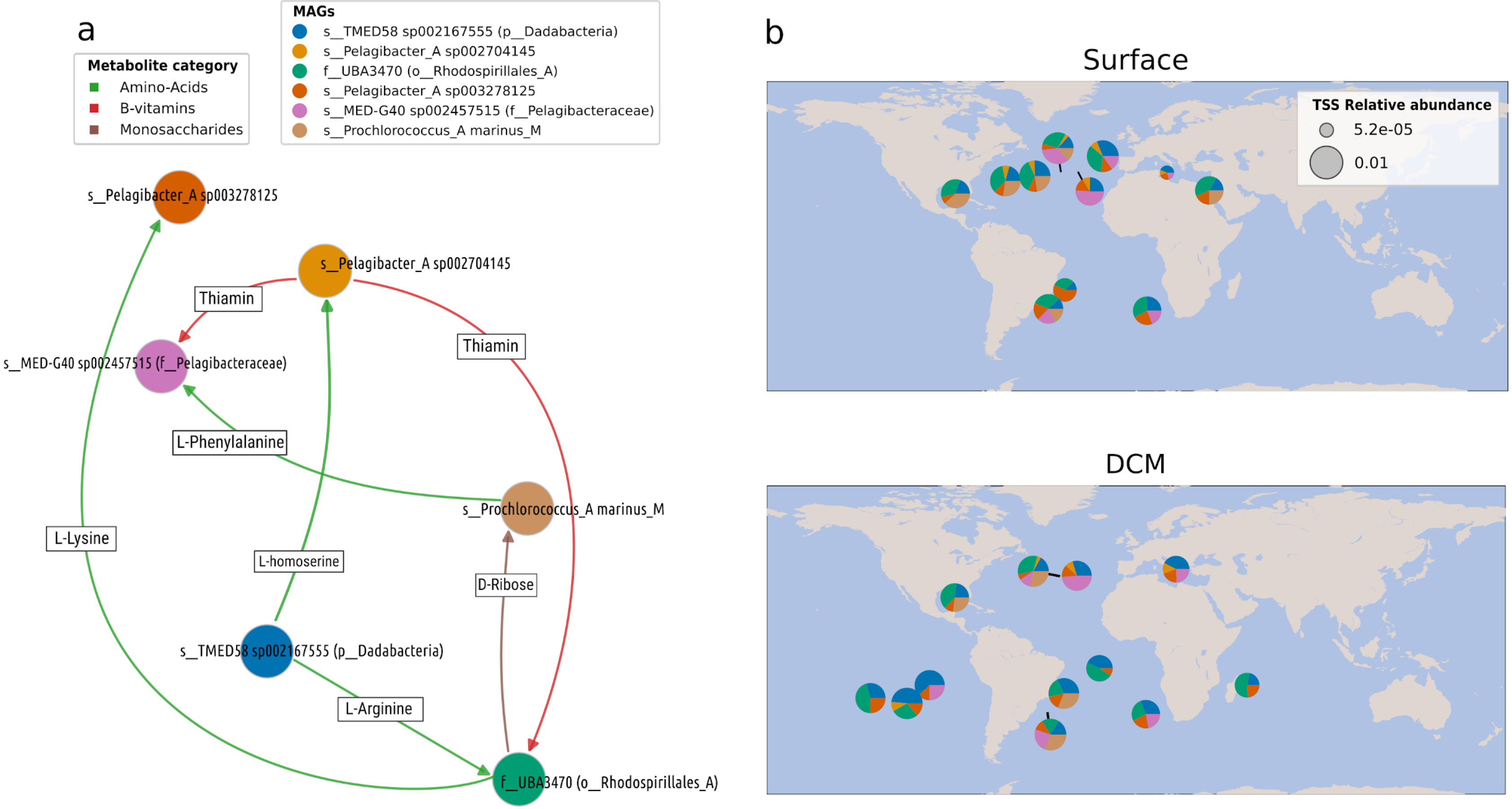
Community metabolic modelling predicts specific metabolic cross-feedings



- ✓ Predicted exchanges of specific amino acids (Glutamic acid and Arginine)
- ✓ Predicted exchanges of B vitamins (B$_1$ and B$_6$)
- ✓ Predicted exchanges of products of B$_{12}$-dependent enzymes (ornithine, glutamate and methionine)
- ➢ **Widespread AAs and group B vitamins interdependencies and auxotrophies shaping bacterioplankton community assembly?**

Giordano, Gaudin et al. Nature Comm. 2024

Zooming on a specific co-active genome community

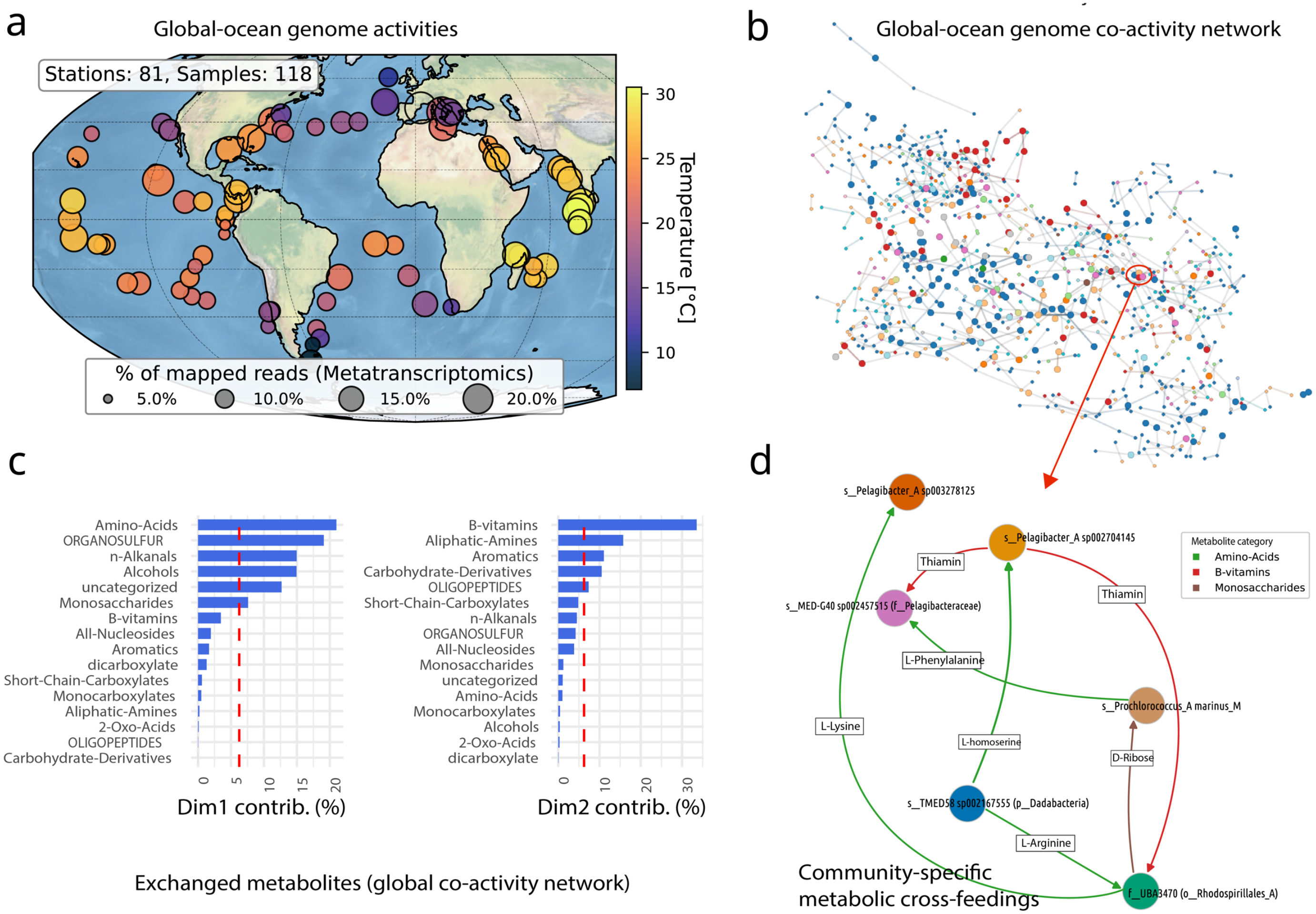


- ➢ Predicted exchanges of vitamin B_1 and several amino acids predicted between these six genomes

Giordano, Gaudin et al. Nature Comm. 2024

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



Exchanged metabolites (global co-activity network)

Community-specific metabolic cross-feedings

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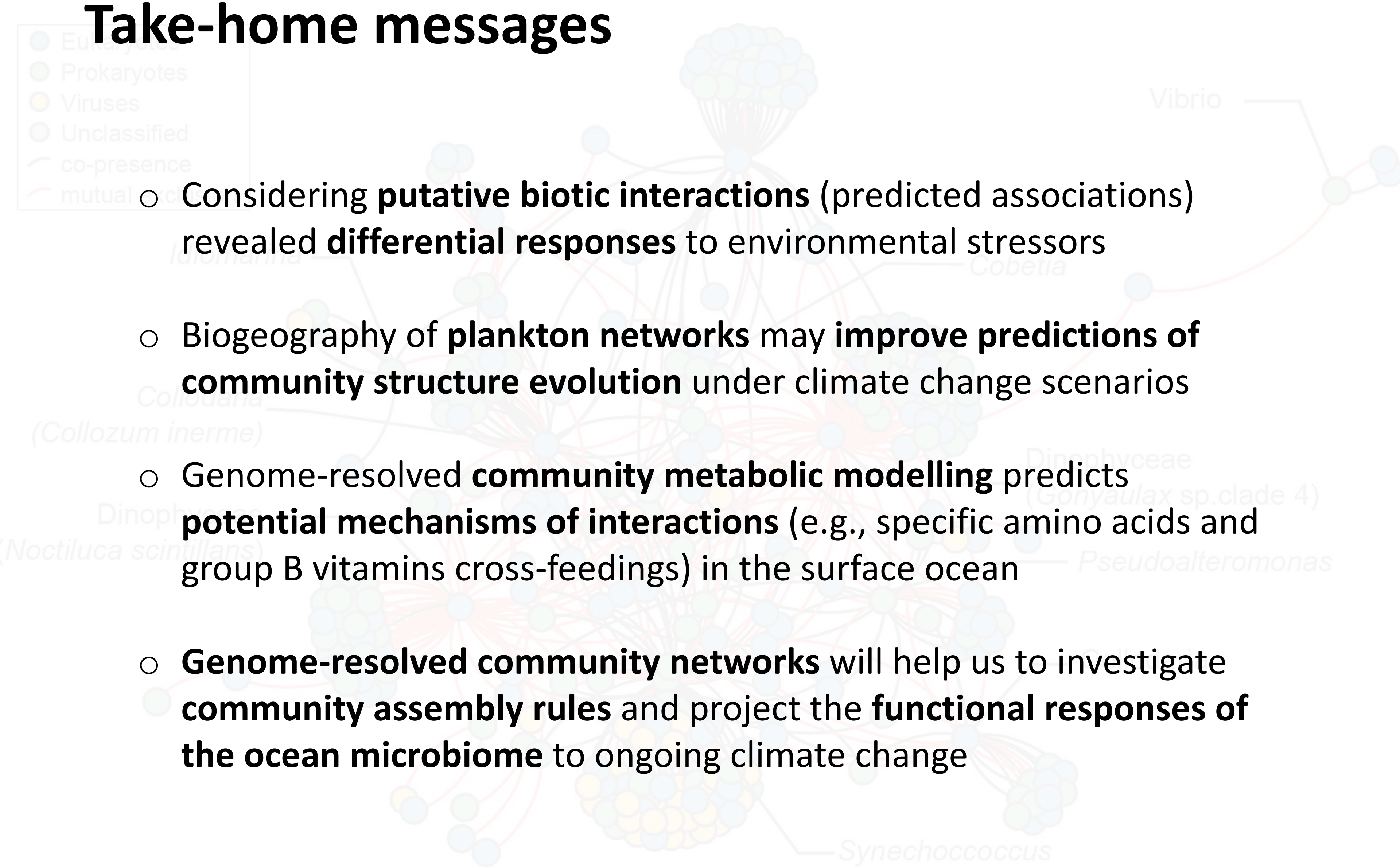
Take-home messages



- Considering **putative biotic interactions** (predicted associations) revealed **differential responses** to environmental stressors

- Biogeography of **plankton networks** may **improve predictions of community structure evolution** under climate change scenarios

- Genome-resolved **community metabolic modelling** predicts **potential mechanisms of interactions** (e.g., specific amino acids and group B vitamins cross-feedings) in the surface ocean

- **Genome-resolved community networks** will help us to investigate **community assembly rules** and project the **functional responses of the ocean microbiome** to ongoing climate change

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