Grasping the invisible ocean life: some new answers to old questions

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EXCELENCIA SEVERO OCHOA

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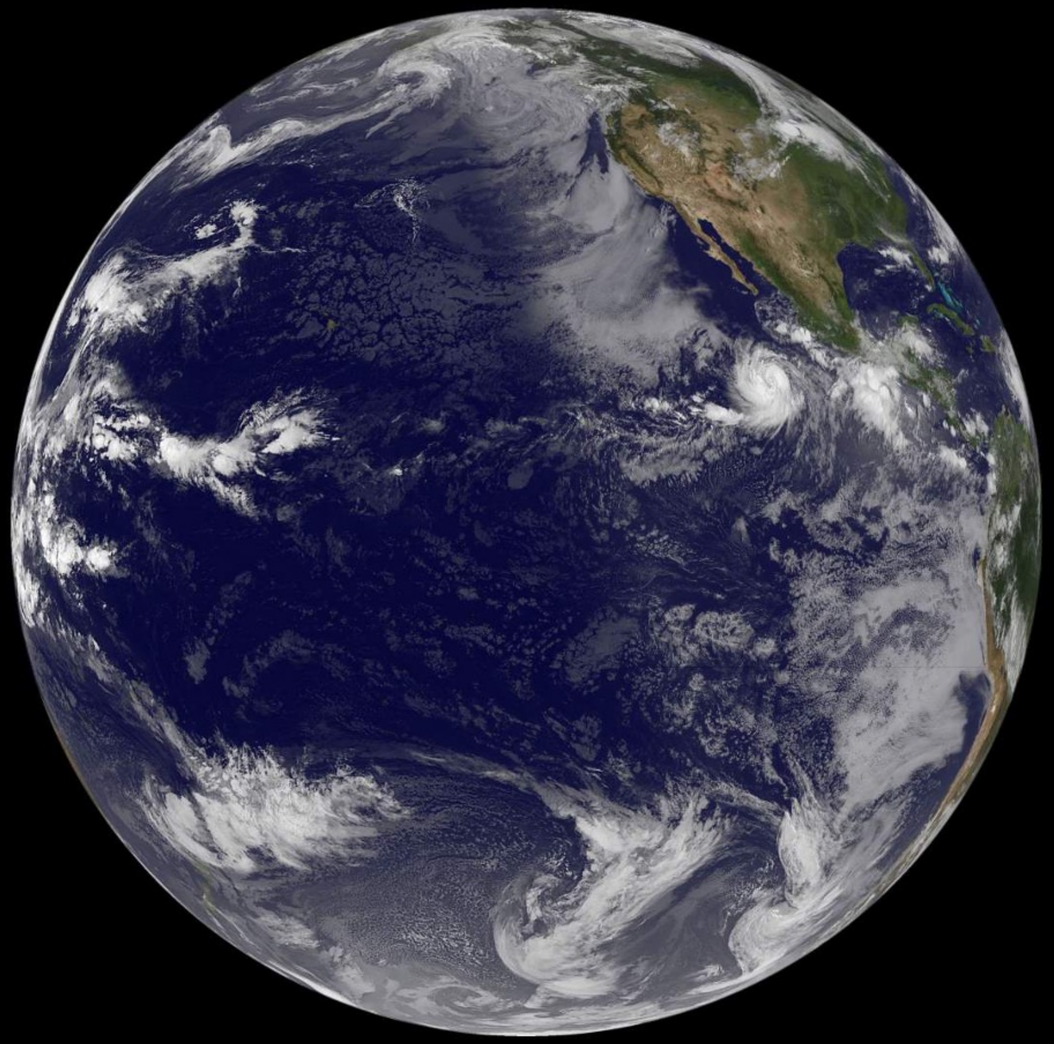
Lidia Montiel

Ina Deutschmann

Anders Krabberød

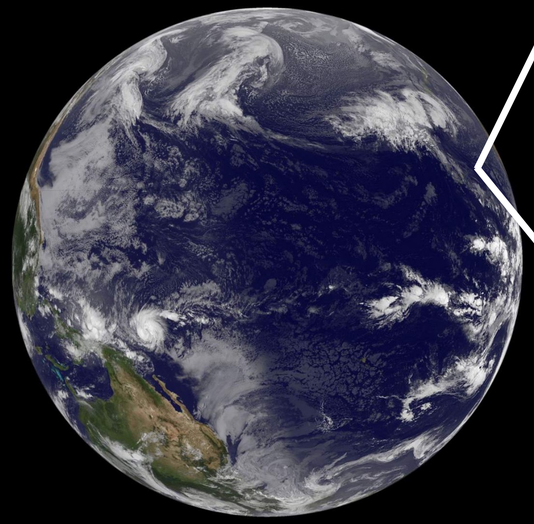
The importance of microbial life in the ocean became evident during the 20th century



A microbial ocean

Cells

- 10^{30} viruses
- 10^{29} prokaryotes
- 10^{28} eukaryotes
- (10^{24} stars in visible universe)



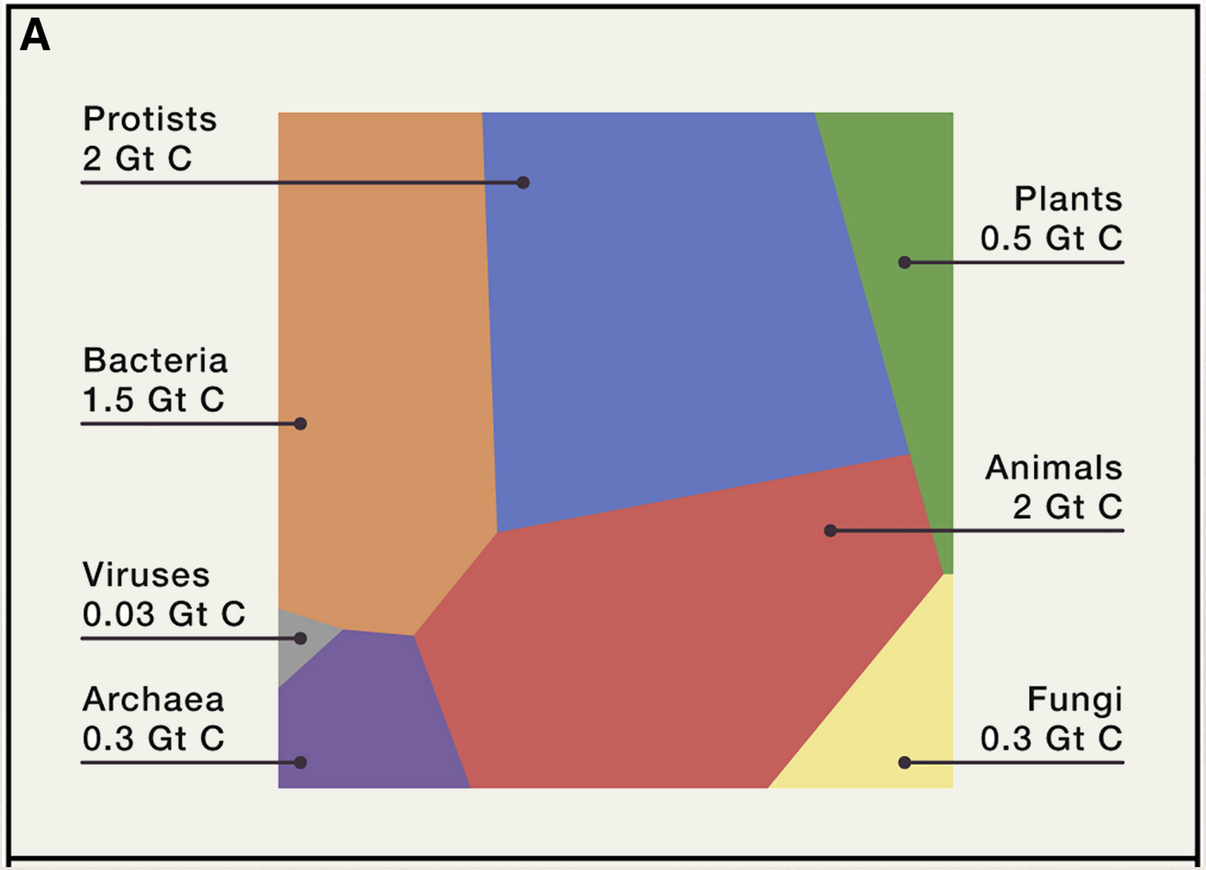
Marine biomass

Protists, bacteria, fungi, viruses:
ca. 70% of the ocean biomass

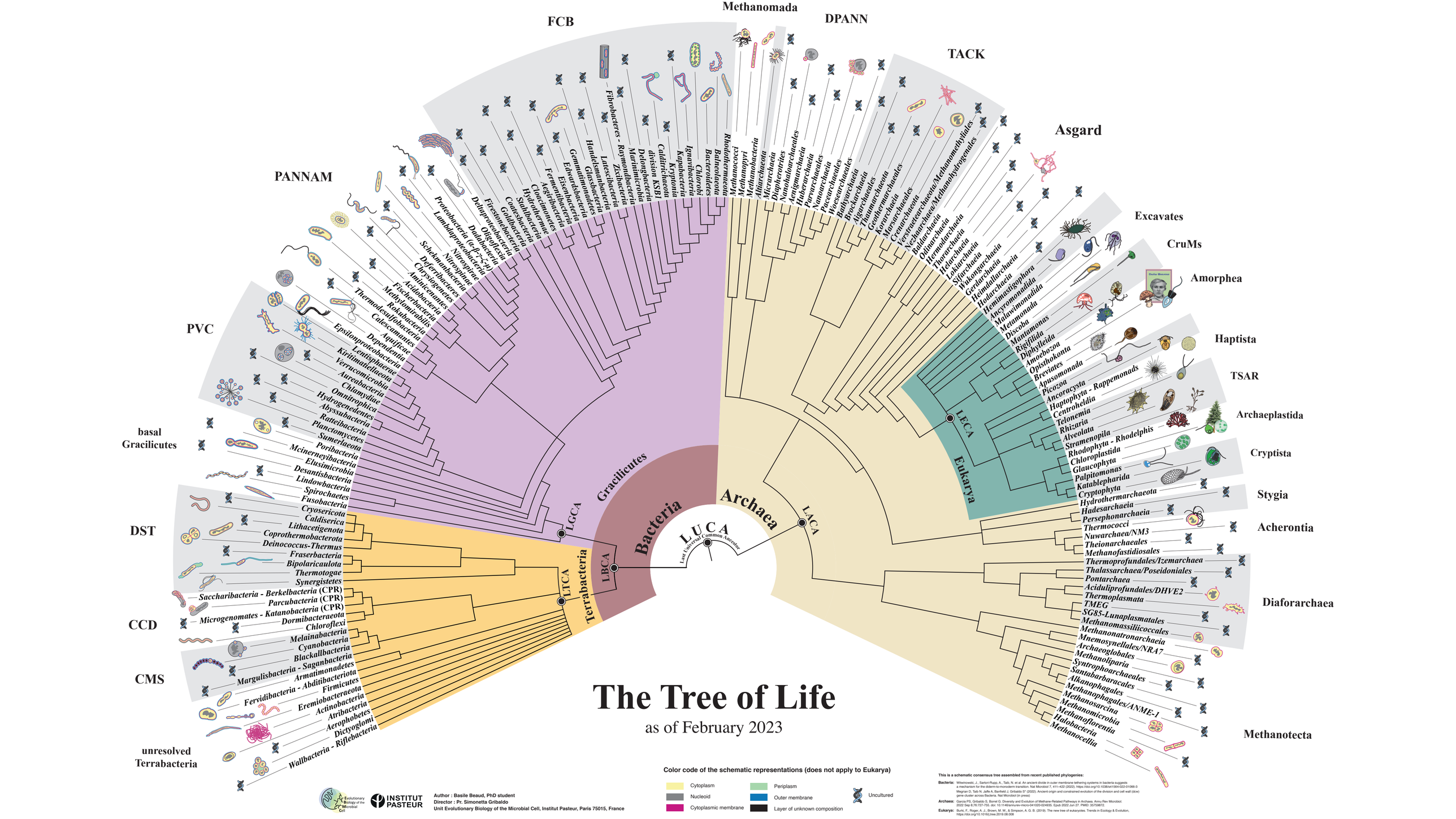
Microbial biomass:

- Protists ca. 50%

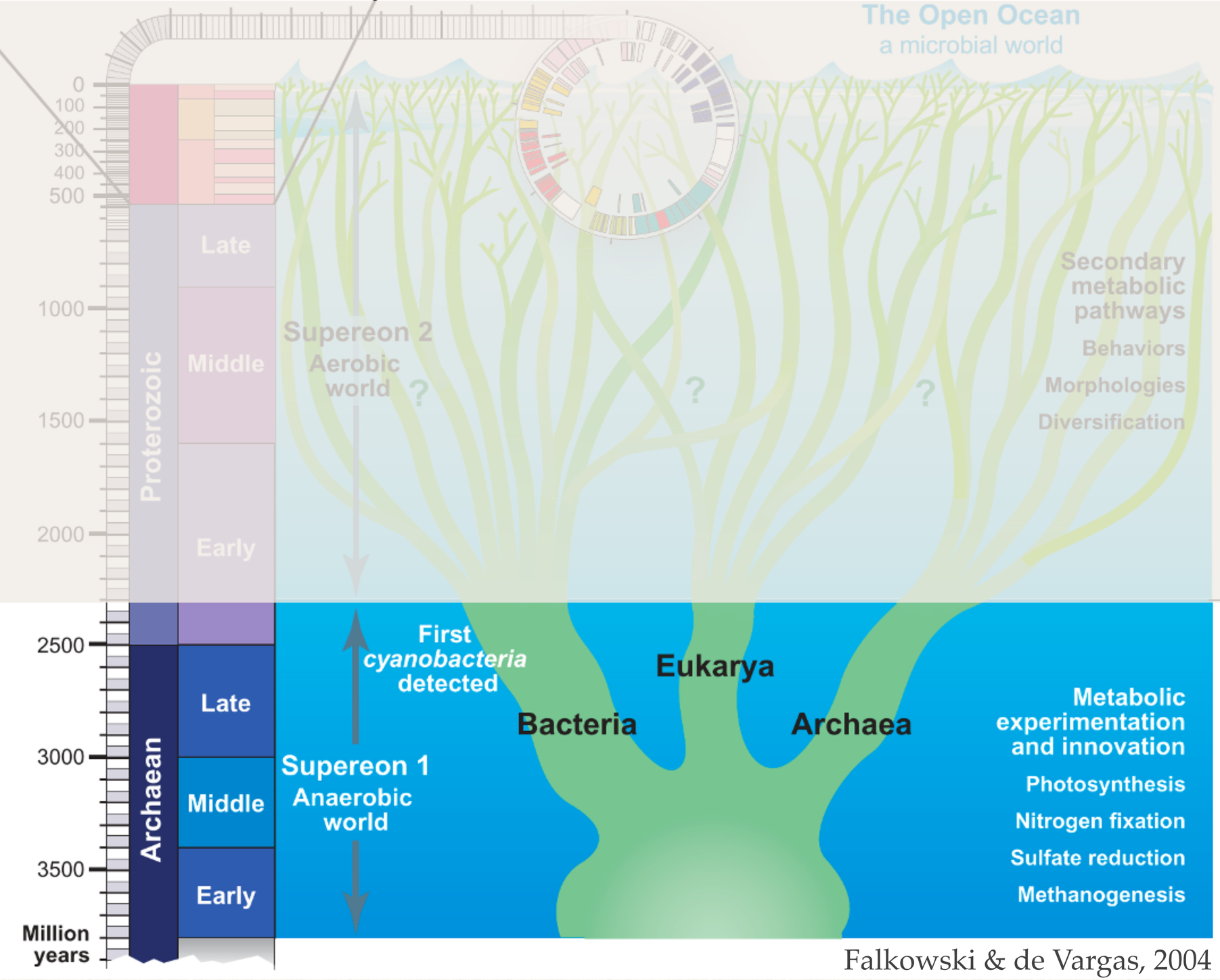
- Prokaryotes ca. 46%



Bar-On & Milo, 2019


The Tree of Life
as of February 2023
LUCA
Last Universal Common Ancestor
Bacteria
Archaea
Eukarya
LBCA
LGCA
LTCA
LACA
LECA
Gracilicutes
Terrabacteria
FCB
PANNAM
PVC
DST
CCD
CMS
basal Gracilicutes
unresolved Terrabacteria
Methanomada
DPANN
TACK
Asgard
Excavates
CruMs
Amorphea
Haptista
TSAR
Archaeplastida
Cryptista
Stygia
Acherontia
Diaforarchaea
Methanotecta
Color code of the schematic representations (does not apply to Eukarya)
Cytoplasm
Nucleoid
Cytoplasmic membrane
Periplasm
Outer membrane
Layer of unknown composition
Uncultured
This is a schematic consensus tree assembled from recent published phylogenies:
Bacteria: Wiewiowski, J., Sartori-Rupp, A., Talb, N. et al. An ancient divide in outer membrane tethering systems in bacteria suggests a mechanism for the diderm-to-monoderm transition. Nat Microbiol 7, 411–422 (2022). https://doi.org/10.1038/s41564-022-01066-3
Magnan D, Tab N, Jaffe A, Blanfield J, Gribaldo S* (2022). Ancient origin and constrained evolution of the division and cell wall (dcw) gene cluster across Bacteria. Nat Microbiol (in press)
Archaea: Garcia PS, Gribaldo S, Borrel G. Diversity and Evolution of Methane-Related Pathways in Archaea. Annu Rev Microbiol. 2022 Sep 8;76:727-755. doi: 10.1146/annurev-micro-041020-024935. Epub 2022 Jun 27. PMID: 35758872.
Eukarya: Burki, F., Roger, A. J., Brown, M. W., & Simpson, A. G. B. (2019). The new tree of eukaryotes. Trends in Ecology & Evolution, https://doi.org/10.1016/j.tree.2019.08.008
Author : Basile Beaud, PhD student
Director : Pr. Simonetta Gribaldo
Unit Evolutionary Biology of the Microbial Cell, Institut Pasteur, Paris 75015, France
Evolutionary Biology of the Microbial Cell
INSTITUT PASTEUR

The emergence of the marine microbiome



Falkowski & de Vargas, 2004

Aerobic world

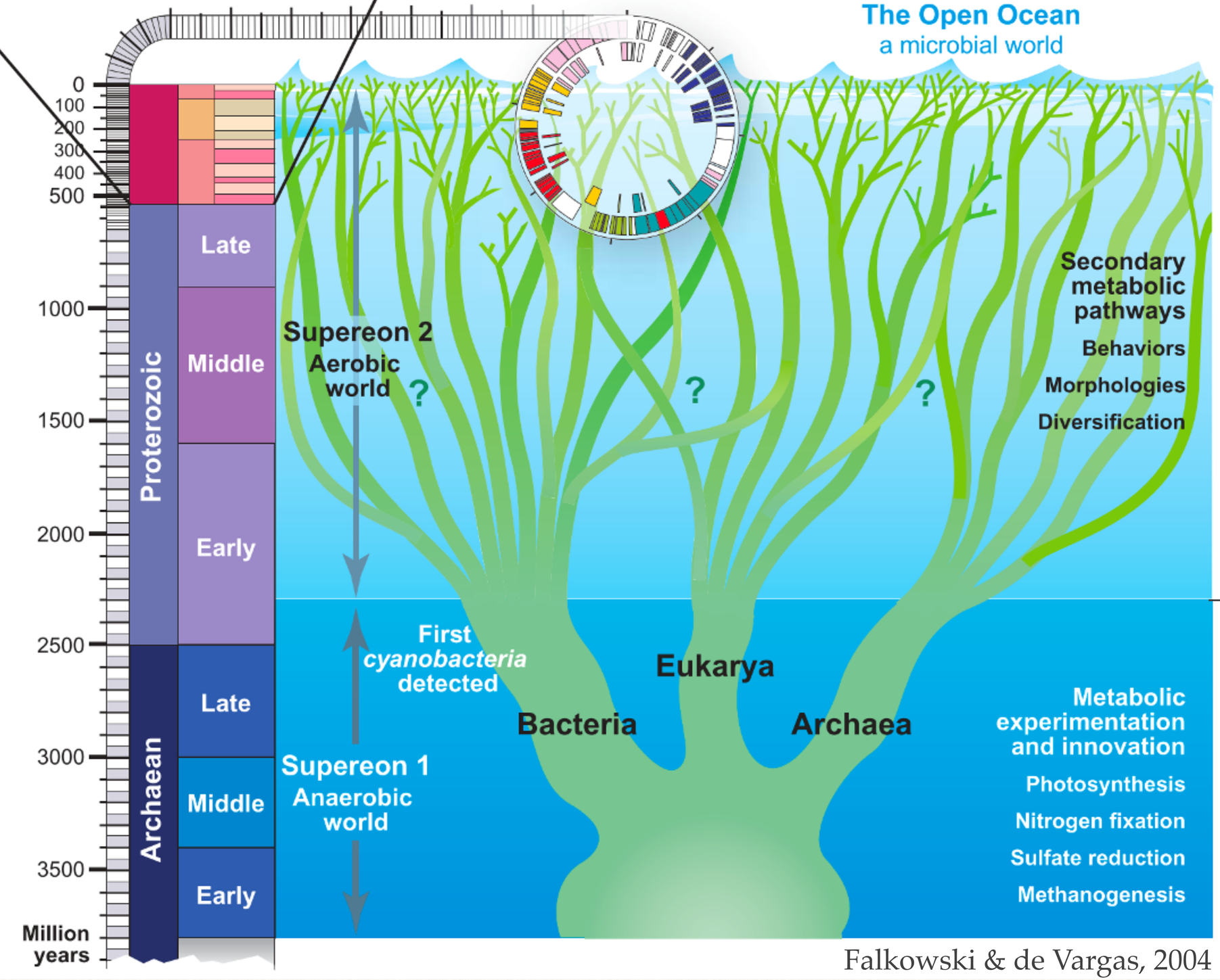
(2,300 MYA-present)

-Diversification:
genes and species
-Interactome complexity

Anaerobic world

(4,400-2,300 MYA)

-Metabolism
-Core genes
-Main lineages



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Anaerobic world

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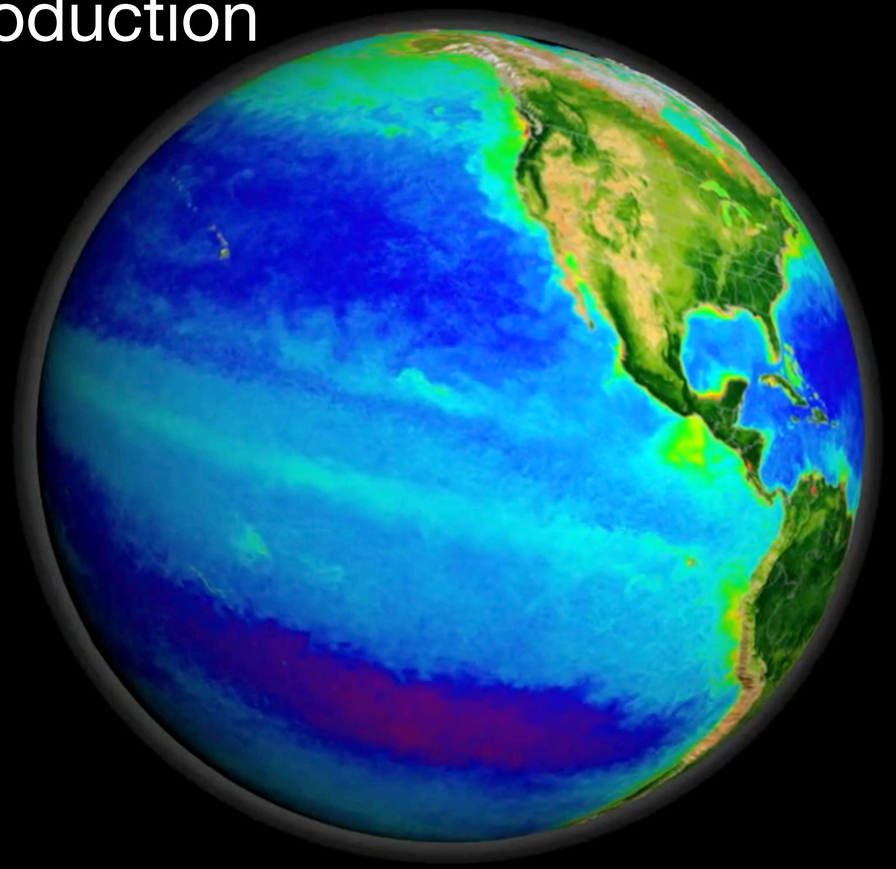
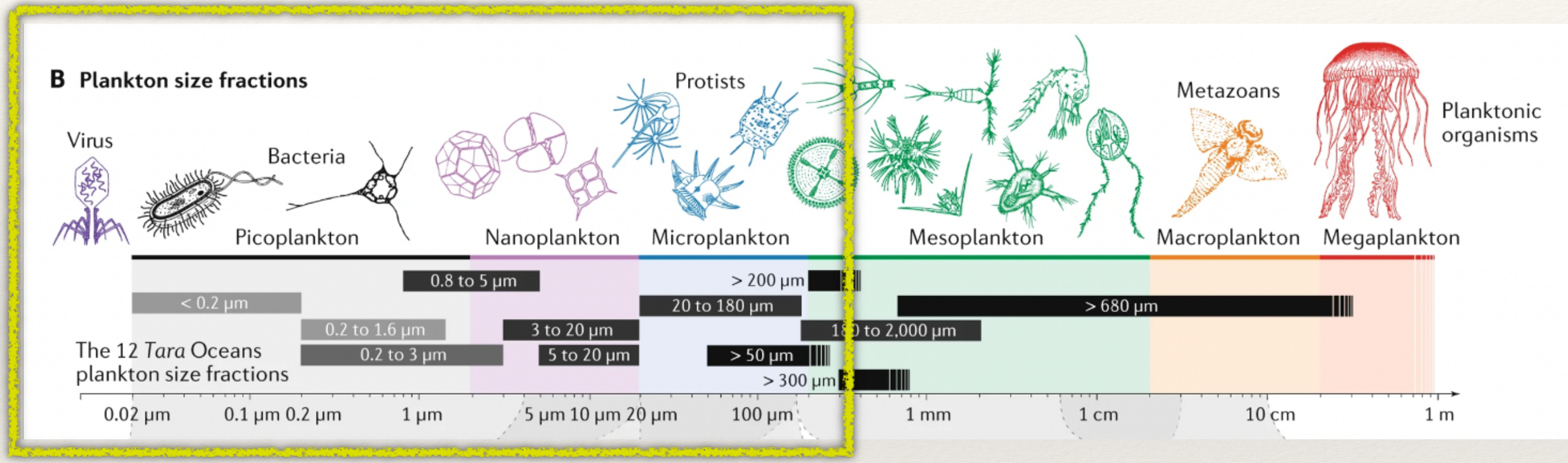
-Main lineages

Marine microbes & ecosystem function

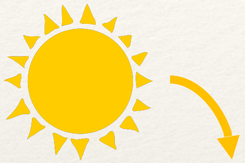
- Responsible for ~50% of the planetary primary production
- Crucial for the marine trophic web
- Fundamental for the biogeochemical cycles

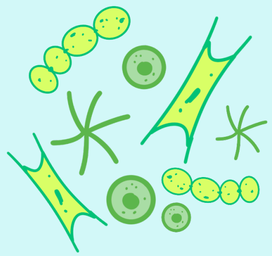


Marine microbial plankton: size



Food web basics

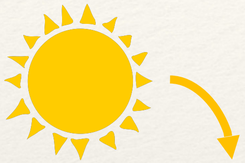


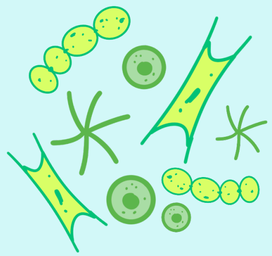


Phytoplankton

- Primary producers
- 50% of the primary production
- Both prokaryotes and eukaryotes

Food web basics





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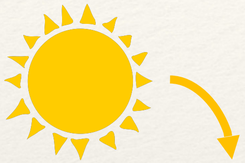
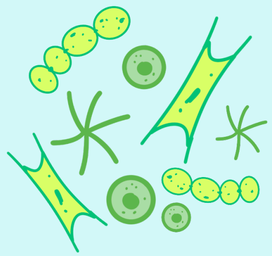




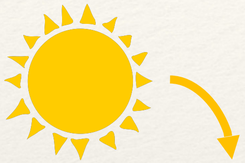
Phytoplankton

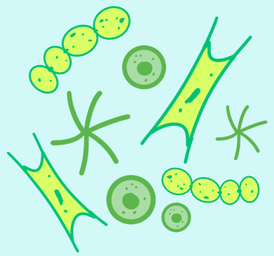
DOM

- Highly abundant and widespread
- Wide metabolic capabilities

Heterotrophic prokaryotes

Food web basics





Phytoplankton

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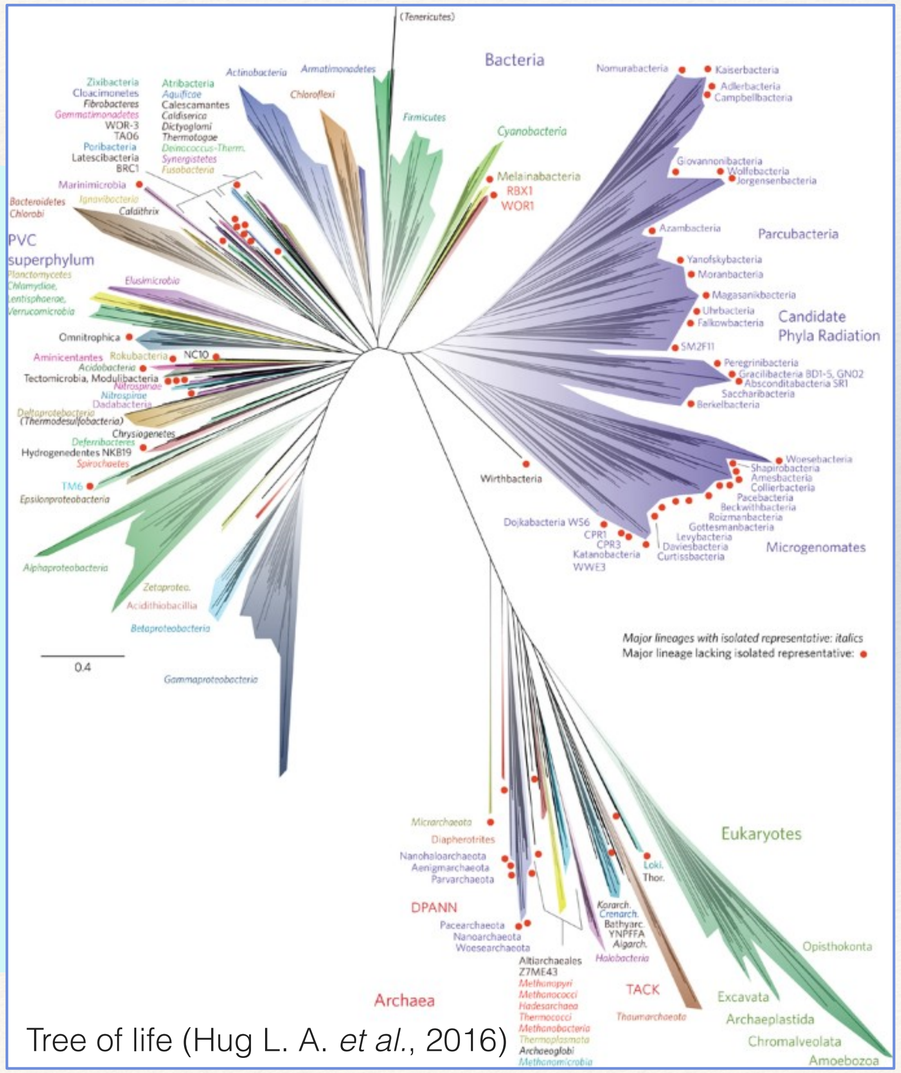
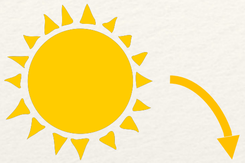
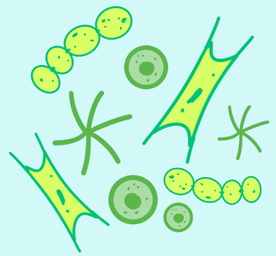
Heterotrophic prokaryotes



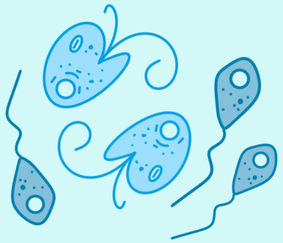
Tree of life (Hug L. A. *et al.*, 2016)

Food web basics





Phytoplankton



Heterotrophic flagellates

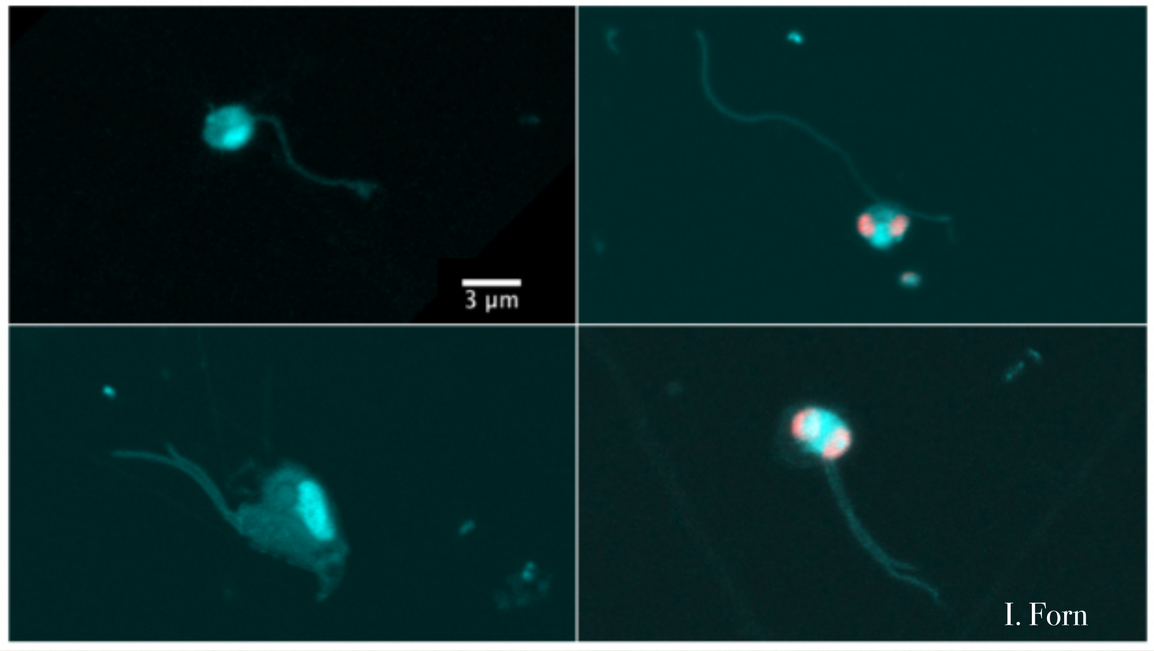
DOM

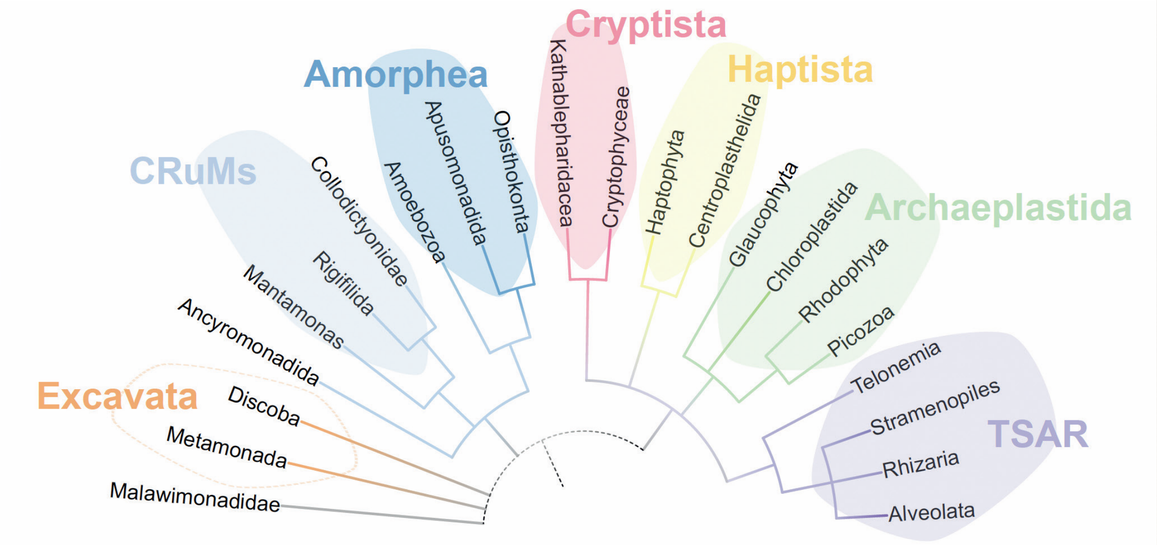
Heterotrophic prokaryotes

- Protists that move or feed with flagella
- Among the least known

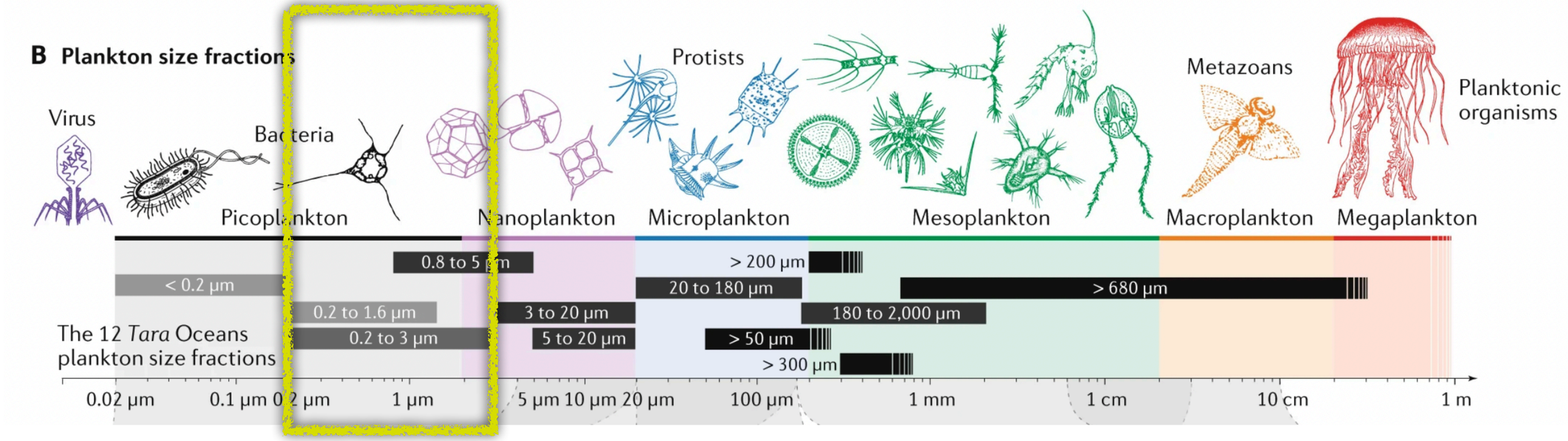
Marine Heterotrophic Flagellates (HFs)

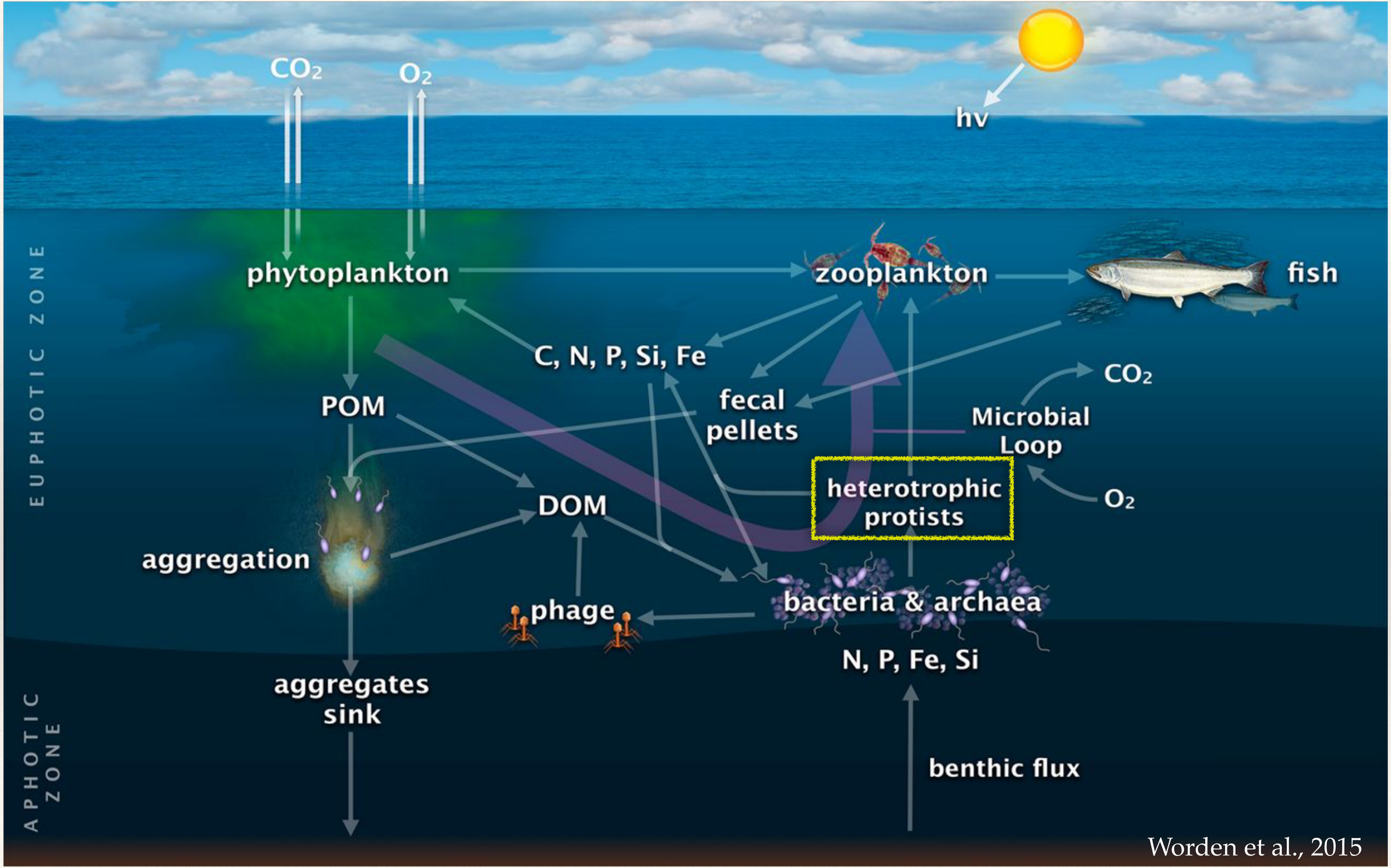
- Colorless cells with flagella
- Grazers
- Present across main lineages
- Most cells with sizes between 1-3 μm
- About 1,000 cells/ml
- Transfer matter and energy to upper trophic levels
- Few cultures and genomes
- Limited recovery using metaomics





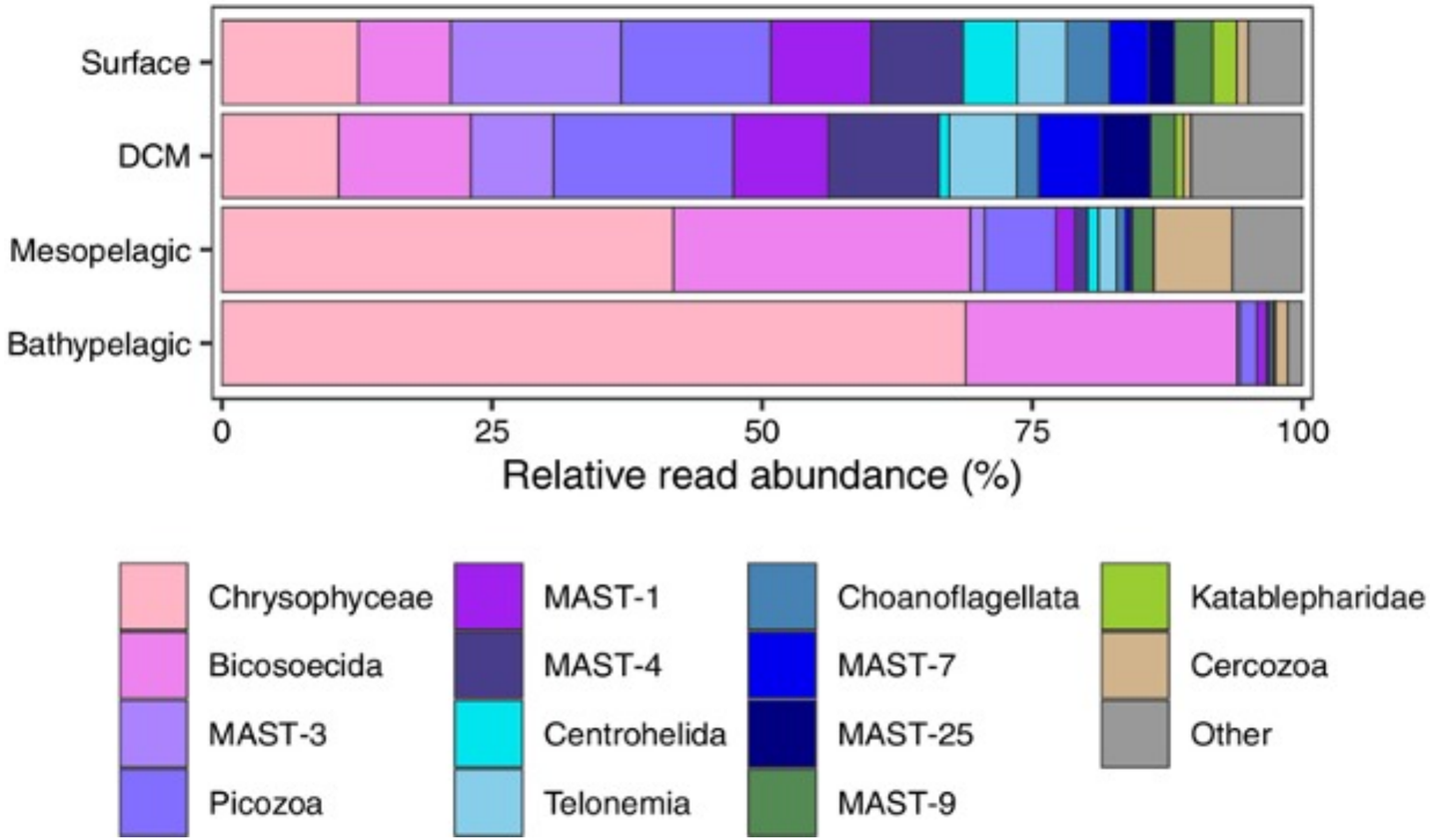
Eukaryotic tree of life (Adapted from Burki *et al.*, 2020)

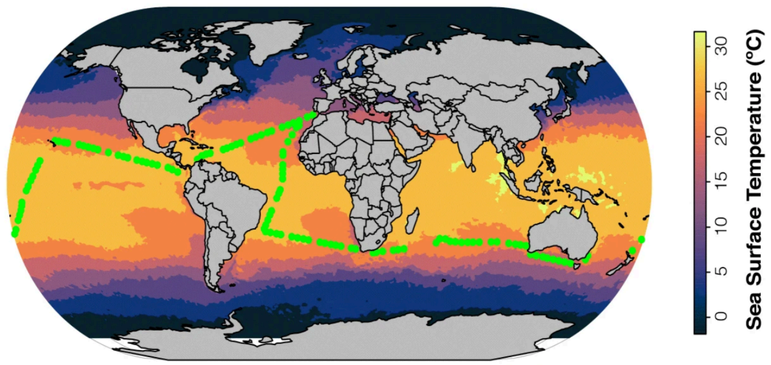

B Plankton size fractions
Virus
Bacteria
Protists
Metazoans
Planktonic organisms
Picoplankton
Nanoplankton
Microplankton
Mesoplankton
Macroplankton
Megaplankton
< 0.2 µm
0.2 to 1.6 µm
0.2 to 3 µm
0.8 to 5 µm
3 to 20 µm
5 to 20 µm
20 to 180 µm
> 200 µm
> 50 µm
> 300 µm
180 to 2,000 µm
> 680 µm
The 12 Tara Oceans plankton size fractions
0.02 µm
0.1 µm
0.2 µm
1 µm
5 µm
10 µm
20 µm
100 µm
1 mm
1 cm
10 cm
1 m



Worden et al., 2015

HFs : A few widespread taxa





Obiol et al. 2021

How do we assess the complexity of the environmental microbiome?

Annu. Rev. Microbiol. 2003. 57:369–94
doi: 10.1146/annurev.micro.57.030502.090759
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THE UNCULTURED MICROBIAL MAJORITY

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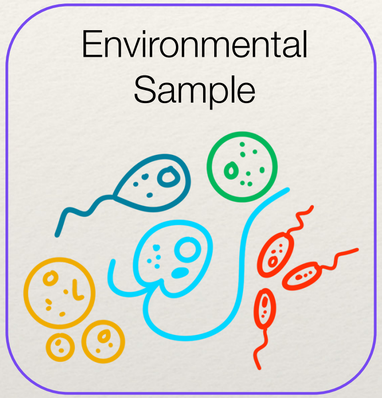
Molecular approaches & Bioinformatics

MOLECULAR APPROACHES



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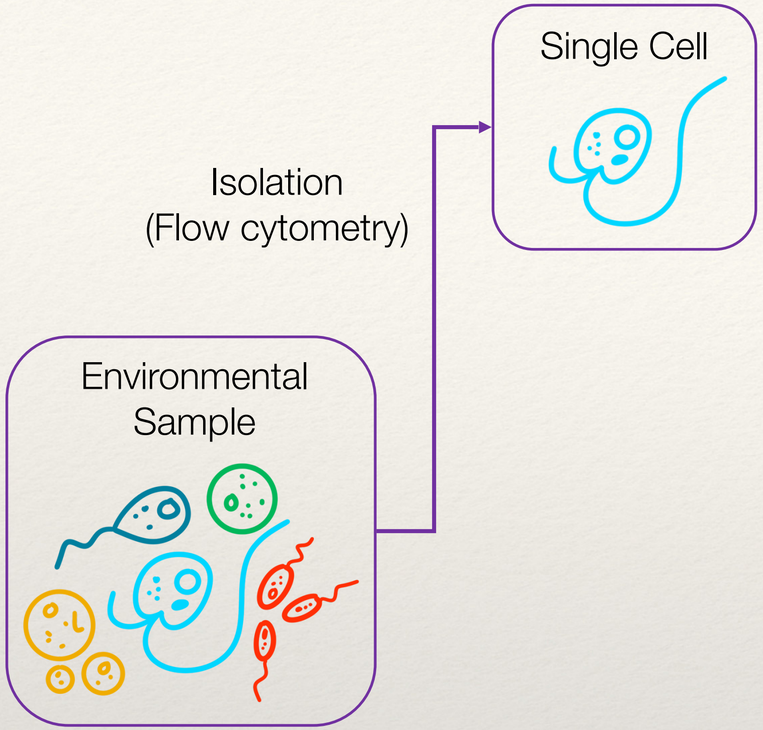

Single-Cell
Genomics
(SCG)

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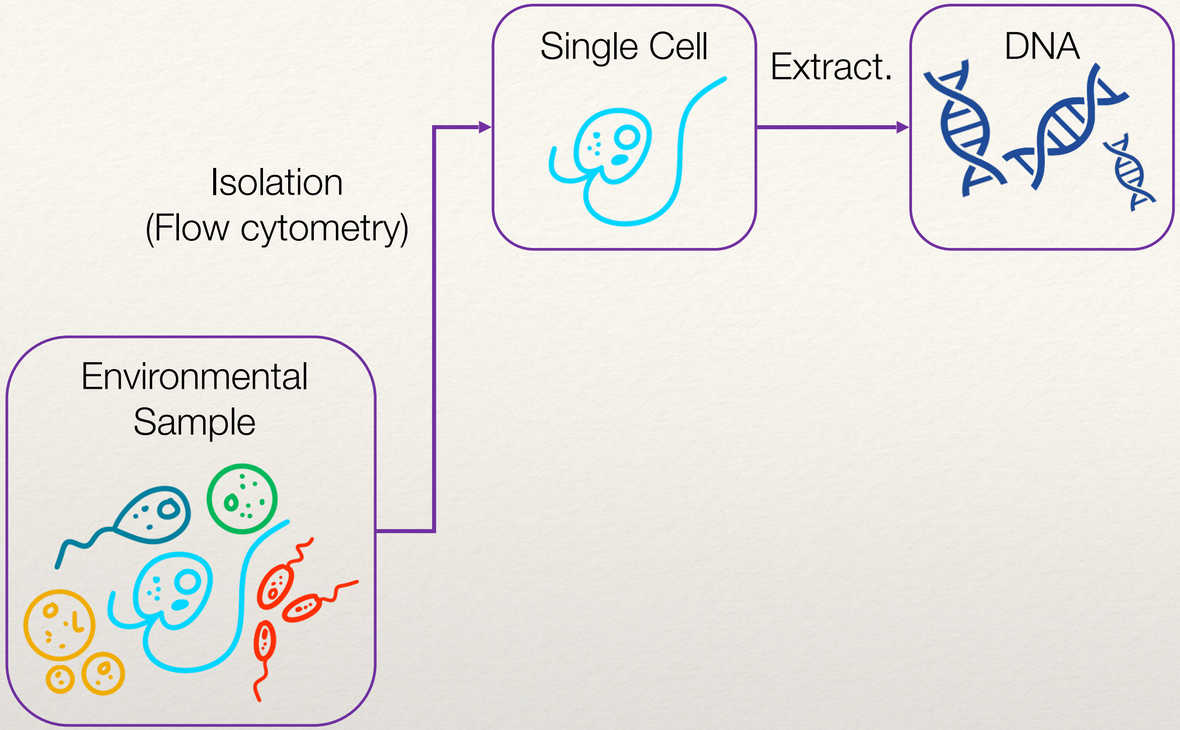

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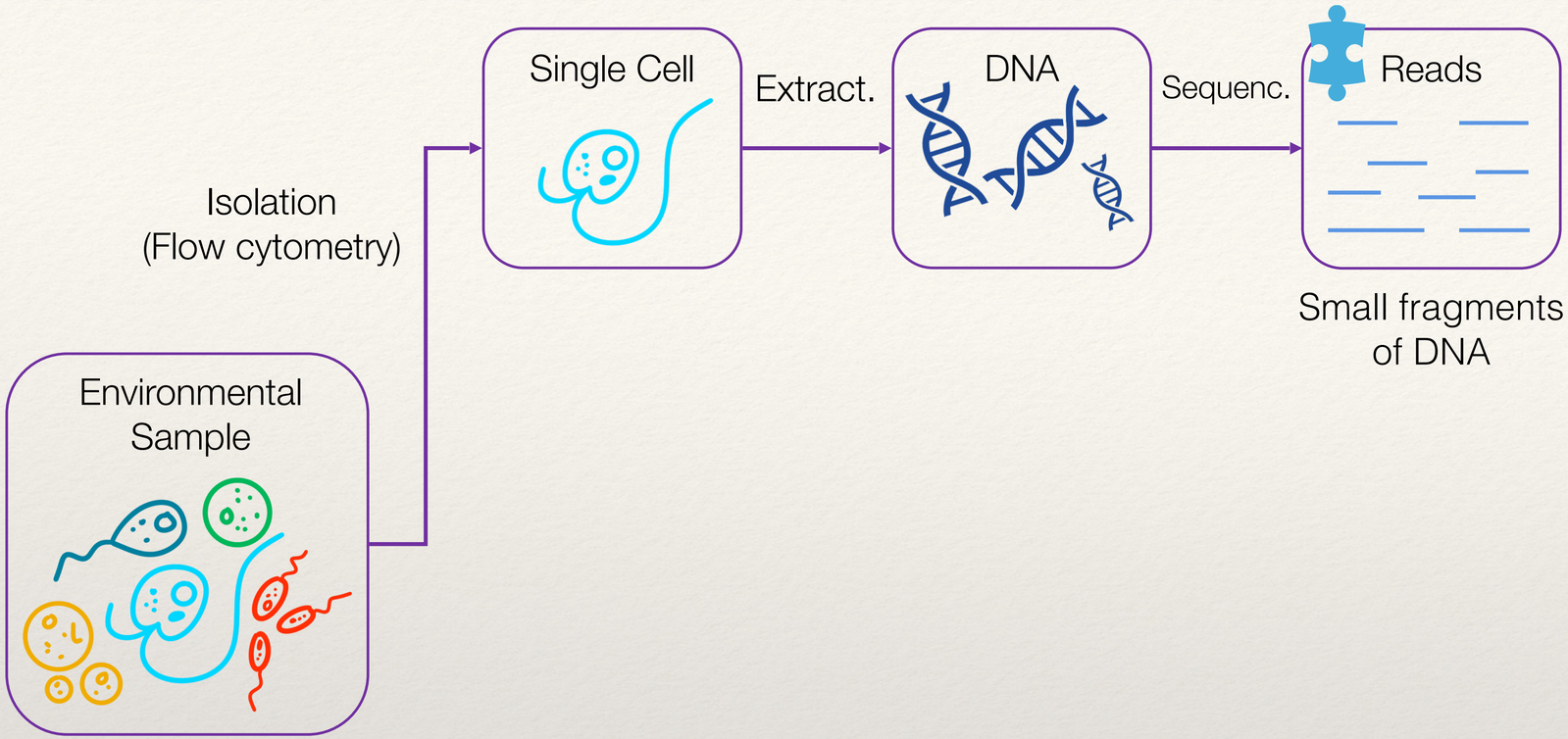

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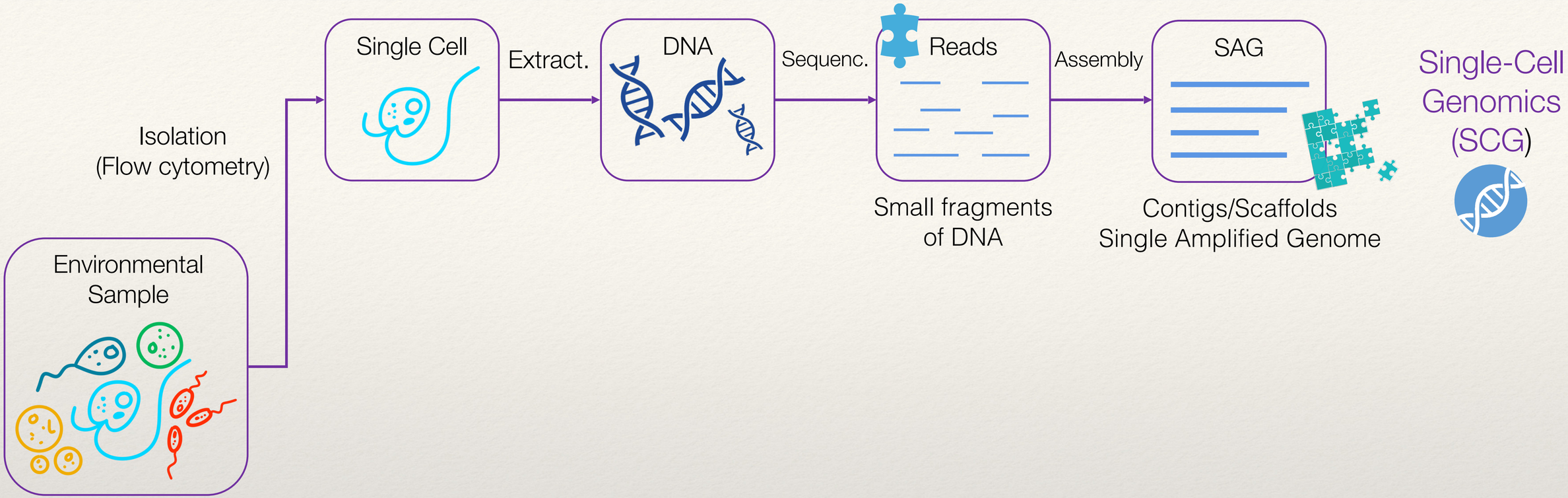

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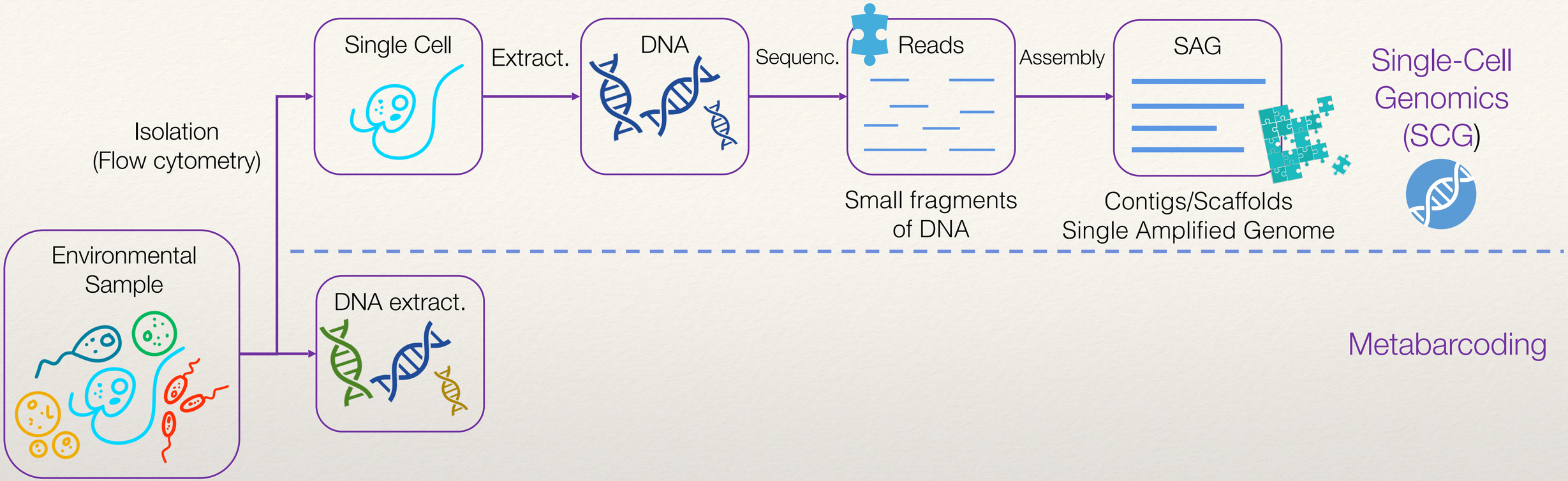

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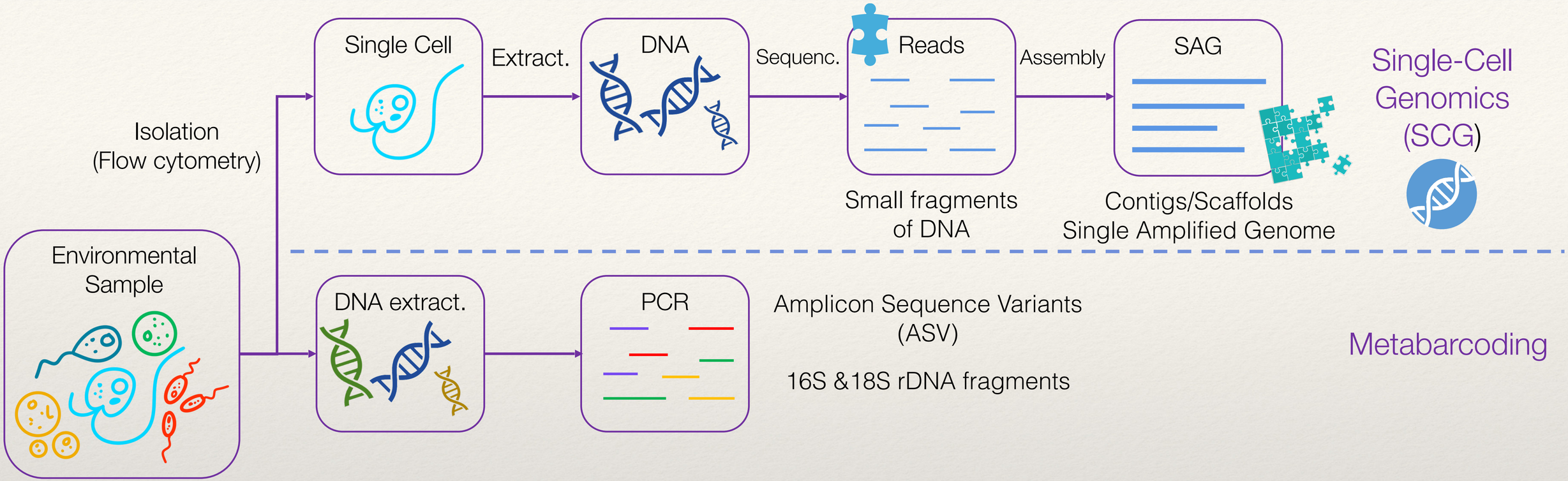

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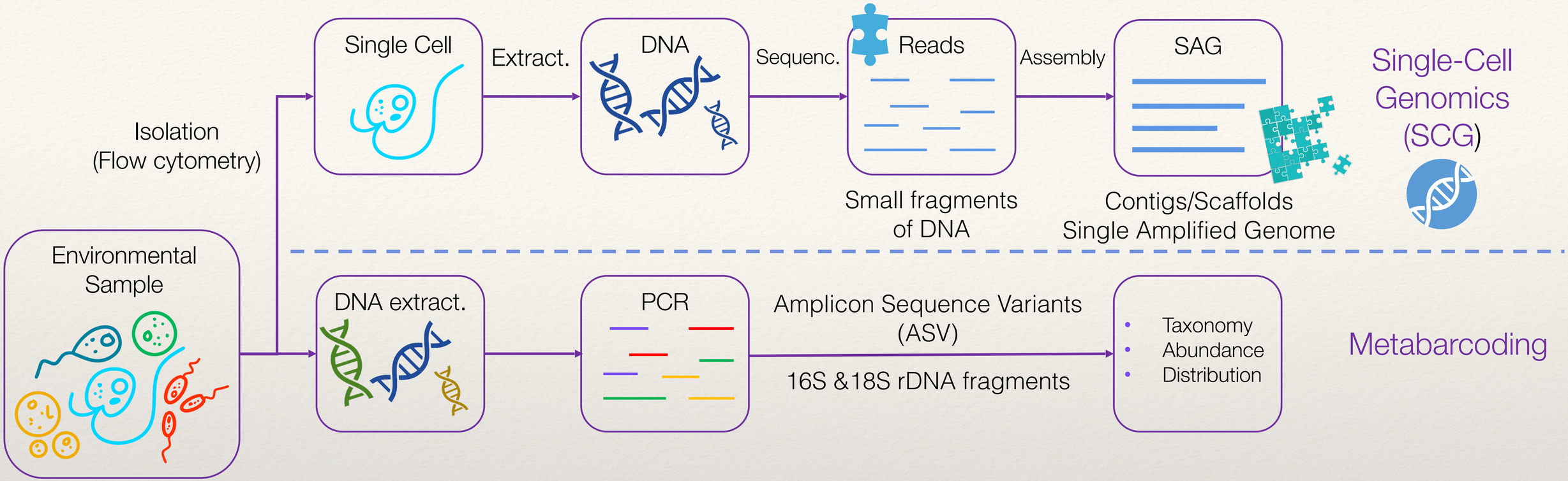

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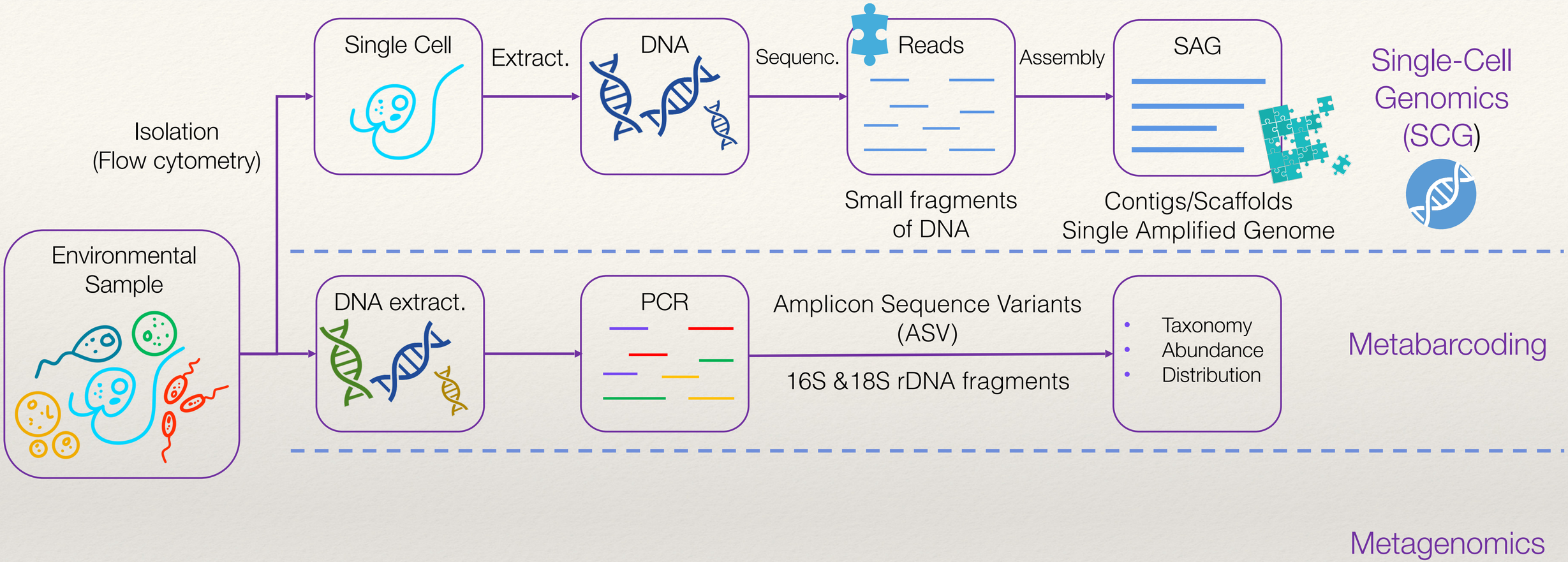

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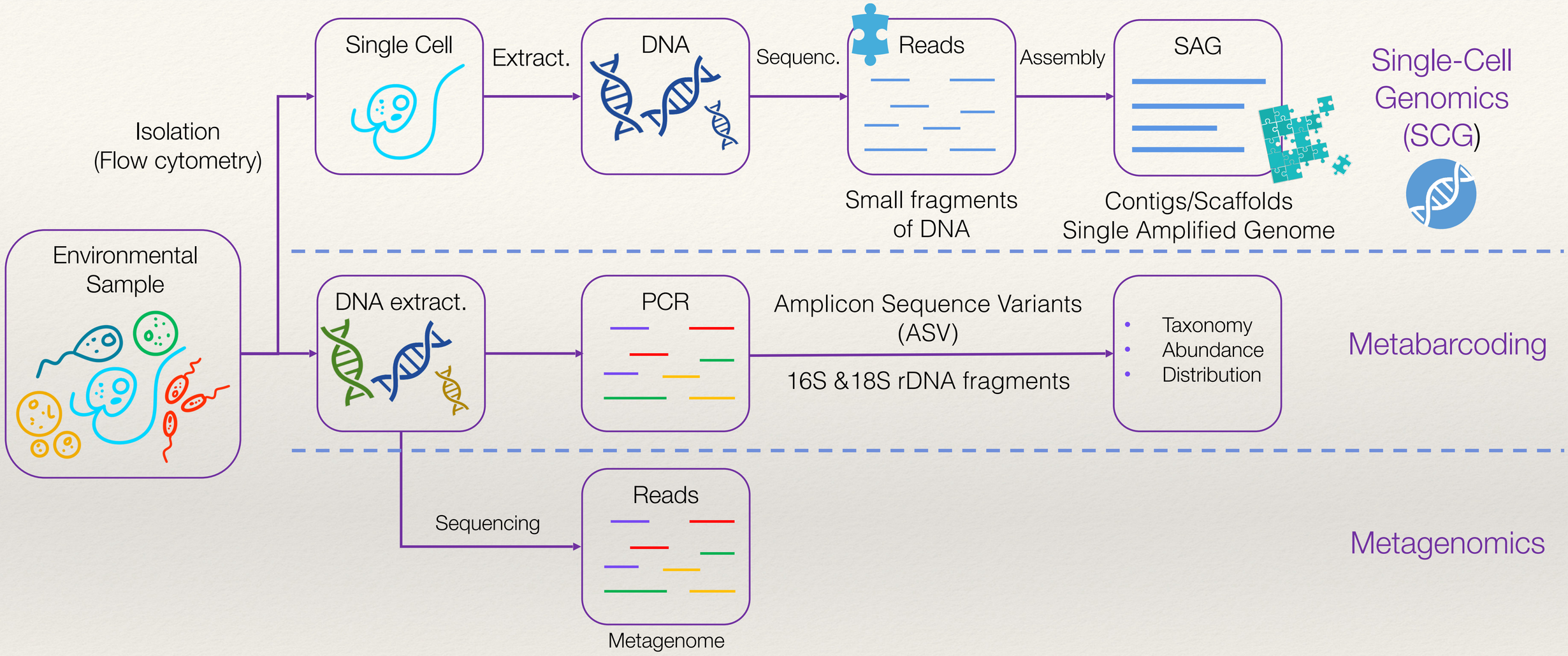

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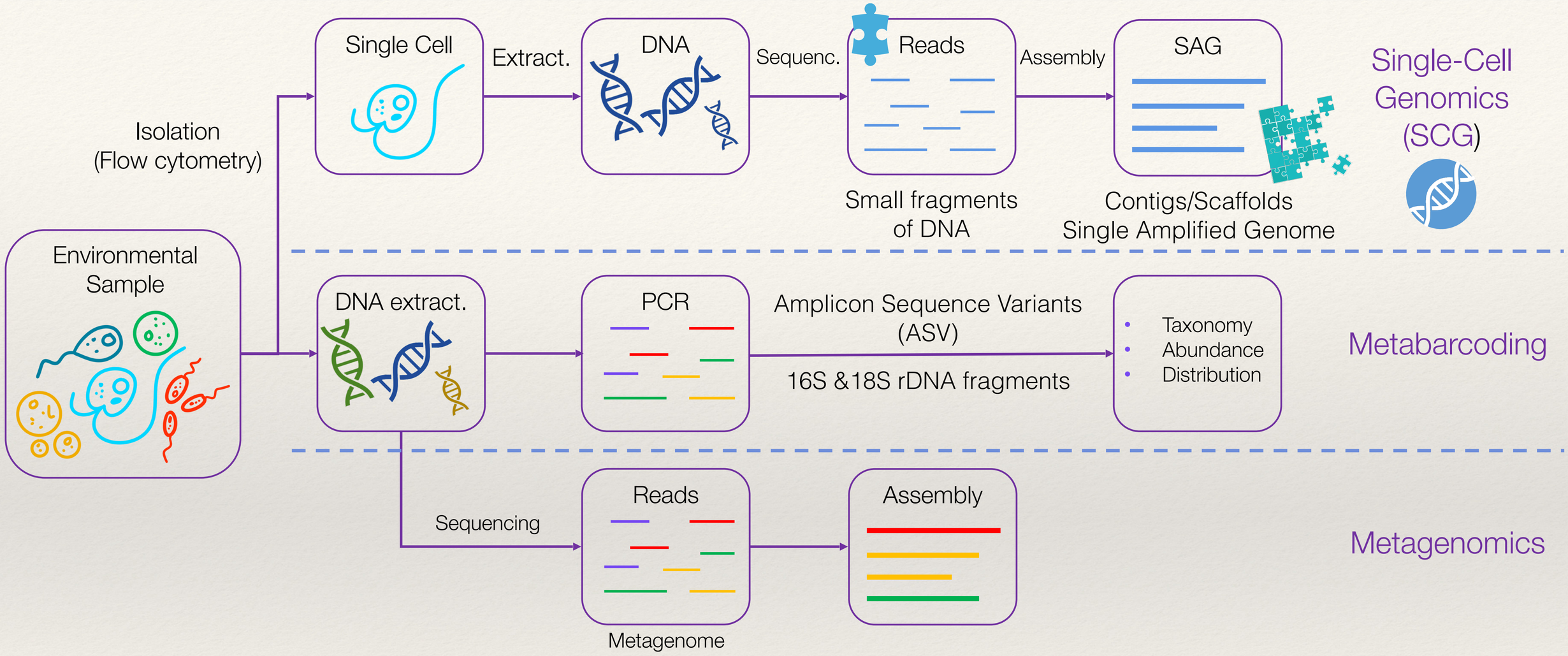

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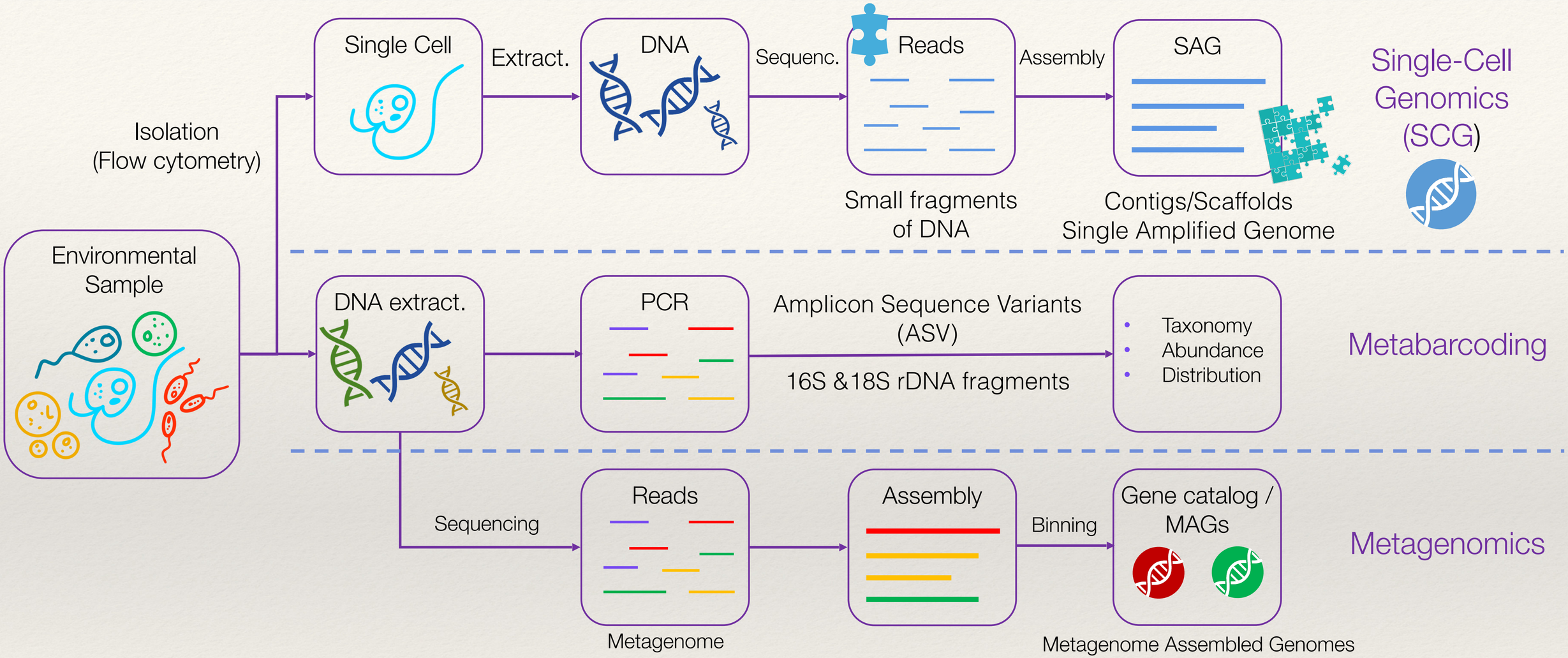

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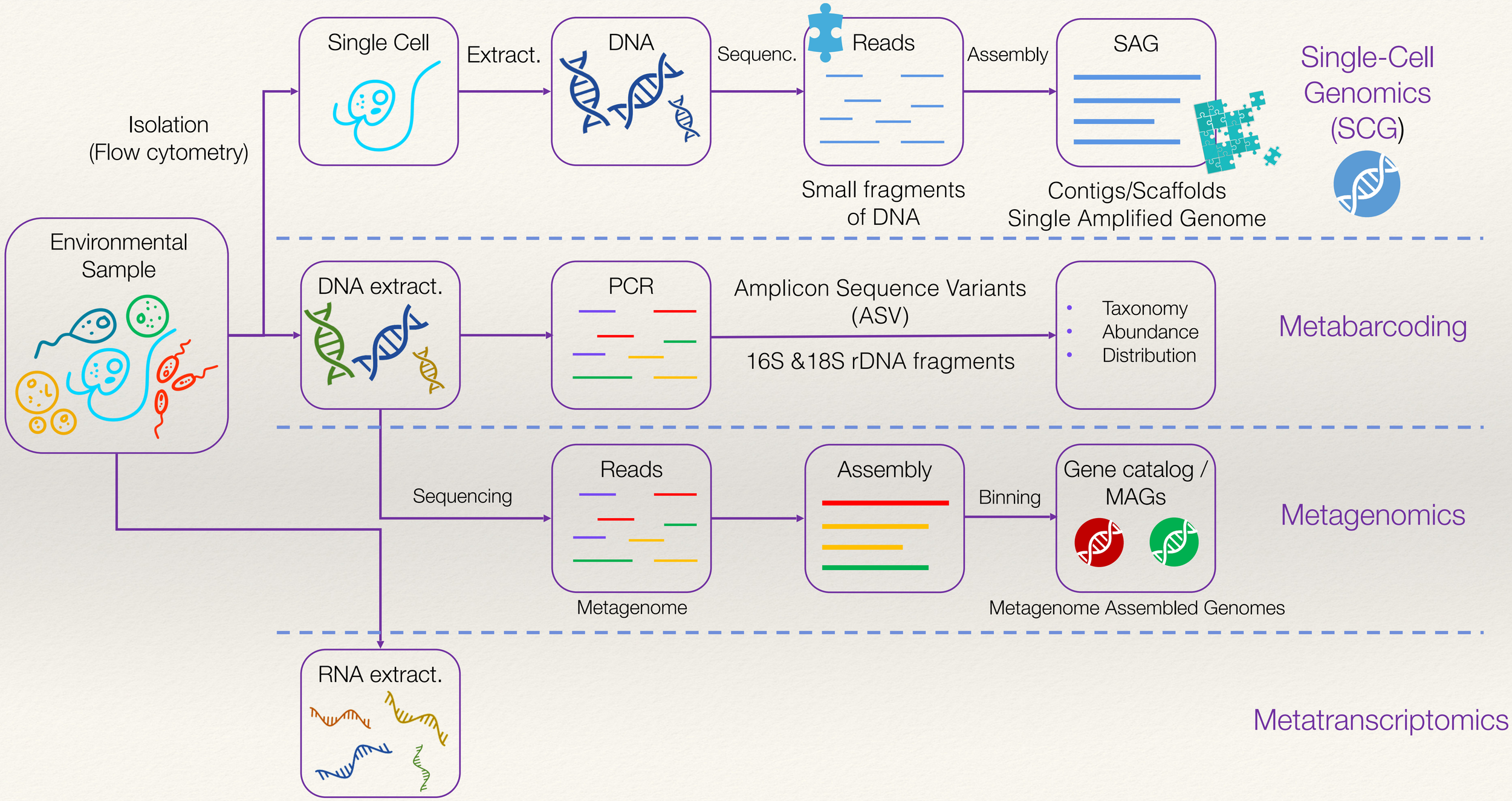

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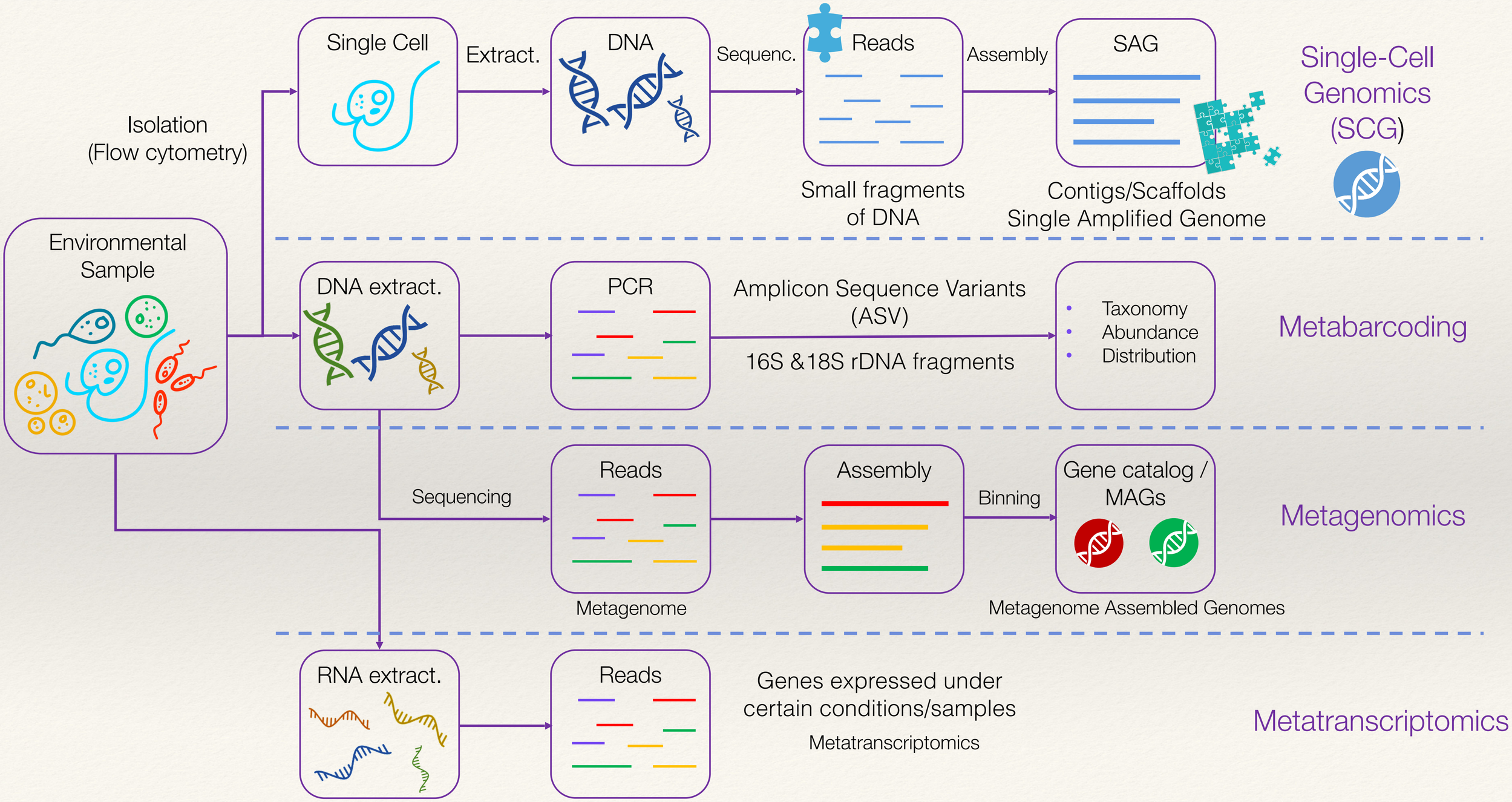

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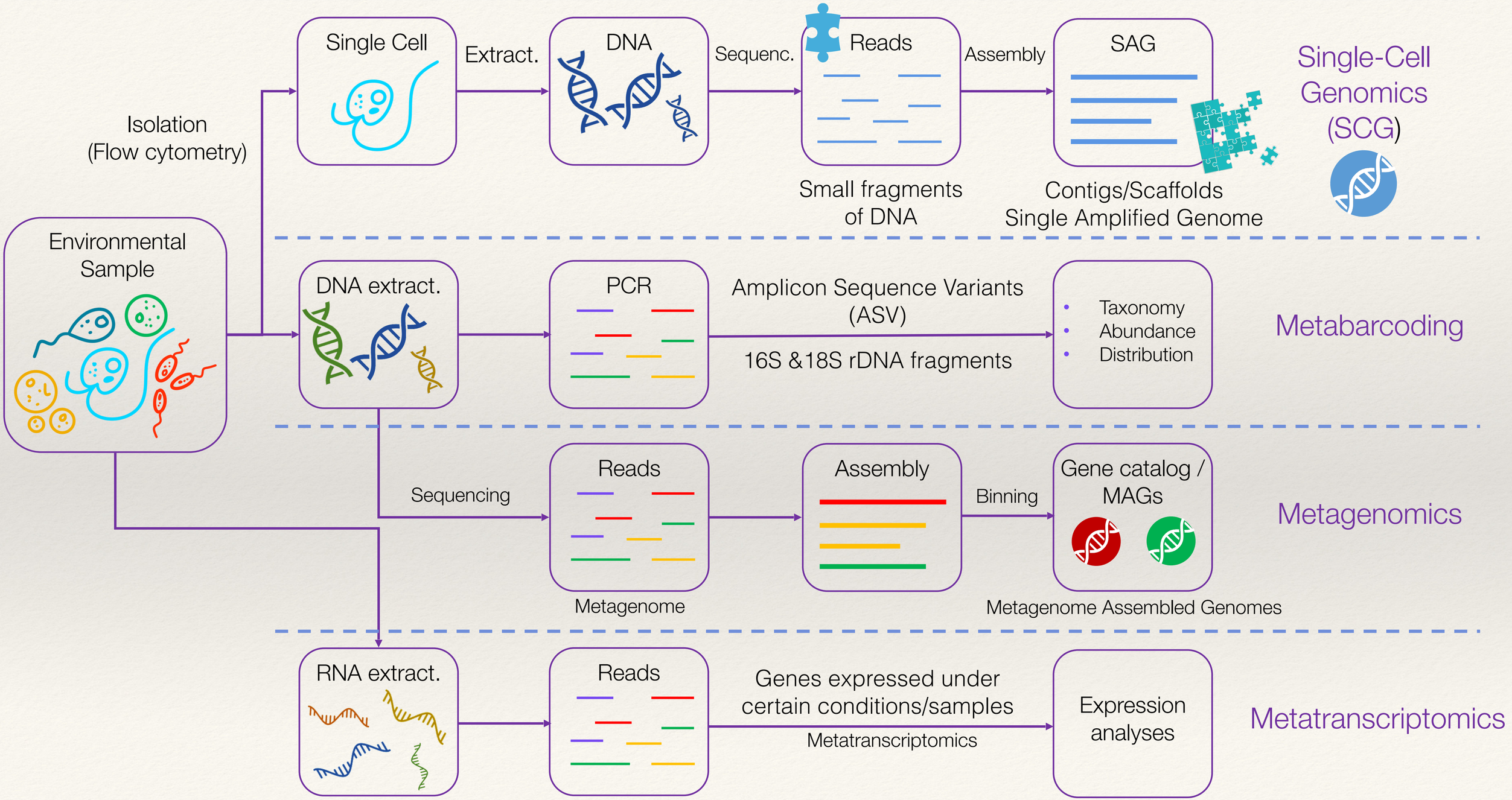
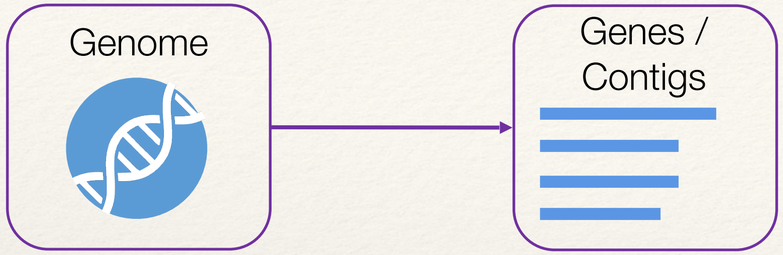


MOLECULAR APPROACHES

How do we assess abundance and expression?



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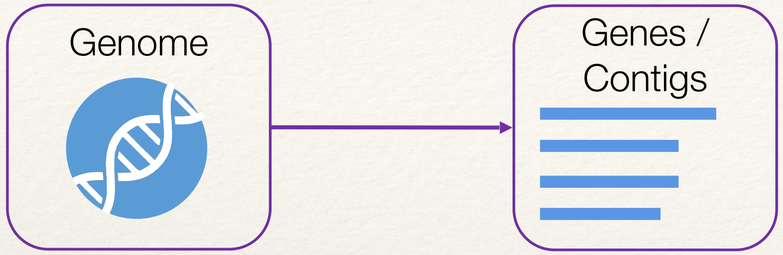
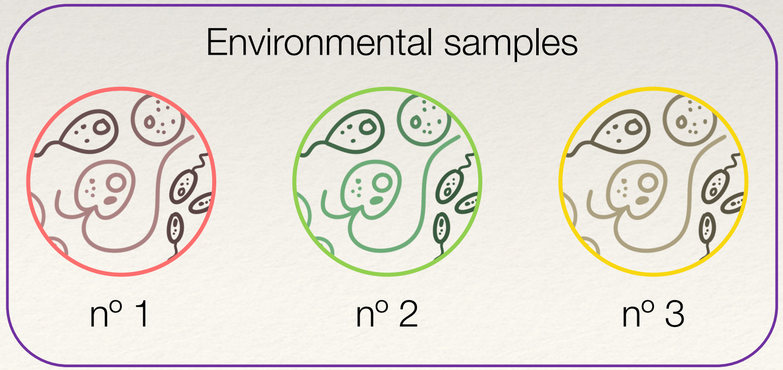
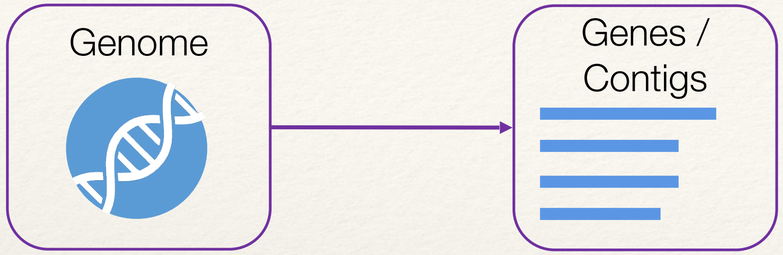
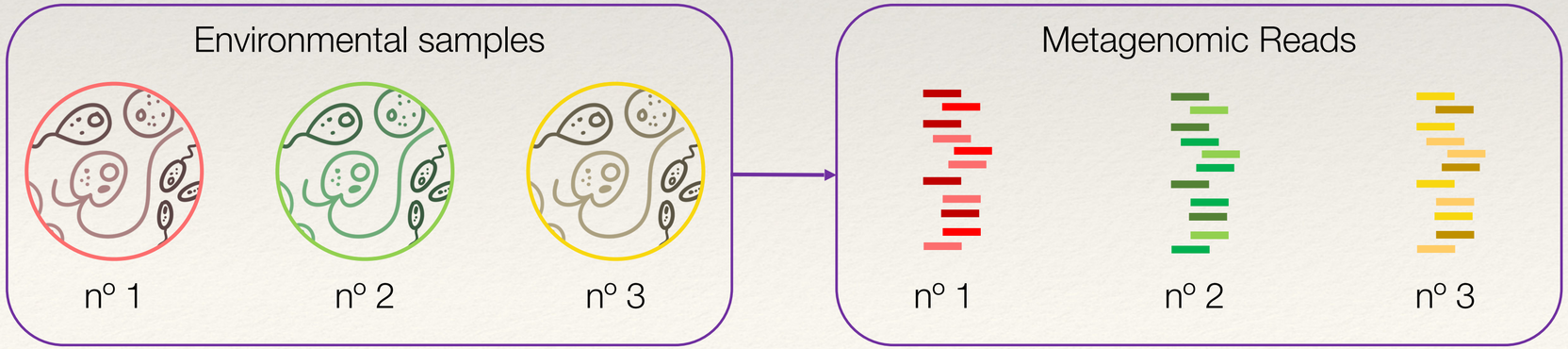




MOLECULAR APPROACHES

How do we assess abundance and expression?





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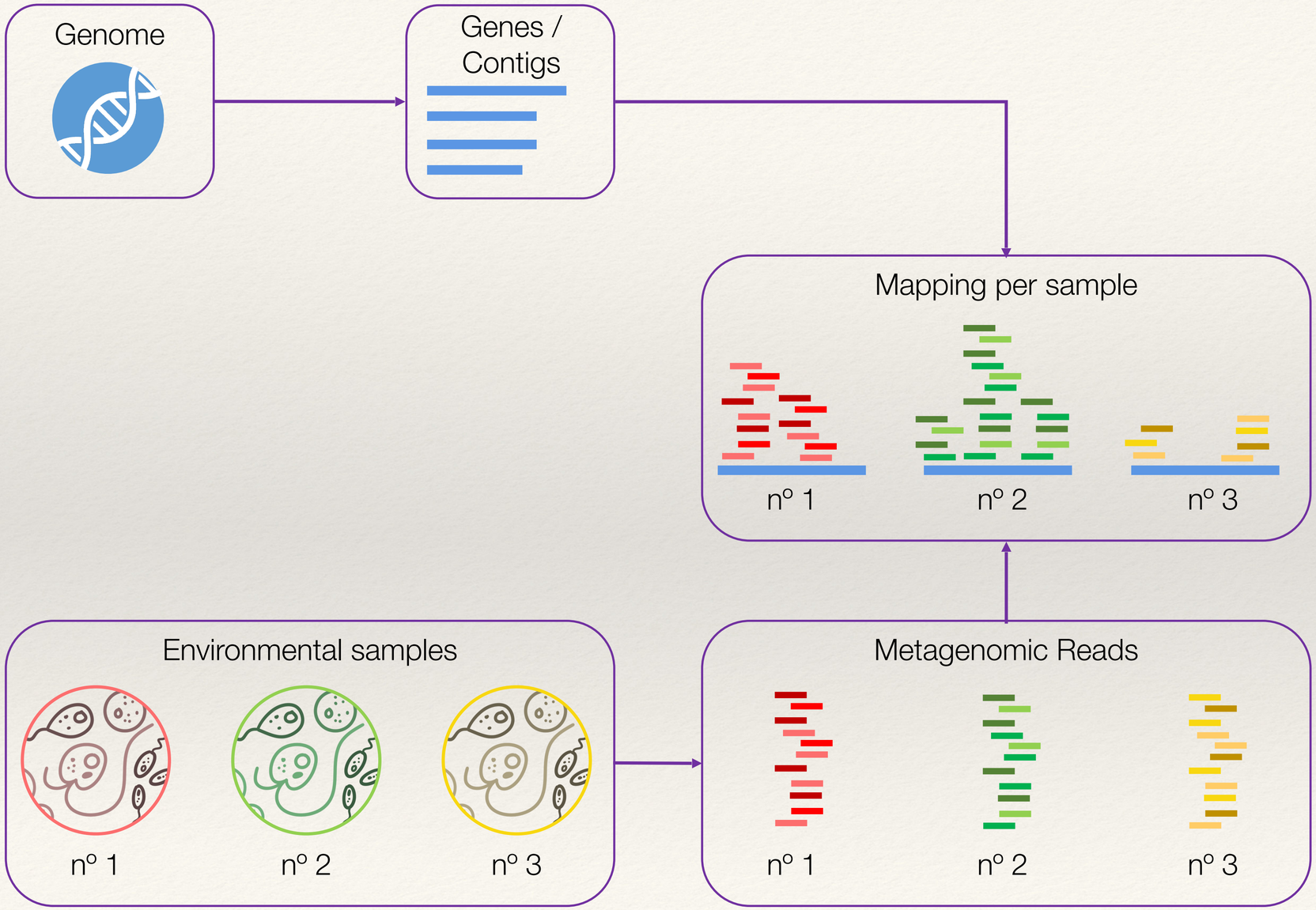

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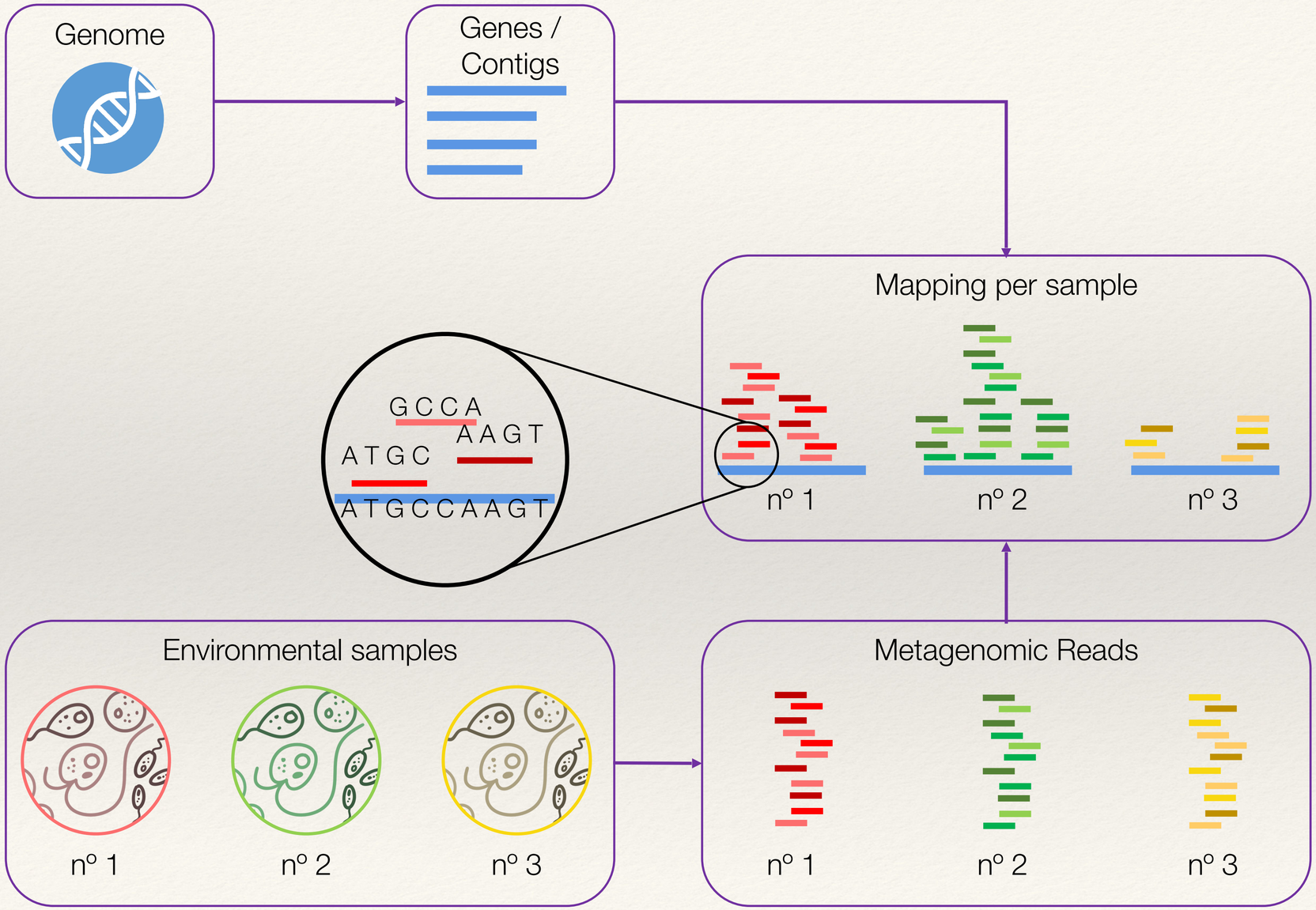

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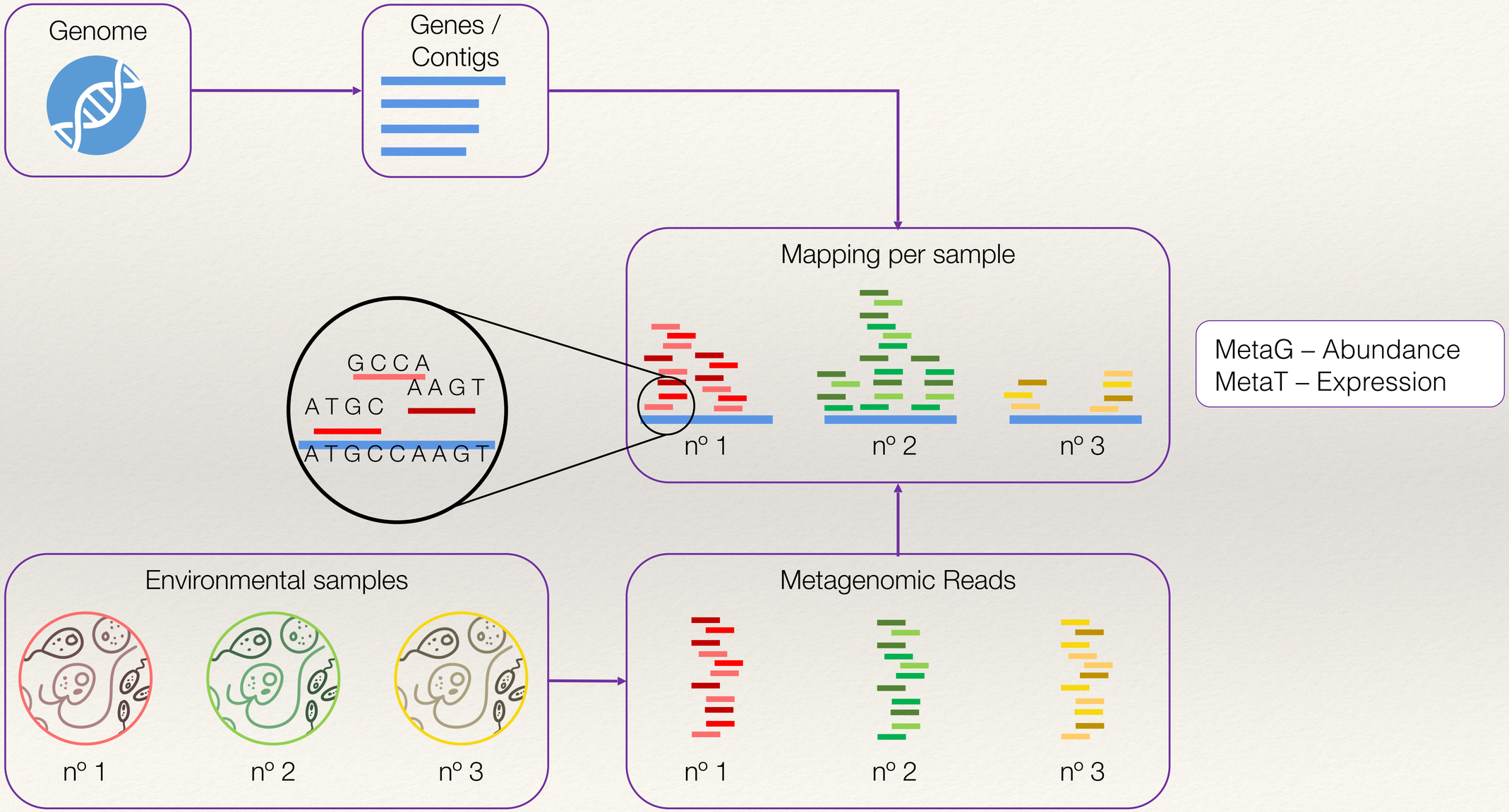
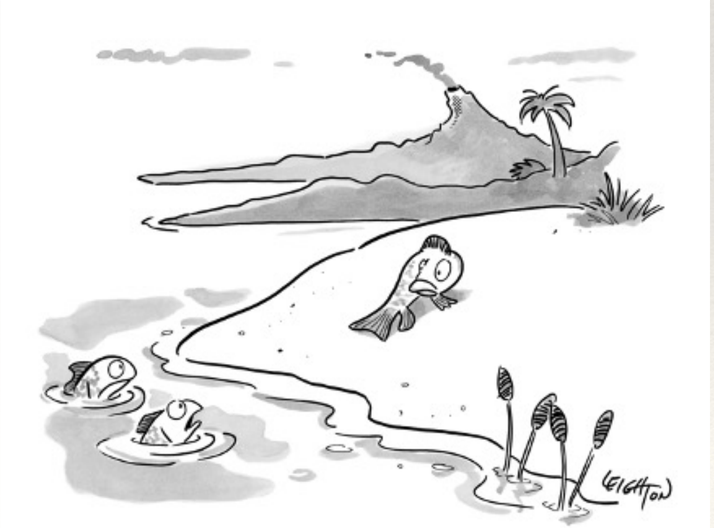


MARBITS
IBM

Long-standing questions we'll try to address

- How do microbes diversify and form new populations and species?

- Which microbes interact and how?



"Go. Evolve. Don't worry about us."

- **How do microbes diversify and form new populations and species?**

- Few examples are available (especially for marine protists)
- Unclear links with drivers and mechanisms (selection, barriers to gene flow)
- Limited understanding of the genomic basis of divergence
- Will contribute to understanding how microbes adapt to different niches

Massive diversification of microbes

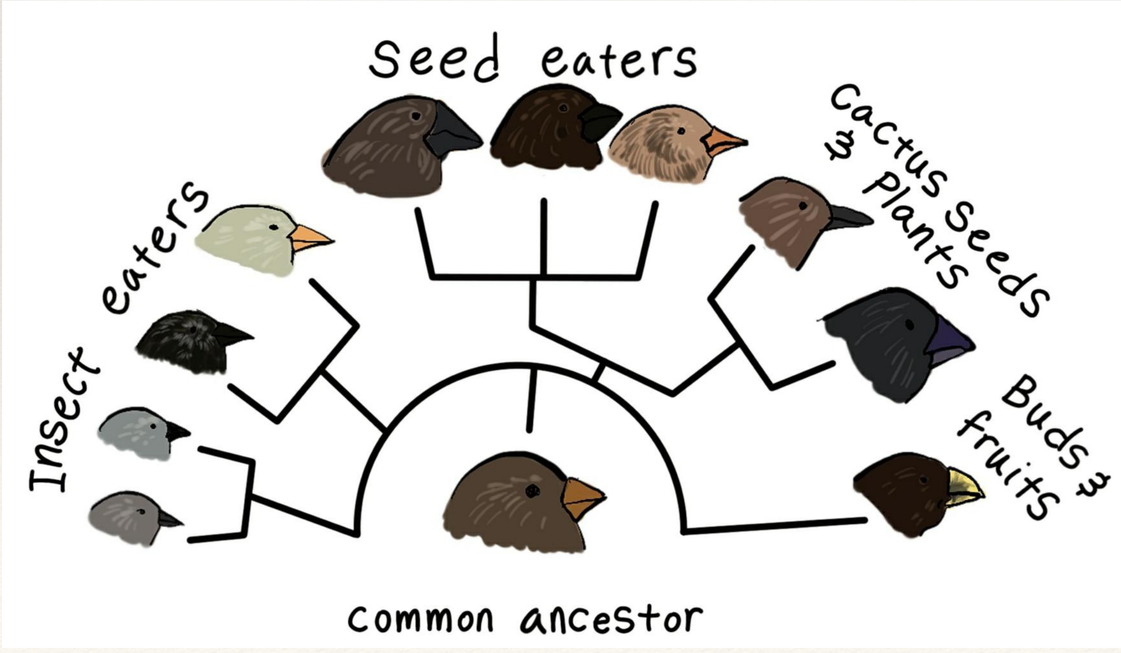
- Species
  - About 10^{10} in the ocean (Locey and Lennon, 2016)
  - Up to 10^{12} prokaryotic species on Earth

- Genes
  - 47 million non-redundant genes in the surface global ocean (TARA) (Salazar et al., 2019)
    - 248 million genes with our pipeline (unpublished)
  - 100 million eukaryotic genes in the surface global ocean (TARA) (Carradec et al., 2018)

Diversification mechanisms

- a) Adaptive diversification
  - Selection drives populations apart, ultimately leading to new species and lineages
    - Facilitated in microbes by:
      - Big population sizes
      - Large population diversity

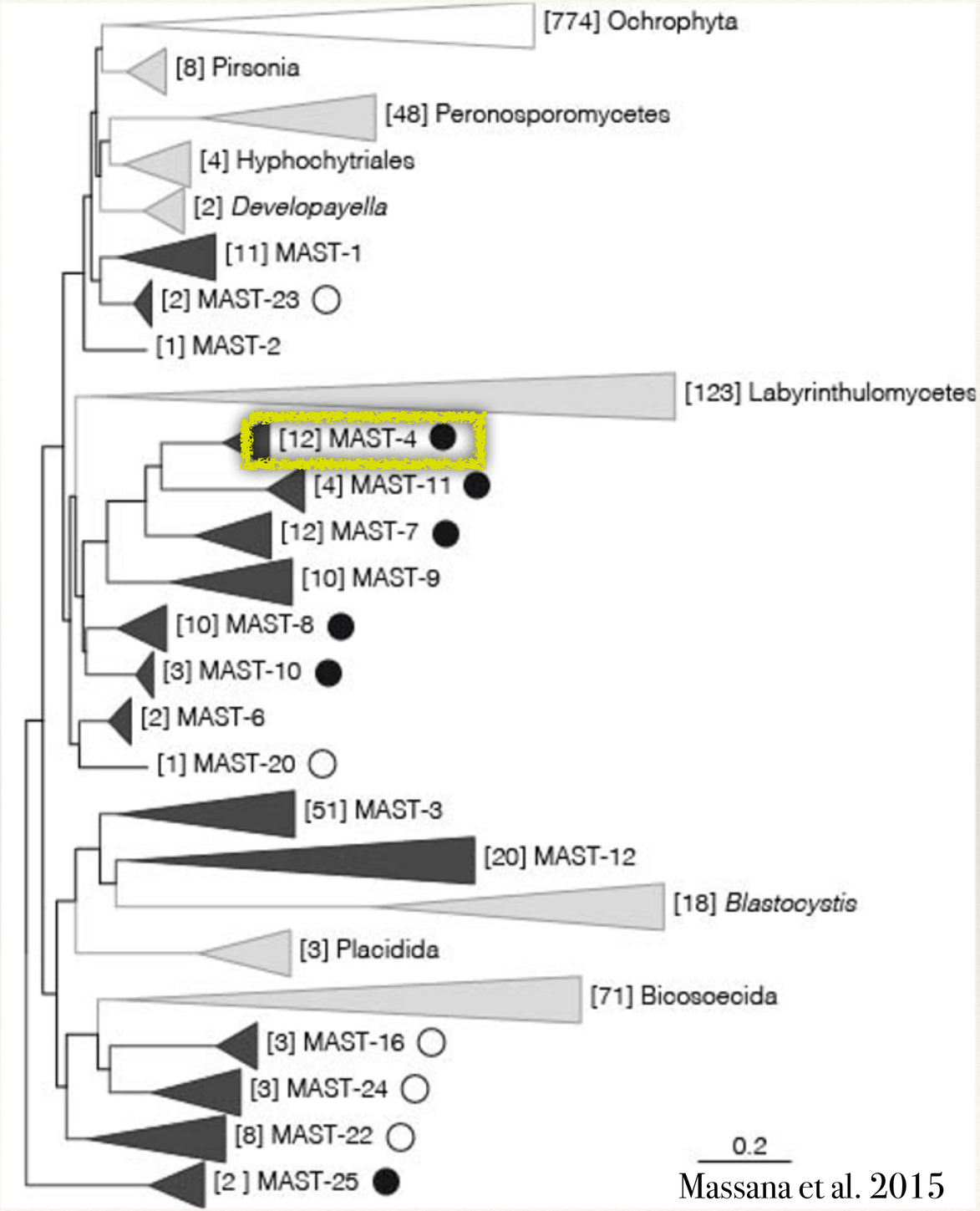
- b) Barriers to gene flow



Diversification of tiny ocean predators

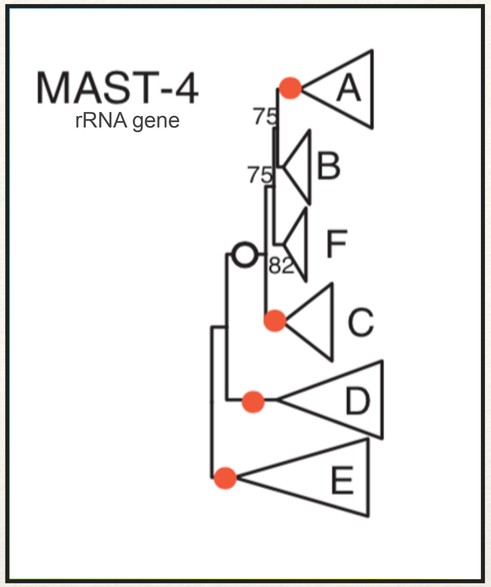
Marine Stramenopiles (MAST)

- 18 identified lineages
- 2-5 μm cell-size
- Mostly planktonic & bacterivorous
- Globally distributed
- Up to 35% of heterotrophic flagellates

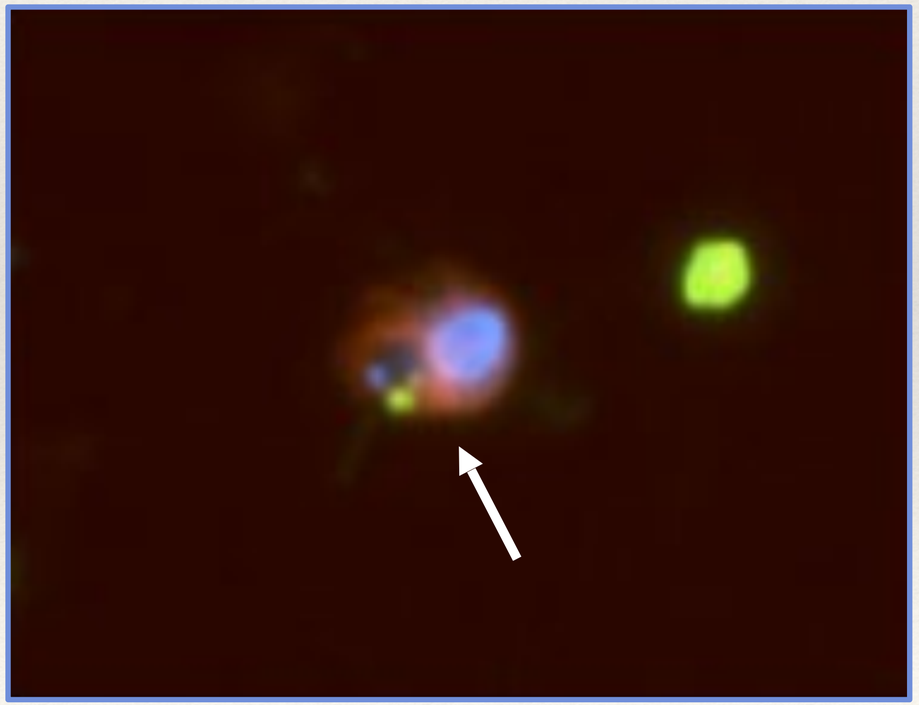


Massana et al. 2015

MAST (Marine Stramenopiles)-4



- Up to 9% of heterotrophic flagellates
- 2-3 μm cell-size
- Important in the marine food web
- Defined species, still closely related



MAST-4 Epifluorescence. Massana *et al.*, 2009 & 2014
Red : Cytoplasm, Blue : Nucleus, Green : Food Bacteria

Main questions

- How different are MAST-4 species at the genome level?
- Did MAST-4 species diverge via niche adaptation?
- Is such adaptation reflected in the MAST-4 genomes?
- Can gene composition and expression provide insights into MAST-4 diversification?

MAST (Marine Stramenopiles)-4

- Up to 9% heterotrophic flagellates

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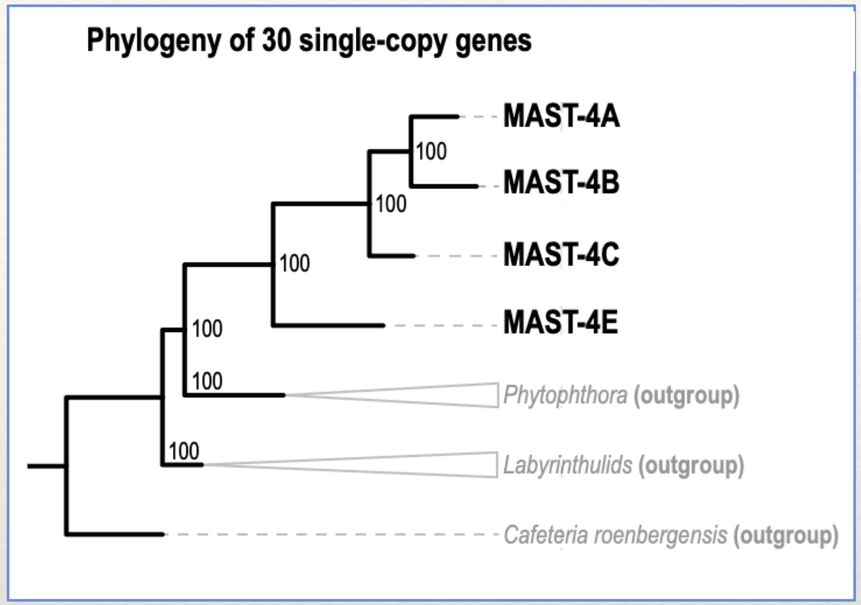
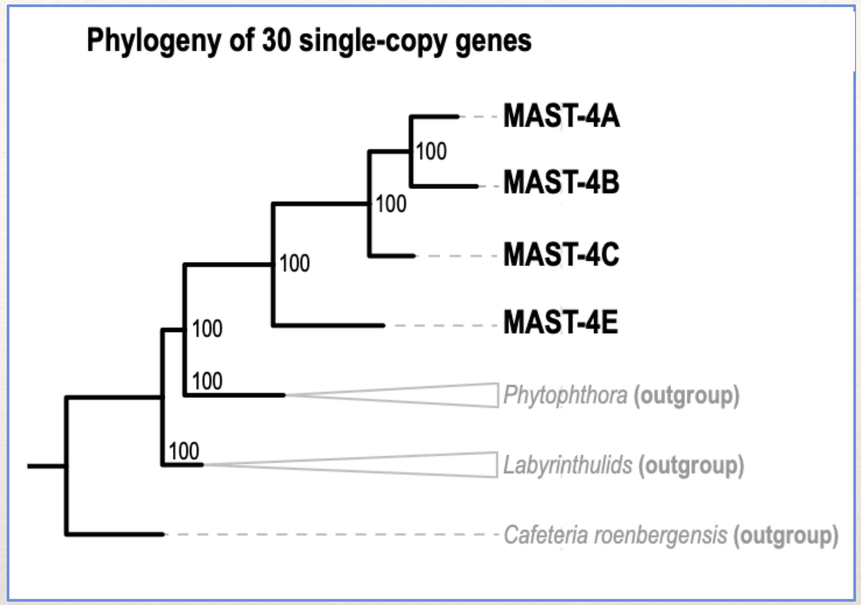


MAST (Marine Stramenopiles)-4

- Up to 9% heterotrophic flagellates
- Originally classified as ecotypes
- Planktonic & bacterivorous



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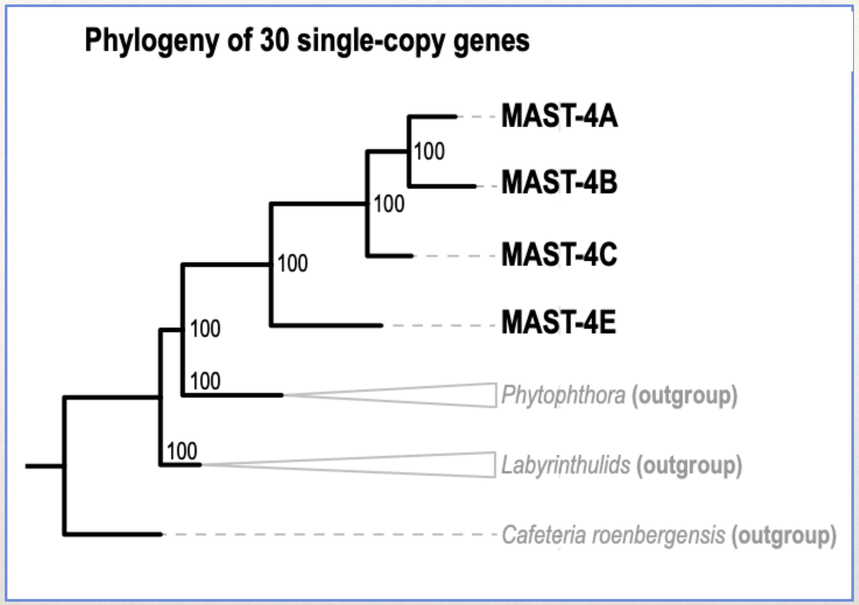

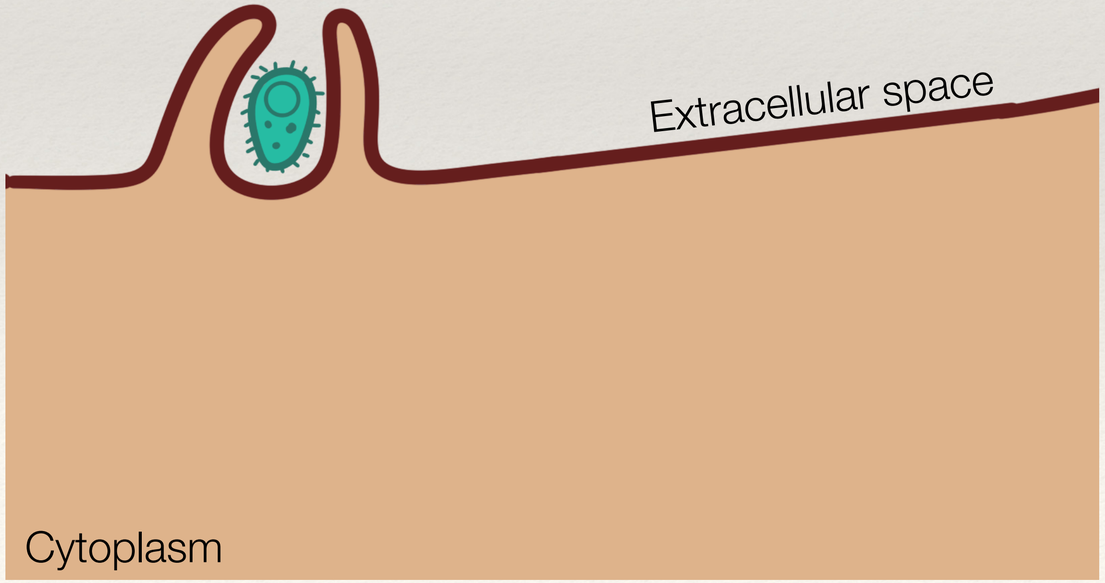

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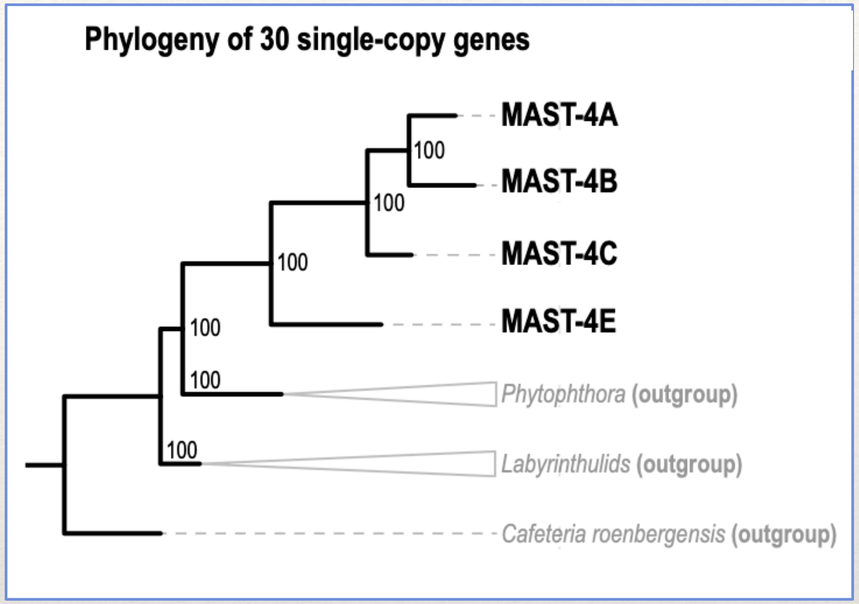

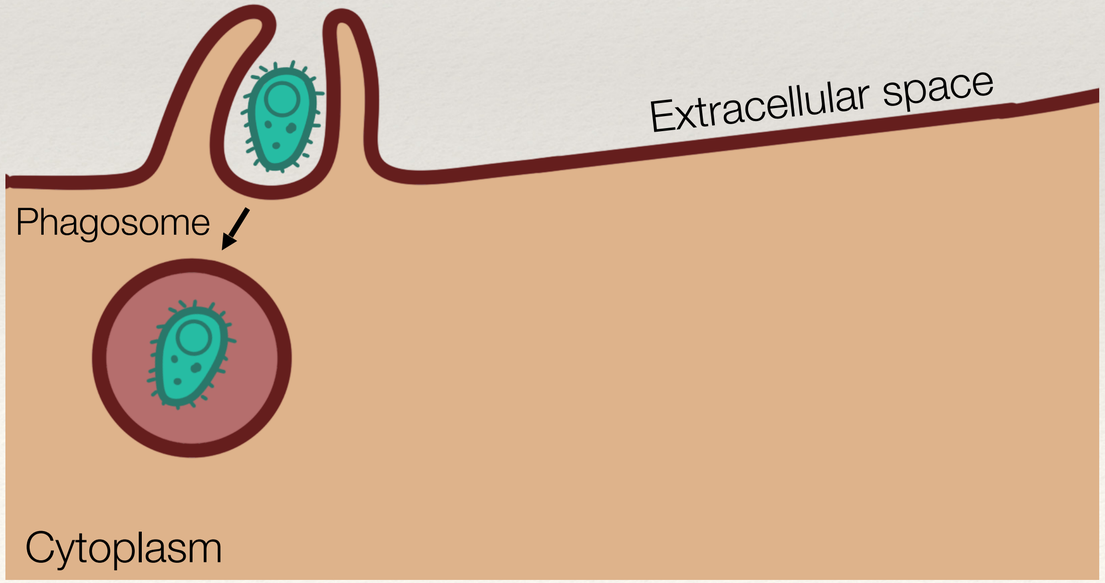

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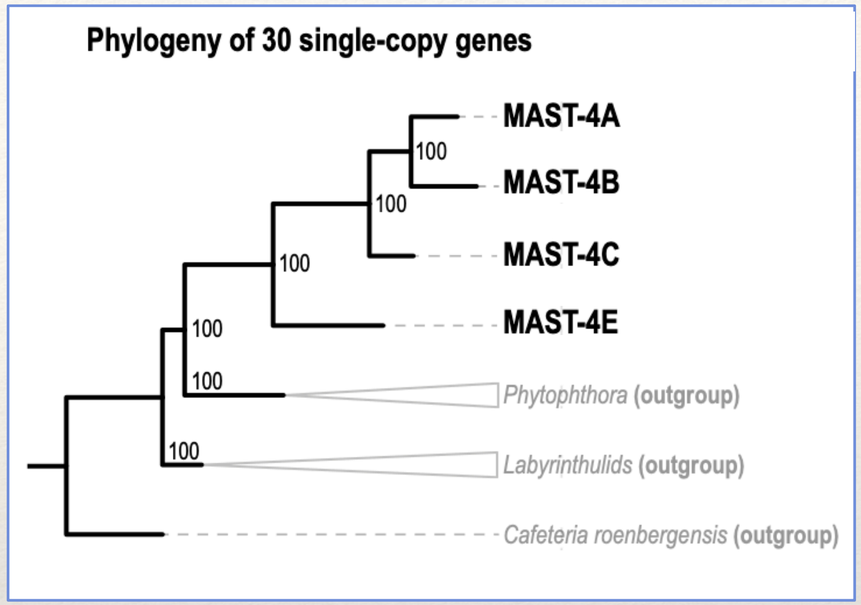

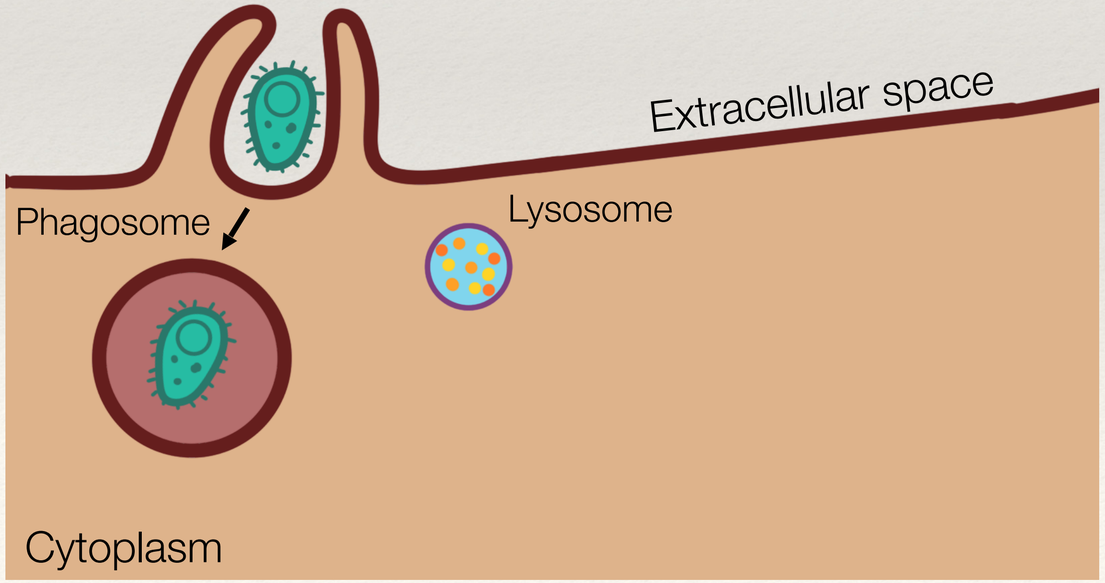

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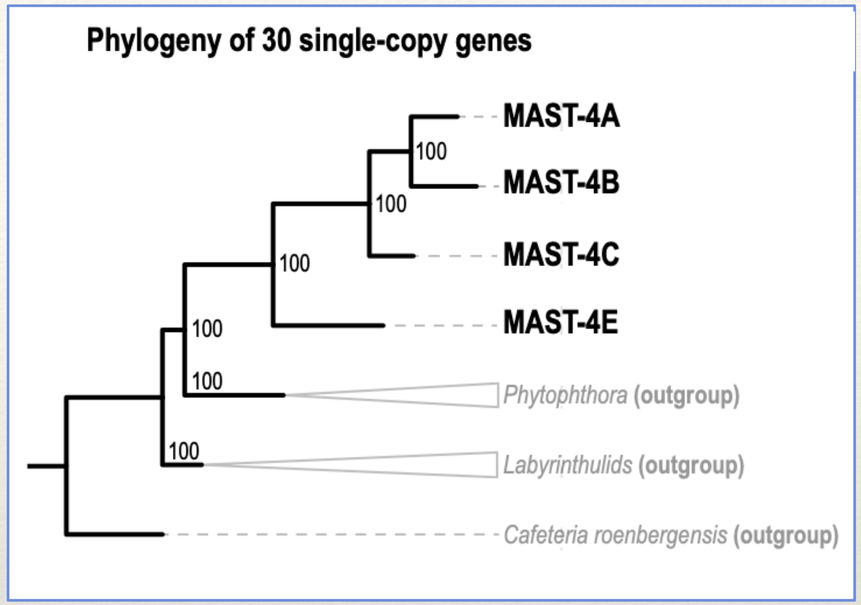

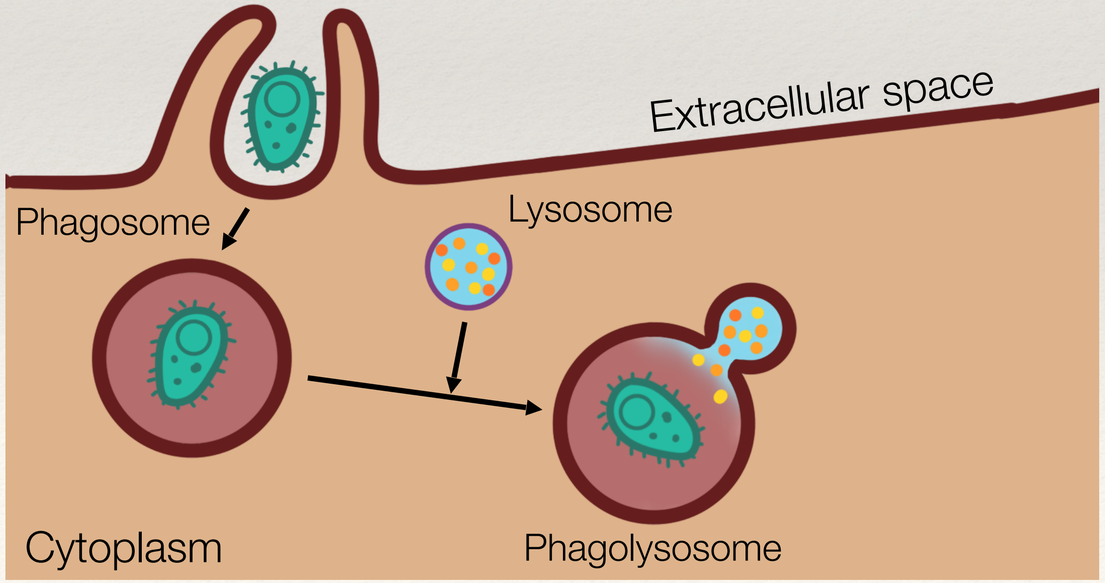

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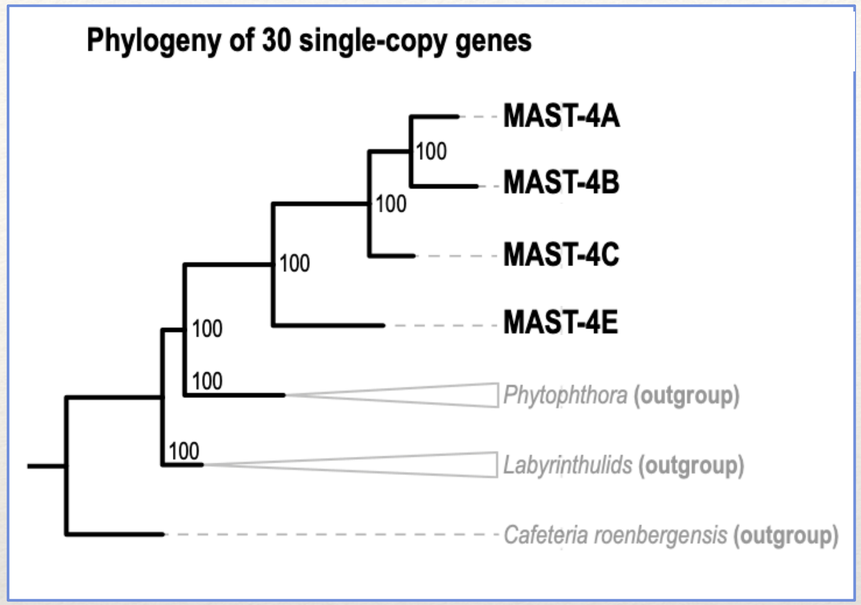

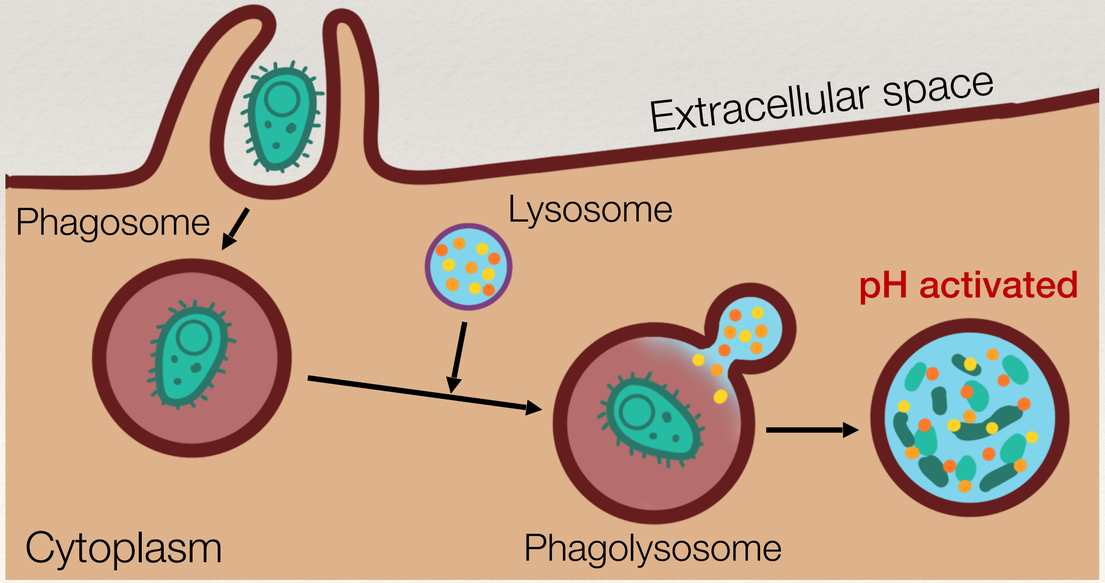

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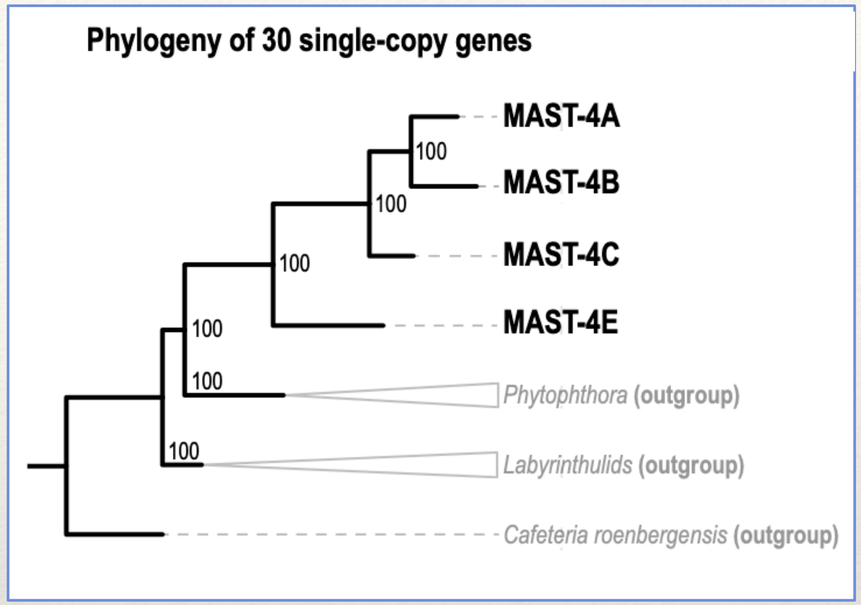

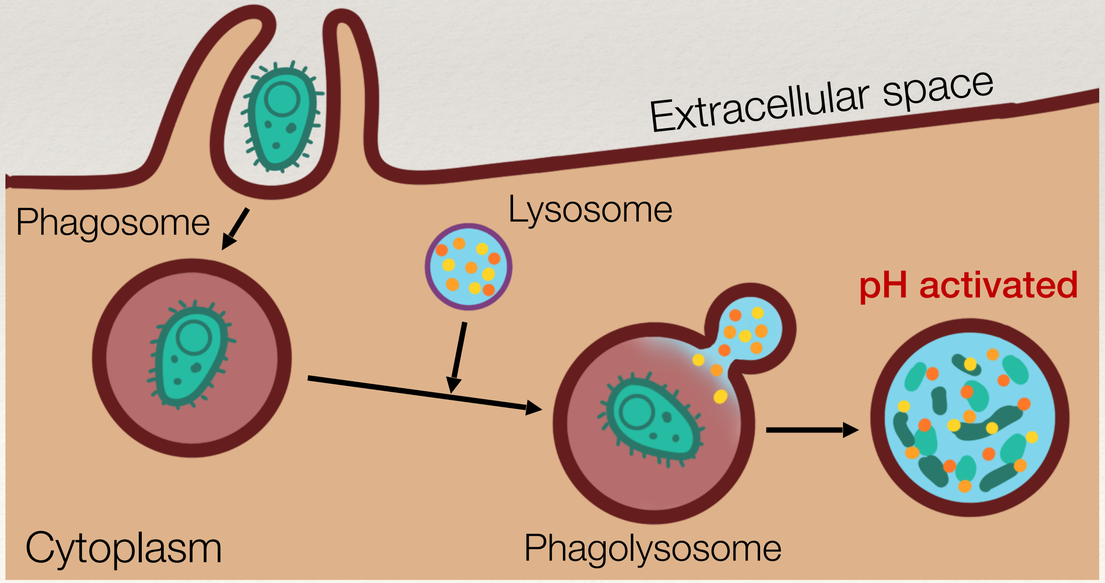

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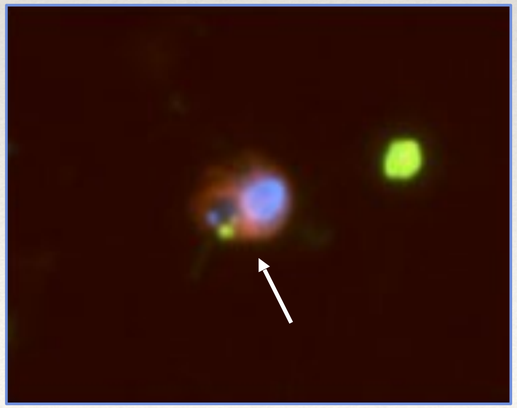
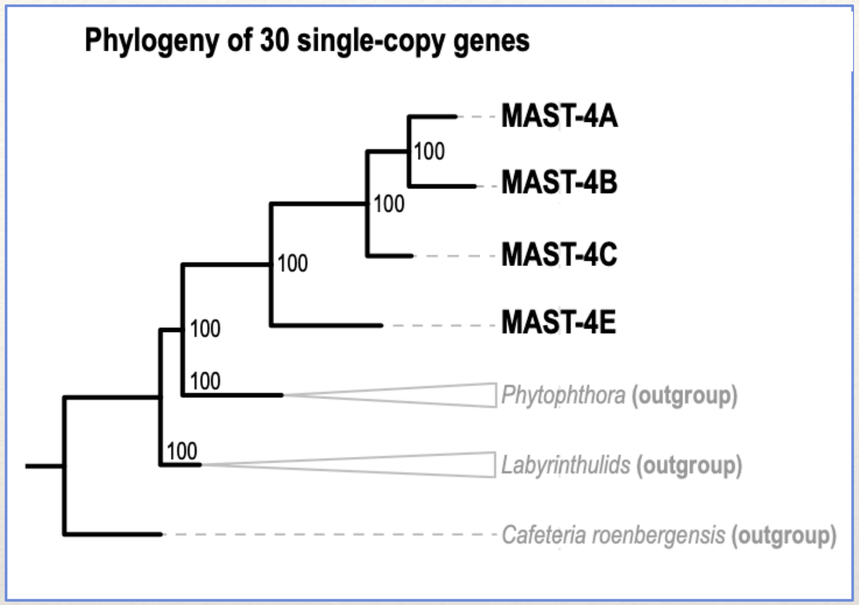
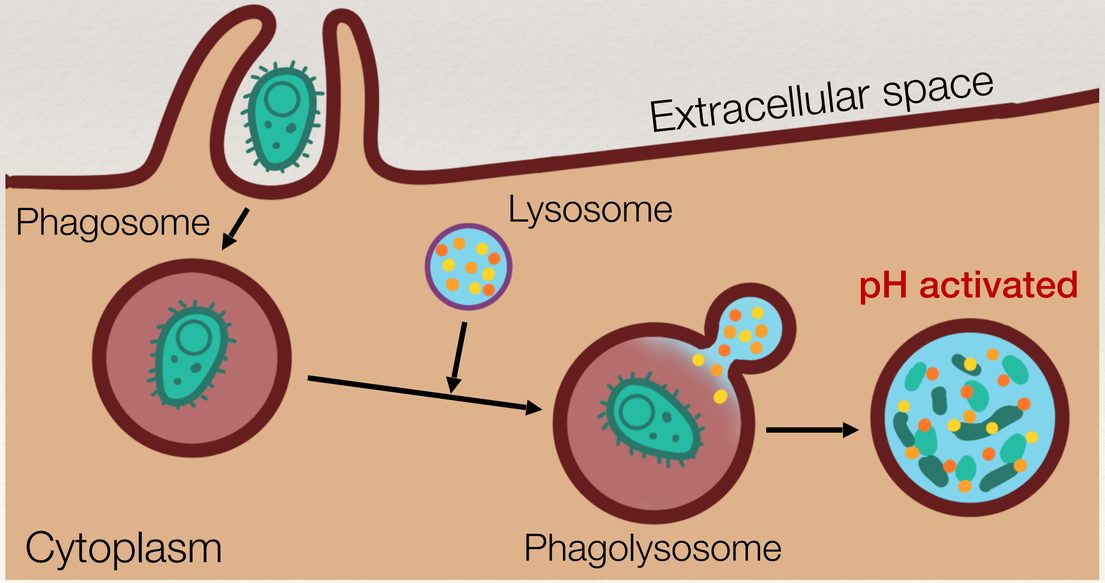


Epifluorescence of MAST-4 (Massana R *et al.*, 2009)

MAST (Marine Stramenopiles)-4

- Up to 9% heterotrophic flagellates
- Originally classified as ecotypes
- Planktonic & bacterivorous
- Model organism





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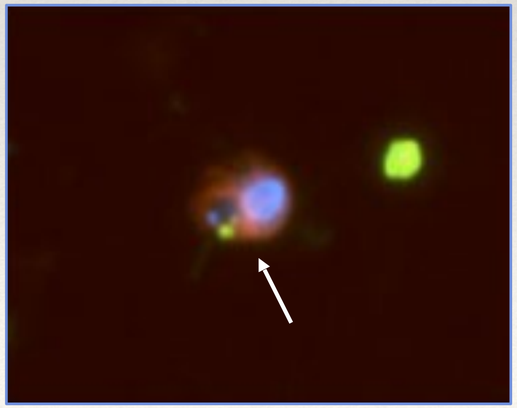
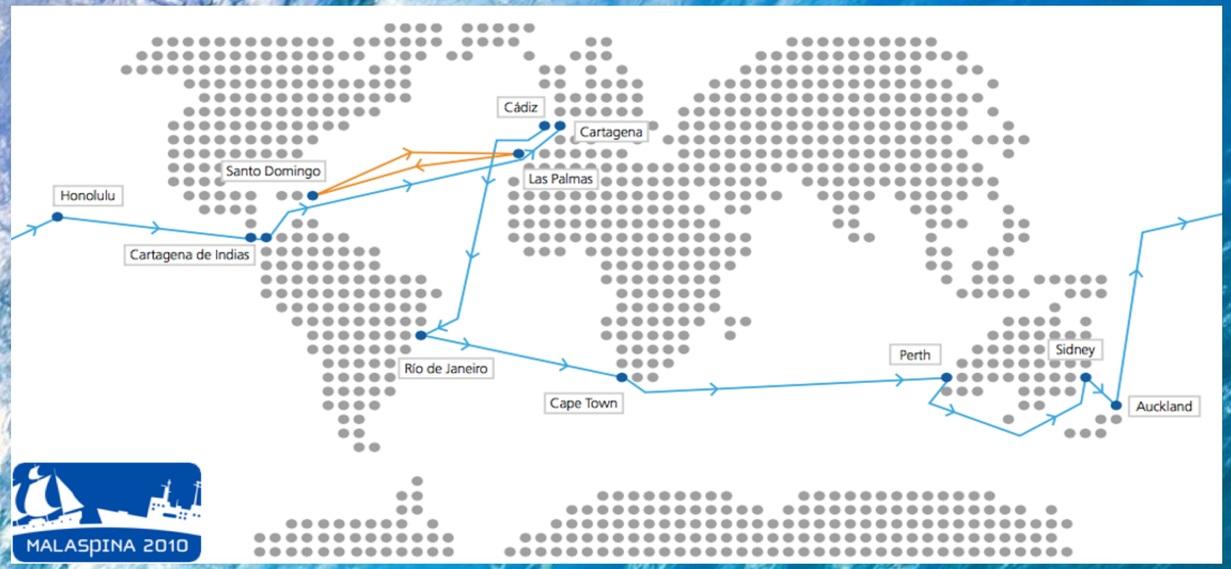
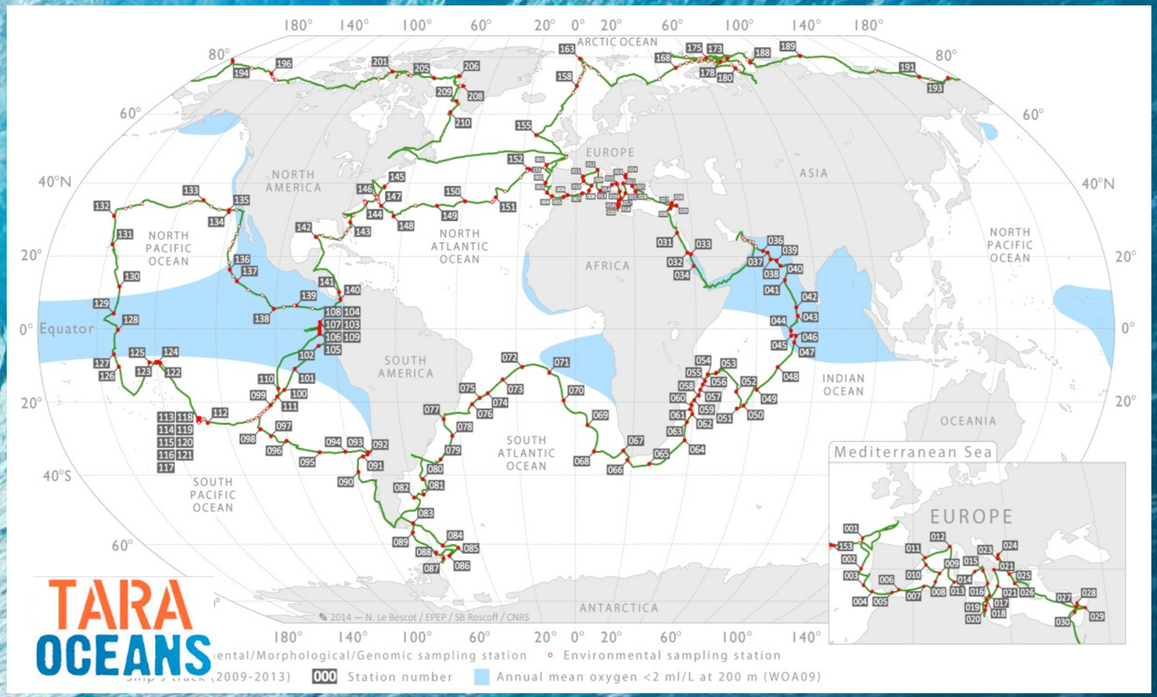


Epifluorescence of MAST-4 (Massana R *et al.*, 2009)

Environmental survey


Cádiz
Cartagena
Santo Domingo
Las Palmas
Honolulu
Cartagena de Indias
Río de Janeiro
Cape Town
Perth
Sidney
Auckland
MALASPINA 2010

TARA
OCEANS
agnès b.
Fondation
VEOLIA


ARCTIC OCEAN
EUROPE
ASIA
NORTH AMERICA
NORTH PACIFIC OCEAN
NORTH ATLANTIC OCEAN
AFRICA
SOUTH AMERICA
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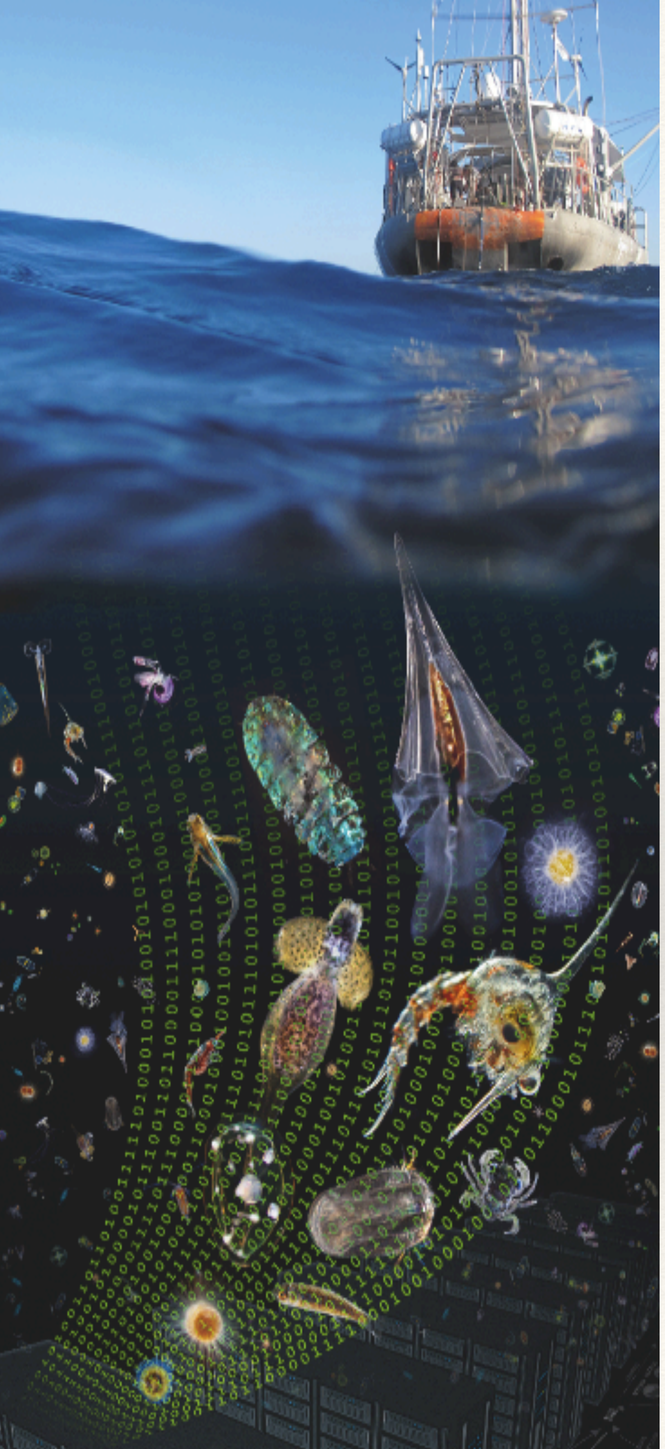
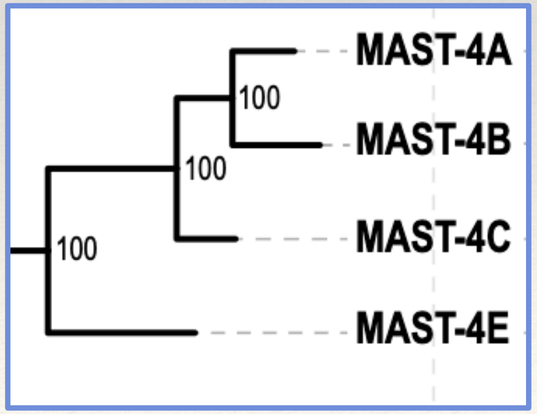
INDIAN OCEAN
OCEANIA
ANTARCTICA
Equator
Mediterranean Sea
TARA
OCEANS
Environmental sampling station
Station number
Annual mean oxygen <2 ml/L at 200 m (WOA09)

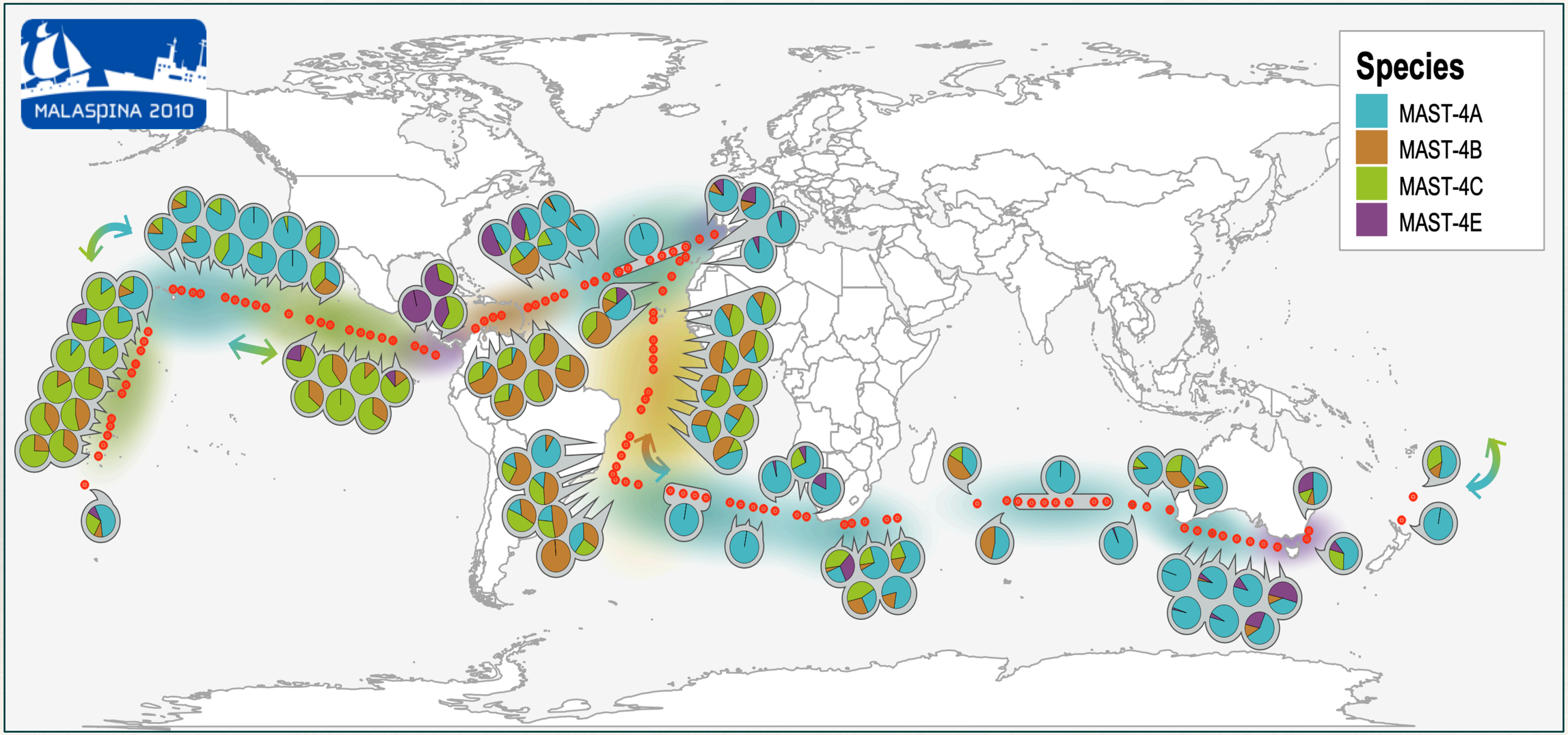


Data gathered

- Amplicons (rRNA gene)
- Single-Amplified Genomes of MAST-4
- Metagenomes
- Metatranscriptomes

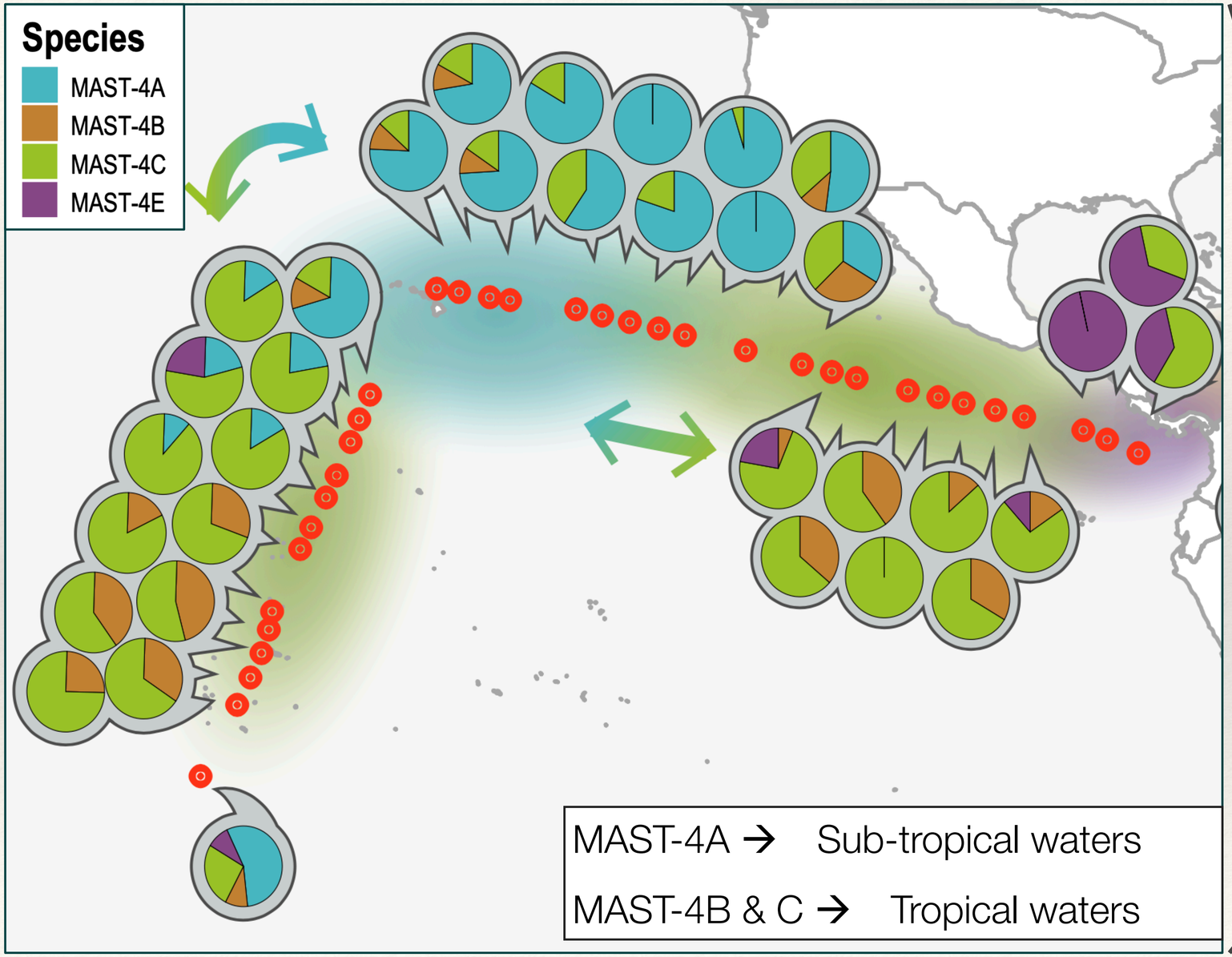


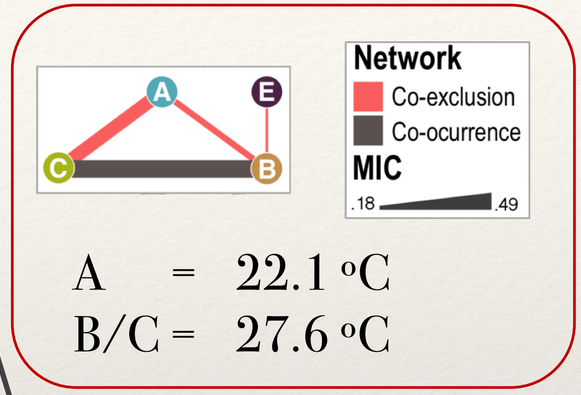
MAST-4 biogeography

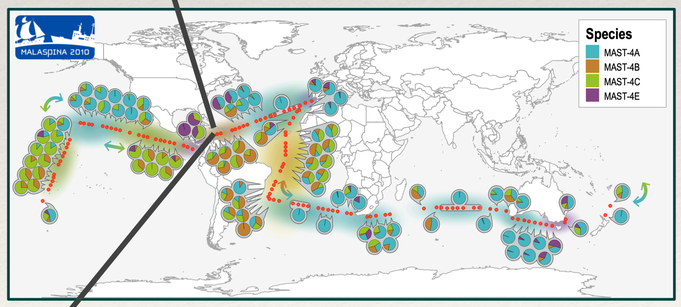


Amplicon Sequence Variants (ASV) from the Malaspina-2010 expedition

MAST-4 biogeography

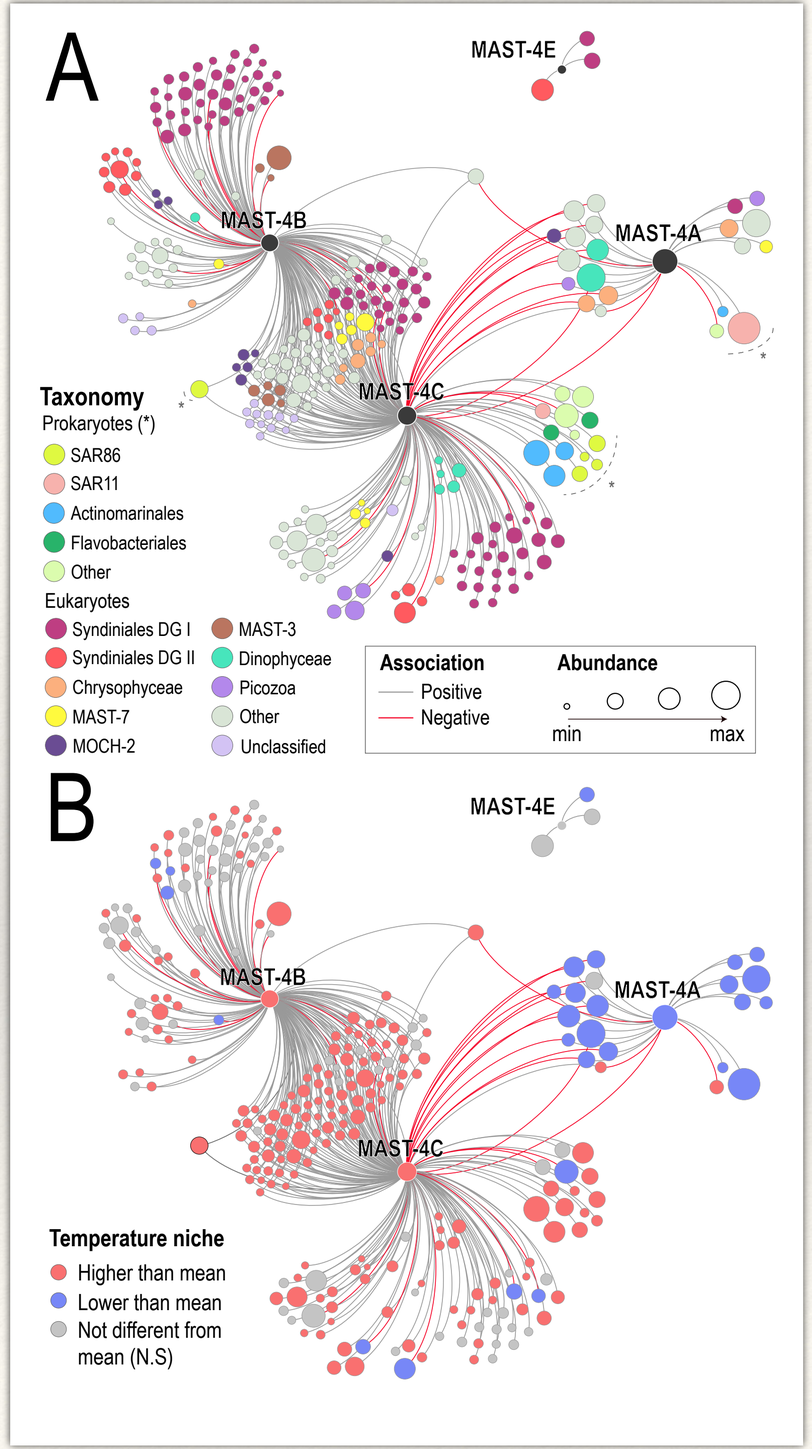


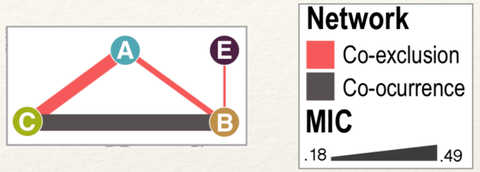




- Species C & B
  - Share positive species associations and the same niche temperature

- Species A
  - Share fewer negative associations with species C and B and a different niche temperature





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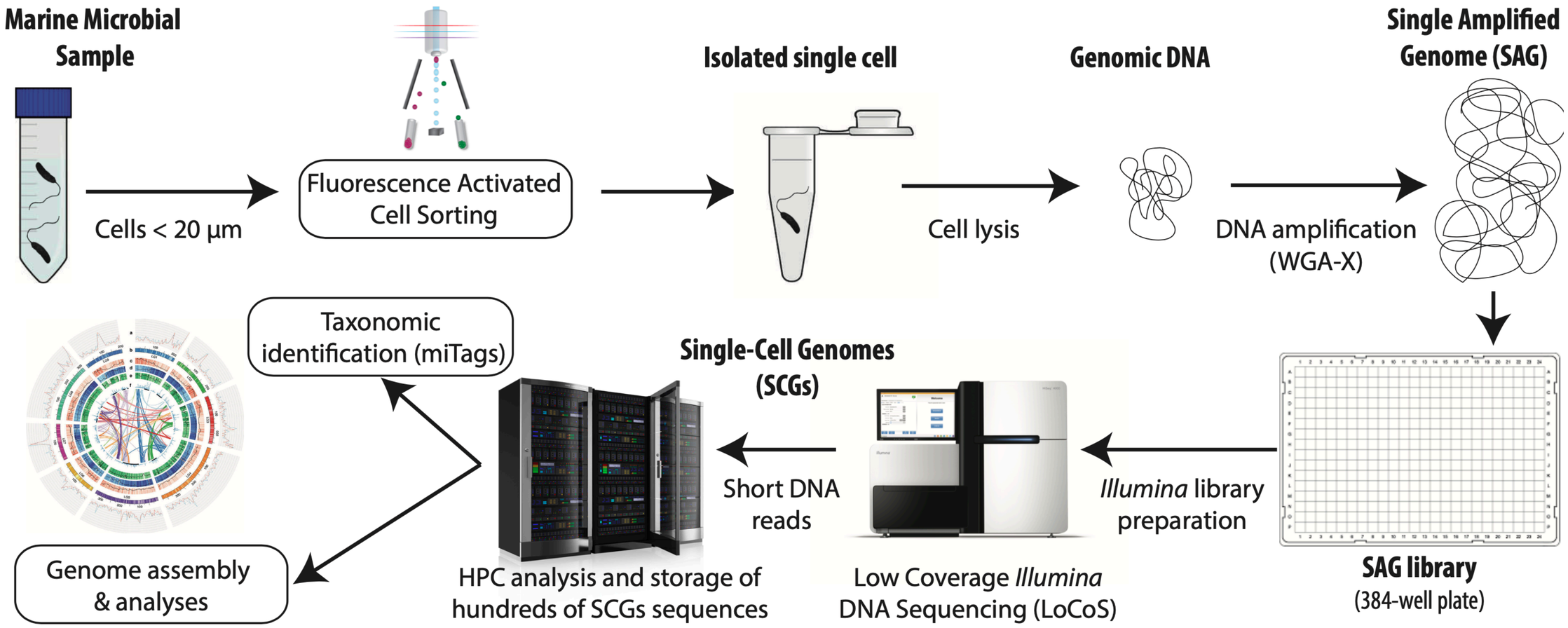
So far, uncultured

Single-Cell Genomics

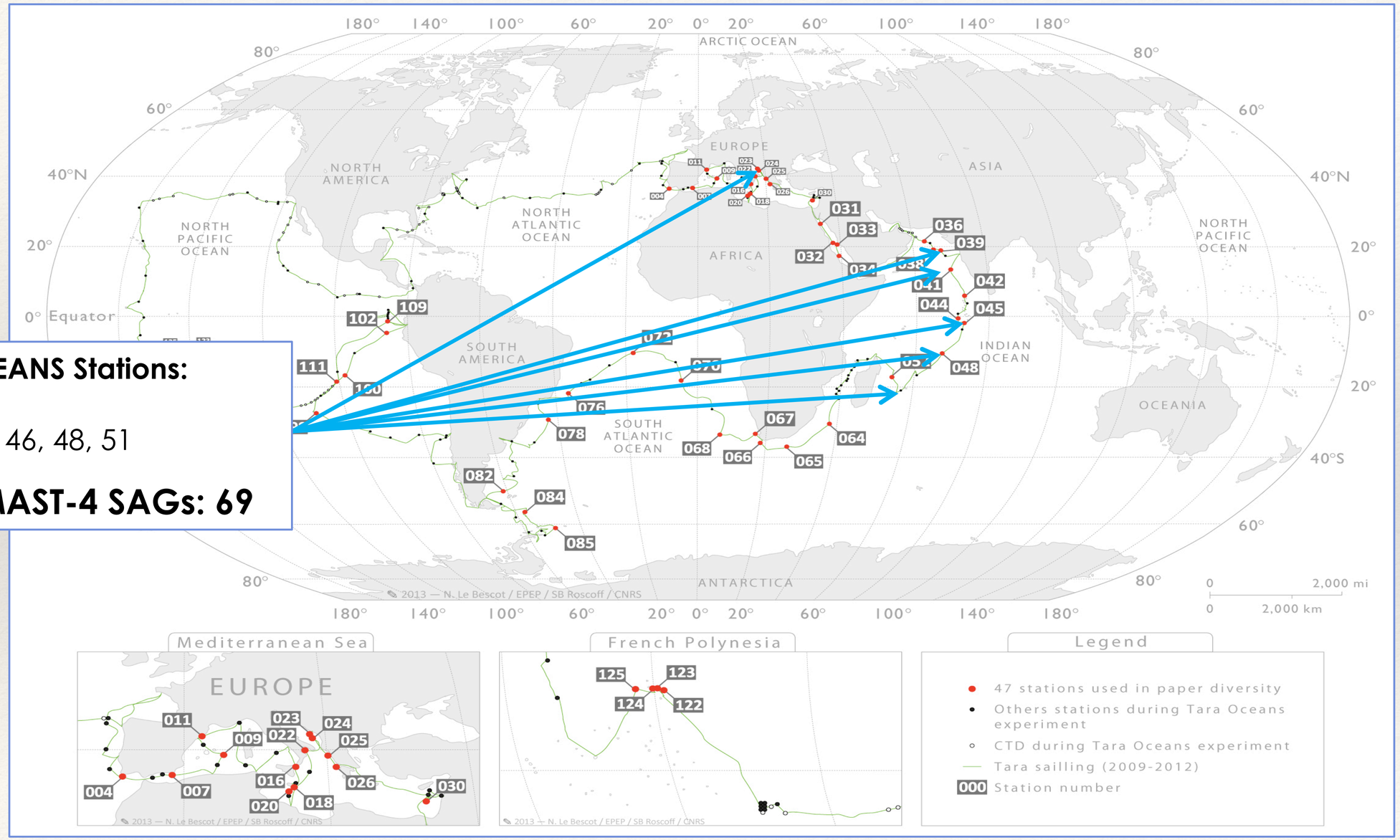


Sample Locations

TARA OCEANS Stations:

23, 39, 41, 46, 48, 51

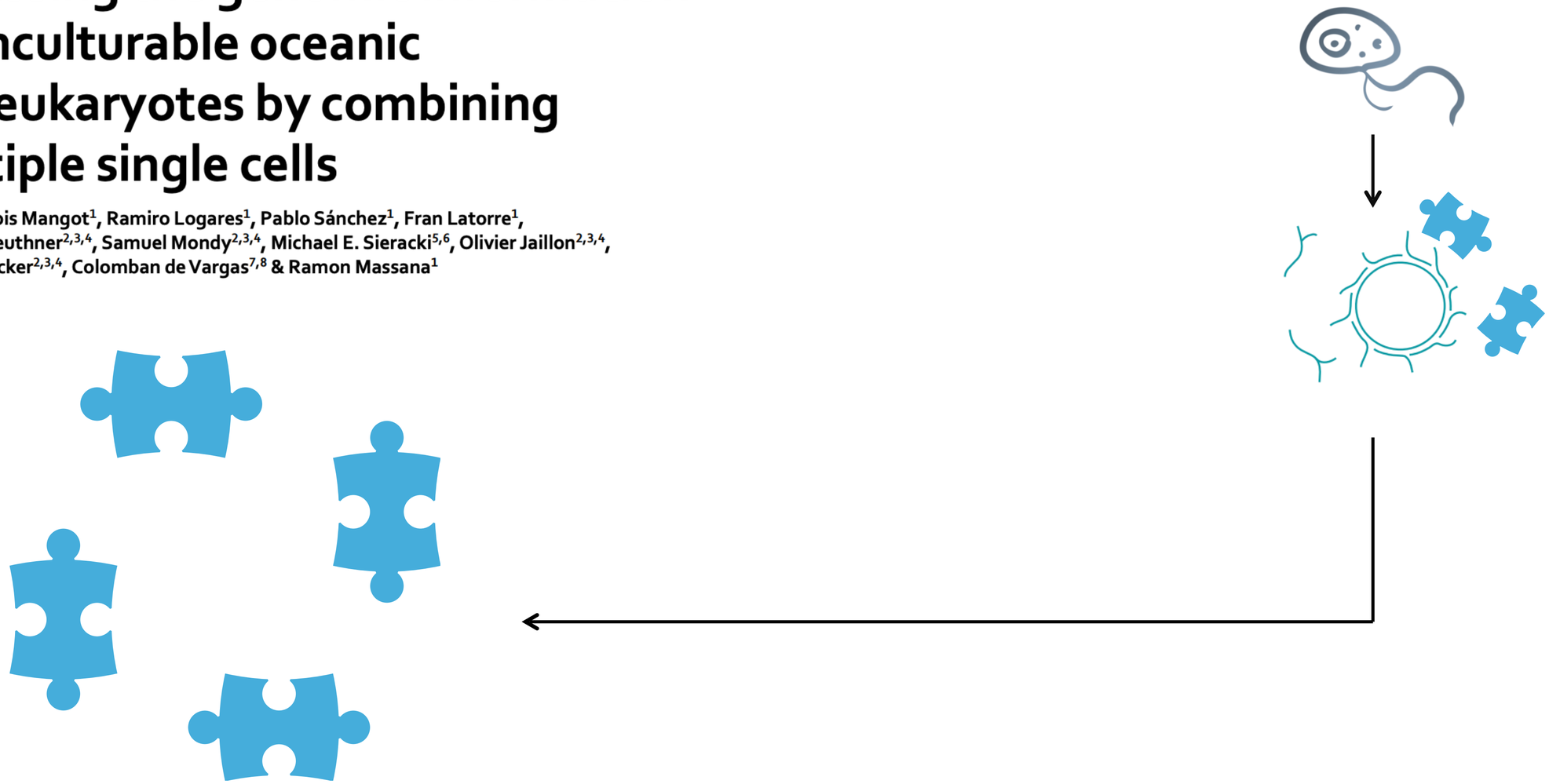
TOTAL MAST-4 SAGs: 69



SCG – Co-assembly strategy

Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells

Jean-François Mangot[1], Ramiro Logares[1], Pablo Sánchez[1], Fran Latorre[1], Yoann Seeleuthner[2,3,4], Samuel Mondy[2,3,4], Michael E. Sieracki[5,6], Olivier Jaillon[2,3,4], Patrick Wincker[2,3,4], Colomban de Vargas[7,8] & Ramon Massana[1]



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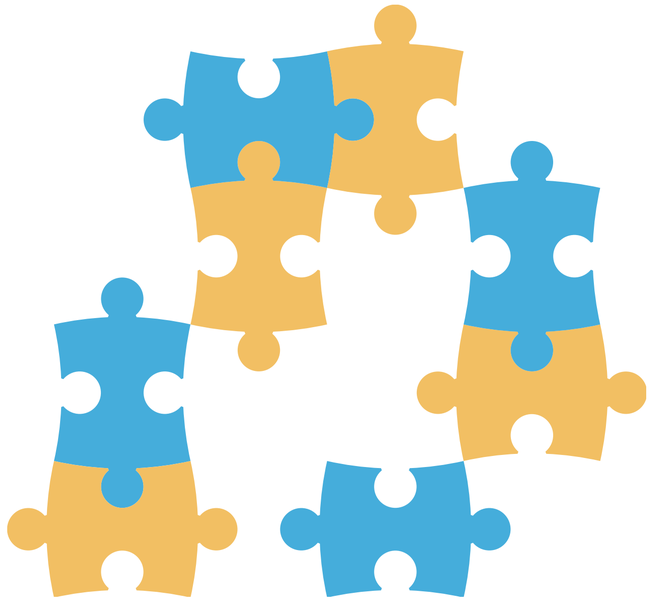

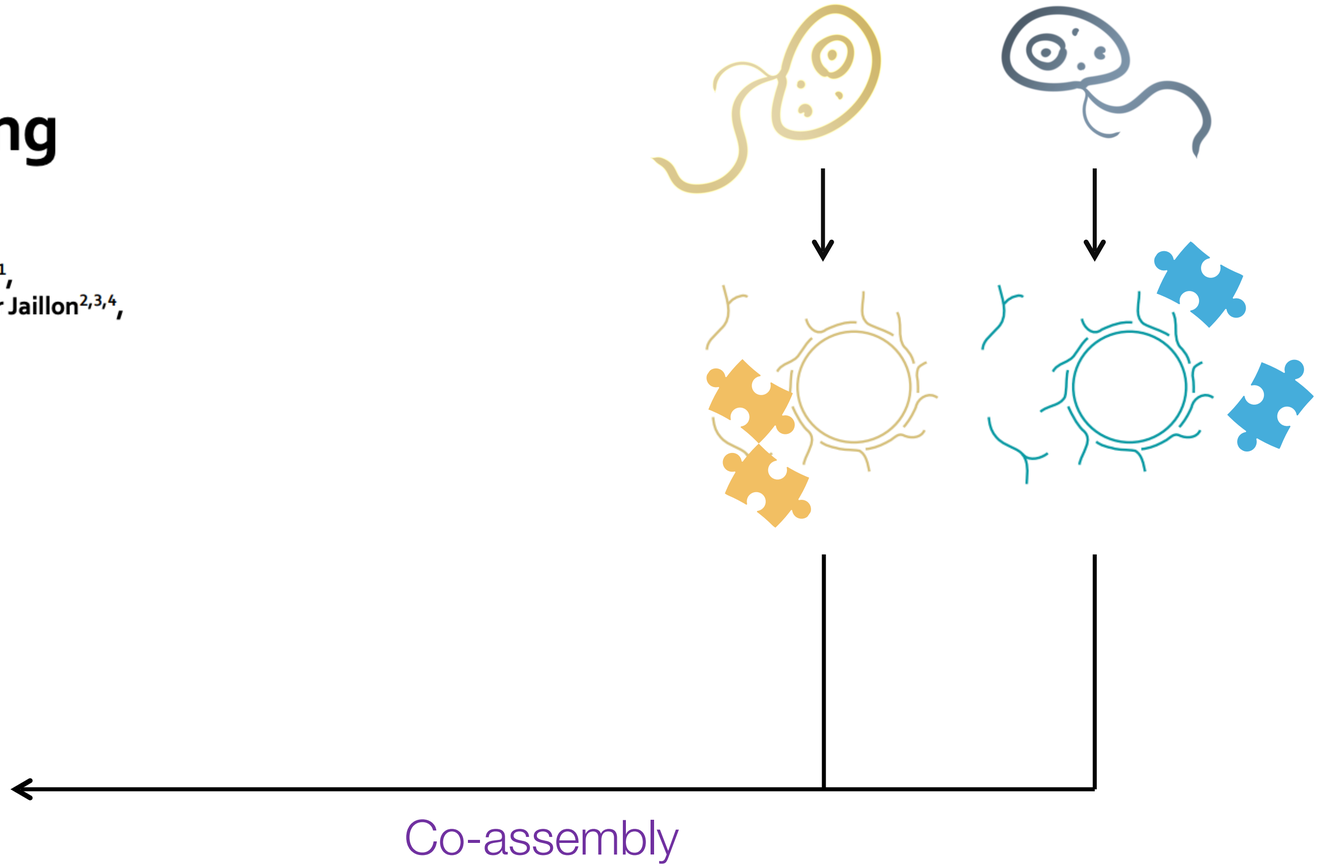

SCG – Co-assembly strategy

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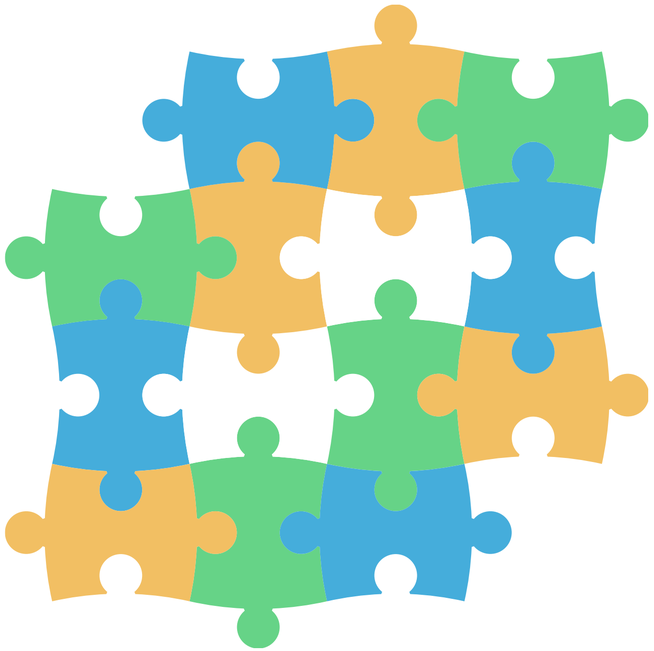

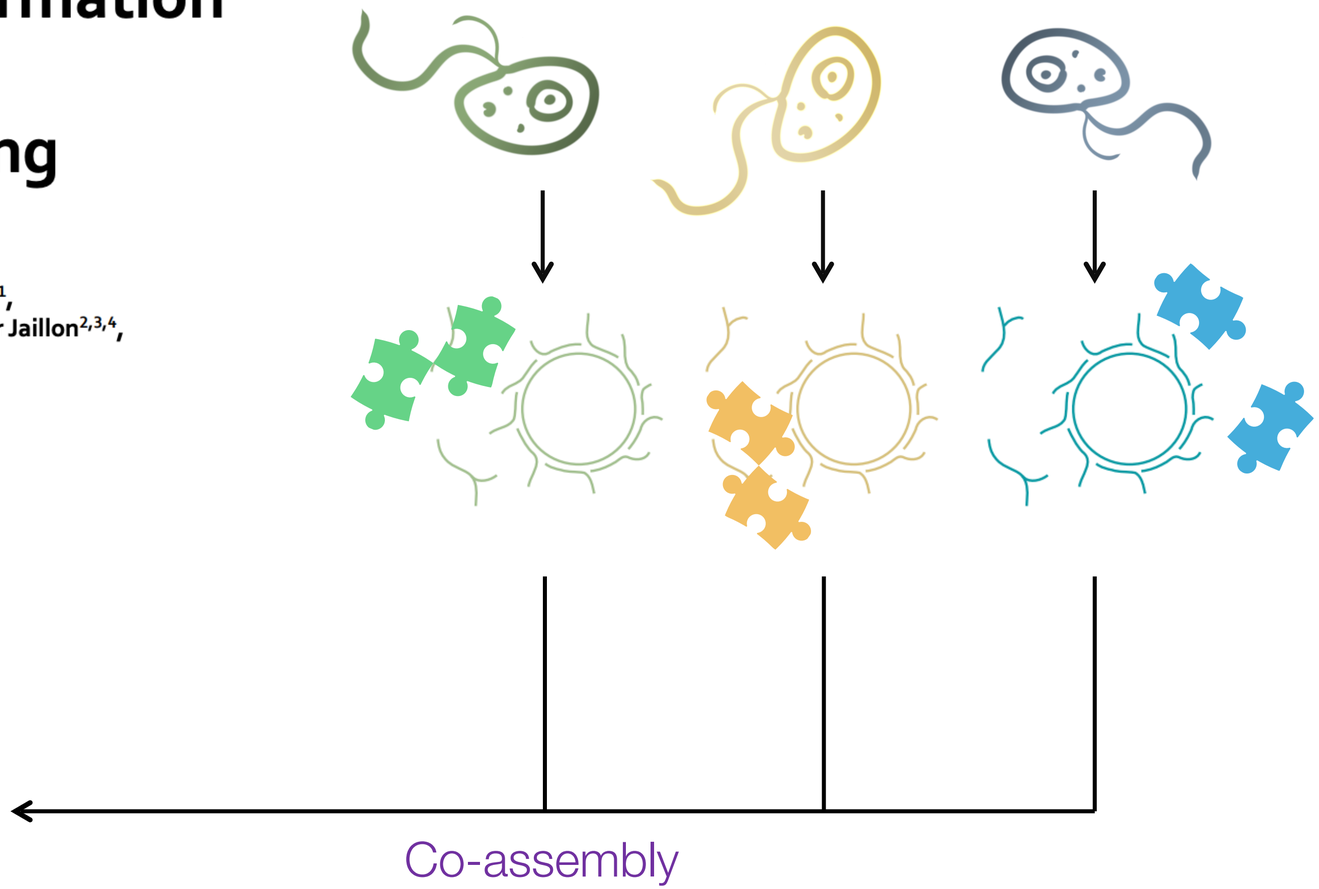

MAST-4 Genomes

	MAST-4A	MAST-4B	MAST-4C	MAST-4E
nº of SAGs coassembl.	23	9	20	17

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Genome Size (Mb)	47.4	29	47.8	31
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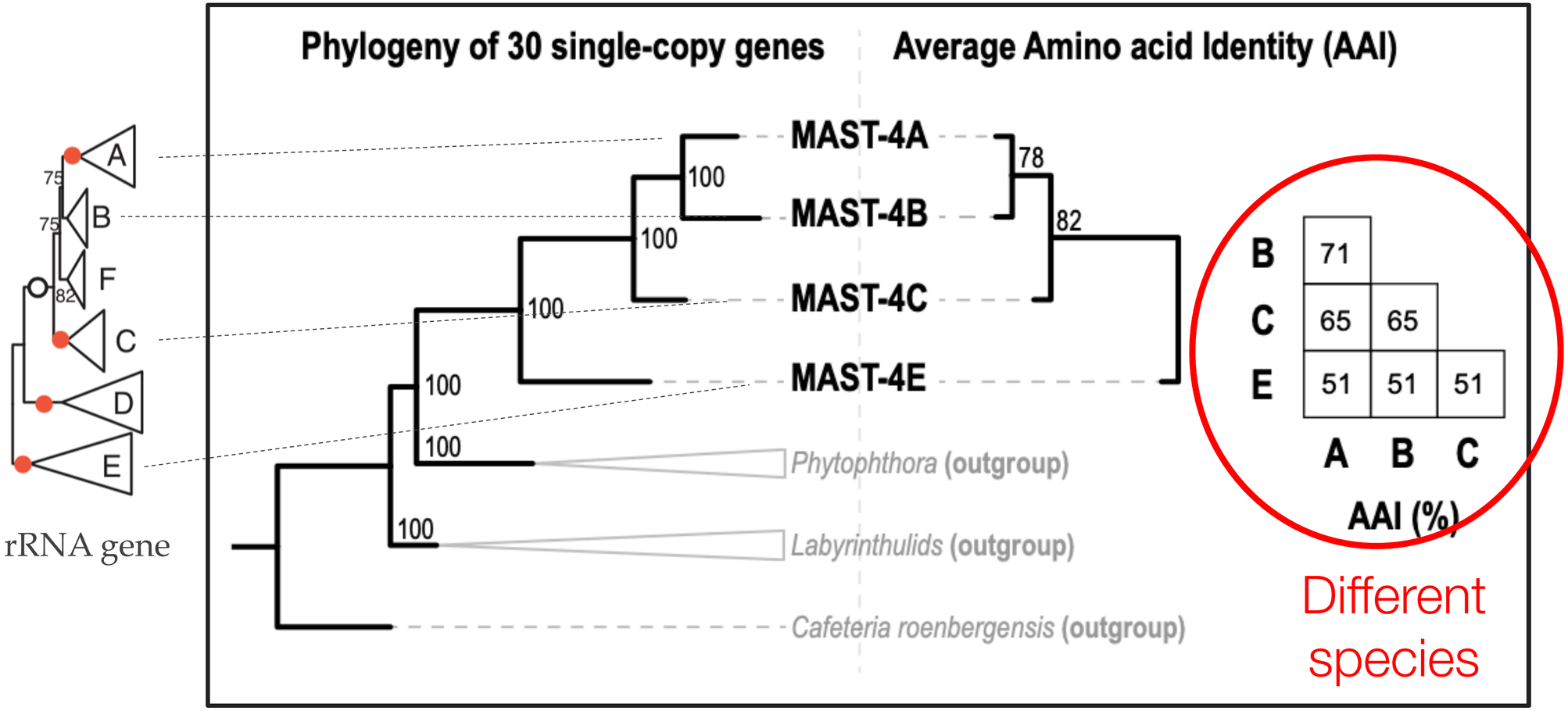
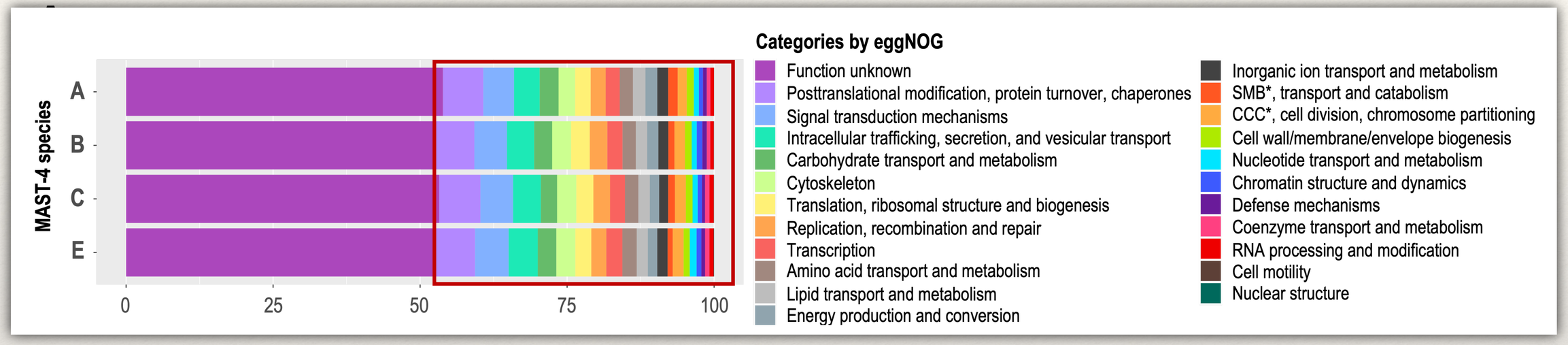
Completeness (%)	80%	67%	84%	71%

Substantial genomic differentiation between species



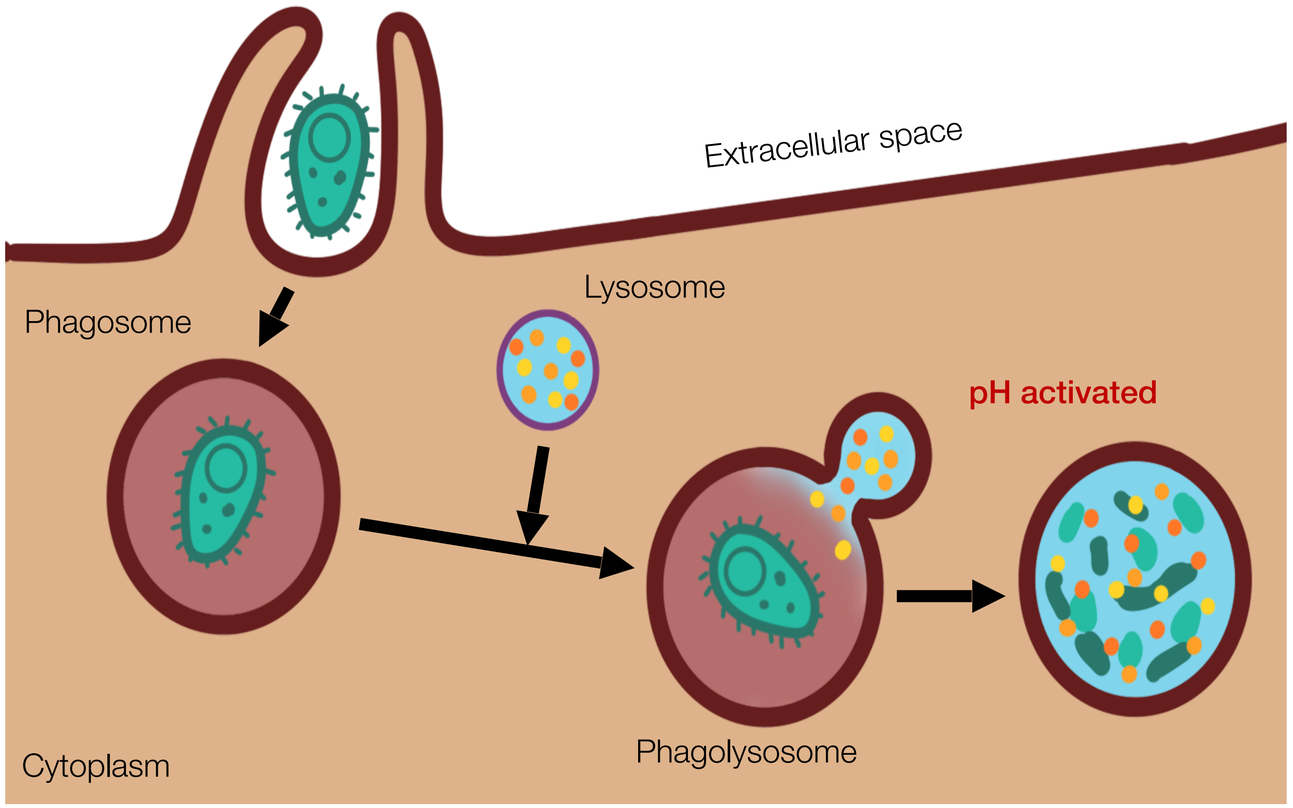
No major differences in general metabolic functions



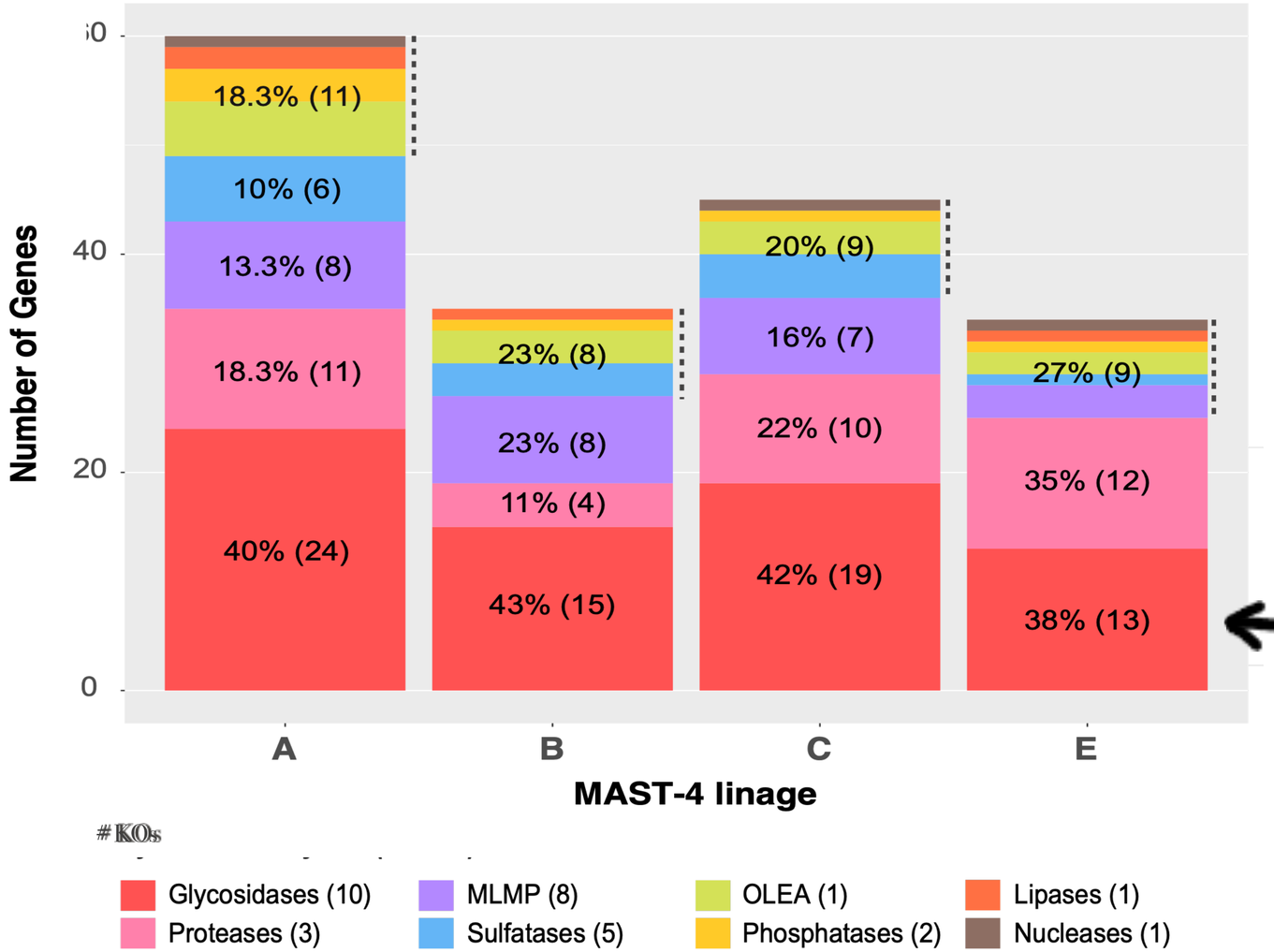
75% of the genes had hits in eggNOG

Focus on ecologically relevant genes

- Lysosomes:
  - Hydrolytic enzymes (~60)
  - Digestion of biomolecules
  - Phagocytosis & autophagy
  - Enzyme composition modulated by different food items?

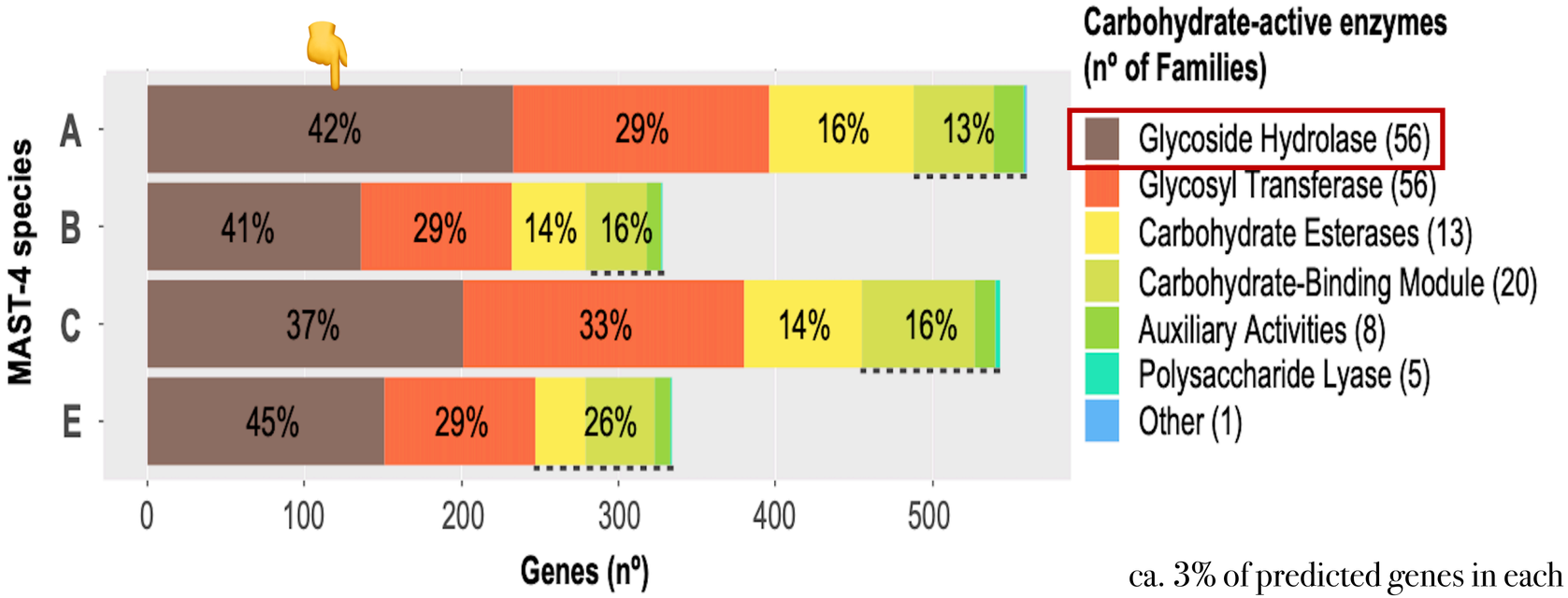


Hydrolytic enzymes



Dominated by
Glycoside Hydrolases

Carbohydrate-active enzymes (CAZymes)

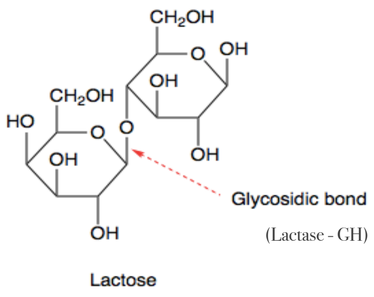


A broad class of enzymes that break, synthesize, or modify carbohydrates

ca. 3% of predicted genes in each MAST-4

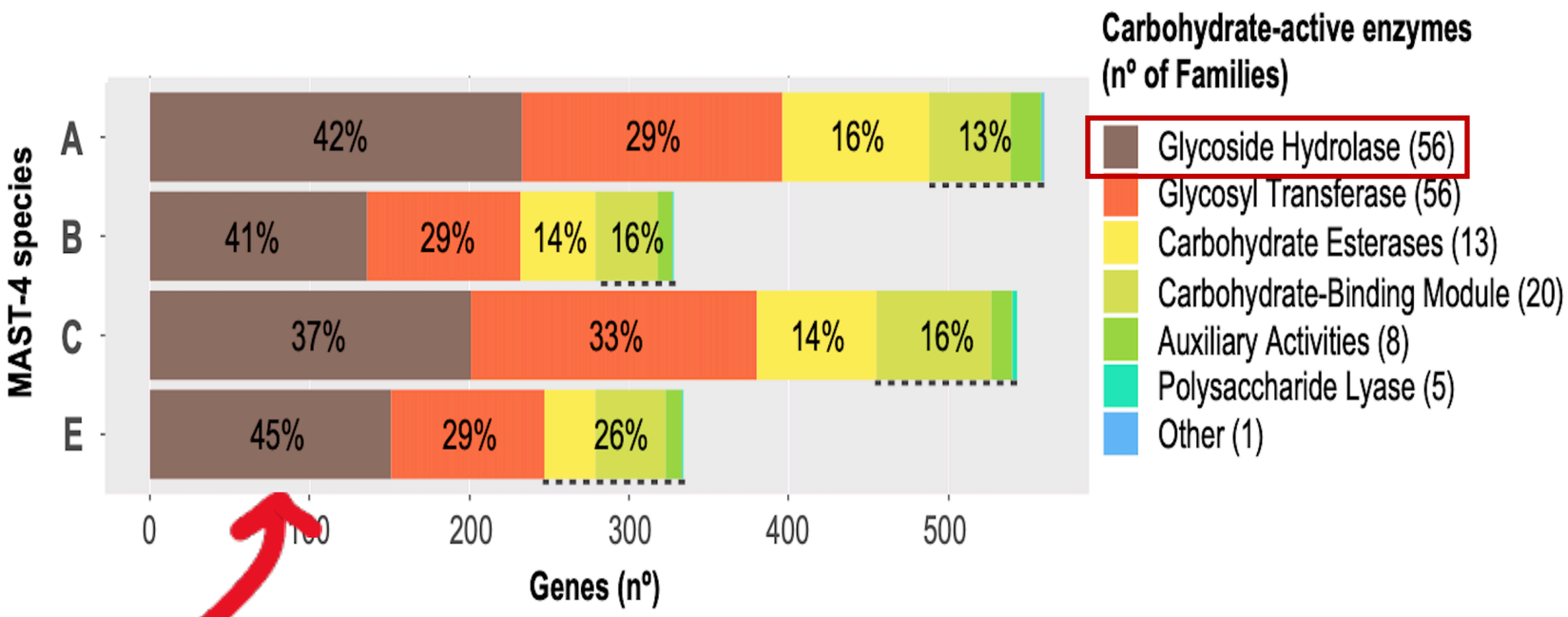
Most important in the digestion of food items:

<u>Glycoside Hydrolases</u> (GHs): Break glycosidic bonds in various carbohydrates



- Digestion of complex carbohydrates from prey into simpler sugars
- Break down organic detritus

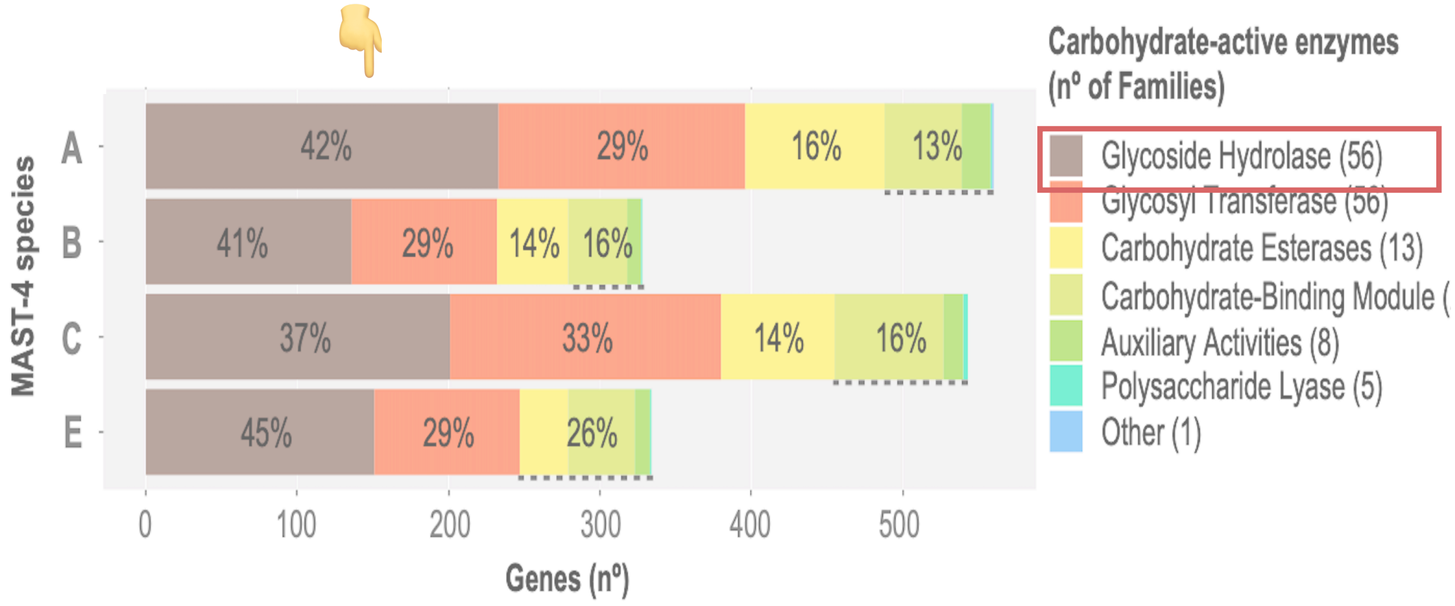
Focus on Glycoside Hydrolases

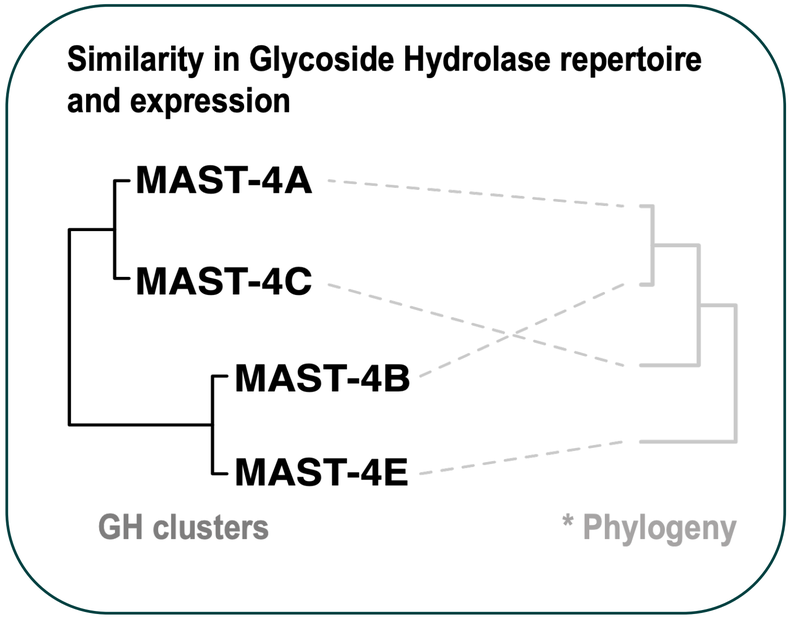


🤔

Could different GH repertoires be linked to different capacities to degrade prey or compounds?

Focus on Glycoside Hydrolases



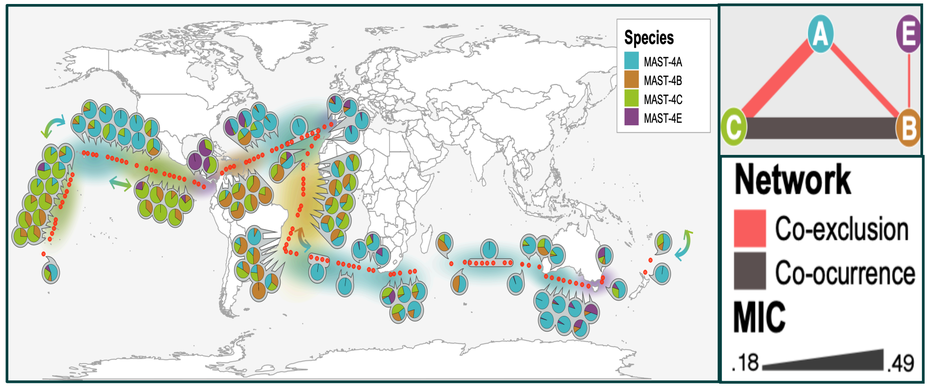


Avoid competition?

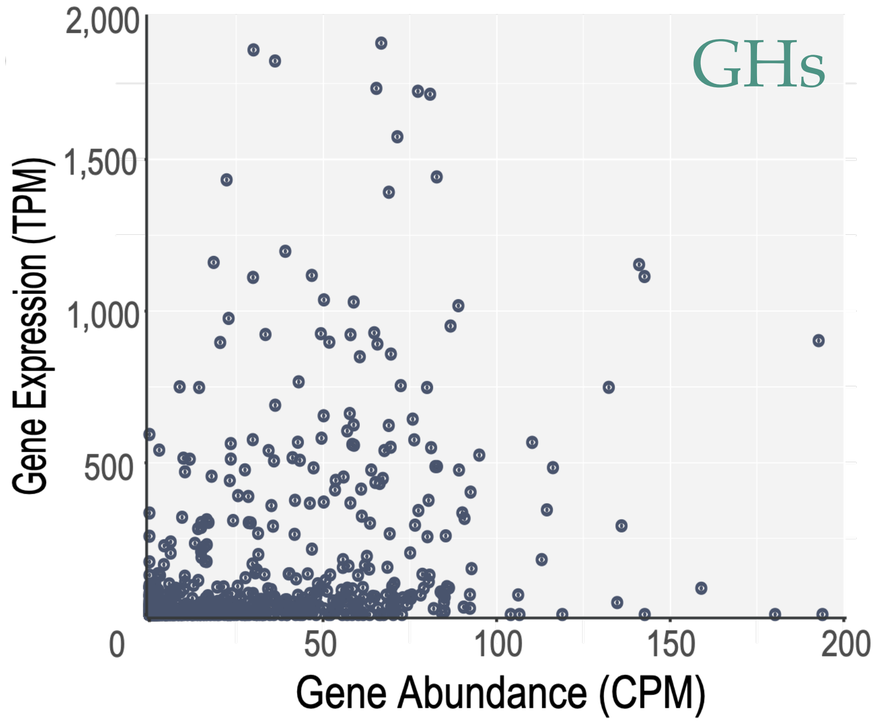
In the global ocean:

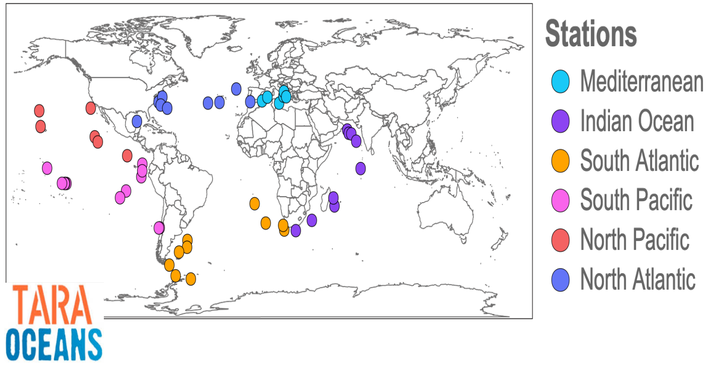
-Species with similar GH repertoire (A-C) co-exclude

-Species with different GH repertoire (C-B) co-occur



Environmental expression of MAST-4's GHs

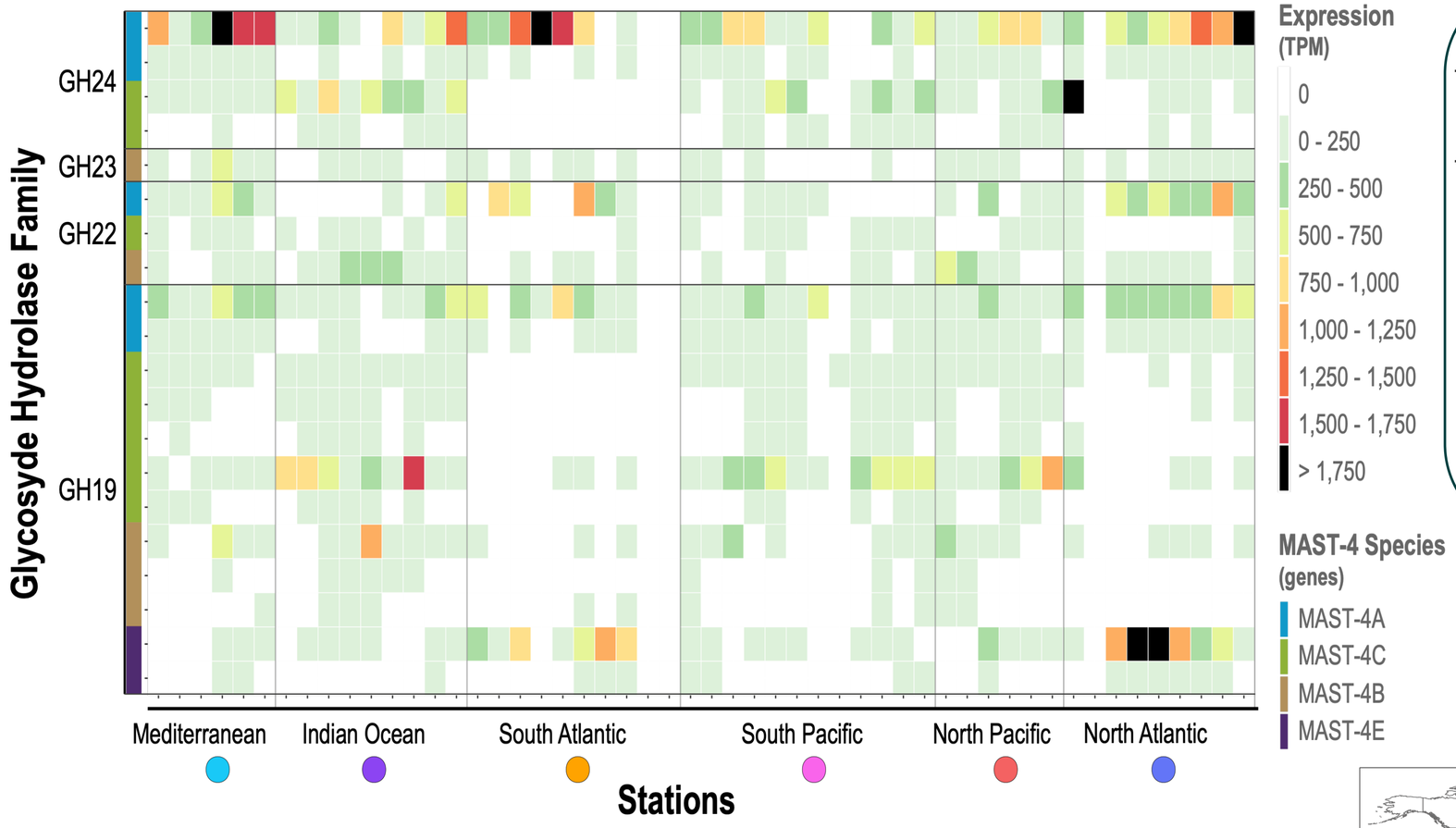




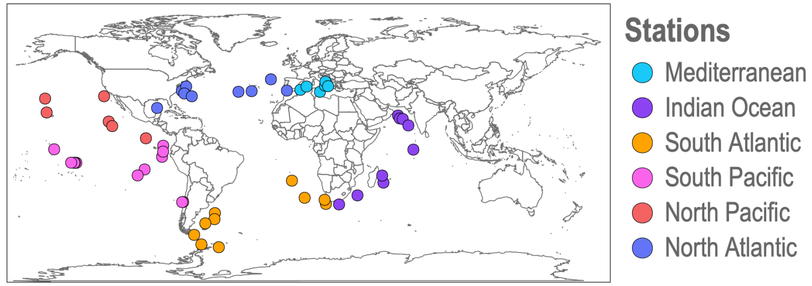
-No relationship between GH gene abundance and expression over the <u>surface</u> global ocean

-Differences in gene expression most likely represent up- or down-regulation of GH genes

MAST-4's GHs expression across stations

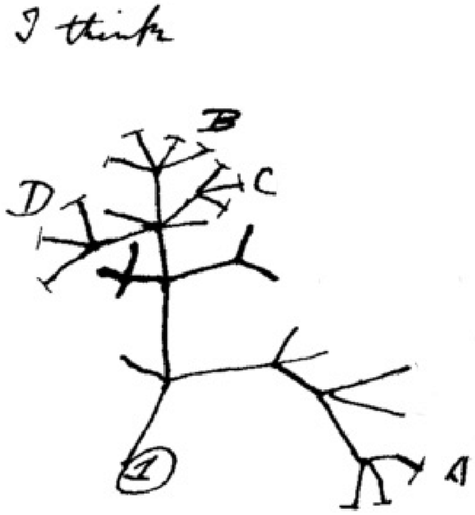


- Heterogeneous expression
- Highest expression
  - Lysozyme families GH22 and GH24 (peptidoglycan degradation)
  - Chitinase family GH19 (chitin degradation)

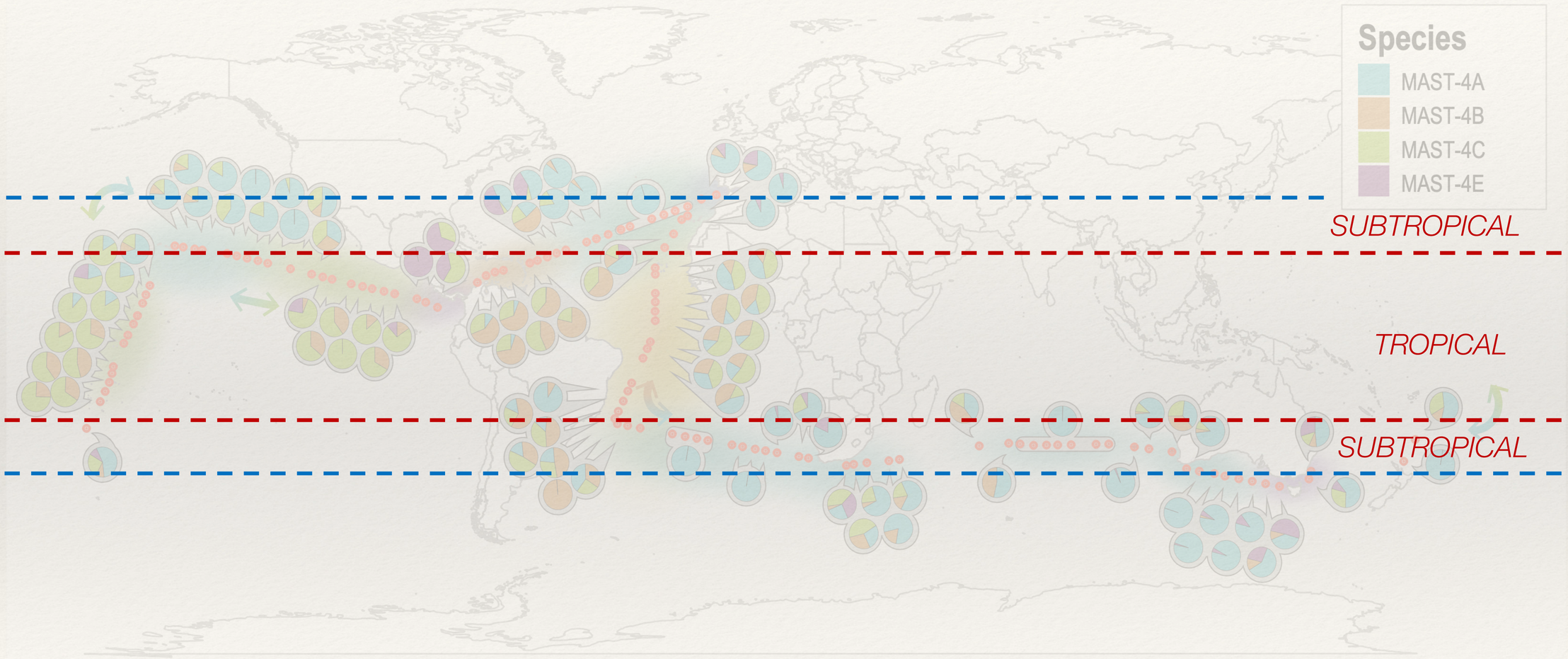


Hypothetical evolutionary diversification of MAST-4

Adaptation to different temperature niches and competition may have determined MAST-4's biogeography & speciation



Possible diversification of MAST-4



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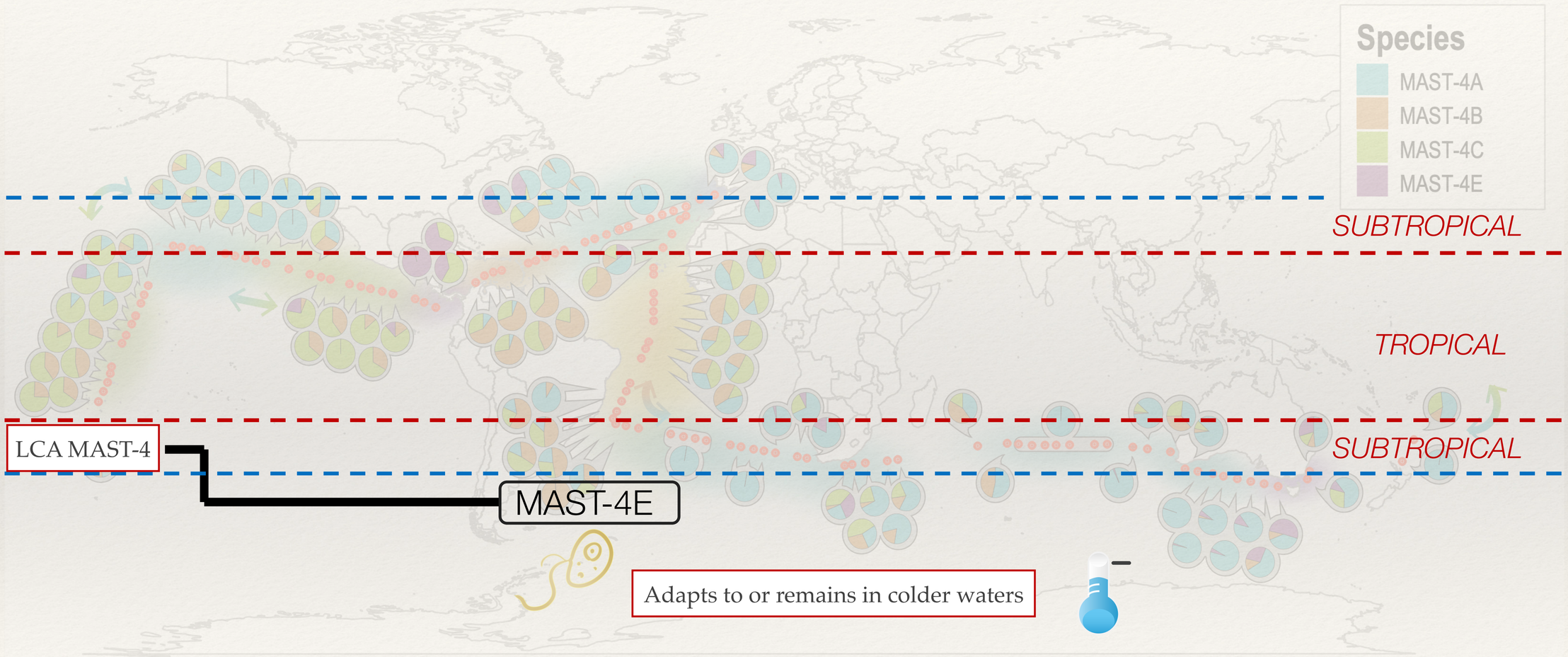

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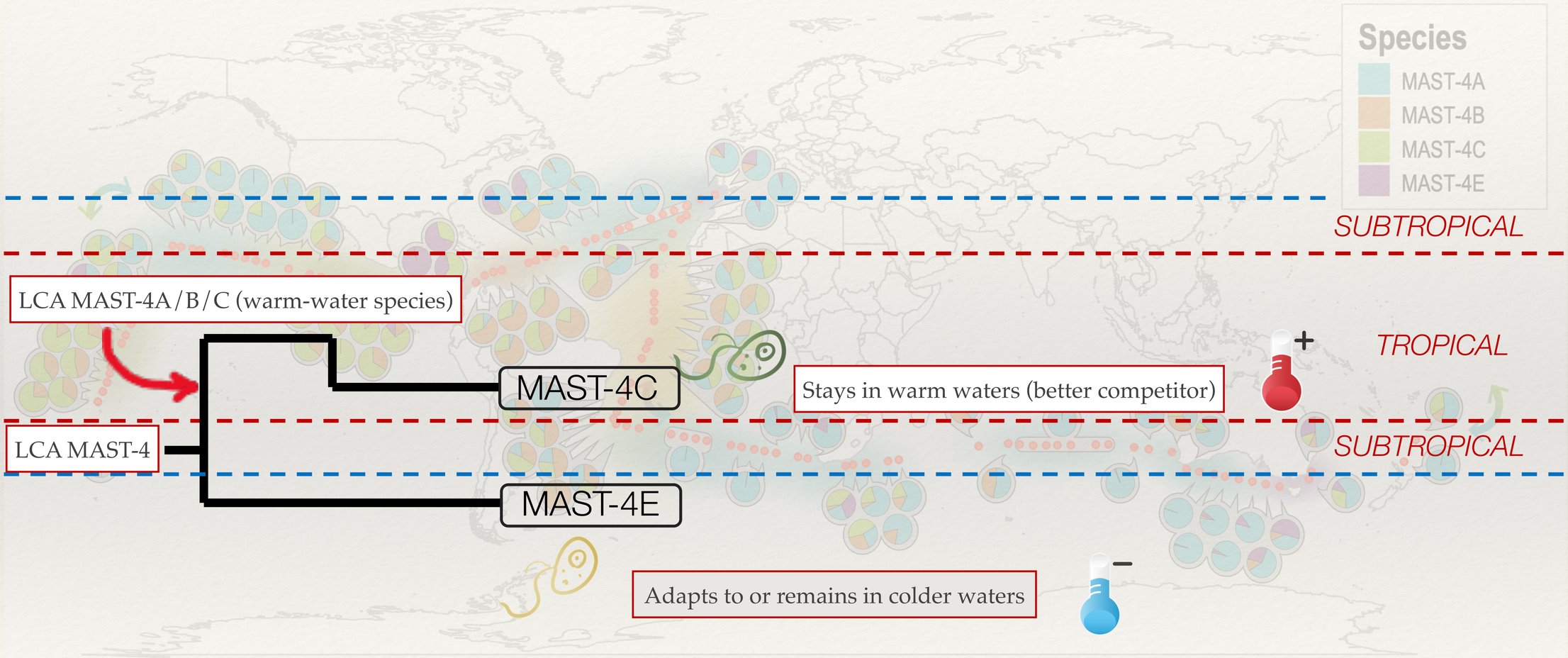

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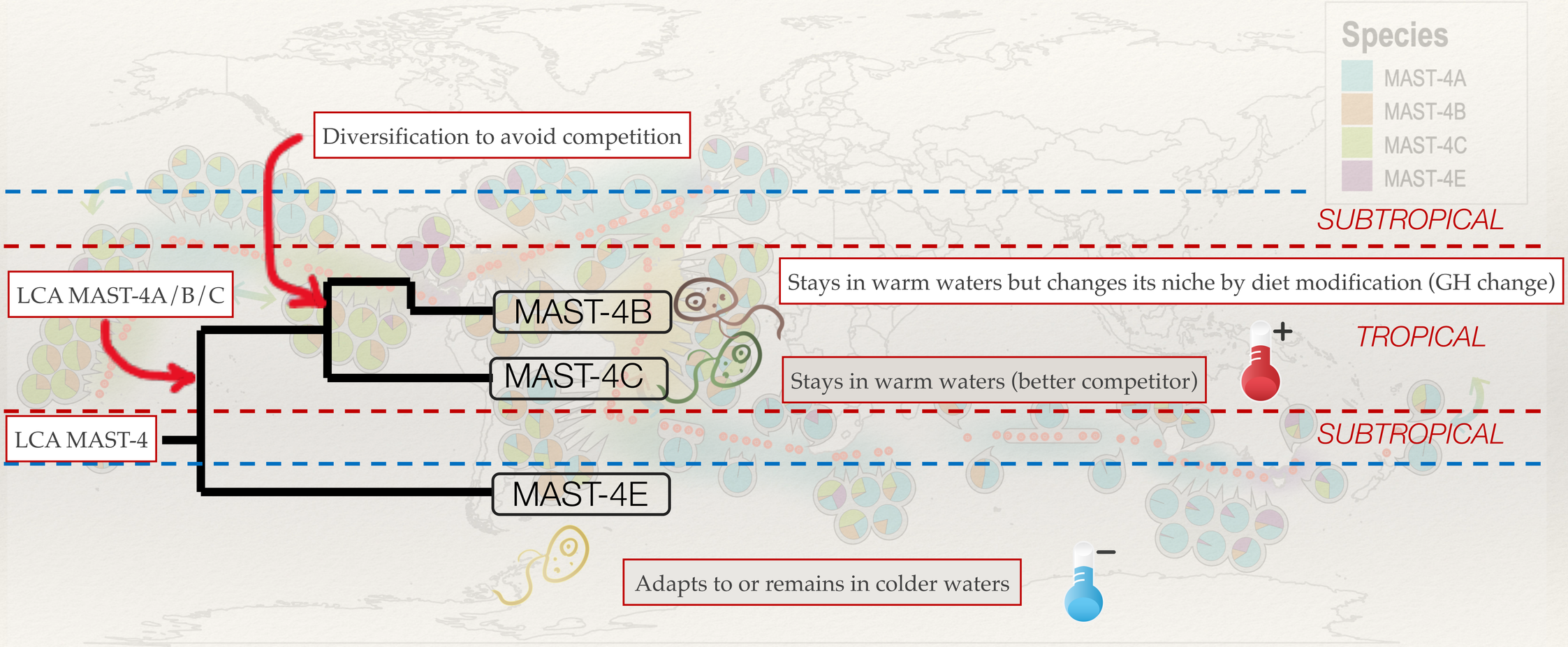

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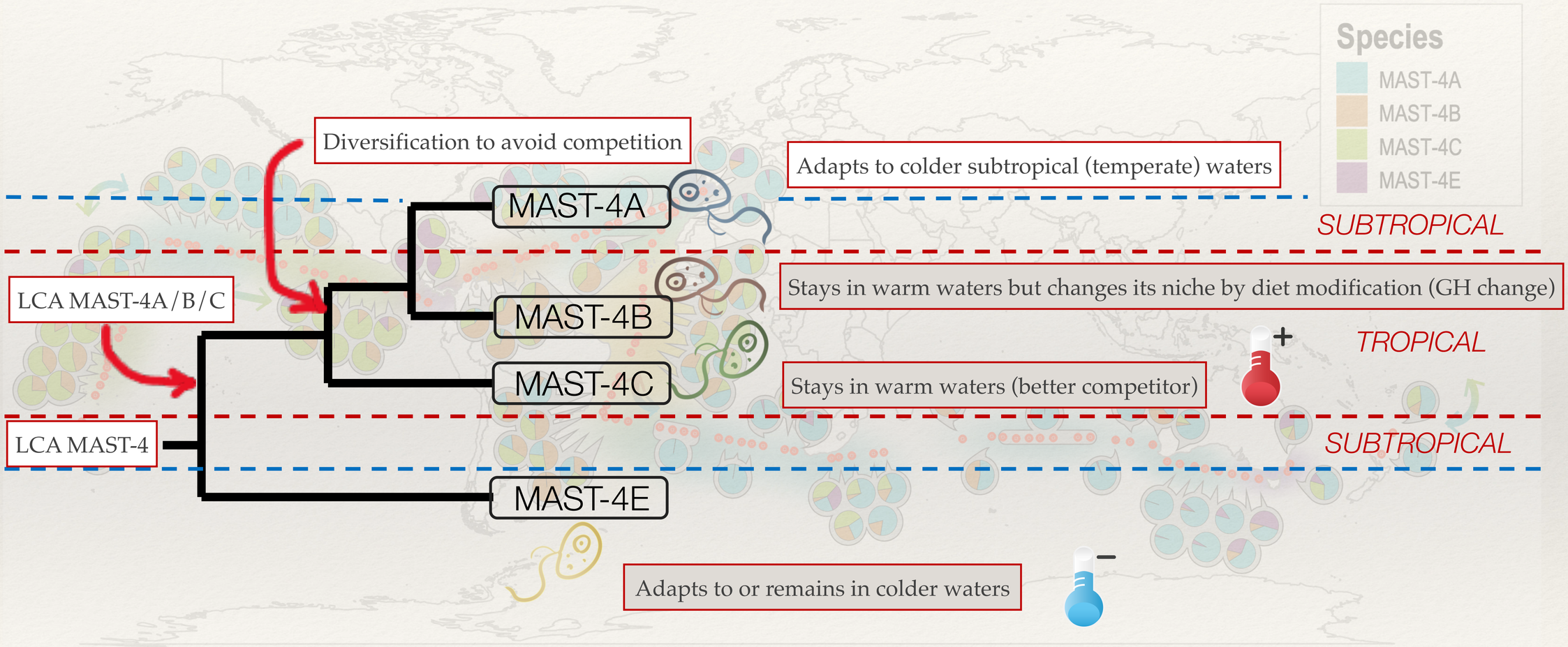

MAIN QUESTIONS

1. How different are MAST-4 species at the genome level?
   - Very different

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1. How different are MAST-4 species at the genome level?
   - Very different
2. Did MAST-4 species diverge via niche adaptation?
   - Based on our results, yes
3. Is such adaptation reflected in the MAST-4 genomes?
4. Can gene composition and expression provide insights on MAST-4 niche diversification?
   - To a certain extent, yes

Niche adaptation promoted the evolutionary diversification of tiny ocean predators **PNAS**

Francisco Latorre, Ina M. Deutschmann, Aurélie Labarre, Aleix Obiol, Anders K. Krabberød, Eric Pelletier, Michael E. Sieracki, Corinne Cruaud, Olivier Jaillon, Ramon Massana, and Ramiro Logares

-7 Authors Info & Affiliations

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What about populations?

Why study populations?

- Fundamental ecological units
  - ”eco-genetic” clusters
  - Limited knowledge

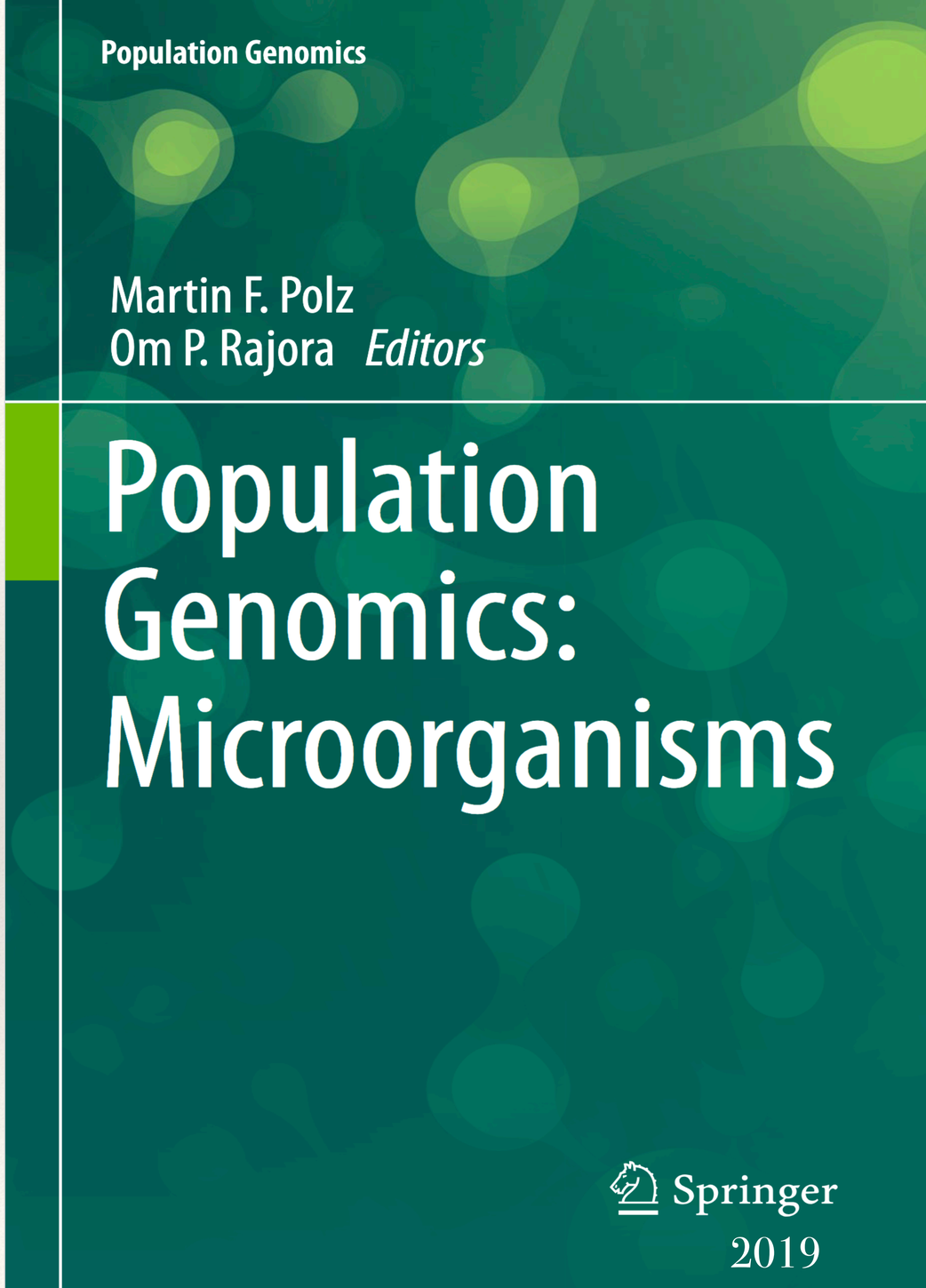
- Important for understanding:
  - Ecosystem function
  - Adaptation
  - Ecological interactions

Before industrial revolution

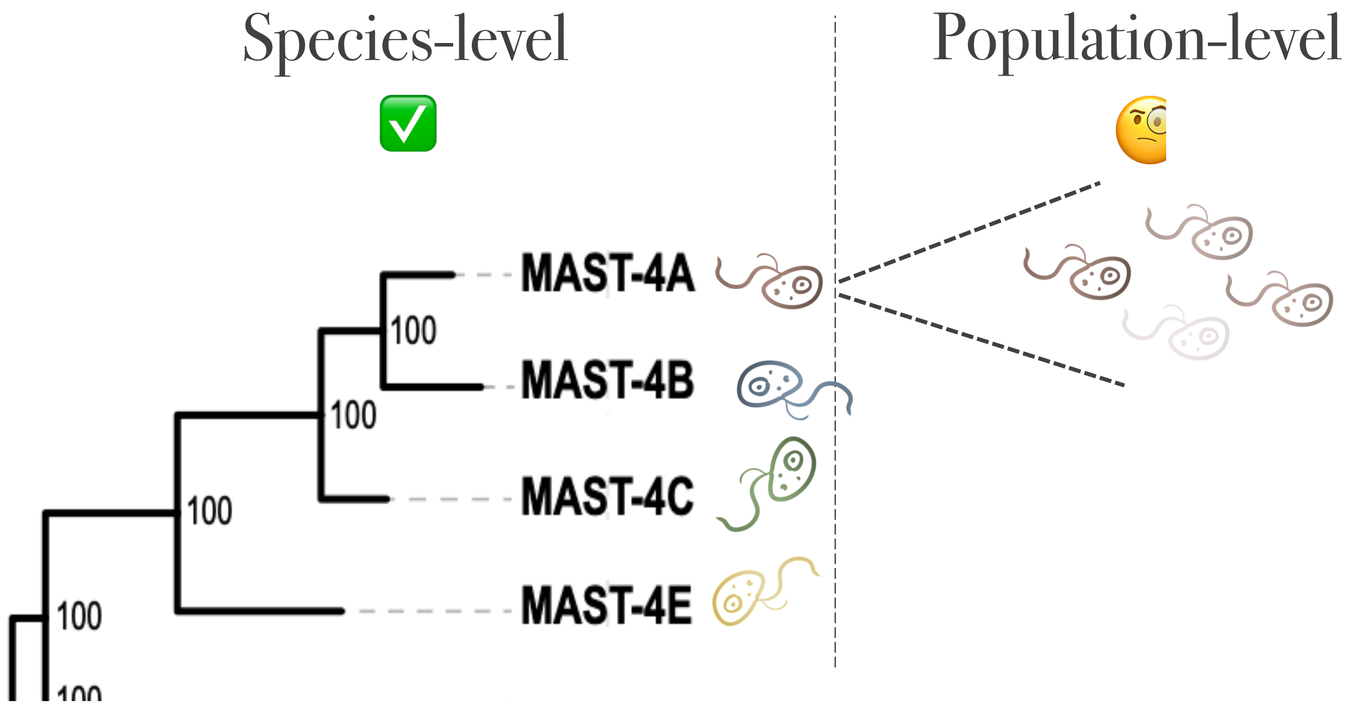
During industrial revolution

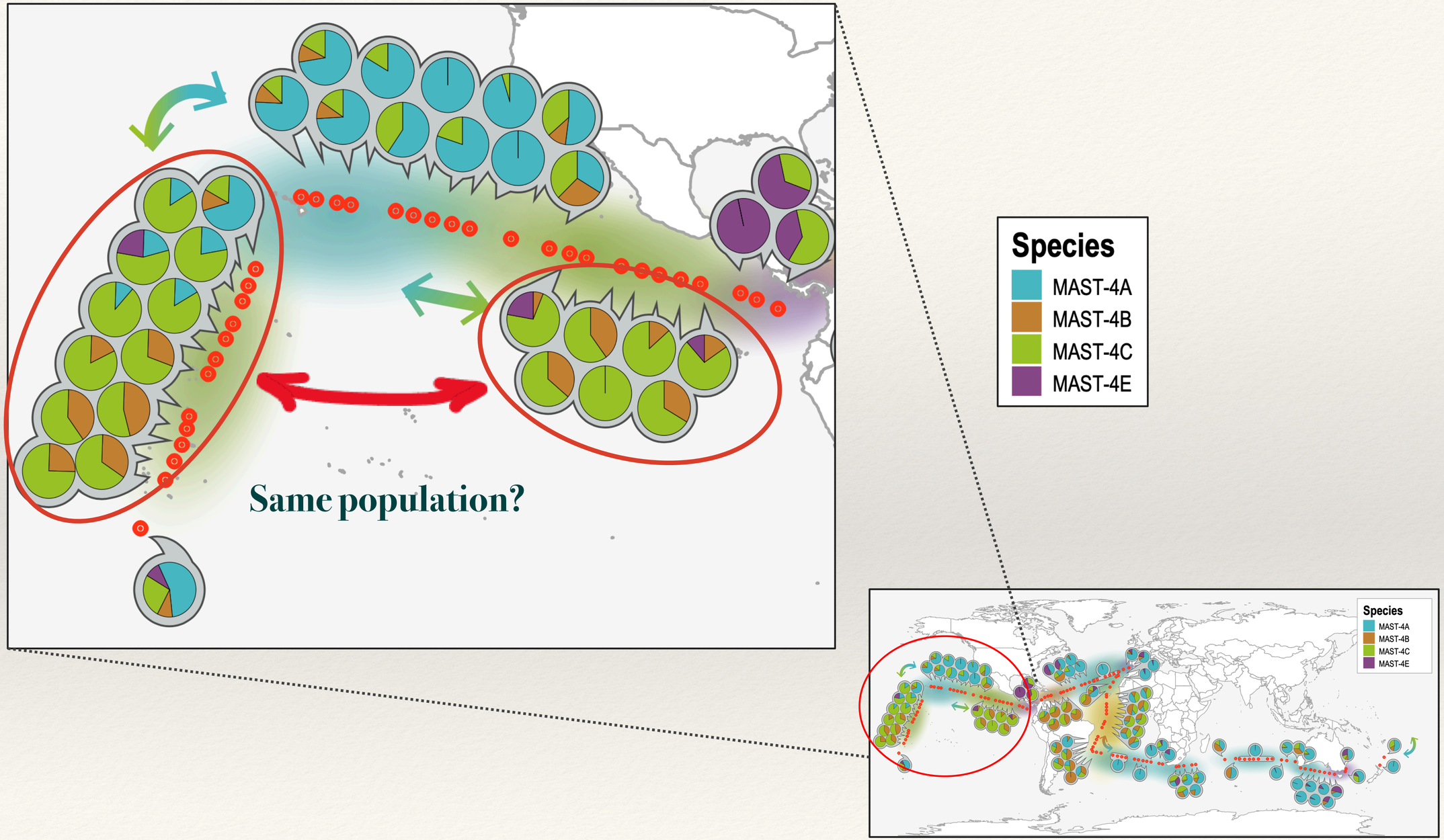
Population genomics of microbes

- "… a nascent field …"
- "…encompass the analysis of entire genomes of closely related individuals…"
- Boosted by decreasing DNA-sequencing costs
- One chapter (only) is dedicated to the population genomics of uncultured organisms



Looking at the population structure of MAST-4 species




Same population?
Species
MAST-4A
MAST-4B
MAST-4C
MAST-4E
Species
MAST-4A
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MAST-4 Population Genomics

MAIN QUESTIONS

1. What amount of intraspecies genomic divergence do MAST-4 species show in the global ocean?

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2. Do they exhibit population structure?
3. What environmental factors promote such a structure?
4. Can we detect genes featuring adaptation to different environmental conditions?

How do we quantify population genomics differences?

MAST-4 Population Genomics

How do we quantify population genomics differences?

- Count and compare mutations in the genome

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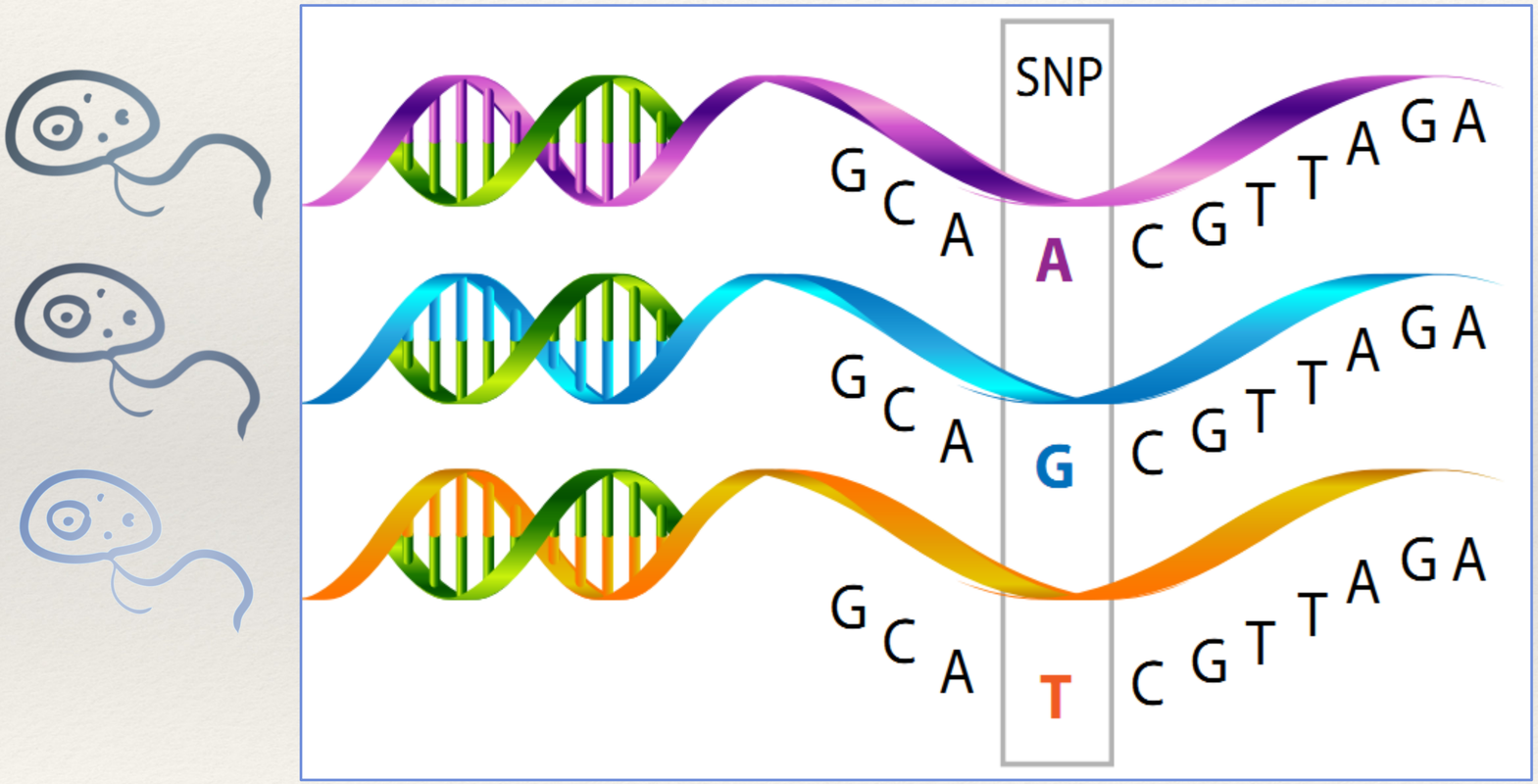
SNV = Single Nucleotide Variant



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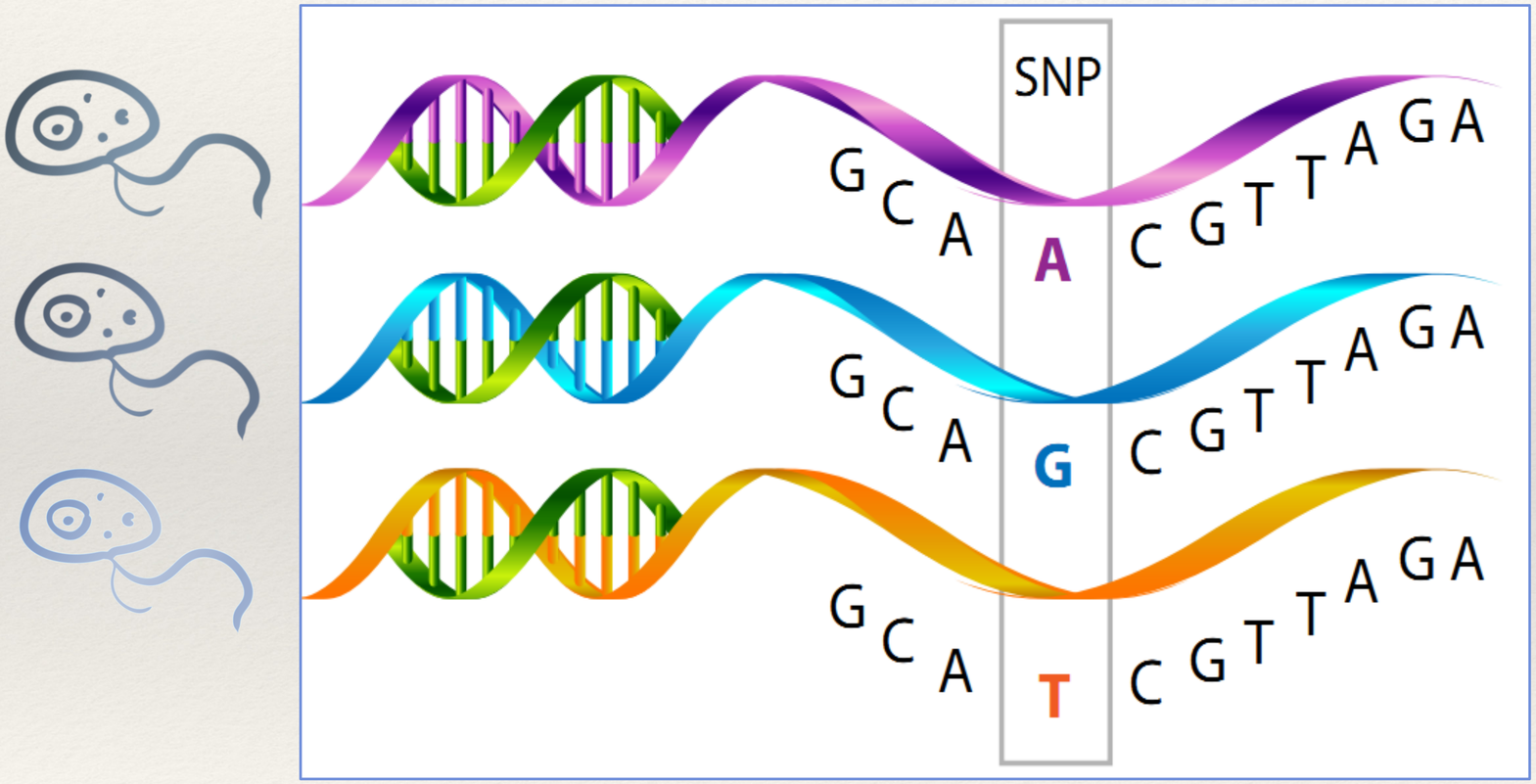


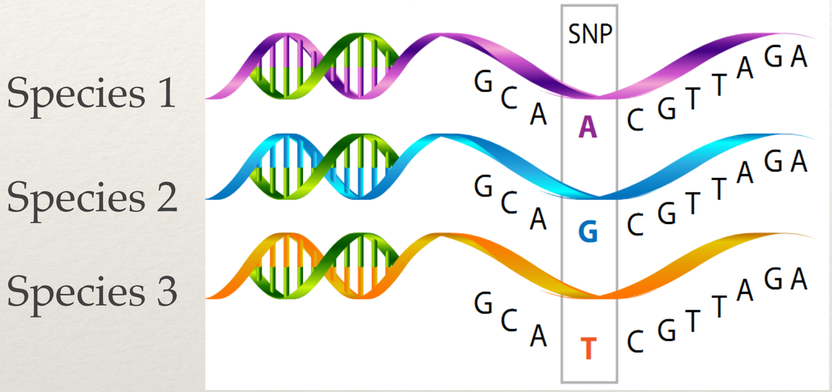
SNVs can…

- Modify the expression of a gene
- Change the structure of a protein
- Change its effectiveness
- Change the function
- Do nothing (silent mutations)

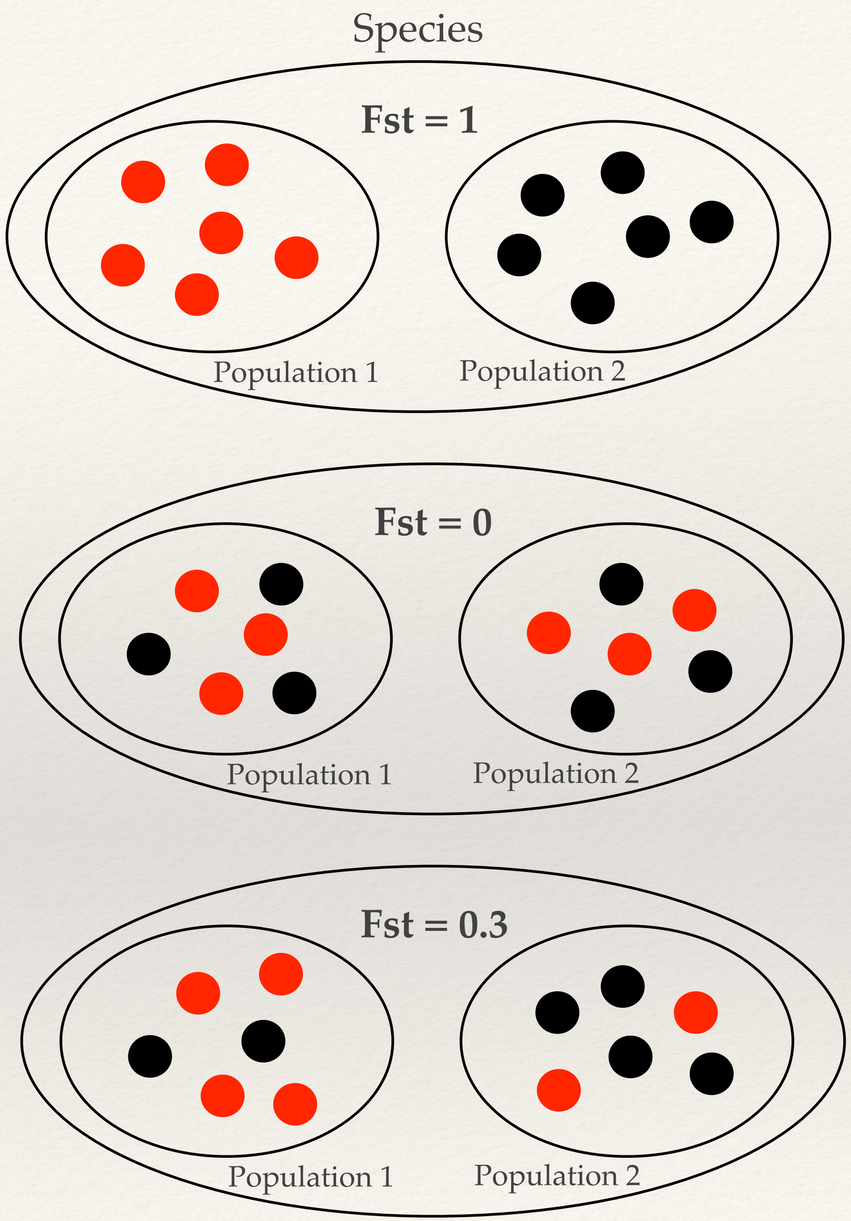
Positive selection – beneficial mutations
Negative selection – deleterious mutations

The Fixation Index (Fst)

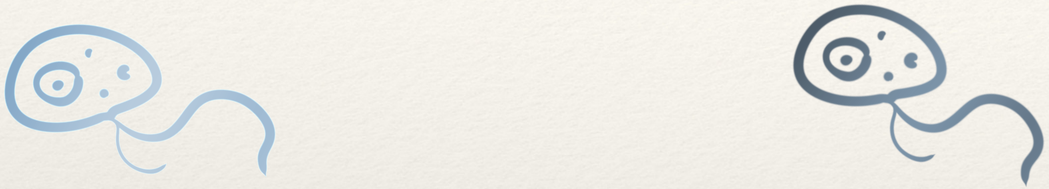
Analysis of Single Nucleotide Variants (SNVs)



$$\frac{Variation\ between\ populations - Variation\ within\ populations}{Variation\ between\ populations} = Fst$$



Quantifying the difference – The Fixation Index



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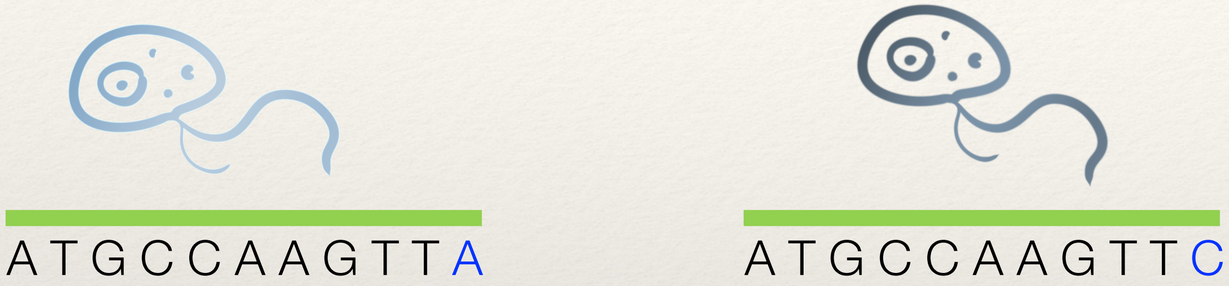

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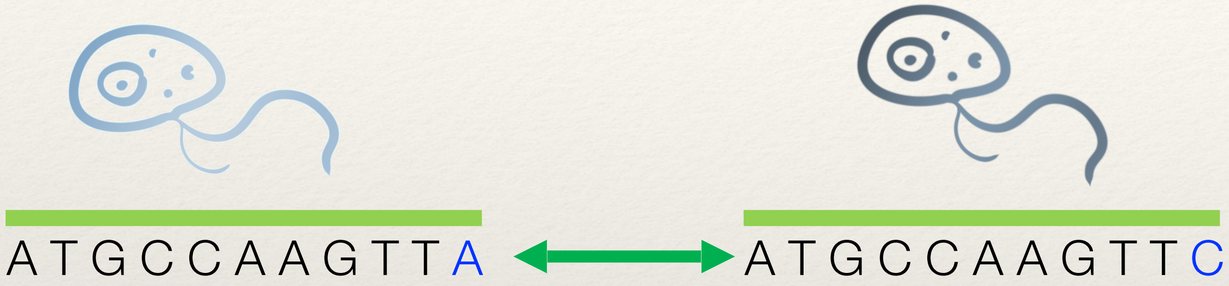
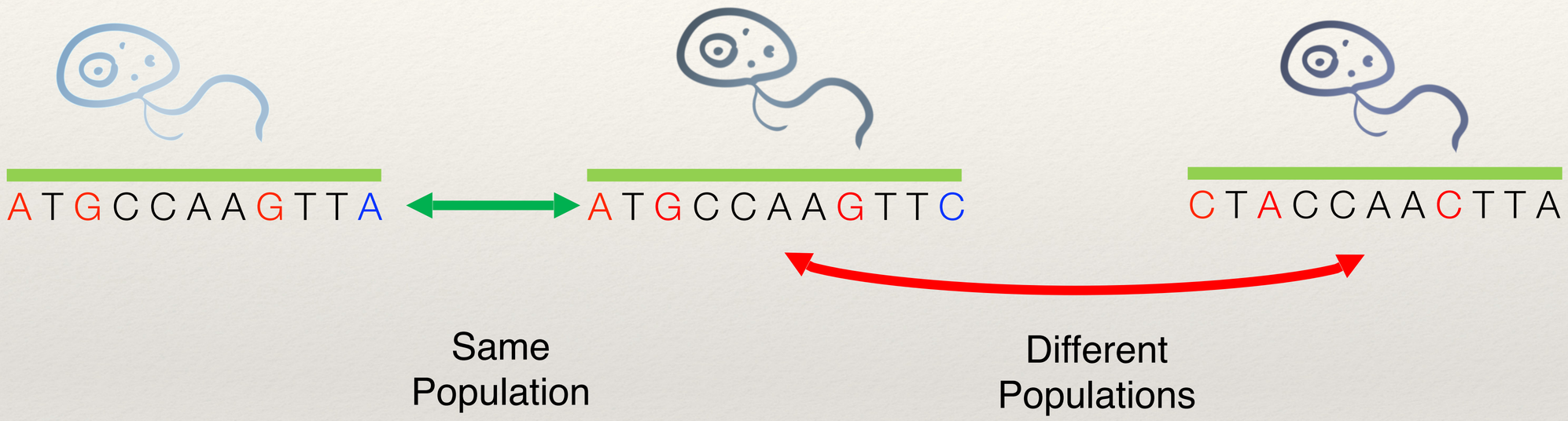


Same
Population

Quantifying the difference – The Fixation Index



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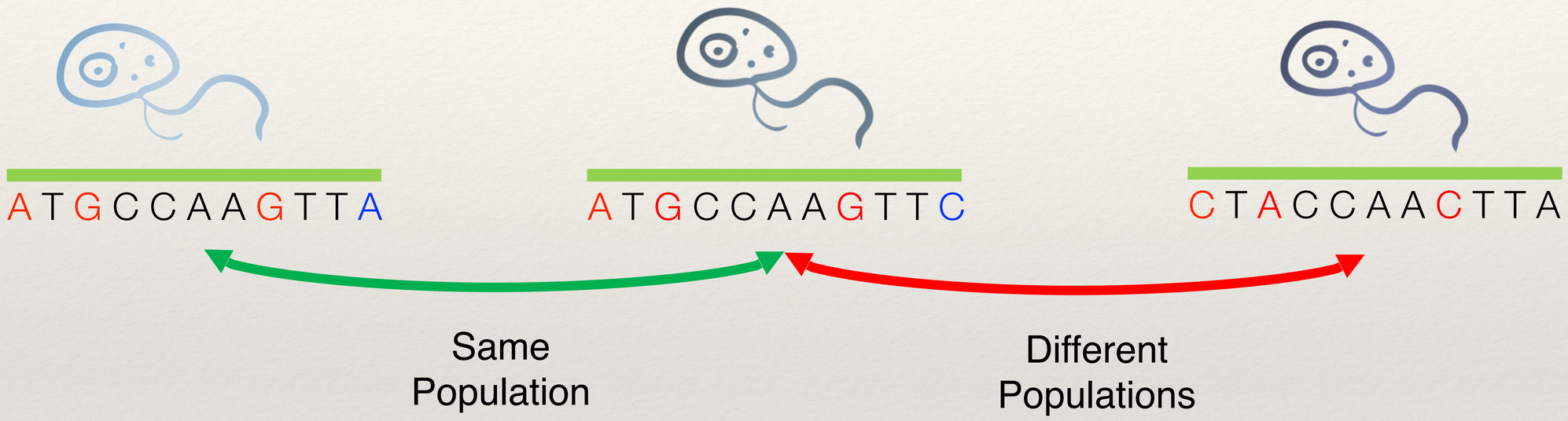
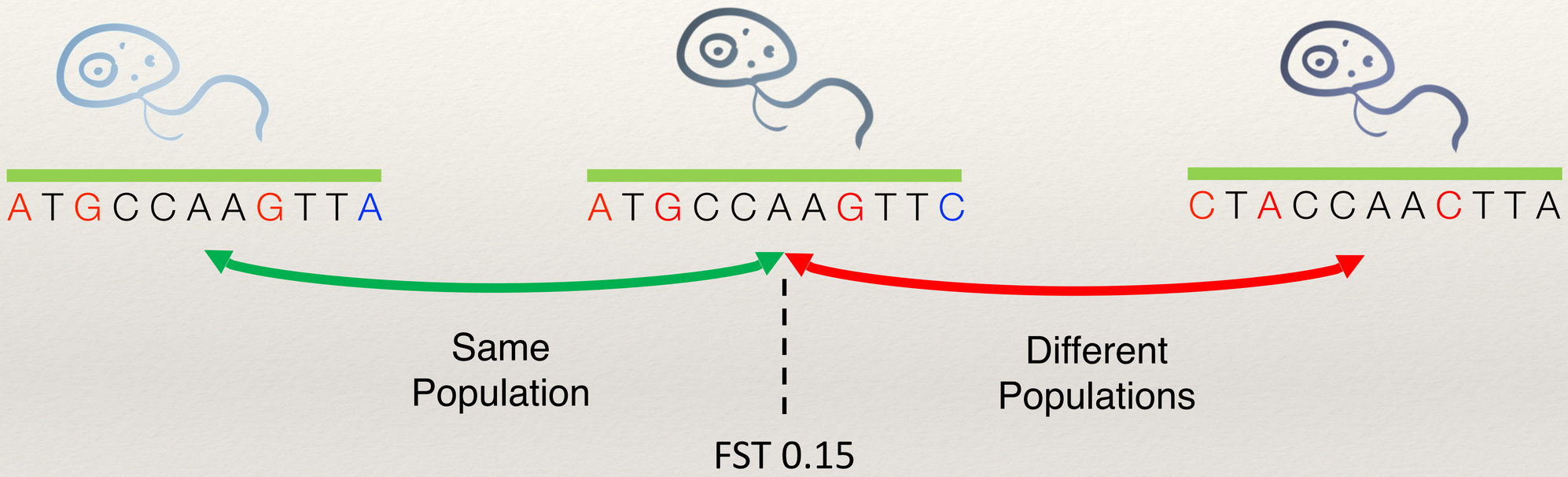


Fixation Index (FST) measures genomic differentiation of two populations based on the SNVs.

- FST = 0 between two samples → identical populations
- FST > 0.3 between two samples → very different fferent populations

Quantifying the difference – The Fixation Index



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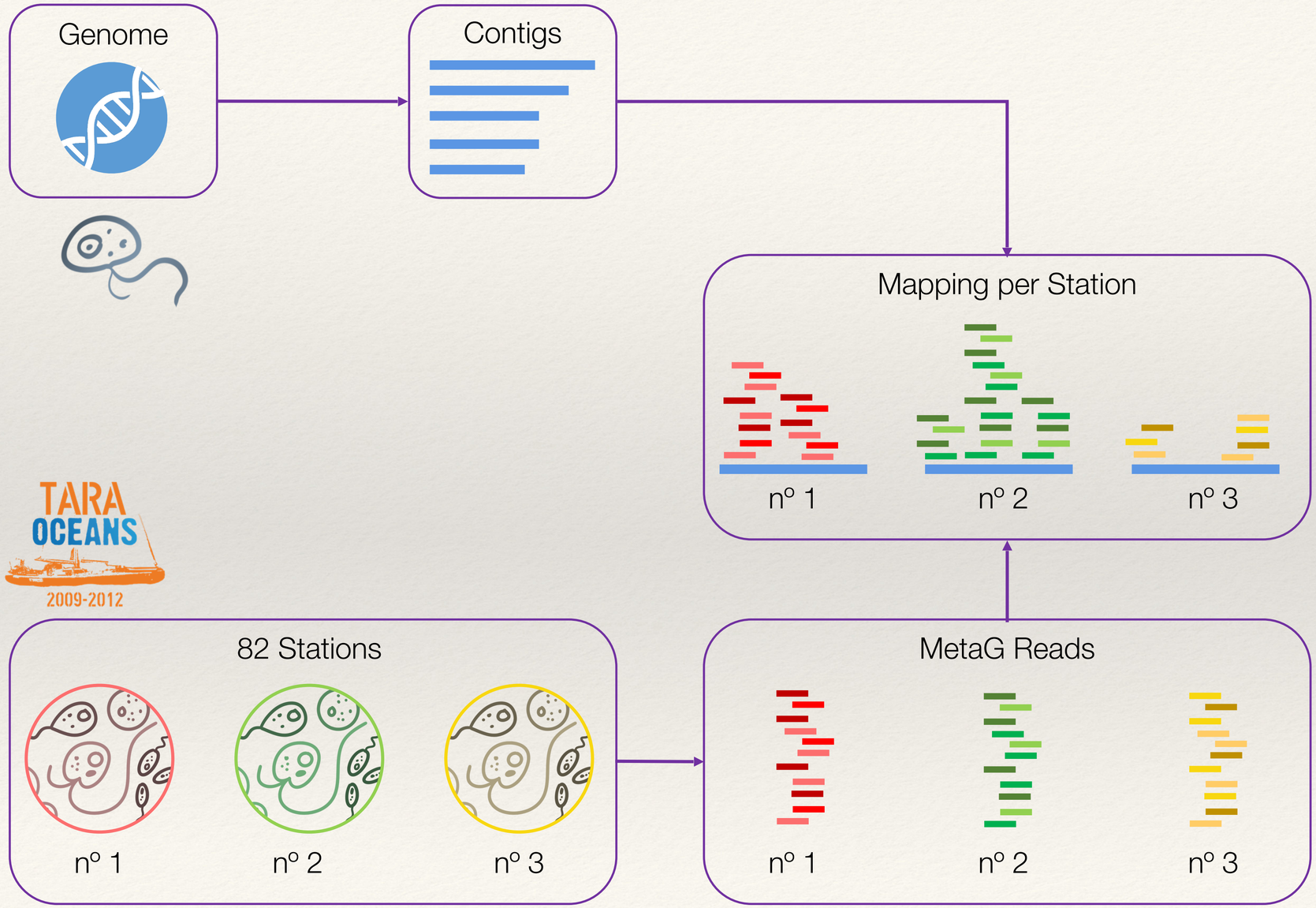
MAST-4 Population Genomics

Data context



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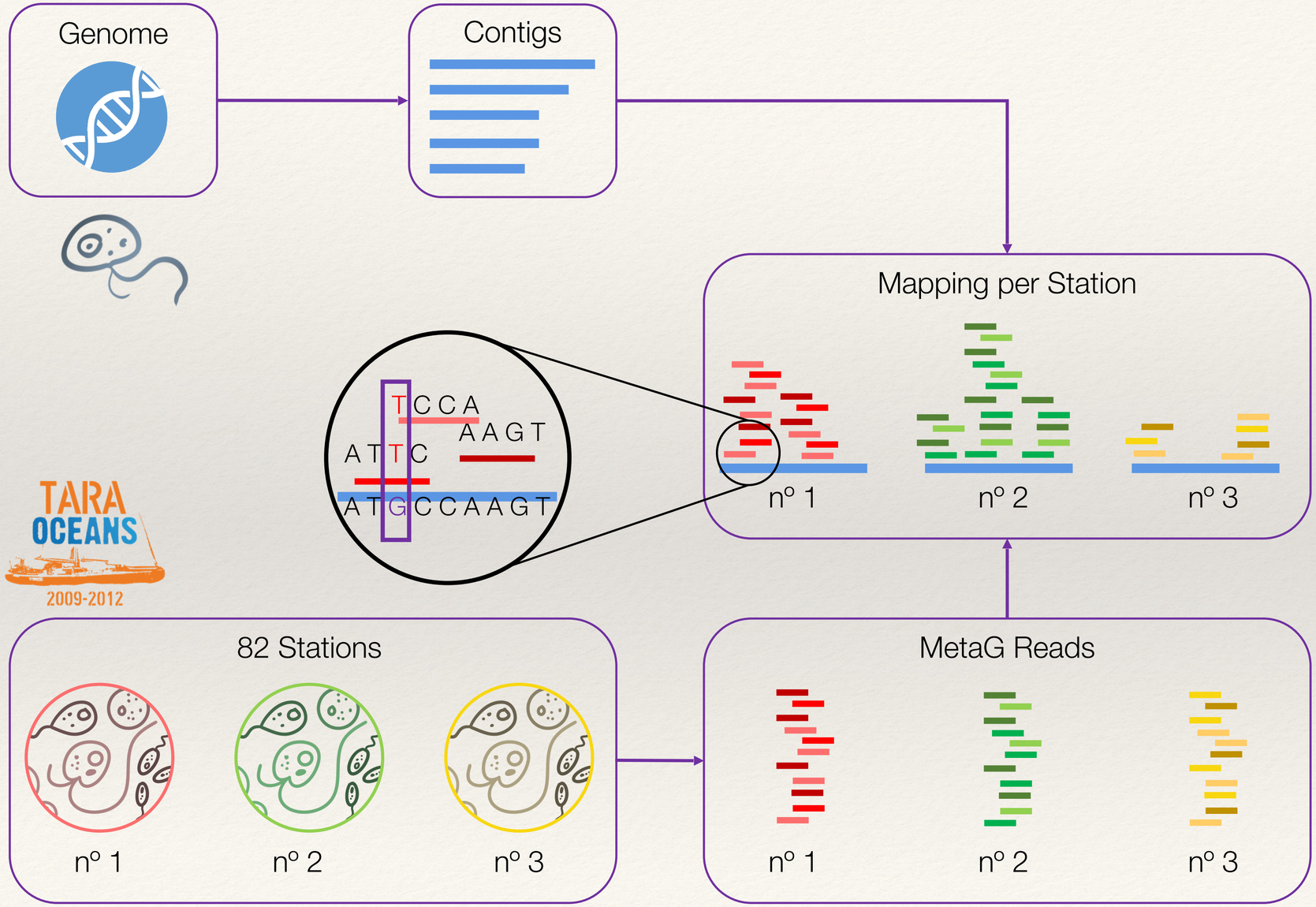

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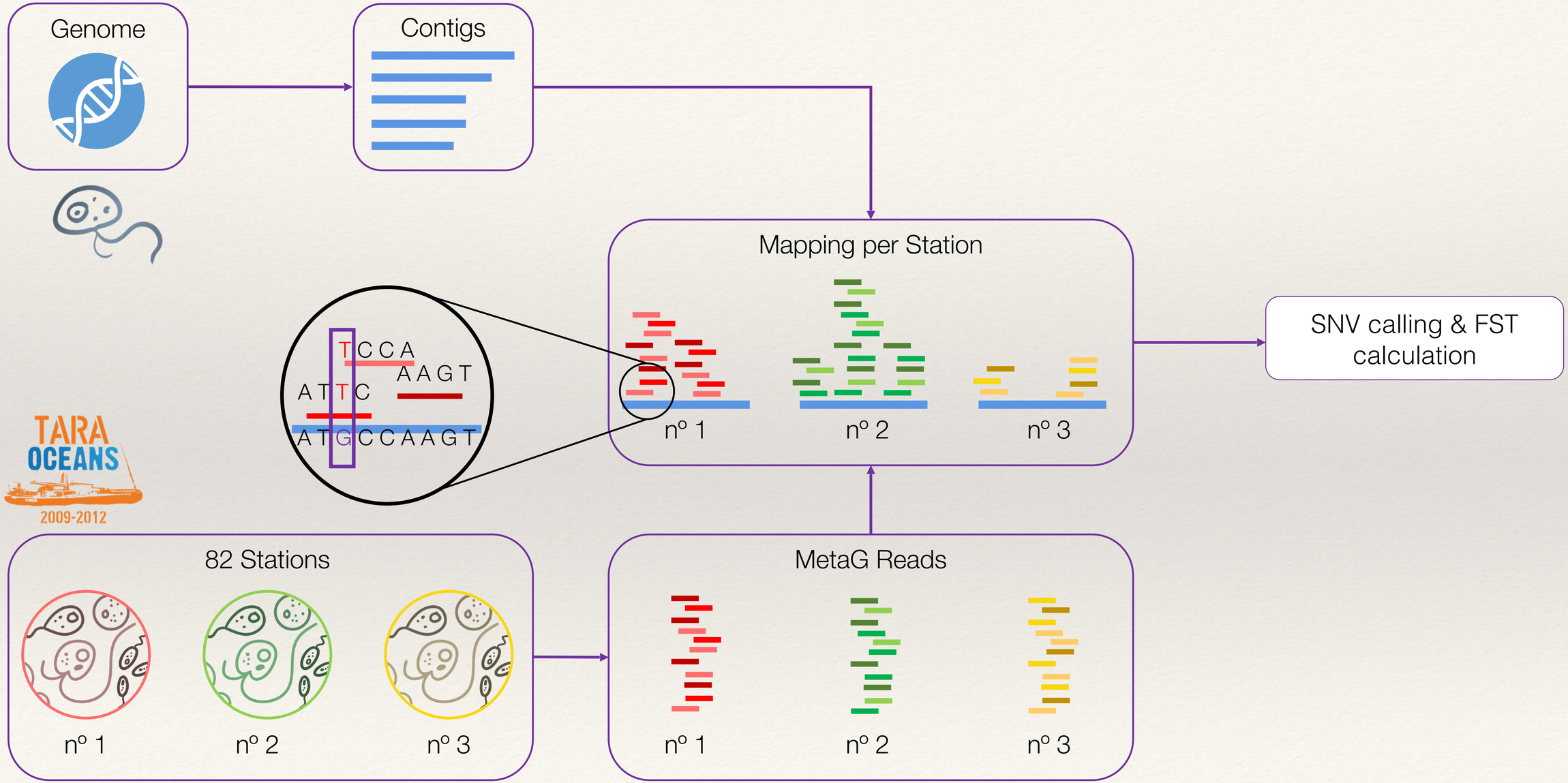
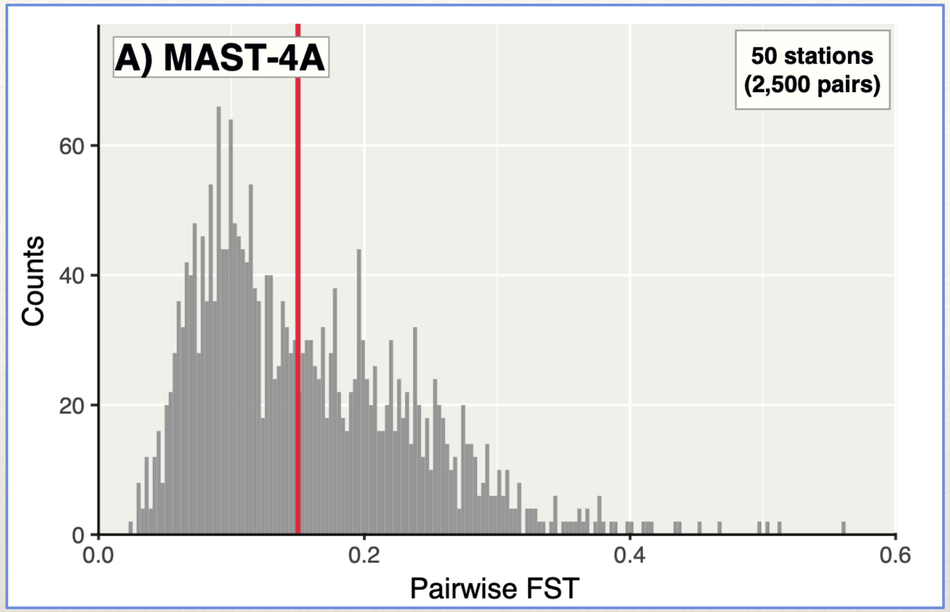


MAST-4 Population Genomics

Genomic Differentiation of MAST-4



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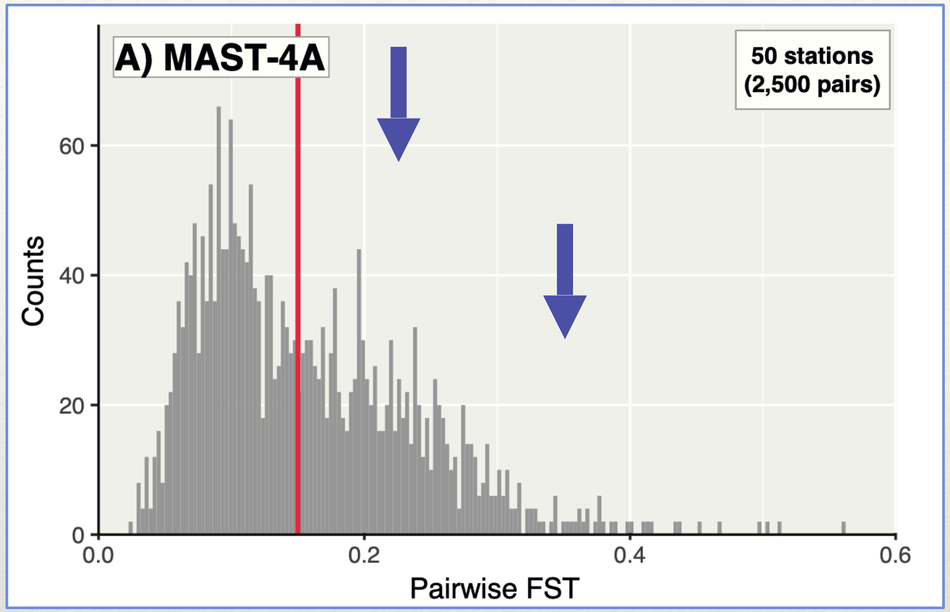

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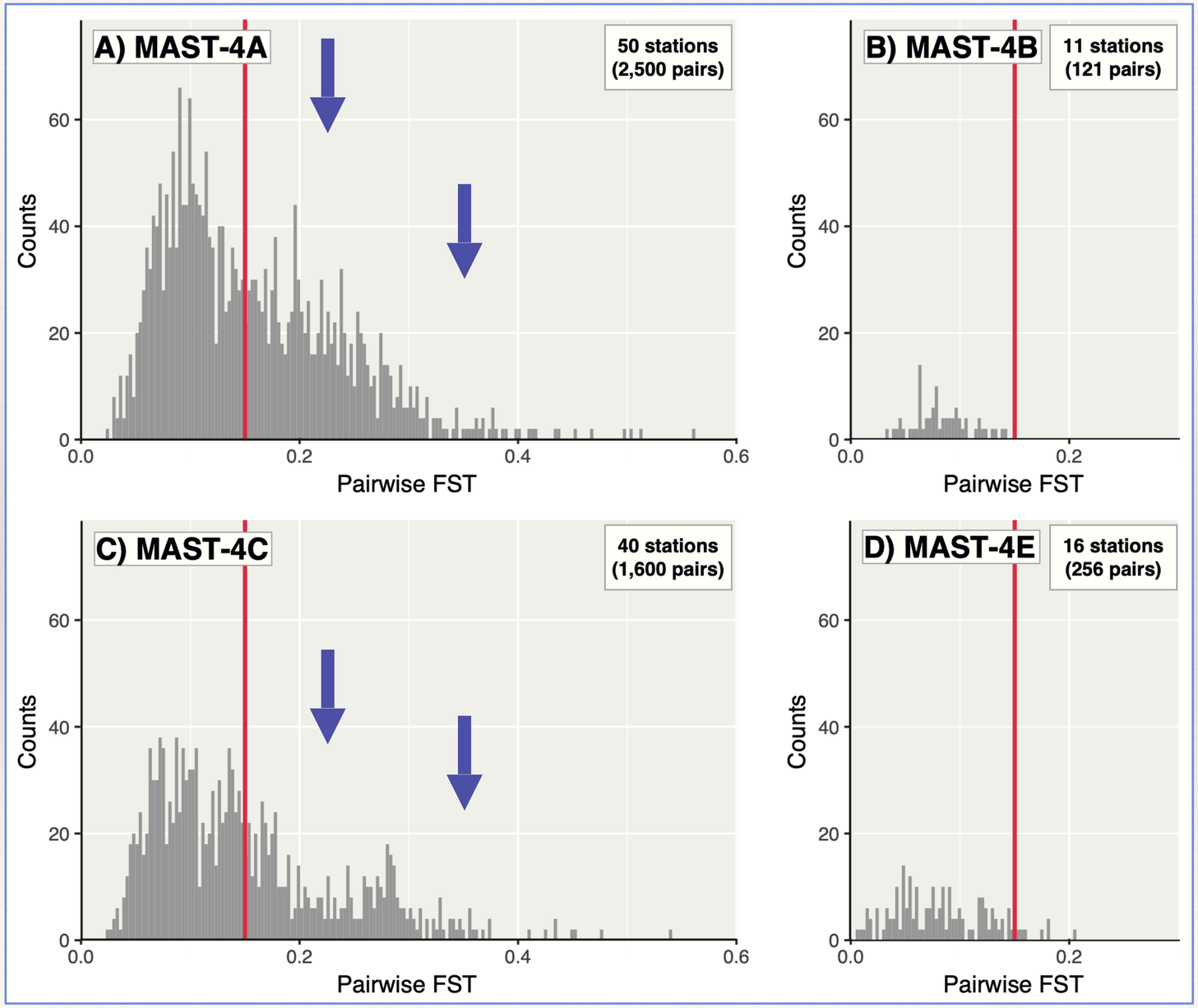

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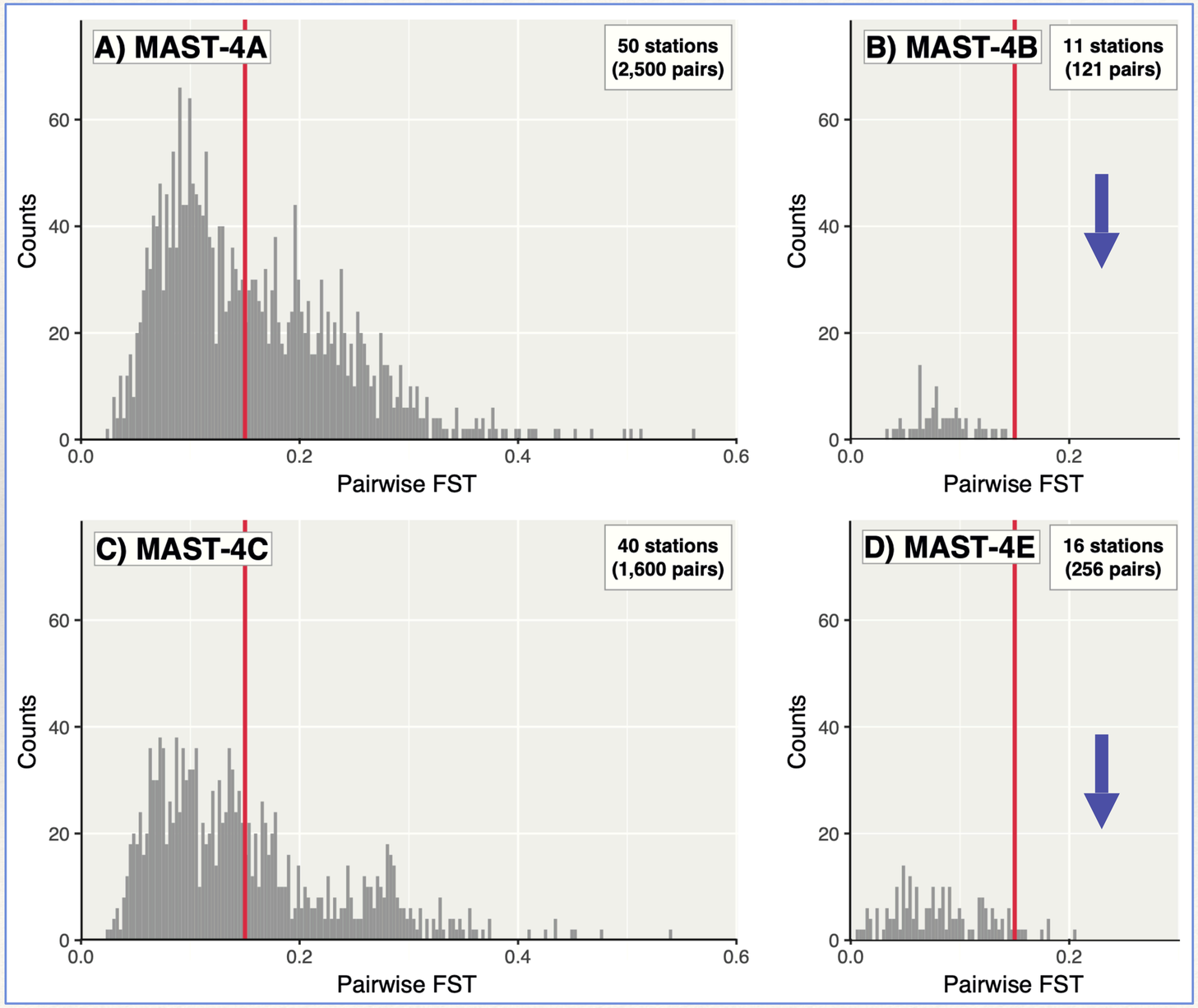
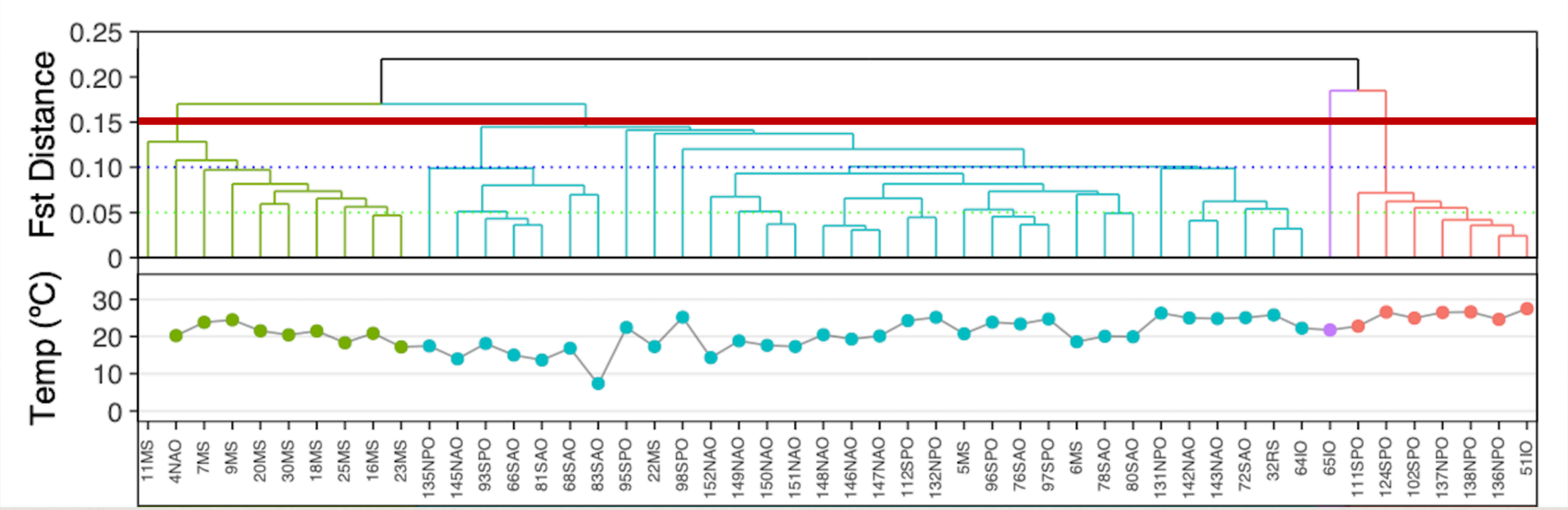


MAST-4 Population Genomics

Inferring Populations in MAST-4



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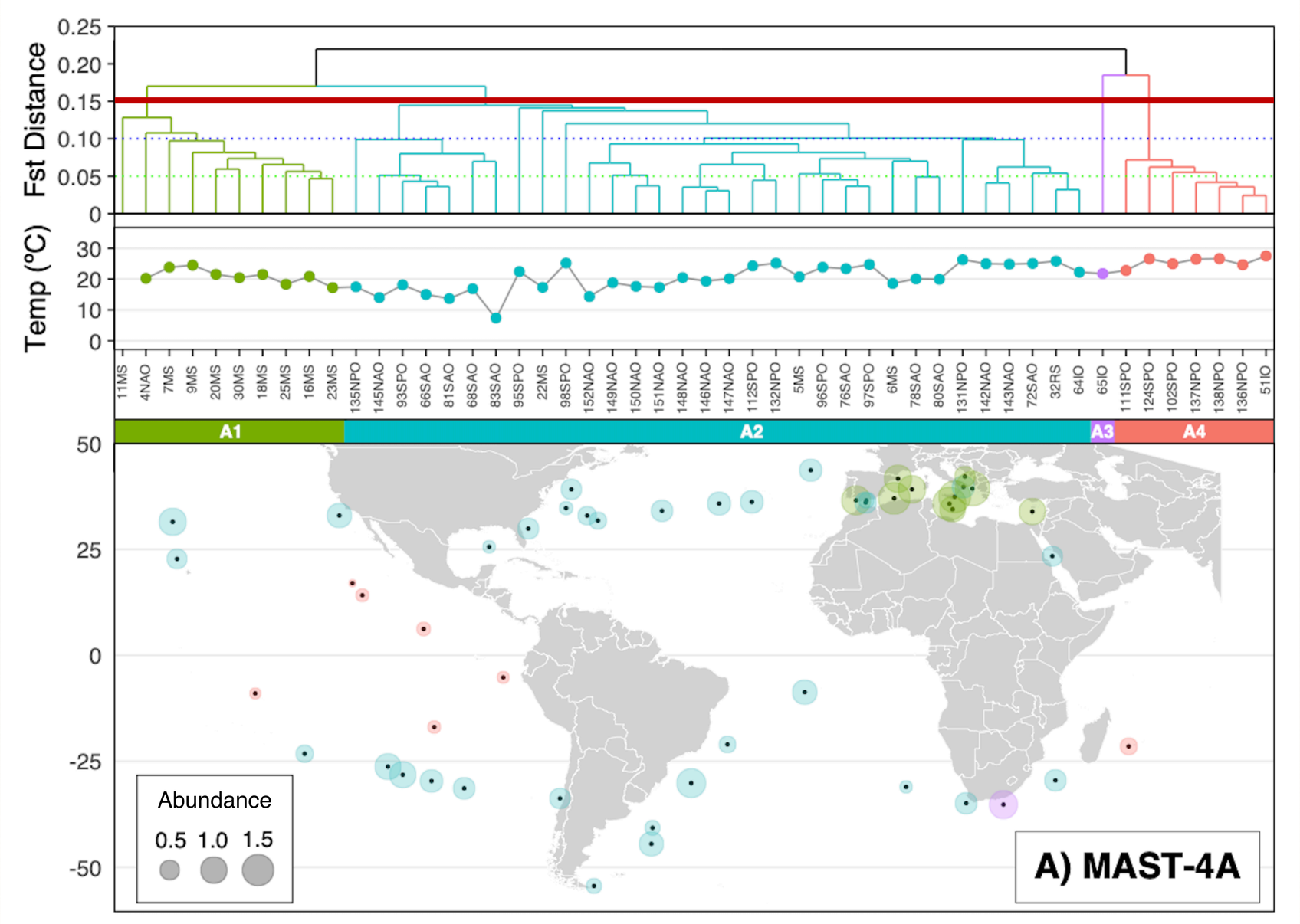

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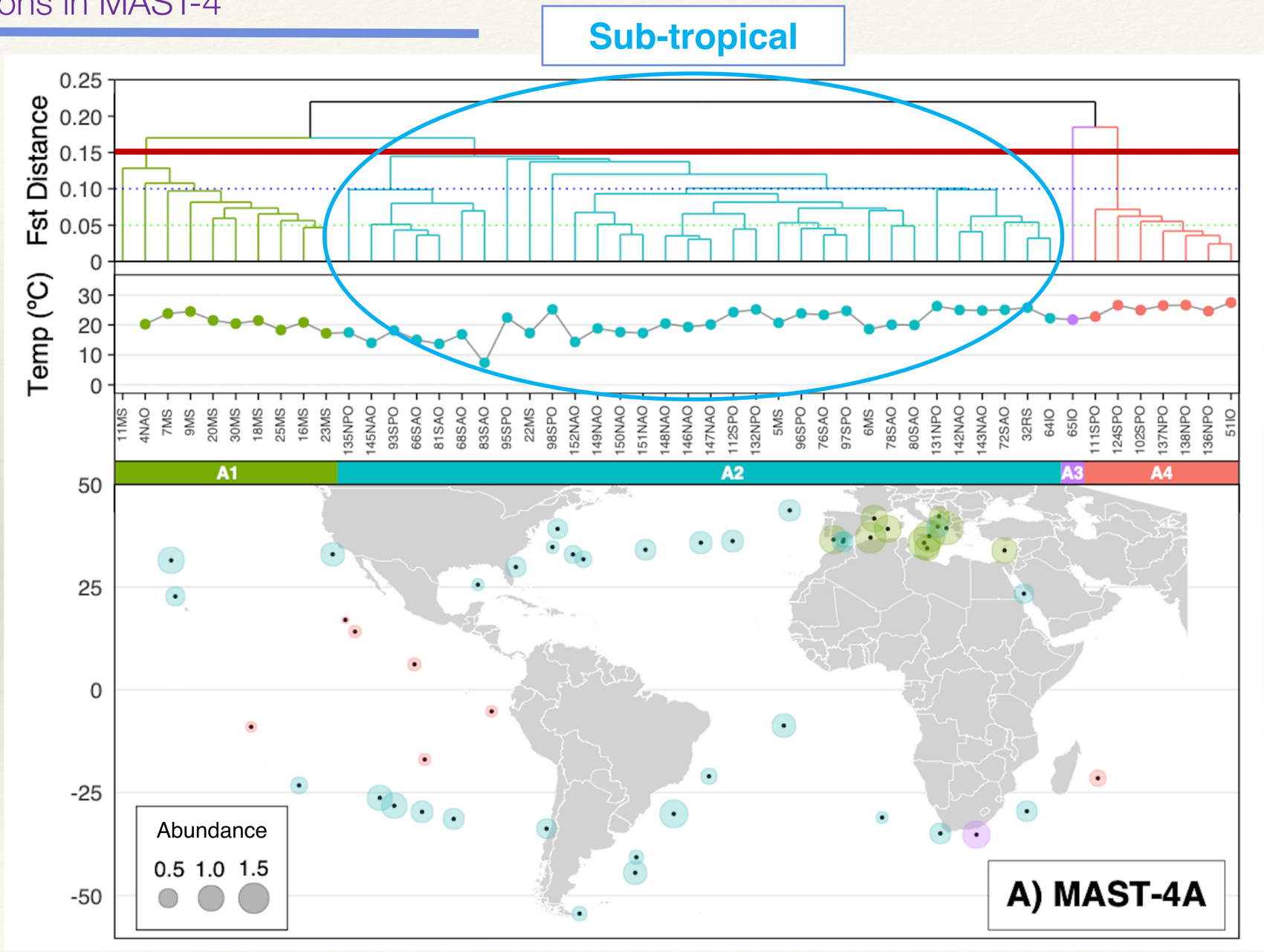

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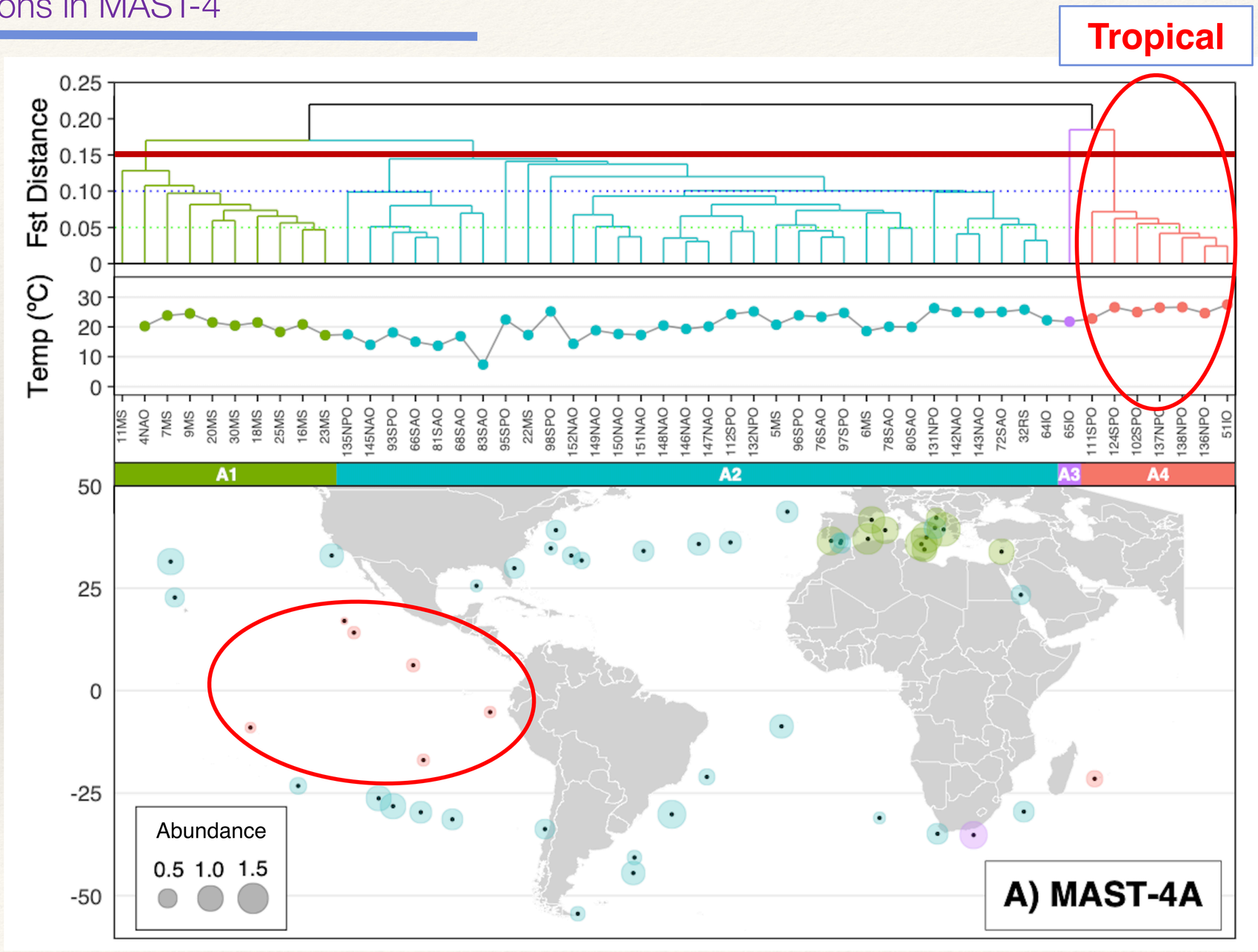

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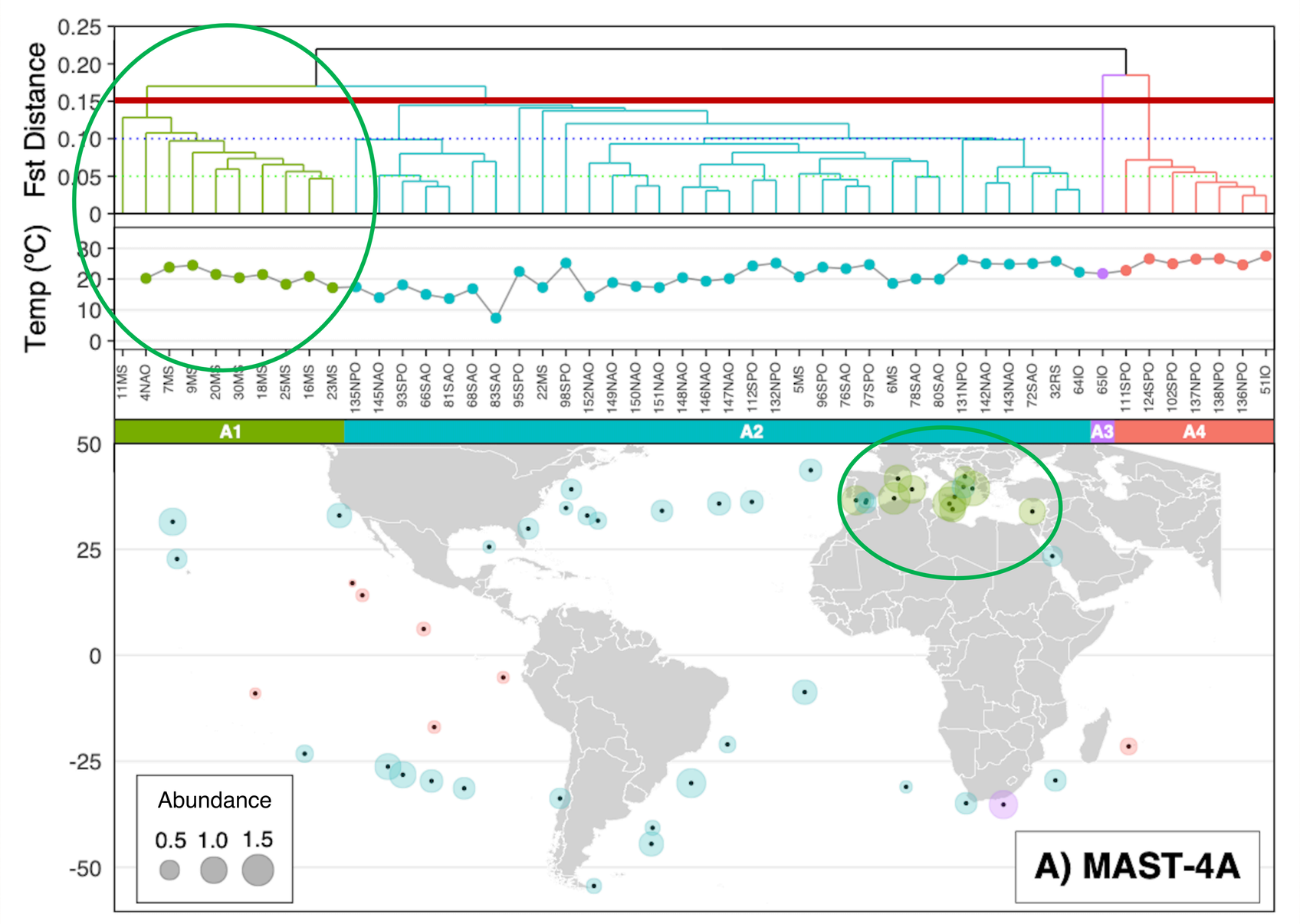

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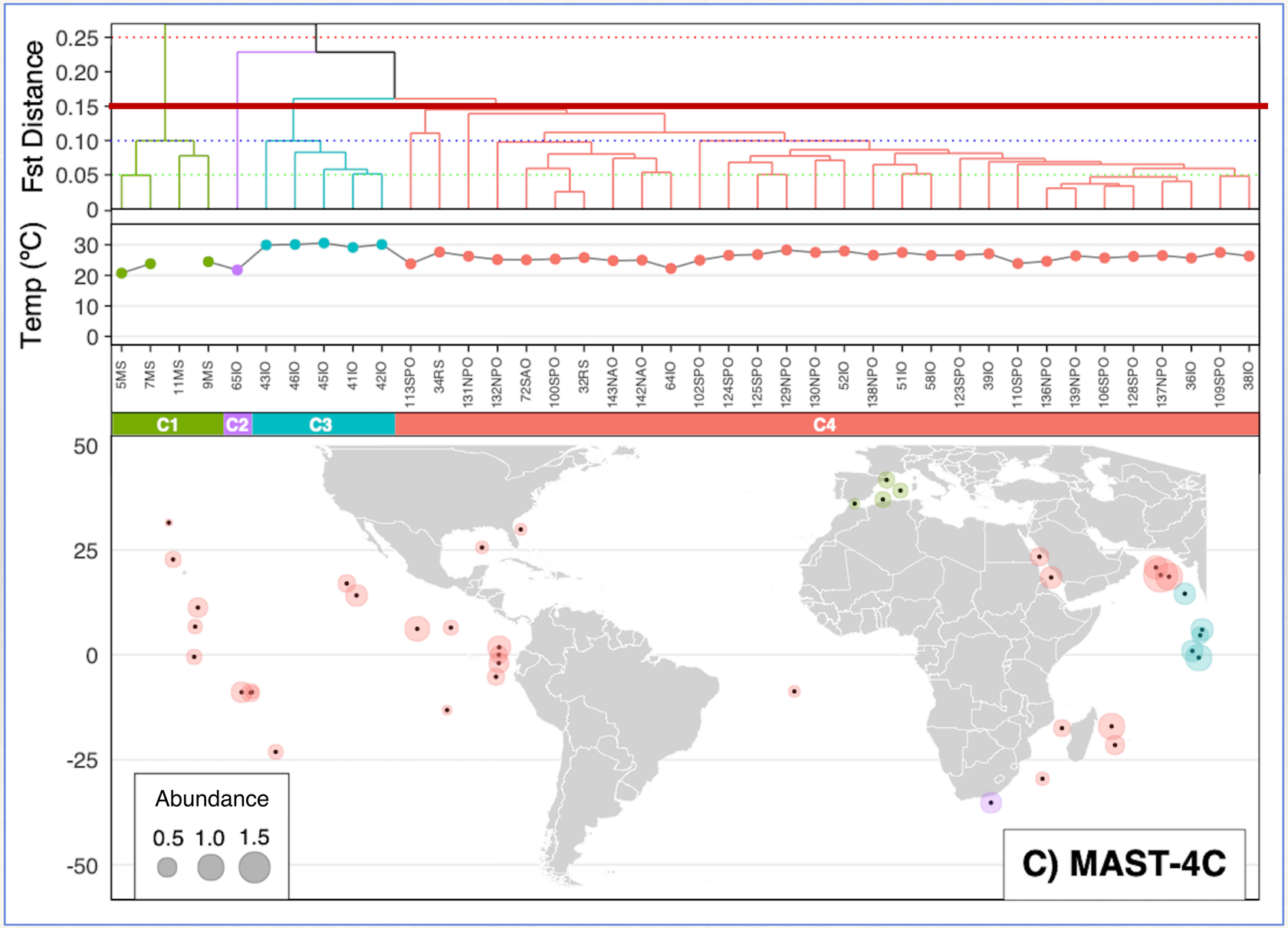

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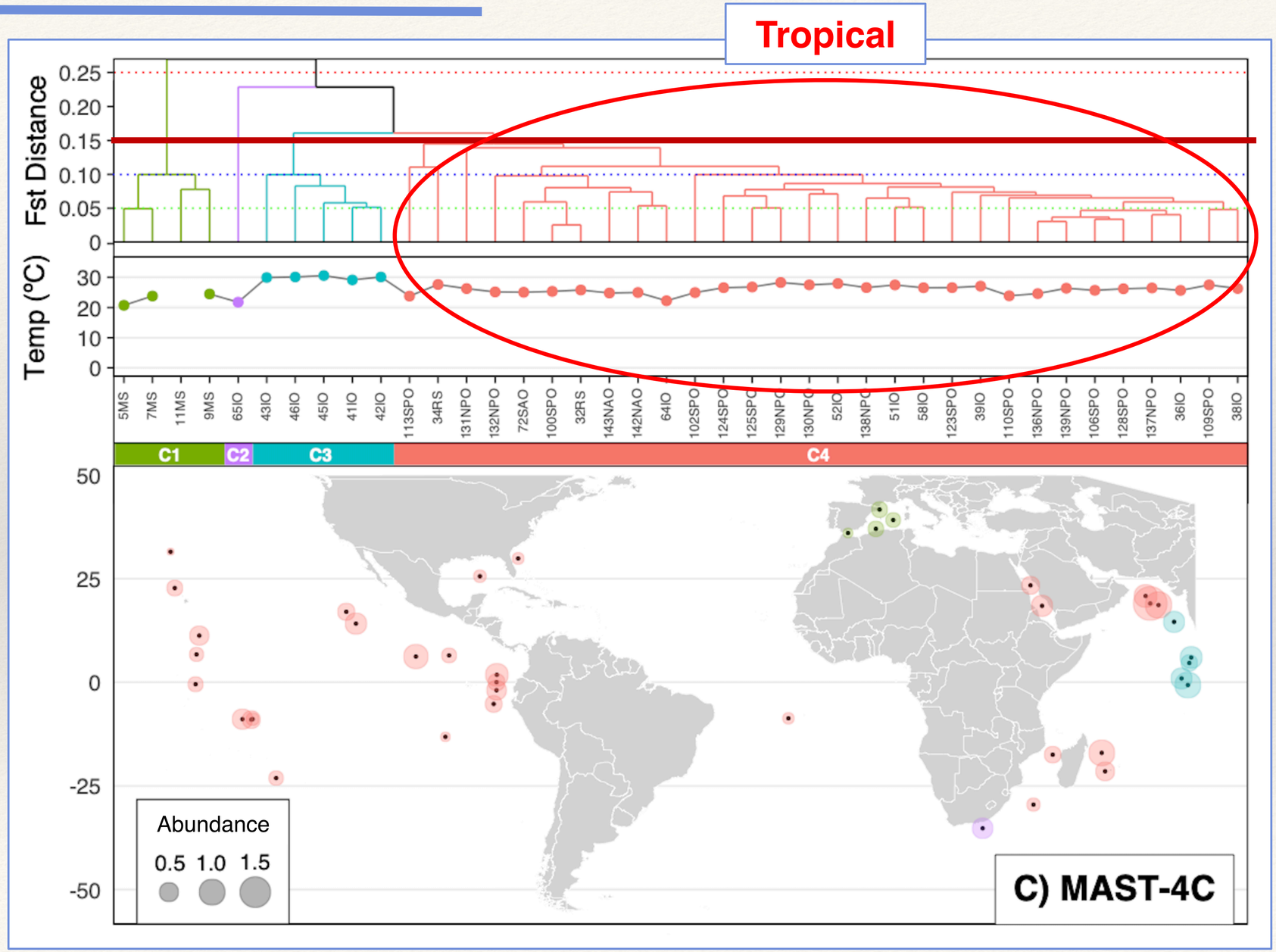

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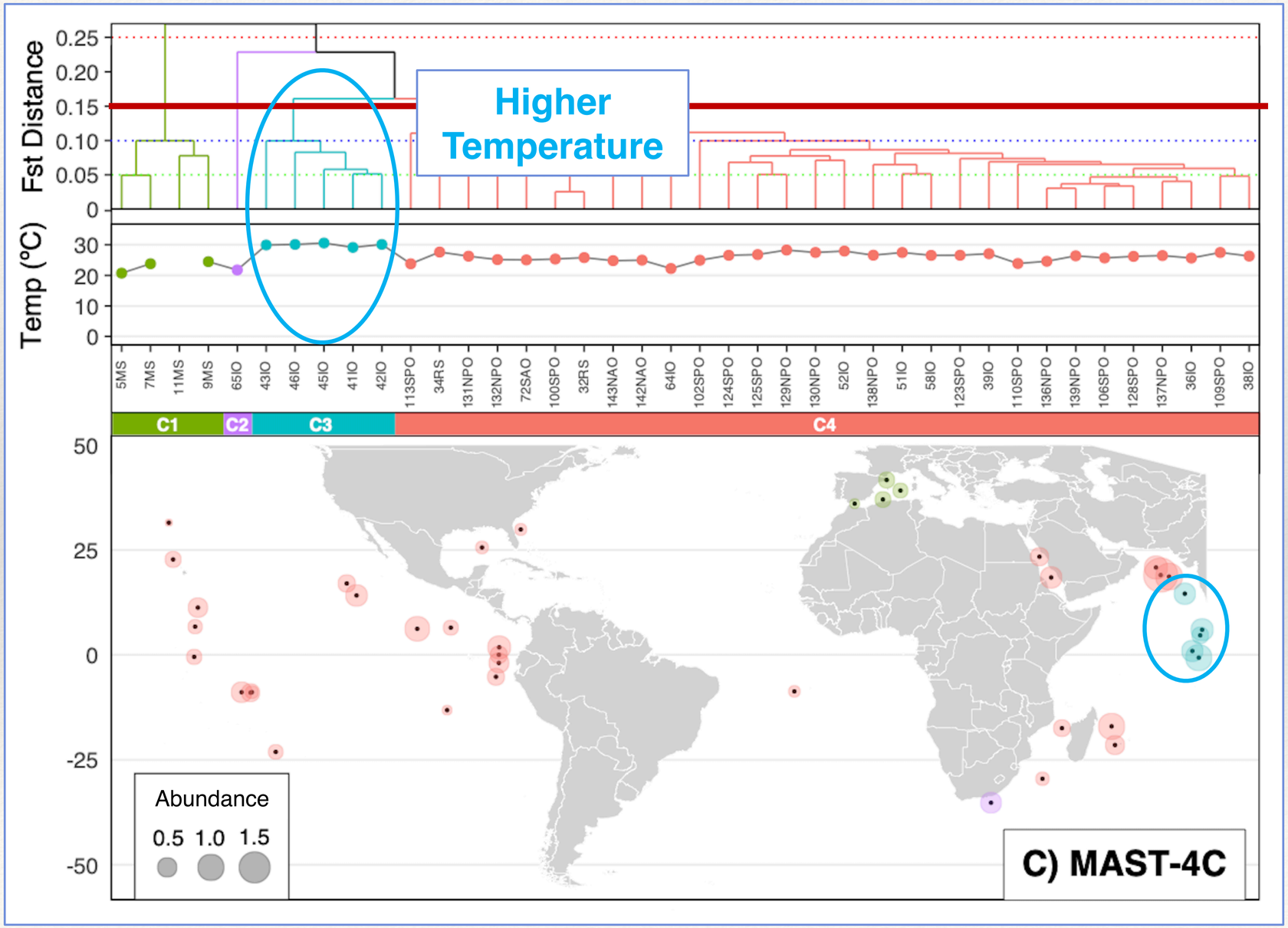
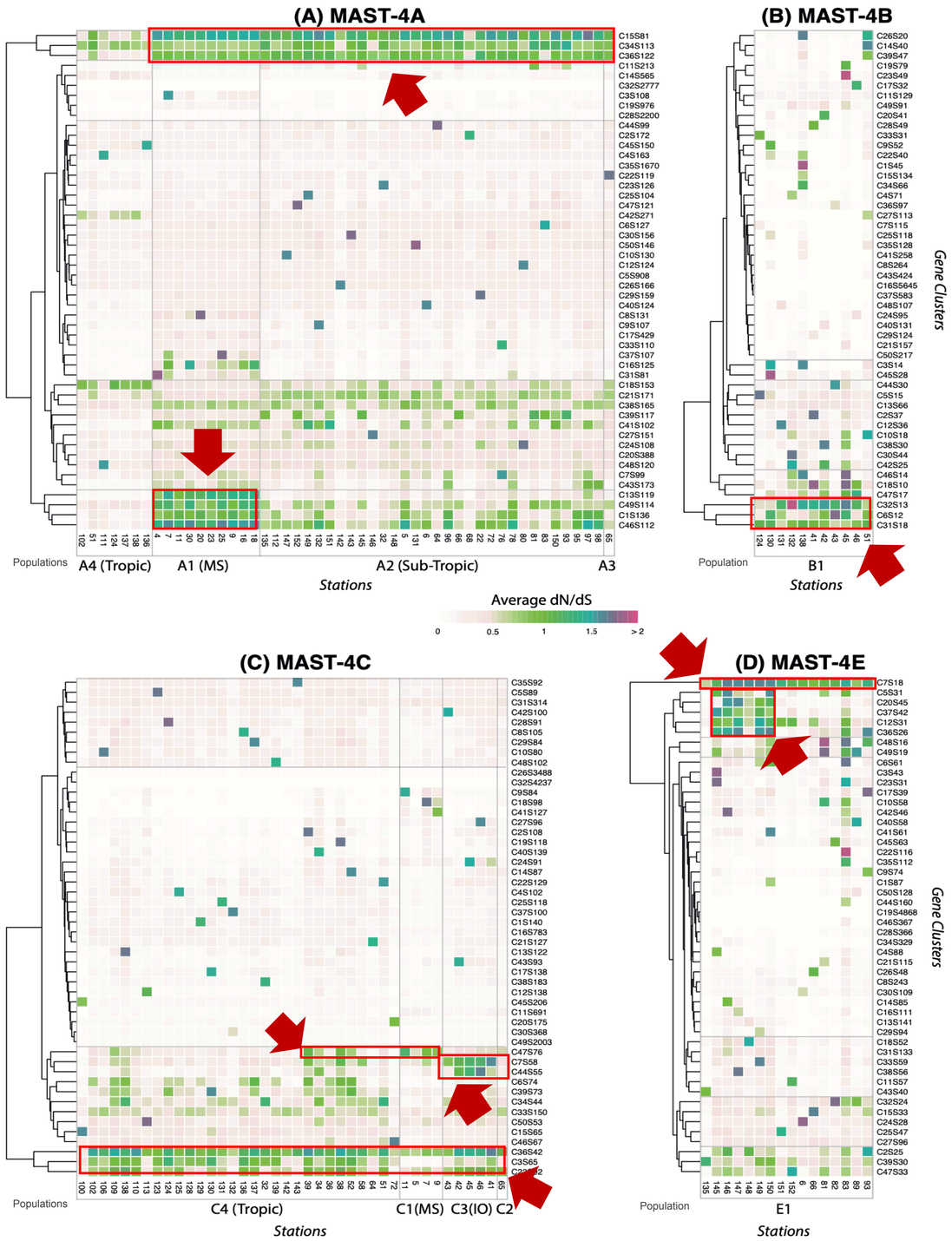


Checking for population adaptation

Gene: $$\frac{Non - Synonymous}{Synonymous} = \frac{pN}{pS}$$ >1 : Selection

1. Selection of genes with mean pN/pS > 1
2. Genes clustered based on pN/pS values across stations



Groups of positively selected clusters of genes detected in one or across populations for the different species

Specific clusters are enriched in metabolic or structural functions

MAST-4 Population Genomics

MAIN QUESTIONS

1. What amount of intraspecies genomic divergence do MAST-4 species show in the global ocean?
   - High genomic divergence in MAST-4A and C

MAST-4 Population Genomics

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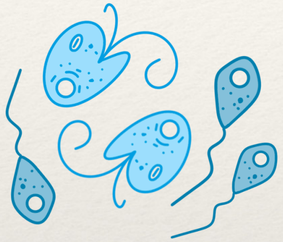
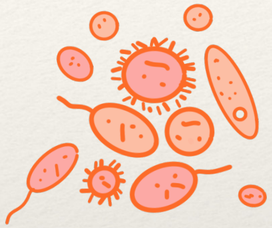
3. What environmental factors promote such a structure?
   - Temperature and salinity mainly
4. Can we detect genes featuring adaptation to different environmental conditions?
   - Yes



Heterotrophic flagellates



Bacteria & Archaea

Population structure of prokaryotes over a decade and across the global ocean

Population genomics of marine prokaryotes

MAIN QUESTIONS

1. How much population-level genomic divergence is present in marine prokaryotic species over large spatiotemporal scales?

Population genomics of marine prokaryotes

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Population genomics of marine prokaryotes

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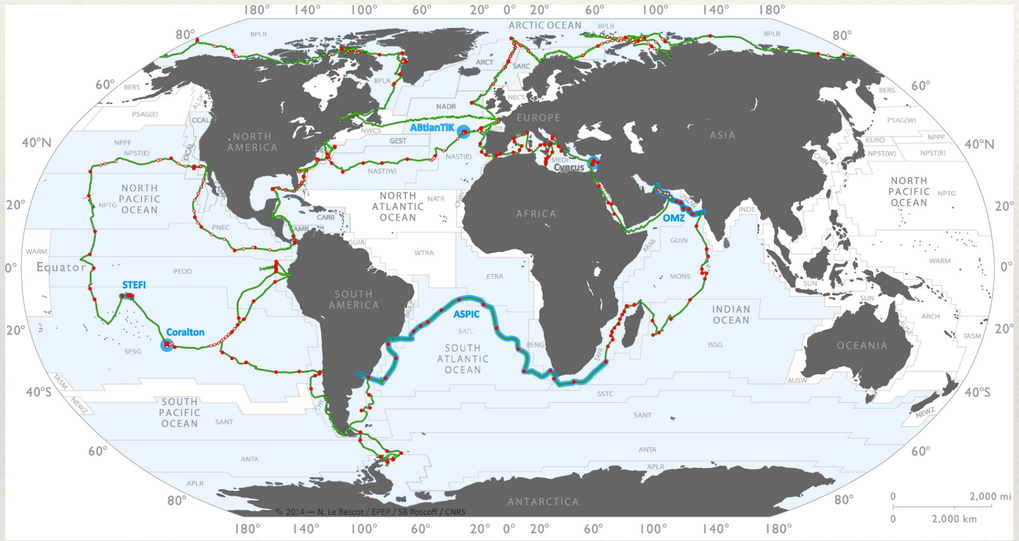
2. Is the genomic divergence structured into populations?
3. What environmental factors may drive population structure?

Population genomics of marine prokaryotes

GLOBAL OCEAN

TARA OCEANS

2009-2012



- Samples from tropical, subtropical, subpolar and polar areas.
- Metagenomes (0.22 – 3 µm) from 82 STATIONS

Population genomics of marine prokaryotes

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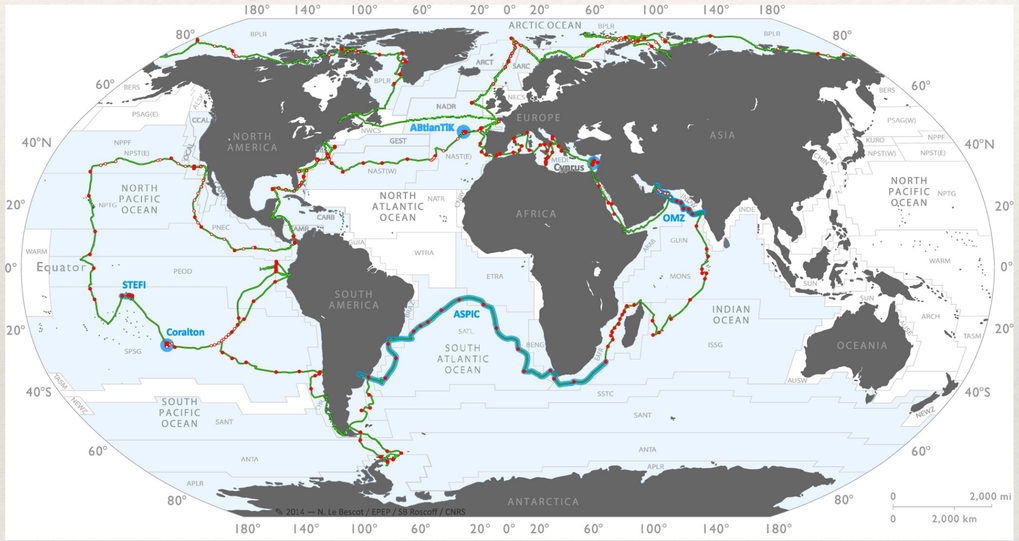

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TIME SERIES

BBMO & SOLA

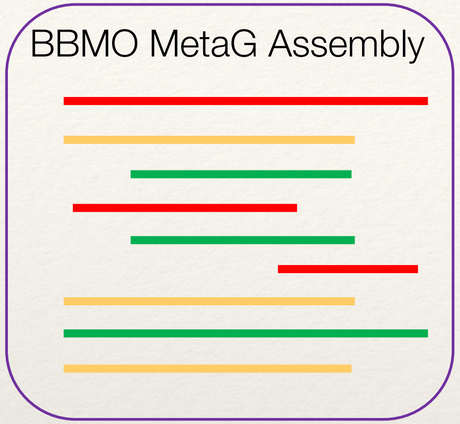
- Monthly metagenomes from 12 and 7 years (140 and 89 samples)
- Jan 2009 – Dec 2020

WINTER & SPRING
COLDER WATERS

SUMMER & FALL
WARMER WATERS

Population genomics of marine prokaryotes

Methods & Sample summary



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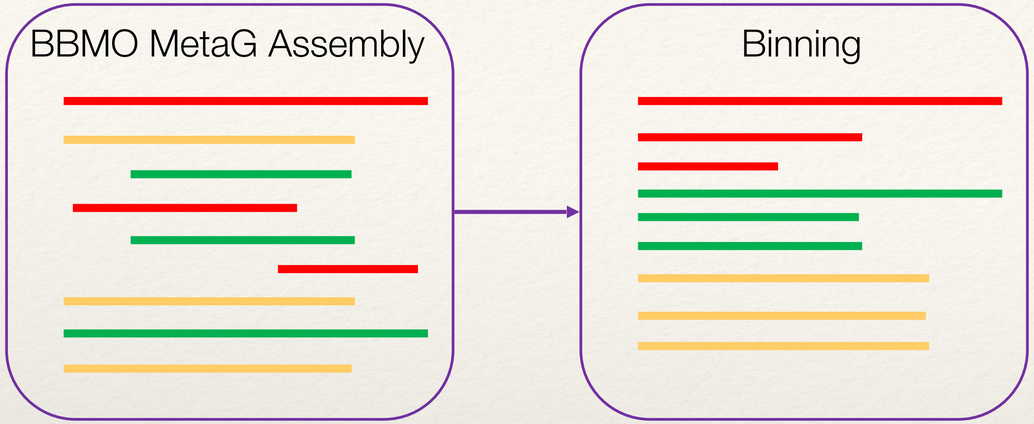

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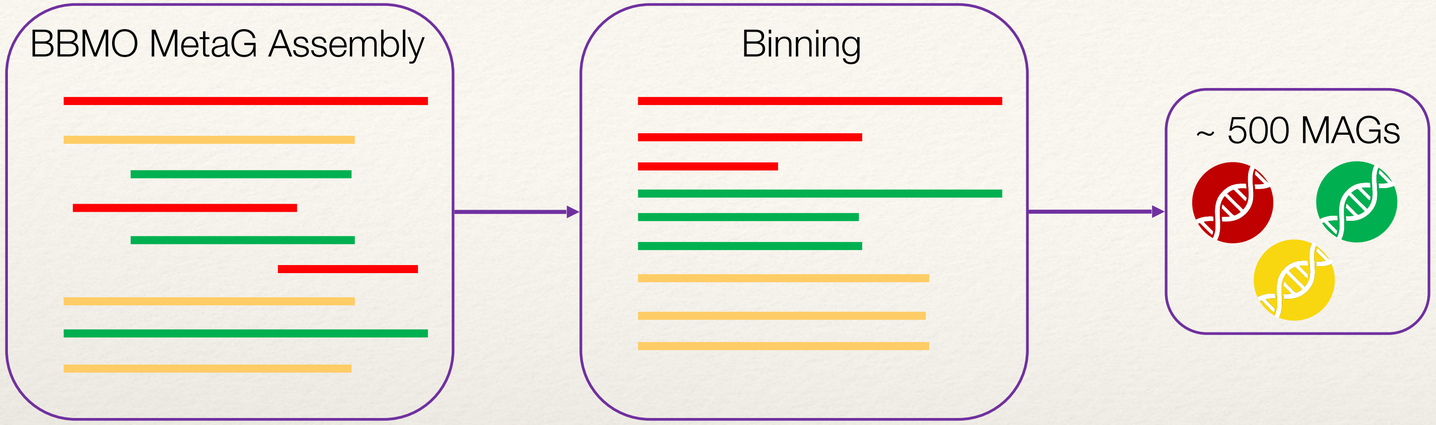

selected MAGs:

- SAR11 (9)
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- SAR116 (47)
- SAR86 (44)
- Balneolales (5)
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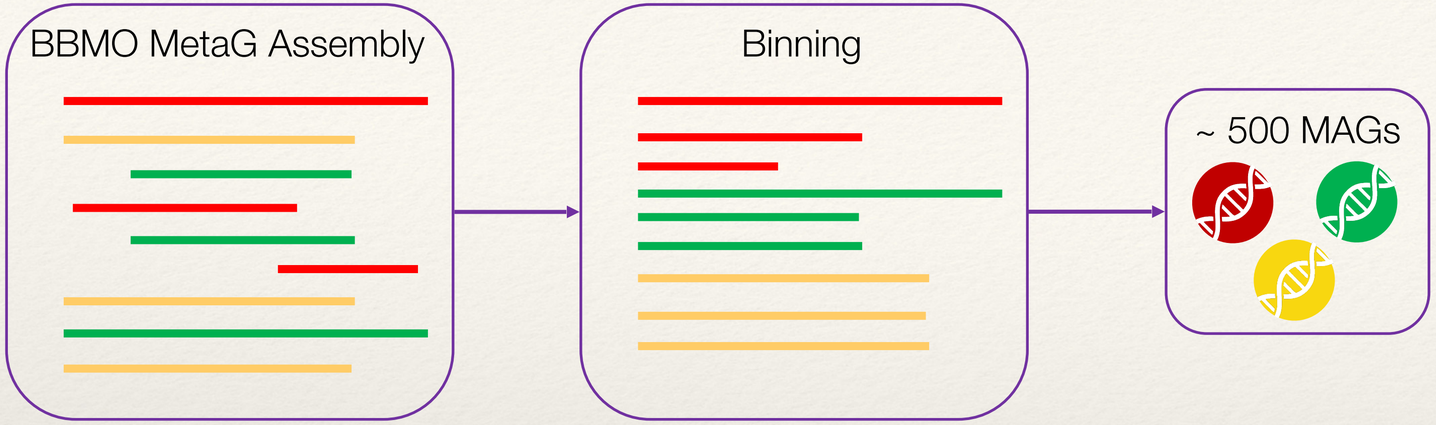

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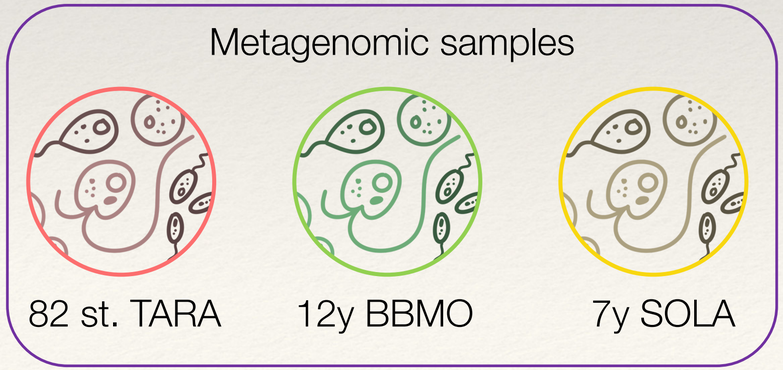

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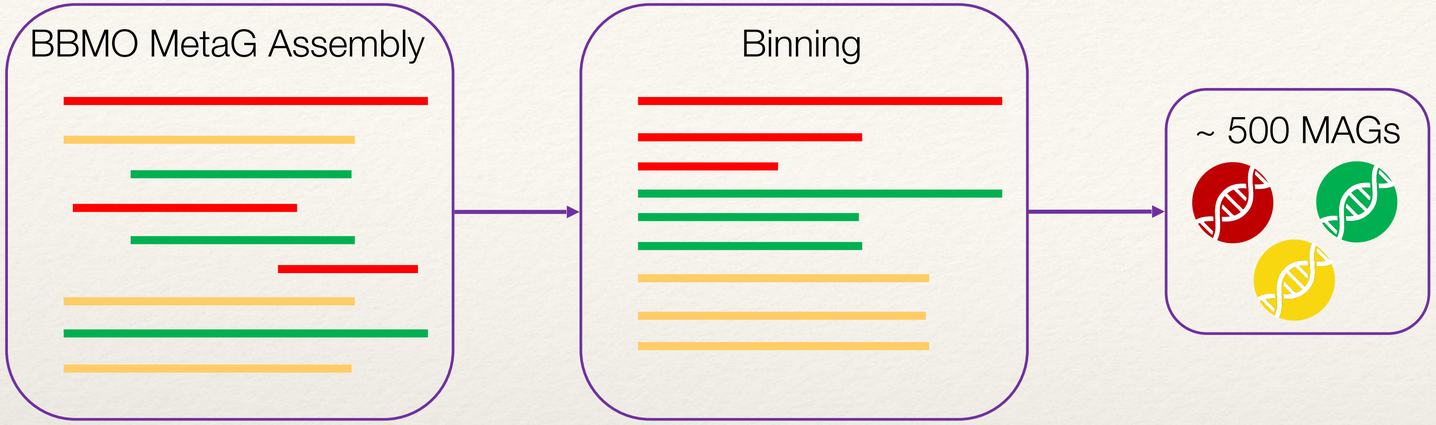

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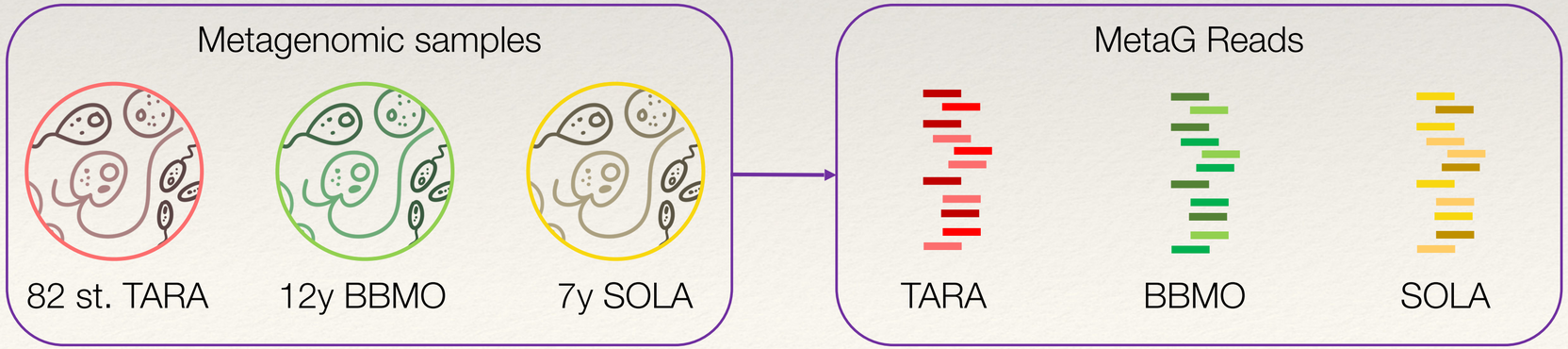

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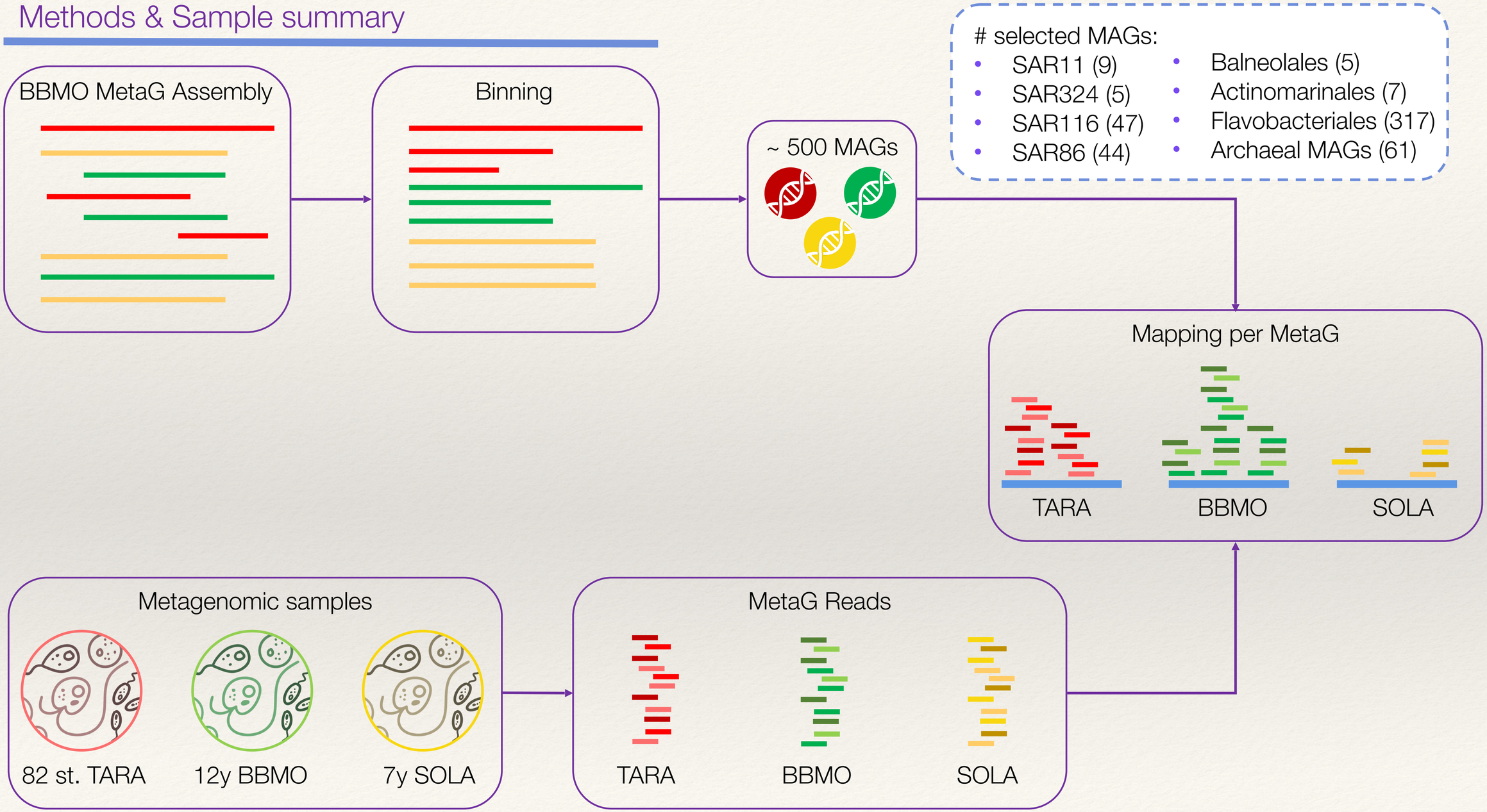

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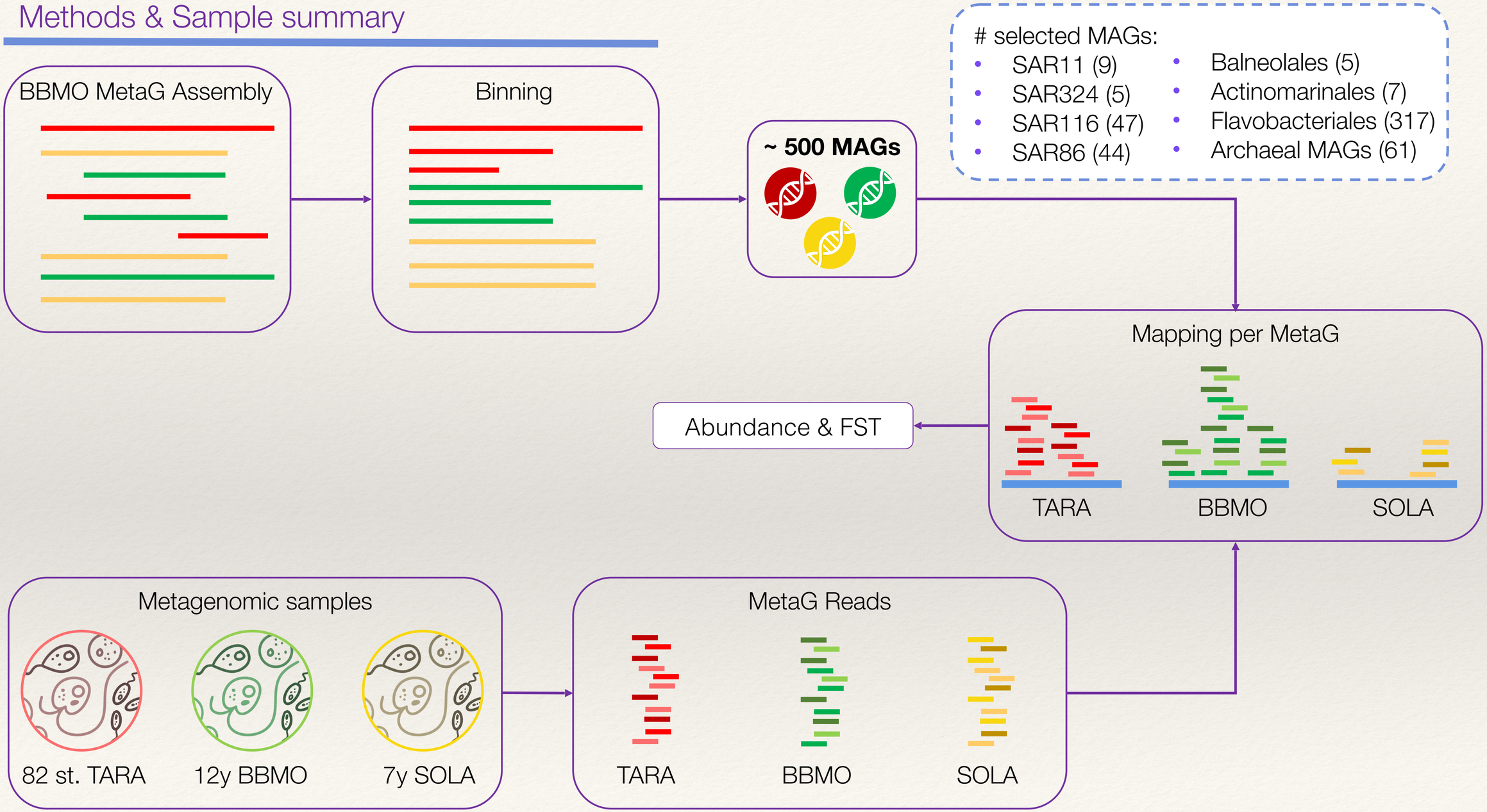
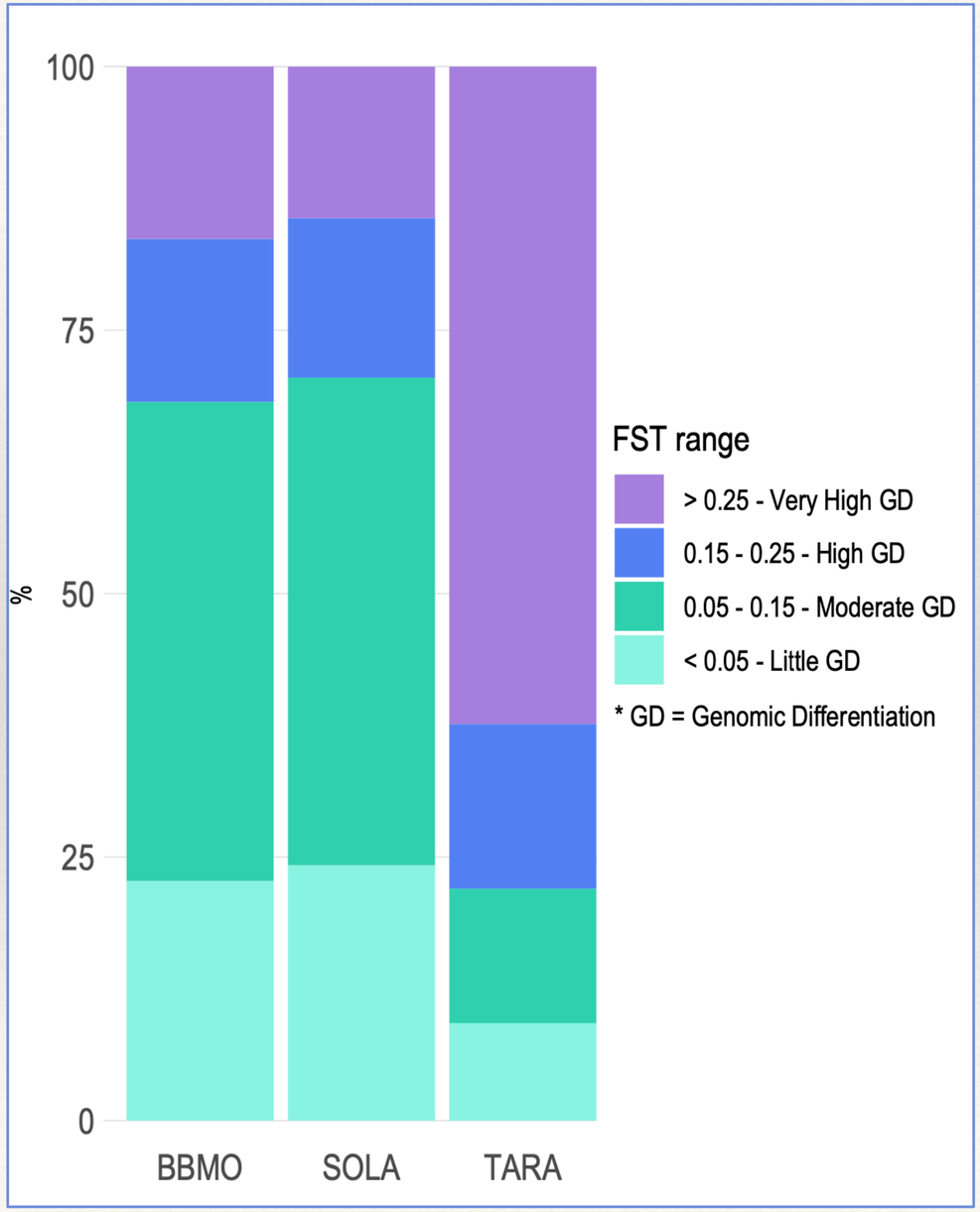


Population genomics of marine prokaryotes

Population-level genomic differentiation at different scales



Proportion of FST of each category in BBMO, SOLA, and TARA for the **495 MAGs**

- Little genetic difference: Fst < 0.05
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Population genomics of marine prokaryotes

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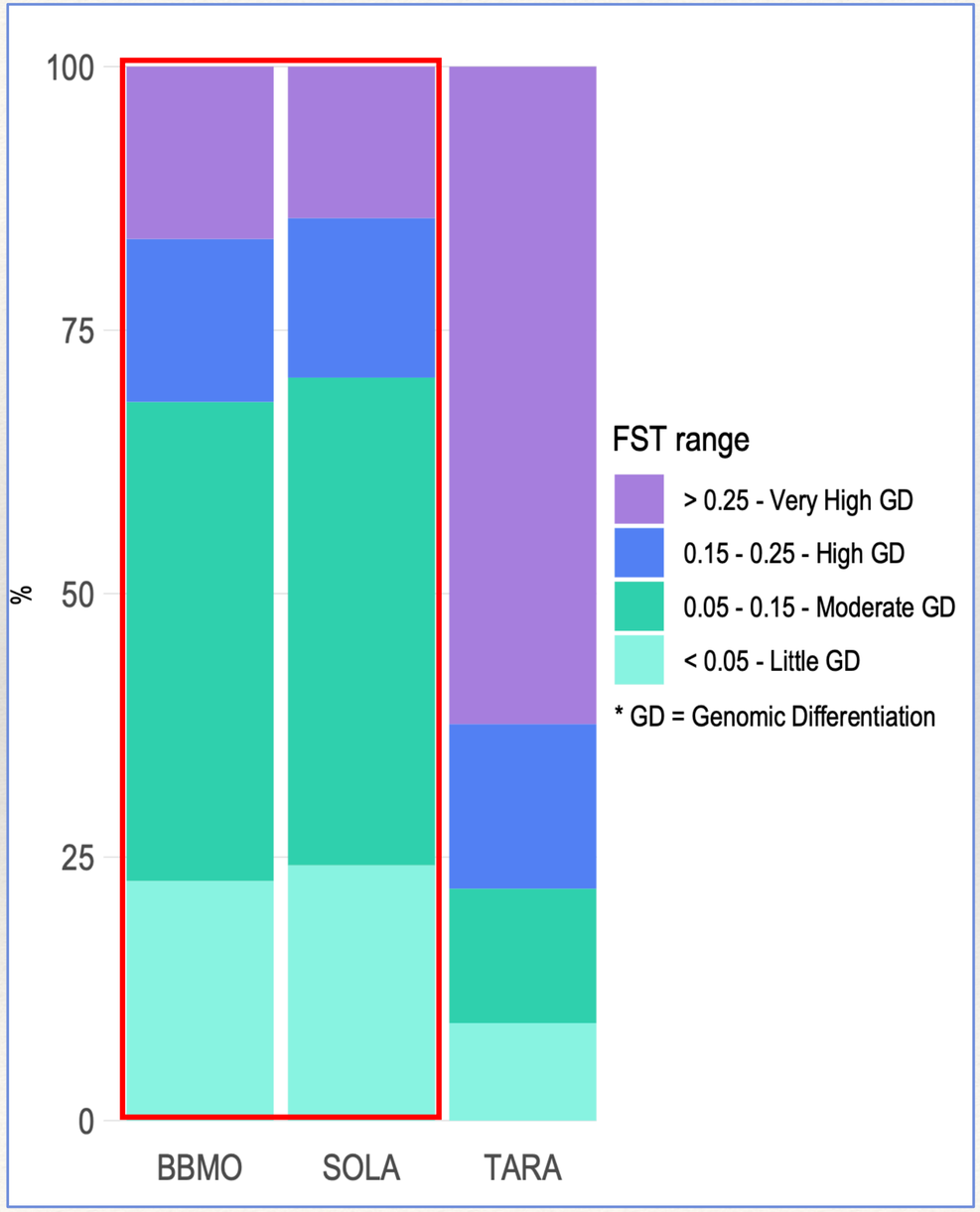

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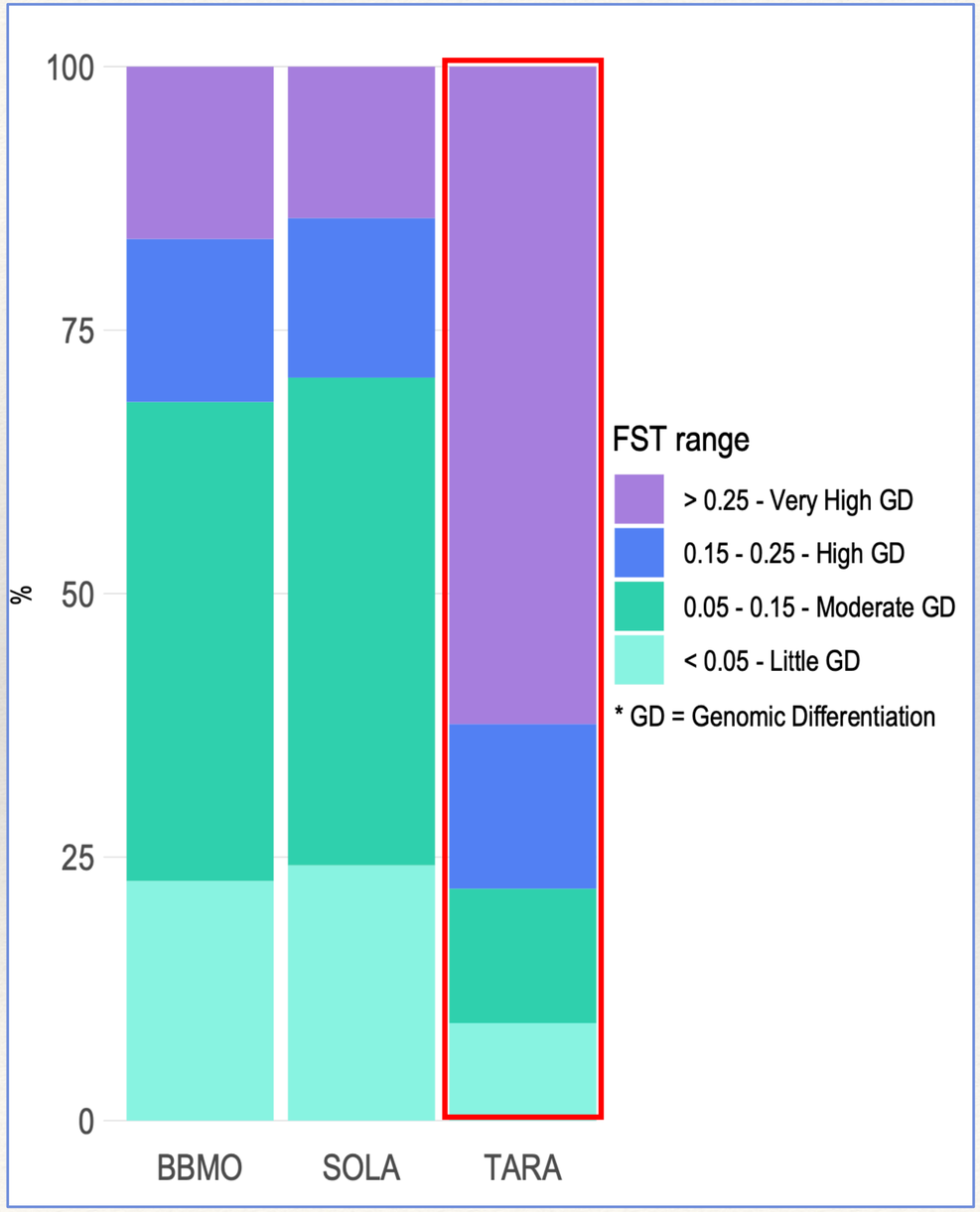

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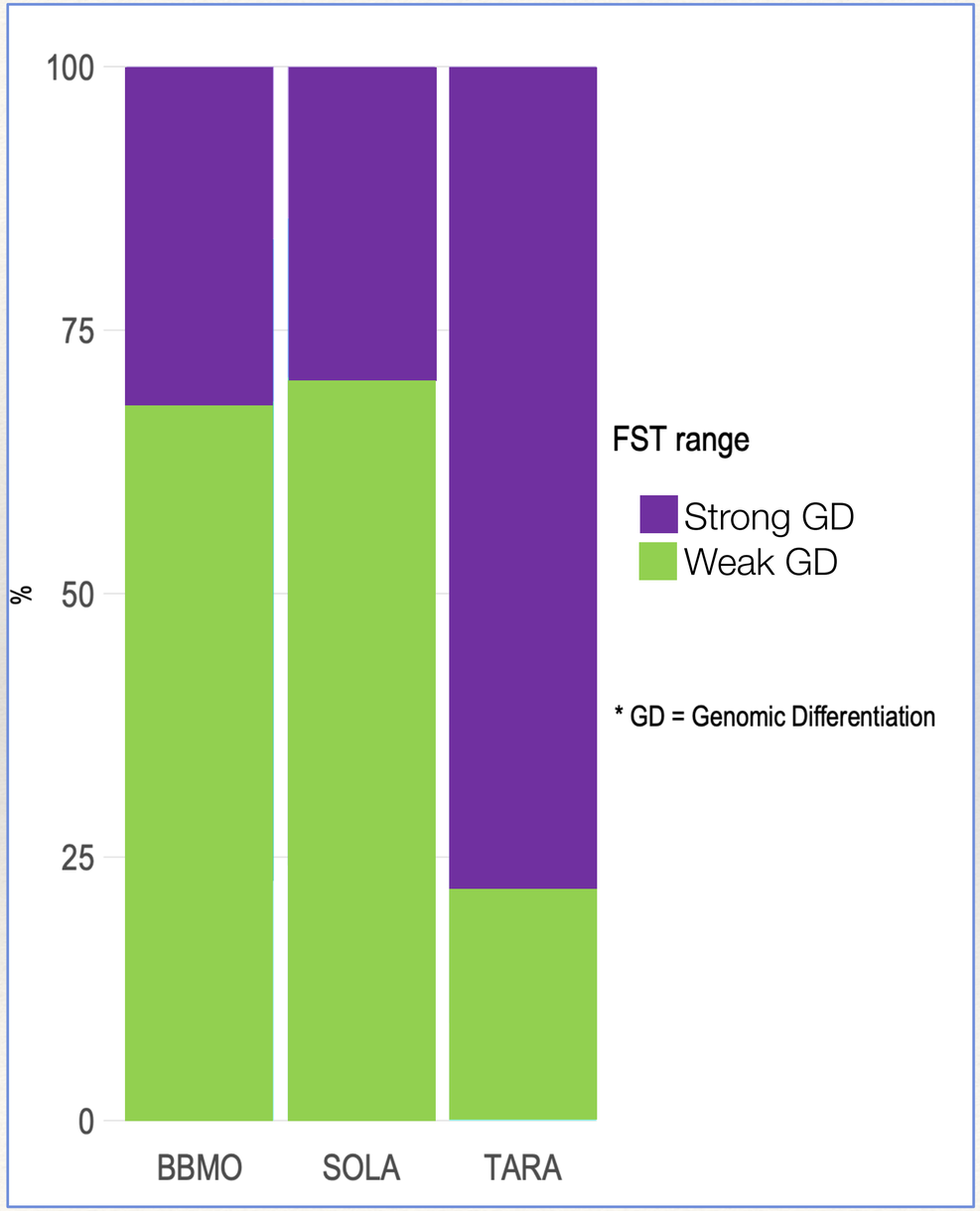
Population genomics of marine prokaryotes

Population-level genomic differentiation at different scales

Strong GD – FST ≥ 0.15
Weak GD – FST < 0.15



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Population genomics of marine prokaryotes

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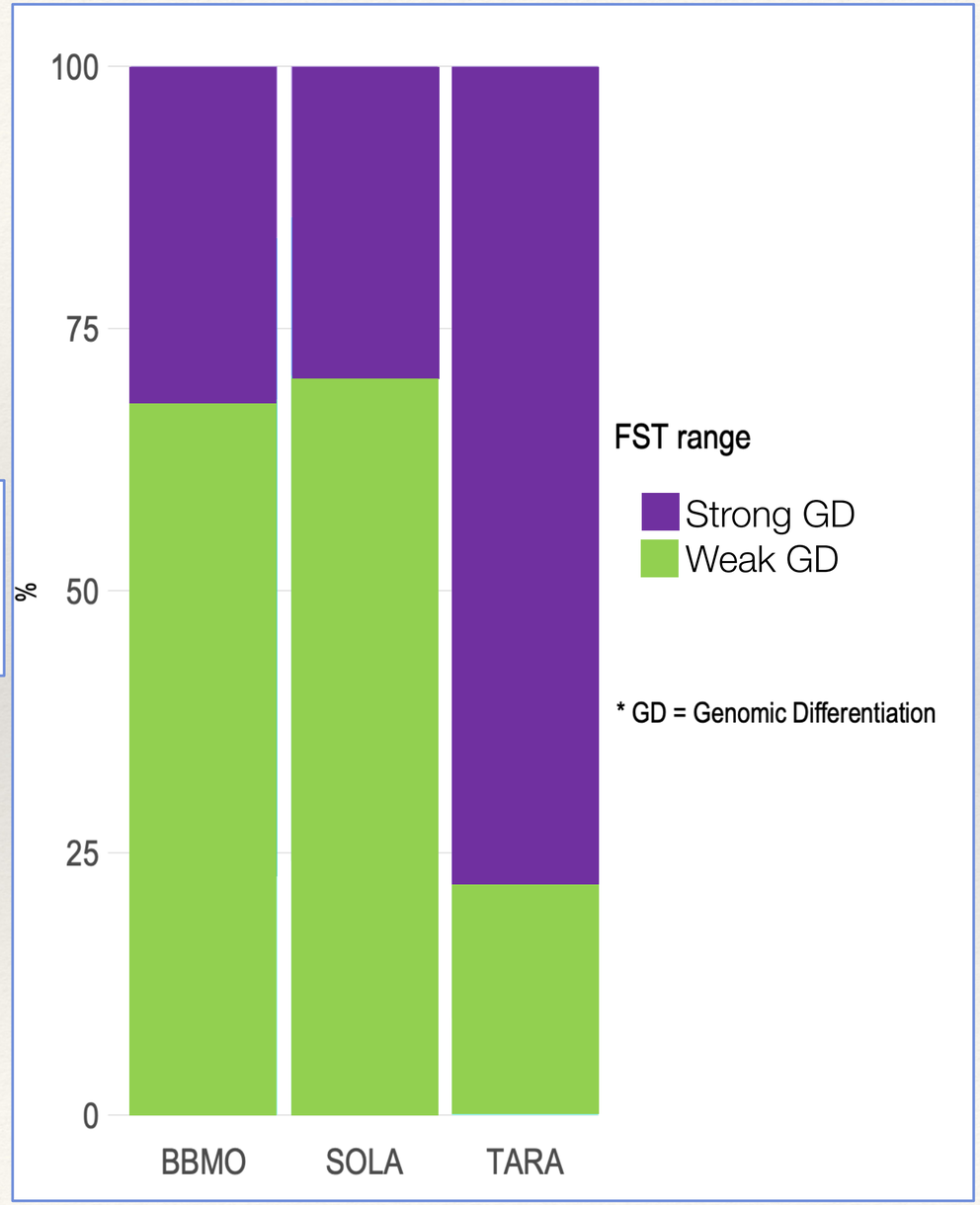

Proportion of FST of each category in BBMO, SOLA, and TARA for the **495 MAGs**

General pattern:

- Stronger spatial differentiation than temporal differentiation

- Higher environmental heterogeneity at the global ocean scale
- But, MAGs are from the Mediterranean…

Examples of main patterns

Population genomics of marine prokaryotes

Specific examples of Genomic differentiation

- Temporal scale – Strong GD
- Global scale – Strong GD

Population genomics of marine prokaryotes

Specific examples of Genomic differentiation

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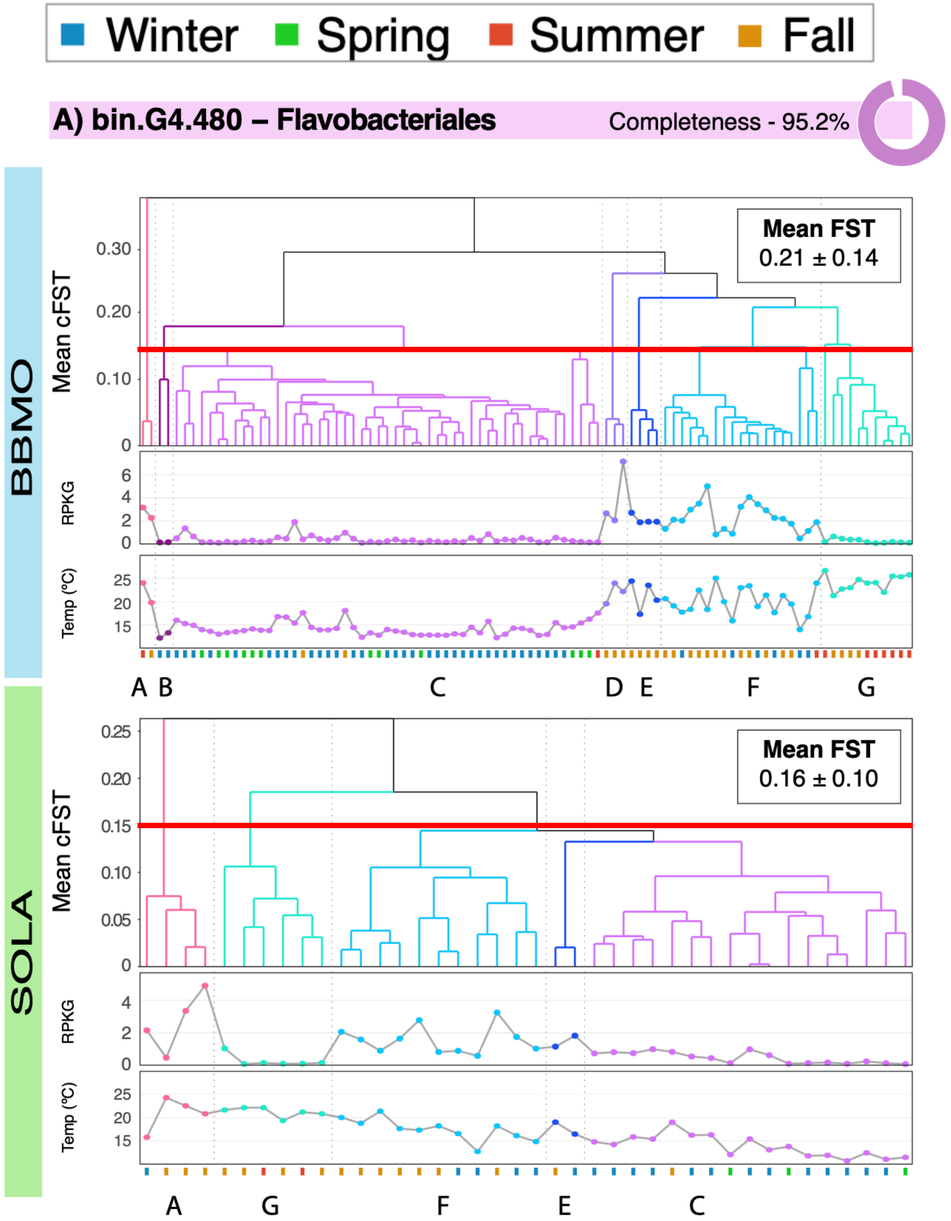

Population genomics of marine prokaryotes

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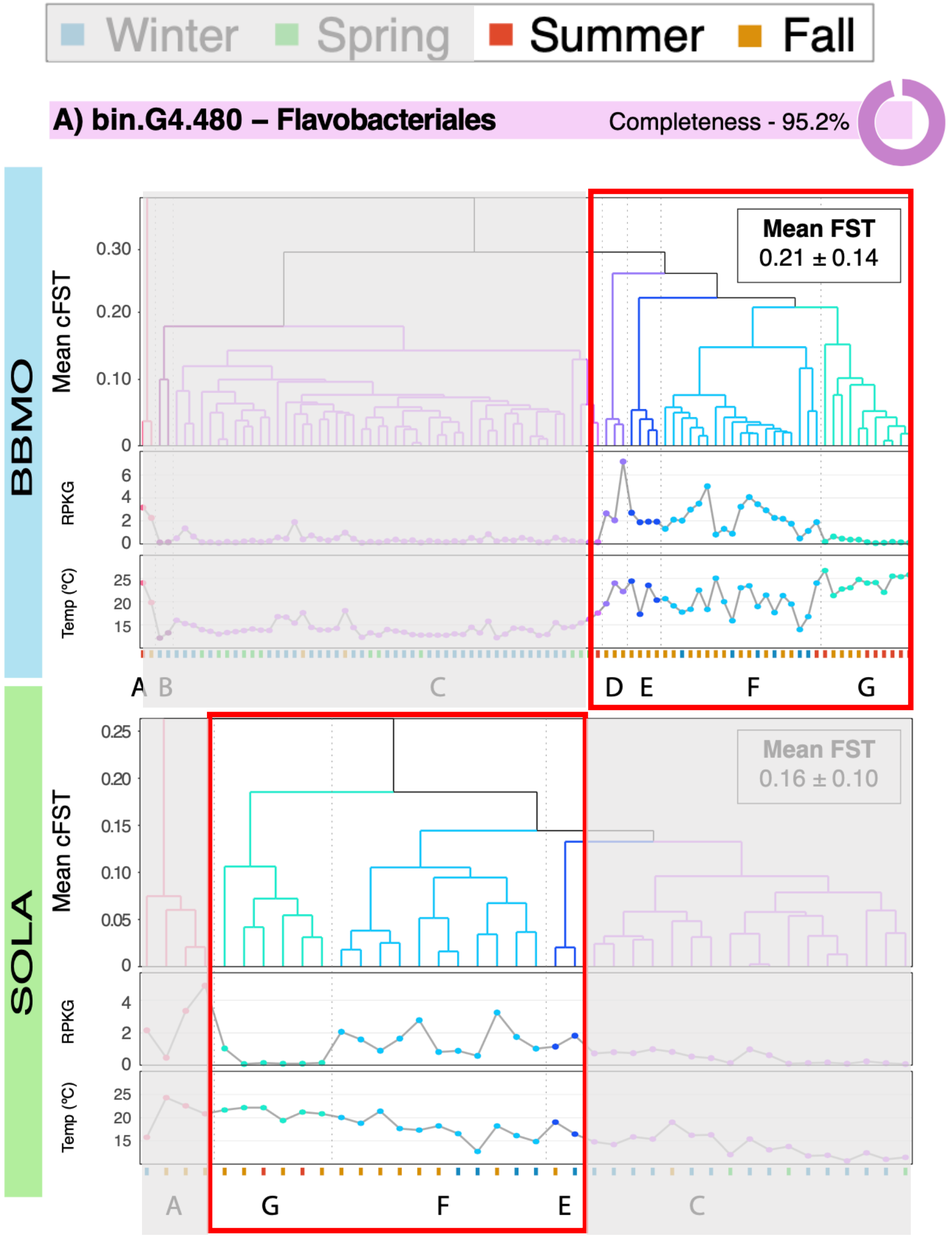

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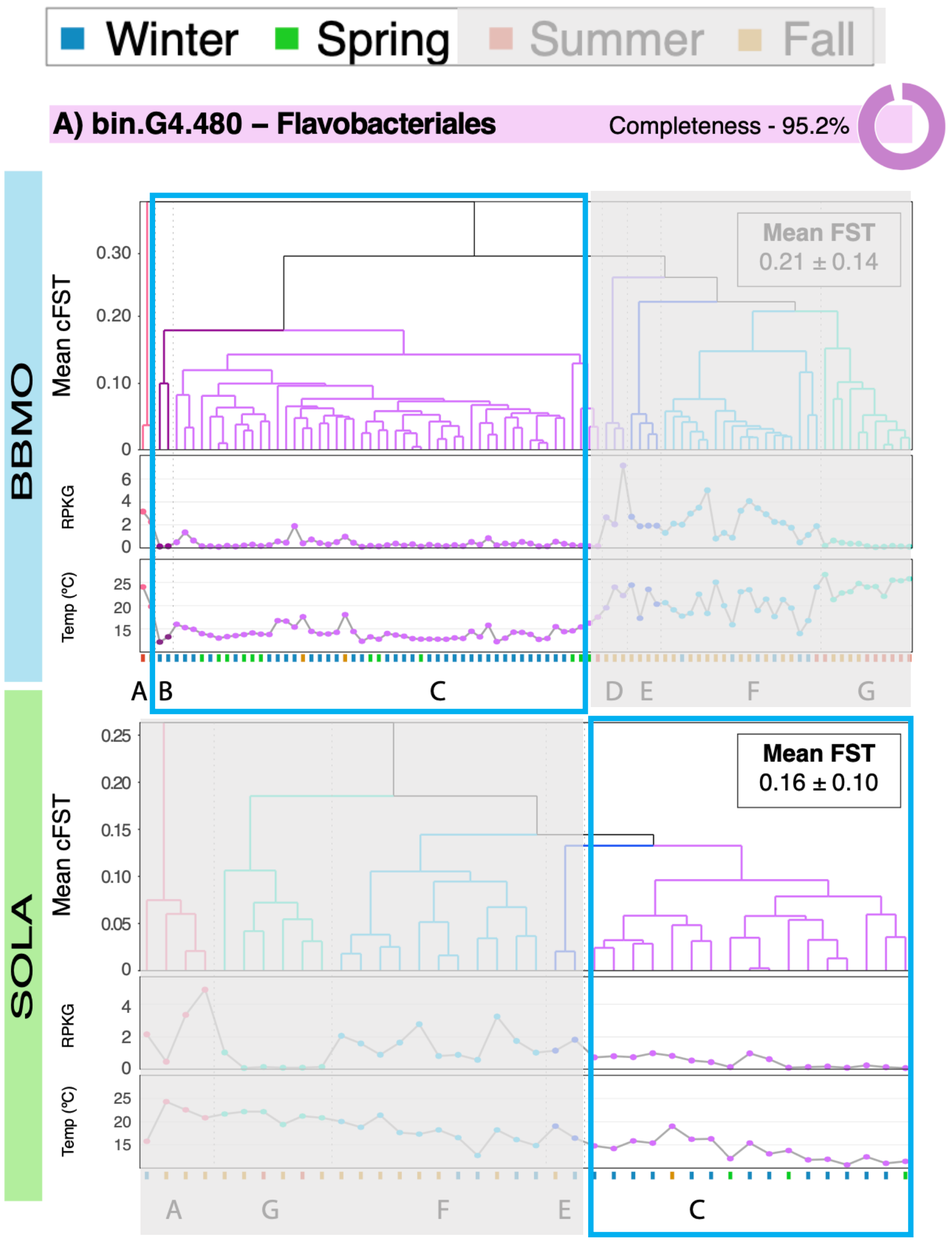

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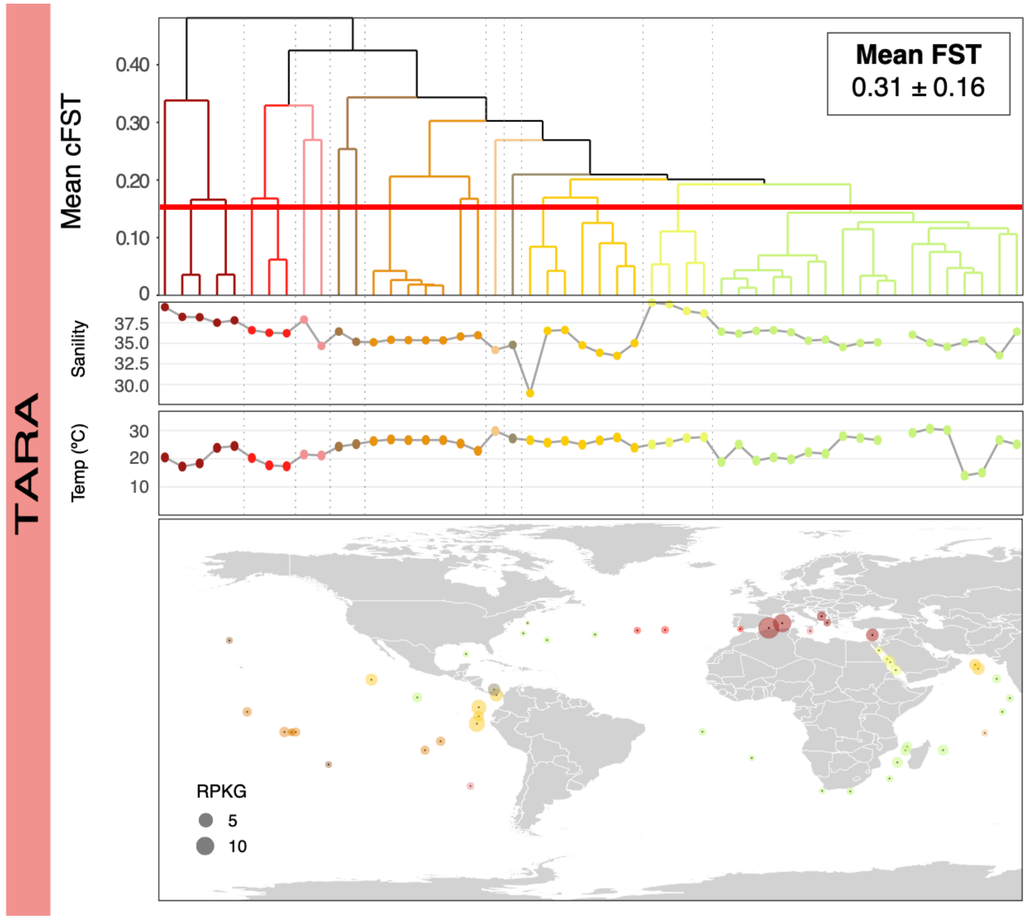

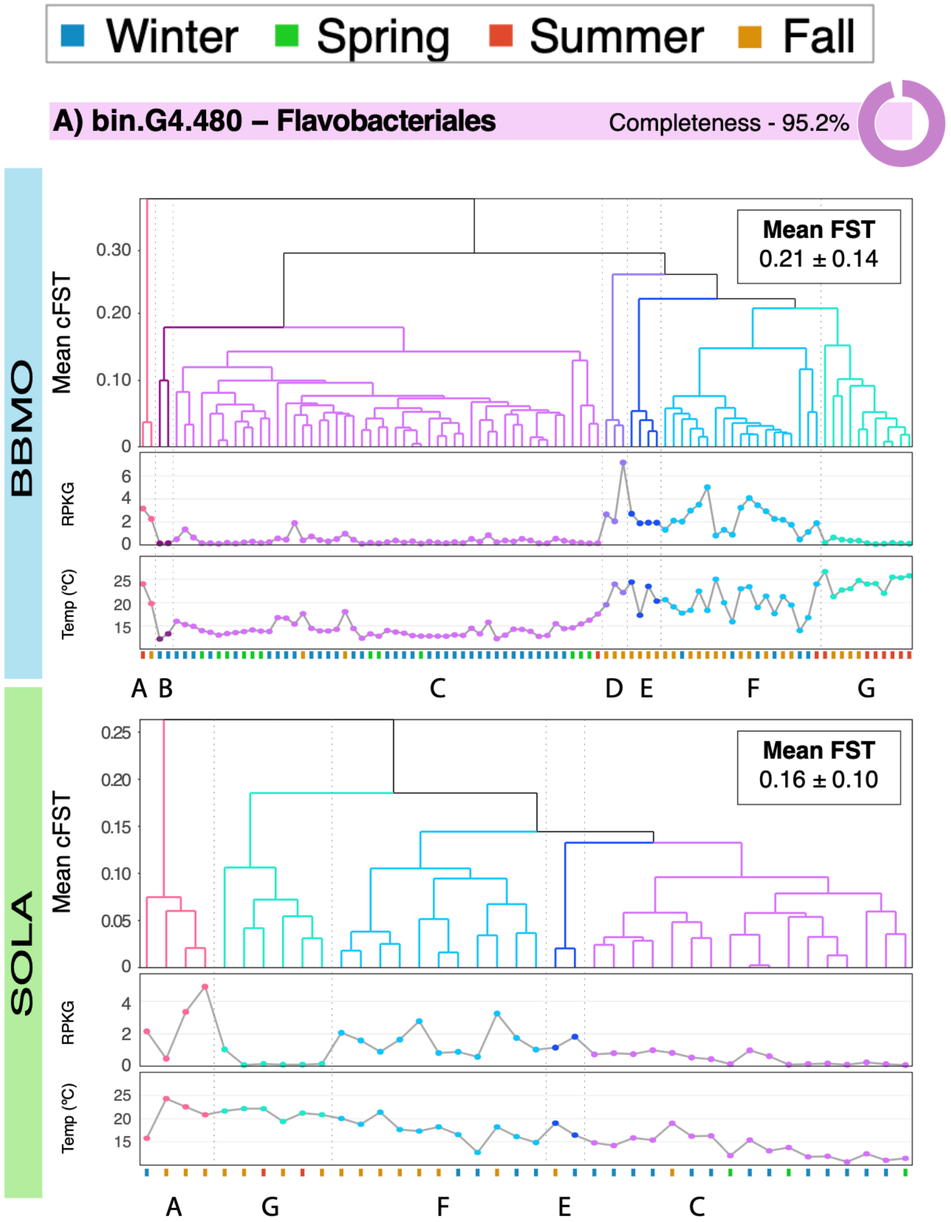

Population genomics of marine prokaryotes

Specific examples of Genomic differentiation

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Population genomics of marine prokaryotes

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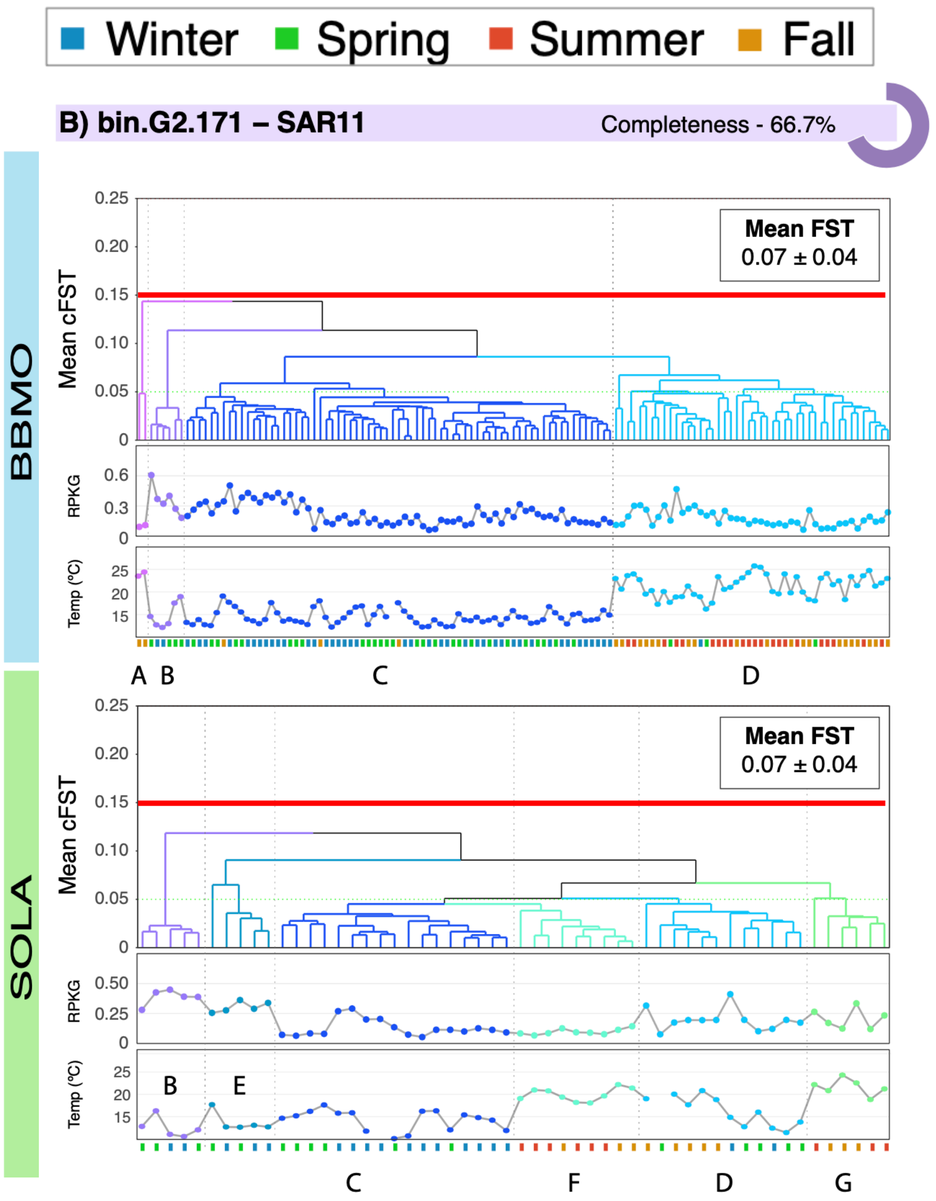

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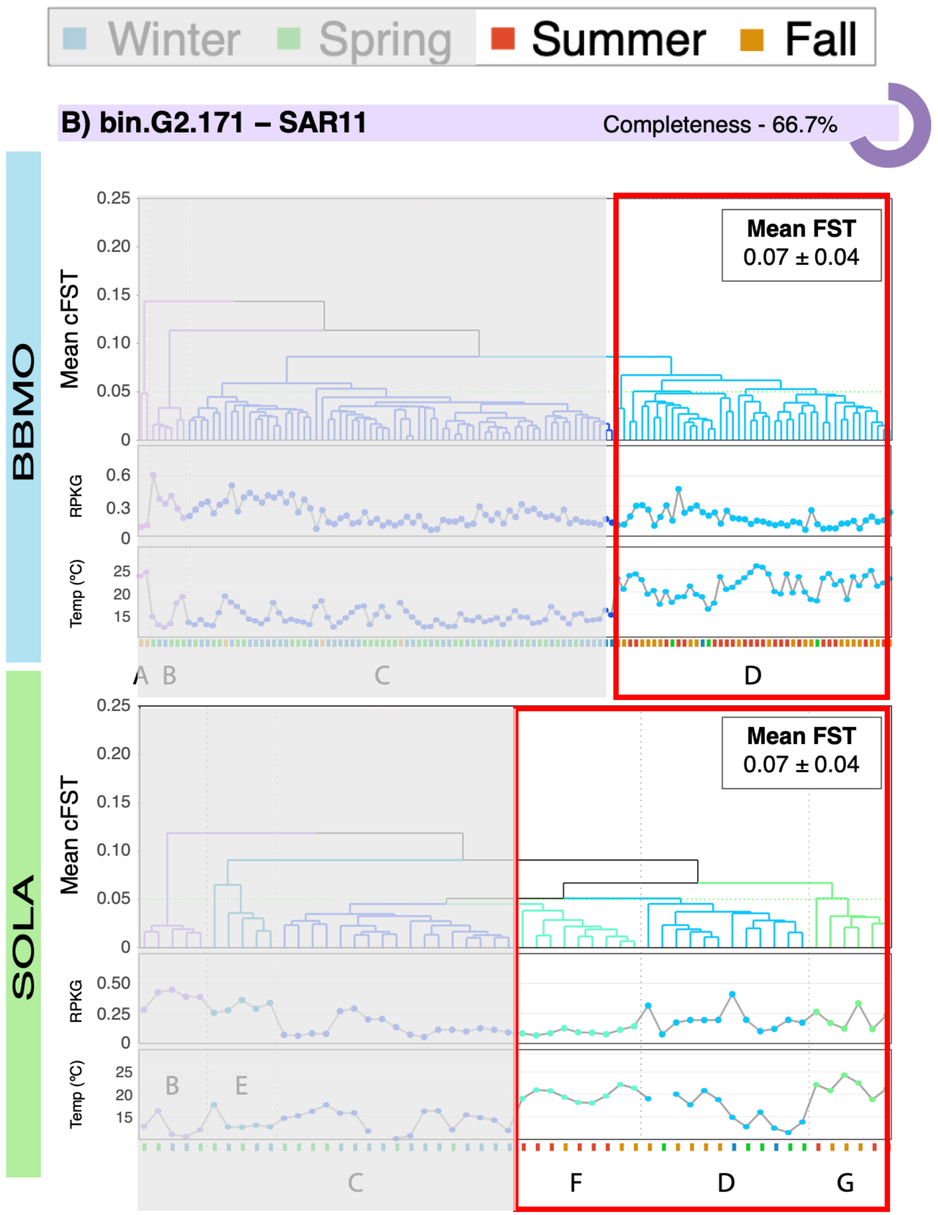

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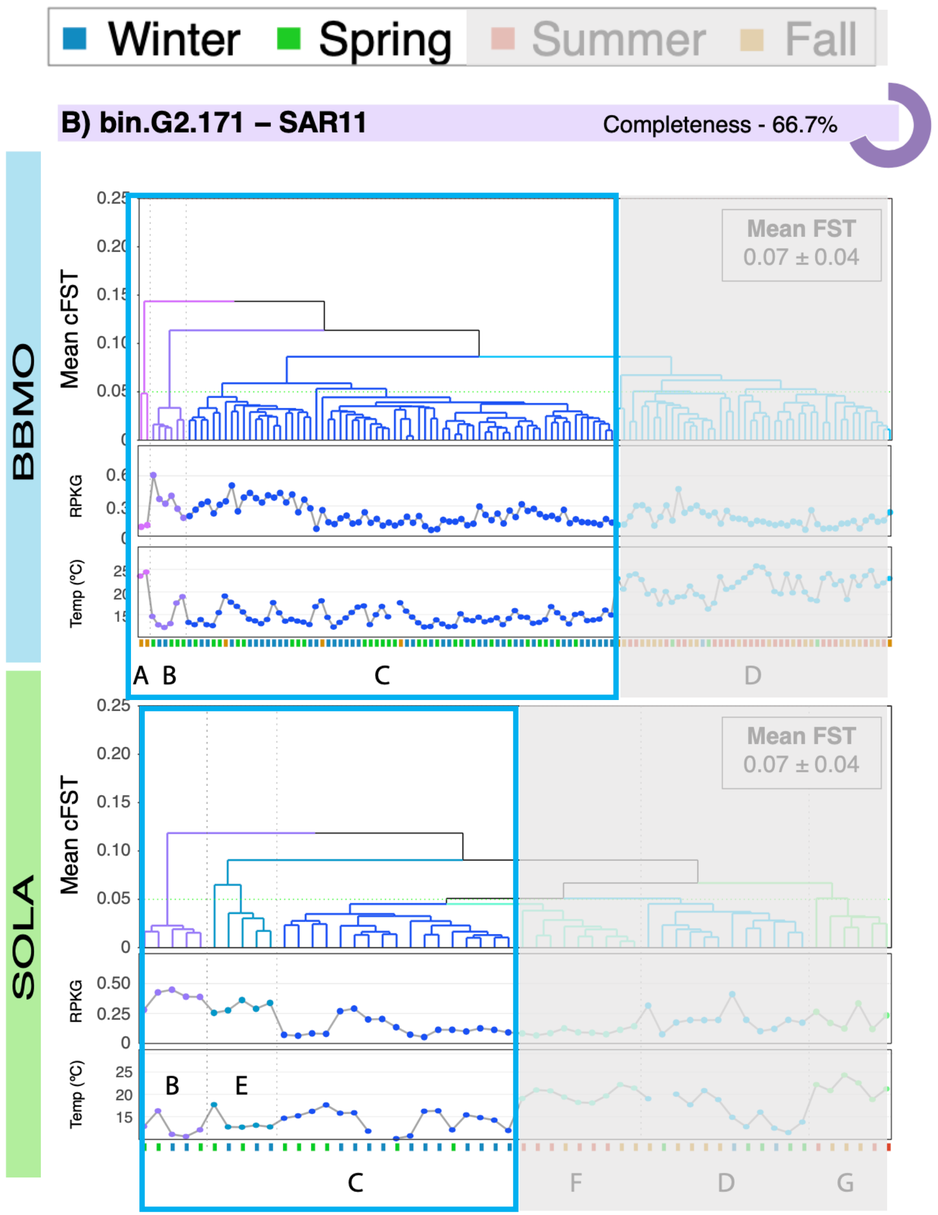

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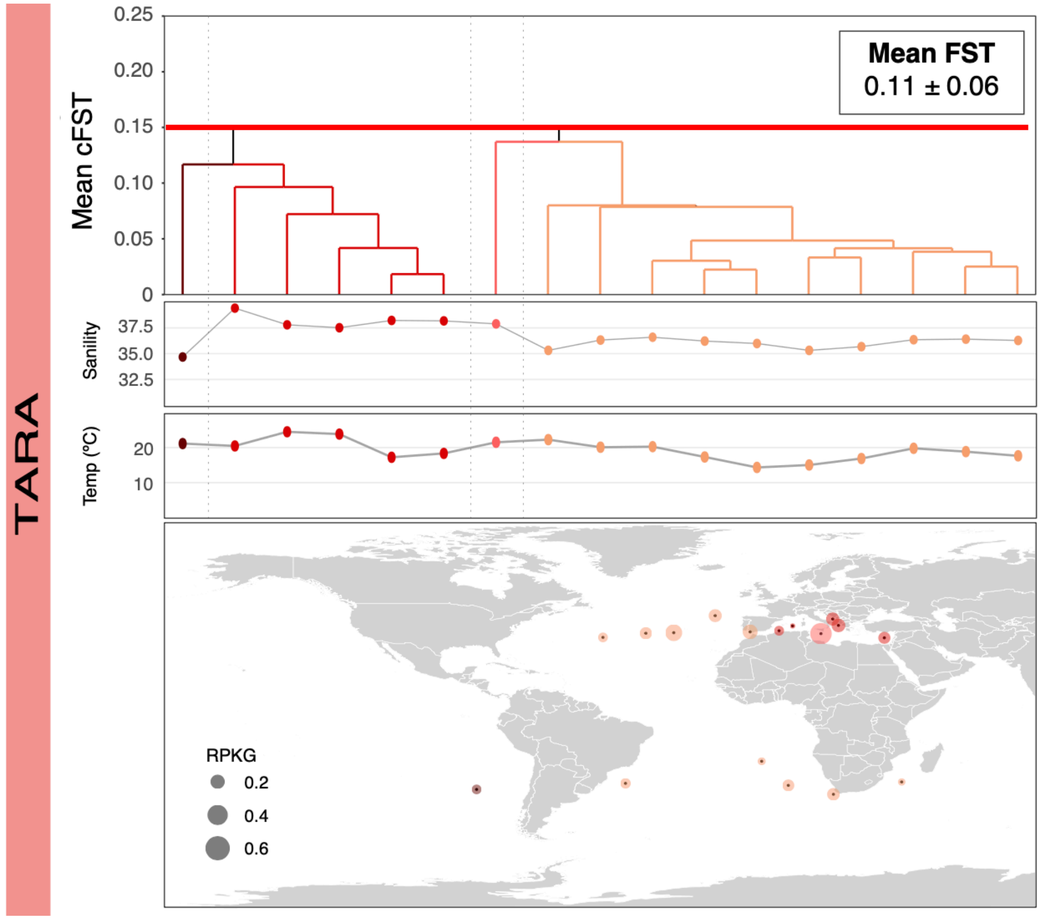

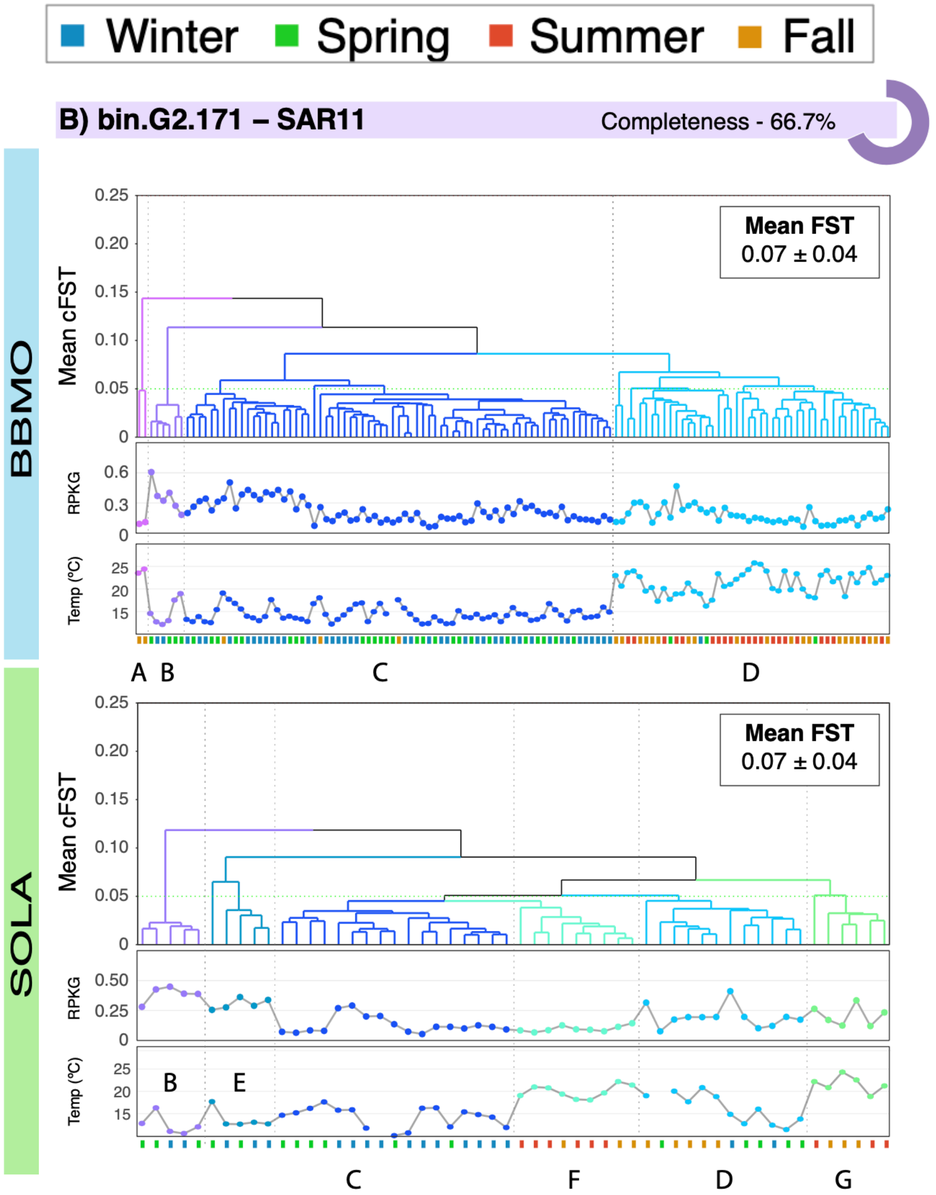

Population genomics of marine prokaryotes

MAIN QUESTIONS

1. How much population-level genomic divergence is present in marine prokaryotic species over a large spatiotemporal scale?
   - Very high differentiation at the global scale and moderate on the long temporal scale for the selected Mediterranean MAGs

Population genomics of marine prokaryotes

MAIN QUESTIONS

1. How much population-level genomic divergence is present in marine prokaryotic species over a large spatiotemporal scale?
   - Very high differentiation at the global scale and moderate on the long temporal scale for the selected Mediterranean MAGs
2. Is the genomic divergence structured into populations?
   - Yes, we find clear population structure for several prokaryotic species

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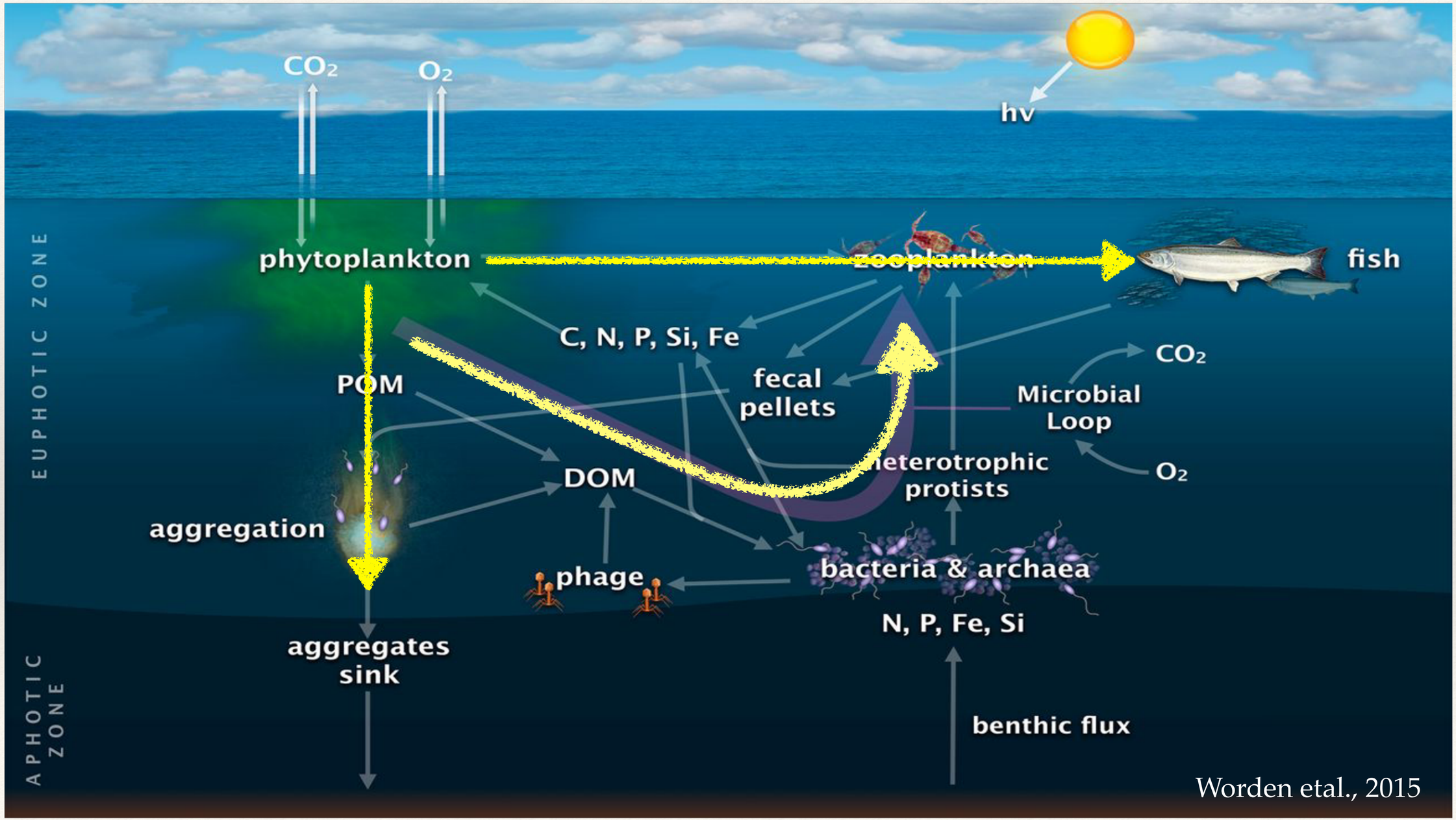
   - Very high differentiation at the global scale and moderate on the long temporal scale for the selected Mediterranean MAGs
2. Is the genomic divergence structured into populations?
   - Yes, we find clear population structure for several prokaryotic species
3. What environmental factors may drive population structure?
   - Temperature (seasonality) in BBMO and SOLA, and Temperature and Salinity in the global ocean

Long-standing questions we'll try to address

- How do microbes diversify and form new populations and species?
- Which microbes interact and how?

Microbial interactions sustain food webs



Worden etal., 2015

We don’t know much about microbial interactions

- Bibliographic search (human based)
- Reported interactions for protists
- ~2500 ecological interactions from ~500 publications,
- Spanning the last 150 years.

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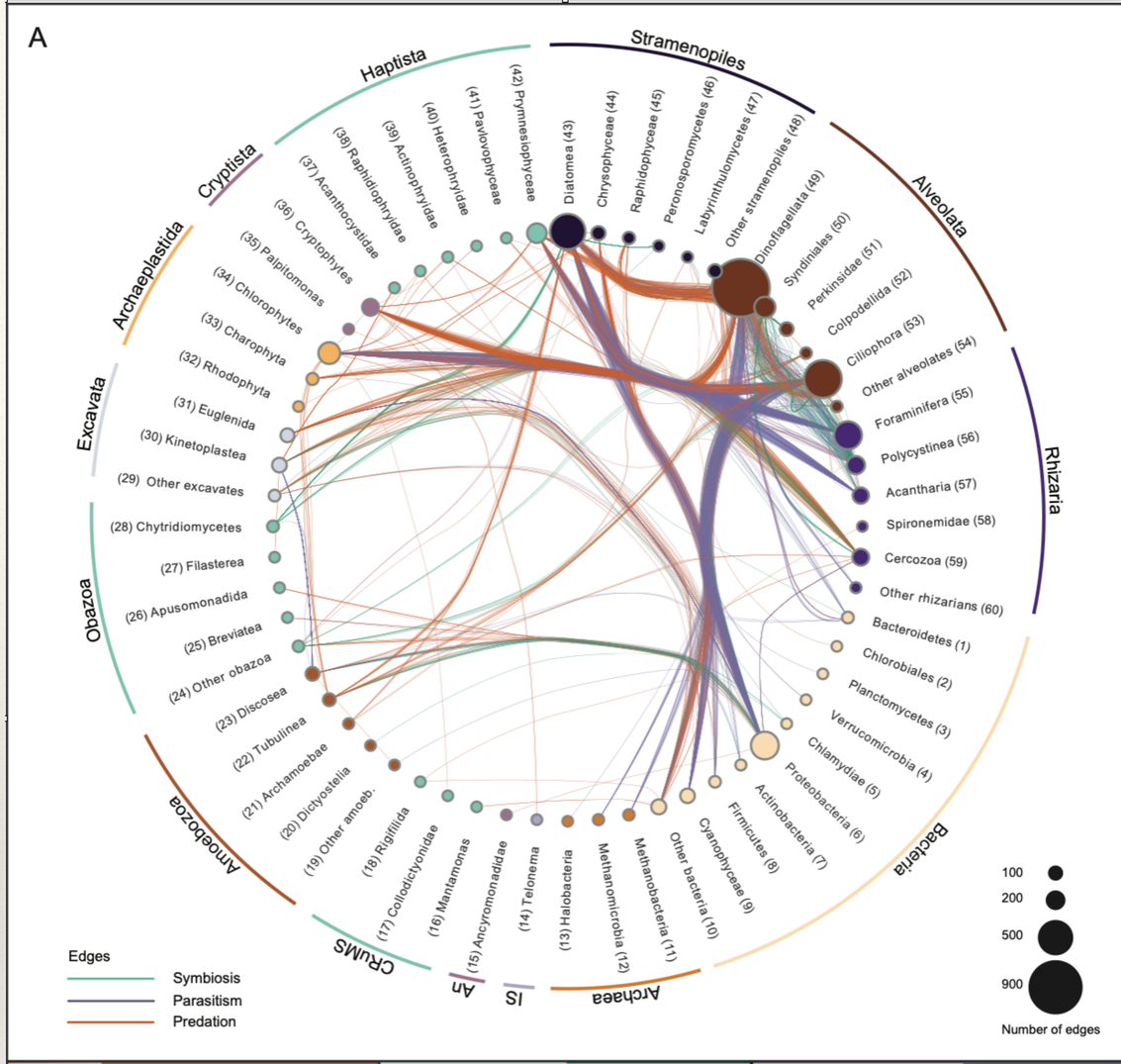
https://doi.org/10.1038/s41396-019-0542-5

ISME

ARTICLE

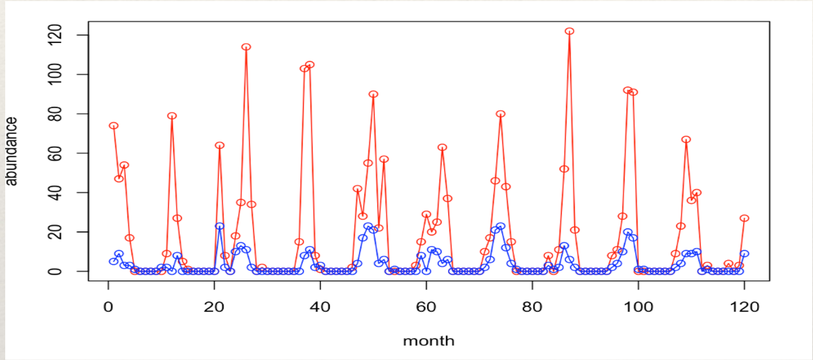
The planktonic protist interactome: where do we stand after a century of research?

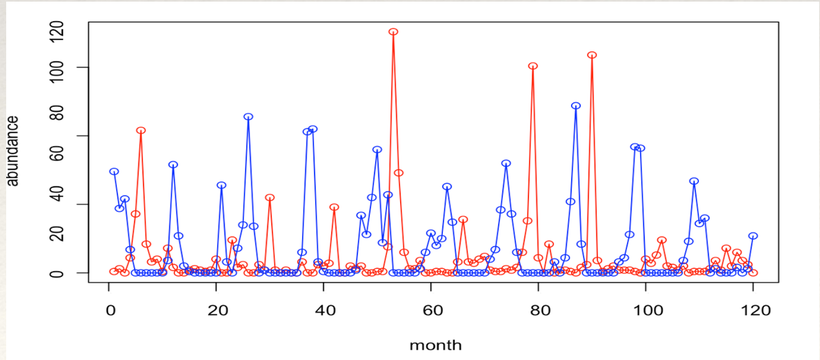
Marit F. Markussen Bjorbækmo[1] · Andreas Evenstad[1] · Line Lieblein Røsæg[1] · Anders K. Krabberød[1] · Ramiro Logares[1,2]



Association networks can help us in this daunting task

Microbial abundance correlations





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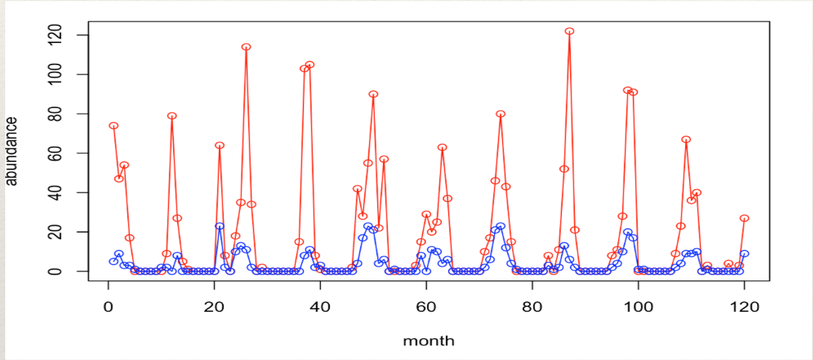

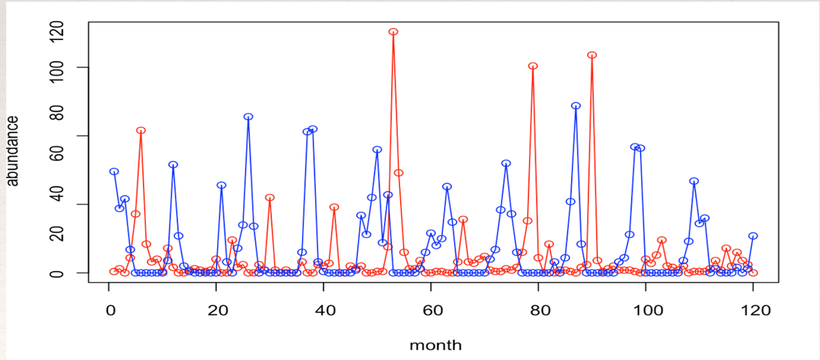

POTENTIAL INTERACTION

Association networks can help in this daunting task

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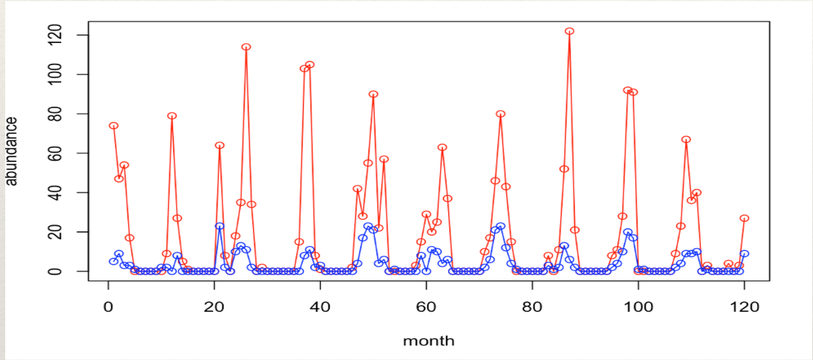
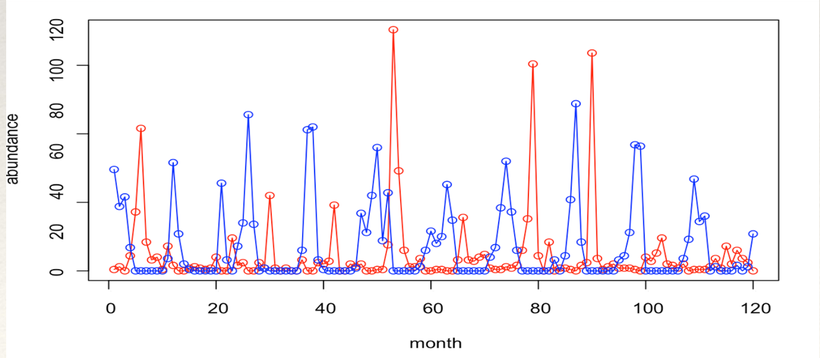
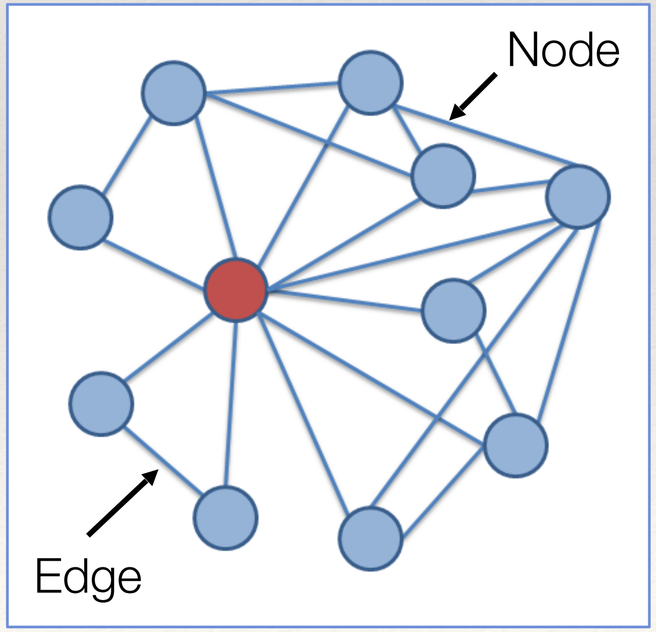




POTENTIAL INTERACTION



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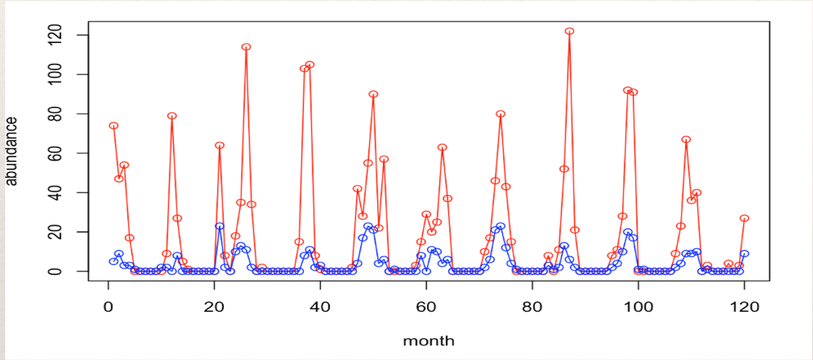
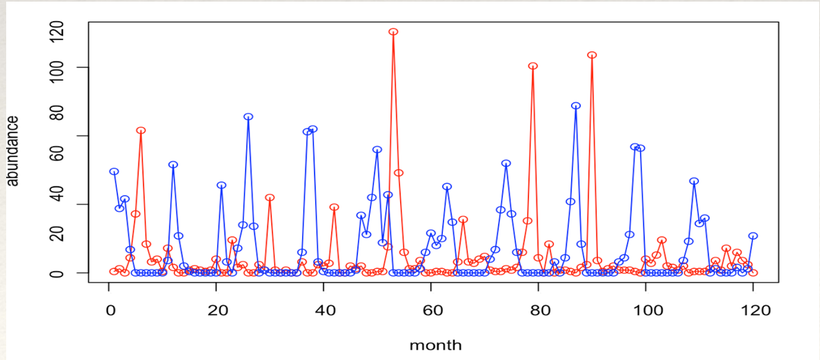
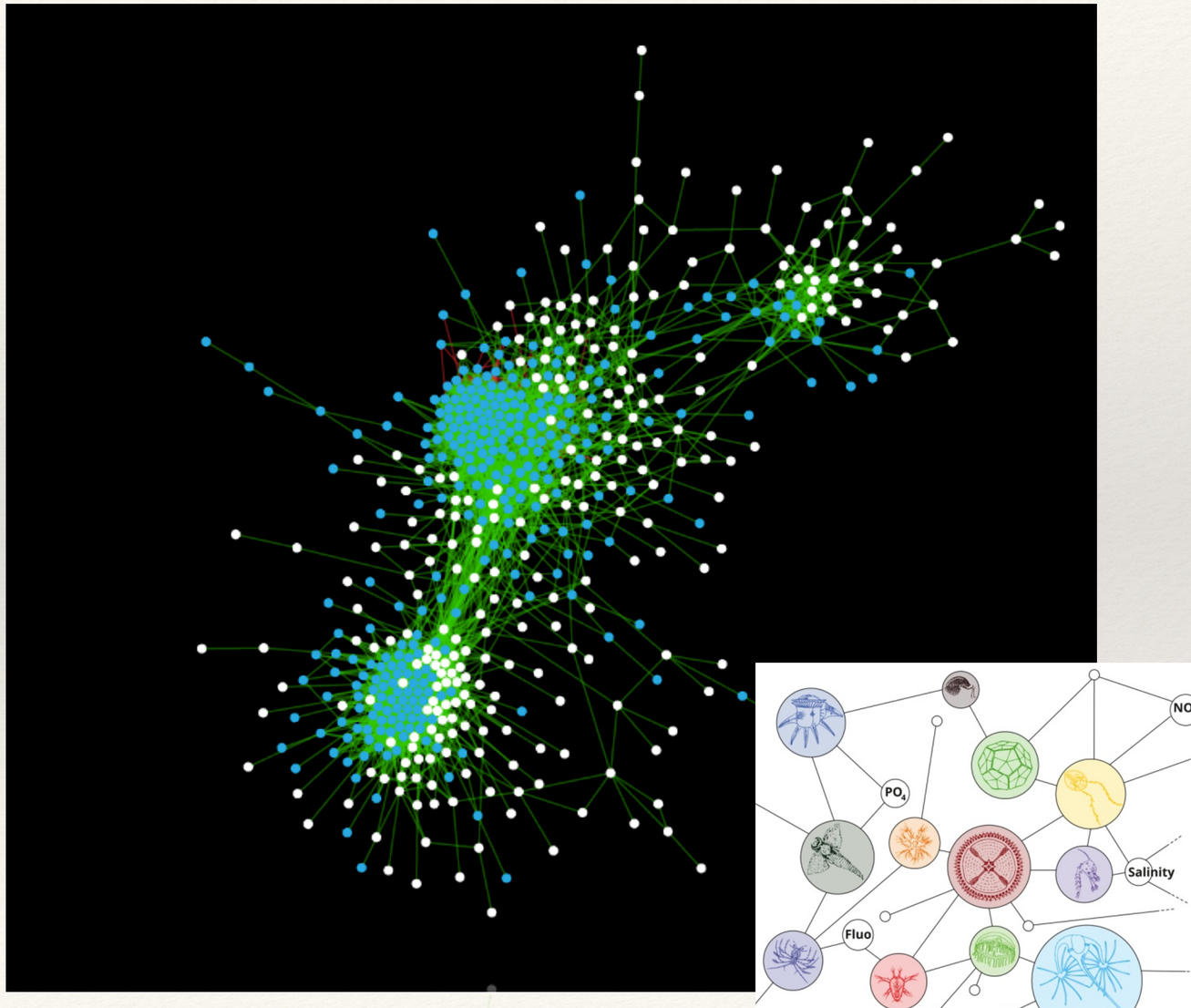






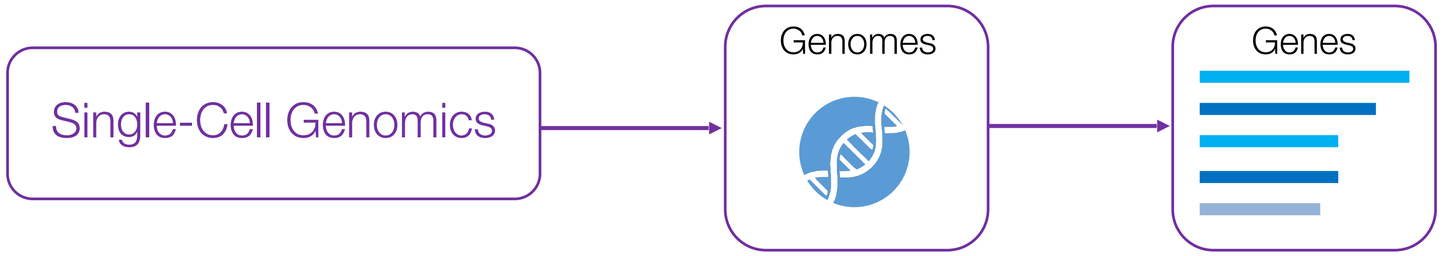
Single-cell genomics can also generate interaction hypotheses

Unveiling *in situ* interactions between marine protists and bacteria through single cell sequencing

Manuel Martinez-Garcia[1], David Brazel[1,2], Nicole J Poulton[1], Brandon K Swan[1], Monica Lluesma Gomez[1], Dashiell Masland[1], Michael E Sieracki[1] and Ramunas Stepanauskas[1]

[1]*Single Cell Genomics Center, Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME, USA and* [2]*Colby College, Waterville, ME, USA*

Using Single-Cell genomics to predict interactions



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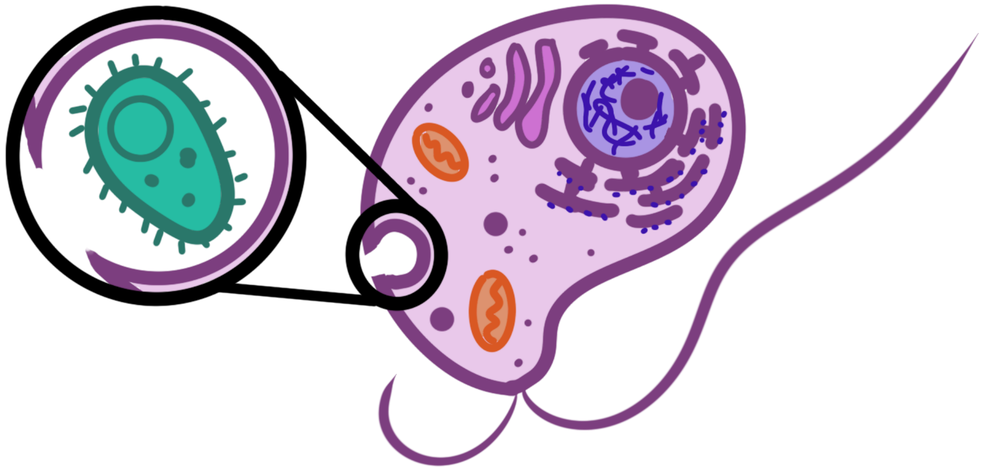

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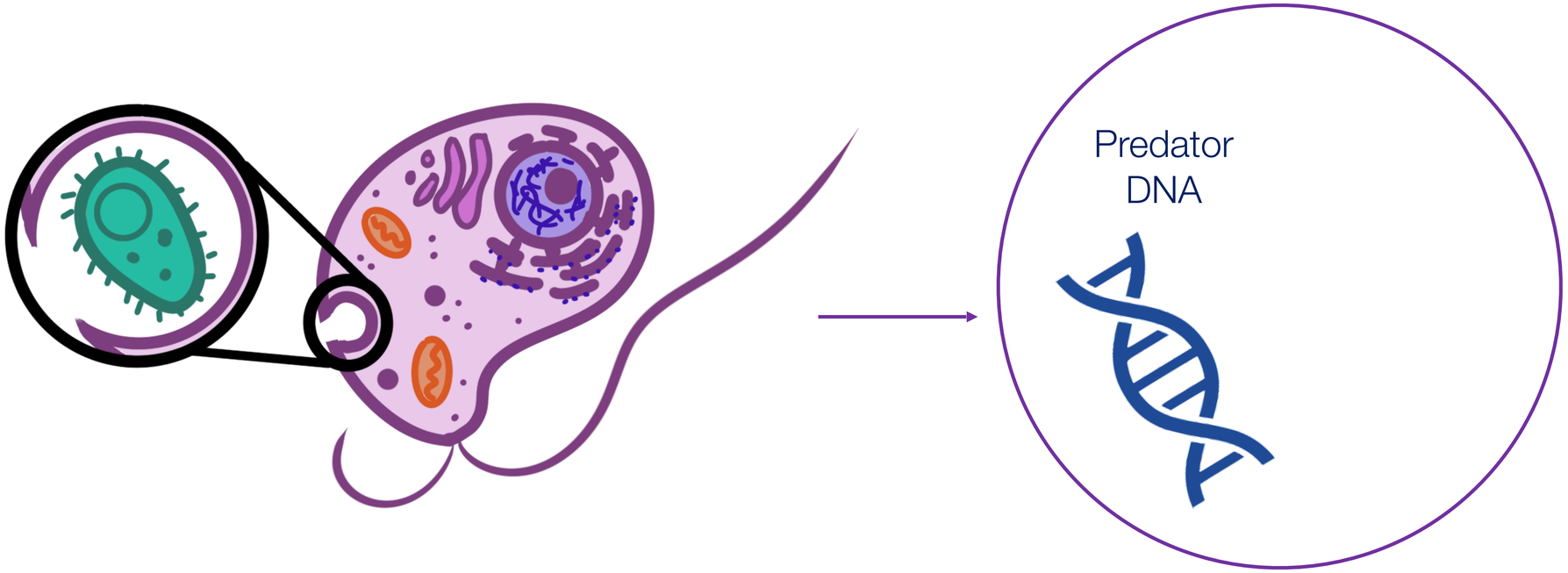

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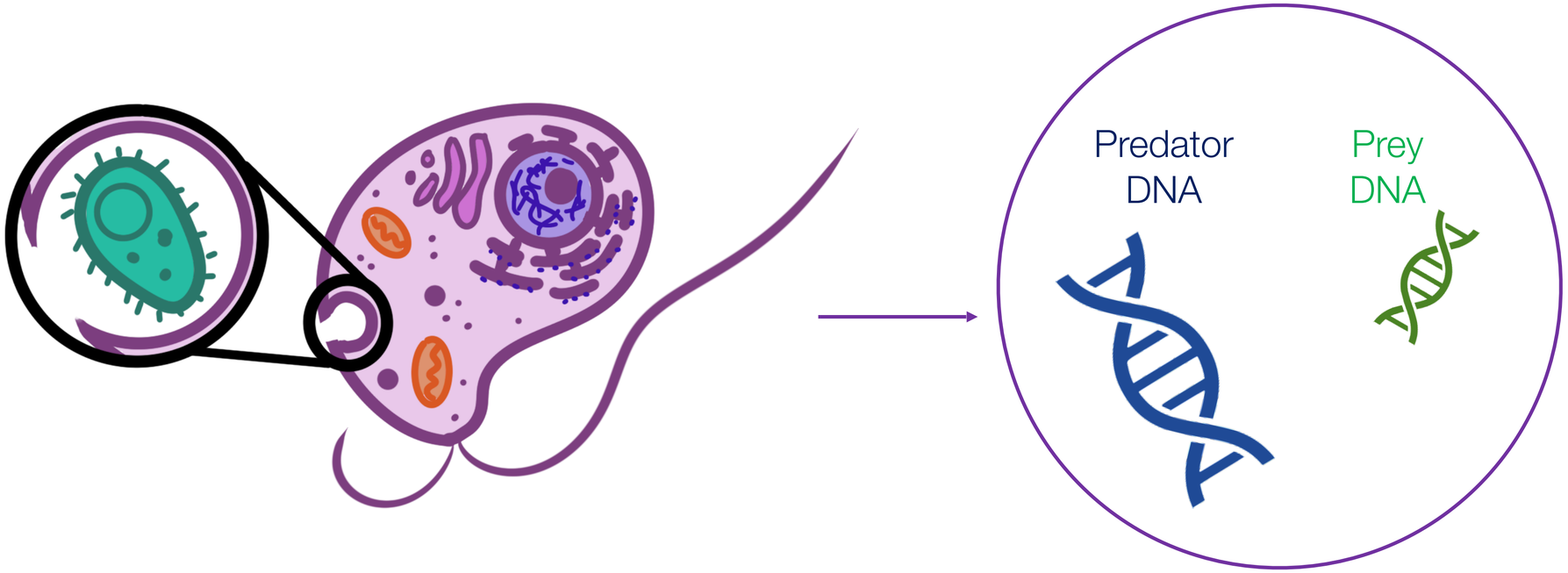

Using Single-Cell genomics to predict interactions

MAIN QUESTIONS

1. What are the most important “potential” interactions in a long time series?

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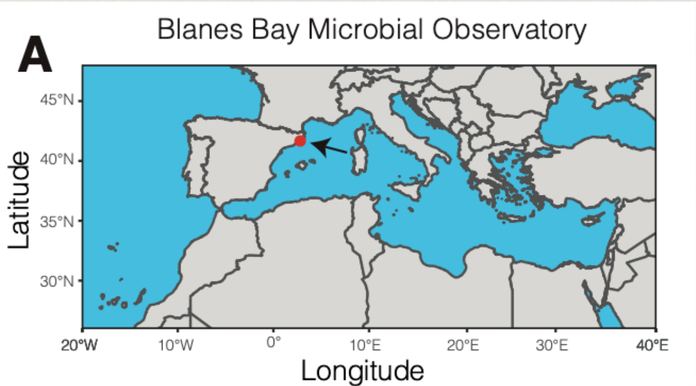
3. Can we use Single Amplified Genomes to survey potential microbial interactions?

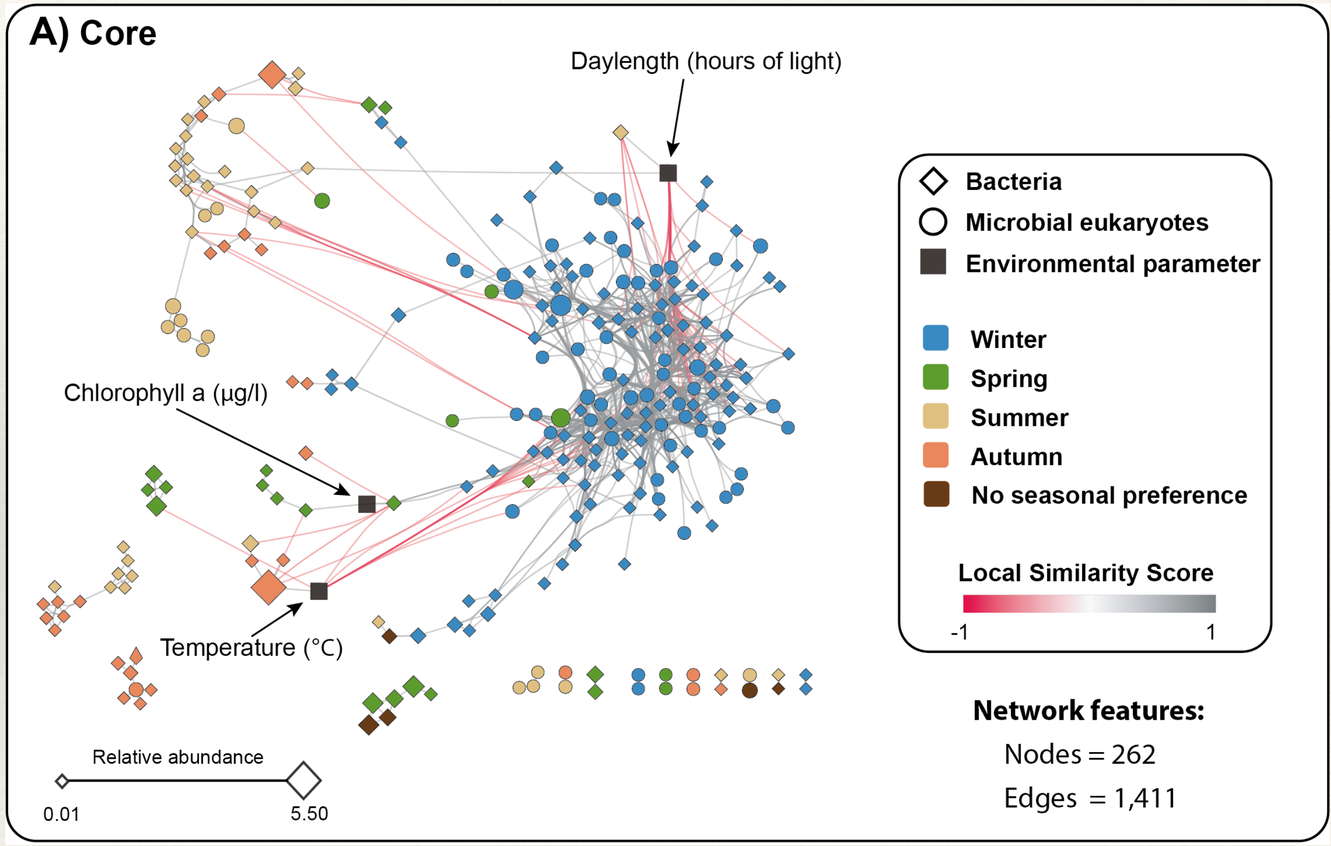
Microbial networks over 10 years

- Prokaryotes and protists
- Pico- and Nanoplankton
- Metabarcoding
- Strongest associations



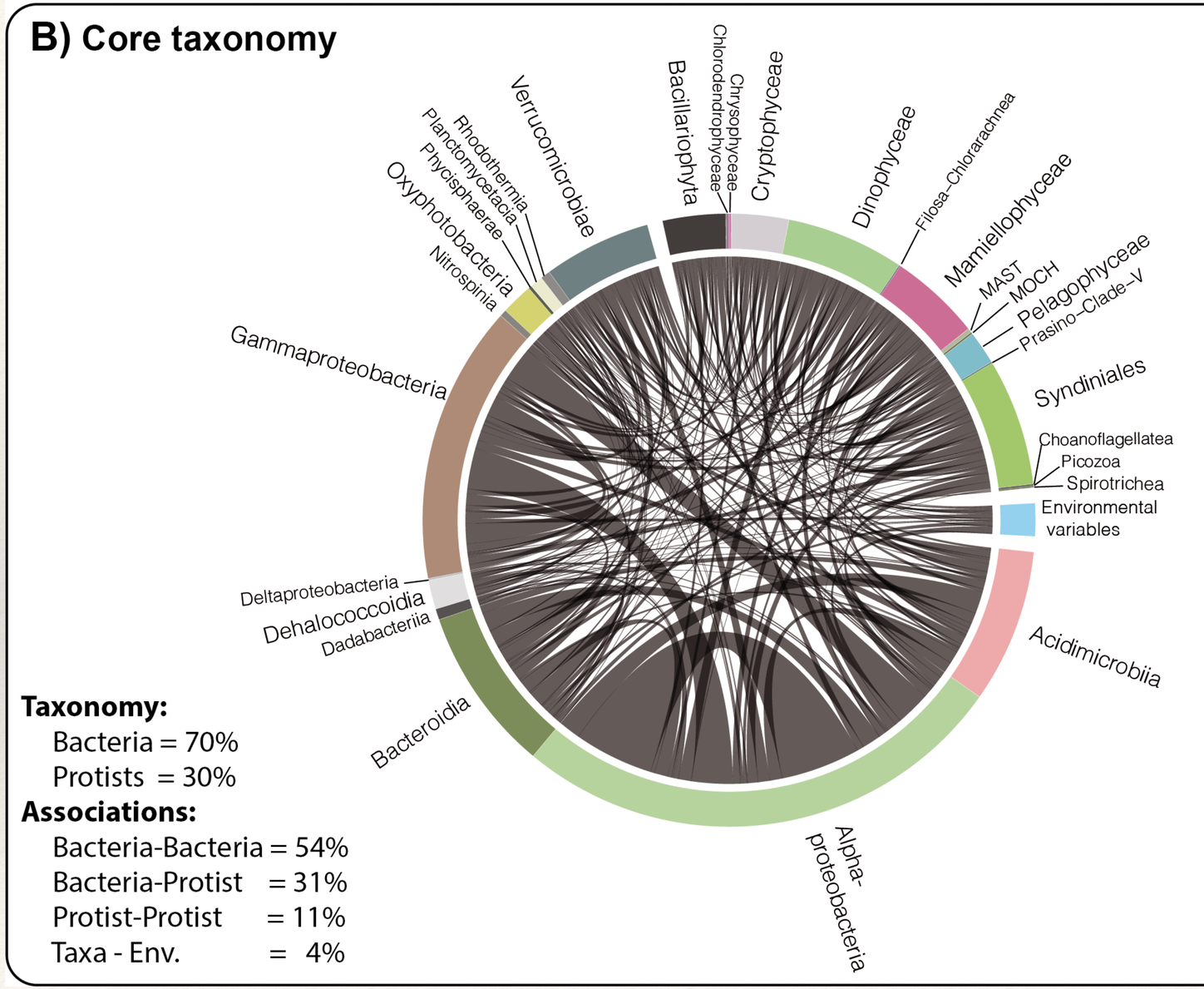
Core network

- 259 species (OTUs) & 1411 associations
- Core OTUs:
  - ~54% read abundance
  - ~9% of richness
  - ~98% seasonal
    - Winter OTUs more prevalent & connected
- Associations: 95% positive (co-occurrences)



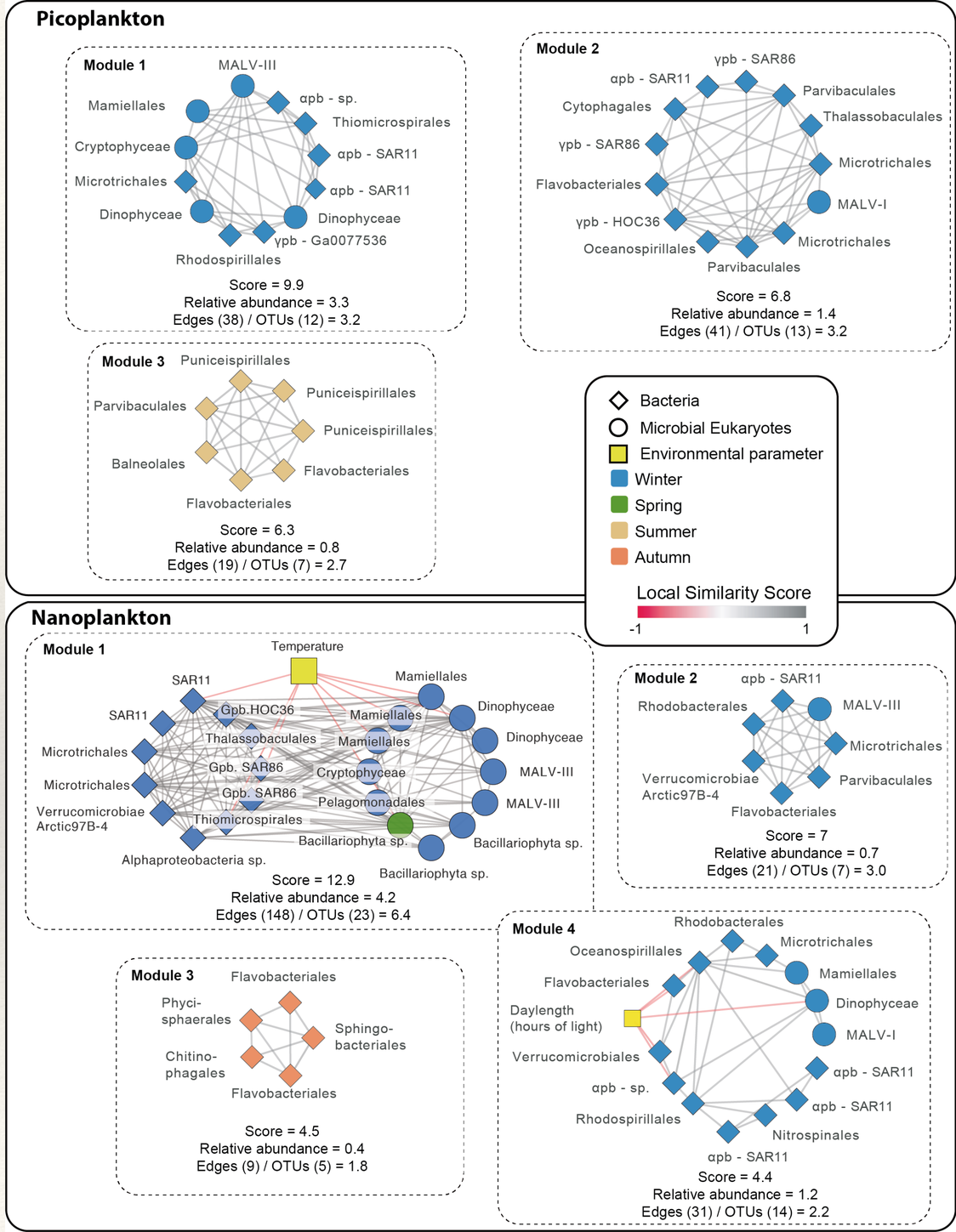
Taxa

- Bacteria ~70% | Protists ~30%
- Bacteria tended to be associated with bacteria
- Protists tended to be associated with bacteria



Modules

- OTUs more connected to each other than to the rest of the network
- Recurrent associations
- Tended to include OTUs from the same season
- Winter modules more prevalent



Central OTUs

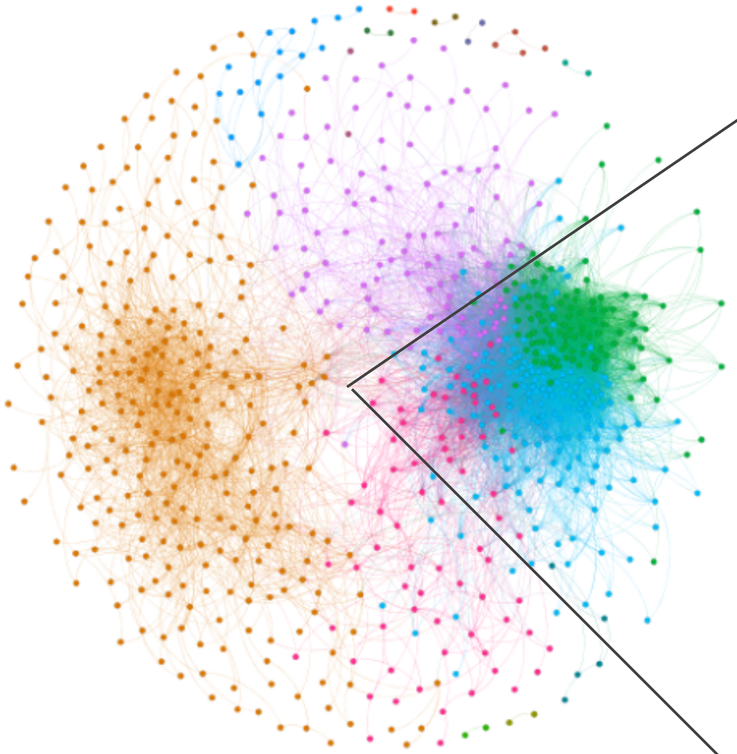
- OTUs with central positions in the network
- So far, unclear role, but likely, ecologically relevant

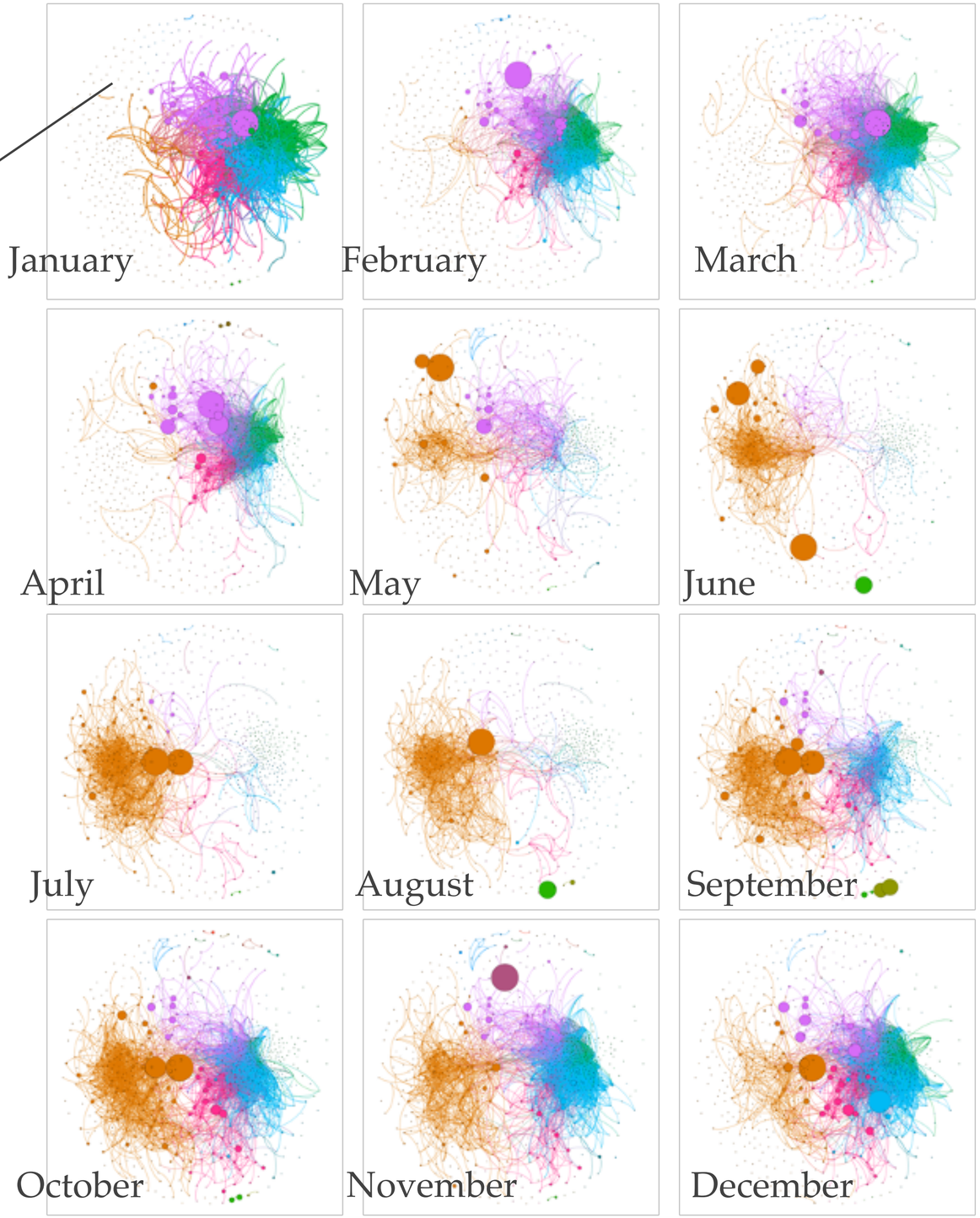
- 13 hub-OTUs (moderate-low abundance, high degree)
  - Associated with winter or spring
- 18 connector OTUs (low degree and high centrality)
  - Mostly associated with summer or autumn
  - May be linked to seasonal transitions of the community
  - Included some abundant OTUs

OTU	Class	Lowest rank taxonomy	Relative Abundance (%)[1]	Degree	Betweenness Centrality	Closeness Centrality	Season
Hubs							
en_00092	Mamiellophyceae	*Bathycoccus*	0.51	42	0.04	0.42	Winter
en_00119	Dinophyceae	-	0.41	50	0.03	0.42	Winter
bp_000037	Alphaproteobacteria	Parvibaculales_OCS116	0.31	45	0.08	0.43	Winter
bp_000039	Gammaproteobacteria	SUP05_cluster	0.28	29	0.12	0.41	Spring
bn_000039	Gammaproteobacteria	SUP05_cluster	0.21	42	0.17	0.44	Spring
bn_000037	Alphaproteobacteria	Parvibaculales_OCS116	0.20	40	0.05	0.42	Spring
bp_000059	Gammaproteobacteria	SAR86	0.20	24	0.09	0.40	Spring
ep_00070	Cryptophyceae	Cryptomonadales_X	0.13	40	0.04	0.42	Winter
bn_000059	Gammaproteobacteria	SAR86	0.12	24	0.03	0.40	Spring
bn_000102	Alphaproteobacteria	Nisaeaceae_OM75	0.09	26	0.03	0.38	Winter
bp_000193	Alphaproteobacteria	-	0.06	37	0.03	0.40	Winter
bn_000170	Acidimicrobiia	Sva0996_marine_group	0.06	59	0.06	0.44	Winter
bn_000226	Gammaproteobacteria	HOC36	0.04	60	0.06	0.43	Winter
Connectors							
bp_ 000001	Oxyphotobacteria	*Synechococcus* (CC9902)	3.79	5	0.05	0.30	Autumn
bp_ 000002	Alphaproteobacteria	SAR11 Clade_Ia	2.26	2	0.40	0.56	Spring
bp_ 000004	Alphaproteobacteria	SAR11 Clade_Ia	2.02	3	0.15	0.63	NA
bp_ 000007	Alphaproteobacteria	SAR11 Clade_Ia	1.38	3	0.60	0.71	NA
bp_ 000008	Alphaproteobacteria	SAR11 Clade_Ia	1.15	3	0.15	0.63	NA
bn_ 000008	Alphaproteobacteria	SAR11 Clade_Ia	0.68	5	0.03	0.27	Winter
en_ 00059	Chlorodendrophyceae	*Tetraselmis*	0.66	4	0.05	0.26	Summer
bn_ 000020	Oxyphotobacteria	-	0.56	3	0.60	0.67	Autumn
en_ 00161	Syndiniales	Syndiniales-Group-I-Clade-4_X	0.42	4	0.80	0.75	Autumn
bn_ 000018	Oxyphotobacteria	*Prochlorococcus* MIT9313	0.41	5	0.04	0.24	Winter
bn_ 000054	Alphaproteobacteria	Puniceispirillales_SAR116	0.11	4	0.14	0.40	Autumn
bn_ 000062	Alphaproteobacteria	Puniceispirillales_SAR116	0.08	3	0.55	0.50	Autumn
bn_ 000077	Rhodothermia	*Balneola*	0.07	3	0.17	0.32	Summer
bn_ 000112	Gammaproteobacteria	KI89A	0.06	4	0.53	0.48	Summer
bn_ 000156	Alphaproteobacteria	Parvibaculales_PS1	0.05	4	0.14	0.40	Summer
bn_ 000281	Bacteroidia	Sphingobacteriales_NS11-12	0.05	5	0.16	0.44	Autumn
bn_ 000221	Alphaproteobacteria	Puniceispirillales_SAR116	0.04	5	0.05	0.30	Winter
ep_ 00269	Chrysophyceae	Clade-I_X	0.04	2	1.00	1.00	Summer

But networks are dynamic…

Static network
10 years

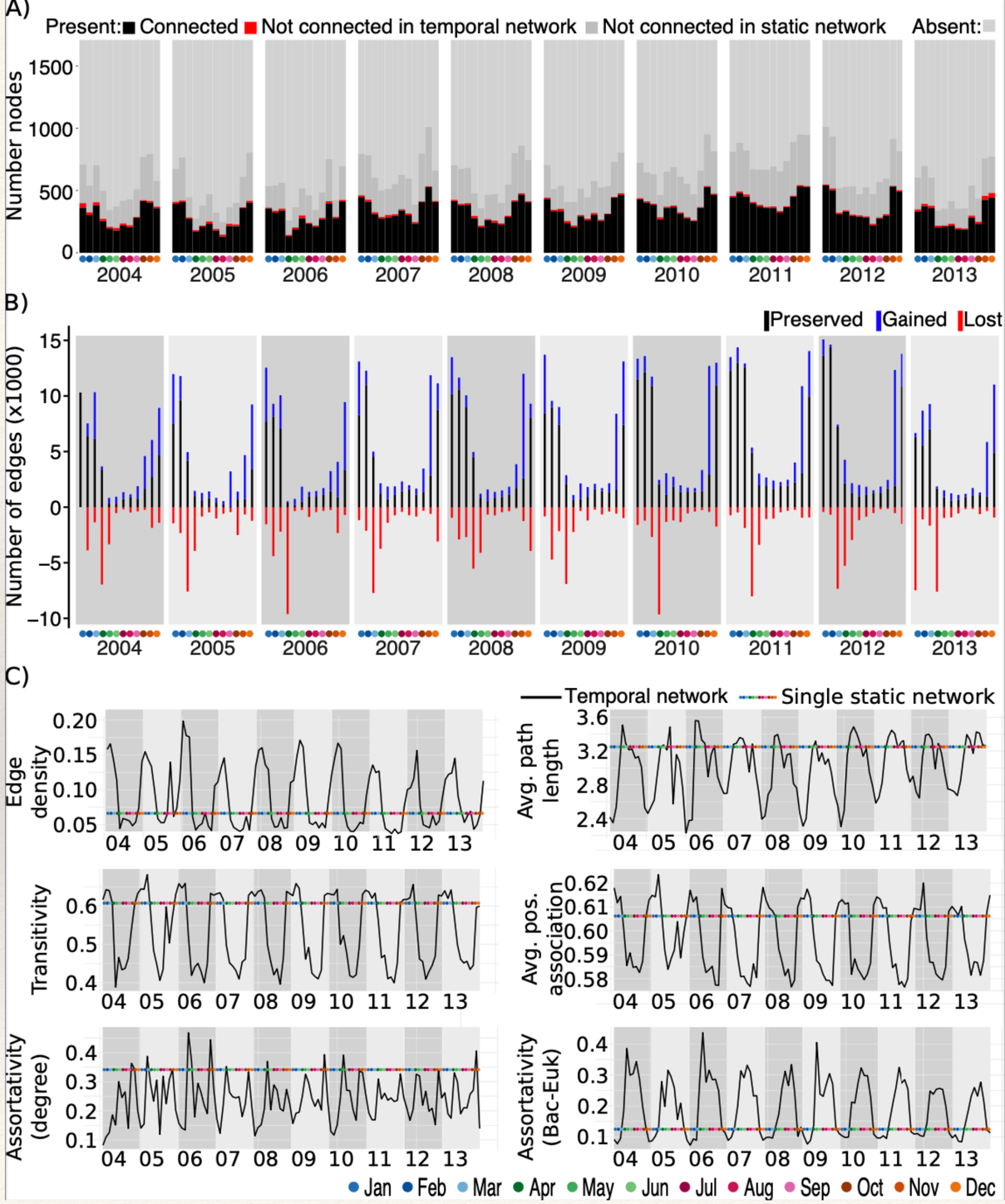




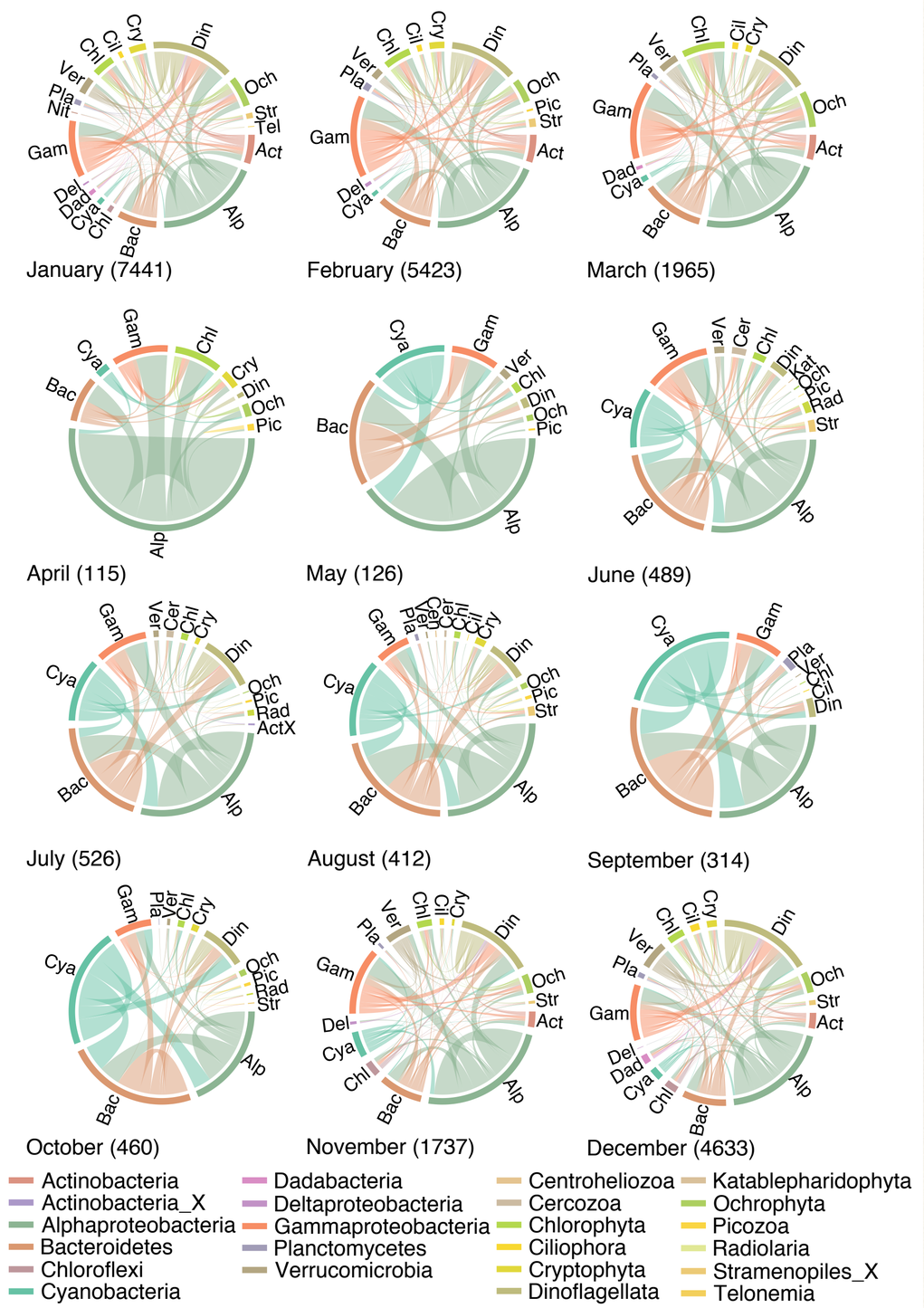
Blanes Bay
Microbial
Observatory

Network dynamics

- Network changes over 10 years and has recurrent features
- Recurrent winter associations
- Seasonal disassembly and reassembly of the network



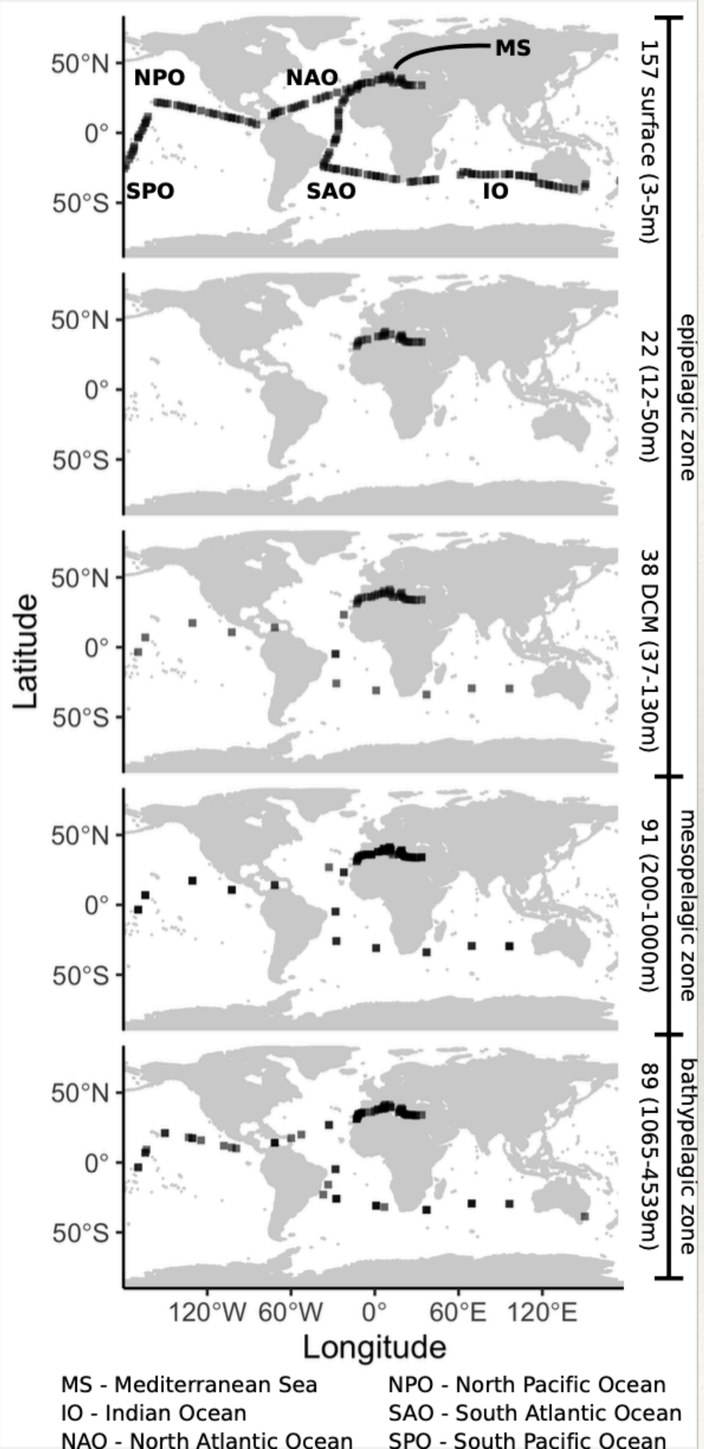
Dynamic taxonomic associations



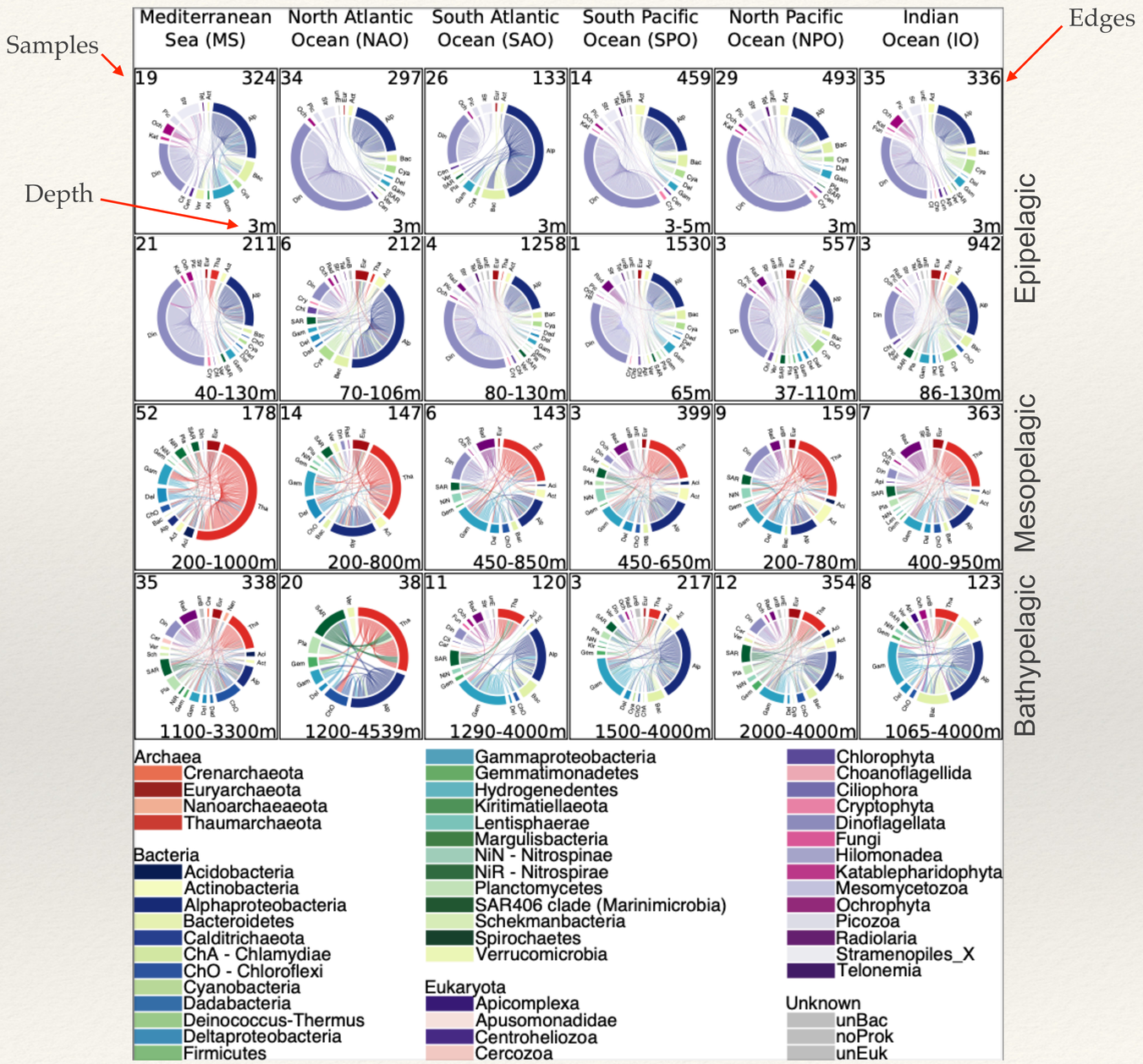
Networks change across space

397 samples

397 networks



Associations in >70% of subnetworks



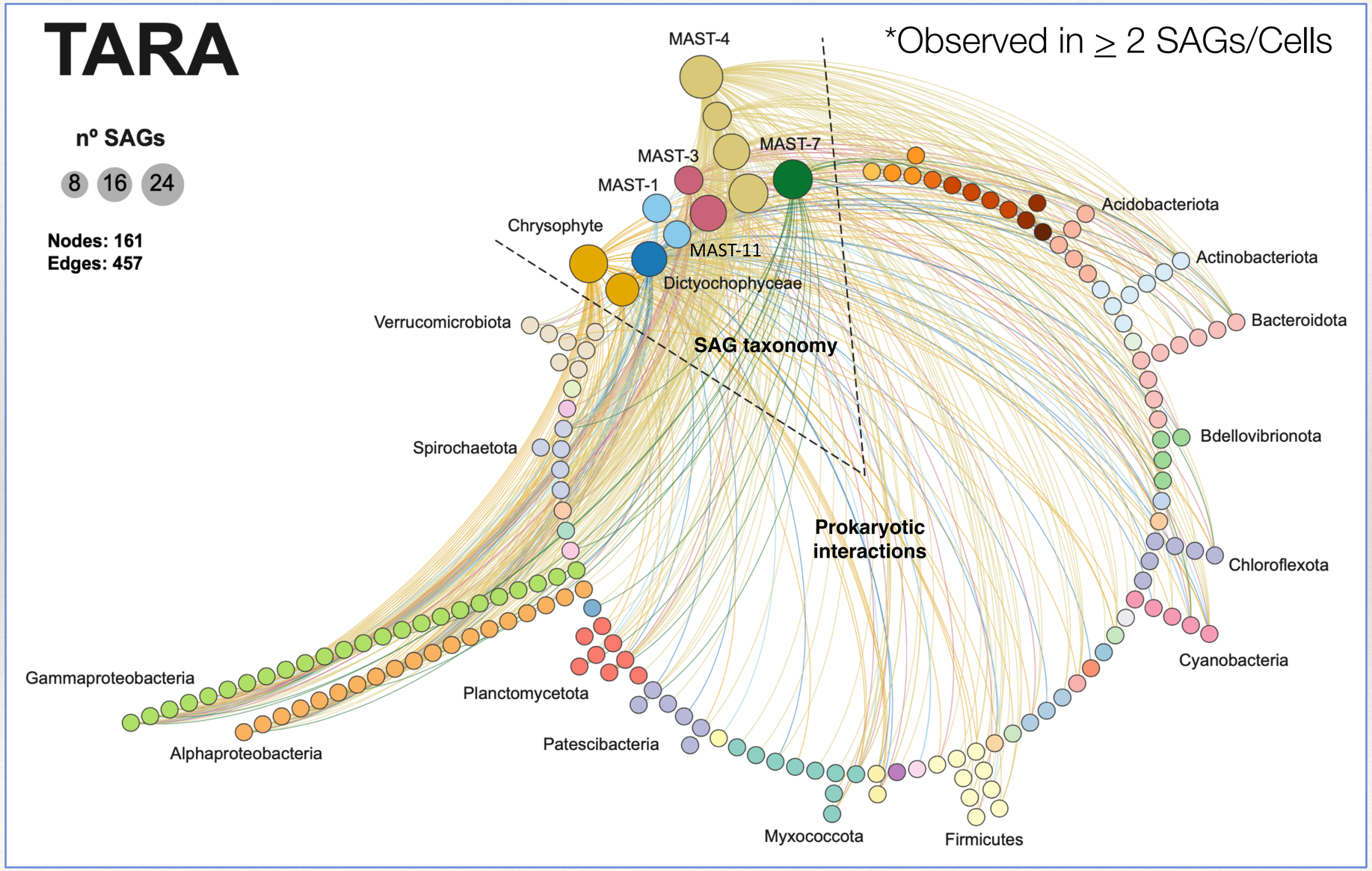
Horizontal and vertical change of networks in the global ocean

Samples location

GoM – Gulf of Maine
BBMO – Blanes Bay
TARA – Indian Ocean & MS

3,015 SAGs of protists

Eukaryotic – Prokaryotic interactions



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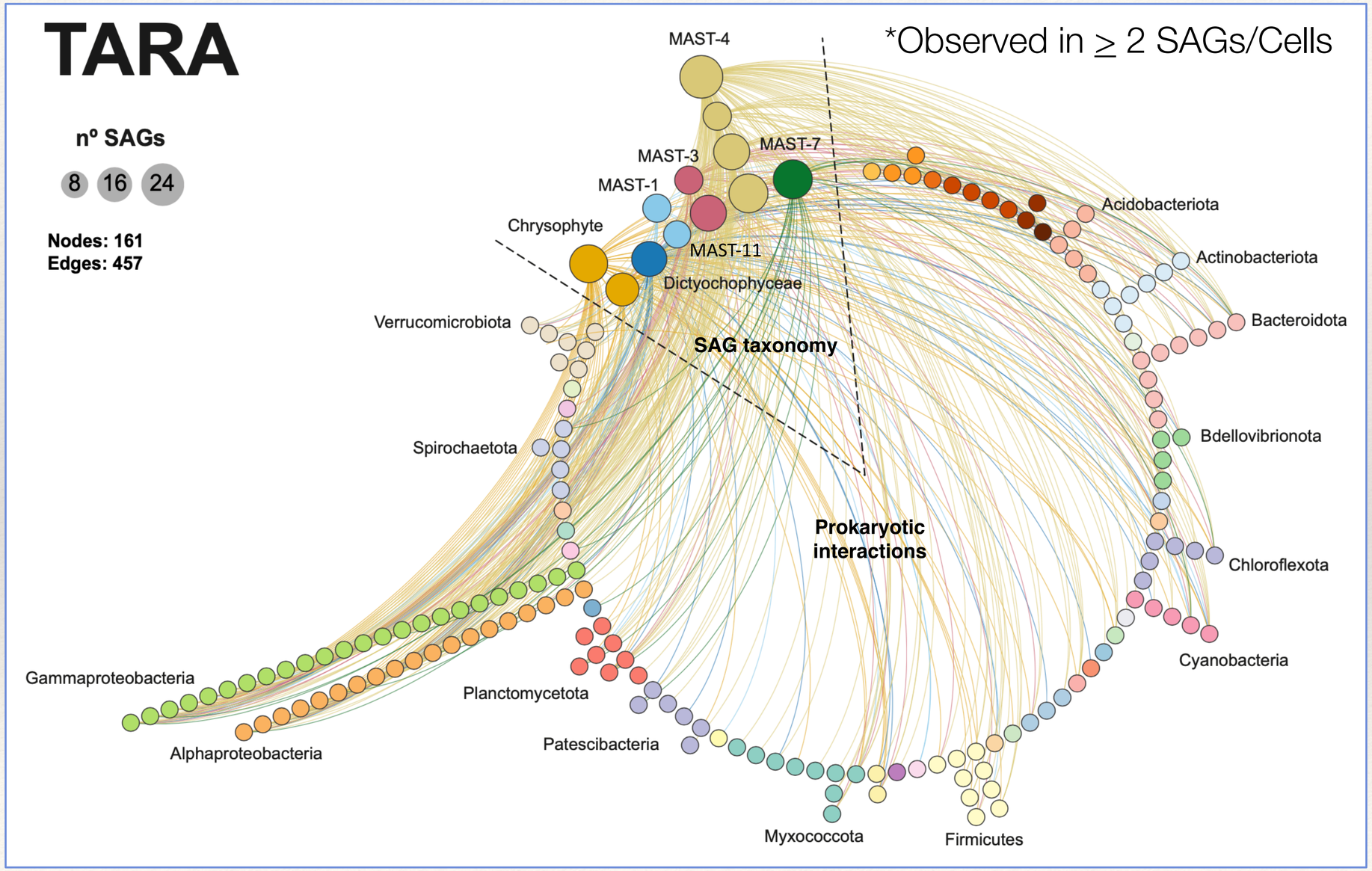
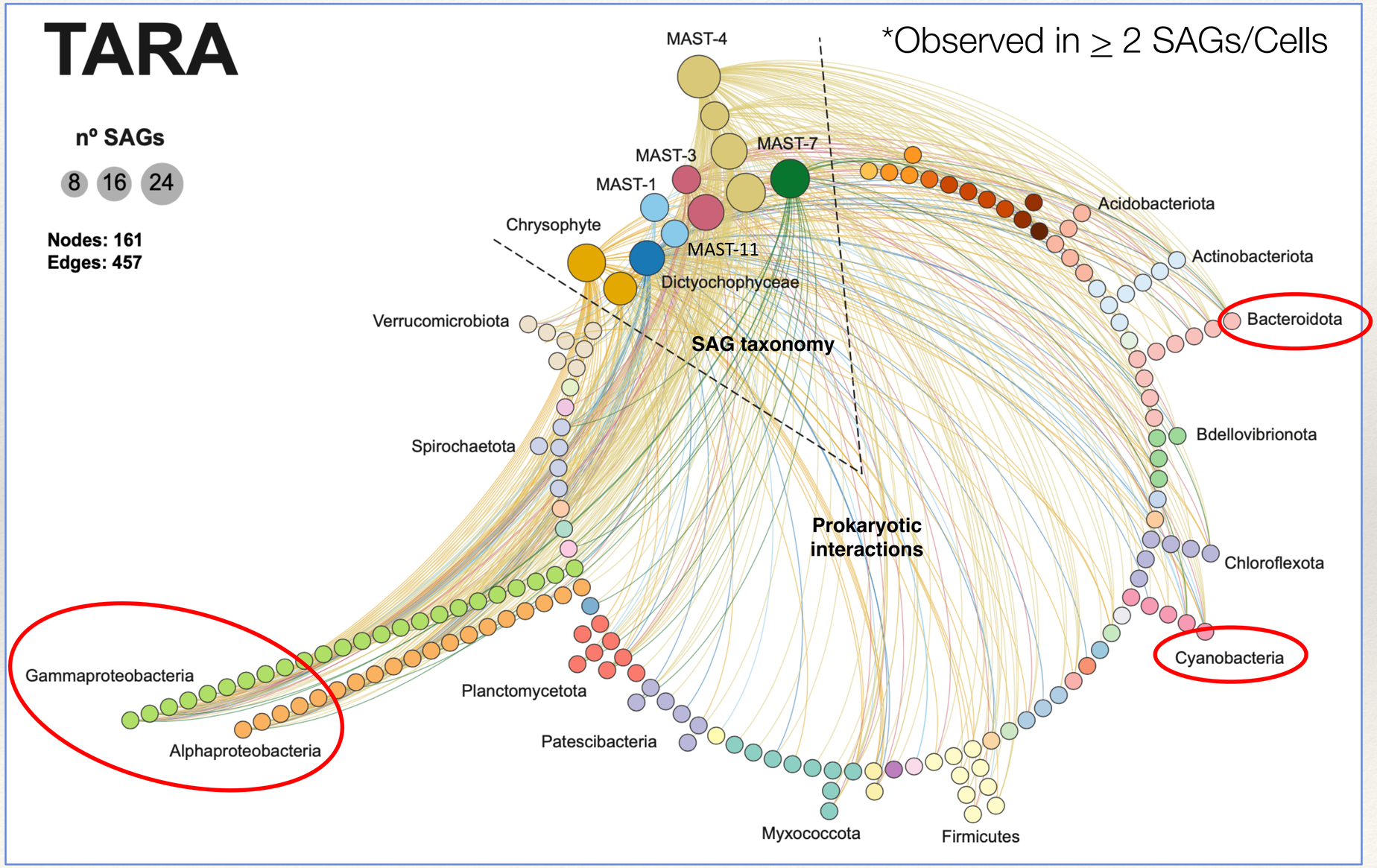


Taxonomy	Nº SAGs	Interactions (Order level)
Chrysophyte-G	14	36
Chrysophyte-H	19	56
Dictyochophyceae	17	38
MAST-11	9	14
MAST-1D	8	10
MAST-3A	17	9
MAST-3F	9	37
MAST-4A	24	115
MAST-4B	9	47
MAST-4C	20	34
MAST-4E	17	44
MAST-7	20	17

Eukaryotic – Prokaryotic interactions



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2. How do association networks change over a decade and across the global ocean?
   - Networks are highly dynamic over large geographic and temporal scales
3. Can we use Single Amplified Genomes to survey potential microbial interactions?
   - Yes, several strong hypotheses emerge when using this approach

Take home messages

- Substantial population structure and differentiation in microbes: we are opening the black box (this was expected)
- But there are also microbes with low population structure/differentiation
- Microbial diversification at species and population levels seems driven by environmental heterogeneity and biotic interactions (not new)
- Microbial association networks can help us identify critical potential interactions
- Microbial networks are dynamic, and we need to understand how they change
- Part of the networks reassemble in a systematic manner
- Single-Cell Genomics emerge as a robust (but expensive) tool to survey microbial interactions

log[lab]

Ecology of Marine Microbes

Institut de Ciències del Mar

Blanes Bay Microbial Observatory

INTERACTOMICS

MALASPINA 2010

TARA OCEANS by TARA EXPEDITIONS www.taraexpeditions.org

minime

MARBITS

CESGA Centro de Supercomputación de Galicia

GENOSCOPE Centre National de Séquençage

BIGELOW LABORATORY FOR OCEAN SCIENCES

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