



From Genes to Pixels: Towards Biodiversity from Space

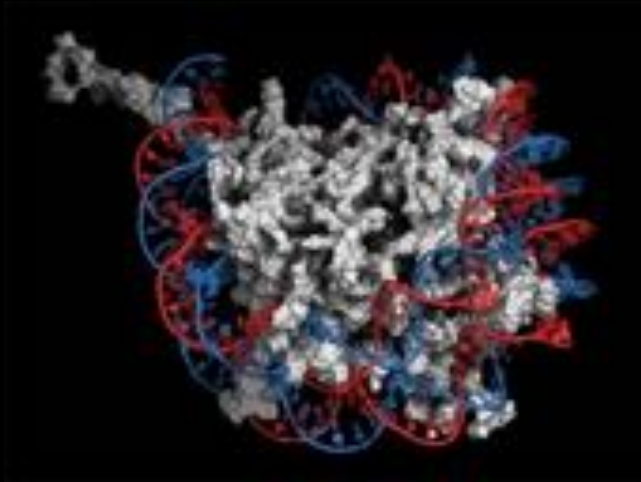
Roy El Hourany, Junior Professor at ULCO-LOG

Contribution: Ziad Sari El Dine, Christophe Guinet, Lucile Duforêt-Gaurier, Hubert Loisel, Cedric Jamet, Marie Montero, Maximiliano Arena, Alain Fumenia, Rimi Kobeissi, Pedro Junger, Juan Pierella Karlusich, Lucie Zinger, Marina Levy, Luther Ollier, Chris Bowler, Lola Daboussy, Colomban de Vargas, Margaux Crédeville, Olivier Jaillon

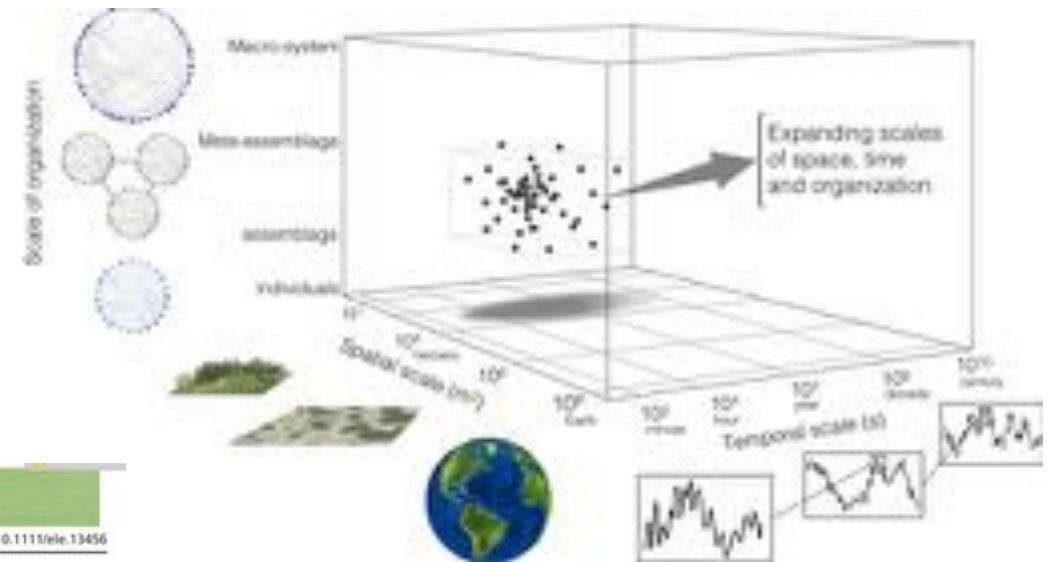
Darmstadt, Germany
1-4 December 2025



Biodiversity Across Scales



Biodiversity Across Scales: From Gene to Globe

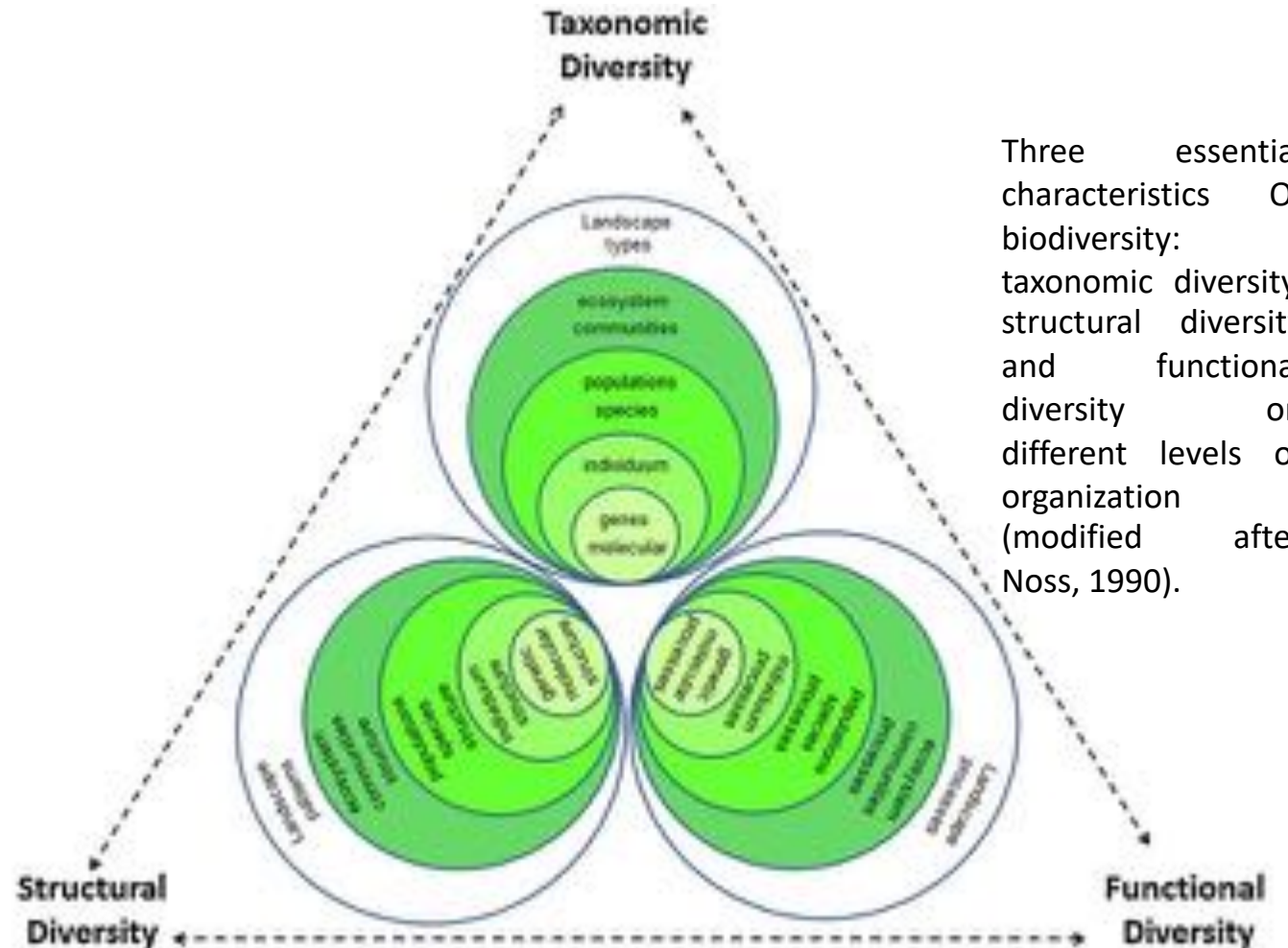
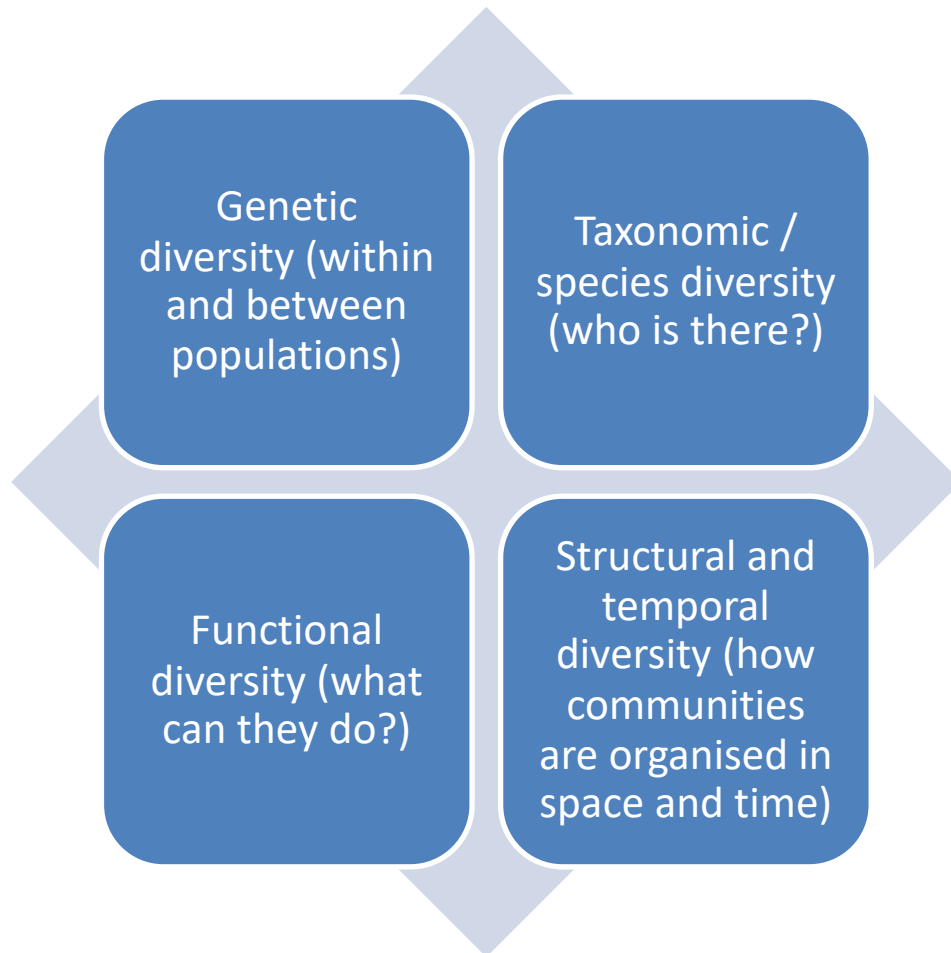


Gonzalez et al. 2020

The three dimensions of scale in Biodiversity-Ecosystem function (BEF) research: time, space and organisation

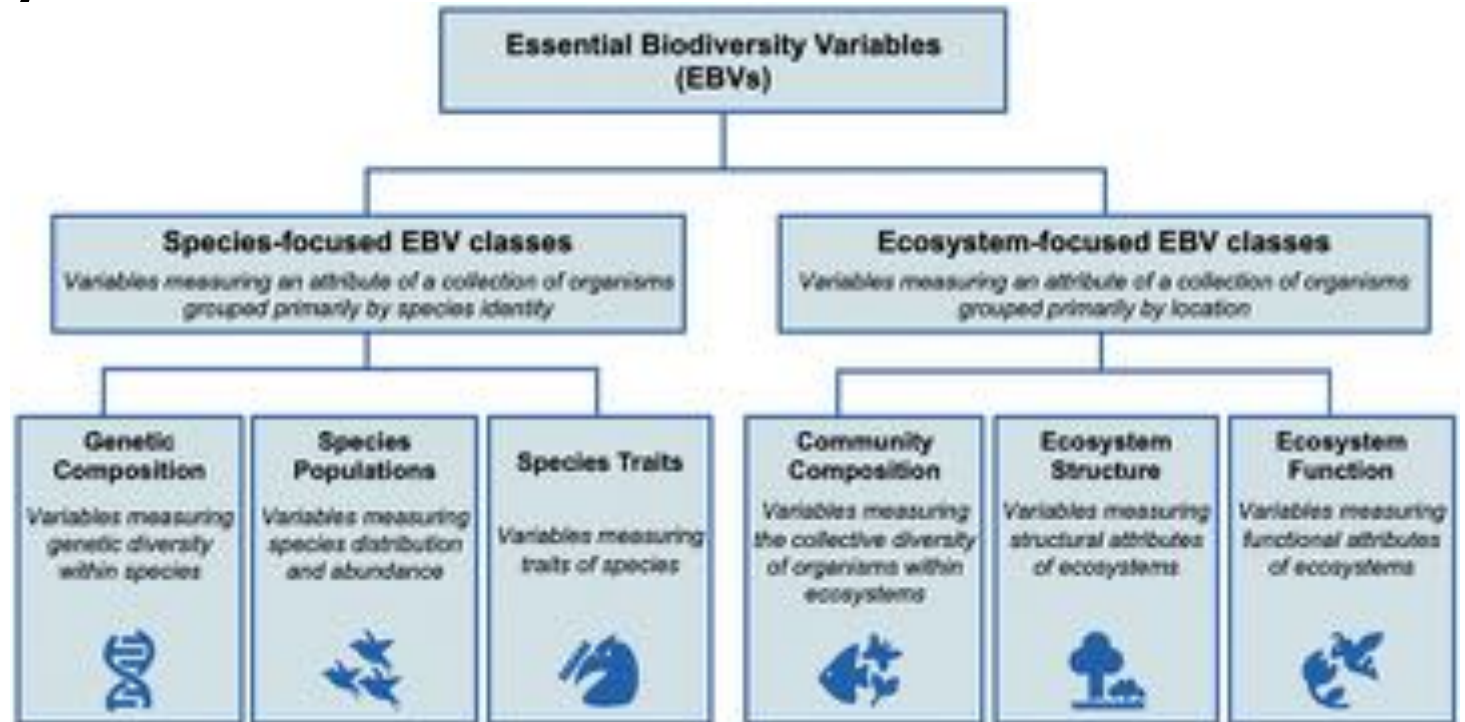
Defining Biodiversity

Biodiversity, the variability among living organisms from all sources, underpins all life on Earth. This includes diversity within species, between species and across ecosystems, representing the genetic makeup of plants, animals, microorganisms and the complexity of ecosystems (WHO, 2025).

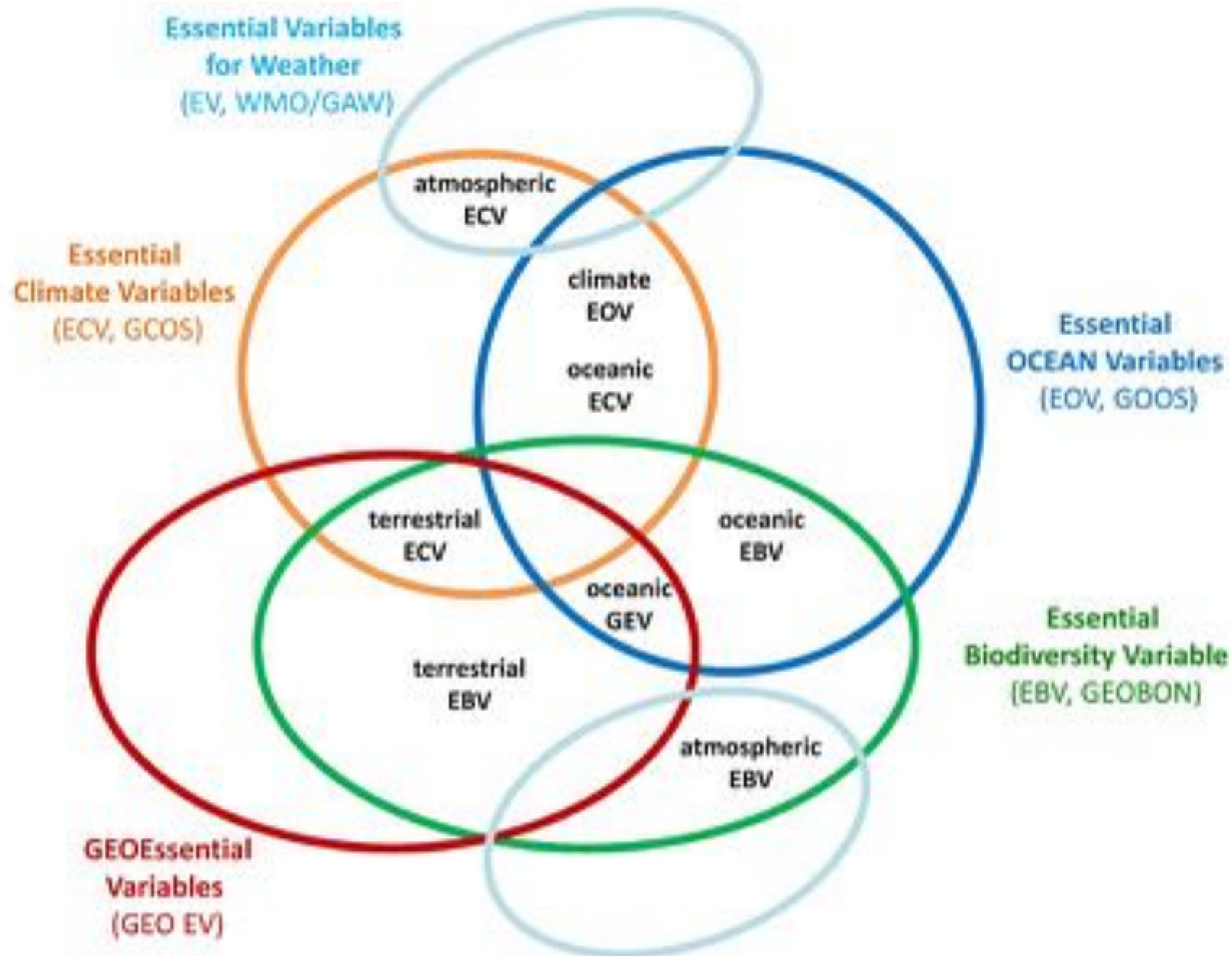


Essential Biodiversity Variables

Essential Biodiversity Variables (EBVs) are a set of standardized biological measurements that help scientists study, report and manage changes in biodiversity across time, space, and biological level. They bridge the gap between raw biodiversity data and derived policy-relevant indicators, and have the potential to serve as a foundation for biodiversity monitoring programs around the world (Pereira et al. 2013).

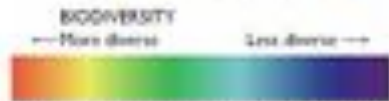
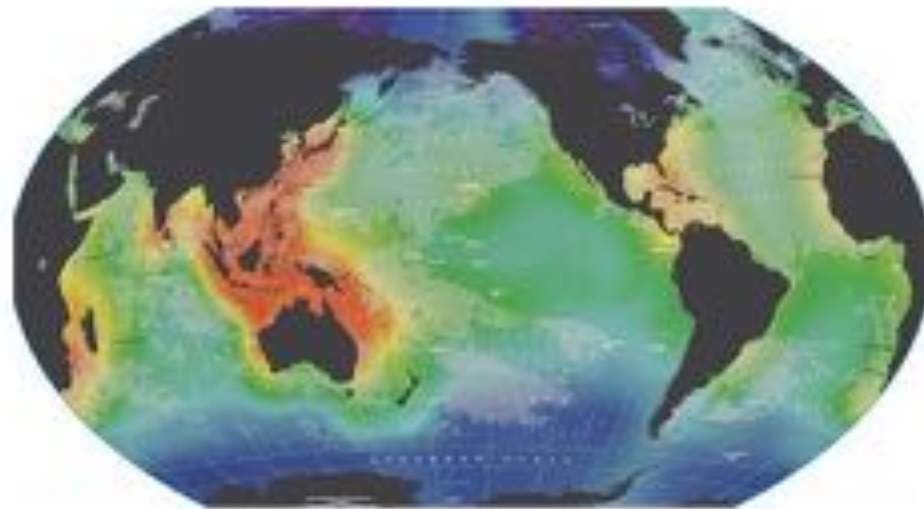


Conceptual overlap of all projects for defining Essential Variables



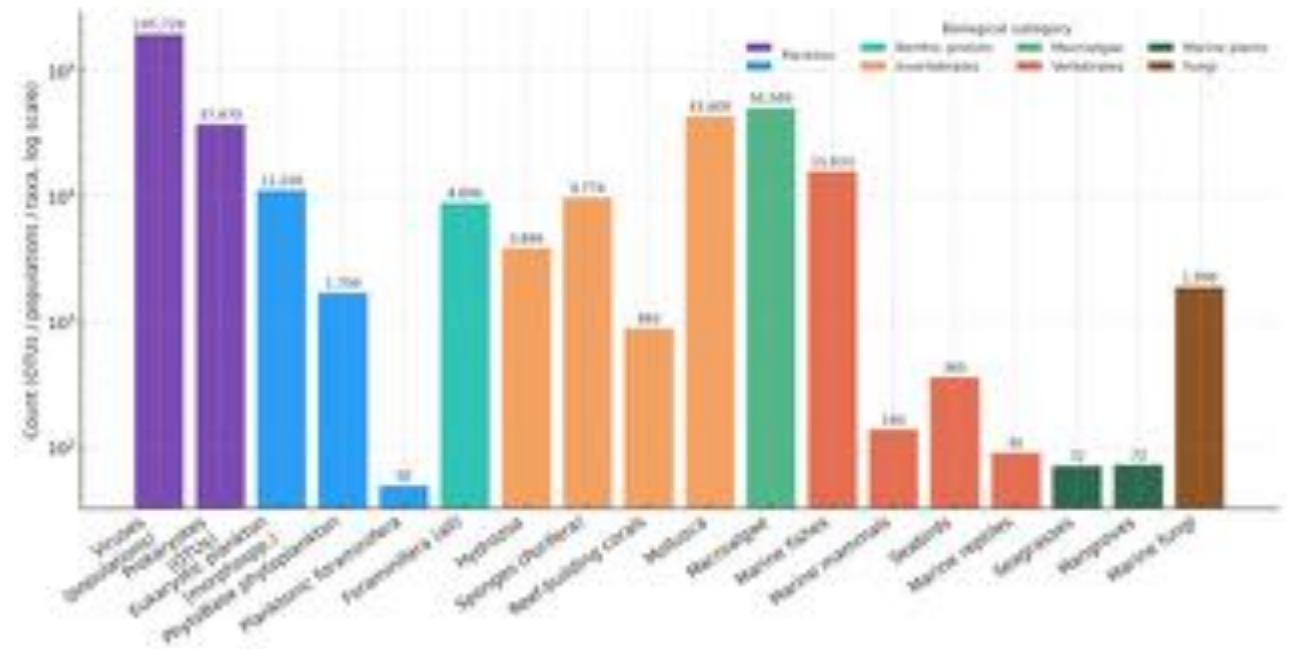
Essential Variables for Weather-EVW, (led by WMO/GAW–World Meteorological Organization/Global Atmosphere Watch, Essential Ocean Variables-EOV (led by the GOOS–Global Ocean Observing System), Essential Climate Variables-ECV (led by GCOS–Global Climate Observing System), Essential Biodiversity Variables-EBV (led by GEOBON–Group on Earth Observations Biodiversity) and the GeoEssential Variables-GEO EV (led by the actual project (<http://www.geoessential.net/>) (modified after Lindstrom et al.).

Distribution of biodiversity in the oceans



The boundaries and names shown and the designations used on this map do not imply official endorsement or acceptance by the United Nations.

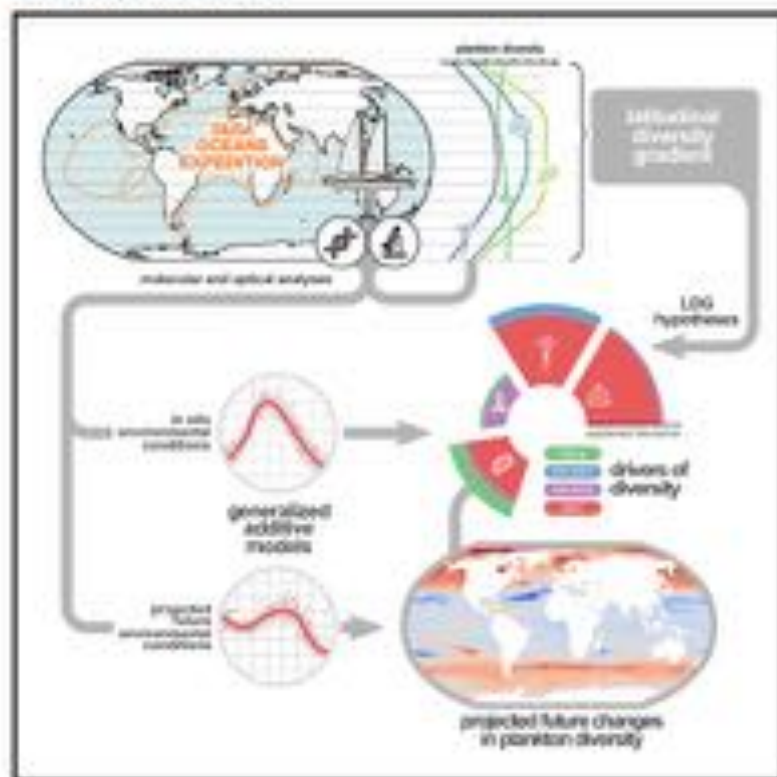
Distribution of biodiversity in the oceans. Biodiversity data: tittensor et al., 2010. Map: census of marine life (2010); ausubel et al. (2010); national geographic society (2010).” Appears in world ocean assessment I, part II, chapter 1: introduction- planet, oceans and life.



de Vargas et al., 2015; Righetti et al., 2020; Righetti et al., 2019; Brummer & Kučera, 2022; Holzmann et al., 2024; World Hydrozoa Database (WoRMS), 2025; Rosenberg, 2014; World Porifera Database (WPD), 2025; IUCN, 2024; Guiry, 2024; Short et al., 2011; West et al., 2016; Duke et al., 1998; Spalding et al., 2010; FAO, 2020; Humphries et al., 2023; BirdLife International, 2025; BirdLife Seabird Tracking Database Team, 2024; Society for Marine Mammalogy Committee on Taxonomy, 2025; Avila et al., 2024; Sunagawa et al., 2015; Gregory et al., 2019.

Global Trends in Marine Plankton Diversity across Kingdoms of Life

Graphical Abstract



Authors

Federico M. Ibarbalz, Nicolas Henry, Manoela C. Brandão, ..., Fabien Lomban, Chris Bowler, Lucie Zinger

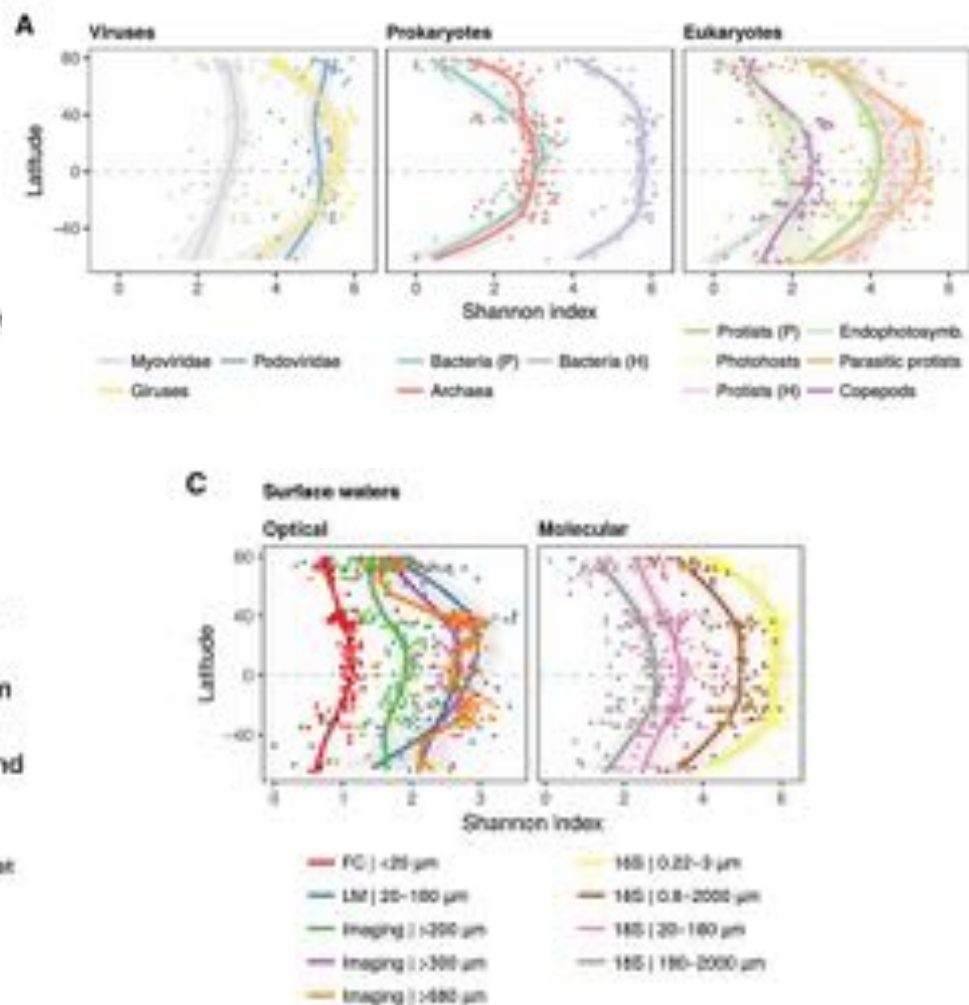
Correspondence

cbowler@biologie.ens.fr (C.B.), lucie@zinger.fr (L.Z.)

In Brief

The drivers of ocean plankton diversity across archaea, bacteria, eukaryotes, and major virus clades are inferred from both molecular and imaging data acquired by the Tara Oceans project and used to predict the effects of severe warming of the surface ocean on this critical ecosystem by the end of the 21st century.

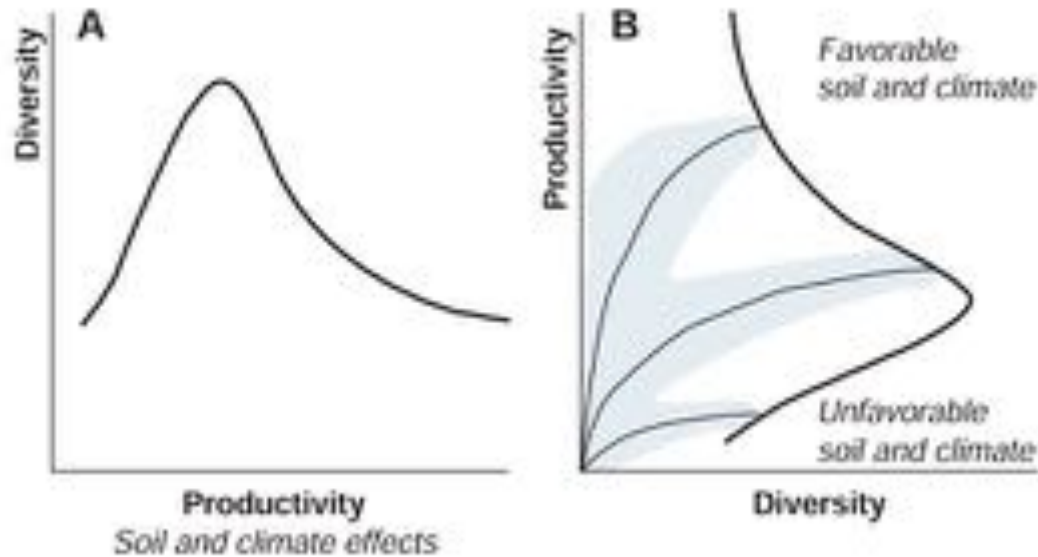
Ibarbalz et al., 2019



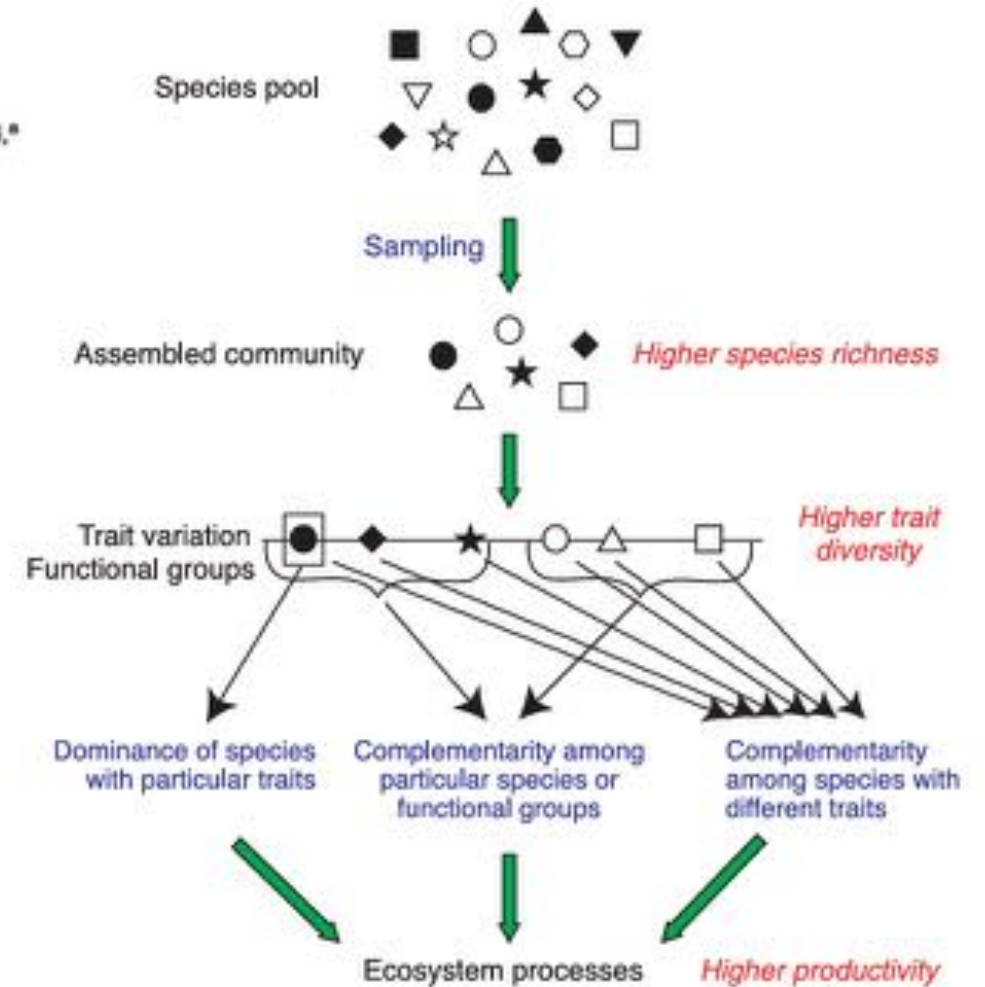


Biodiversity and Ecosystem Functioning: Current Knowledge and Future Challenges

M. Loreau,^{1*} S. Naeem,² P. Inchausti,¹ J. Bengtsson,³ J. P. Grime,⁴ A. Hector,⁵ D. U. Hooper,⁶ M. A. Huston,⁷ D. Raffaelli,⁸ B. Schmid,⁹ D. Tilman,¹⁰ D. A. Wardle⁴

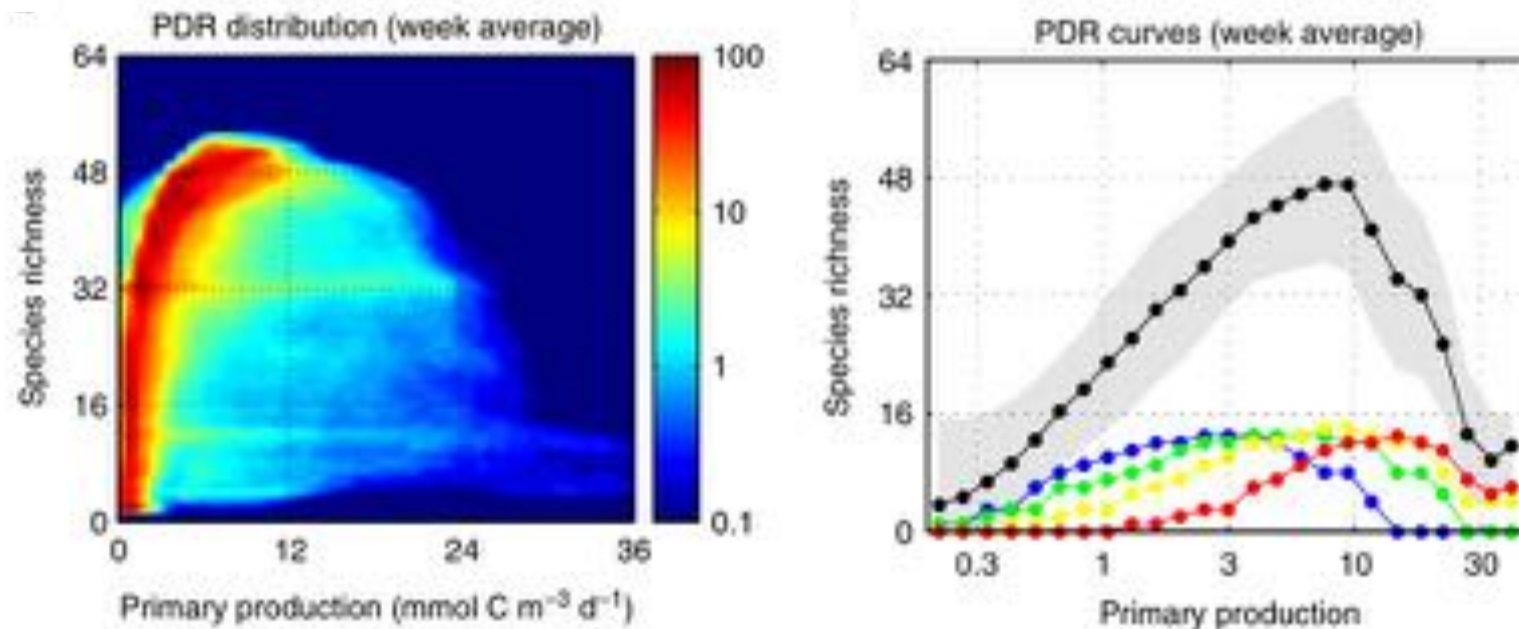


Hypothesized relationships between (A) diversity productivity patterns driven by environmental conditions across sites, and (B) the local effect of species diversity on productivity in a grassland ecosystem.



Global relationship between phytoplankton diversity and productivity in the ocean

S.M. Vallina^{1,2}, M.J. Follows¹, S. Dutkiewicz¹, J.M. Montoya², P. Cermeno² & M. Loreau³



Global PDR distribution of model outputs using weekly averaged data. Units: primary production (mmol C m³ d⁻¹); phytoplankton diversity (# species) (contributing 41% total biomass). **Global PDR curve of model outputs using equally spaced log₁₀ bins of primary production using weekly averaged data.** Units: primary production (mmol C m³ d⁻¹); phytoplankton diversity (# species) (contributing 41% total biomass). Colour legend: Prochlorococcus (blue line), Synechococcus (green line), f lagellates (yellow line) and diatoms (red line).

Observing Tools Along the Biodiversity Scale Ladder



Omics: genes, cells, organisms,
function, communities



Microscopy, cytometry,
pigments, optics: cells, traits,
organisms, communities



Autonomous platforms &
animal-borne sensors: 4D
context and behavior



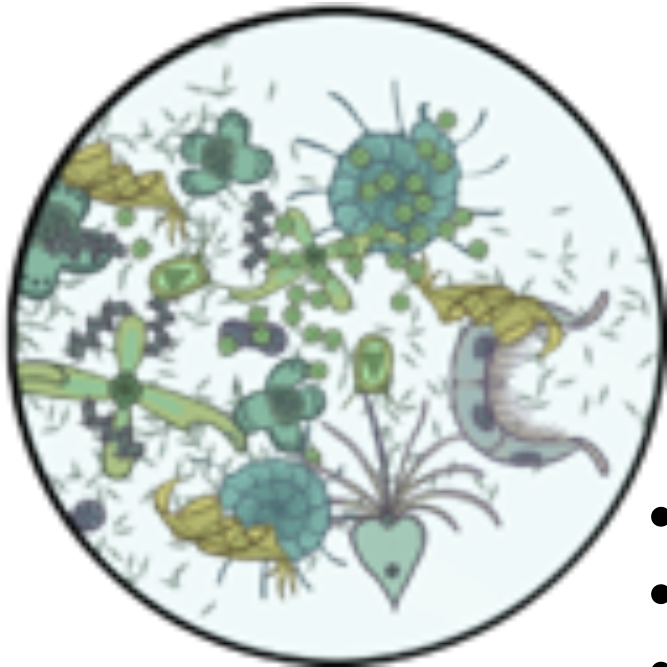
Satellites: continuous coverage
of surface environment and
optical properties

What Satellites OC Actually Measure

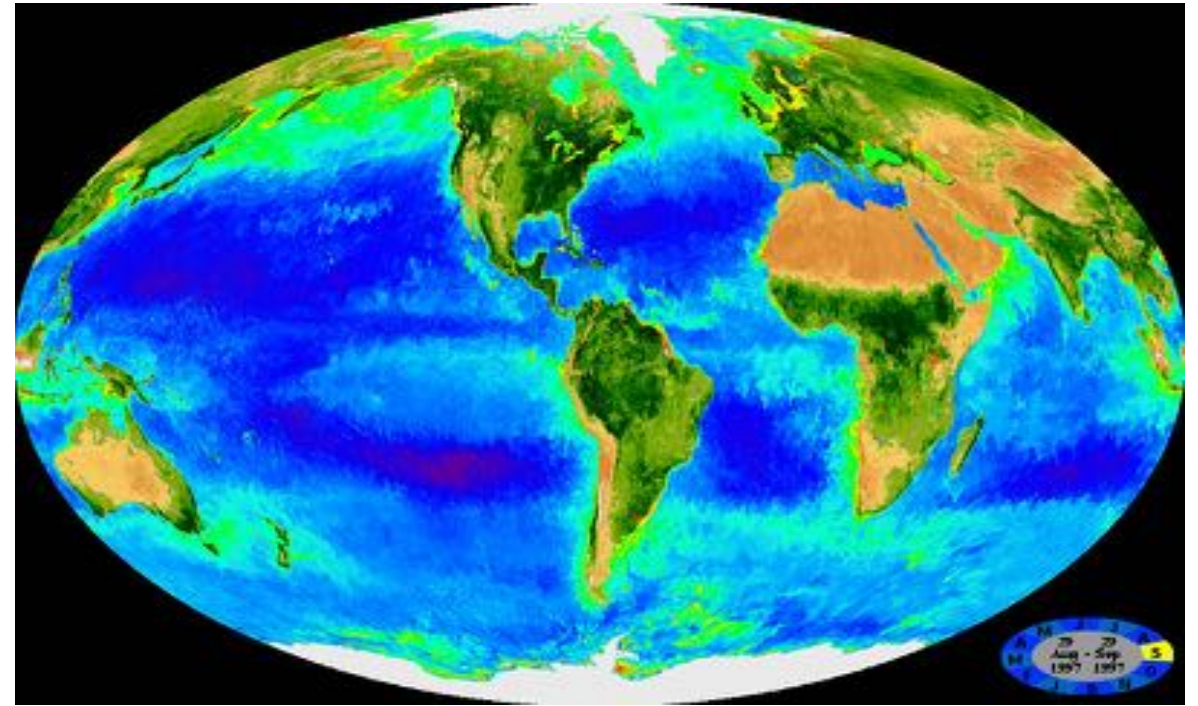
Satellites see proxies and context for biodiversity, not species directly

- **Spectral reflectance**
- Derived environmental variables: PAR temperature,
- Derived optical properties (a , b_b),
- Derived biogeochemical variables (Chl a , K_d , SPM, POC...)

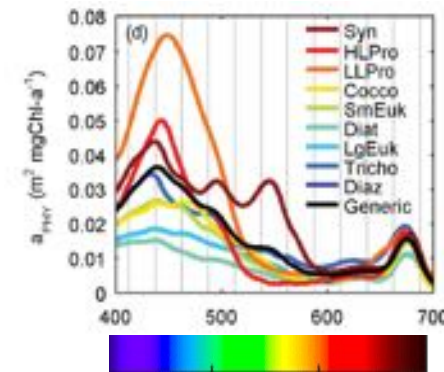
Phytoplankton interaction with light depends on:



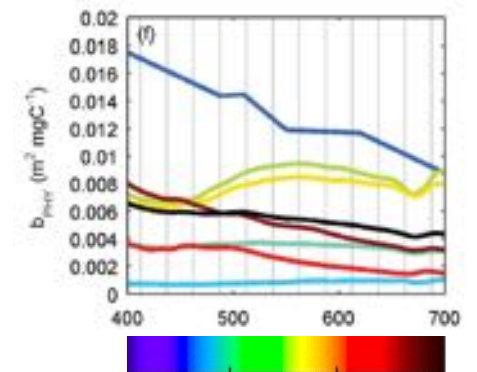
- Cell Concentration
- Pigment composition
- Taxonomic composition
- Size, morphology and physiology.



Absorption



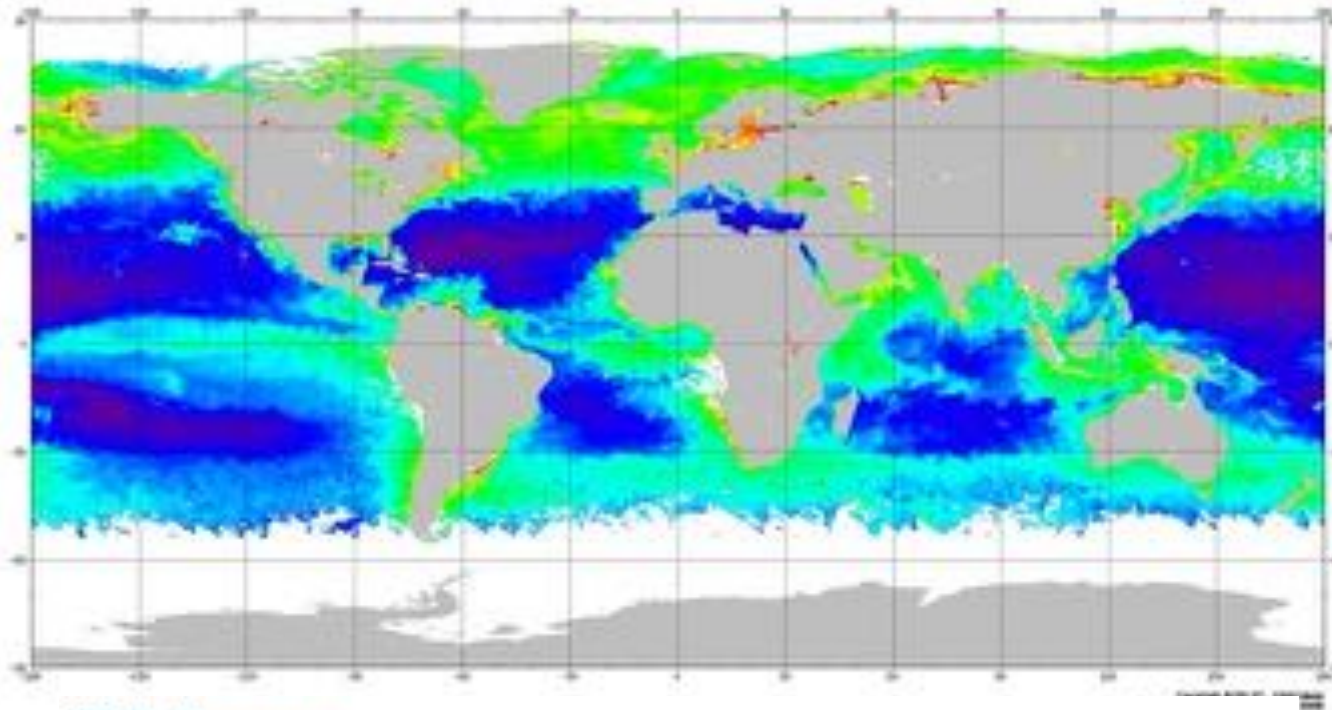
Back-scatter



Dutkiewicz et al., 2015

Beyond Chlorophyll-a

OC2v3 CHL1 - OC4v3
 Global Colour monthly Level-3 product
 2013-08-01 to 2013-08-31



JGR Oceans

RESEARCH ARTICLE
 10.1029/2013JC004450

Key Points:

- The dynamics of phytoplankton communities can be observed while reconstructing secondary pigment variability from ocean color observations
- Self-organizing maps allow an accurate retrieval of different phytoplankton pigment concentrations from satellite observations

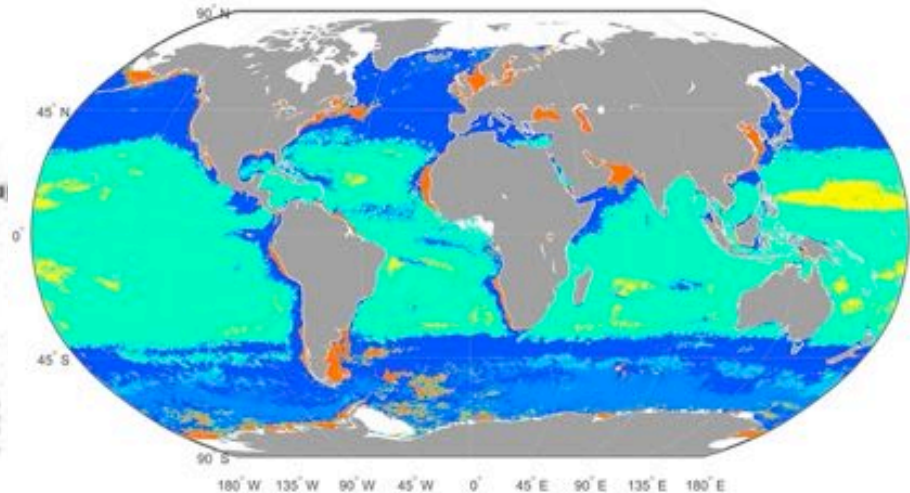
Estimation of Secondary Phytoplankton Pigments From Satellite Observations Using Self-Organizing Maps (SOMs)

Roy El Hourany^{1,2}, Marie Abboud-Abi Saab³, Ghaleb Faour², Olivier Aumont⁴, Michel Crépon¹, and Sylvie Thiria^{1,4}

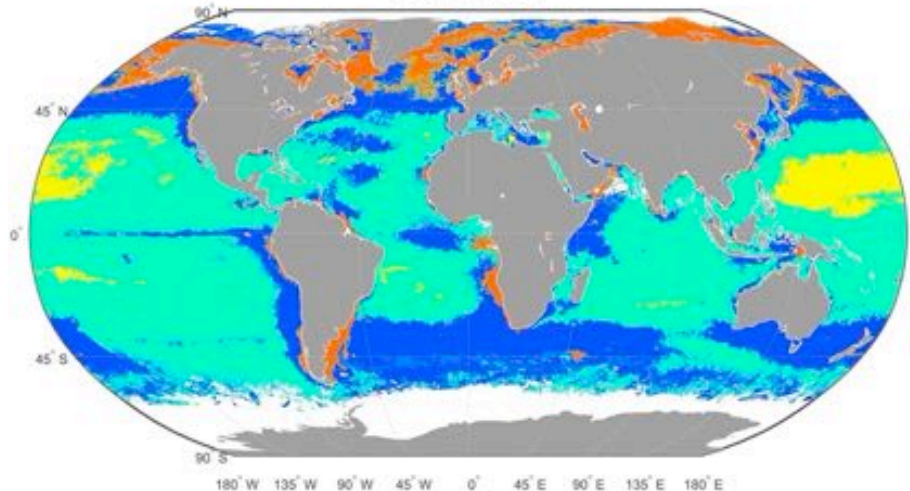
¹IPSL/LOCEAN, Sorbonne Université (Université Paris VI, CNRS, IRD, MNERG), Paris, France, ²National Center for Remote Sensing, National Council for the Scientific Research, Beirut, Lebanon, ³National Center for Marine Sciences, National Council for the Scientific Research, Batroun, Lebanon, ⁴Observatoire de Versailles Saint-Quentin-en-Yvelines (OVVSQ) Versailles Saint-Quentin-en-Yvelines University, Versailles, France

CHL1
 (mg/m3)

Winter



Summer



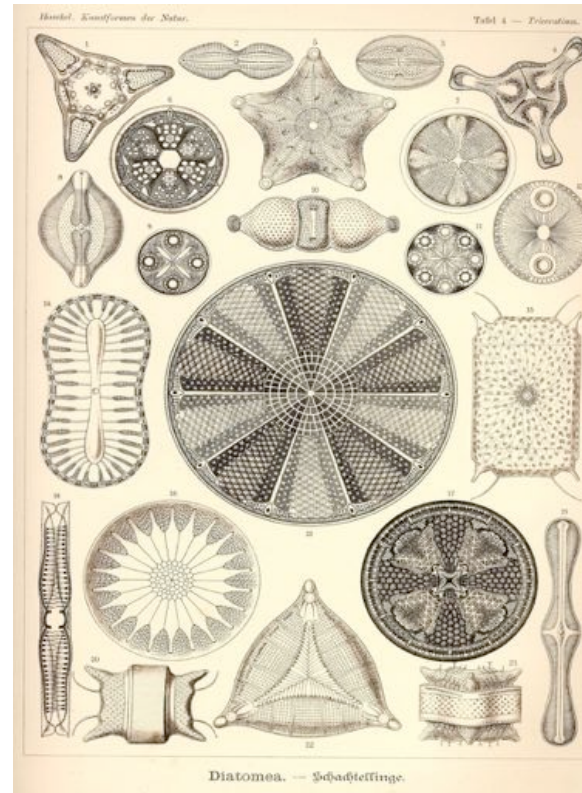
Fuco
 Perid
 DVChl_a
 DVChl_b
 Zea
 19BF
 Allo
 Chl_b
 19HF

Phytoplankton Community structure

PG =Phytoplankton Groups

Taxonomic groups PG

Diatoms
Dinoflagellates
Green Algae
Haptophytes
Cyanobacteria...



Ernst Haeckel,
“Kunstformen der
Natur” (Art forms
of nature),1904

Phytoplankton Community structure

Taxonomic groups PG

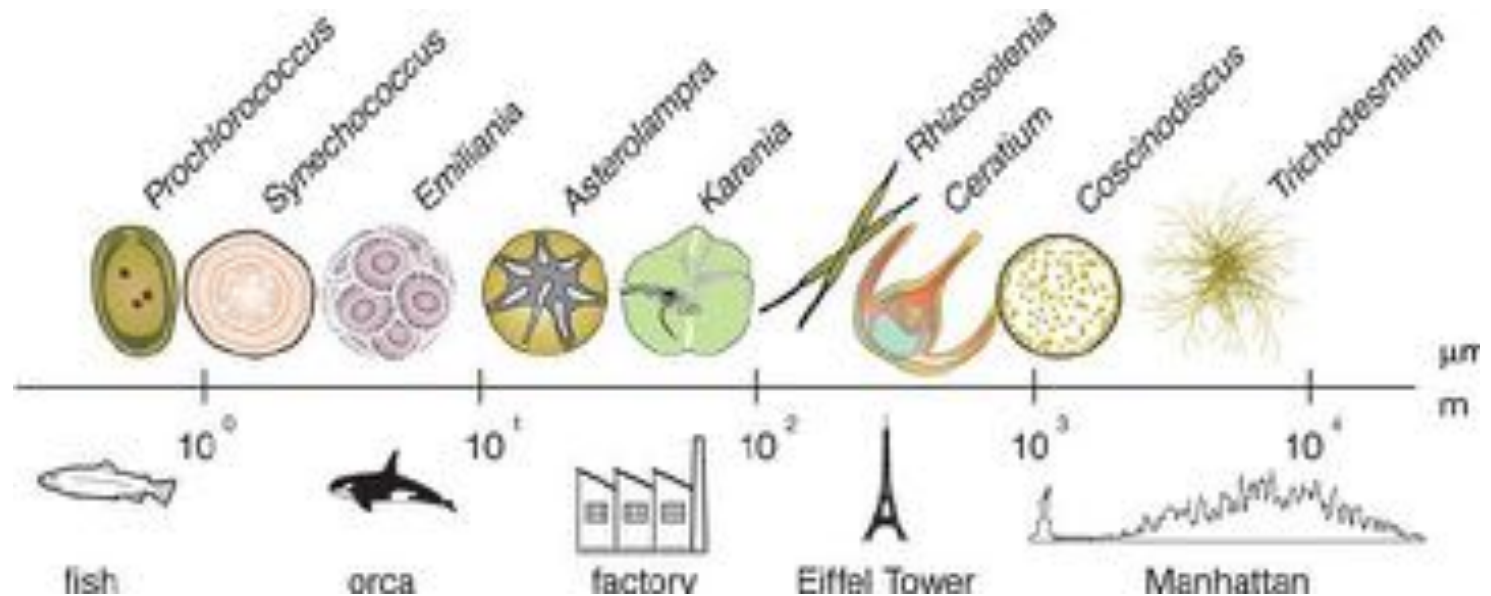
Diatoms
Dinoflagellates
Green Algae
Haptophytes
Cyanobacteria...

Size ranges PSC

Micro-phytoplankton 20 - 200 μm
Nano-phytoplankton 2 - 20 μm
Pico-phytoplankton 0.2 - 2 μm

PG =Phytoplankton Groups

PSC =Phytoplankton Size Classes



Finkel et al. 2010

Phytoplankton Community structure

Taxonomic groups PG

Diatoms
Dinoflagellates
Green Algae
Haptophytes
Cyanobacteria...

Size ranges PSC

Micro-phytoplankton 20 - 200 μm
Nano-phytoplankton 2 - 20 μm
Pico-phytoplankton 0.2 - 2 μm

Ecosystem functions PFT

Primary producers
Silicifiers
Calcifiers
N₂ fixer etc...

PG =Phytoplankton Groups

PSC =Phytoplankton Size Classes

PFT =Phytoplankton Functional Types



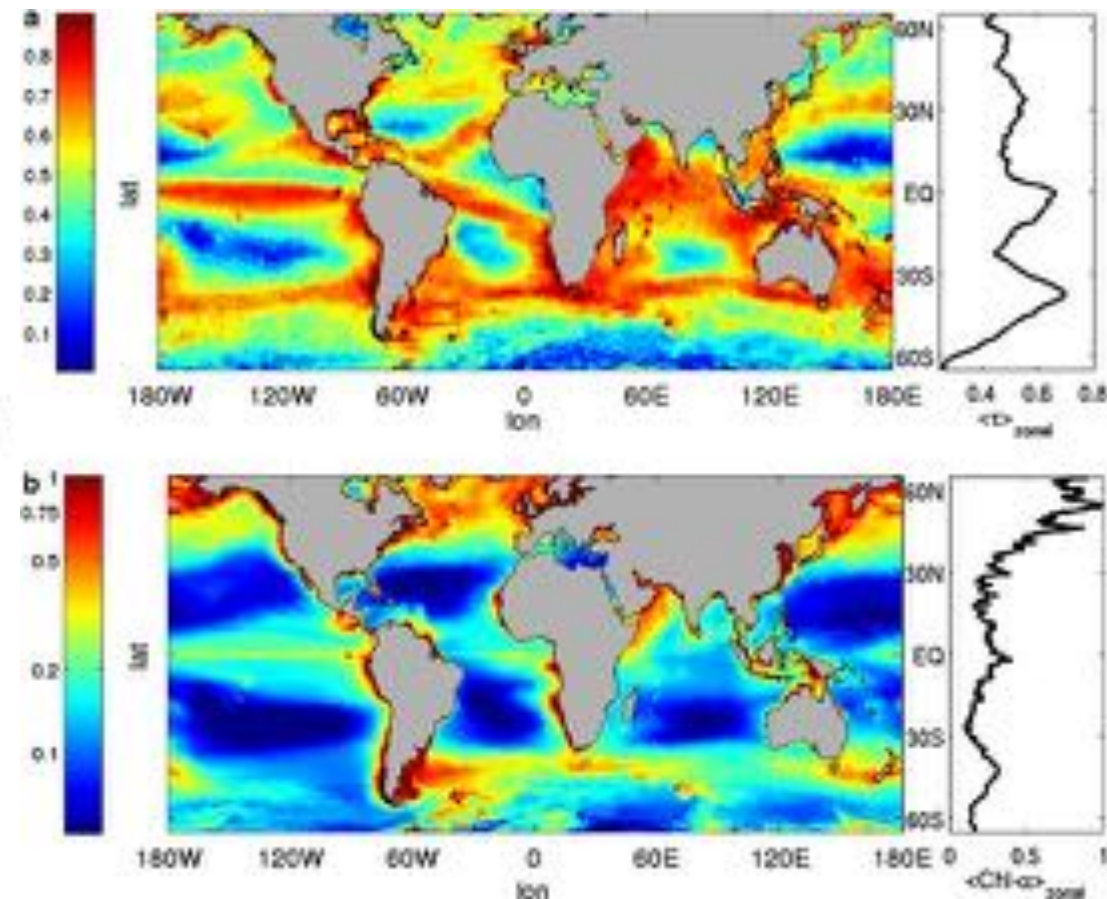
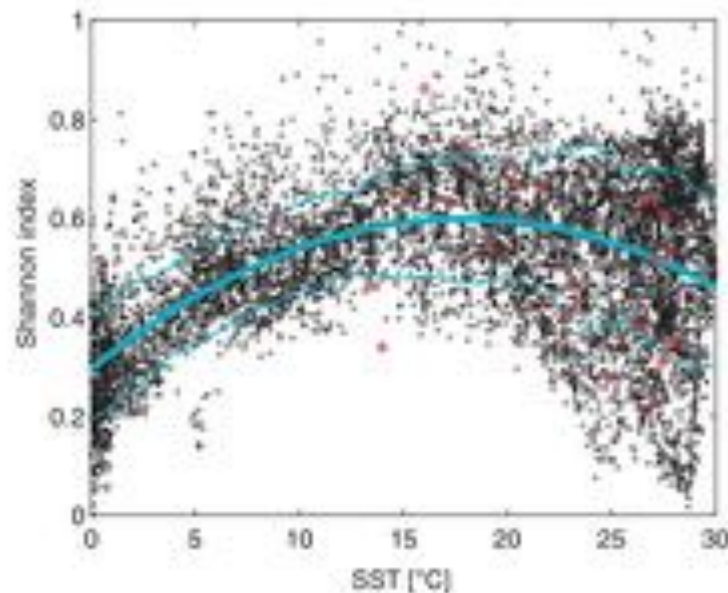
SHORT COMMUNICATION

Can we detect oceanic biodiversity hotspots from space?

Silvia De Monte^{1,2,3}, Alice Soccodato⁴, Séverine Alvain⁵ and Francesco d'Ovidio⁶

¹Ecole Normale Supérieure, Ecologie et Evolution, Paris, France; ²Université Pierre et Marie Curie-Paris 6, Ecologie et Evolution, Paris, France; ³CNRS, Ecologie et Evolution, Paris, France; ⁴Laboratoire d'Océanographie et du Climat: Expérimentation et Approches Numériques, LOCEAN-IPSL, CNRS/MNHN/IRD/UPMC, Paris, France and ⁵Laboratoire d'Océanologie et de Géosciences, CNRS-ULCO-Université Lille Nord de France, Wimereux, France

De Monte et al., 2013



(a) Shannon Index for the global ocean: average of daily maps of the index computed over 7-day composites of PHYSAT data for the period 2003–2010. The hotspots emerging from this analysis characterize regions with a standing representation of several nearby communities, as identified by their dominant phytoplankton types (PHYSAT algorithm applied to SeaWiFS radiances). (b) Average of daily chlorophyll-a maps (SeaWiFS, 2003–2010).



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Deep-Sea Research I 52 (2005) 1989–2004

DEEP-SEA RESEARCH
Part I

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Remote sensing of phytoplankton groups in case 1 waters from global SeaWiFS imagery

S. Alvain^a, C. Moulin^{a,*}, Y. Dandonneau^b, F.M. Bréon^a

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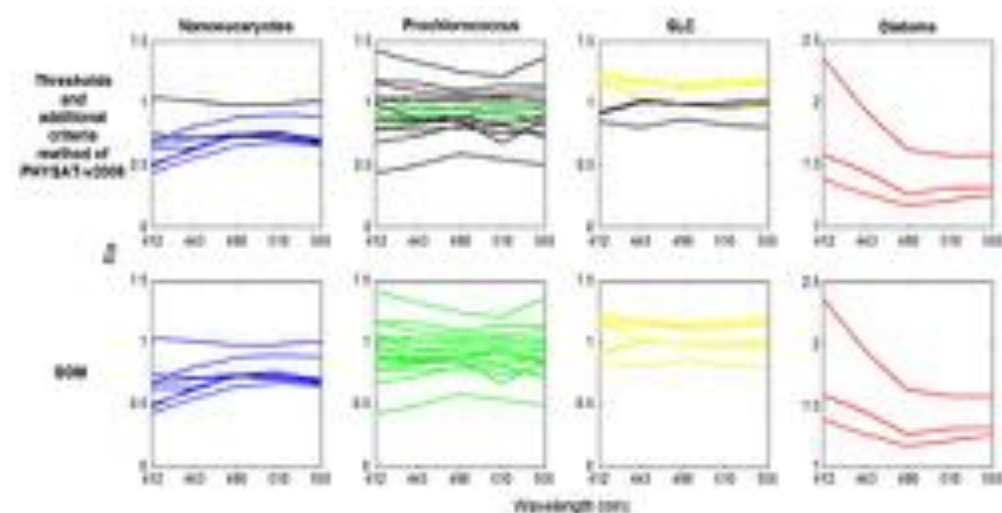


Automatic classification of water-leaving radiance anomalies from global SeaWiFS imagery: Application to the detection of phytoplankton groups in open ocean waters

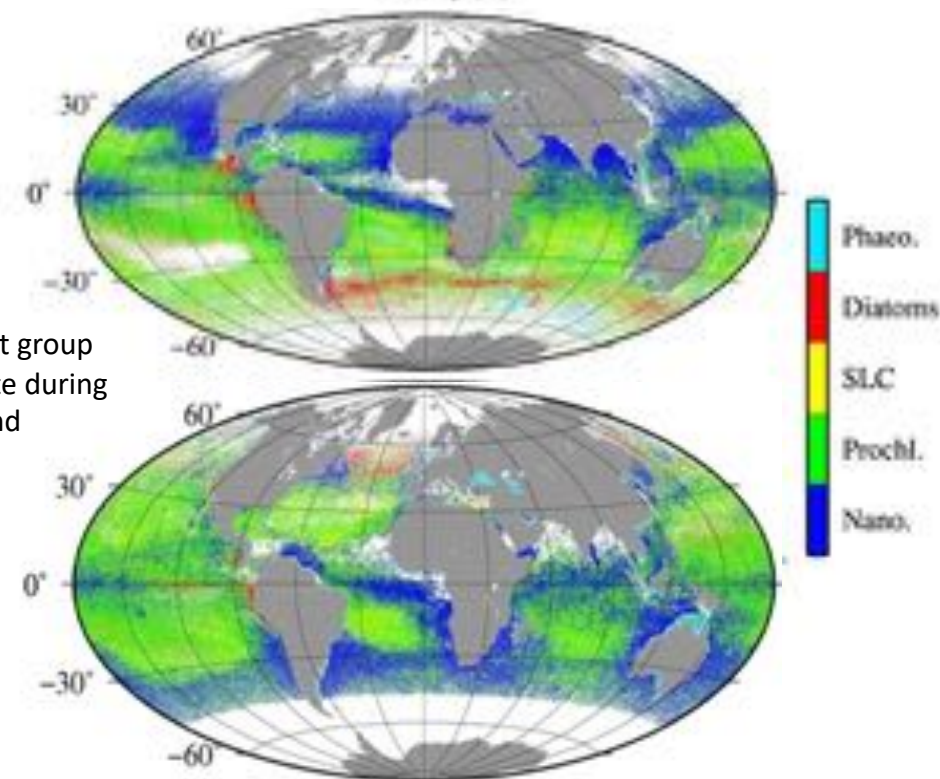
Zied Ben Mustapha, Séverine Alvain^{*}, Cédric Jamet, Hubert Loisel, David Dessailly

OSL, Unité Labo Nord de l'océan, UMR 5175 CNRS, F-42000 Saint-Nazaire, France

Water leaving anomaly per dominant group



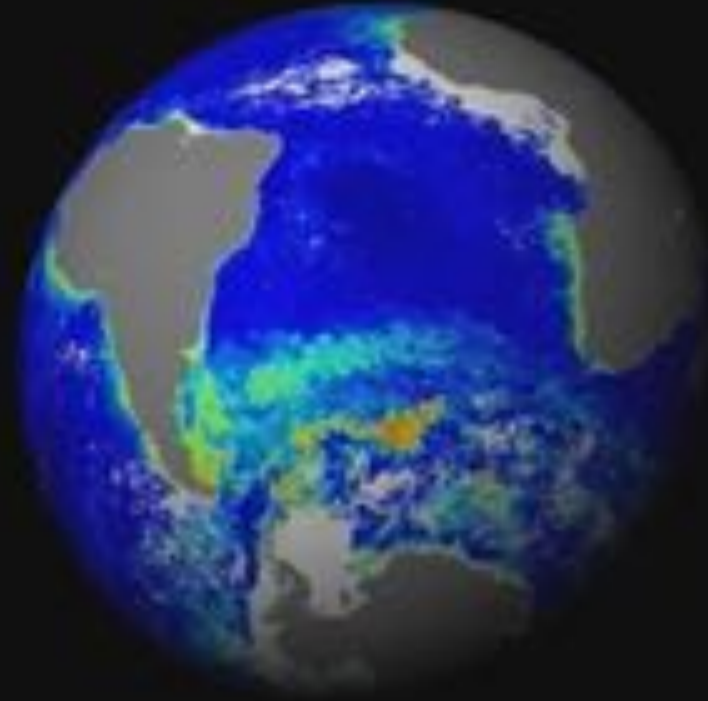
Dominant group composite during winter and summer



Alvain et al., 2005, Ben Mustapha et al., 2014

Taxonomic groups seen from space

El Hourany, R. *et al.*, 2019



Phytoplankton community structure from space: integration of diagnostic pigment concept in ocean color studies

Compilation of published algorithms to assess phytoplankton community composition

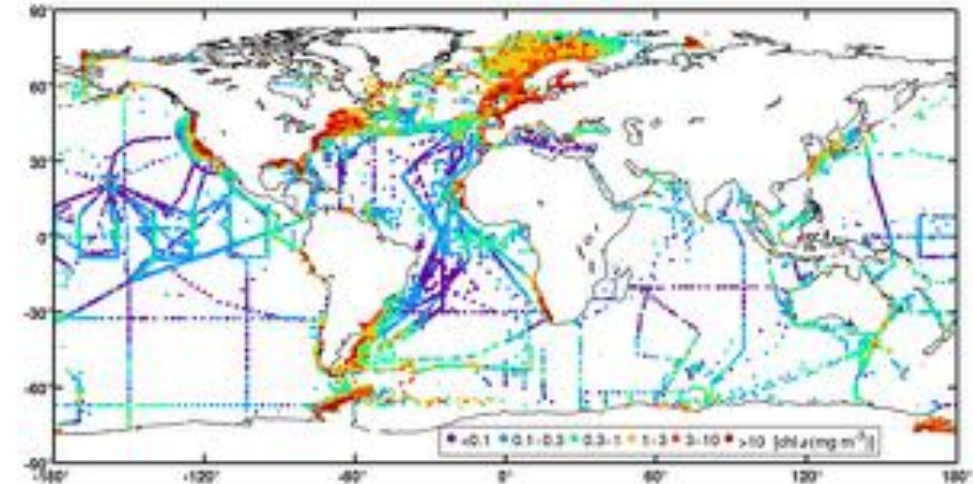
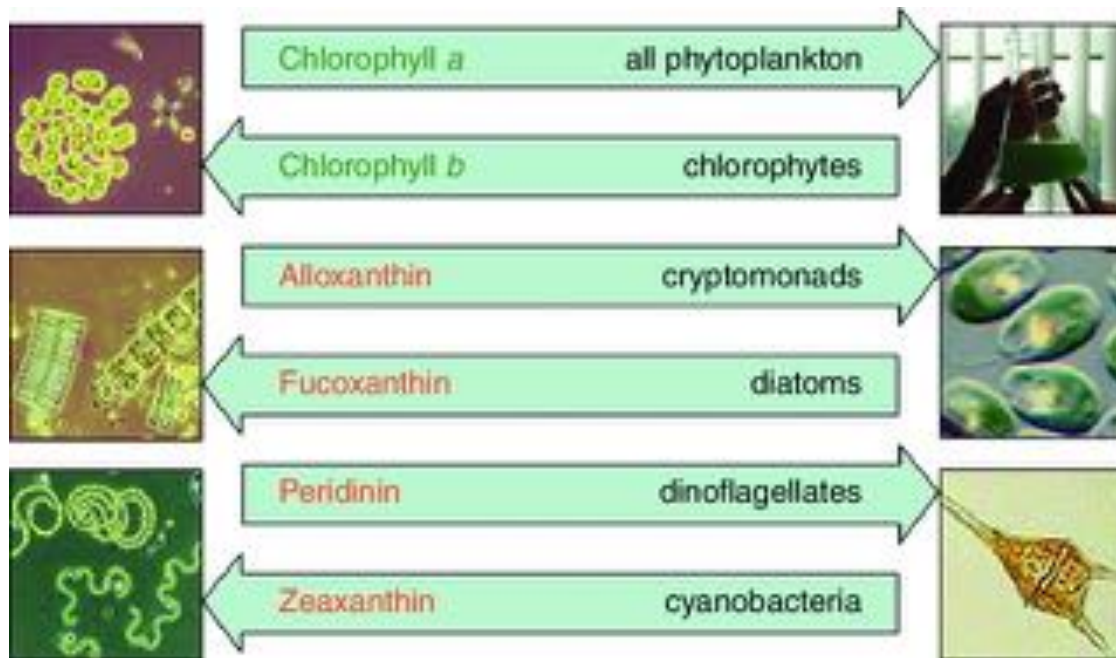
>70% PCC studies from satellite are based on pigments

Application	PCC product(s)	Algorithm validation data	Remote sensing approaches
Global	Taxonomic group(s)	Direct cell observation (cultures and/or field microscopy)	Subramaniam et al. (2001); Westberry et al. (2005) Subramaniam and Carpenter (1994)
		Pigment concentrations	Alvain et al. (2005); Alvain et al. (2008); Ben Muntapha et al. (2014); Bracher et al. (2008); Hirata et al. (2011); Lora et al. (2017); Moore et al. (2012); Palacz et al. (2013); Sadeghi et al. (2012); Seppa et al. (2014); Xi et al. (2020)
		Spectral signatures	Brown and Yoder (1994)
	Size classes, size index, or PSD	Pigment concentrations	Brewin et al. (2010); Brewin et al. (2015); Devred et al. (2006); Devred et al. (2011); Fujiwara et al. (2011); Hirata et al. (2008); Hirata et al. (2011); Kostadinov et al. (2010); Li et al. (2013); Moore and Brown (2020); Mouw and Yoder (2010); Roy et al. (2013, spectral a _{ph} also used in development); Ulitz et al. (2006)
		Mie modeling, Coated Spheres model	Kostadinov et al. (2009); Kostadinov et al. (2022)
		Spectral signatures	Bricaud et al. (2012)
	Accessory pigments	Pigment concentrations	O'Shea et al. (2021); Wang et al. (2018)
Regional /Local	Taxonomic group(s)	Direct cell observation (microscopy of cultures and/or field data or imaging-in-flow cytometry)	Chase et al. (2022); Raitos et al. (2008) R��ve-Lamarche et al. (2017)
		Pigment concentrations	Di Cicco et al. (2017); Kramer et al. (2018); Pallacios et al. (2015); Sathyendranath et al. (2004); Werdell et al. (2014)
		Spectral signatures	
	Size classes, size index, or PSD	Pigment concentrations	Gittings et al. (2019)
		Spectral signatures	Clotti and Bricaud (2006)
	Accessory pigments	Pigment concentrations	Bracher et al. (2015); Pan et al. (2010); Sun et al. (2022)

Phytoplankton community structure from space: integration of diagnostic pigment concept in ocean color studies

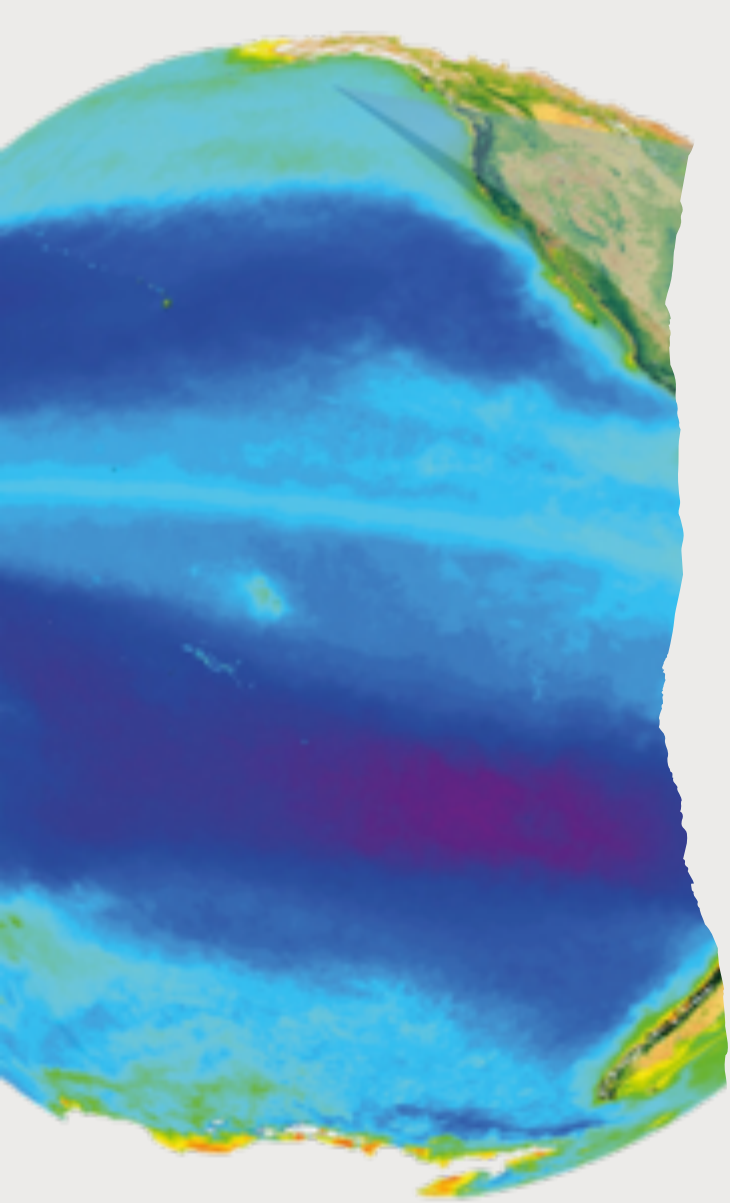
A methodology covering Prok to Euk phytoplankton

Over 20K obs compiled HPLC dataset of Chla and several pigments measured at the surface (<30m), (Valente et al., 2019; Kramer et al., 2019)

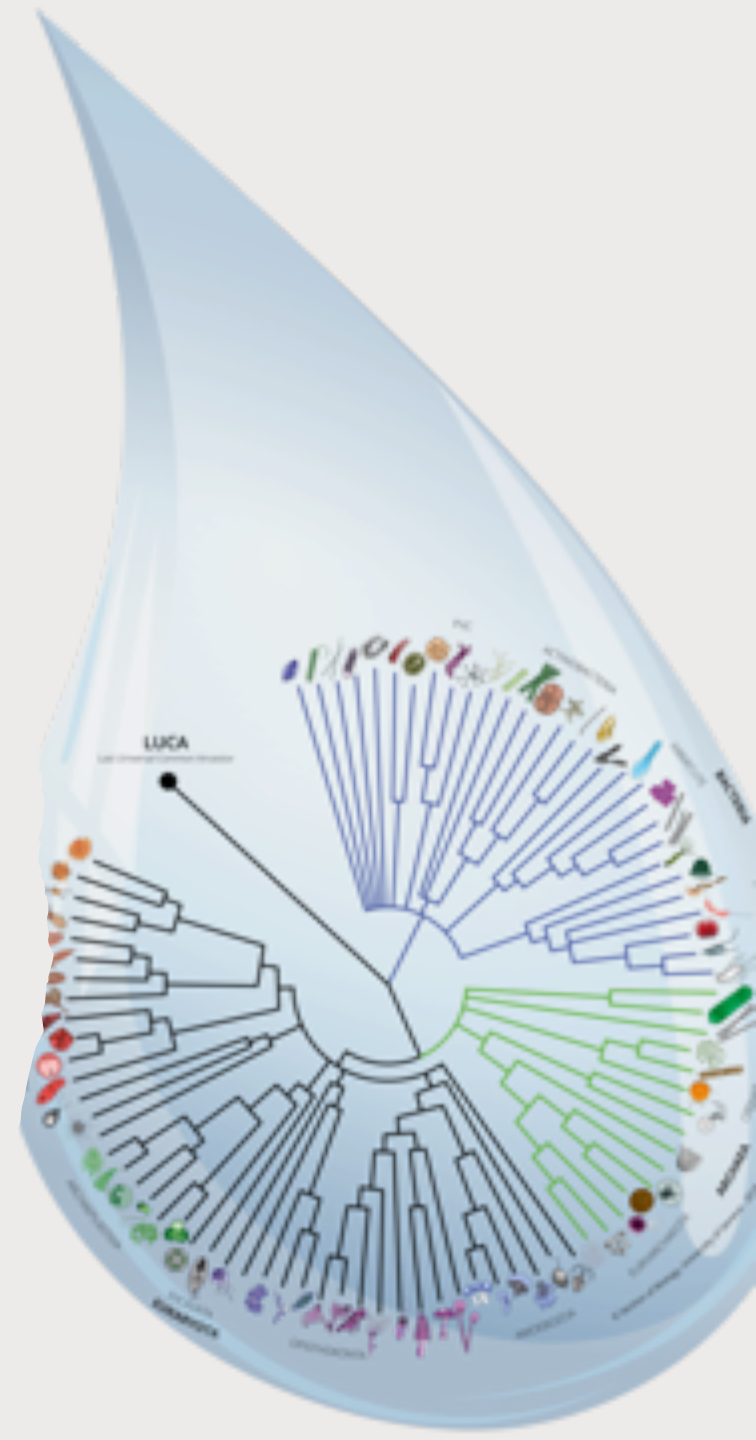


Examples of the major phytoplankton groups and their diagnostic photopigments. From Paerl, H.W., Valdes, L.M., Pinckney, J.L., Piehler, M.F., Dyble, J., Moisander, P.H., 2003. Phytoplankton photopigments as indicators of estuarine and coastal eutrophication. *BioScience* 53 (10), 953-964.

Broad taxonomic resolution, physiology-dependent



Complexity in a drop: The Omics Toolbox

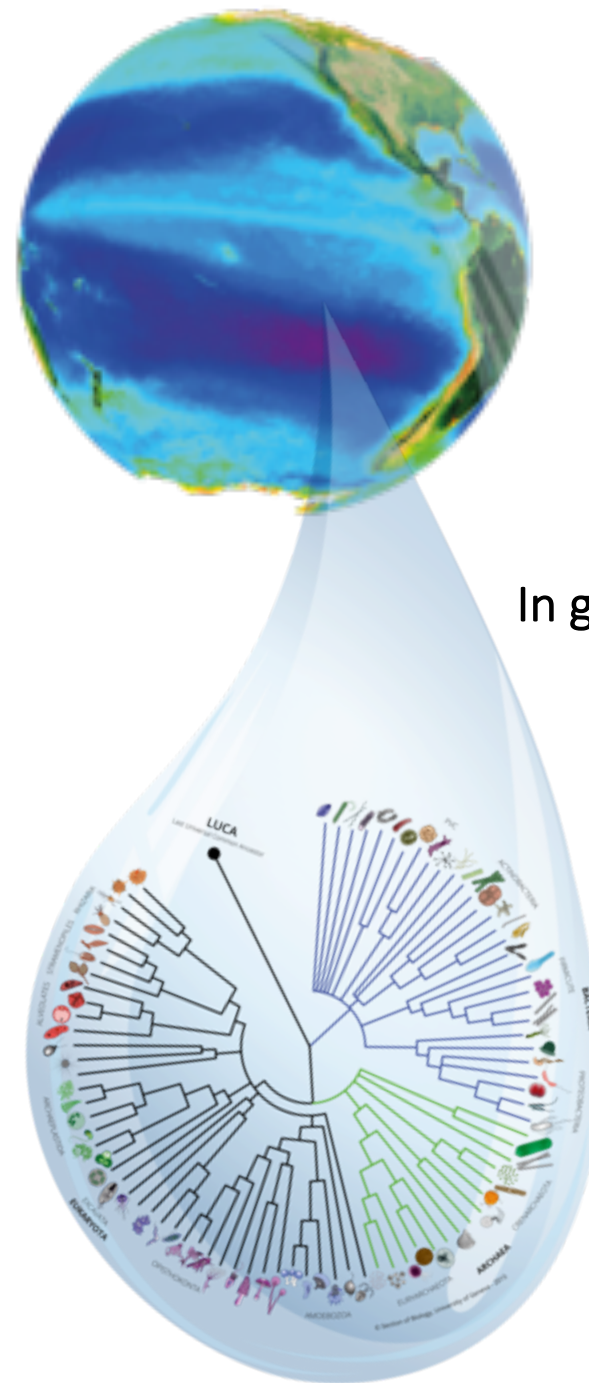




The Omics Toolbox



MetaBarcoding MetaGenomics MetaTranscriptomics

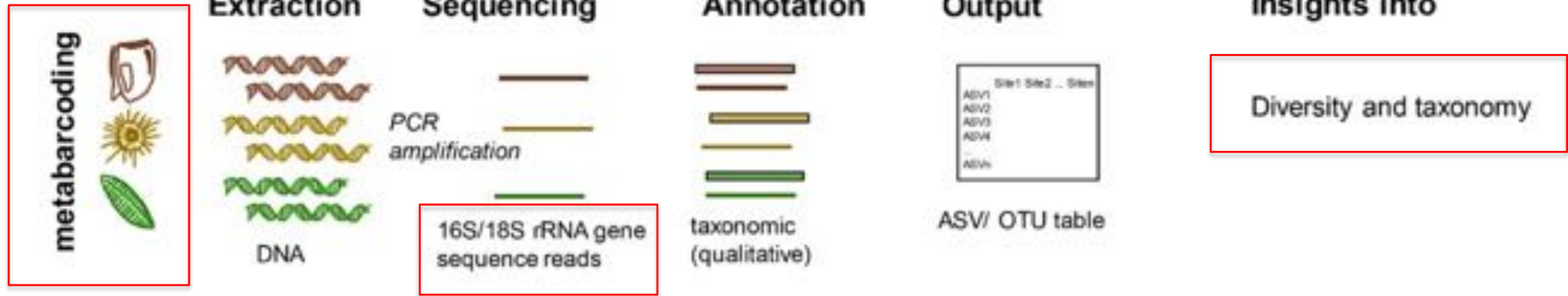


Diversity uncovered

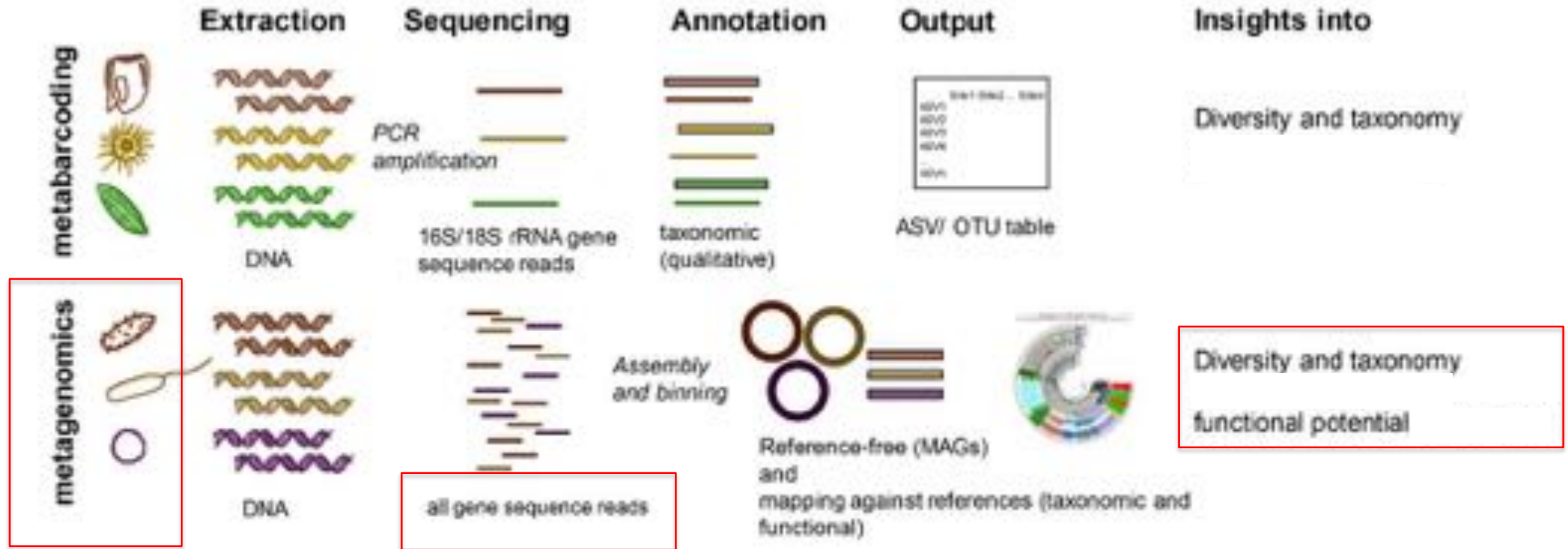
In global ocean surface waters:

- ✓ Hundred thousands of DNA and RNA virus 'species'.
- ✓ Hundred thousands of eukaryotic genera
- ✓ Tens of millions of prokaryotic genes
- ✓ Hundreds of millions of eukaryotic genes
- ✓ Billions of metabolites

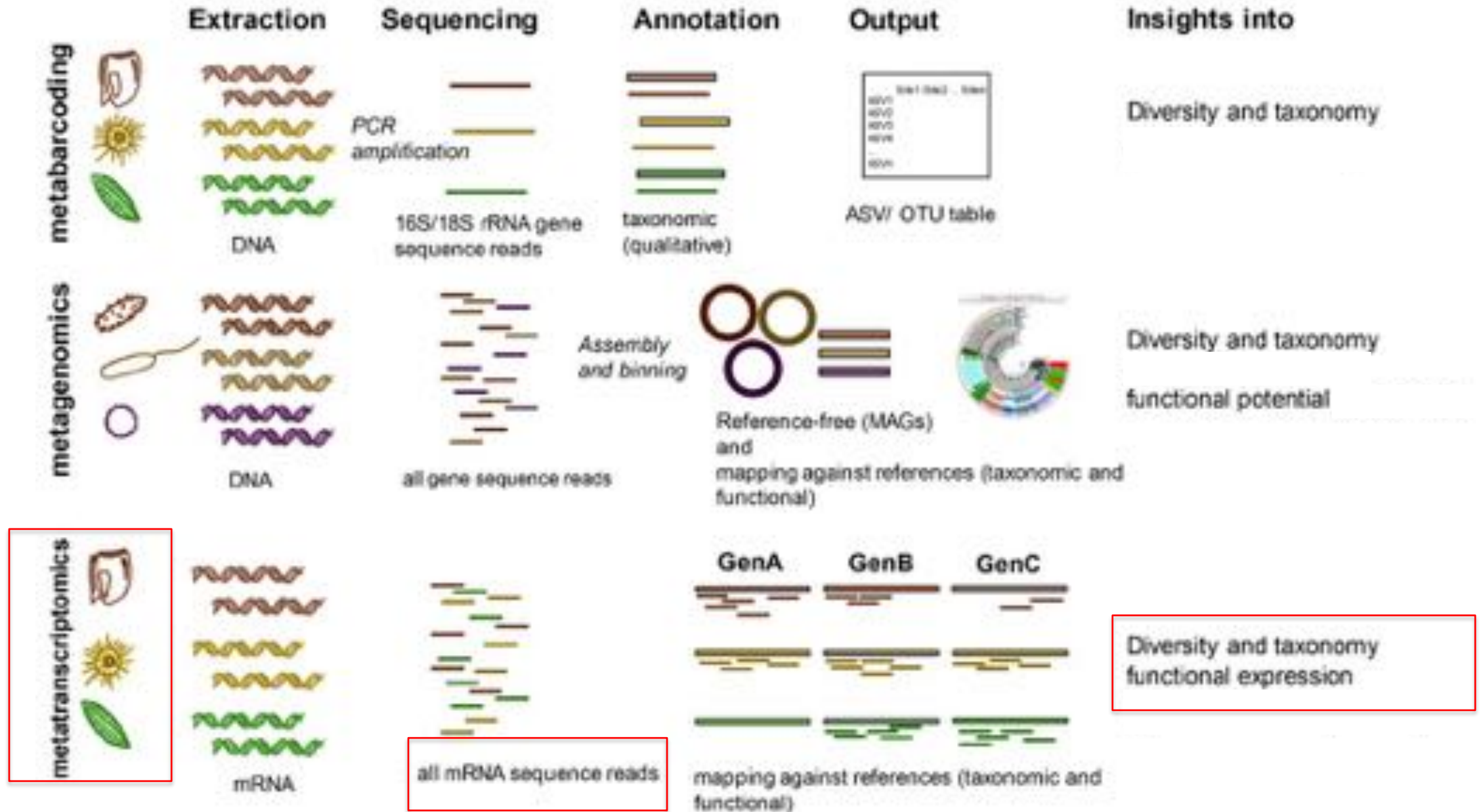
Metabarcoding, Metagenomics and Metatranscriptomics



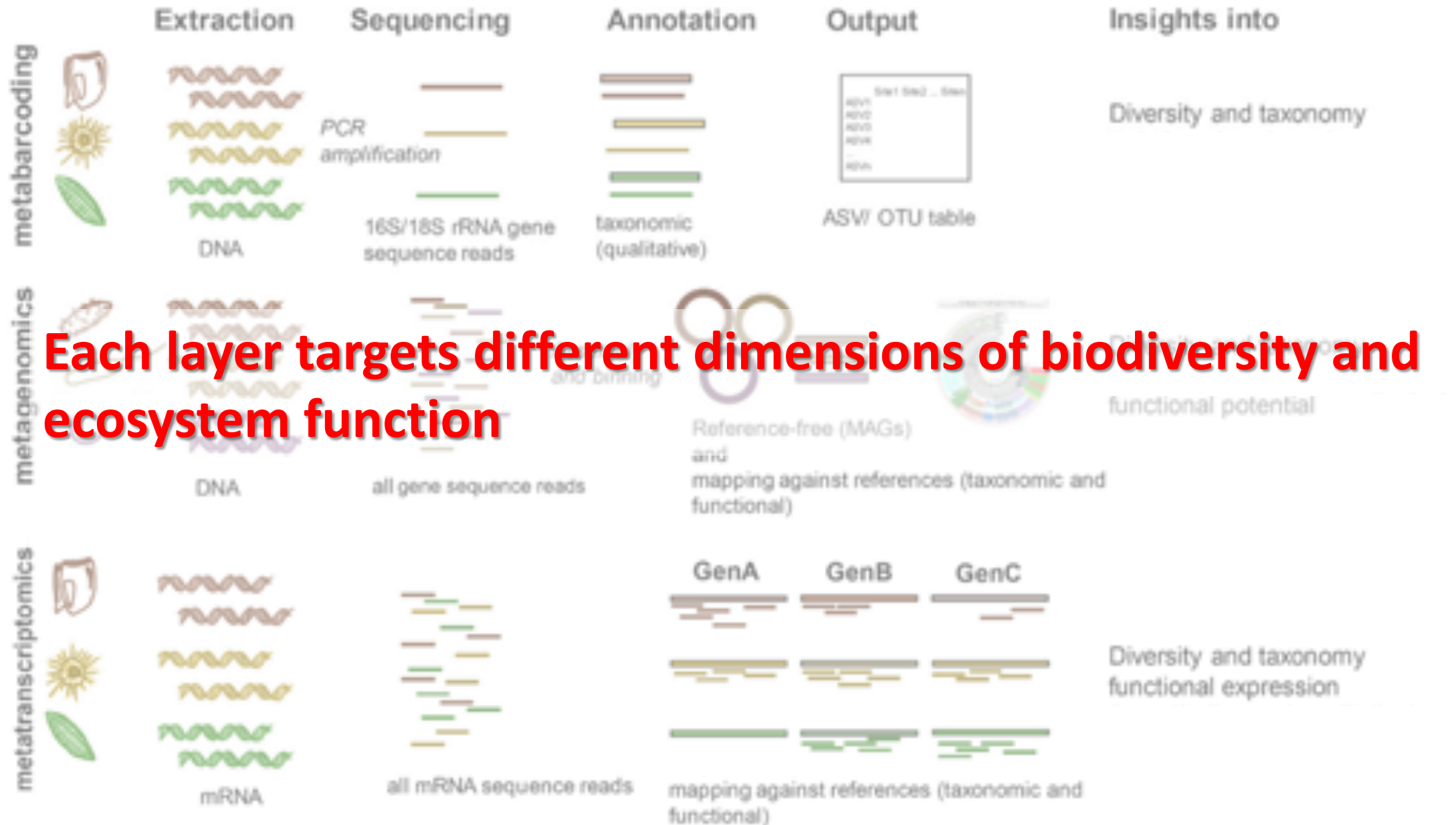
Metabarcoding, Metagenomics and Metatranscriptomics



Metabarcoding, Metagenomics and Metatranscriptomics

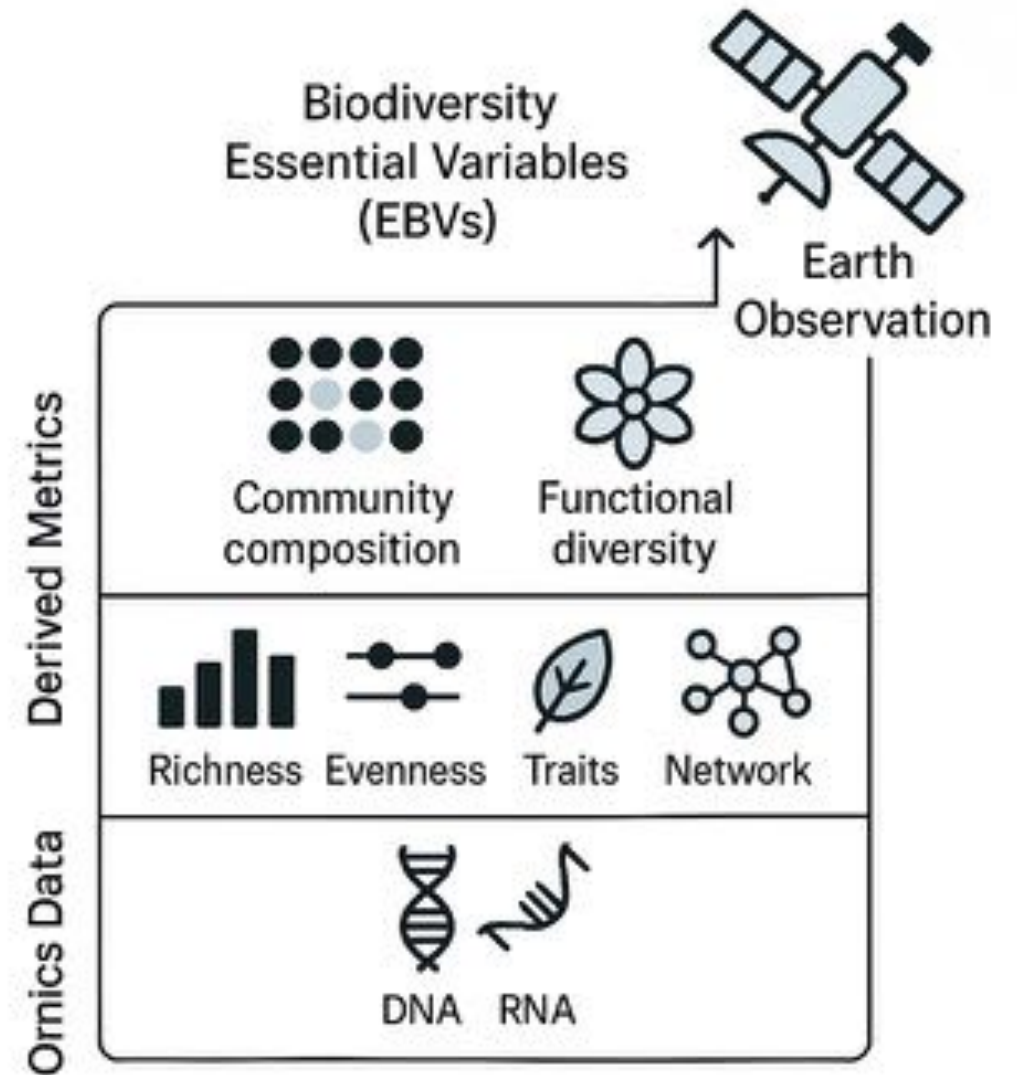


Metabarcoding, Metagenomics and Metatranscriptomics



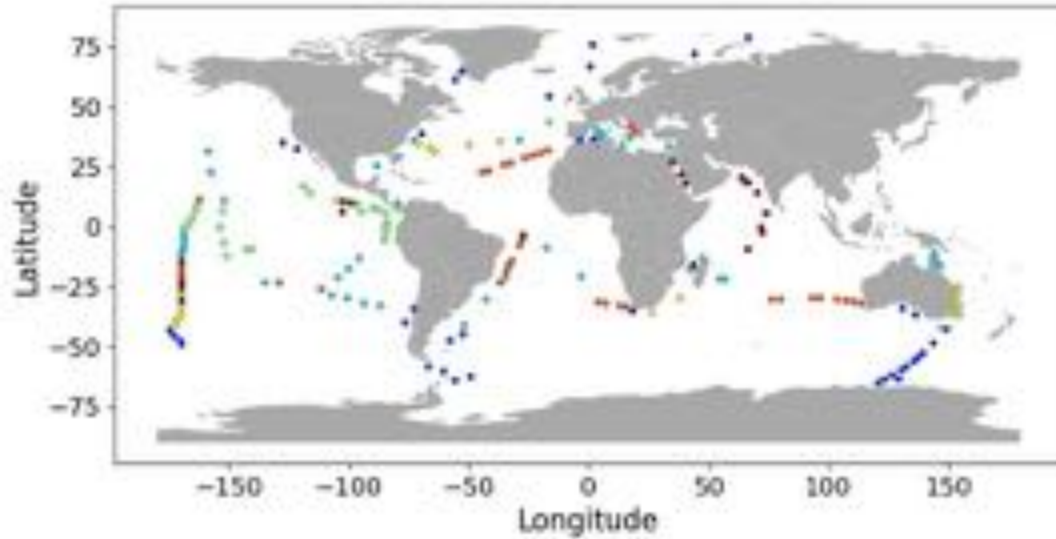
From Sequences to Satellites

- **Derive metrics:** richness, evenness, traits, network structure, functional diversity, and Translate these metrics into candidate EBVs (e.g., community composition),
- These omics-derived metrics become training data for EO-driven models



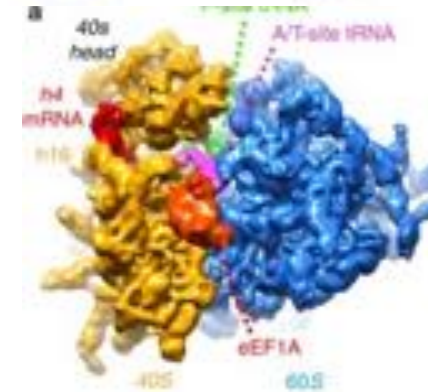
Linking Omics and Satellites: Metabarcoding approach

- Global 18S rRNA gene, decodes a part of the ribosomal RNA in **eukaryotes**, collocated with satellite data,



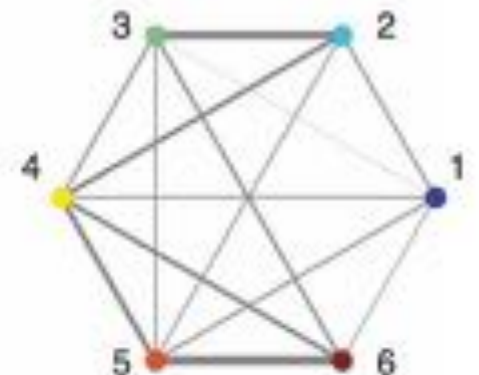
Predicting global distributions of eukaryotic plankton communities from satellite data

Hiroto Kaneko¹, Hisashi Endo¹, Nicolas Henry^{2,3}, Cédric Berney^{2,4}, Frédéric Mahé^{1,6}, Julie Poulain⁷, Karine Labadie⁸, Odette Beluche⁹, Roy El Hourany^{2,10}, Tara Oceans Coordinators*, Samuel Chaffron^{1,11}, Patrick Wincker², Ryosuke Nakamura¹², Lee Karp-Boss¹³, Emmanuel Boss¹³, Chris Bowler^{2,10}, Colomán de Vargas^{2,6}, Kentaro Tomii^{14,15} and Hiroyuki Ogata^{1,16}



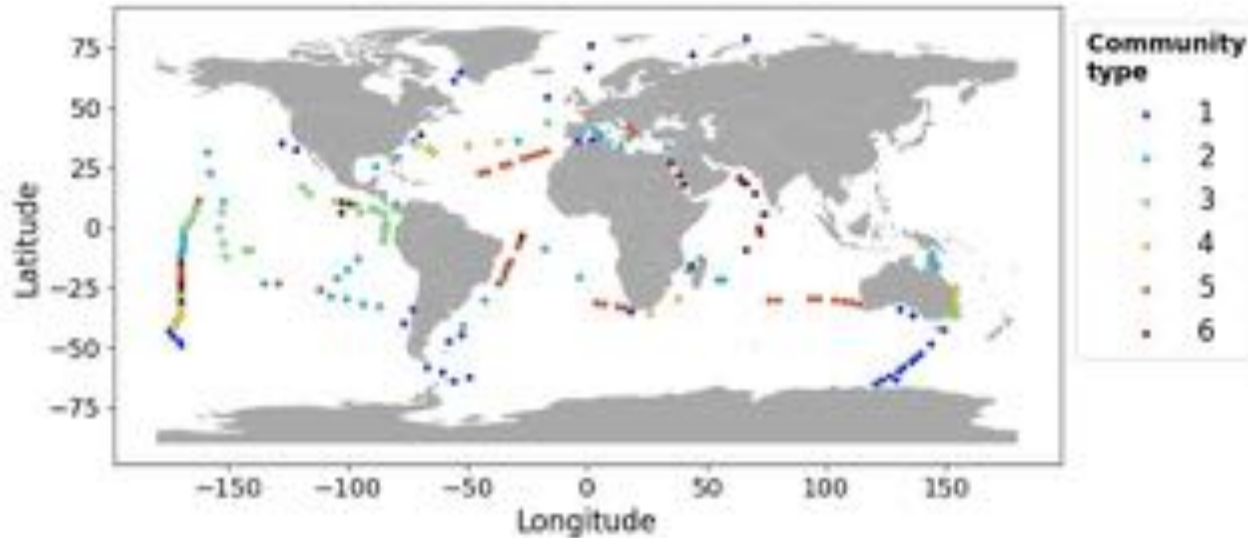
Module
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Linking Omics and Satellites: Metabarcoding approach

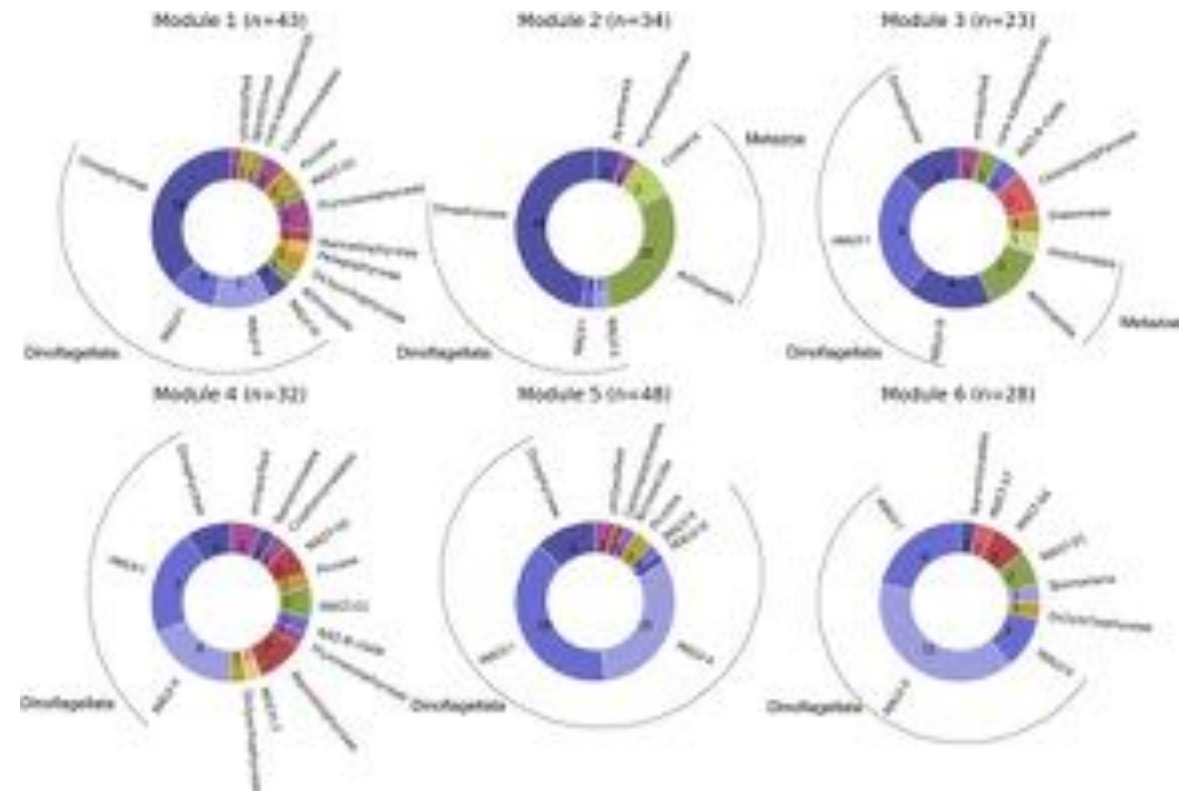
- Global 18S rRNA gene, decodes a part of the ribosomal RNA in **eukaryotes**, collocated with satellite data,



653 samples, 177 monthly matchups with 17 satellite variables from MODIS: Rrs(412), Rrs(443), Rrs(469), Rrs(488), Rrs(531), Rrs(547), Rrs(555), Rrs(645), Rrs(667), Rrs(678), Chla, Kd490, POC, PIC, PAR, nFLH, SST

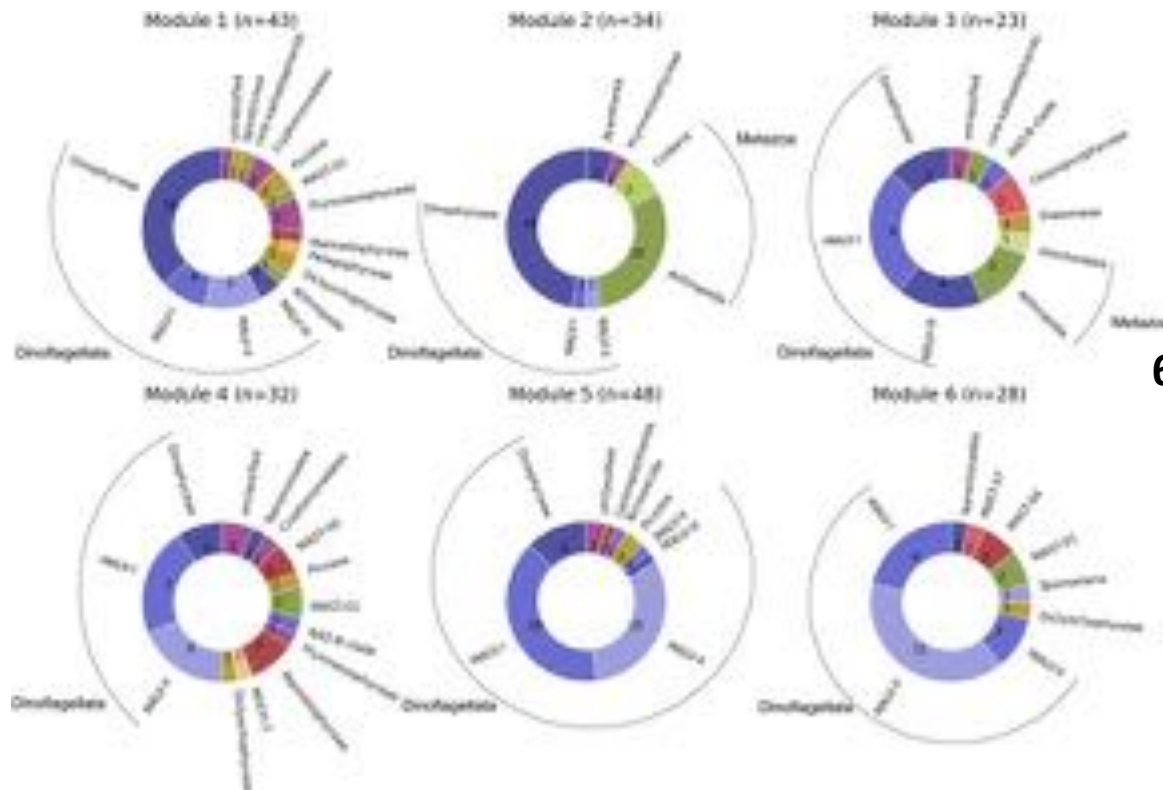
Predicting global distributions of eukaryotic plankton communities from satellite data

Hiroto Kaneko¹, Hisashi Endo¹, Nicolas Henry^{2,3}, Cédric Berney^{2,4}, Frédéric Mahé^{1,5}, Julie Poulain⁷, Karine Labadie⁸, Odette Beluche⁹, Roy El Hourany^{9,10}, Tara Oceans Coordinators*, Samuel Chaffron^{1,11}, Patrick Wincker¹², Ryosuke Nakamura¹², Lee Karp-Boss¹³, Emmanuel Boss¹³, Chris Bowler^{3,10}, Colomán de Vargas^{1,2,6}, Kentaro Tomii^{14,15} and Hiroyuki Ogata^{1,16}

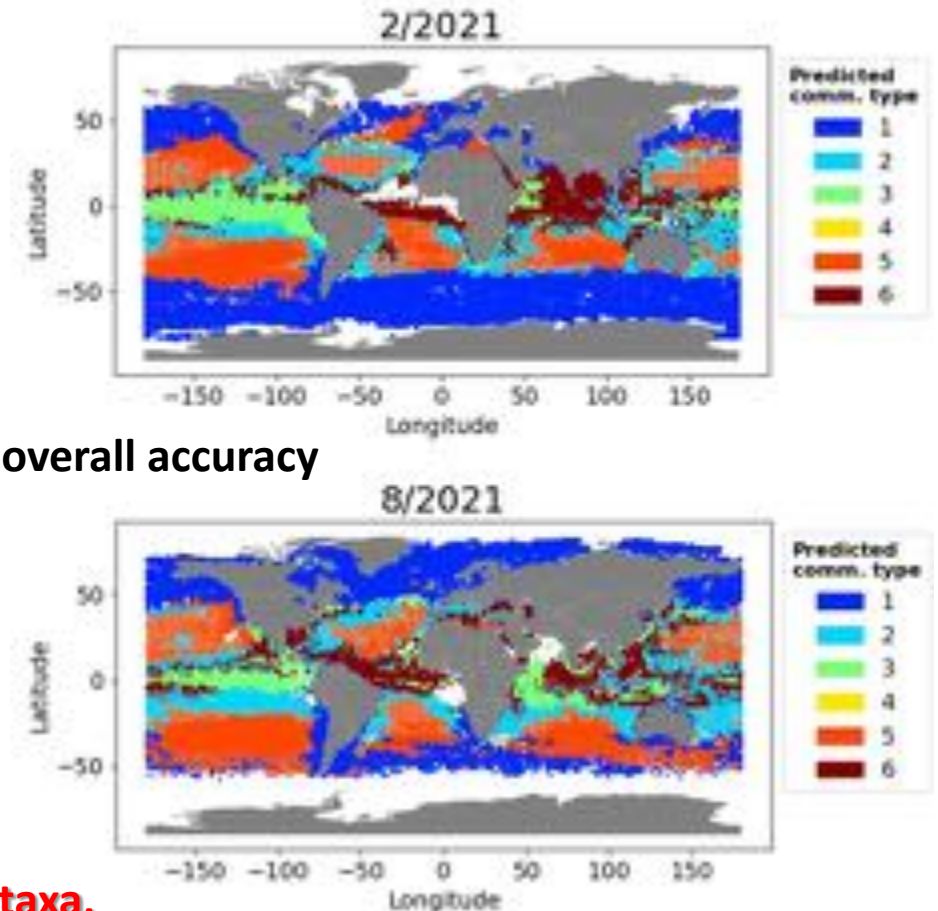


Linking Omics and Satellites: Metabarcoding approach

- Global 18S rRNA gene, decodes a part of the ribosomal RNA in **eukaryotes**, collocated with satellite data,
- Classification ML algorithm to predict plankton community types Produces maps of community type,
- Demonstrates feasibility of EO-informed biodiversity predictions.



67 % overall accuracy



18S read counts are distorted by huge copy-number differences between taxa, so they don't scale linearly with cell abundance.

Linking Omics and Satellites: Searching for an unbiased approach using metagenomics

The *psbO* protein; a core subunit of photosystem II (PSII), **unique to organisms that carry out oxygenic photosynthesis**.

The *psbO* is* a **single-copy gene**, present in both eukaryotes and prokaryotes groups

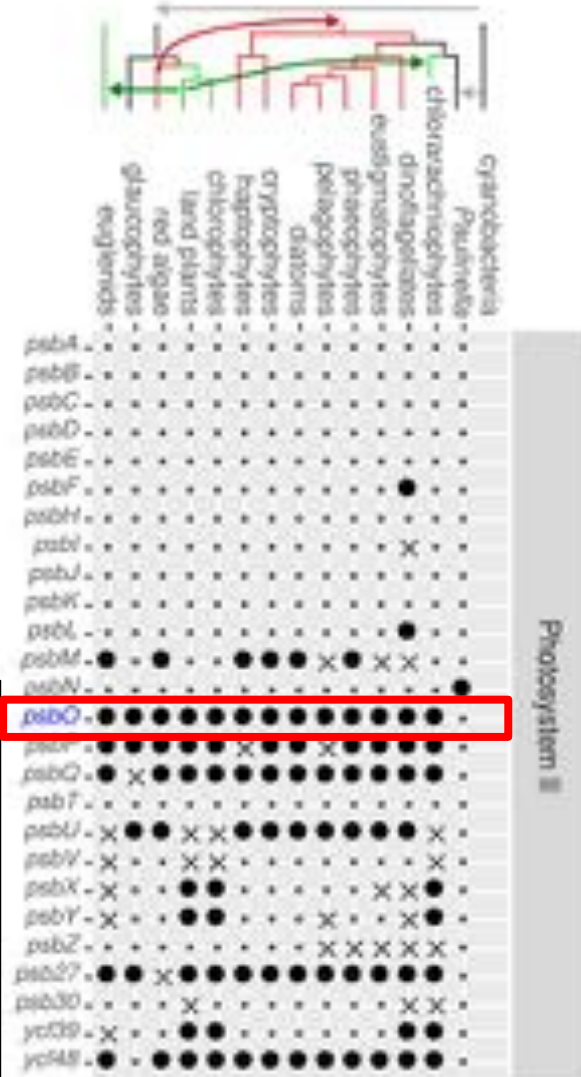
= Proxy of cell abundance



FROM THE COVER

A robust approach to estimate relative phytoplankton cell abundances from metagenomes

Juan José Pierella Karlusch^{1,2} | Eric Pelletier^{2,3} | Lucie Zinger^{1,2} | Fabien Lombard^{2,4,5} | Adriana Zingone⁶ | Sébastien Colin^{7,8,9} | Josep M. Gasol¹⁰ | Richard G. Dorrell¹ | Nicolas Henry^{2,11} | Eleonora Scalco⁶ | Silvia G. Acinas¹⁰ | Patrick Wincker^{2,3} | Colomán de Vargas^{2,8} | Chris Bowler^{1,2}



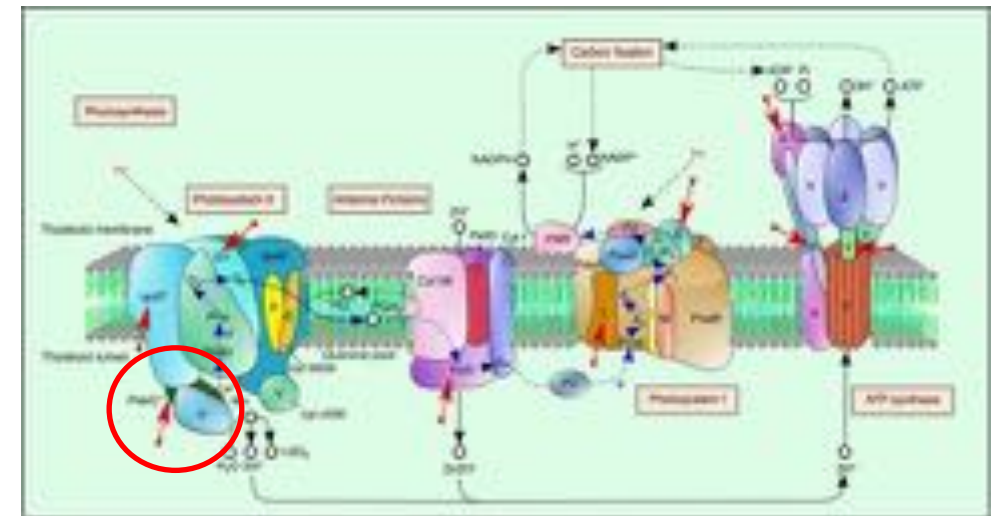
Received: 19 September 2021 | Revised: 9 January 2022 | Accepted: 25 January 2022
DOI: 10.1111/1755-0998.13592

FROM THE COVER

MOLECULAR ECOLOGY
RESOURCES WILEY

A robust approach to estimate relative phytoplankton cell abundances from metagenomes

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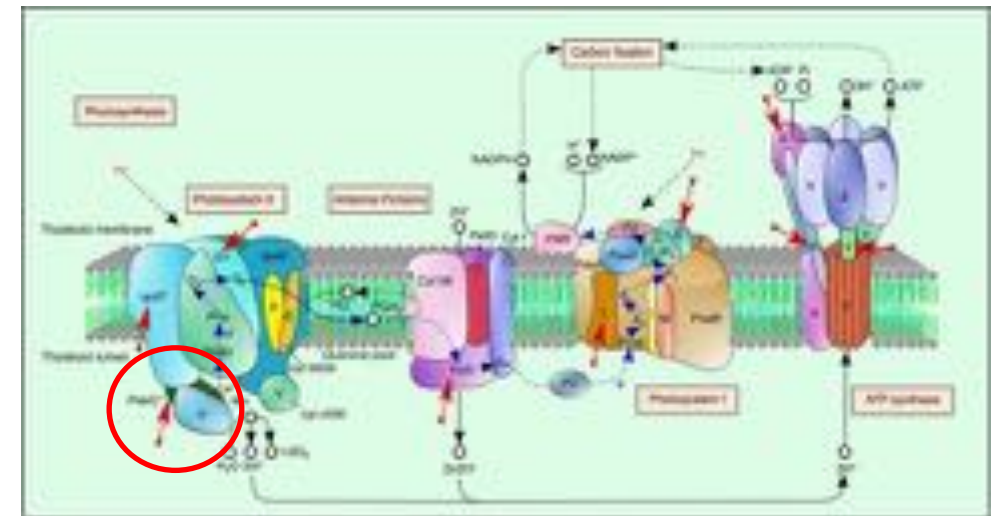
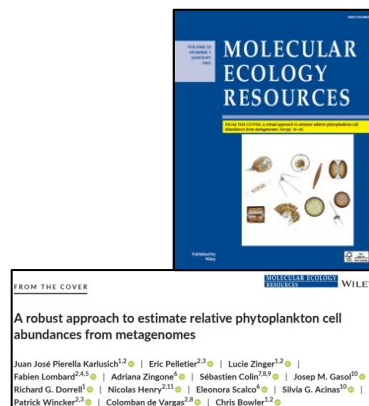
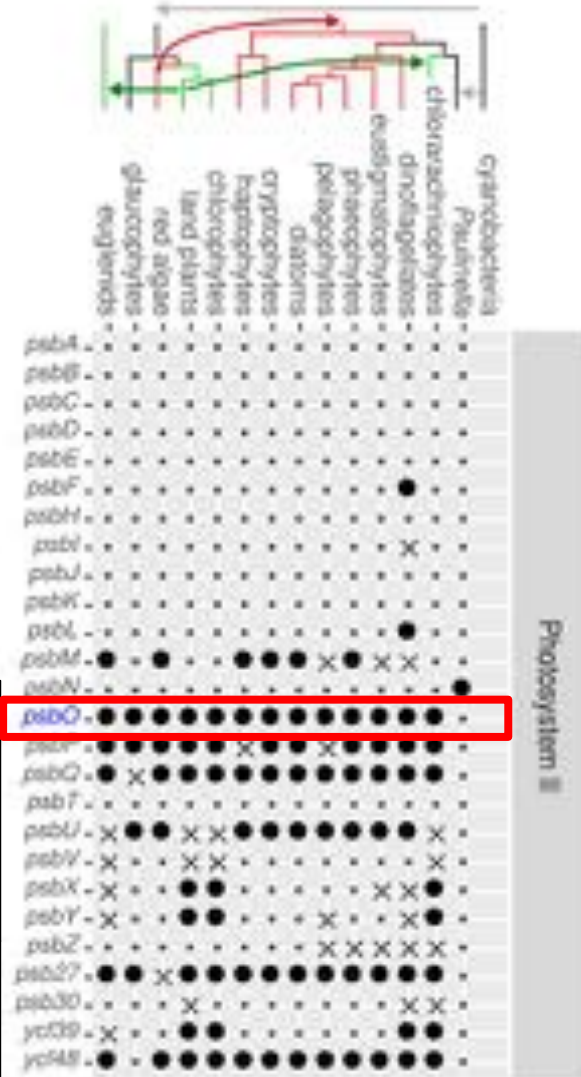
Pierella et al., 2022, <https://doi.org/10.1111/1755-0998.13592>

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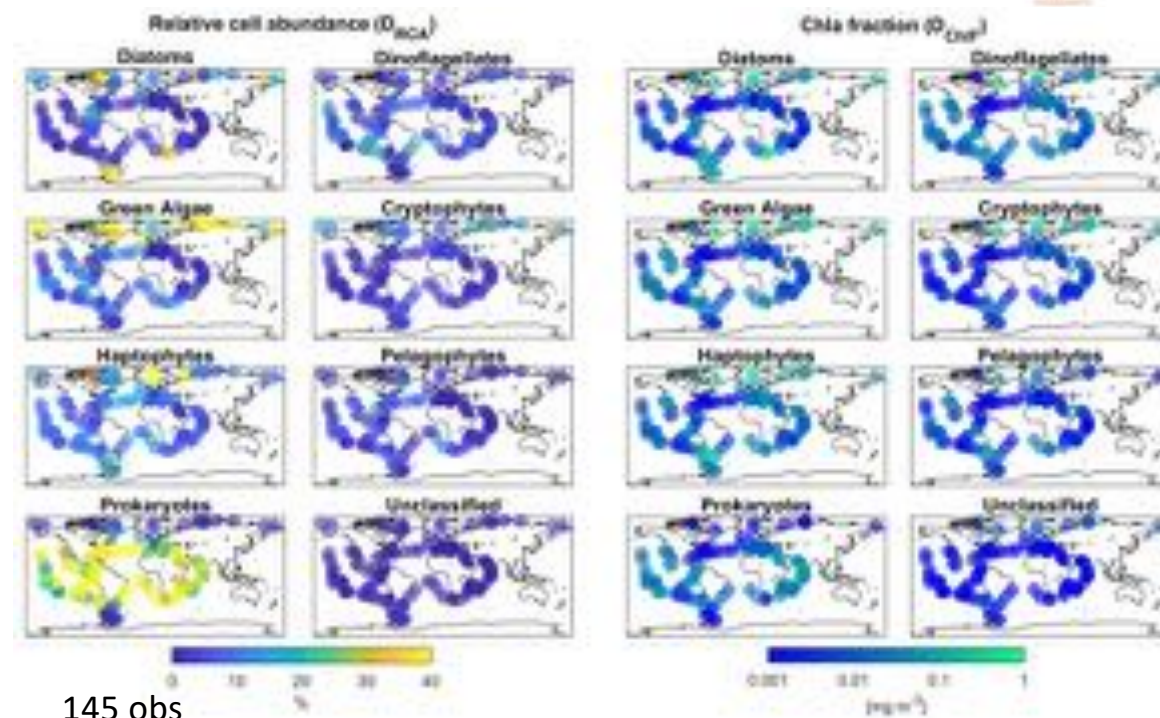
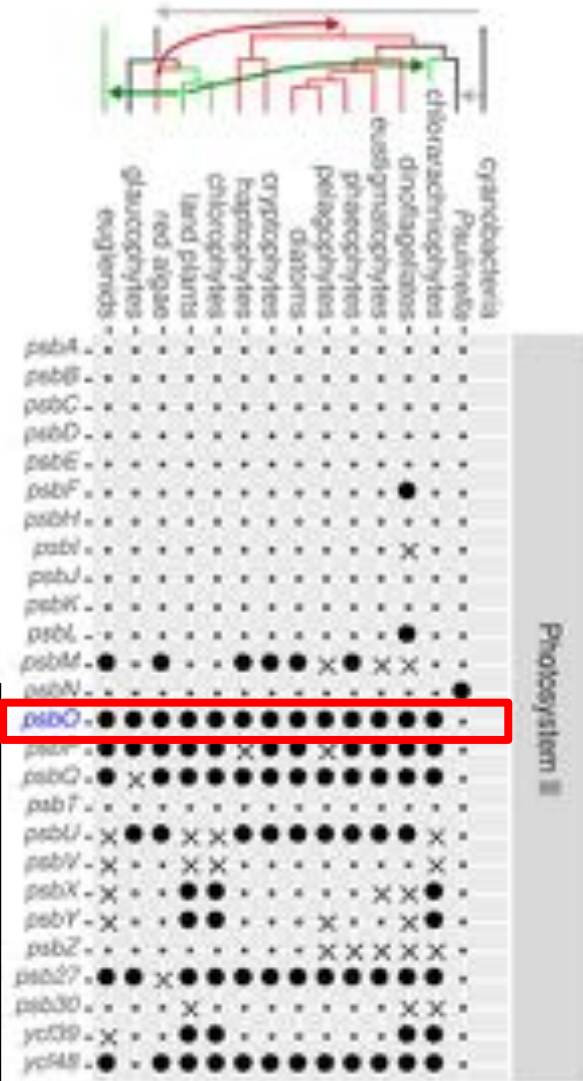
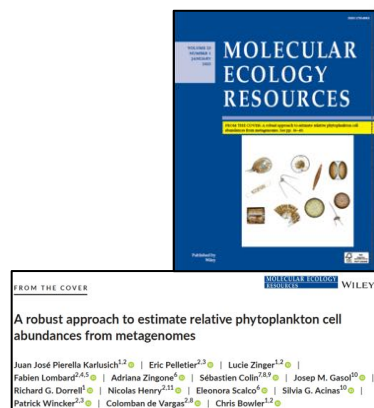
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145 obs

*integrating size fractions (4 sizes)

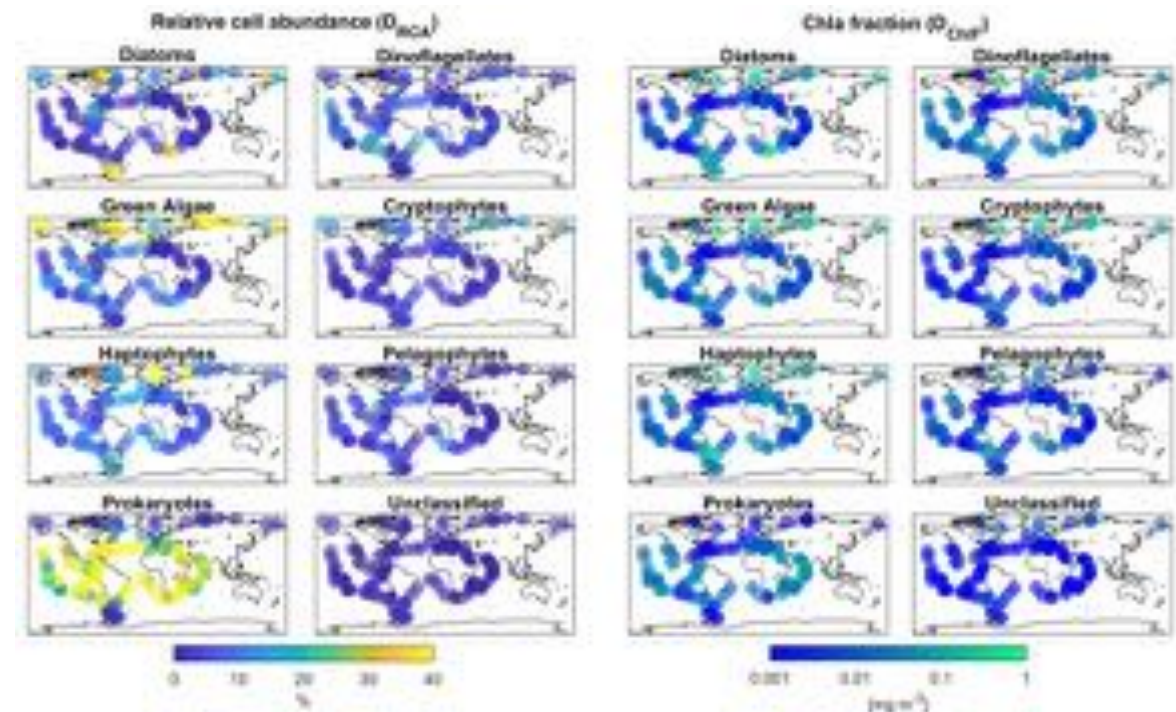
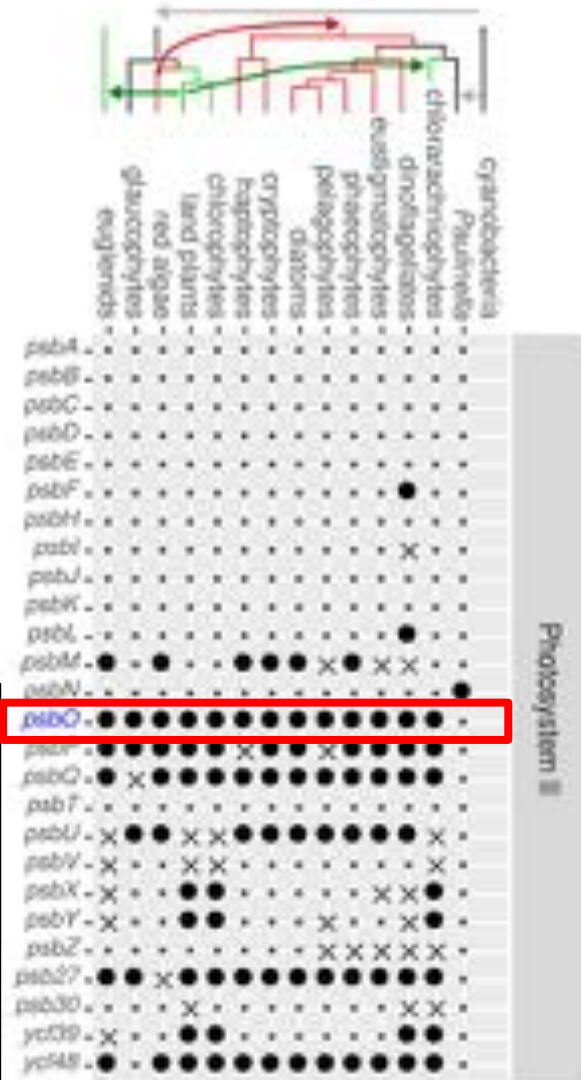
El Hourany, R., 2024,
Zenodo. <https://doi.org/10.5281/zenodo.10361485>

Linking Omics and Satellites: Searching for an unbiased approach using metagenomics

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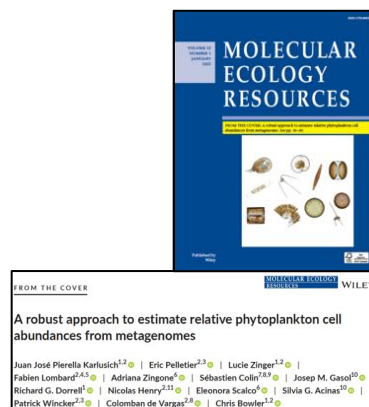
= Proxy of cell abundance



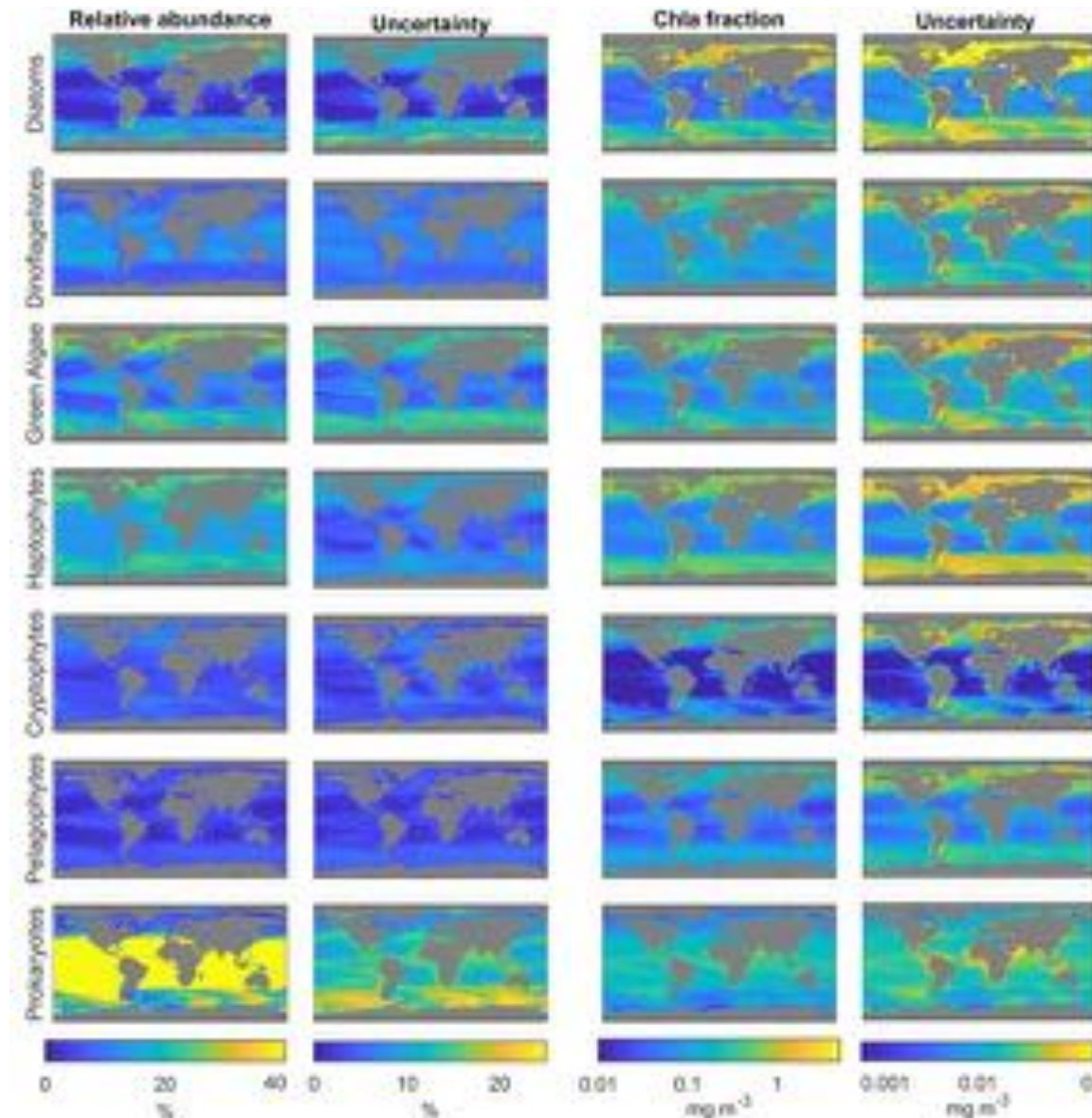
145 obs

Satellite matchups (at daily or ± 3 days, 4km resolution)

(Reflectance at several wavelengths, Chlorophyll-a, sea surface temperature, PAR, Fluorescence, bbp (443), attenuation coefficient)



Linking Omics and Satellites: Searching for an unbiased approach using metagenomics

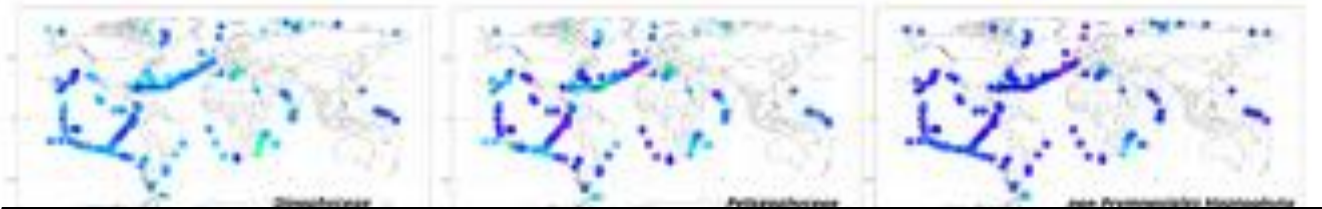
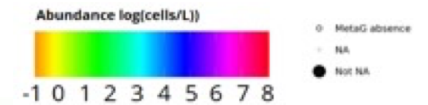
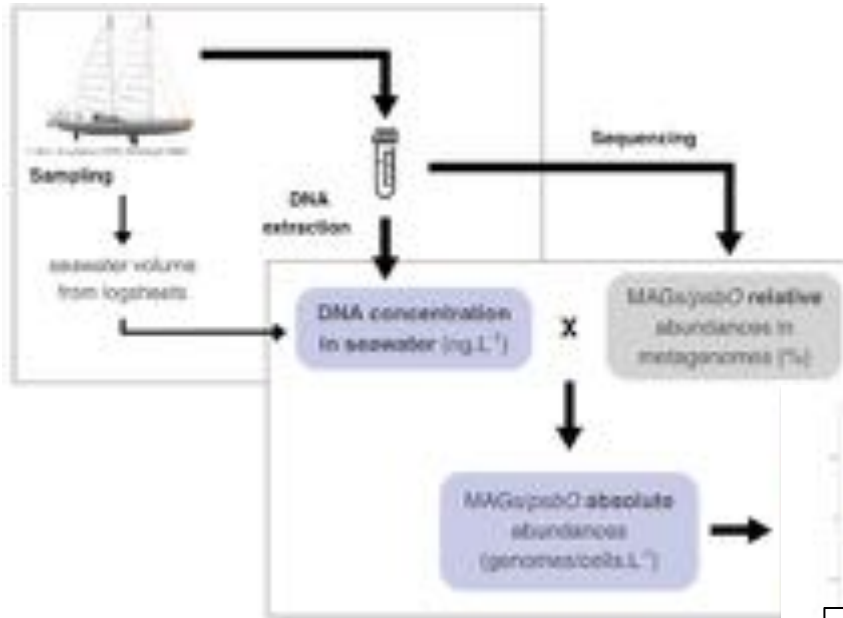


65 % overall accuracy

El Hourany, R. et al., Linking satellites to genes with machine learning to estimate phytoplankton community structure from space, *Ocean Sci.*, 20, 217–239, <https://doi.org/10.5194/os-20-217-2024>, 2024.

From DNA to Cell abundance

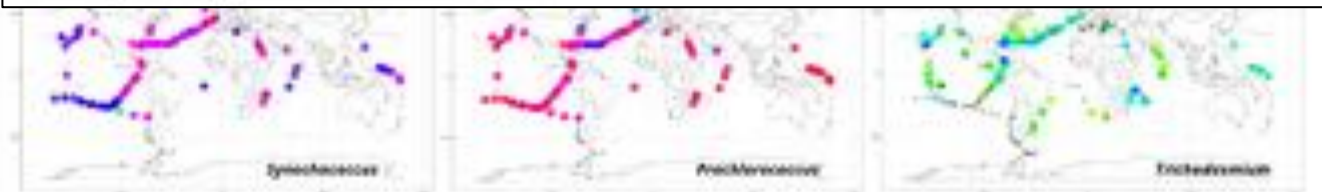
- Convert DNA concentration into absolute cell concentrations per lineage
- Focus on psbO marker gene to quantify 17 photosynthetic lineages over 3 size filters



Genomics-based quantitative biogeography of marine plankton

Margaux Crédeville, Roy El Hourany, Swan L. S. Sow, Julie Poulain, Manon Depaty, Eric Pelletier, Zoé Mériguet, Marie-Fanny Racault, Genoscope Sequencing Team, Aude Perdereau, Laurie Bertrand, Frédérick Gavory, Priscillia Gourvil, Céline Orvain, Morgane Ratin, Laurence Garczarek, Tom O Delmont, Adrien Thurotte, Corinne Le Quéré, Juan J Pierella Karlusich, Chris Bowler, Samuel Chaffron, Patrick Wincker, Fabien Lombard, Olivier Jaillon

doi: <https://doi.org/10.1101/2025.10.25.684415>



TARA
OCEANS

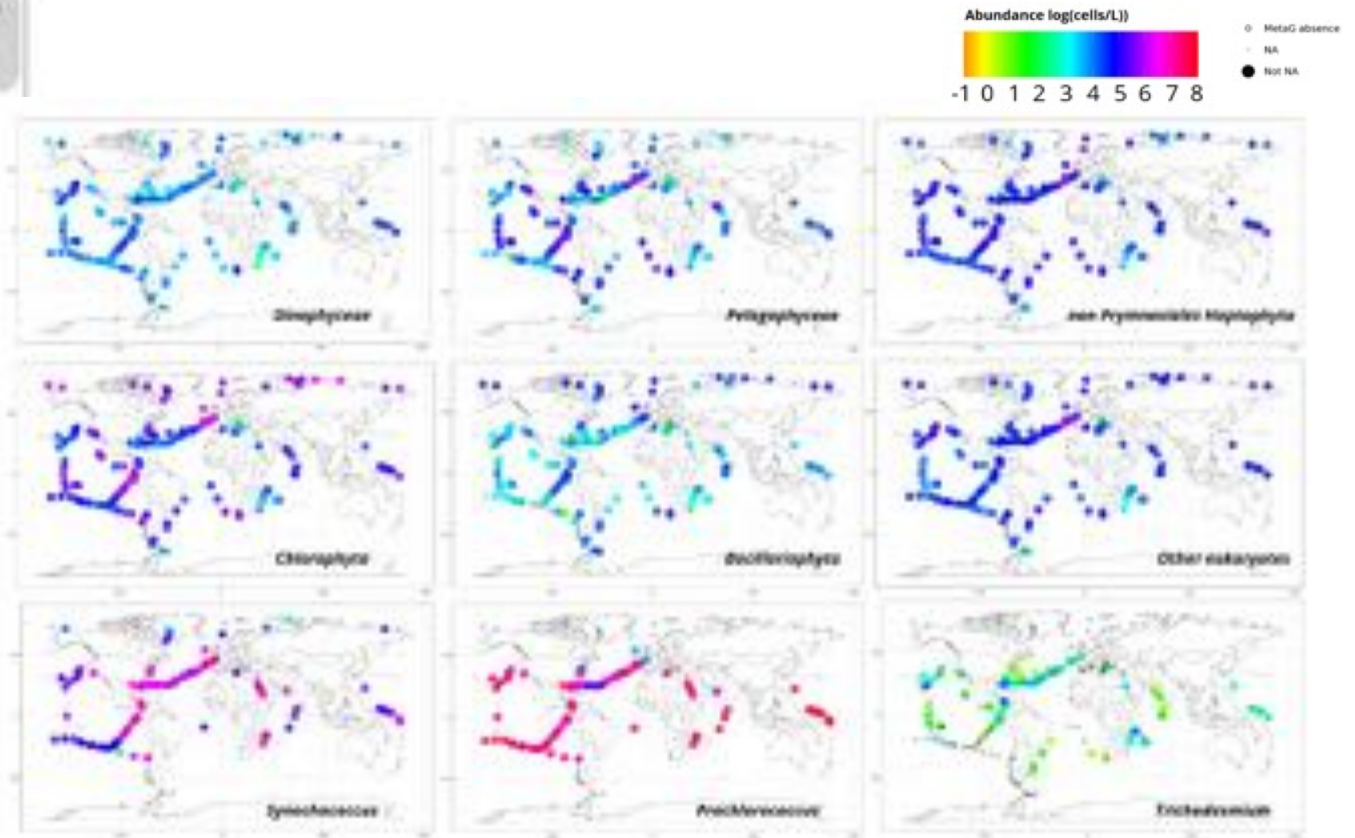
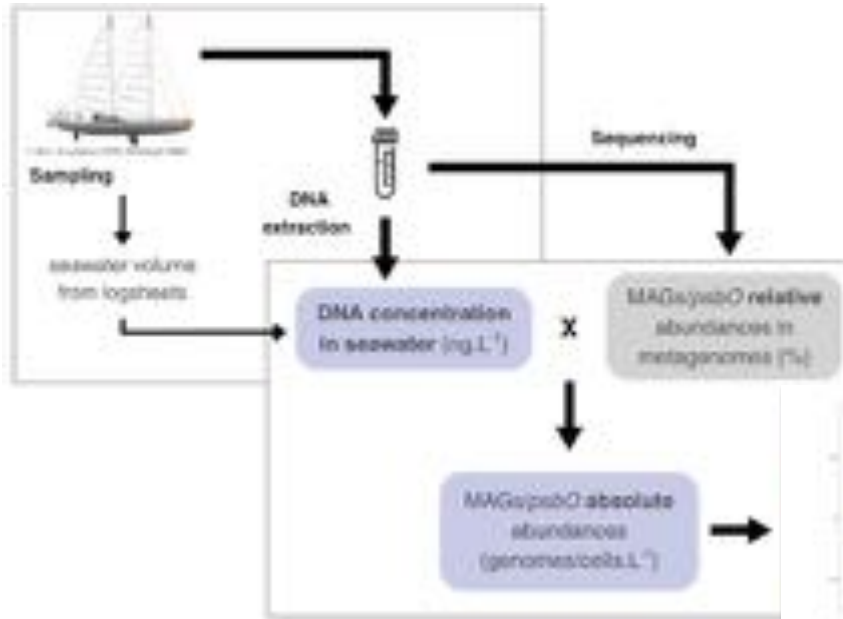
tara
PACIFIC

2009 - 2014 2016 - 2018

Crédeville, El Hourany, Jaillon et al, Genomics-based quantitative biogeography of marine plankton
bioRxiv 2025.10.25.684415; doi: <https://doi.org/10.1101/2025.10.25.684415>

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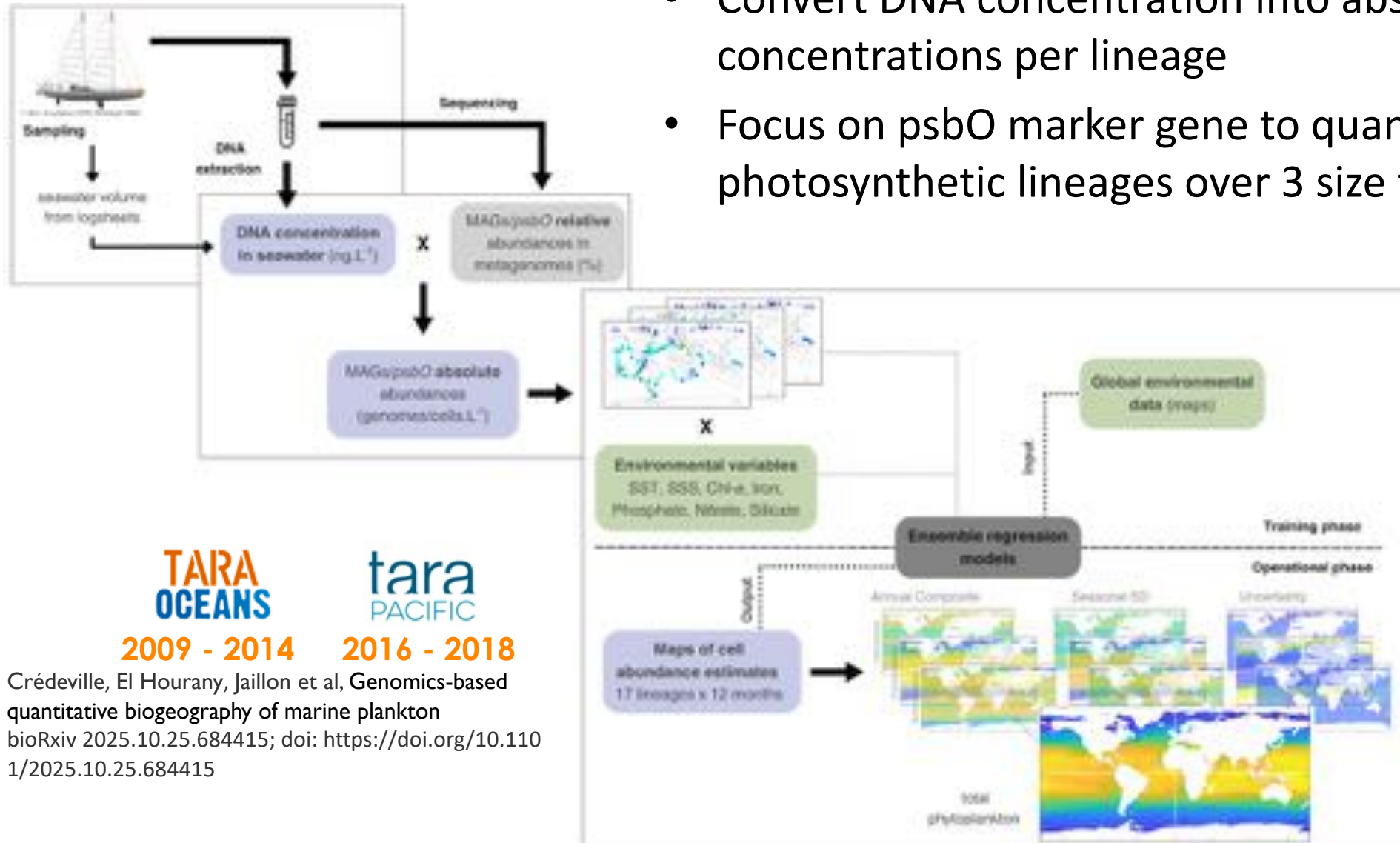
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OCEANS

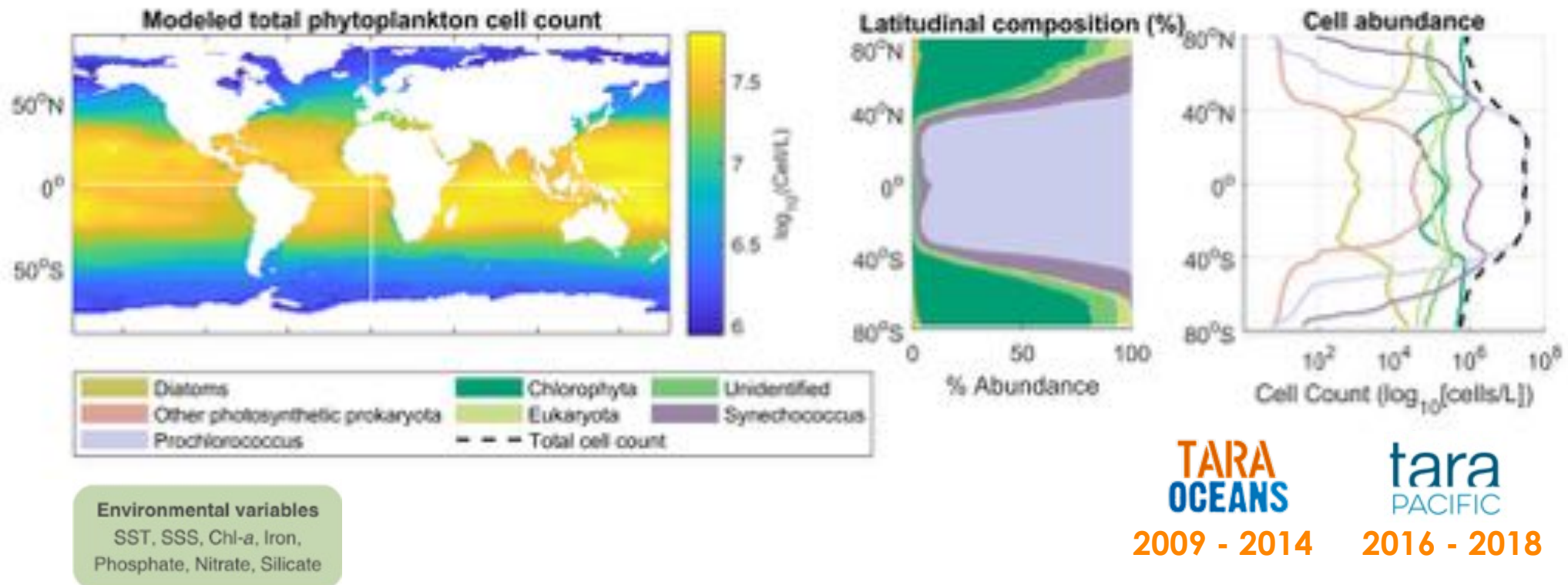
tara
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quantitative biogeography of marine plankton
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From DNA to Cell abundance

Build phytoplankton community maps based on absolute cell abundance



Crédeville, El Hourany, Jaillon et al, Genomics-based quantitative biogeography of marine plankton
bioRxiv 2025.10.25.684415; doi: <https://doi.org/10.1101/2025.10.25.684415>

From DNA to Cell abundance to Carbon

Latitudinal variation in phytoplankton community composition derived from metagenomic-based quantification of *psbO*-lineages, estimated cell abundance, and carbon biomass across global ocean regions, revealing differing patterns among the three metagenomic-based estimates.

Integrated over the 0.2–2,000 μm plankton size range at surface stations from Tara Oceans, Tara Oceans Polar Circle, and Tara Pacific.

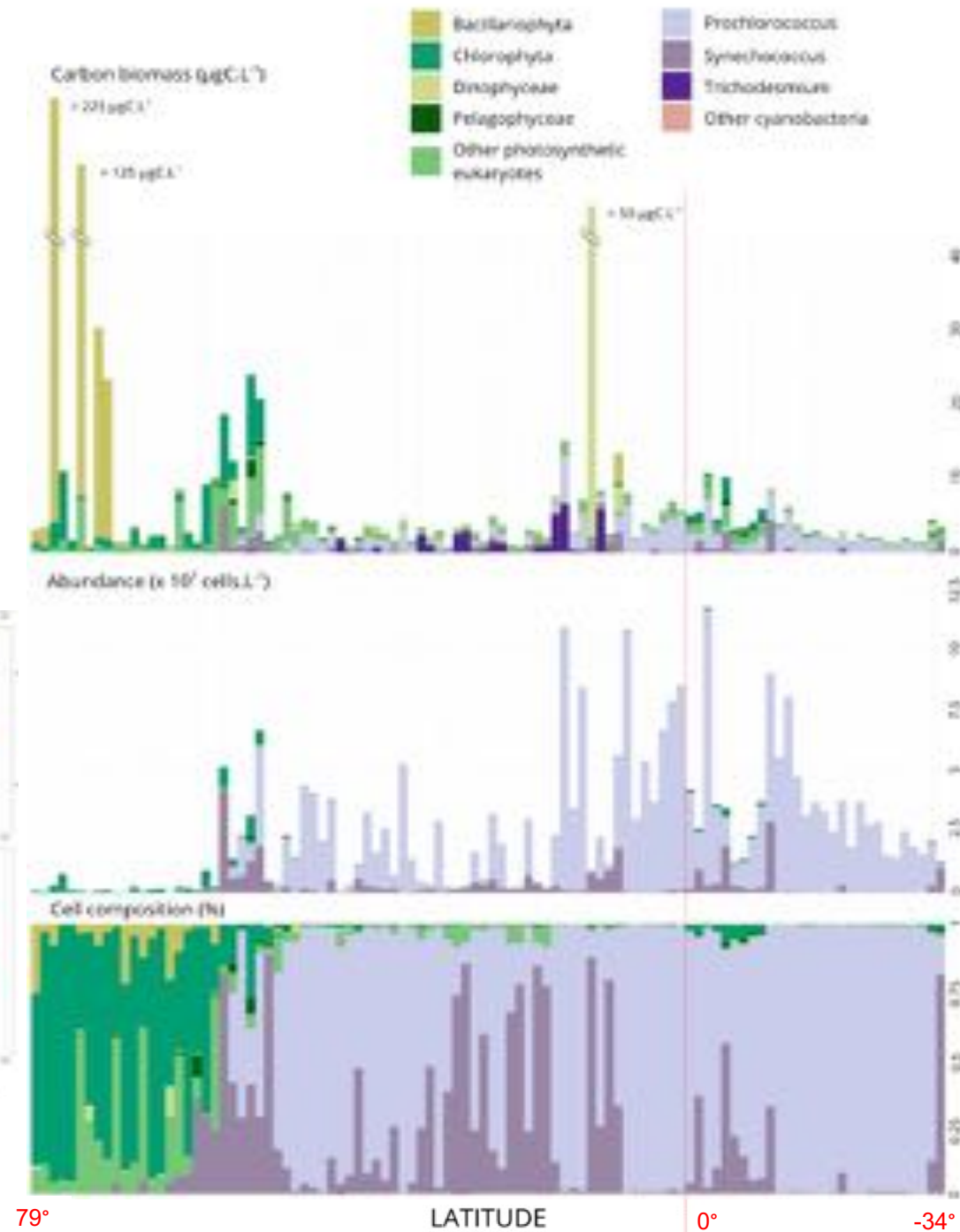
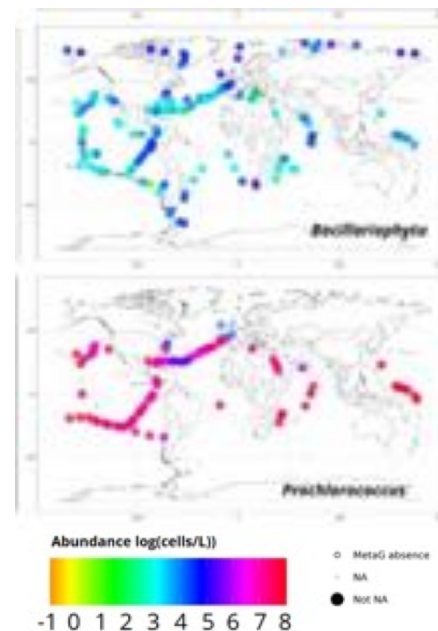
TARA
OCEANS

2009 - 2014

tara
PACIFIC

2016 - 2018

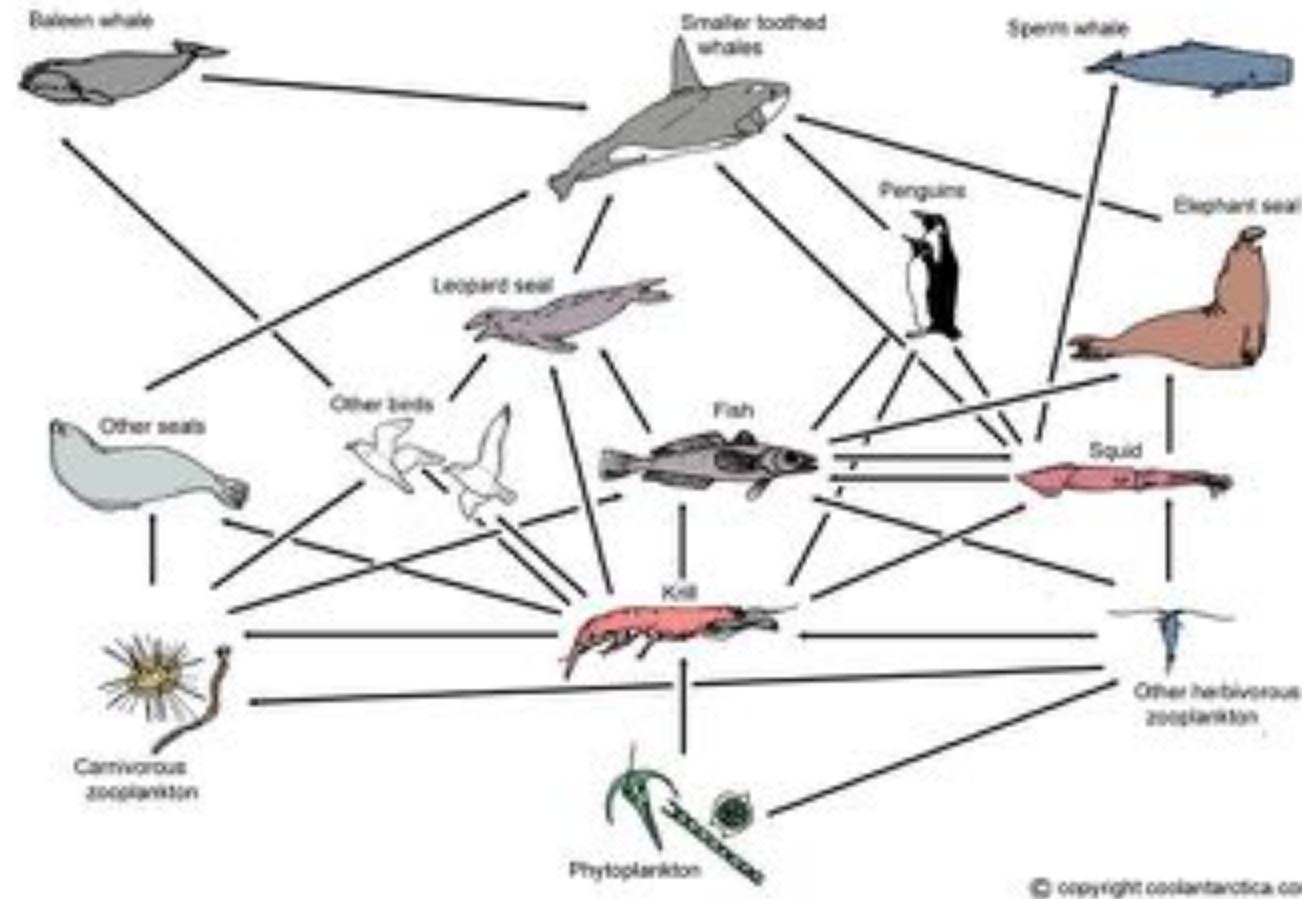
Crédeville, El Hourany, Jaillon et al, Genomics-based quantitative biogeography of marine plankton bioRxiv 2025.10.25.684415; doi: <https://doi.org/10.1101/2025.10.25.684415>





**Where are we
going with this?**

From phytoplankton to predators: can community composition from space tell us about the food web?



Can PCC, mapped from satellites, tell us something about the trophic state of the system and the potential for higher trophic levels?

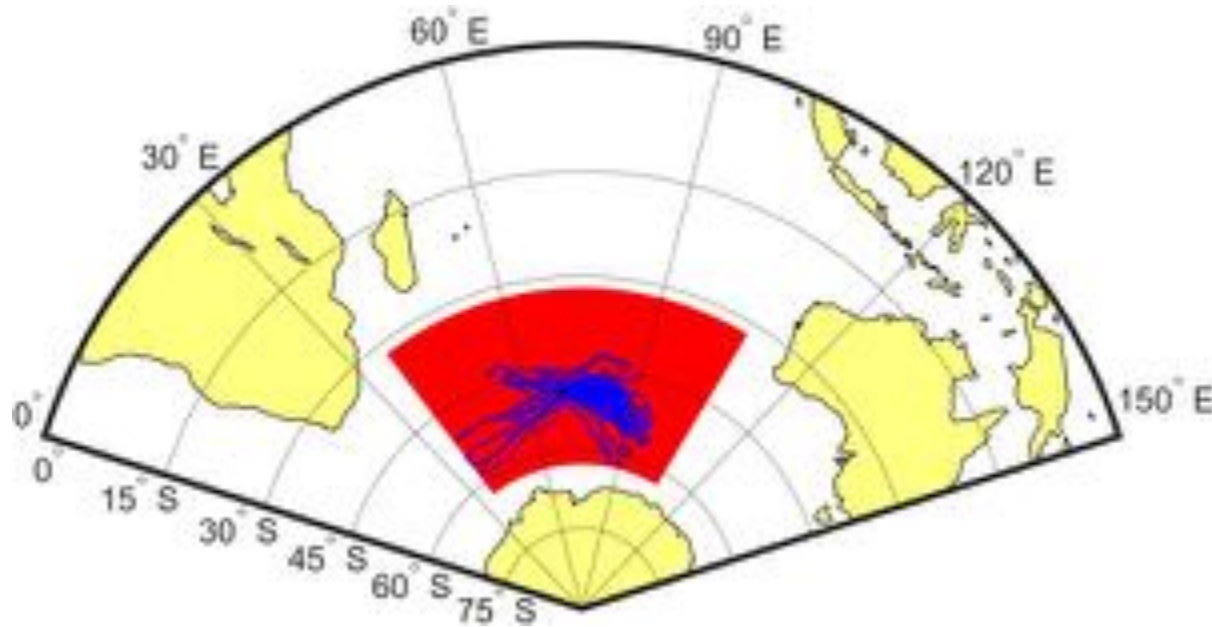
From phytoplankton to predators: can community composition from space tell us about the food web?



Sari El Dine, et al., 2025, Influence of the phytoplankton community structure on the southern elephant seals' foraging activity within the Southern Ocean, Comm Biology

From phytoplankton to predators: can community composition from space tell us about the food web?

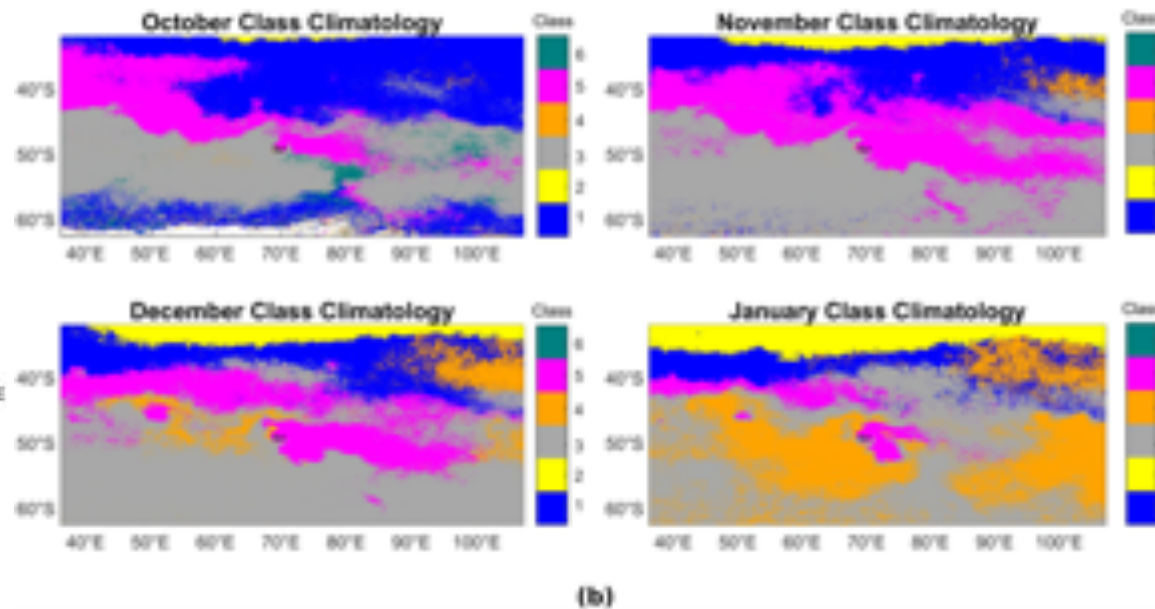
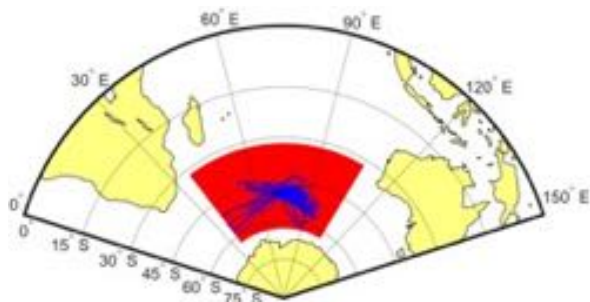
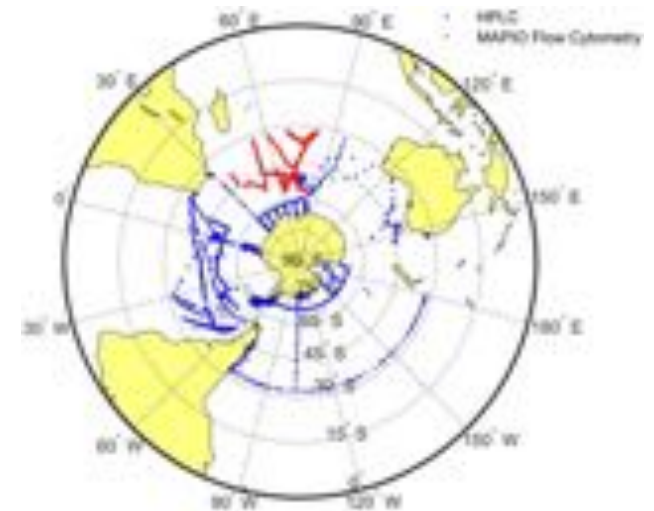
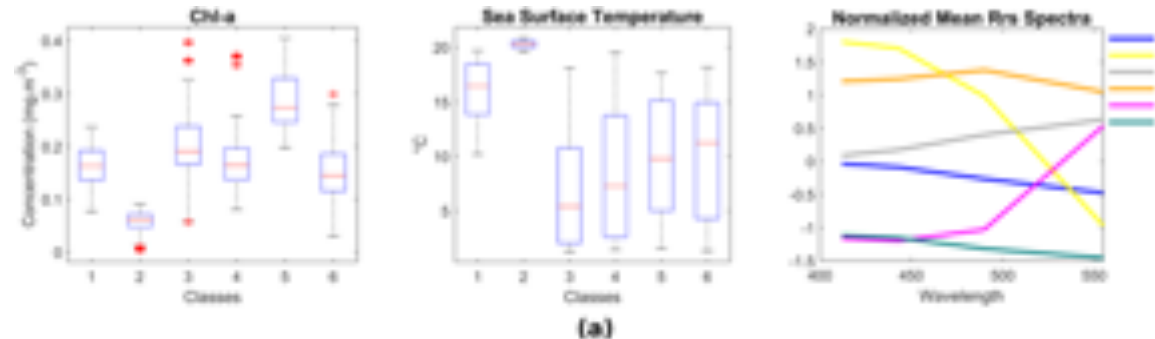
Accelerometer data from October to January for each year from 2010 to 2020.



Sari El Dine, et al., 2025, Influence of the phytoplankton community structure on the southern elephant seals' foraging activity within the Southern Ocean, Comm Biology

From phytoplankton to predators: can community composition from space tell us about the food web?

Characterization of the water-type classes in terms of the satellite data in addition to a monthly class climatology over the area of interest.



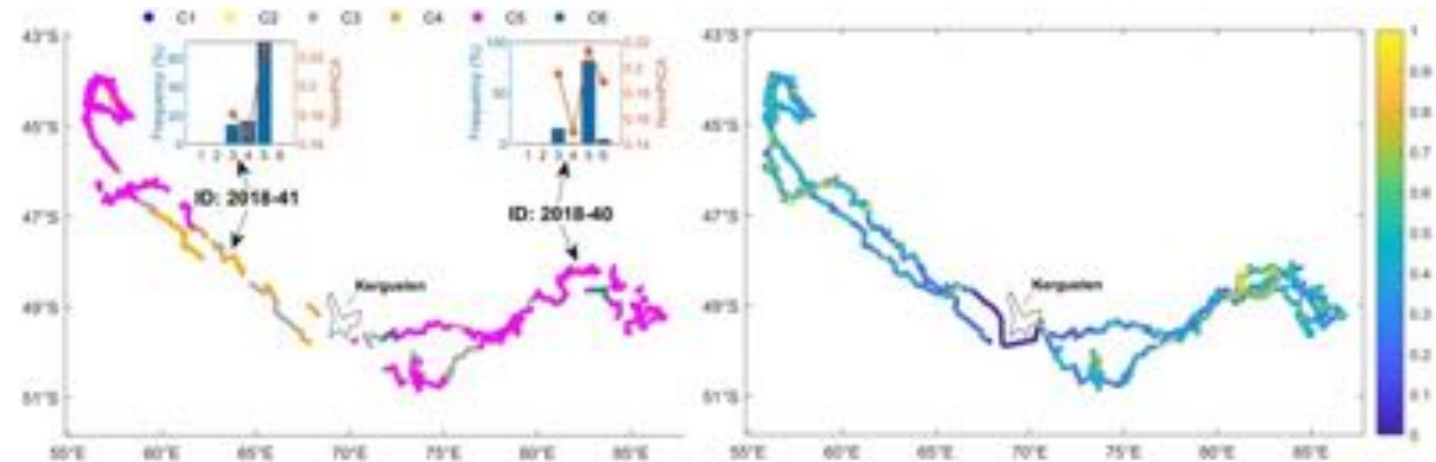
From HPLC and Cytometry data: C5= Productive waters, Diatom-dominated

Sari El Dine, et al., 2025, Influence of the phytoplankton community structure on the southern elephant seals' foraging activity within the Southern Ocean, Comm Biology

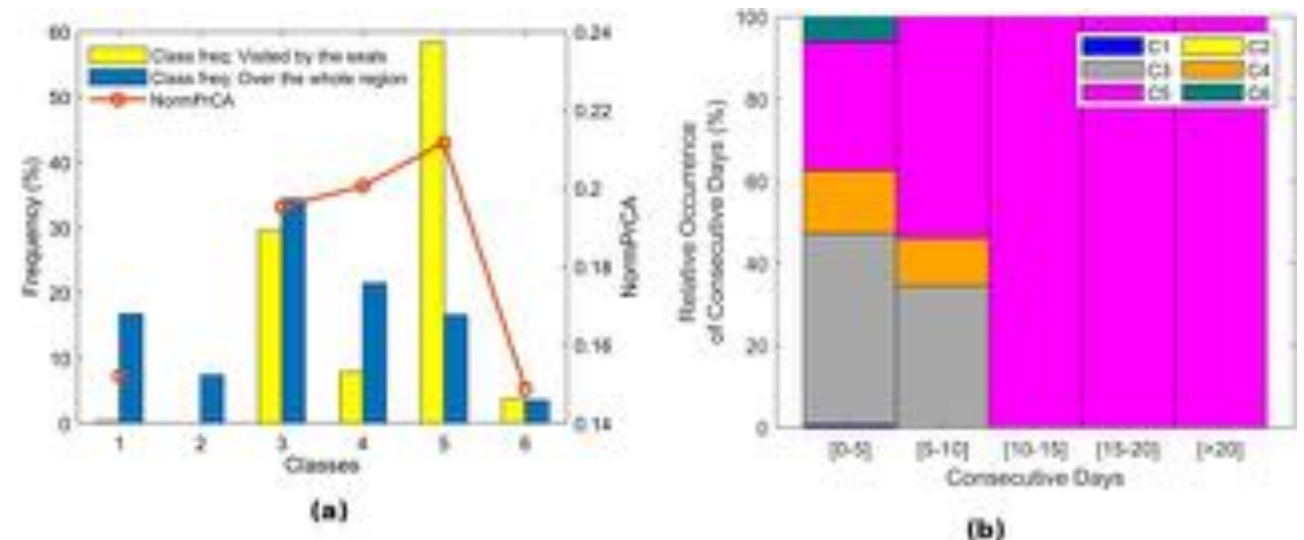
From phytoplankton to predators: can community composition from space tell us about the food web?

Southern Elephant Seals tend to:

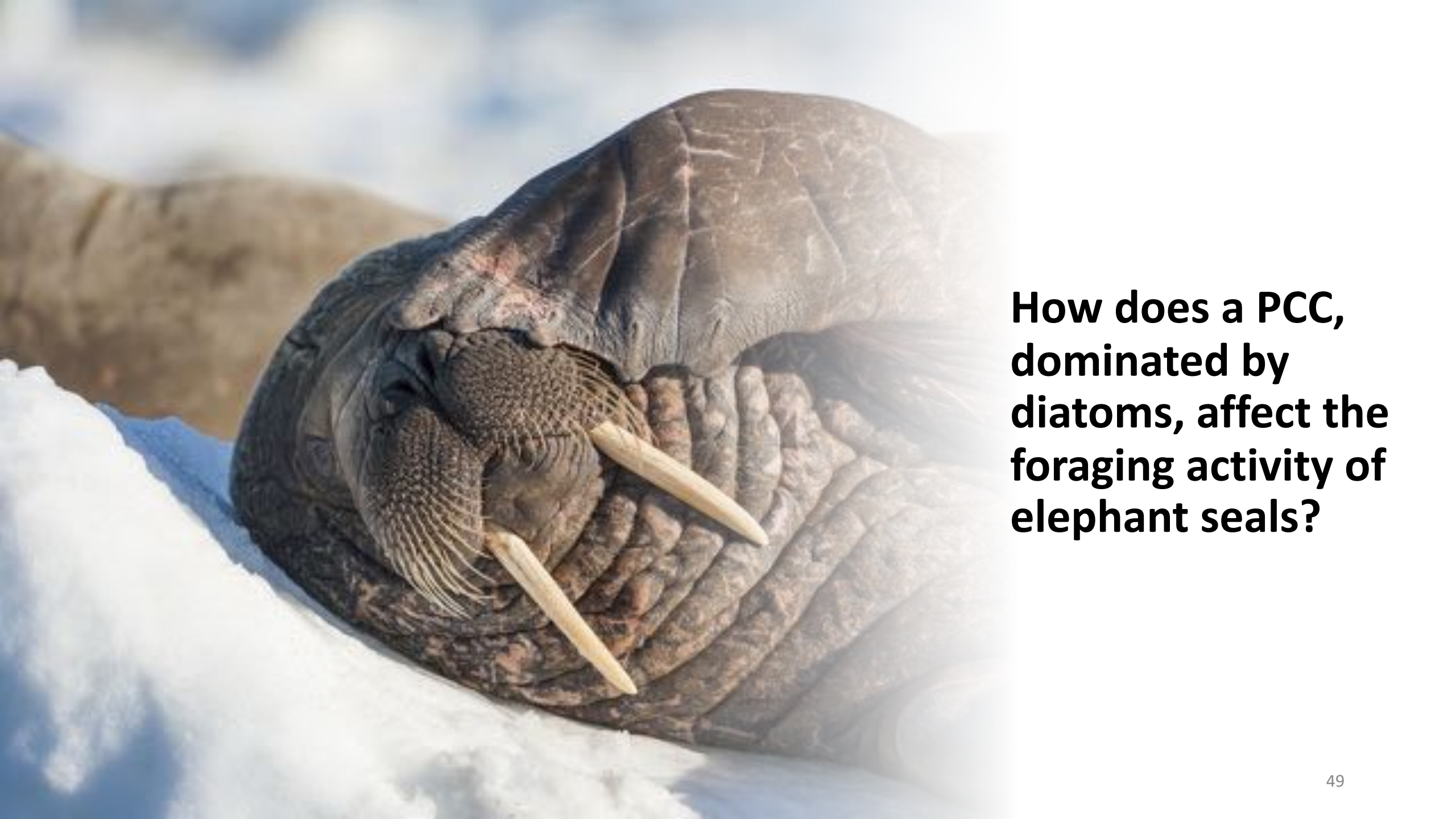
1. Seek productive waters, dominated by diatoms
2. Forage significantly well in such waters
3. Stay in them for an extended period.



(a). The frequency of class occurrence in the whole region (blue bars) and in the regions visited by the seals (yellow bars) in addition to the average normalized PrCA per class. (b). The relative occurrence of consecutive days per class, based on 79 SES.



Sari El Dine, et al., 2025, Influence of the phytoplankton community structure on the southern elephant seals' foraging activity within the Southern Ocean, Comm Biology,



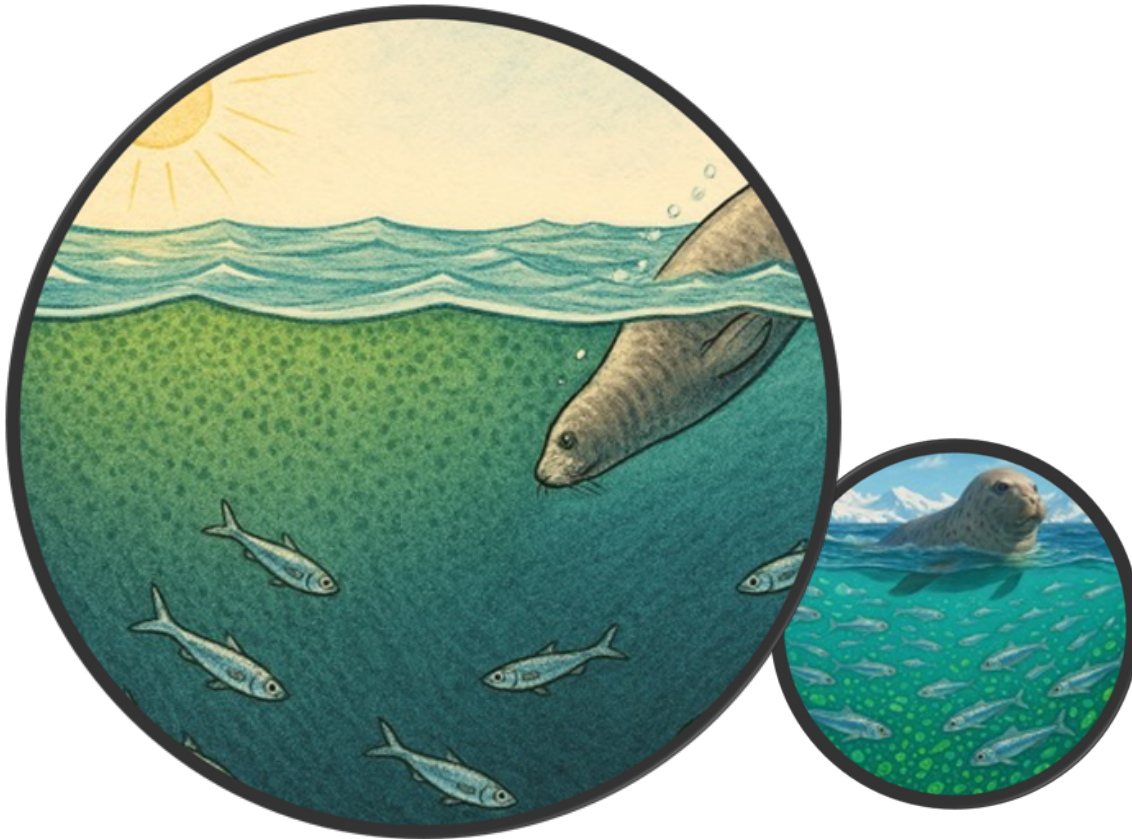
**How does a PCC,
dominated by
diatoms, affect the
foraging activity of
elephant seals?**

How does a PCC, dominated by diatoms, affect the foraging activity of elephant seals?



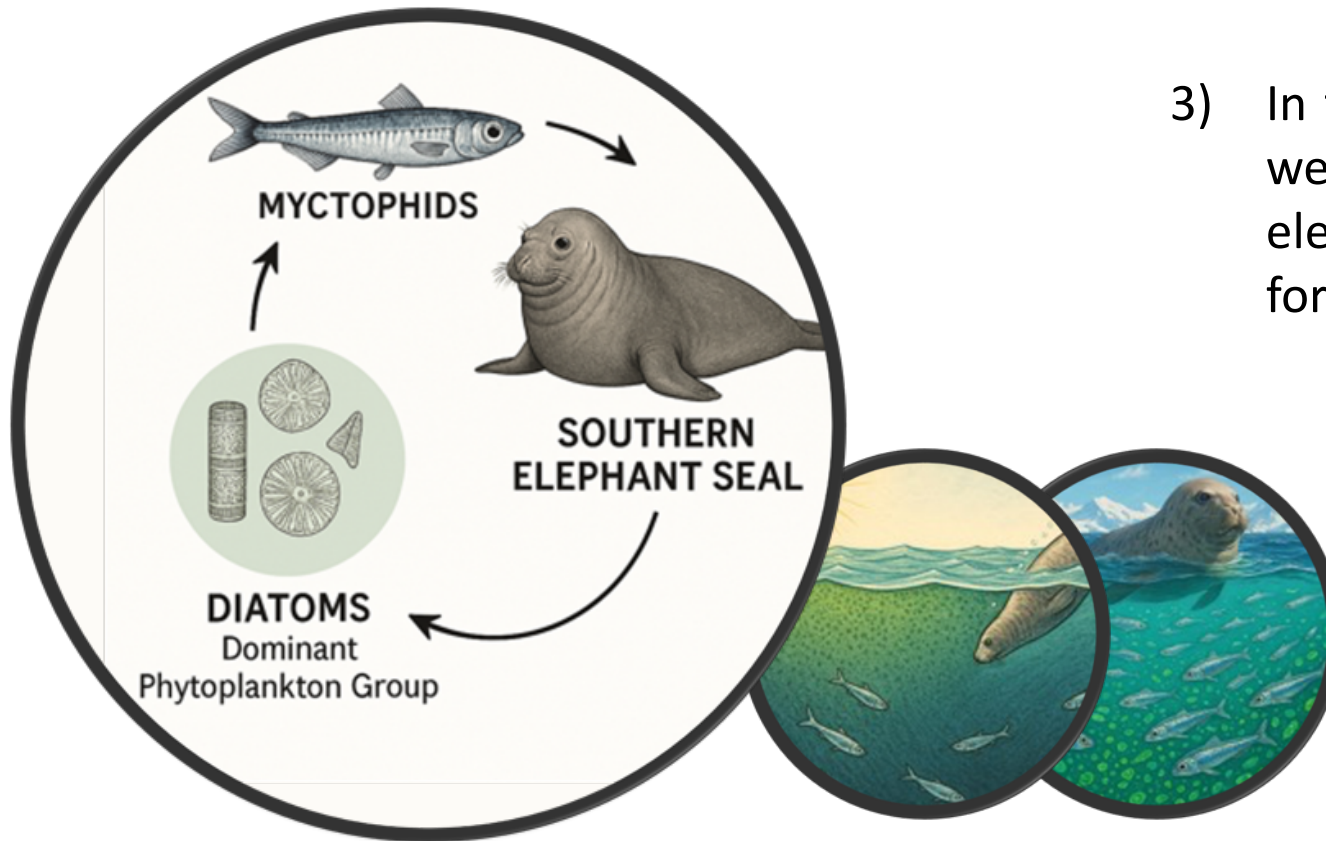
- 1) An increase in phytoplankton biomass increases the availability of prey to the SES

How does a PCC, dominated by diatoms, affect the foraging activity of elephant seals?



- 2) Increases in the phytoplankton abundance result in a shading effect underneath the surface and draw myctophids, the main prey of SES, to shallower depths, thus facilitating the vertical access to prey for the seals during the day.

How does a PCC, dominated by diatoms, affect the foraging activity of elephant seals?

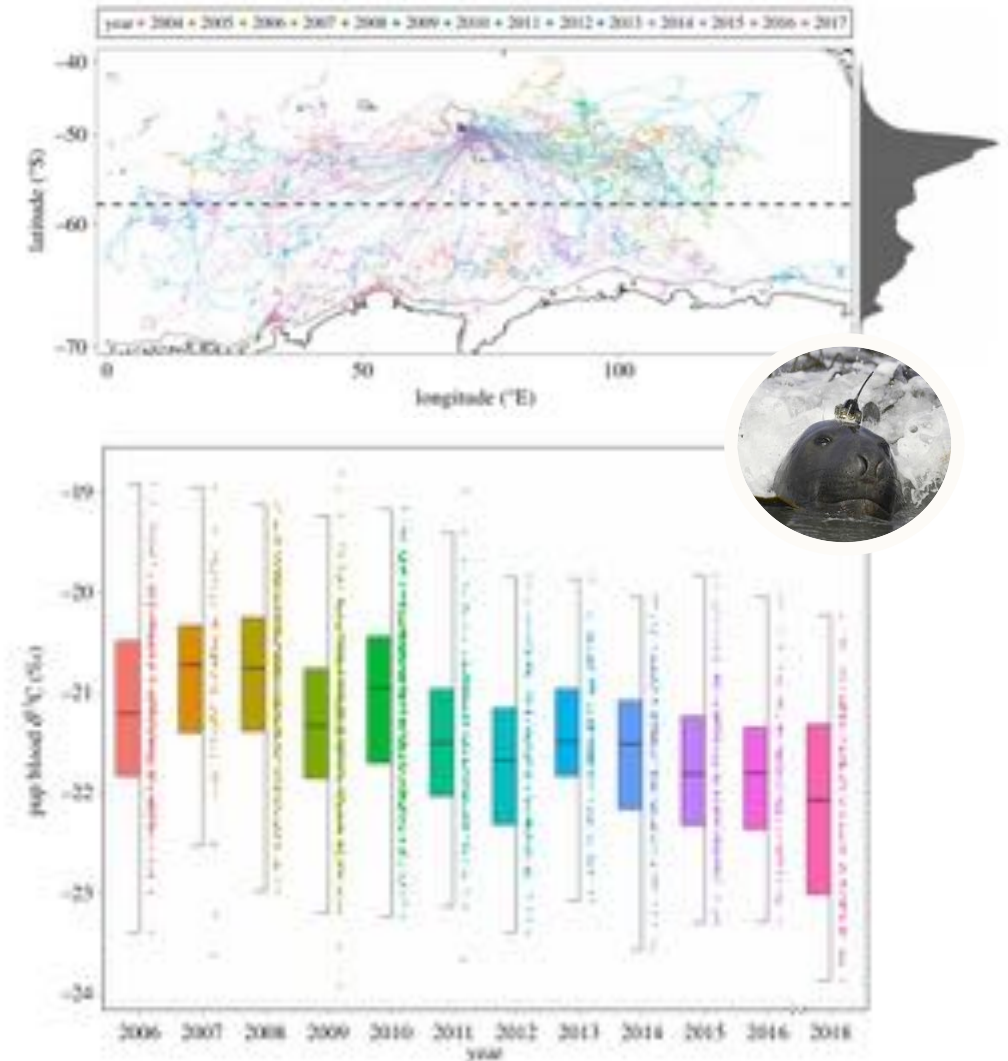


- 3) In the presence of diatoms, a food web more favorable to the elephant seals is formed and better foraging conditions are observed.

Decadal changes in blood $\delta^{13}\text{C}$ values, at-sea distribution, and weaning mass of southern elephant seals from Kerguelen Islands

Julie Mestre^{1,2}, Matthieu Authier^{3,4}, Yves Cherel¹, Rob Harcourt⁵, Clive R. McMahon^{5,6,7}, Mark A. Hindell⁷, Jean-Benoît Charrassin⁸ and Christophe Guinet¹

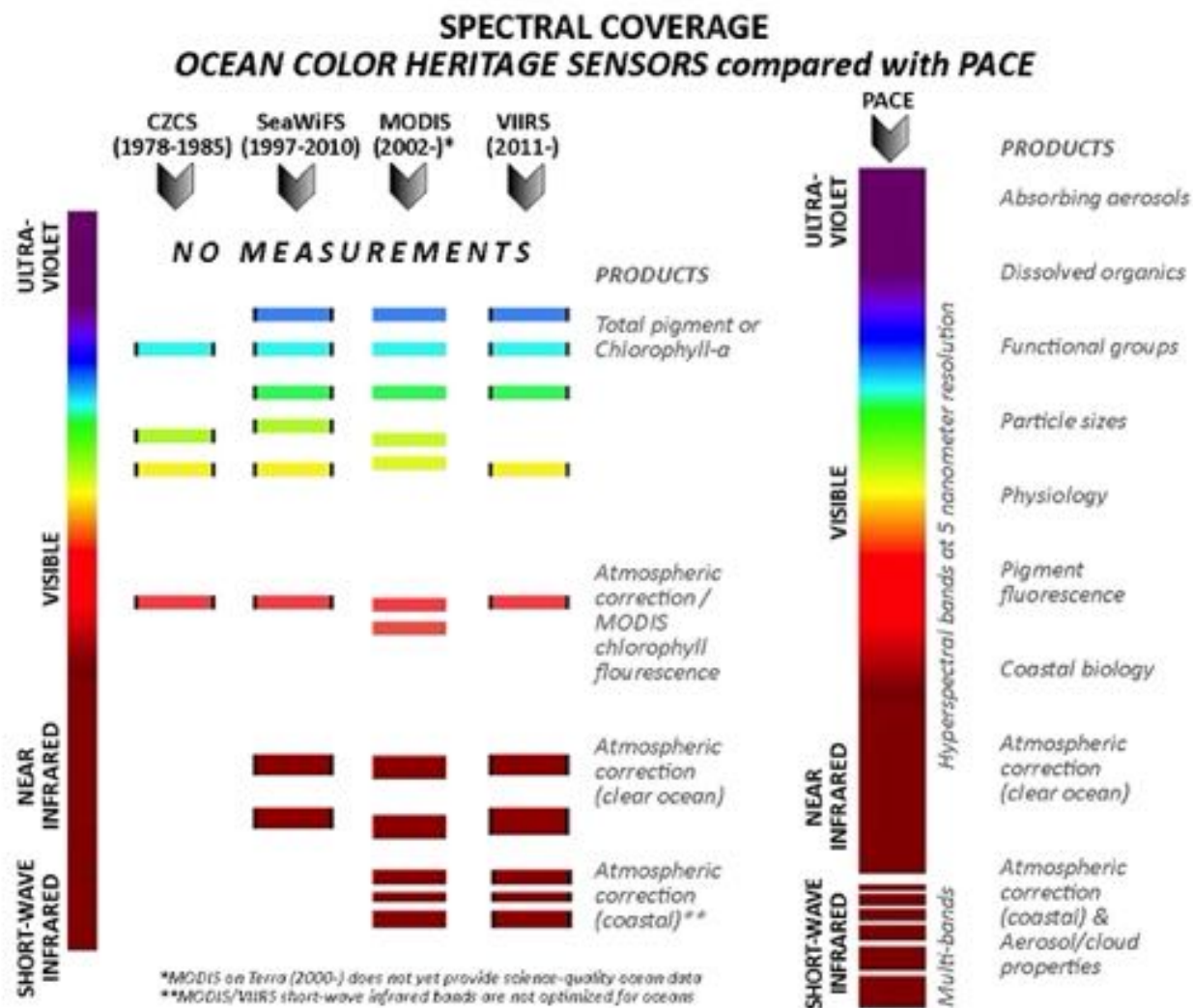
- Suggesting that **changes in primary production and/or the composition of phytoplankton communities** could be driving the $\delta^{13}\text{C}$ decrease,
- especially **which phytoplankton groups dominate:**
 ^{13}C -rich diatoms vs ^{13}C -depleted nano- and picophytoplankton





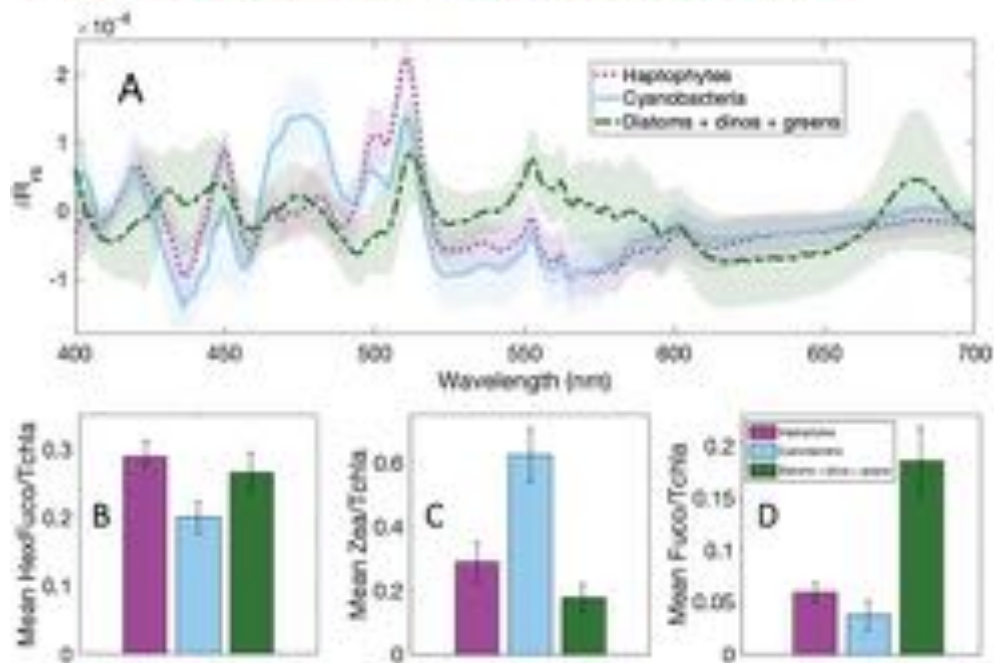
The hyperspectral era

The hyperspectral era

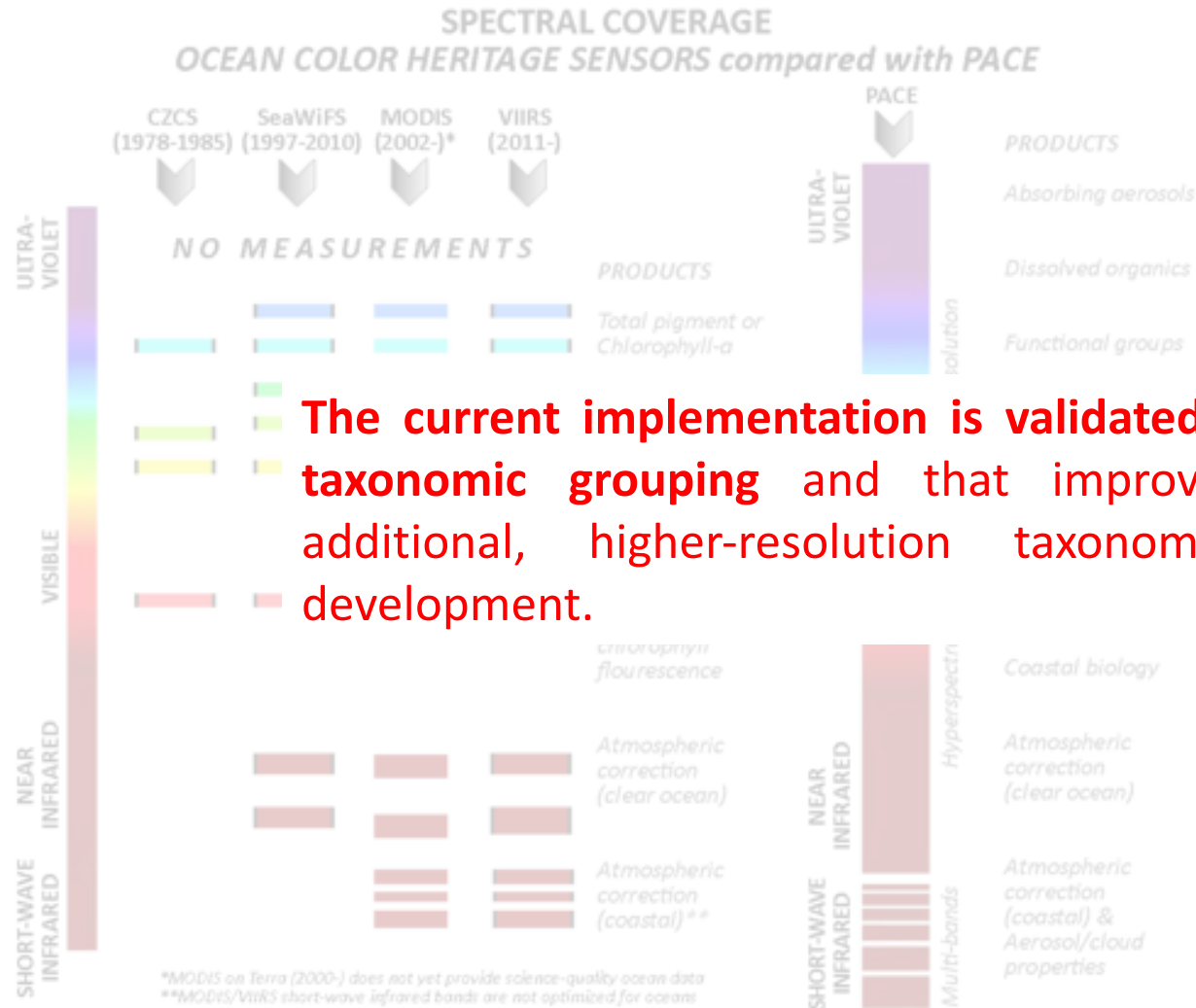


Phytoplankton communities quantified from hyperspectral ocean reflectance correspond to pigment-based communities

SASHA J. KRAMER,^{1,*} STÉPHANE MARITORENA,² IVONA CETINIĆ,^{3,4} P. JEREMY WERDELL,³ AND DAVID A. SIEGEL²



The hyperspectral era



The current implementation is validated only for a three-community, broad taxonomic grouping and that improving taxonomic resolution requires additional, higher-resolution taxonomic data and further algorithm development.

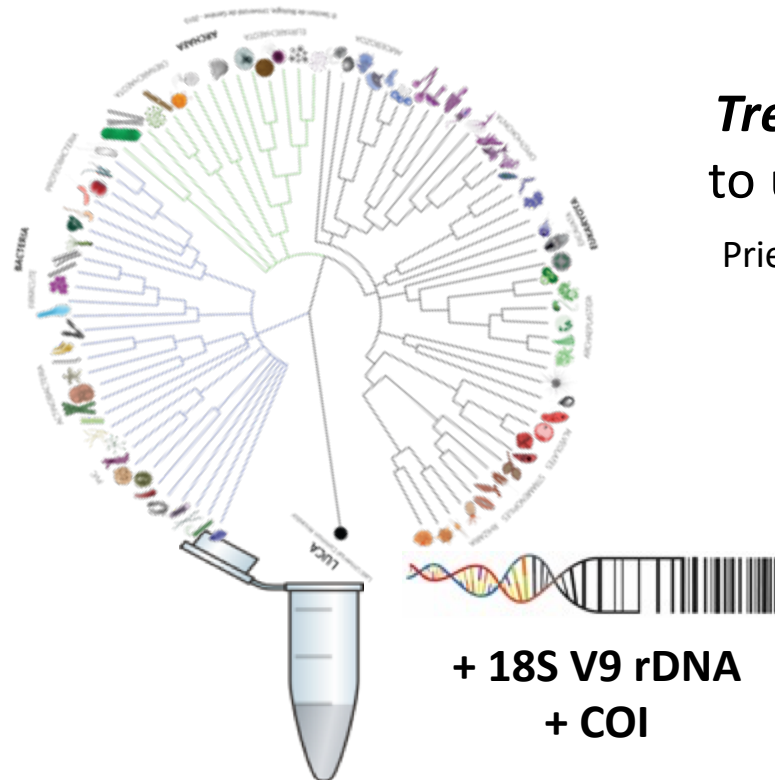
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Towards Hyperspectral - Genomics Synergy

- Co-located omics, optics and environmental measurements for algorithm development
- Testbeds for future operational 'biodiversity from space' products

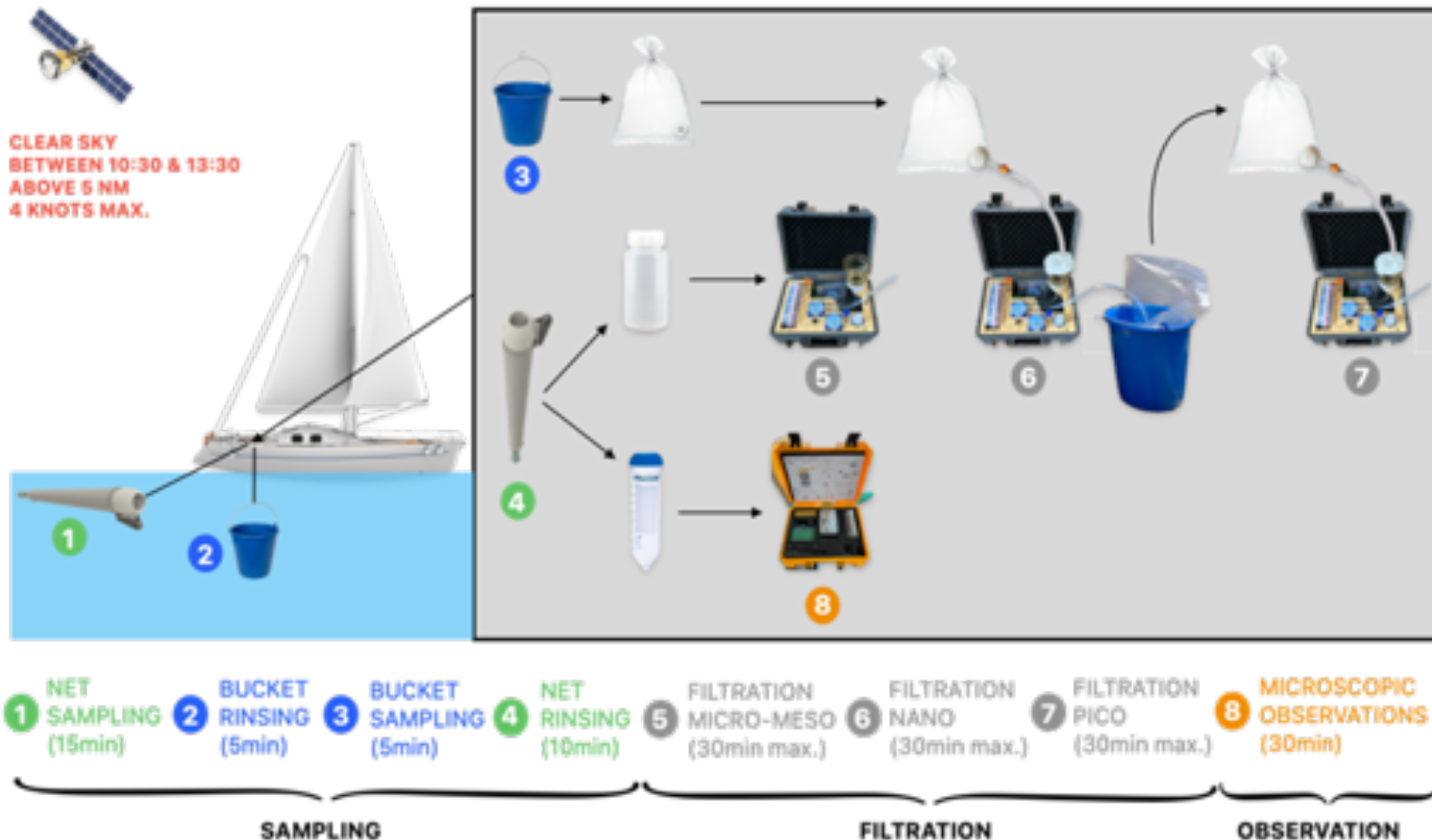


The JEDI marker
***Tree-of-life* scale single-PCR**
to uncover total biodiversity.
Priest, Henry, et al. 2025





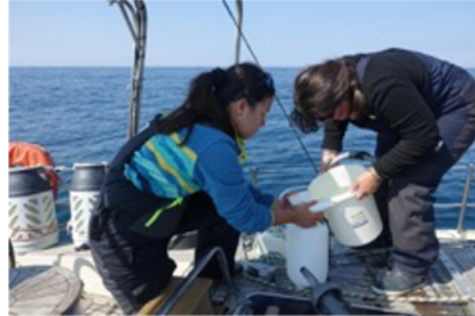
20 kits for 2 years

'matchup' *in-situ* biodiversity datasets from c.a. 1,200 sites covering the world ocean

Optimizing global environmental sampling vs cost

Poster #190

WORKING
WITH
SEATIZENS



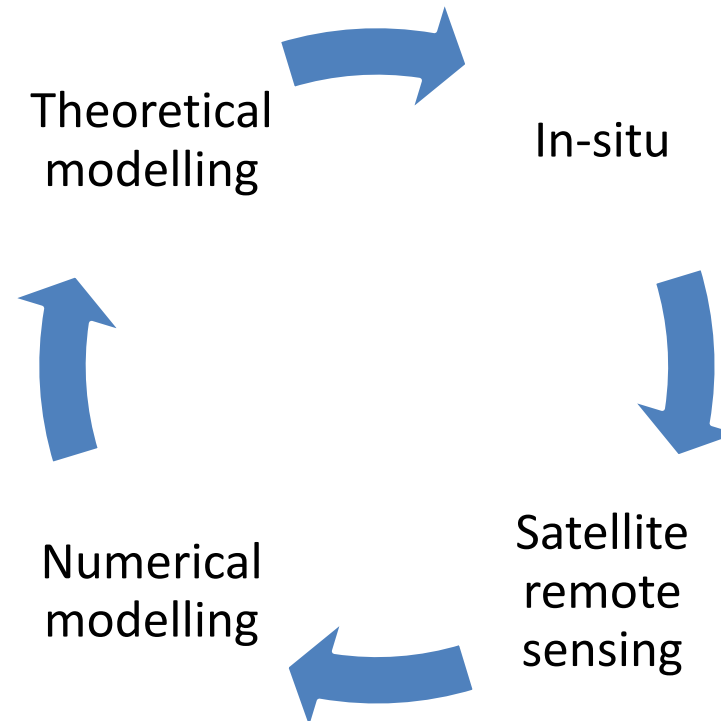
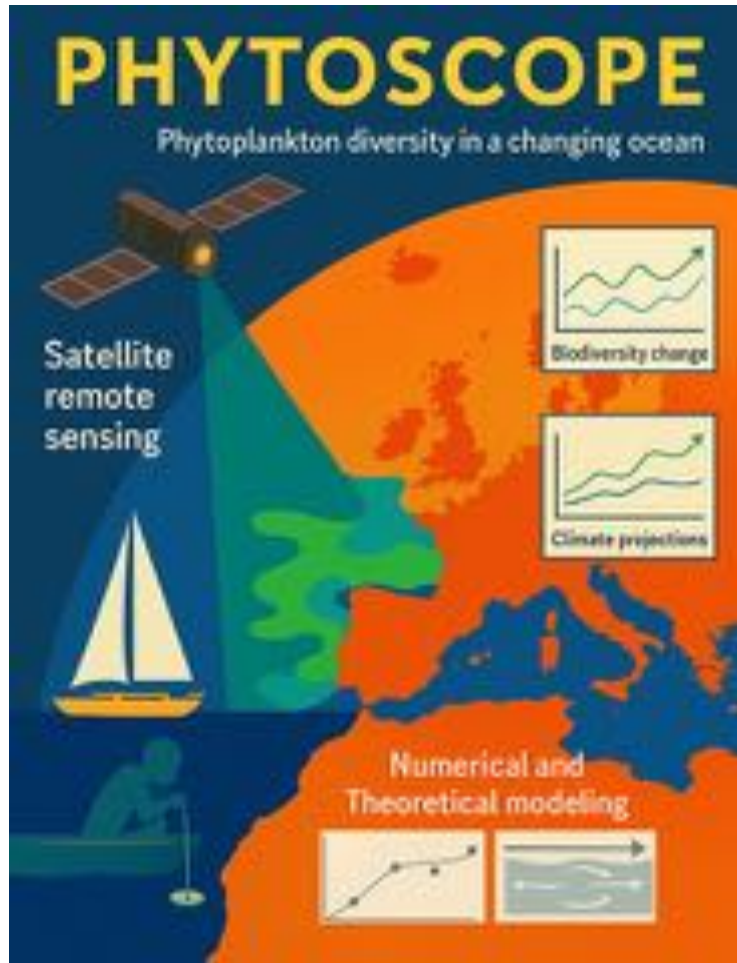
Tutorial videos and
pedagogical contents

https://www.youtube.com/watch?v=n_bQNYxE-2ww



PHYTOSCOPE & ODPE–AASTRES: New Data for Phytoplankton Biodiversity

PHYTOSCOPE (2026-2029), funded by the BNP Paribas Climate and biodiversity initiative, integrates in-situ, satellites, models and theory to understand and predict climate-driven shifts in phytoplankton communities.



THE SECCHI DISK
FOUNDATION



PHYTOSCOPE & ODPE–AASTRES: New Data for Phytoplankton Biodiversity



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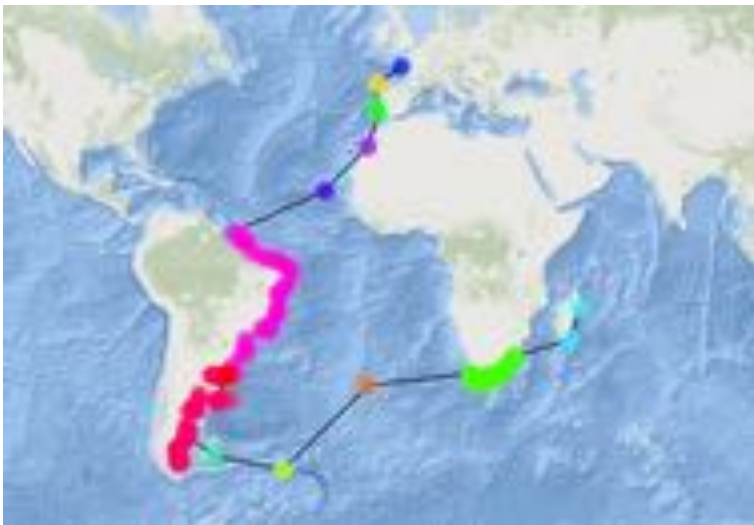


AASTRES sailing campaign 2026: 5–6-month



High-resolution in situ measurements along the route:

- Flow cytometry, Fluoroprobe, metabarcoding (PlanktoSpace kit)
- CTD profiles, nutrients, T/S, chlorophyll-a
- Hyperspectral radiometry



AASTRES campaign stations map

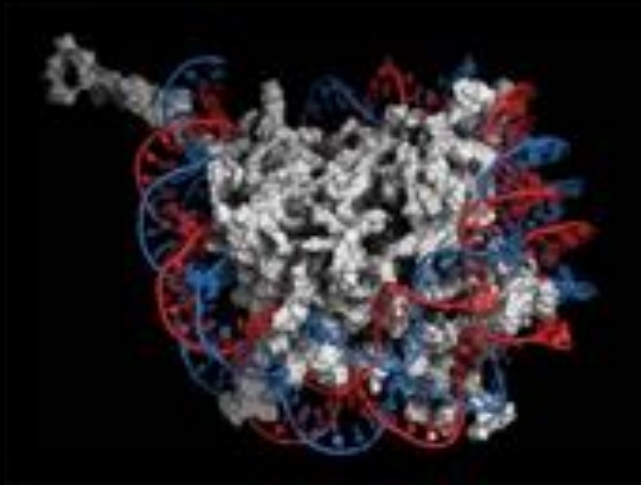
Biodiversity is multi-dimensional and multi-scale: no single observing system is sufficient.



Open Questions and recommendations for Biodiversity from Space

- Which marine biodiversity Essential Variables can we robustly and routinely infer from EO?
- How do we turn these advances into actionable services for conservation and management?
- Importance of an open, cross-disciplinary consortium, merging biology, ecology, physics, data science, and modeling expertise

From genes to satellite pixels,
biodiversity is irreducibly multidimensional, and hierarchical, showing
a different face every time we change scale, perspective, or question.

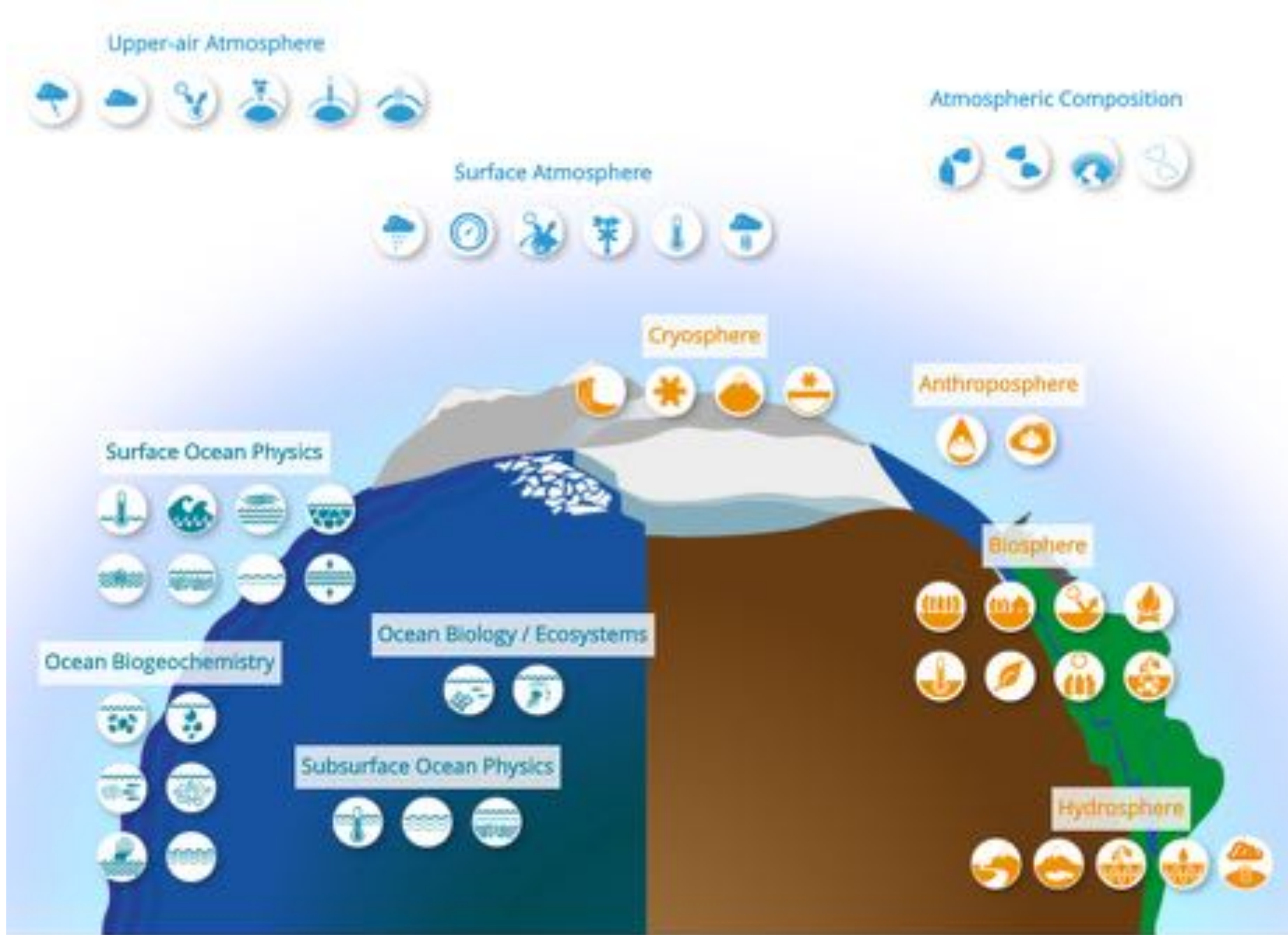




International
Ocean Colour Science
Meeting 2025
Advancing Global Ocean Colour Observations

Thank you!

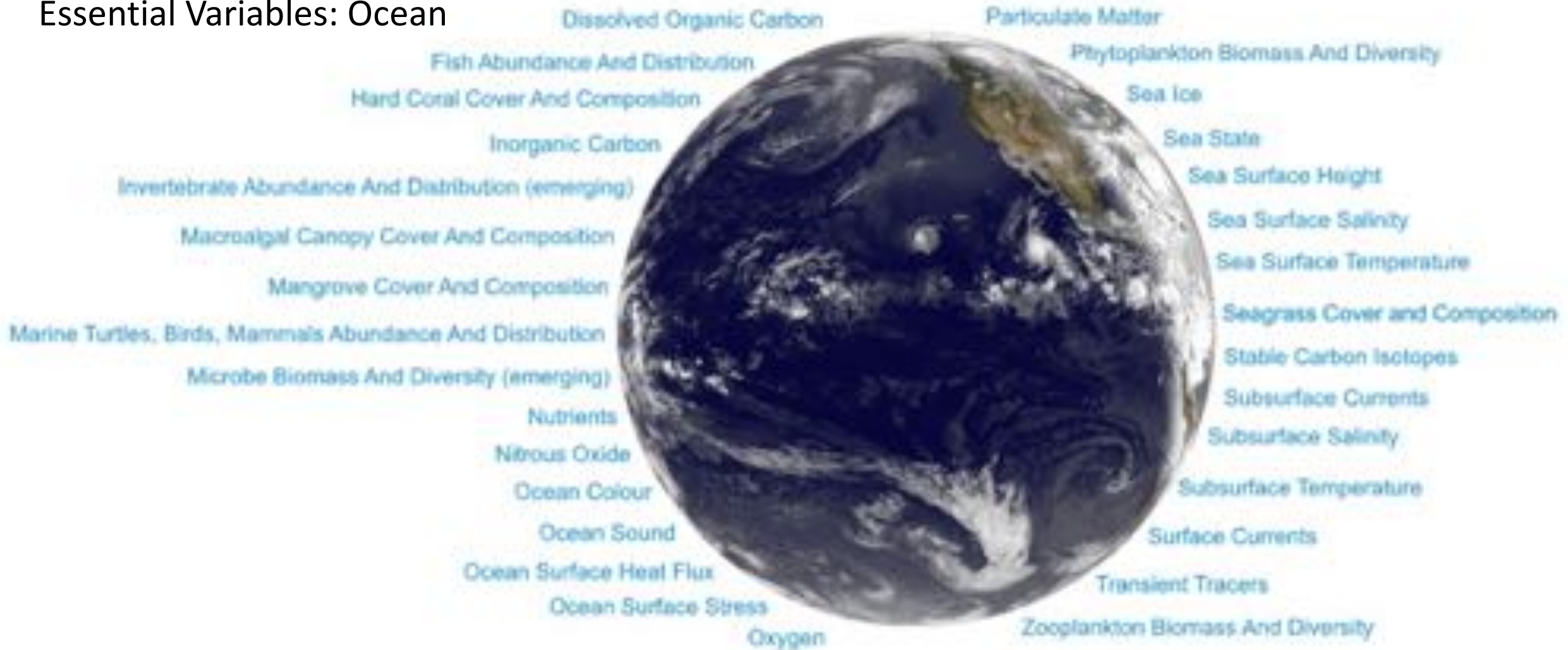
Questions and Answers



From Essential Climate Variables to Biodiversity Essential Variables: Climate

Essential Climate Variables as defined by the Global Climate Observing System; there are 54 focused on the atmosphere, cryosphere, ocean, anthroposphere, biosphere, and the hydrosphere.

From Essential Climate Variables to Biodiversity Essential Variables: Ocean



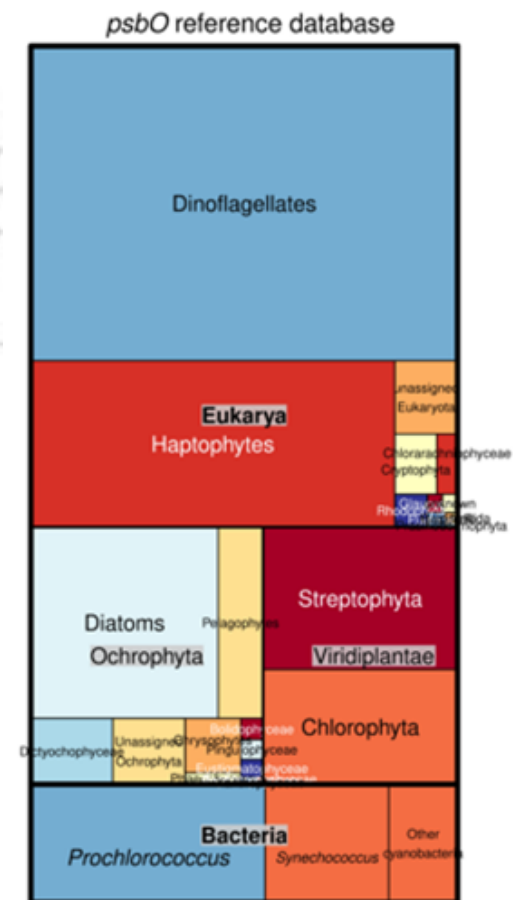
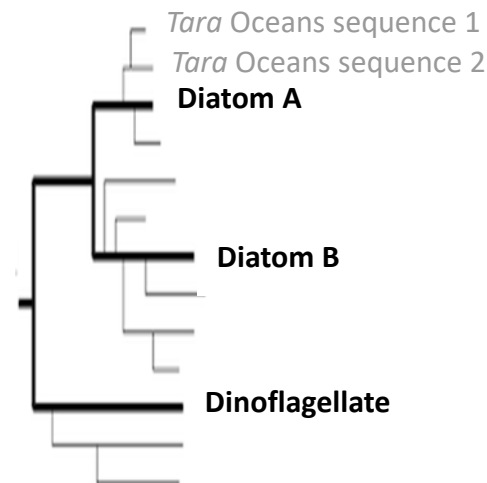
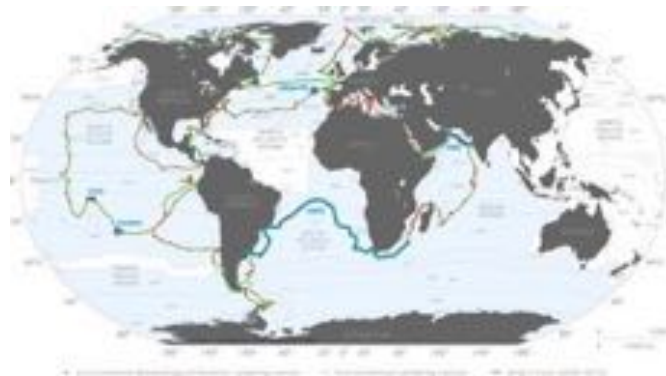
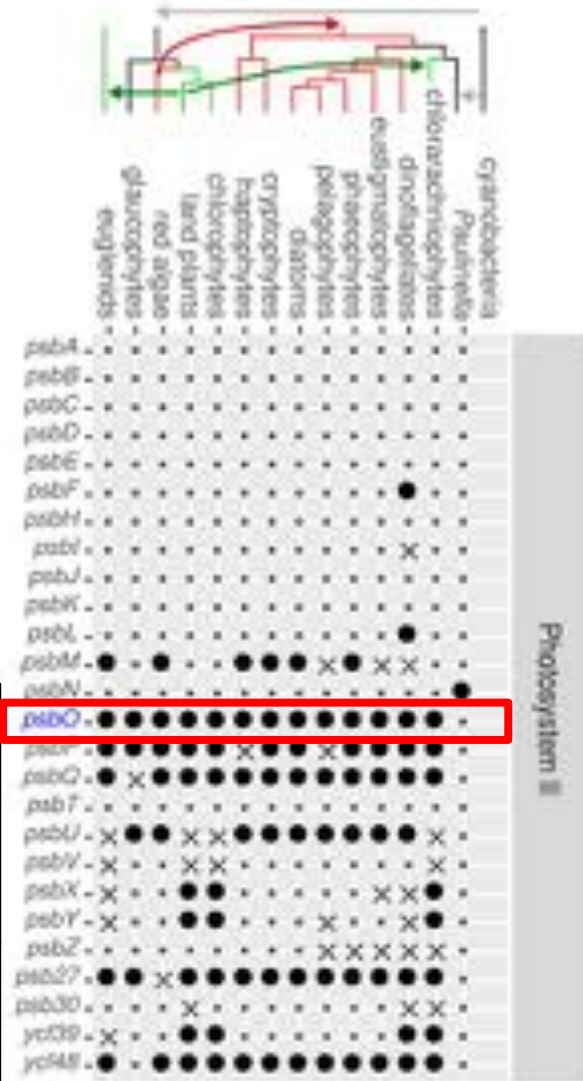
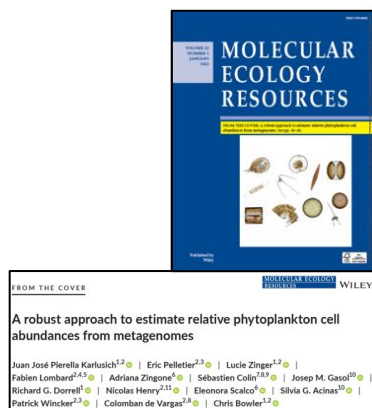
EOVs are focused on the physics of the ocean system, the biogeochemistry, and the biology and ecosystems.

Linking Omics and Satellites: Searching for an unbiased approach using metagenomics

The *psbO* protein; a core subunit of photosystem II (PSII), **unique to organisms that carry out oxygenic photosynthesis**.

The *psbO* is a **single-copy gene**, present in both eukaryotes and prokaryotes groups

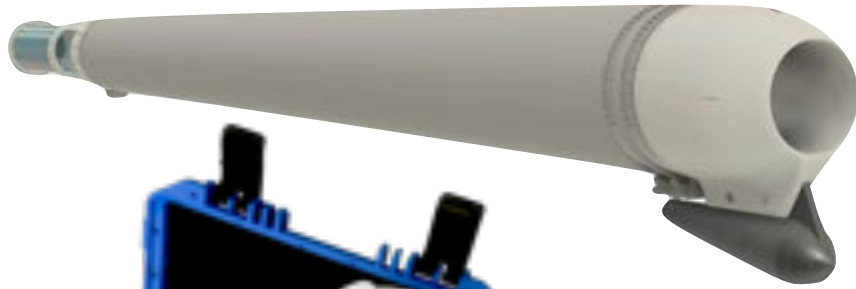
= Proxy of cell abundance



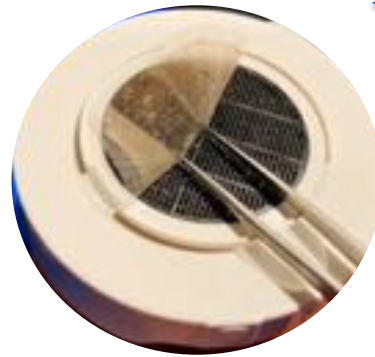
Curated database of >18k unique *psbO* sequences

Pierella et al., 2022, <https://doi.org/10.1111/1755-0998.13592>

pico- / nano-



micro- / meso-



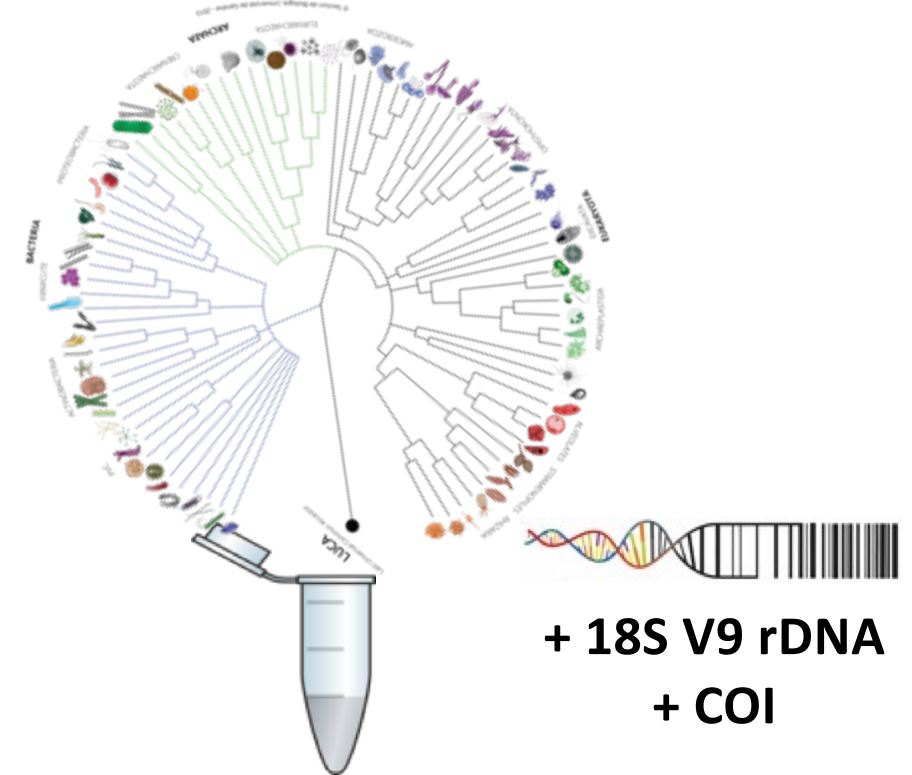
organismal size

taxonomy

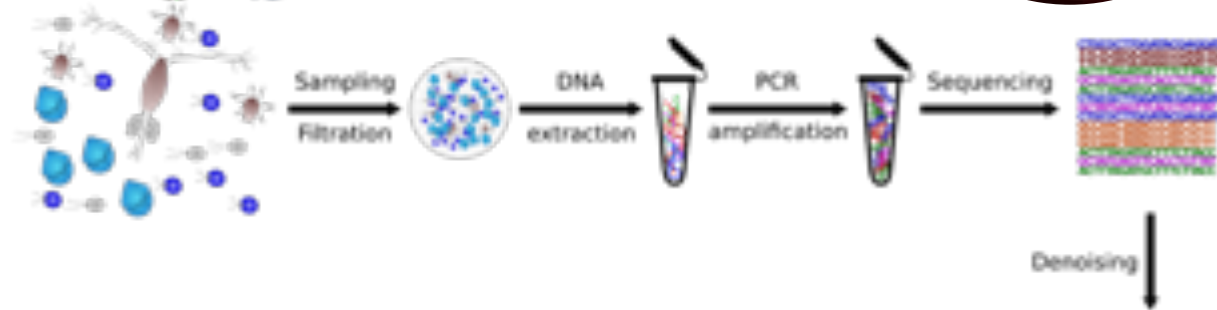
TREE-OF-LIFE SCALE BIODIVERSITY DATA

The JEDI marker

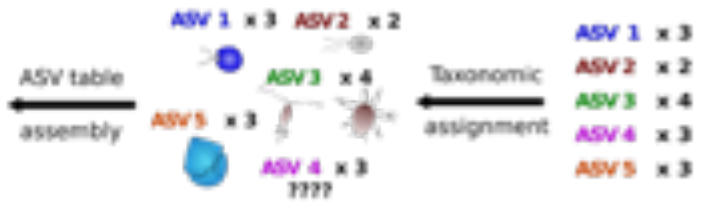
Tree-of-life scale single-PCR to
uncover total biodiversity.



+ 18S V9 rDNA
+ COI



taxonomy	sample 1	sample 2	sample 3
ASV 1 <i>Planocystis</i> sp.	3	0	10
ASV 2 <i>Tetrahymena</i> sp.	2	5	1
ASV 3 <i>Offionema</i> name	4	2	1
ASV 4 ?????	3	1	1
ASV 5 <i>Blattellidreum</i> sp.	3	8	1



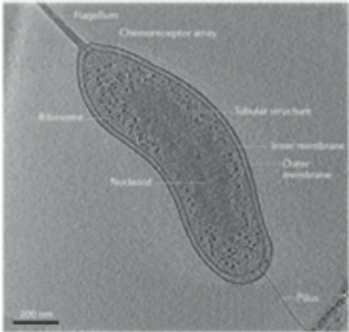
The JEDI marker as a universal measure of planetary biodiversity
Priest, Henry, et al. 2025

<https://www.biorxiv.org/content/10.1101/2025.08.11.669668v1>

The JEDI marker as a universal measure of planetary biodiversity

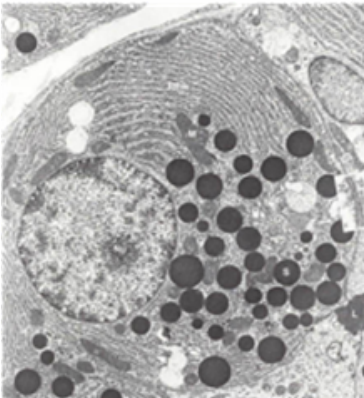
✉ Taylor Priest, ✉ Nicolas Henry, ✉ Thomas Weber, ✉ Laurine Planat, ✉ Coralie Rousseau, ✉ Simon M. Dittami, ✉ Yi-Chun Yeh, ✉ David M. Needham, ✉ Hans-Joachim Ruscheweyh, ✉ Fabienne Rigaut-Jalabert, ✉ Nathalie Simon, ✉ Sarah Romac, ✉ Florence Le Gall, ✉ Thomas Beavis, ✉ Kevin Moog, ✉ Alice Moussy, ✉ Corinne Da Silva, ✉ Caroline Belser, ECOMAP team, TREC expedition team, Mobile Laboratory team, ✉ Jan Korbel, ✉ Raffaele Siano, ✉ Julie Poulain, ✉ Patrick Wincker, ✉ Paola Bertucci, ✉ Peer Bork, ✉ Jed A. Fuhrman, ✉ Flora Vincent, ✉ Shinichi Sunagawa, ✉ Colomban de Vargas

doi: <https://doi.org/10.1101/2025.08.11.669668>



Une cellule de *Vibrio* imagée cryo-microscopie électronique (Oikonomou et al. 2016)

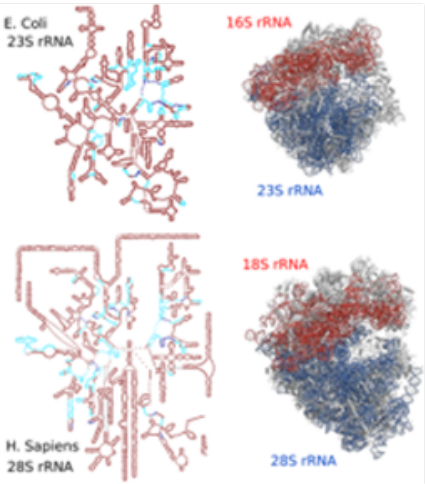
Une cellule animale du pancréas



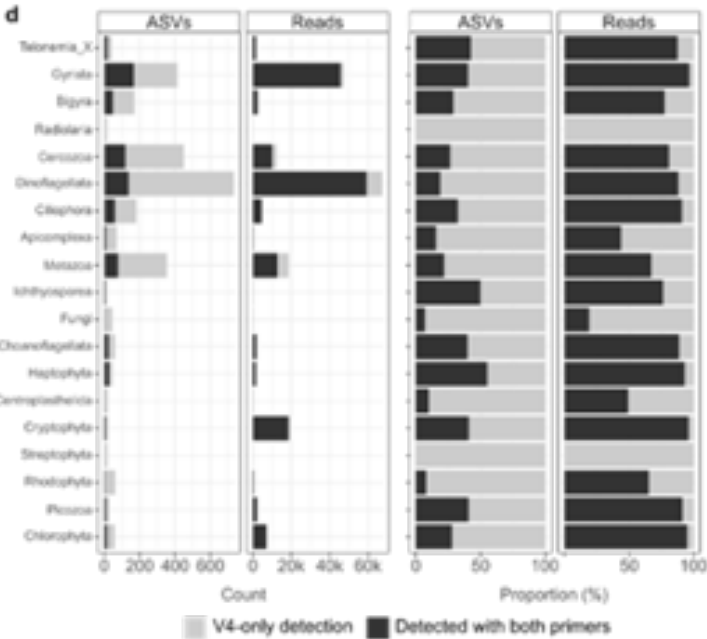
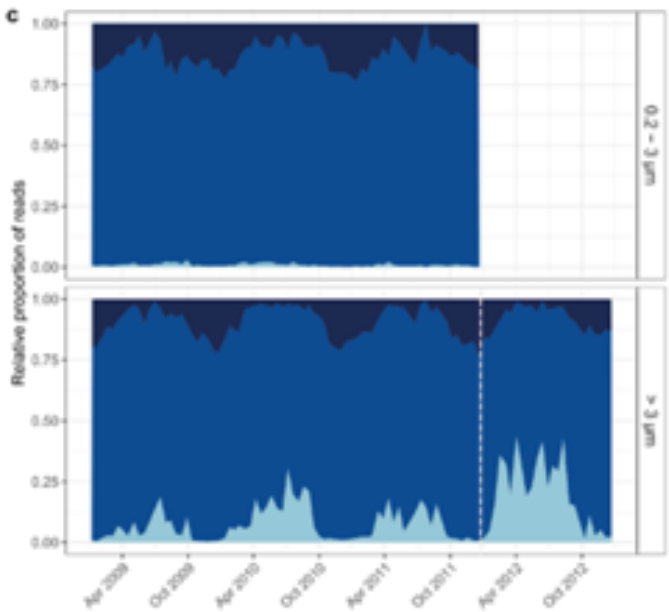
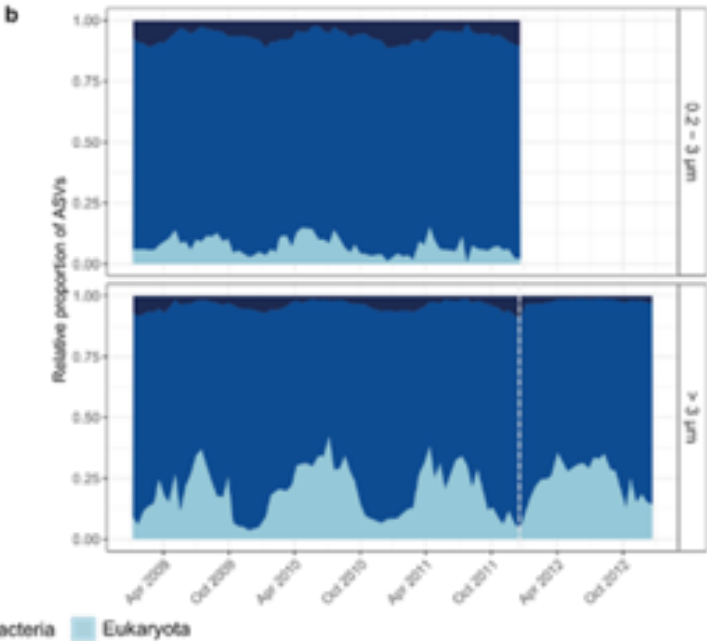
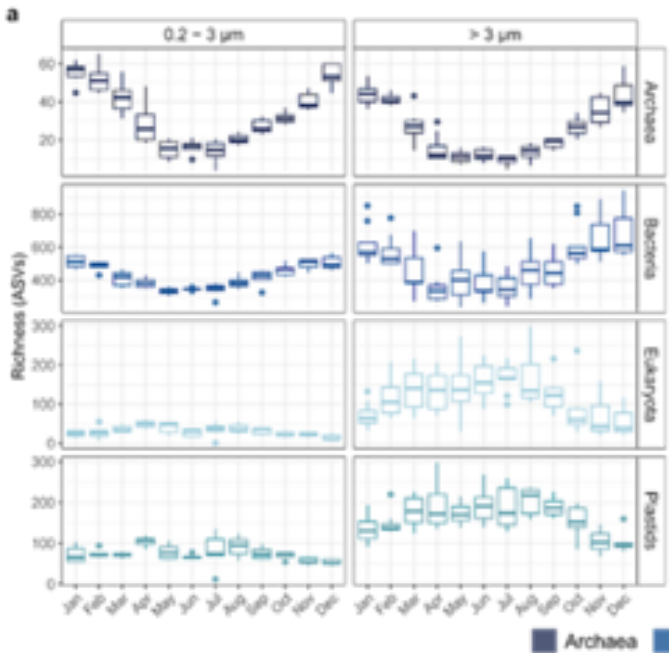
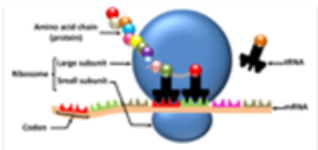
Ribosome .. La molécule universelle du vivant

Structure secondaire de la séquence d'ARN

Structure 3D



Poitevin et al. 2020



Linking oceanographic conditions to foraging behaviour of southern elephant seals by characterising mid-trophic levels with an animal-borne echosounder

Marius Molinet^{a,b,c,*}, Antoine-Pe  o Uhart^a, Nad  ge Fonvicille^{a,b}, Jade Chevassu^a, Cl  ment Castrec^a, Martin Tournier^a, Didier Goulet-Tran^a, Mathilde Chevallay^a, Ziad Sari El Dine^{a,c}, Baptiste Picard^a, Roy El Hourany^c, David Nerini^b, Christophe Guinet^a

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