

Tara Oceans: Eco-Systems Biology at Planetary Scale

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Co-directed by
Etienne Bourgois
and Eric Karsenti



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The Plankton

THE INVISIBLE MULTITUDE

- ✓ BASIS OF THE OCEANIC FOOD WEB
- ✓ SEQUESTER ATMOSPHERIC CO₂ IN THE OCEAN
- ✓ GENERATE THE OXYGEN WE BREATHE
- ✓ THE MOST IMPORTANT BIOLOGICAL CARBON PUMP ON THE PLANET
- ✓ AFFECT AND ARE AFFECTED BY CLIMATE CHANGE

>90% of the biomass in the ocean

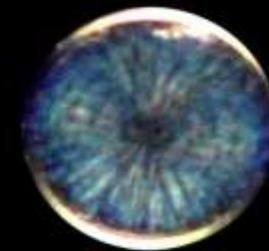
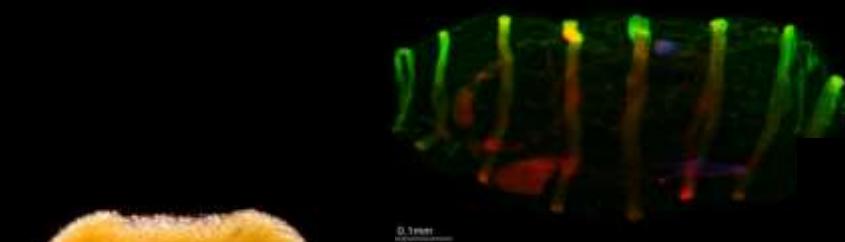
Protists:

0.1-10 million/litre

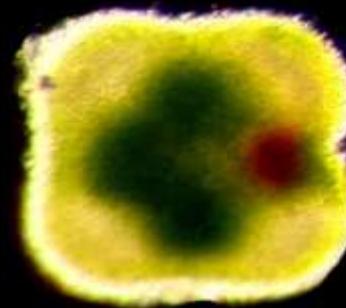




Zooplankton:
0.1-100/litre



E.Reynaud, UCD, Dublin



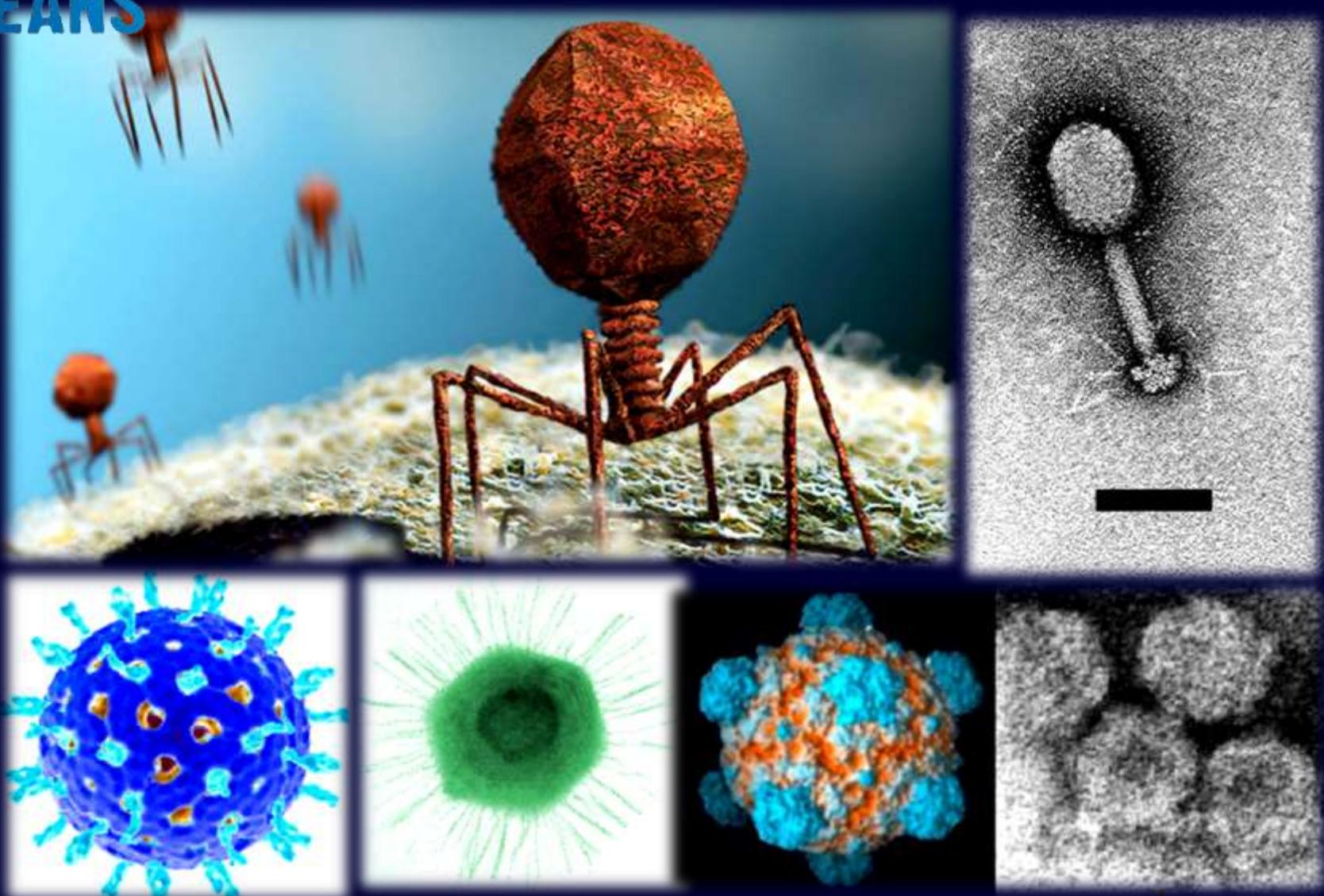
E.Reynaud, UCD, I

Bacteria/Archaea:

0.1-1 billion/litre



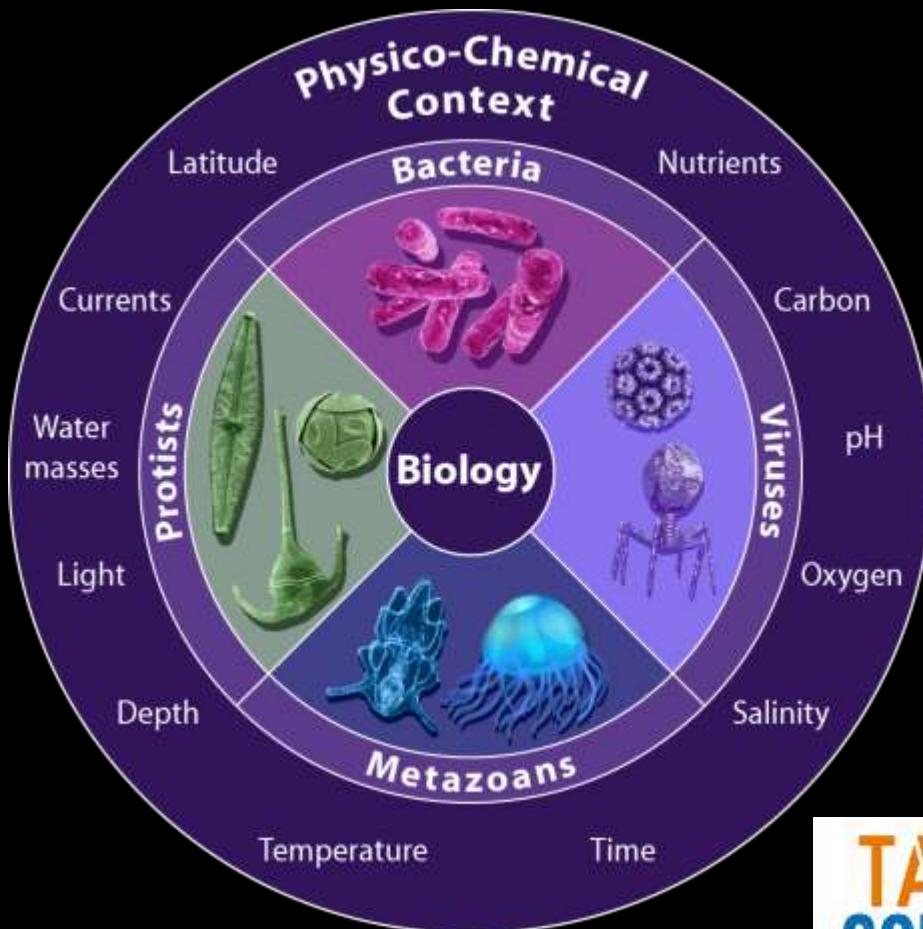
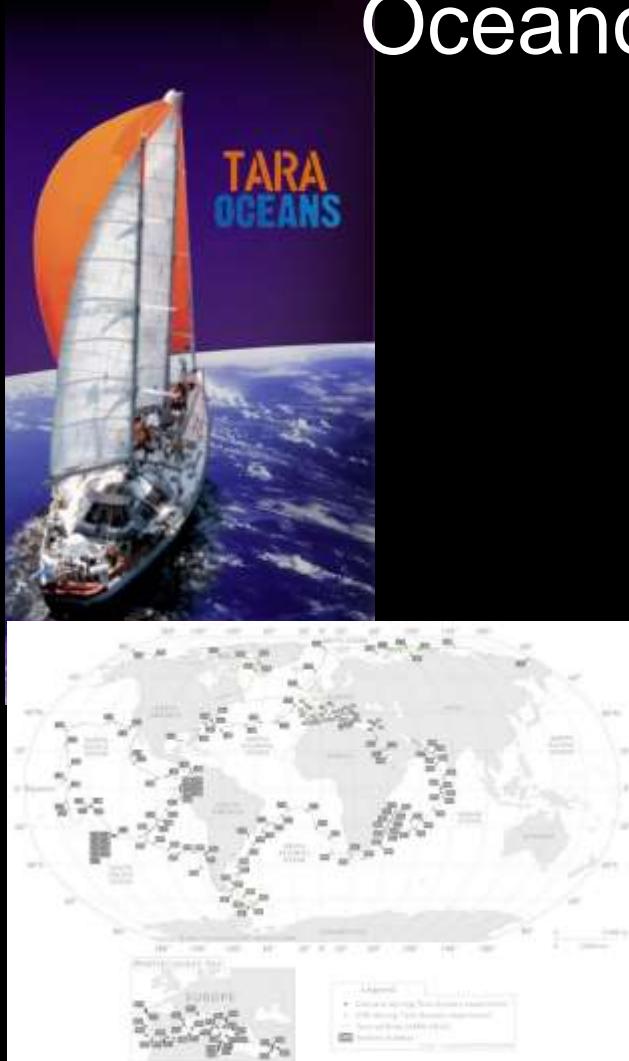
Viruses and giruses: 1-10 billion/litre





1.33W x 3.33H

Adding Biological Parameters into Oceanographic Research



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TARA OCEANS

2009 - 2013

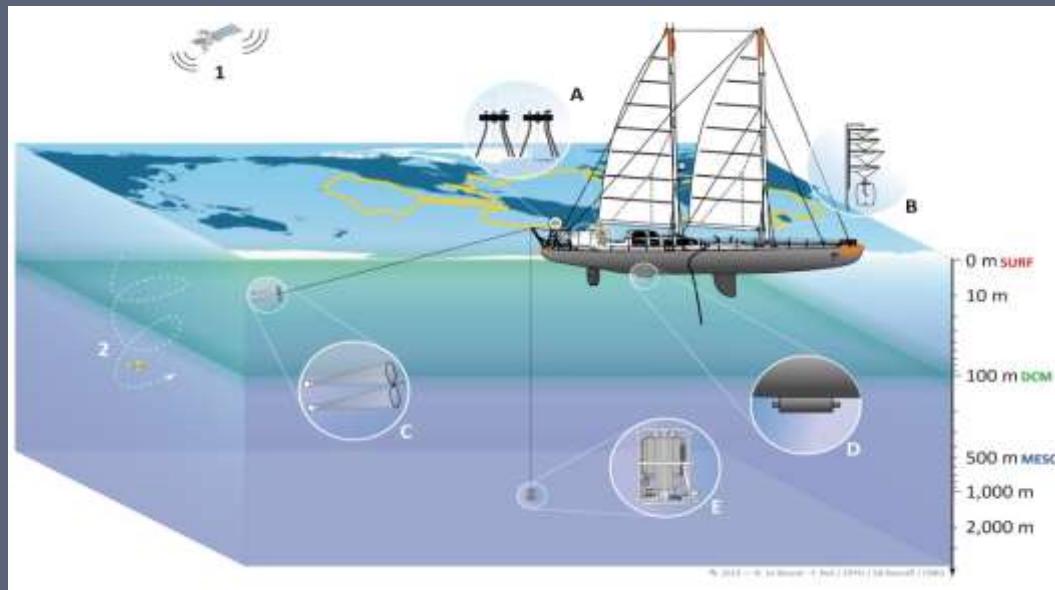


© 2015 — N. Le Bescot / EPEP / SB Roscoff / CNRS



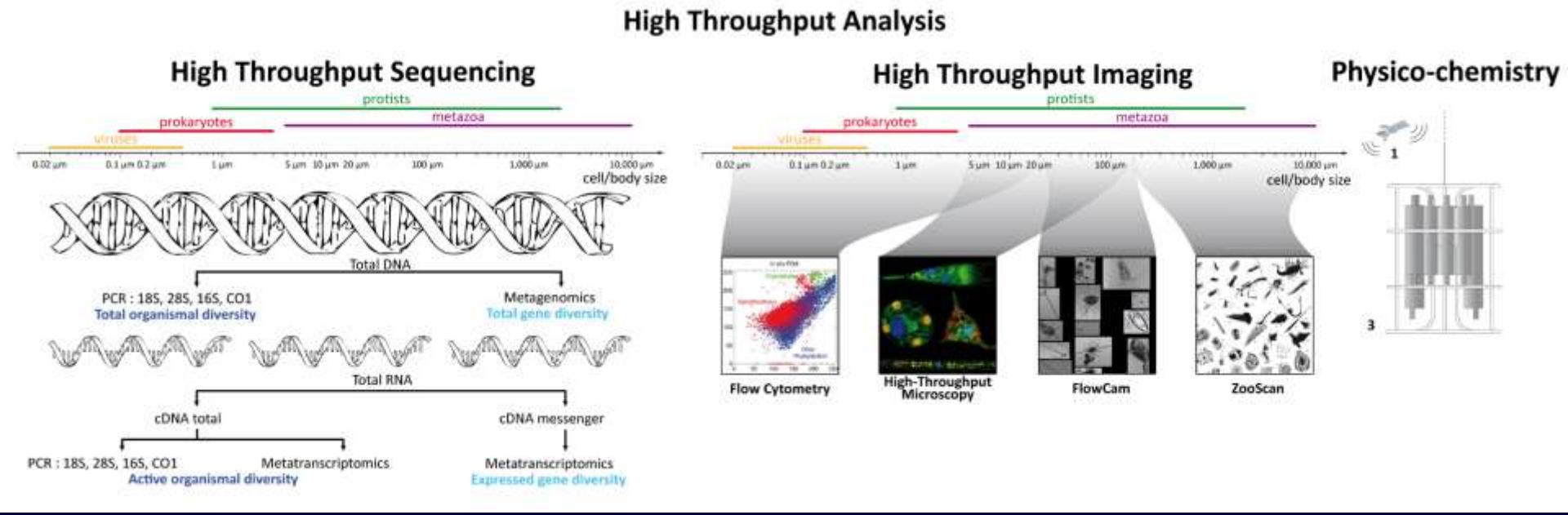
Tara Oceans Global Sampling

September 2009 – October 2013



- 210 stations
- 40,000 samples for biology
 - Surface, DCM, meso
 - DNA, RNA sequencing
 - Microscopy
 - Flow cytometry
- > 1,500 CTD profiles
- Underway measurements
 - TSG, Ac-S, FRRF, Alfa
- > 2,000 nutrient samples
- > 1,800 HPLC samples
- > 900 carbonate samples

The *Tara Oceans* Analysis Pipeline who is there, what do they do, with whom, and why ?



OPEN ACCESS Freely available online

PLOS BIOLOGY

Community Page

A Holistic Approach to Marine Eco-Systems Biology

Eric Karsenti^{1*}, Silvia G. Acinas², Peer Bork¹, Chris Bowler^{3,4}, Colombe De Vargas^{3,5,6}, Jeroen Raes^{7,8}, Matthew Sullivan⁹, Detlev Arendt¹, Francesca Benzoni¹⁰, Jean-Michel Claverie^{3,11}, Mick Follows¹², Gaby Gorsky^{3,6,13}, Pascal Hingamp^{3,11}, Daniele Iudicone¹⁴, Olivier Jaillon¹⁵, Stefanie Kandels-Lewis¹, Uros Krzic¹, Fabrice Not^{3,5,6}, Hiroyuki Ogata^{3,11}, Stéphane Pesant^{16,17}, Emmanuel Georges Reynaud¹⁸, Christian Sardet^{3,6,19}, Michael E. Sieracki²⁰, Sabrina Speich²¹, Didier Velayoudon²², Jean Weissenbach¹⁵, Patrick Wincker¹⁵, the *Tara Oceans* Consortium¹

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Ocean Microbial Reference Gene Catalog

A Tara Oceans sampling stations



Global representation

68 stations

40 million genes : Gene catalog is close to saturation

3 depths

1,000 times more sequence than GOS sequence

sequence

Equivalent to 135 fully sequenced human genomes

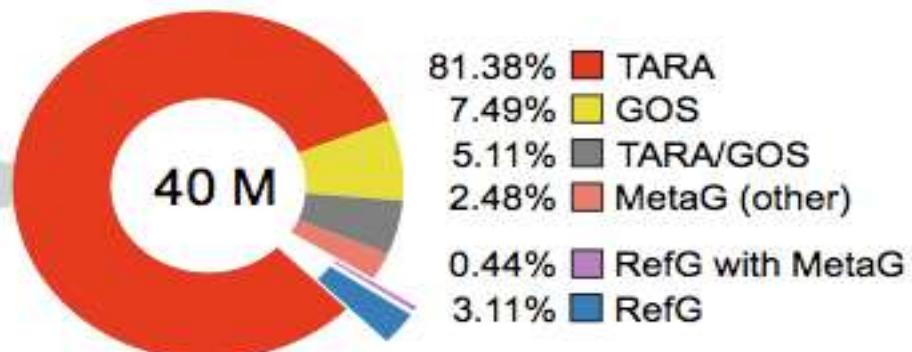
Ocean microbiome

| 68 sites

| 243 samples

111.5 M predicted genes
+ 26 M external genes

Clustering



Of 40M genes, 28% no annotation, rest (60%) mainly bacteria

Sunagawa et al.
Science (2015)

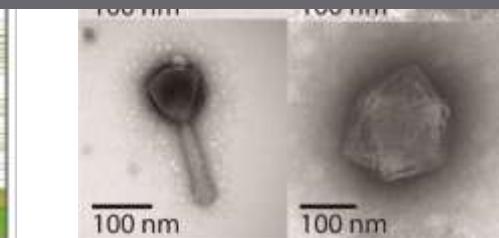
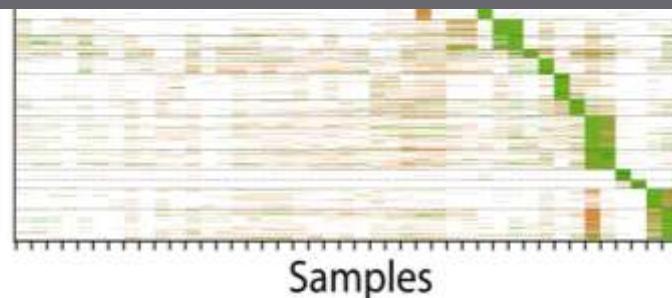
Assessment of global viral communities



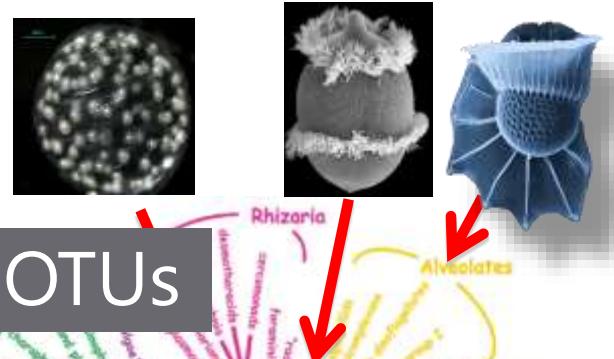
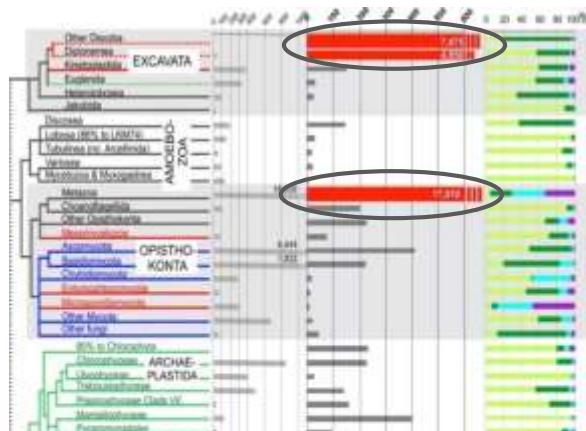
5,476 Viral communities. Only 39 previously known

Viral populations are regionally dominant, but widespread

Data supports seed-bank hypothesis for viral ecology



A new world of marine protists



Saturation at around 130,000 OTUs

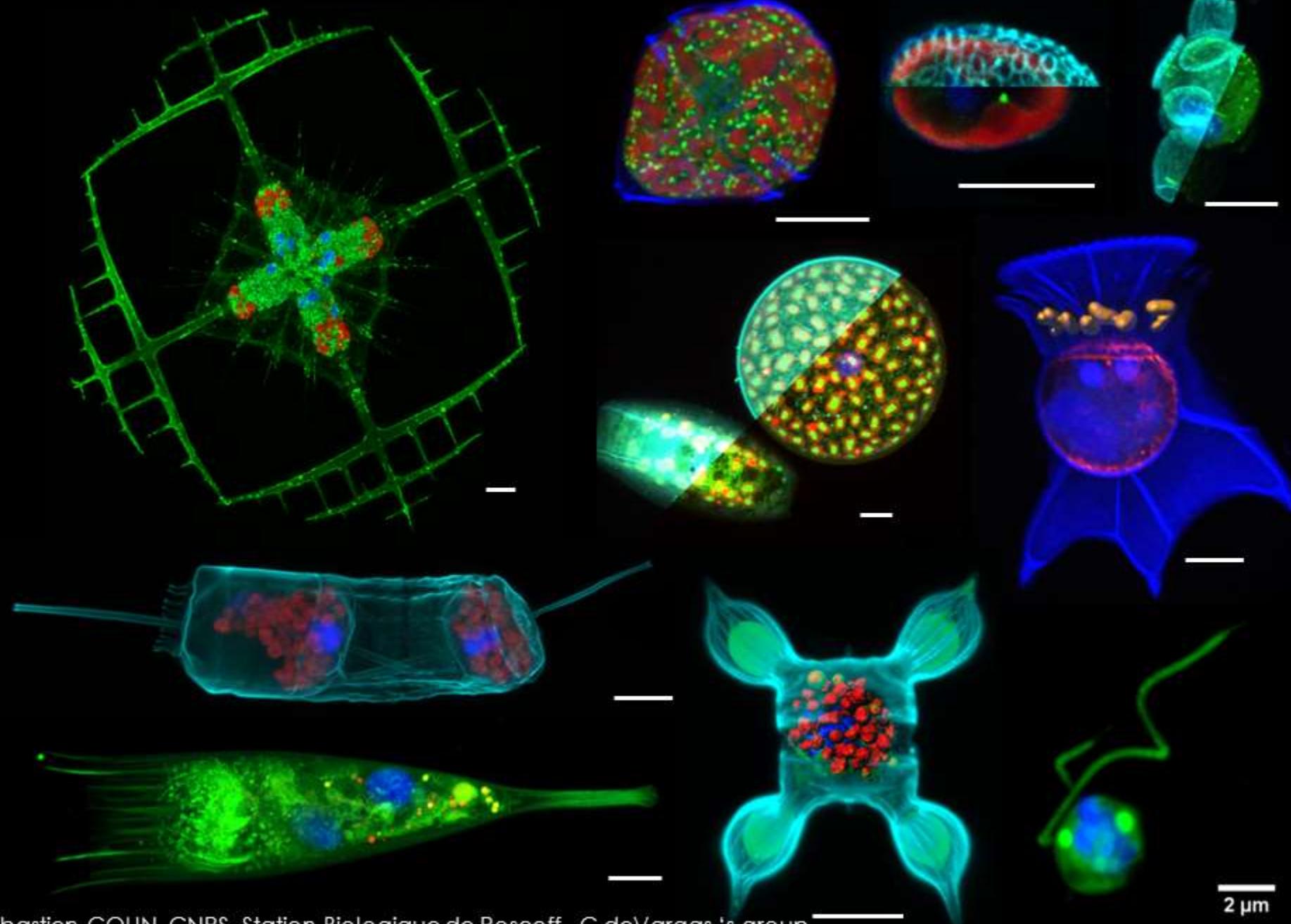
More than 10 times higher than the number of formally described marine eukaryotic plankton



Around one third cannot be assigned to any known taxonomic group



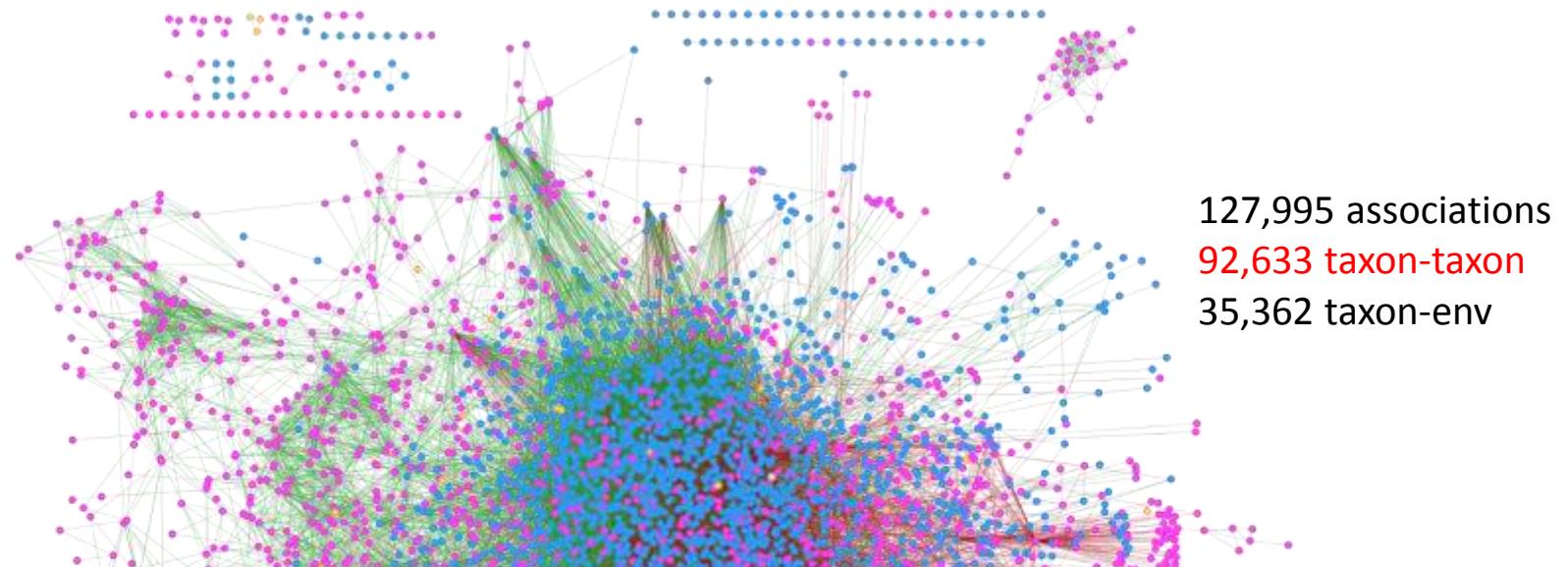
Scale bar 10µm



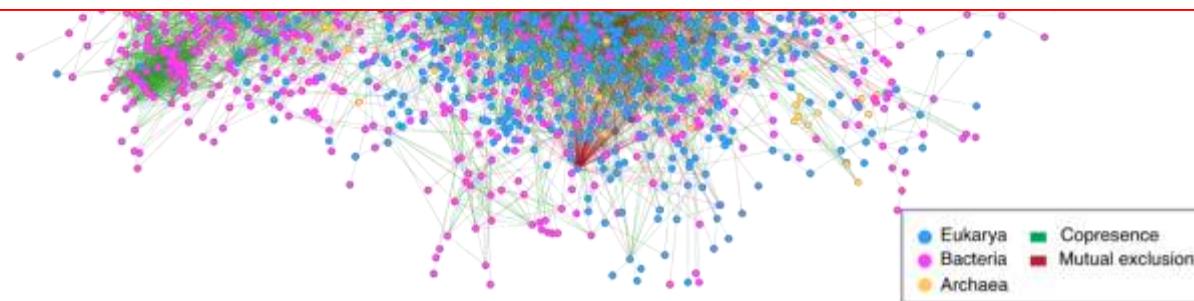
Determinants of community structure in the global ocean interactome

a.k.a The Ocean's facebook

The global plankton interactome – an integrated “network of networks”

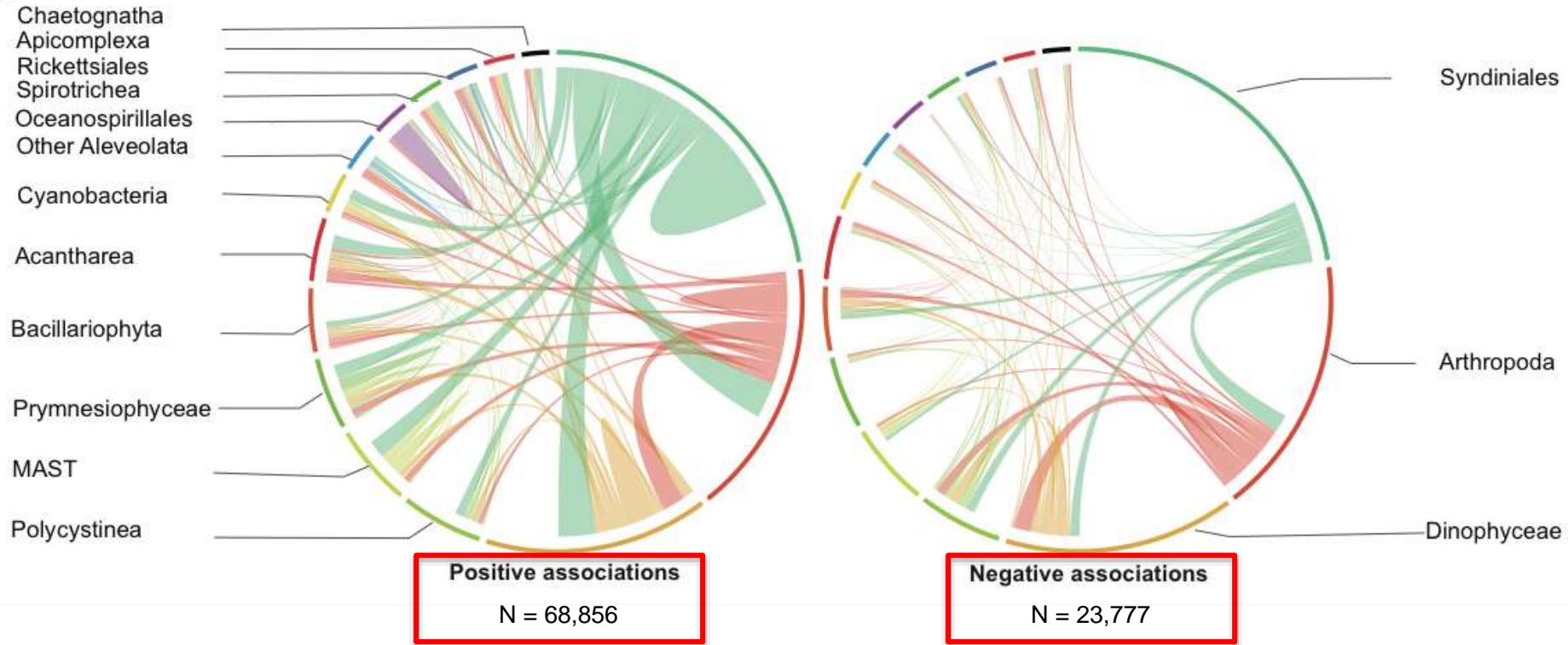


Biotic interactions more important than abiotic interactions



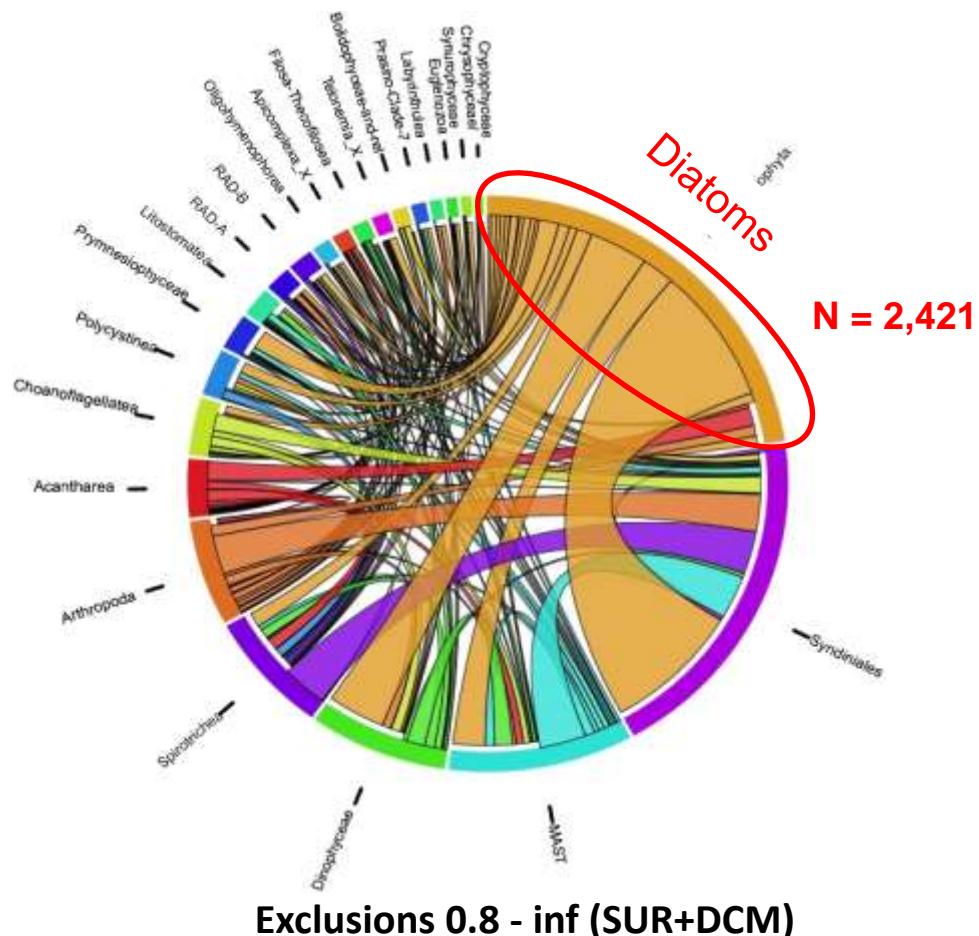
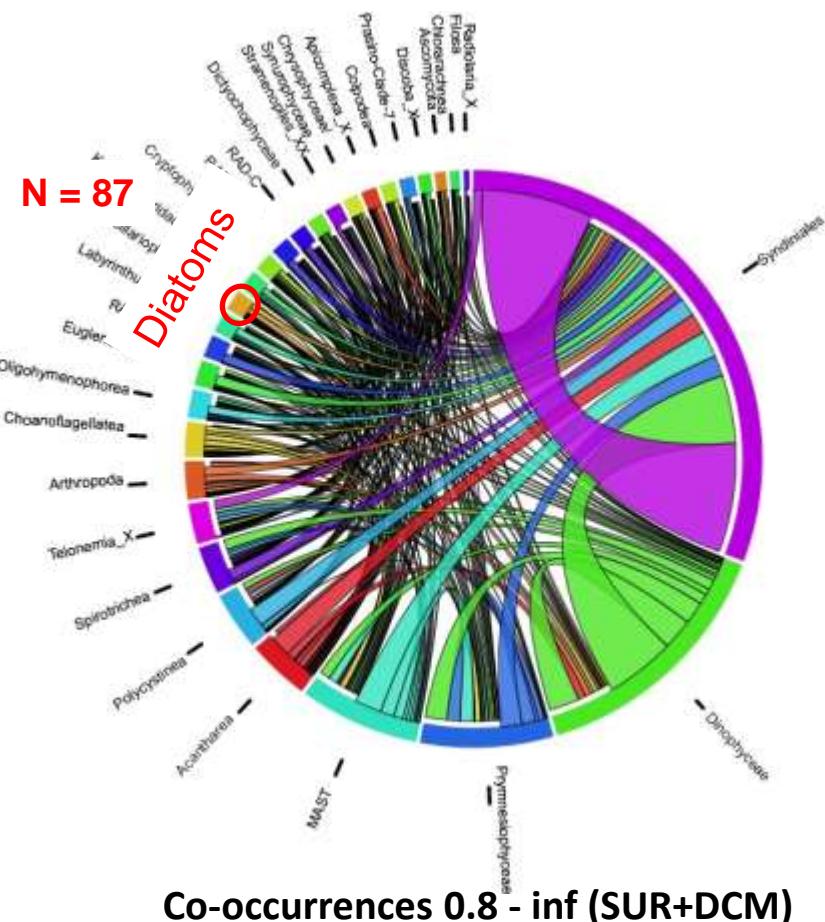
Most interactions are positive ...

A



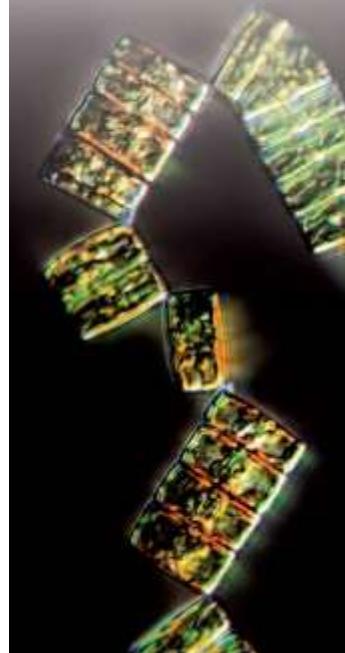
Cooperation is more important than competition

... but diatoms are antisocial

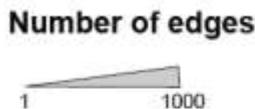


Diatoms have few friends and they keep their competitors at bay !

The co-
occurrence
network can be
superimpose
on food chain
and can predict
parasitoid-ho
interactions



Parasites
0.8-5



Zooplankton



phytoplankton

idae

Kinsea

Metazoa

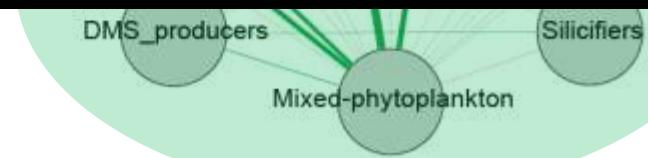
MALV-V

MALV-IV

MALV-III

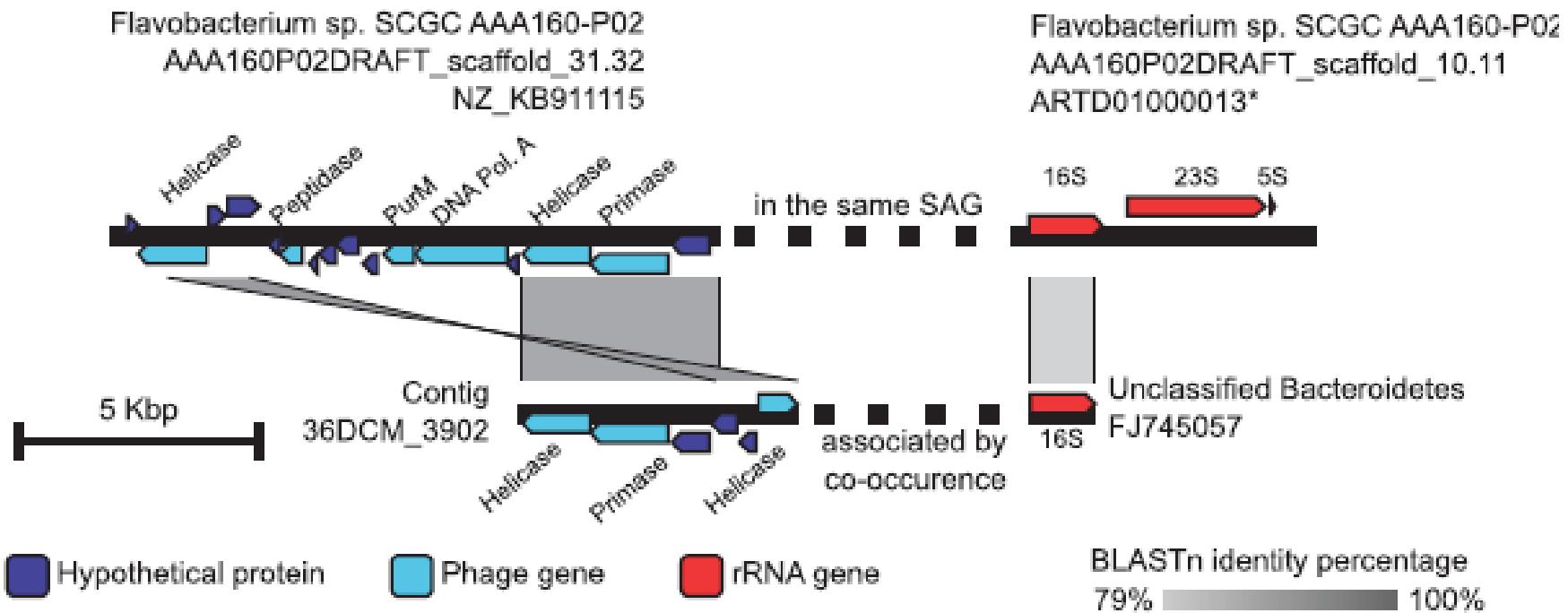
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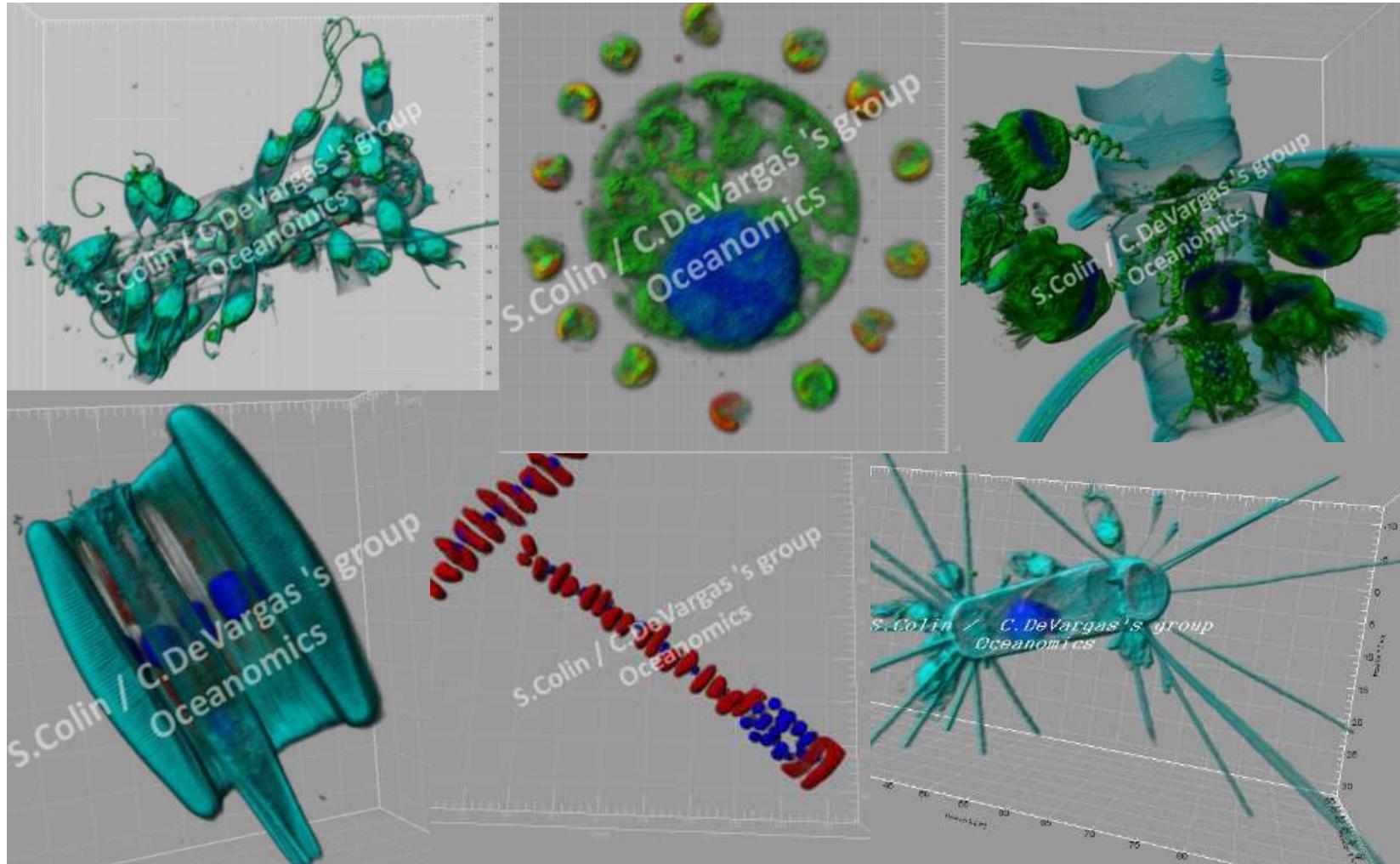
Lima-Mendez et al.
Science (2015)

The co-occurrence network can predict host-phage interactions that can be verified in metagenomes



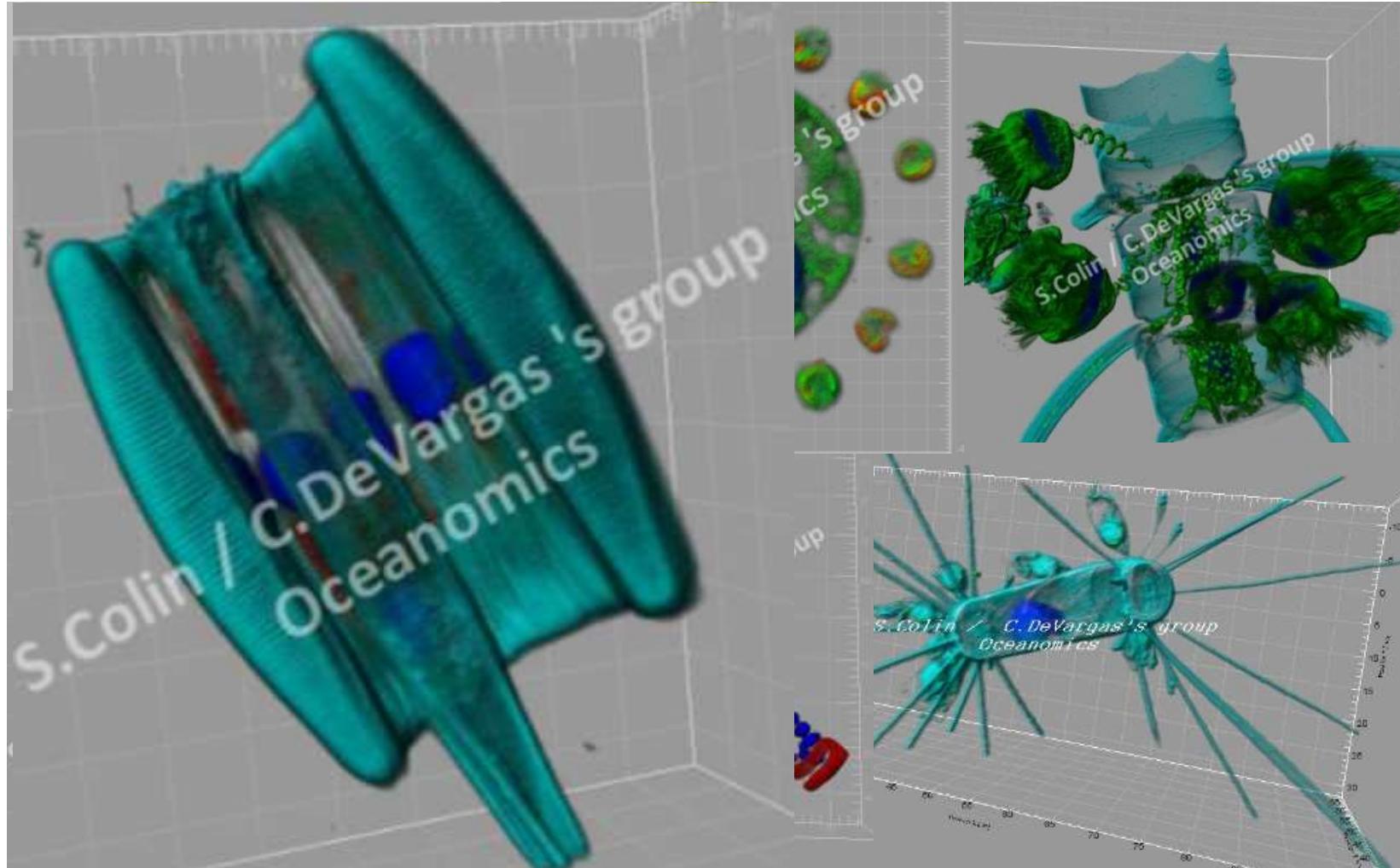
From the global ocean to the single cell and back again

A case study : Diatom interactions with other plankton

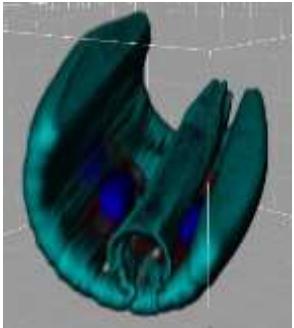


Flora Vincent (IBENS), in collaboration with Colomban de Vargas (Roscoff) and Rainer Pepperkok (EMBL)

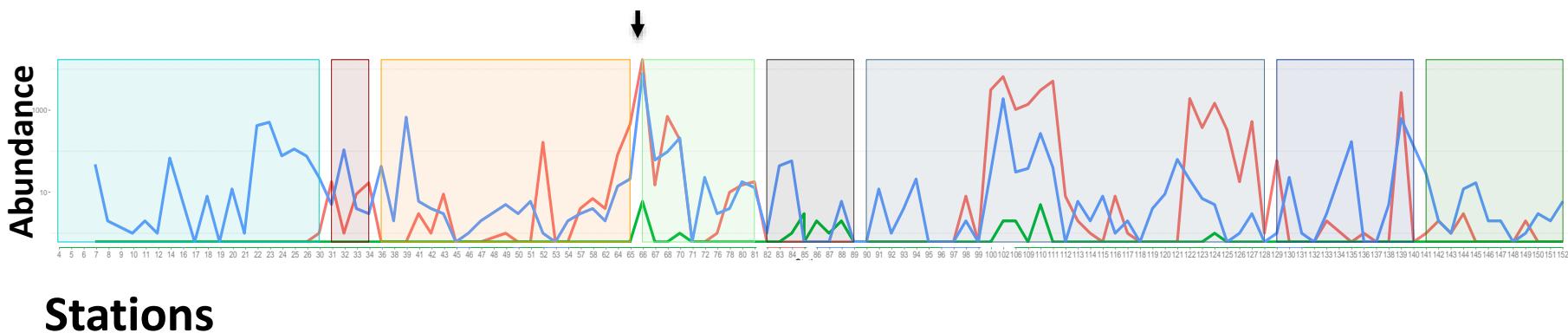
An unorthodox collaboration between a diatom (*Fragillariopsis*) and a ciliate (*Salpingella*)



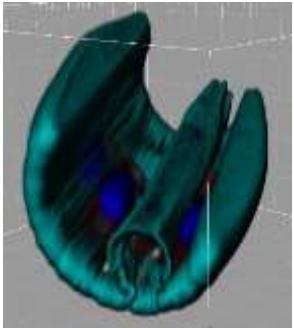
Flora Vincent (IBENS), in collaboration with Colomban de Vargas (Roscoff) and Rainer Pepperkok (EMBL)



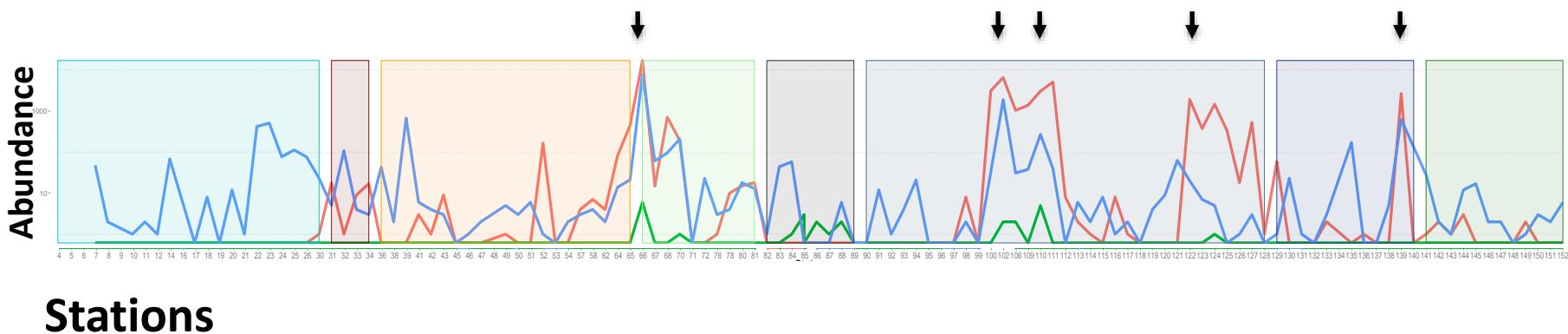
An unorthodox collaboration between a diatom (*Fragillariopsis*) and a ciliate (*Salpingella*)



Stations

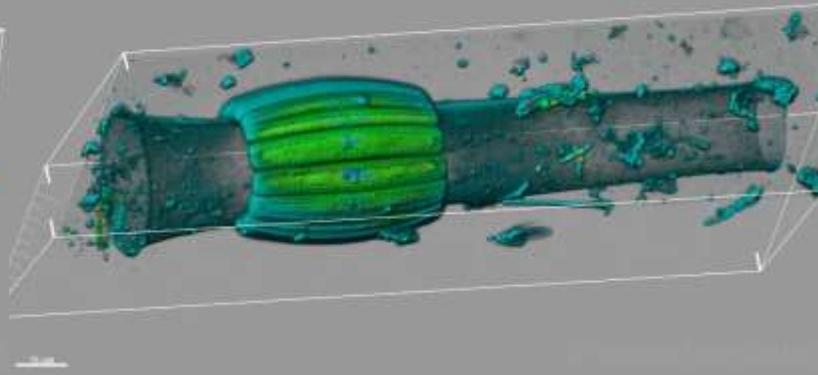
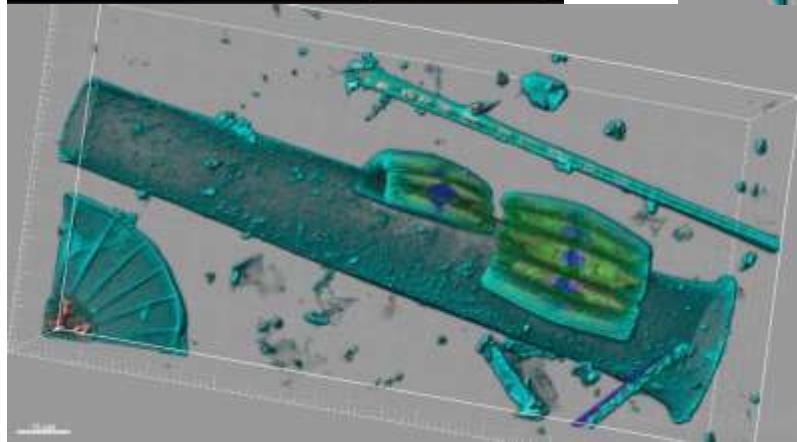
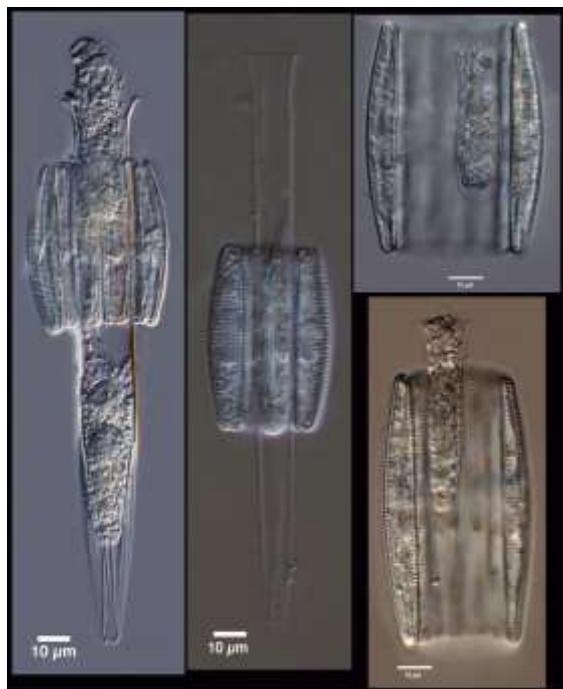


An unorthodox collaboration between a diatom (*Fragillariopsis*) and a ciliate (*Salpingella*)



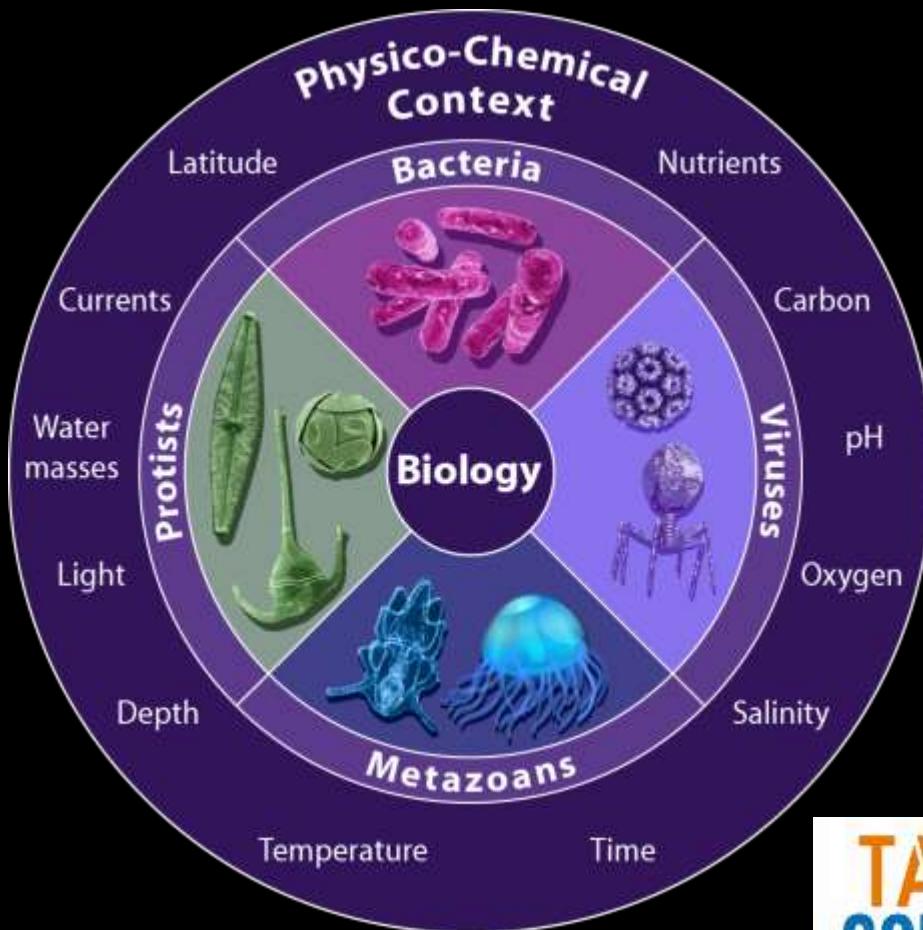
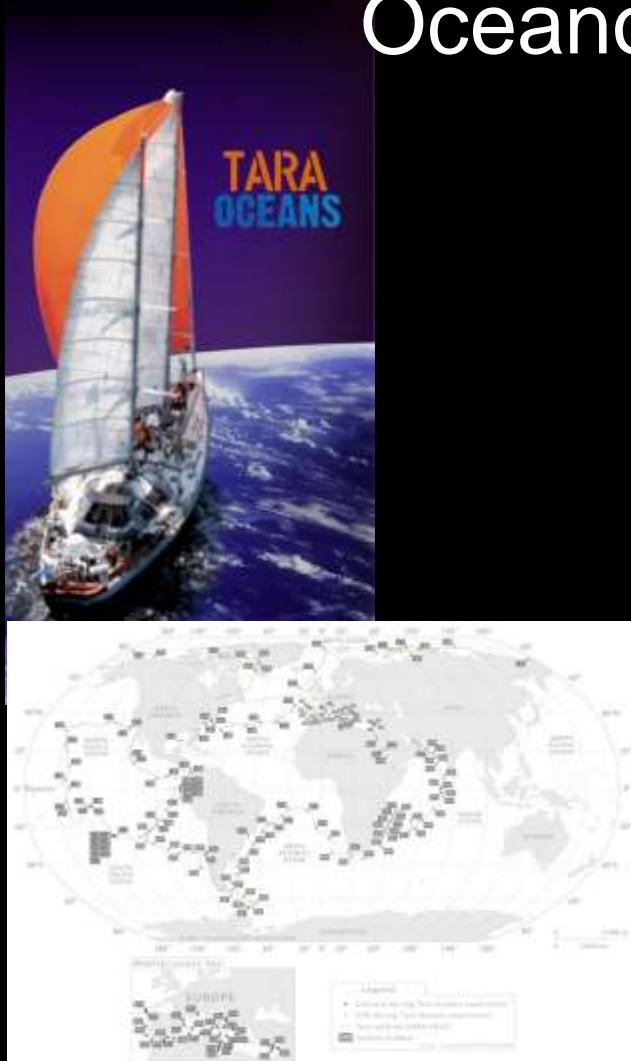
Stations

Identification of new morphotypes at other sampling sites



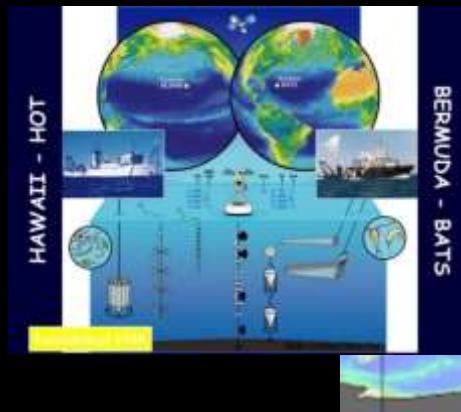
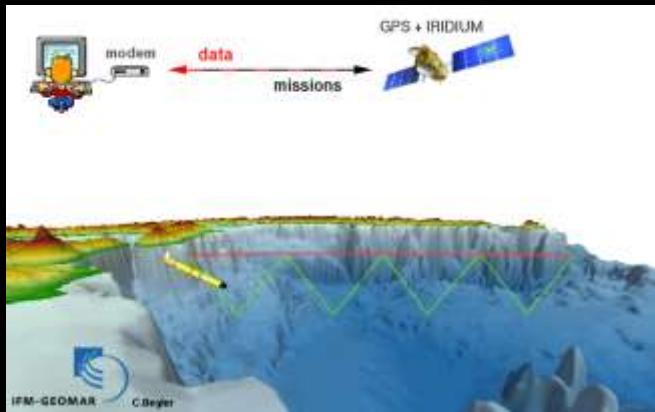
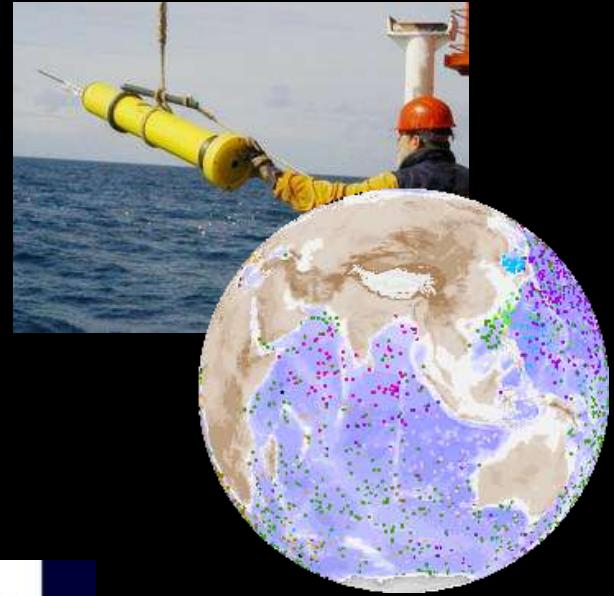
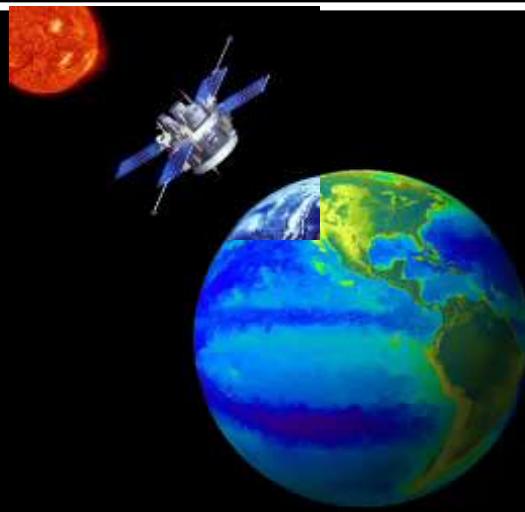
Colin, Vincent,
Dolan; Unpublished

Adding Biological Parameters into Oceanographic Research

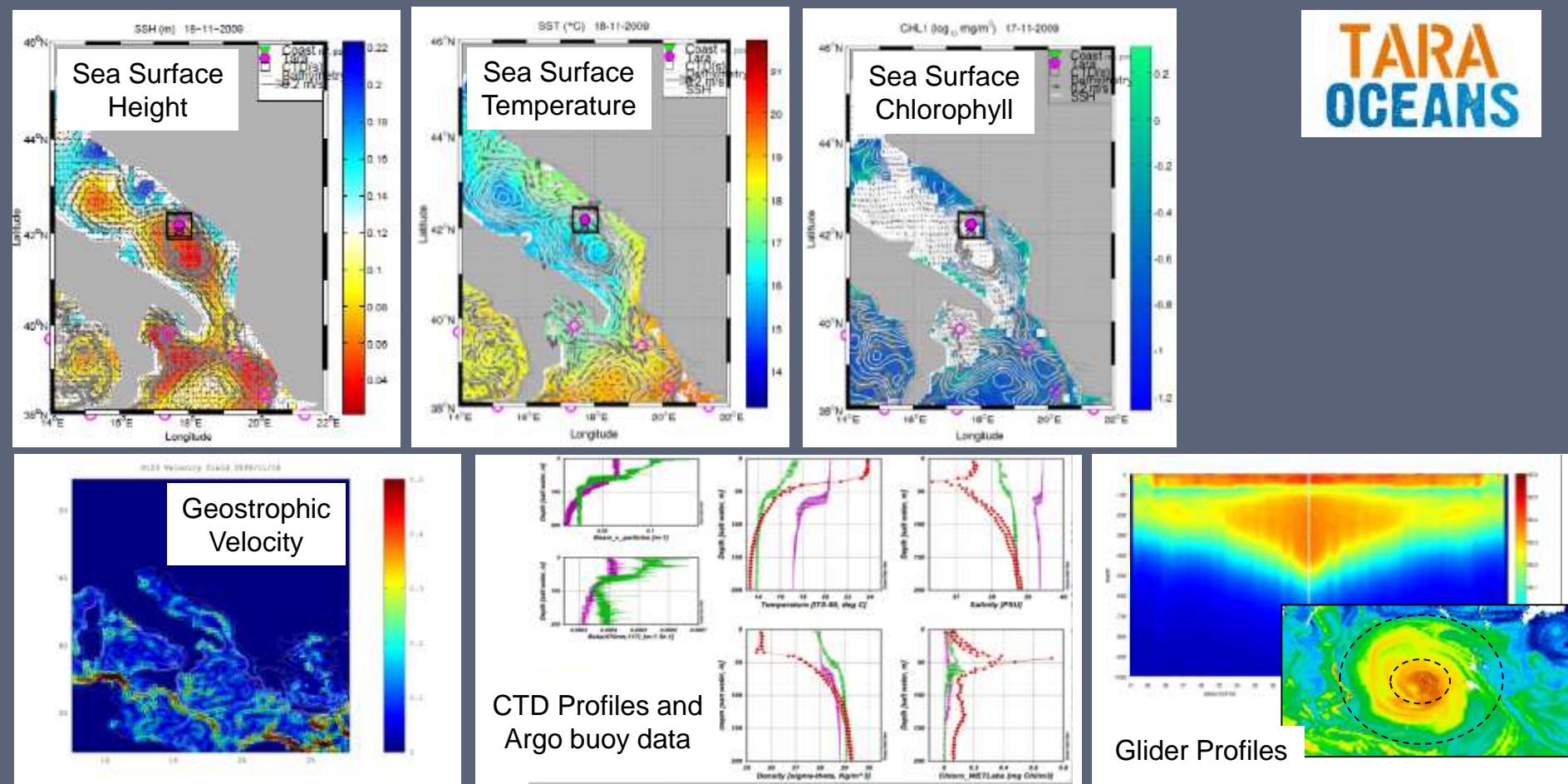


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Real-Time Remote Sensing of Ocean Processes

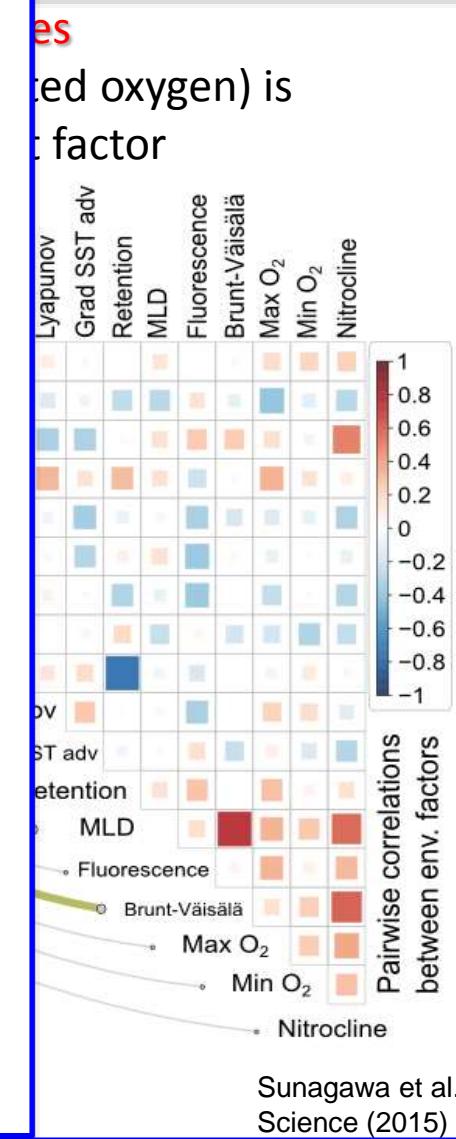
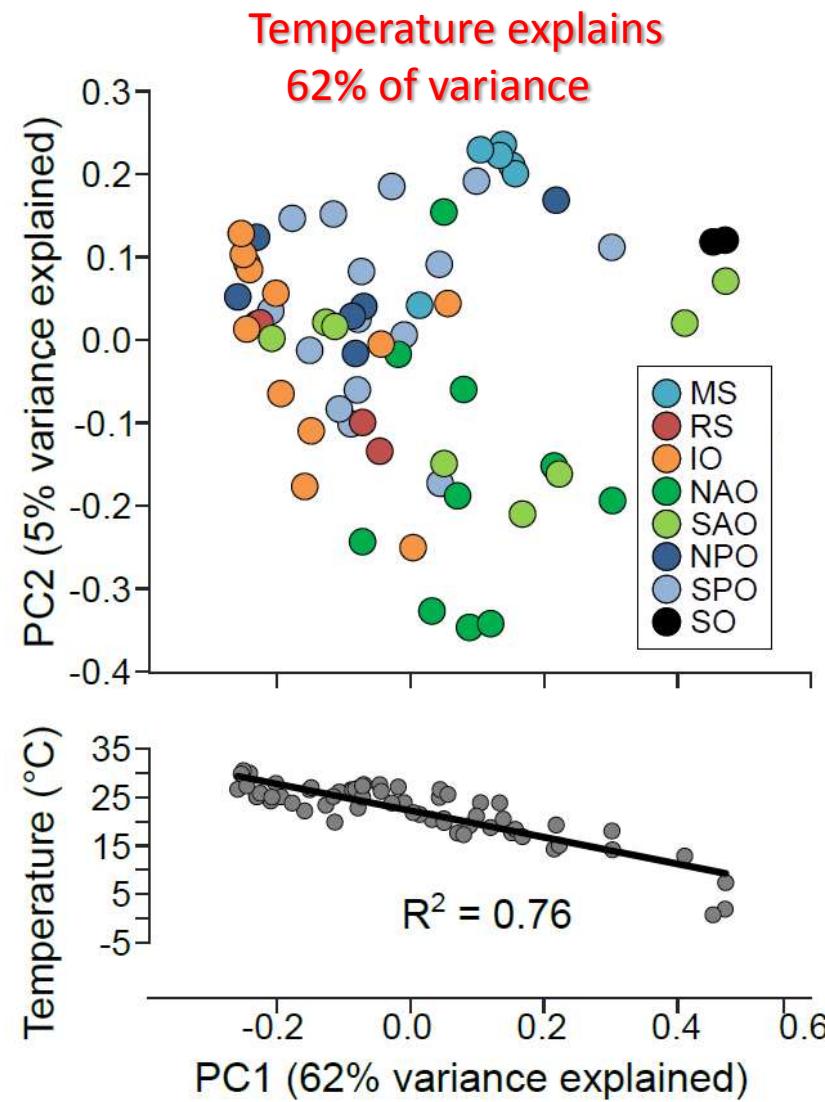
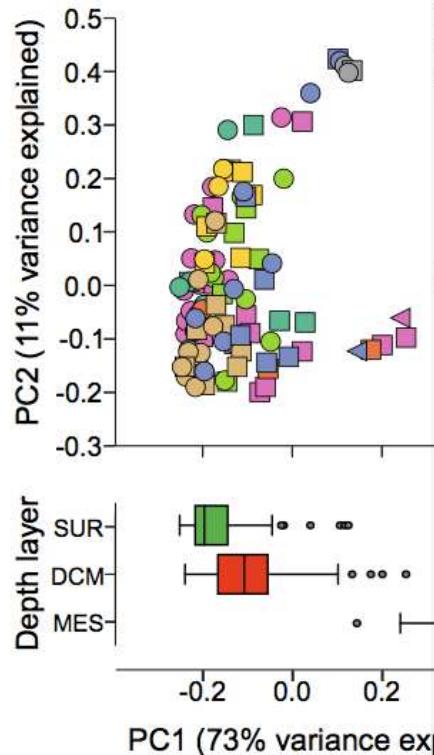


Contextual Data from Sampling, Satellite, Argo Buoys, On-Board Instruments and Gliders



Temperature is the main driver of microbial community structure

All depths
Communities stratify by depth rather than region (all depths)



Principal conclusions of the papers so far :

- The first end-to-end description of a continuous global ecosystem.
- Ocean microbiome consists of ~35,000 OTUs (mostly known) and 40 million genes (mostly unknown).
- Diversity of eukaryotic plankton is huge (~130,000 OTUs) but is finite. Around 90% are new and there is a considerable unknown component.
- More than 5,000 viral communities described; >99% are new. Their distribution supports seed bank hypothesis.
- Biotic interactions are more important than environmental drivers. Most interactions between plankton are positive.
- Bacterial community composition driven largely by temperature.
- All the data are public.
- The analyses were performed on only 579 samples; the data deluge is coming !



All *Tara* Oceans data are public

40 million
genes

Largest-ever DNA sequencing effort for ocean science.

Genetic sequences collected could represent tens of thousands of new species and ecosystem interactions.

Considering the size of the world's ocean, there is much, much more to discover.

11,535
gigabytes

Size of the *Tara* datasets in the European Nucleotide Archive as of May 2015. This represents 12,581 gigabases - roughly equivalent to 135 fully sequenced human genomes.

Unlimited

Potential to discover new knowledge about life in the world's ocean.



A three year expedition

- To explore marine planktonic ecosystems and their sensitivity to climate change-induced modifications to the ocean
- To popularize science
- To educate



September 5th 2009: Departure from Lorient



March 31st 2012: Return to Lorient





Visit of UN Secretary General Ban-Ki Moon: Informing Policy makers about the Key Role of Ocean Life



School kids and TARA OCEANS



Nice



Naples



Beirut



Tangiers



Tripoli



COP21 and the Paris Treaty have recognized the importance of the ocean !



United Nations

FCCC/CP/2015/L.9



Framework Convention on

greenhouse gases referred to in the Convention,

Distr.: Limited

Noting the importance of ensuring the integrity of all ecosystems, including oceans, and the protection of biodiversity, recognized by some cultures as Mother Earth, and noting the importance for some of the concept of “climate justice”, when taking action to address climate change,

Affirming the importance of education, training, public awareness, public participation, public access to

Conference of the Parties

Twenty-first session

Paris, 30 November to 11 December 2015

Agenda item 4(b)

Durban Platform for Enhanced Action (decision 1/CP.17)

Adoption of a protocol, another legal instrument, or an
agreed outcome with legal force under the Convention
applicable to all Parties



ADOPTION OF THE PARIS AGREEMENT



ocean-climate.org



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- NOFIMA

LABORATORIES

- Station Biologique Roscoff
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Thank you !

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