Using co-activity networks to reveal the structure of planktonic symbioses in the global ocean

Nils Giordano, Samuel Chaffron

Computational Biology team (COMBI)
Laboratoire des Sciences du Numérique de Nantes (LS2N, UMR 6004)

International Conference on Ecological Sciences
October 23th, 2018 (Rennes)

LABORATOIRE
DES SCIENCES
DU NUMÉRIQUE
DE NANTES

ENVIRONMENTAL GENOMICS

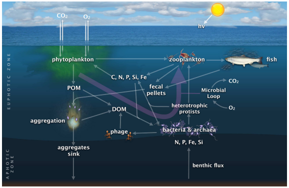
Microbes

- Everywhere, but >90% not cultivable
- Various ecological roles (biogeochemistry, host-nutrition and development, ...)
- Live in complex communities

ENVIRONMENTAL GENOMICS

Microbes

- Everywhere, but >90% not cultivable
- Various ecological roles (biogeochemistry, host-nutrition and development, ...)
- Live in complex communities

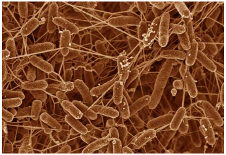


Worden *et al*, Science 2015

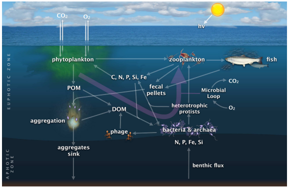
ENVIRONMENTAL GENOMICS

Microbes

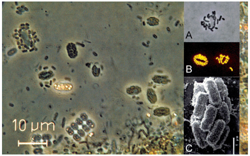
- Everywhere, but >90% not cultivable
- Various ecological roles (biogeochemistry, host-nutrition and development, ...)
- Live in complex communities



Electrically conductive nanowires in *Shewanella oneidensis*.
Photo by R. Bencheikhand B. Arey



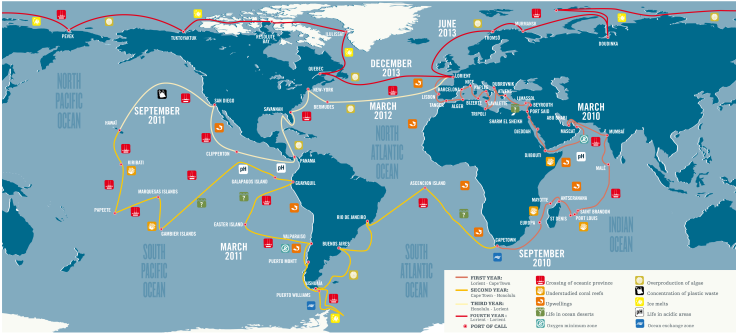
Worden *et al*, Science 2015



Chemocline bacterial community of Lake Dagow. Overmann & van Germeden 2000

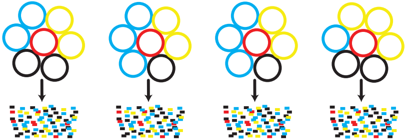
LAST DECADE EFFORTS: "PLANET-SCALE" SAMPLING

Tara Oceans expeditions (sampling of marine microbiome)



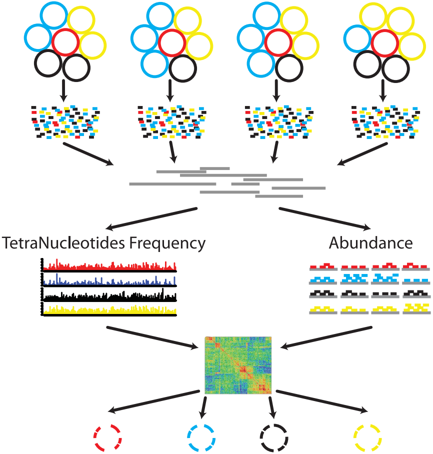
But also Host-associated (Human Microbiome Project), Soil, Oilseep, Hydrothermal...

ENVIRONMENTAL GENOMES CAN BE ASSEMBLED FROM METAGENOMES



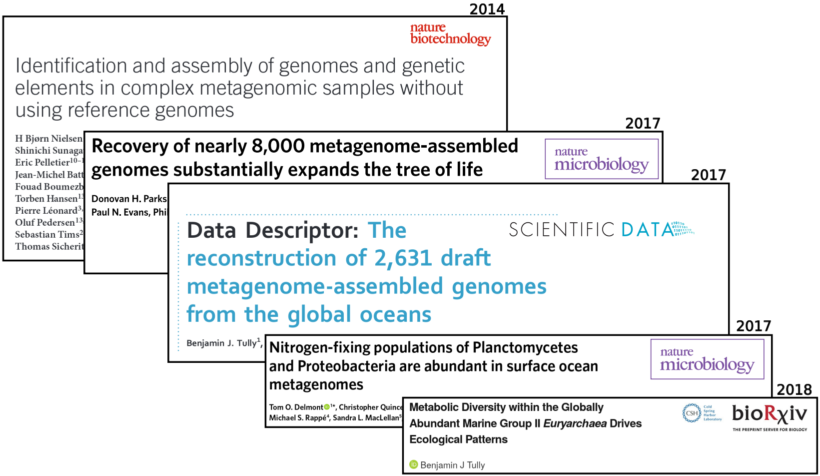
Adapted from Kang *et al*, PeerJ 2015

ENVIRONMENTAL GENOMES CAN BE ASSEMBLED FROM METAGENOMES



Adapted from Kang *et al*, PeerJ 2015

LITERATURE IS FILLED WITH NEW METAGENOME ASSEMBLED GENOMES (MAGS)



2014

nature biotechnology

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

H Bjørn Nielsen
Shinichi Sunaga
Eric Pelletier10–1
Jean-Michel Batt
Fouad Boumezb
Torben Hansen13
Pierre Léonard3,
Oluf Pedersen13
Sebastian Tims2
Thomas Sicherit

2017

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

nature microbiology

Donovan H. Parks
Paul N. Evans, Phi

2017

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

SCIENTIFIC DATA

Benjamin J. Tully[1],

2017

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

nature microbiology

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

2018

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

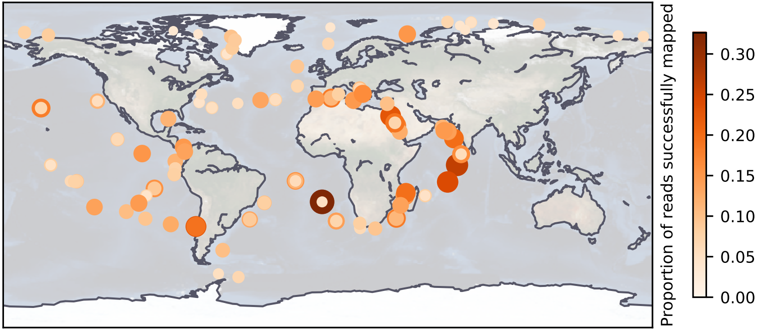
CSH Cold Spring Harbor Laboratory

bioRχiv THE PREPRINT SERVER FOR BIOLOGY

Benjamin J Tully

High-quality MAGs extracted from Tara Oceans expeditions

90% completeness, $< 5\%$ contamination

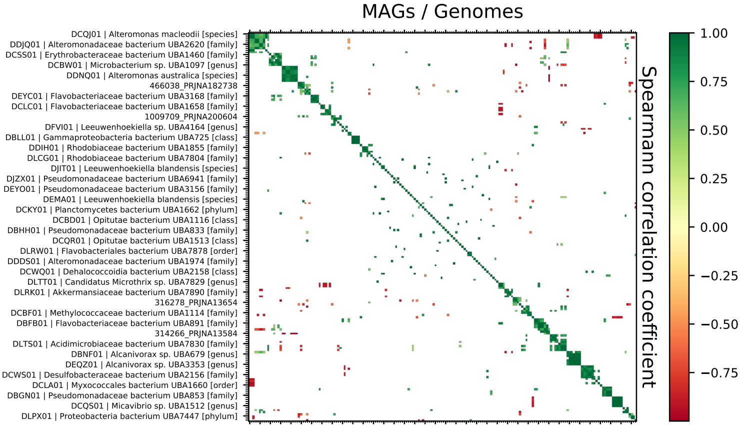


Can we predict, characterize and explain the communities of environmental genomes?

CO-OCCURENCE: WHO LIVES WITH WHOM?

Data: Parks *et al*, Nature Microbiology 2017; Mende *et al*, Nucleic Acids Res 2017; Tara Oceans samples

CO-OCCURENCE: WHO LIVES WITH WHOM?

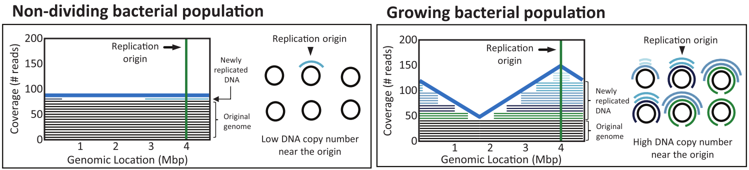


Data: Parks *et al*, Nature Microbiology 2017; Mende *et al*, Nucleic Acids Res 2017; Tara Oceans samples

CAN WE DO BETTER? ADDING THE "GROWTH TRAIT"

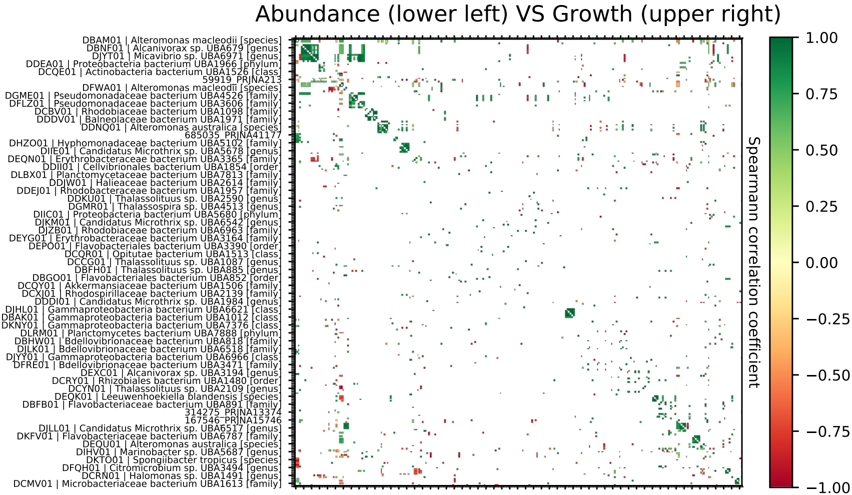
Tools

- **Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples**
  Korem et al, Science 2015
- **Measurement of bacterial replication rates in microbial communities**
  Brown et al, Nature Biotechnology 2016



Korem *et al*, Science 2015

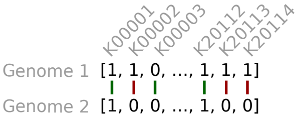
GROWTH CORRELATION BETWEEN MAGS



Work in progress...

NICHE OVERLAP OR REAL INTERACTIONS?

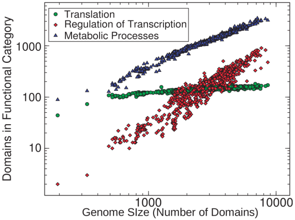
Jaccard distance:



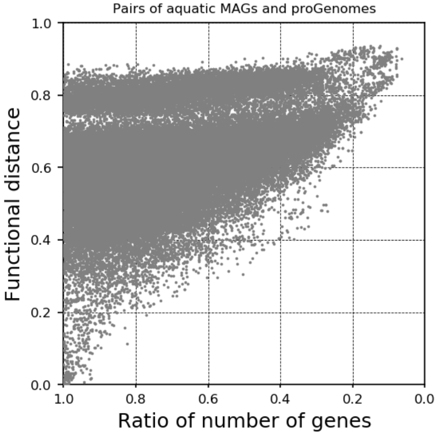
K00001 K00002 K00003 K20112 K20113 K20114

Genome 1 [1, 1, 0, ..., 1, 1, 1]

Genome 2 [1, 0, 0, ..., 1, 0, 0]

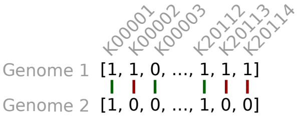


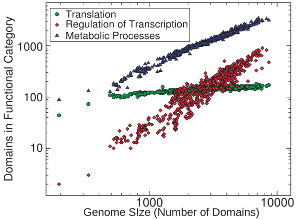
Grilli *et al*, Nucleic Acid Research 2012



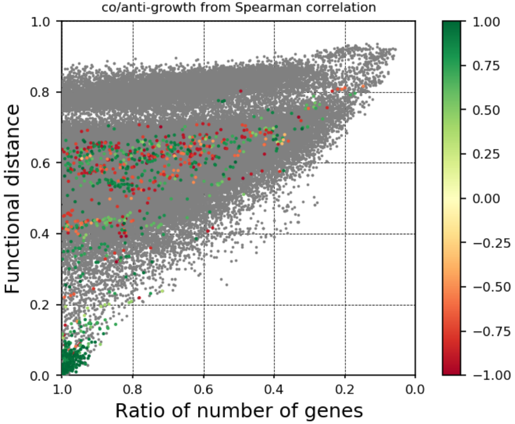
NICHE OVERLAP OR REAL INTERACTIONS?

Jaccard distance:





Grilli *et al*, Nucleic Acid Research 2012



WRAPPING UP

- Microbial diversity is largely unknown
- Intensive experimental (sampling and sequencing) and theoretical (genome prediction) research efforts to uncover new *environmental genomes*
- We try to combine growth and functional content as clues to predict interactions

Perspective

- Co-metabolic modeling to explain the microbe social network
- Revisit scaling laws with environmental genomes
- Functional analysis with metatranscriptomic data

THANK YOU FOR YOUR ATTENTION

Close collaborators

- Samuel Chaffron
- Damien Eveillard
- Marko Budinich Abarca

LS2N LABORATOIRE DES SCIENCES DU NUMÉRIQUE DE NANTES TARA OCEANS Plateforme BiRD Nantes

Funding

UNIVERSITE BRETAGNE LOIRE

RECHERCHE FORMATION INNOVATION en Pays de la Loire