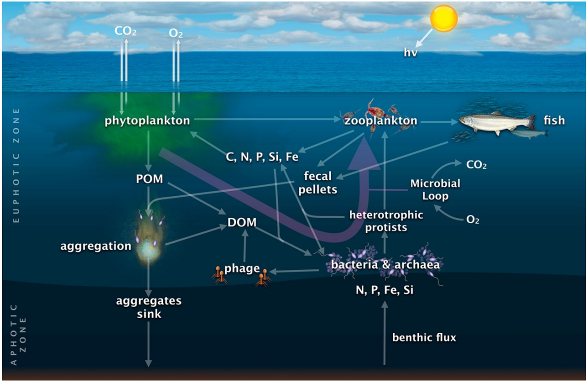
Co-activity networks reveal the structure of planktonic symbiosis in the global ocean

Nils Giordano, Samuel Chaffron

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

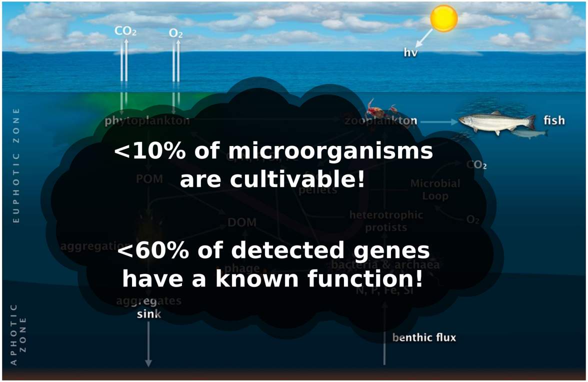
JOBIM 2019: Omics Dark Matter
July 3rd, 2019 (Nantes)

MARINE MICROBIAL COMMUNITIES PLAY CRUCIAL ECOLOGICAL ROLES



Worden *et al*, Science 2015

MARINE MICROBIAL COMMUNITIES PLAY CRUCIAL ECOLOGICAL ROLES



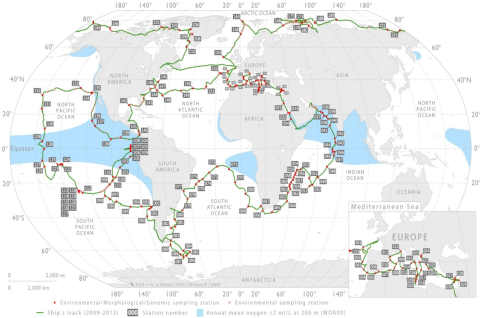
<10% of microorganisms are cultivable!

<60% of detected genes have a known function!

Worden *et al*, Science 2015

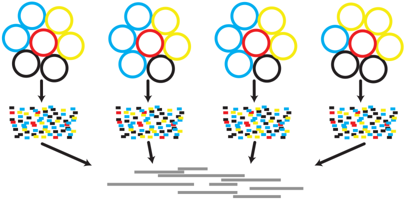
PLANET-SCALE MARINE SAMPLING

Tara expeditions dataset (2009-2013)



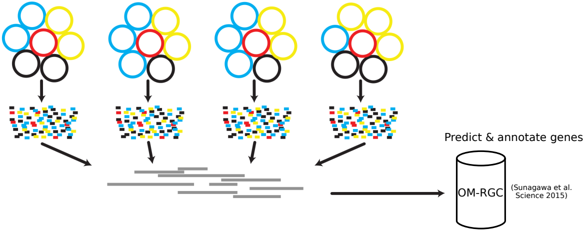
- >200 stations across all oceans
- 3 depth (SUR, DCM, MES)
- Size-filtered samples
- Amplified 16S rRNA, MetaDNA, MetaRNA, ...

RECOVERING GENOMES FROM SHORT DNA FRAGMENTS



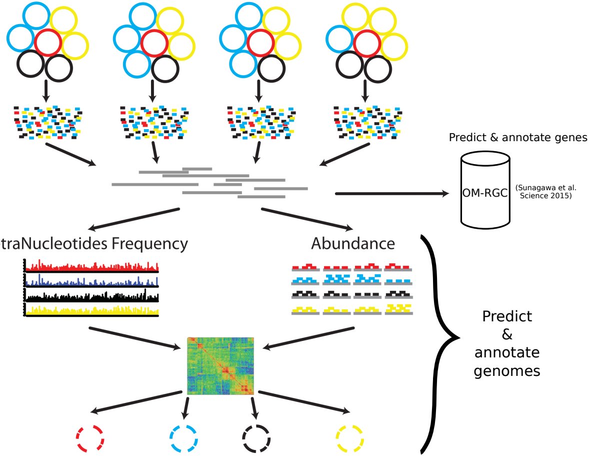
Adapted from Kang *et al*, PeerJ 2015

RECOVERING GENOMES FROM SHORT DNA FRAGMENTS



Adapted from Kang *et al*, PeerJ 2015

RECOVERING GENOMES FROM SHORT DNA FRAGMENTS



Predict & annotate genes

OM-RGC

(Sunagawa et al. Science 2015)

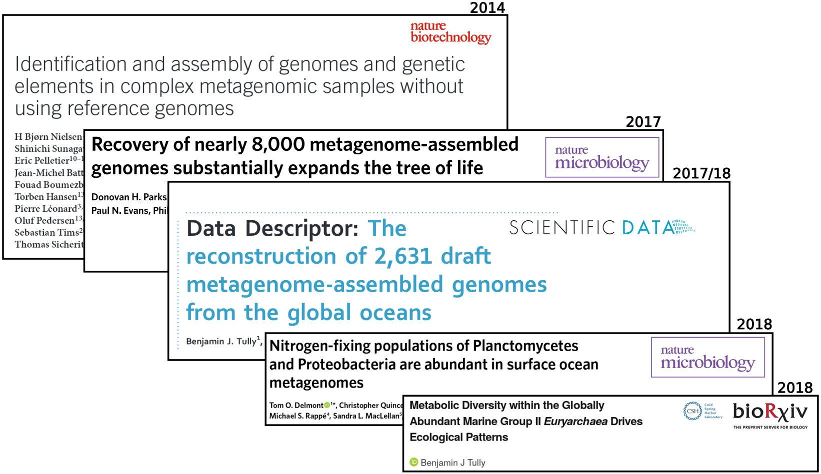
TetraNucleotides Frequency

Abundance

Predict & annotate genomes

Adapted from Kang *et al*, PeerJ 2015

LITERATURE IS FILLING 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 Pelletier[10–1
Jean-Michel Batt
Fouad Boumezb
Torben Hansen[13
Pierre Léonard[3,
Oluf Pedersen[13,
Sebastian Tims[2
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

2017/18

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

SCIENTIFIC DATA

Benjamin J. Tully[1],

2018

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]

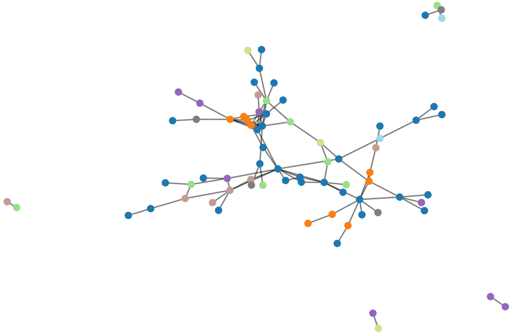
2018

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

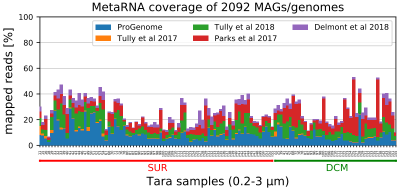
CSH Cold Spring Harbor Laboratory bioRχiv THE PREPRINT SERVER FOR BIOLOGY

Benjamin J Tully

Can we use Metagenome Assembled Genomes (MAGs) to predict, characterize and explain the communities of non-cultivable marine microorganisms?



CO-ACTIVE GENOMES TO INFER PUTATIVE INTERACTIONS



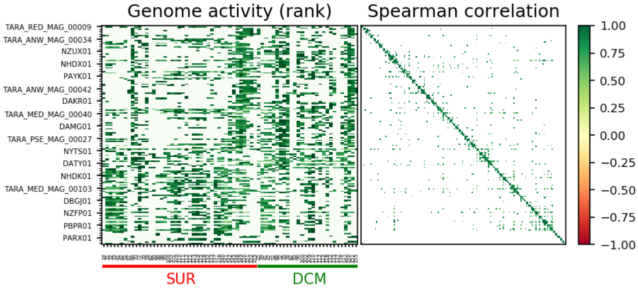
Published MAGs:

- 5319 MAGs+ 566 reference genomes (proGenome 2017)
- After quality filtering and dereplication (95% ANI): **2092 genomes**

71 samples of depleted MetaRNA

- Euphotic zone, 0.2-3 μm filter (free living prokaryotes)
- Normalization by TSS and 10 constitutively expressed genes (Milanese et al. Nature Comm. 2019)

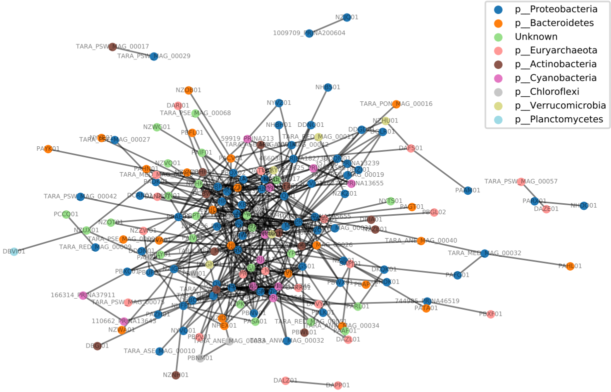
TRANSCRIPTOMIC CO-ACTIVITY CLUSTERING



- Overlapping values in at least 10% of samples (N=8)
- Benjamini-Hochberg FDR correction ($FDR < 0.01$)

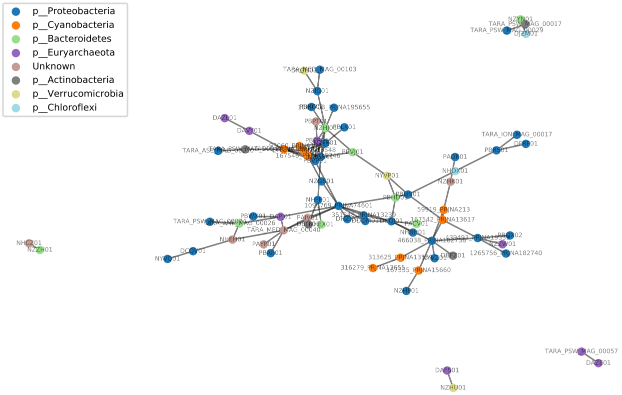
→ **176 genomes** with at least 1 significant correlation!

COMMUNITIES OF CO-ACTIVE MAGS CAN BE IDENTIFIED



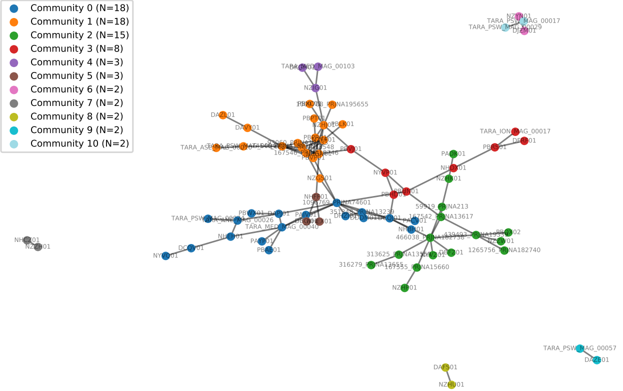
- FDR < 0.01 (176 nodes)

COMMUNITIES OF CO-ACTIVE MAGS CAN BE IDENTIFIED



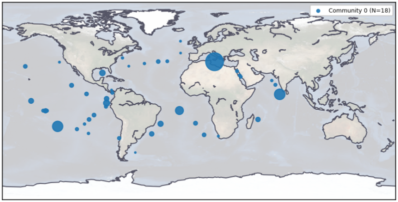
- FDR < 0.001 (76 nodes)

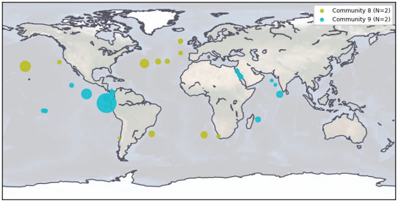
COMMUNITIES OF CO-ACTIVE MAGS CAN BE IDENTIFIED

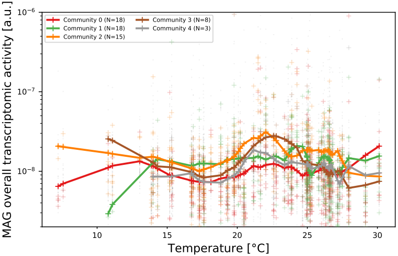


- FDR < 0.001 (76 nodes) (Clauset-Newman-Moore greedy modularity)

LINKING COMMUNITIES TO ENVIRONMENTAL PARAMETERS



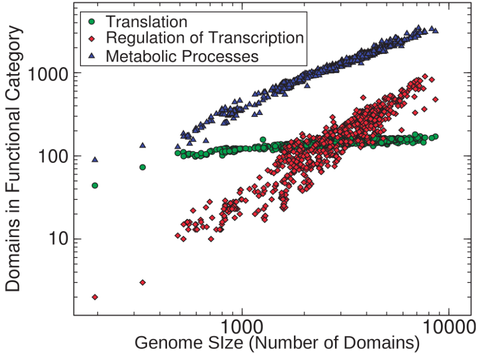




- Global/local communities
- Ecological niches

In progress...

ARE MAGS REALLY DIFFERENT FROM LAB-CULTIVATED GENOMES?



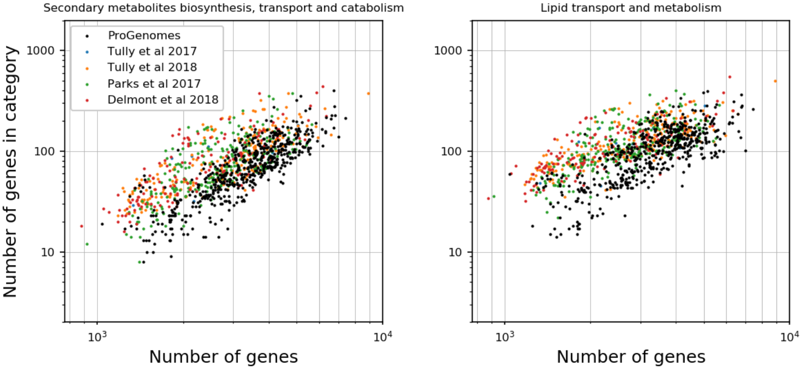
Functional scaling laws:

$$n_c \propto n_{tot}^{\alpha_c}$$

Annotation of MAGs with Prodigal + EggNOG

Grilli *et al*, Nucleic Acid Research 2012

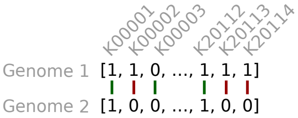
ARE MAGS REALLY DIFFERENT FROM LAB-CULTIVATED GENOMES?

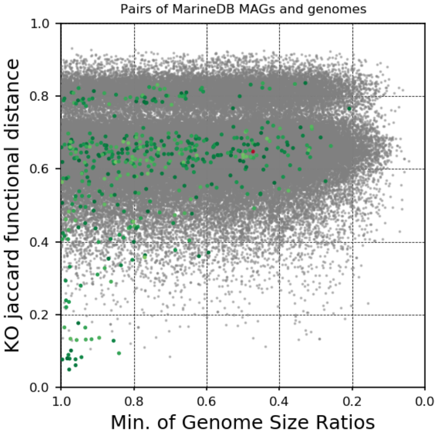


Cross-feeding widespread in non-cultivable organisms?

COMBINING FUNCTIONAL DISTANCE AND CO-ACTIVITY NETWORK

Jaccard distance:

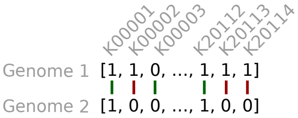




Most predicted interactions are between functionally distant organisms!

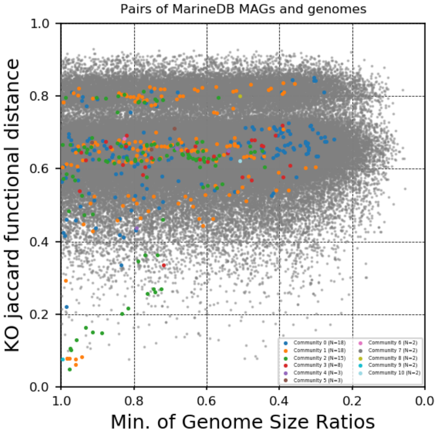
COMBINING FUNCTIONAL DISTANCE AND CO-ACTIVITY NETWORK

Jaccard distance:



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

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



Most predicted interactions are between functionally distant organisms!

WRAPPING UP

- Marine microbial diversity is largely unknown...
- ... but ”environmental” genomes can be predicted...
- ... and putative communities can be infered from co-activity networks (e.g. transcriptomic activity)

Perspective

- Co(mmunity)-metabolic modeling to infer interactions (secondary metabolites cross-feeding)
- Analysis of larger size fractions (aggregates) and interactions with Eukaryotes?
- Co-replication network based on differential coverage (Korem et al, Science 2015)

THANK YOU FOR YOUR ATTENTION

Collaborators

- **Samuel Chaffron**
- Benjamin Churcheward
- Damien Eveillard
- Marko Budinich Abarca
- Tara Oceans consortium

TARA OCEANS

Plateforme BiRD
Nantes

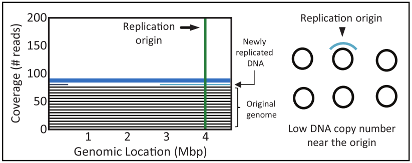
Funding

UNIVERSITE
BRETAGNE
LOIRE

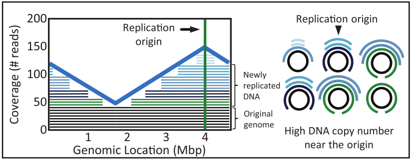
RECHERCHE
FORMATION
INNOVATION
en Pays
de la Loire

WHAT ABOUT CO-GROWTH? (REPLICATION)

Non-dividing bacterial population



Growing bacterial population



$$\frac{\texttt{Ori}_{cov}}{\texttt{Ter}_{cov}} \geqslant 1$$

A growing interest...

- Korem et al, Science 2015
- Brown et al, Nature Biotechnology 2016
- Emiola et al, Nature Communications 2018
- Gao et Li, Nature Methods 2018

BUILDING A DATABASE OF MARINE MAGS

Authors	Total nb.	HQ nb.	Samples	Techniques
Parks et al 2017	1765	673	Tara (all size fractions), others	SA+Metabat (no DC)
Tully et al 2017	290	24	Tara (MED only)	SA+Merging+Metabat
Tully et al 2018	2307	378	Tara (all depth/size fractions)	SA+Merging+Metabat
Delmont et al 2018	957	197	Tara (SUR+DCM, prok. only)	CA+CONCOCT/Anvio
ProGenomes 2017	566	526	(Aquatic representatives)	
Total	5885	1798