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

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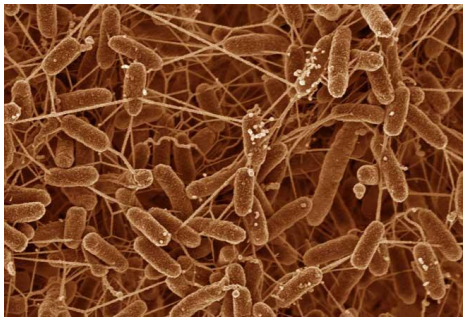
# Environmental genomics

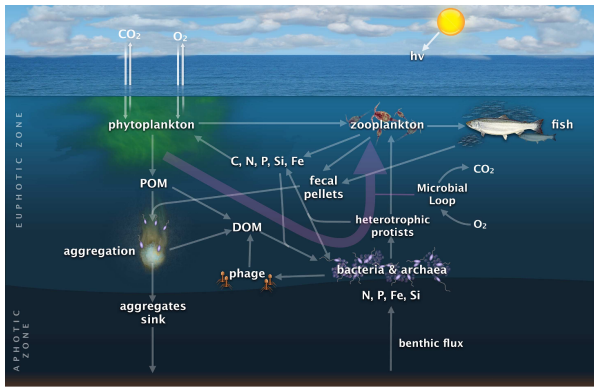
## Microbes

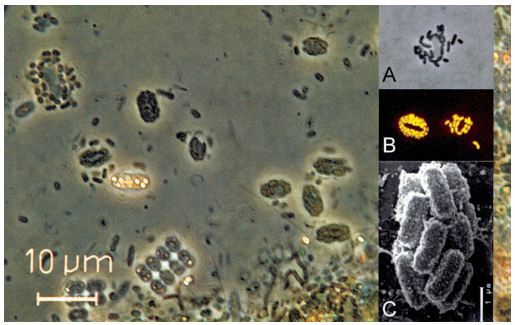
- Everywhere, but >90% not cultivable
- Live in complex communities
- Various ecological roles (biogeochemistry, host-nutrition and development, ...)



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

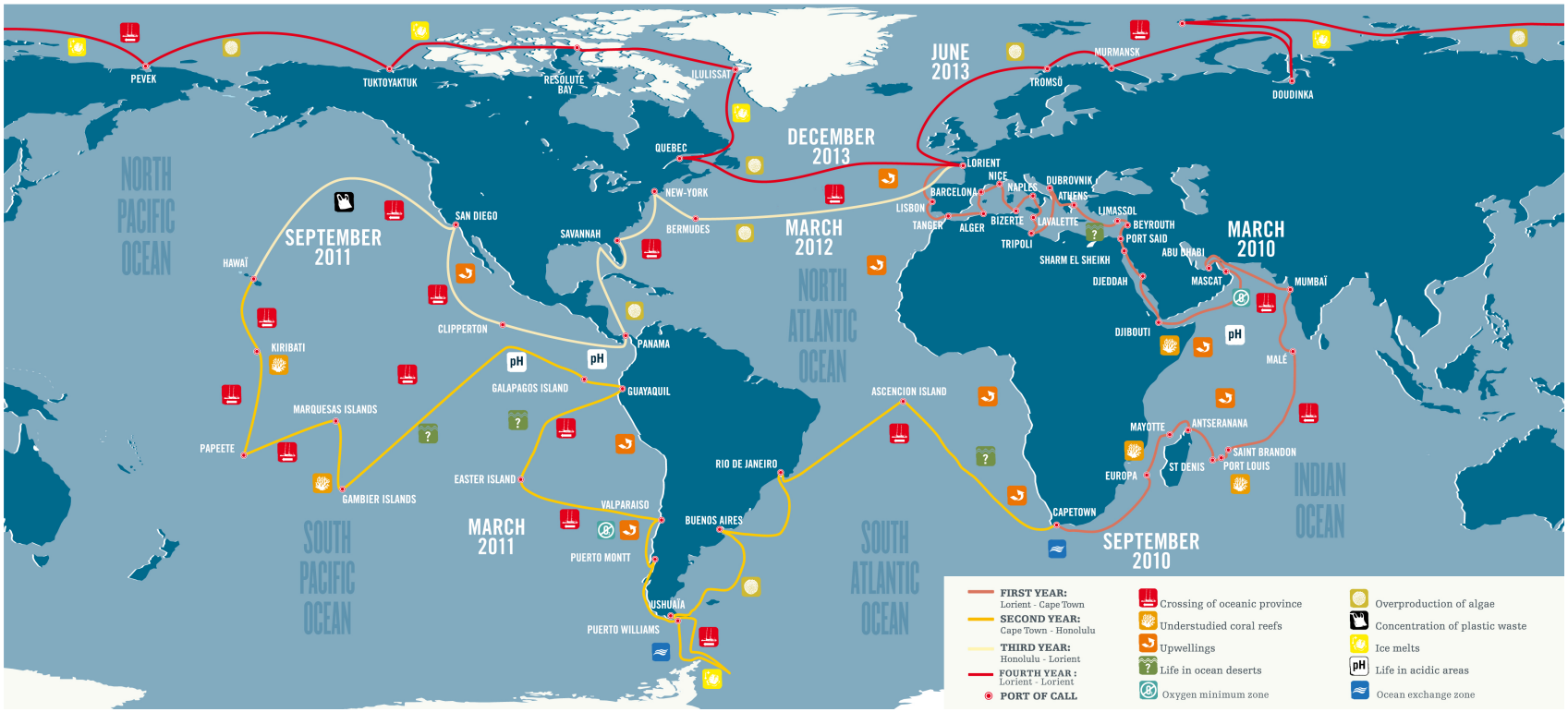
Worden *et al*, Science 2015




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

# Last decade efforts: "planet-scale" sampling

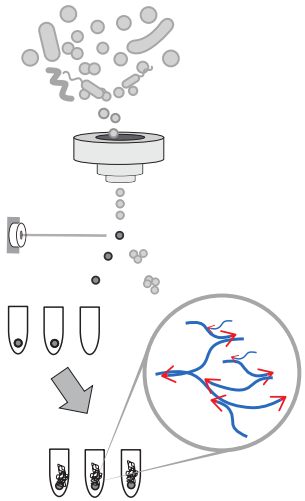



Tara Oceans expeditions for the sampling of marine microbiome

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

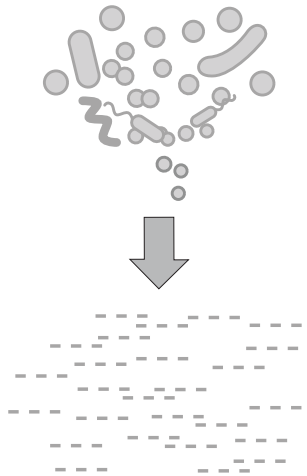
# ENVIRONMENTAL GENOMES

## Single Amplified Genomes



- Experimentally challenging
- Amplification
- Incomplete genomes

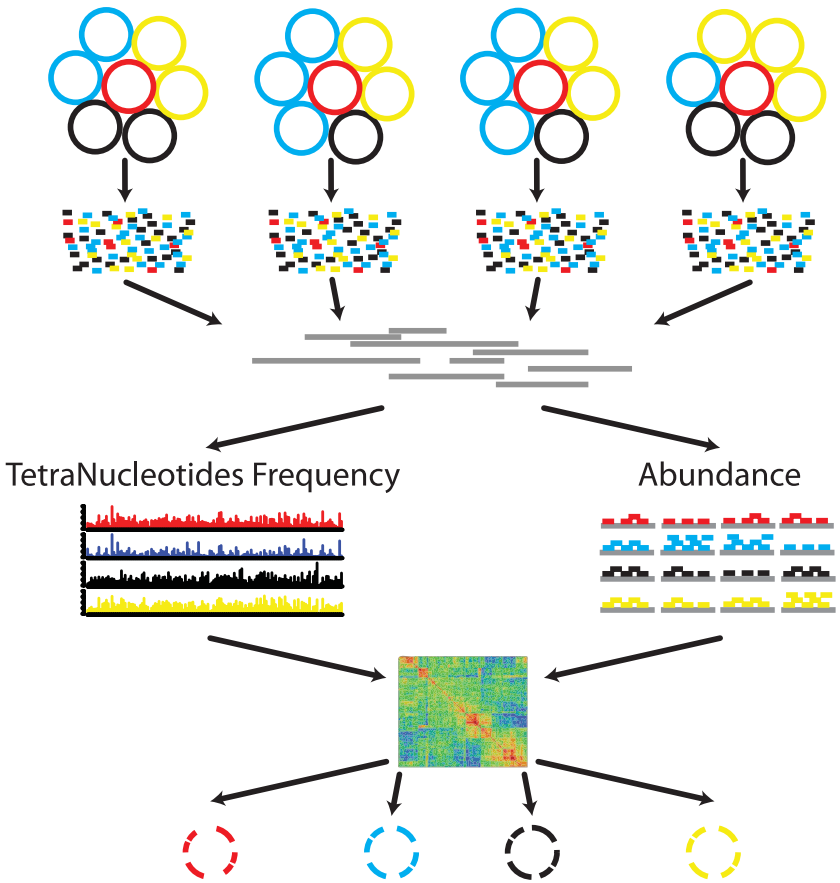
## Metagenome Assembled Genomes



- Shotgun sequencing (cheap)
- Already available data
- Contamination

Adapted from Rinke *et al*, Nature 2013

# METAGENOMES ASSEMBLED GENOMES (MAGS): EXAMPLE OF METABAT




**Preprocessing**

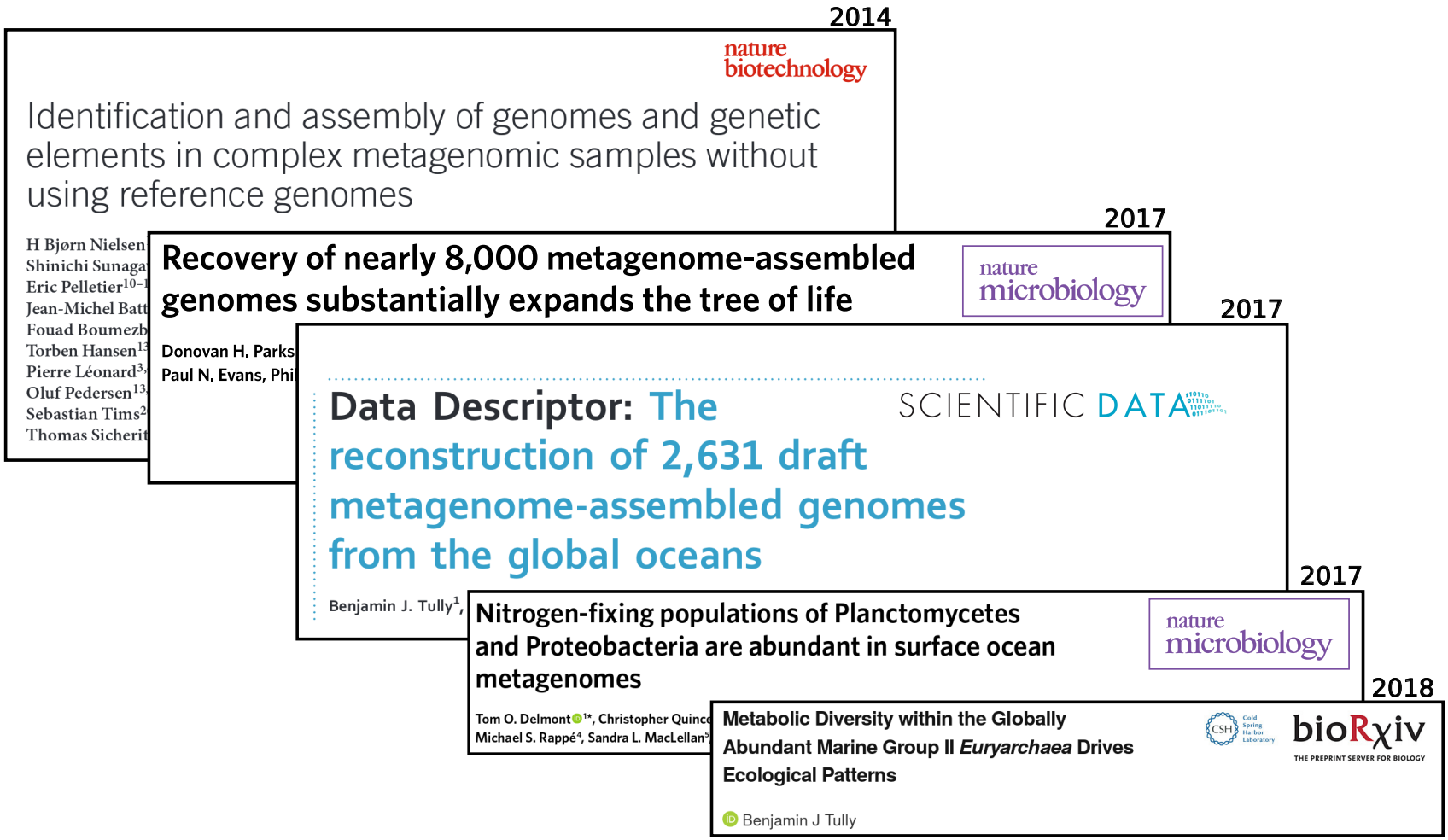
1. Samples from multiple sites or times
2. Metagenome libraries
3. Initial de-novo assembly using the combined library

**MetaBAT**

4. Calculate TNF for each contig
5. Calculate Abundance per library for each contig
6. Calculate the pairwise distance matrix using pre-trained probabilistic models
7. Forming genome bins iteratively

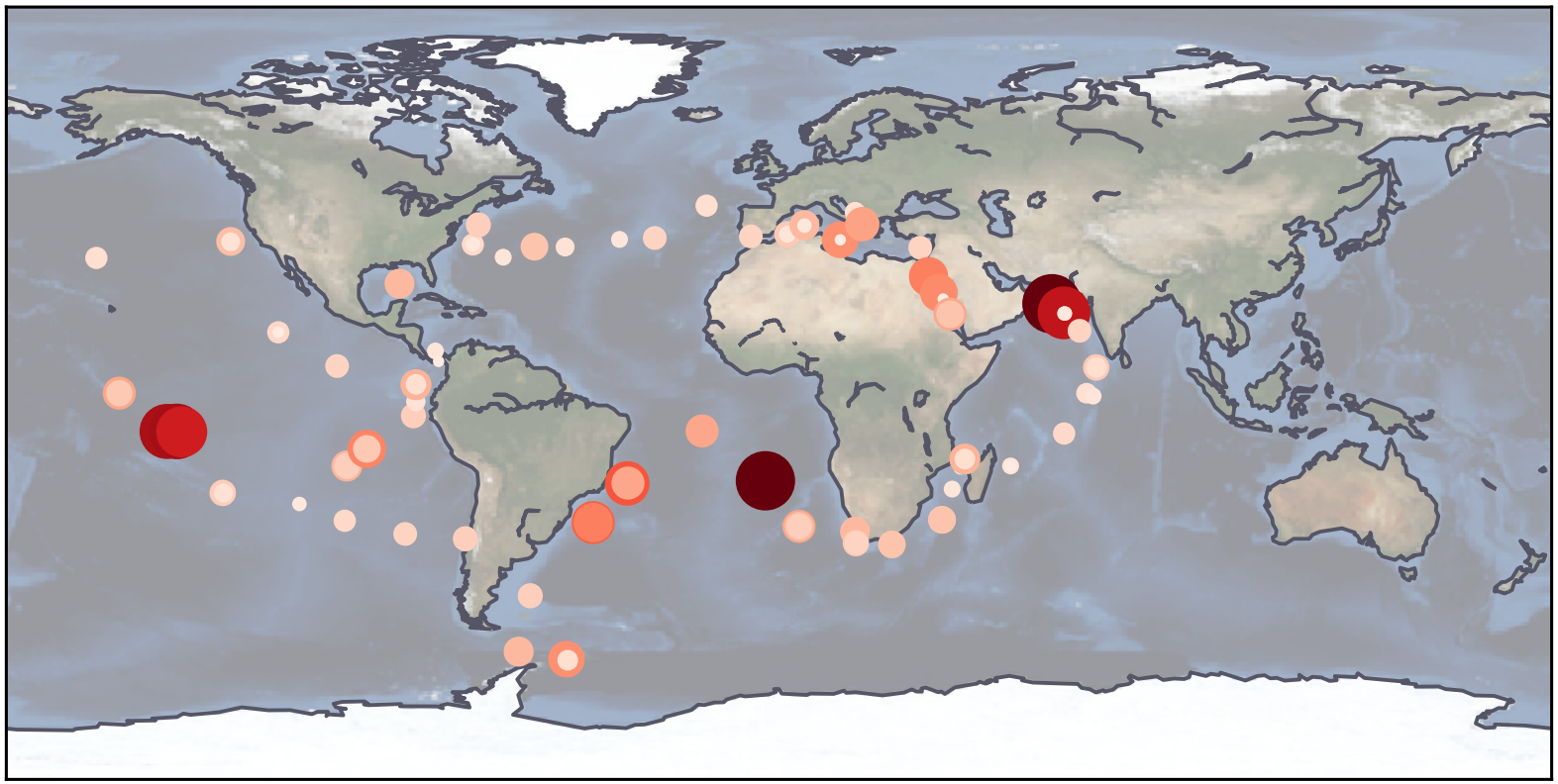
Kang *et al*, PeerJ 2015

# List of MAGs publications



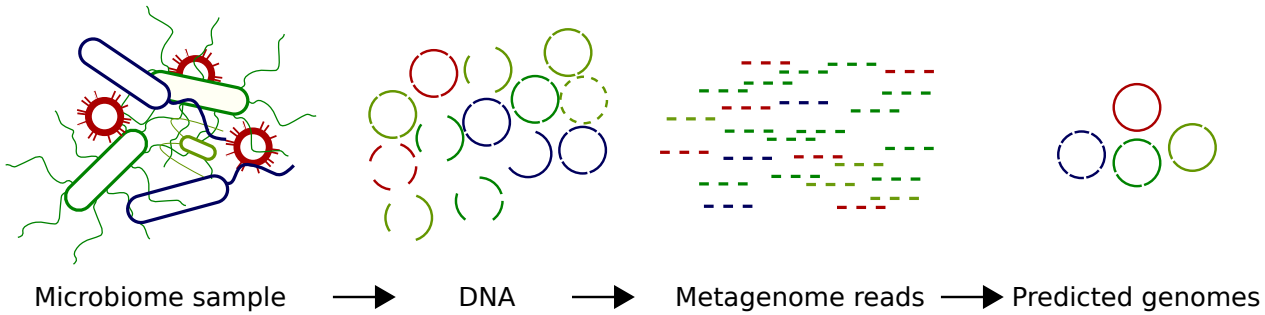

Intense filling of databases, but not so much is currently done with this new information

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



Repartition of 1378 MAGs extracted from Tara Ocean (→2015)

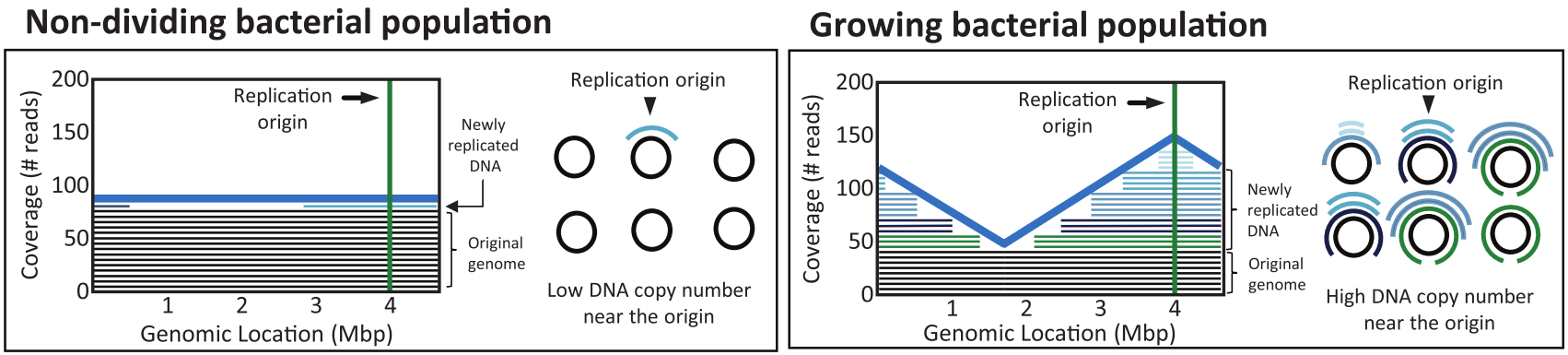
# CO-ACTIVITY: WHO GROWS WITH WHOM?




## Tools

- **Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples**
  *Korem et al, Science 2015*
  → only complete genomes, code not available
- **Measurement of bacterial replication rates in microbial communities**
  *Brown et al, Nature Biotechnology 2016*
  → adapted for draft-quality genomes, code on Github

# Inference of microbial growth directly from metagenomic samples

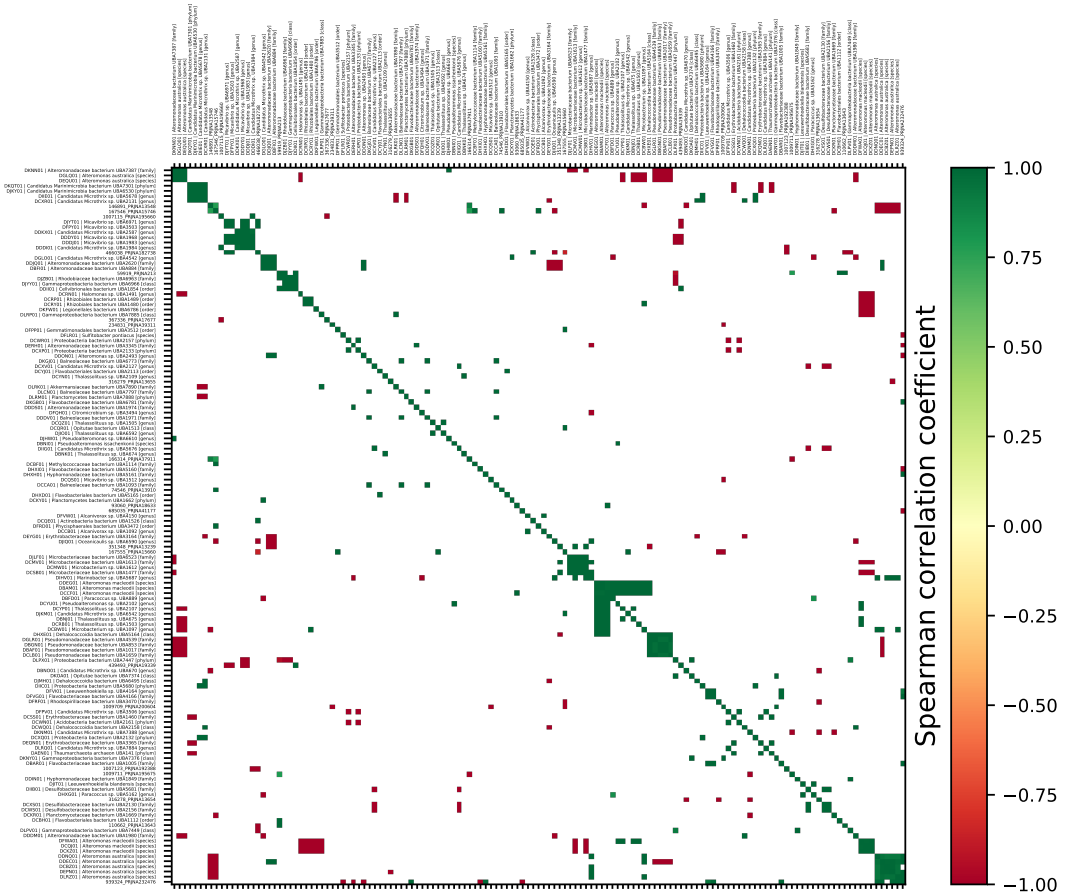



$$PTR = iRep = \frac{\texttt{Ori}_{cov}}{\texttt{Ter}_{cov}} \geq 1$$

Quantitative *in situ* measurement of the replication rate

Korem *et al*, Science 2015

# Growth correlation between 556 MAGs in 172 Tara samples




Data: *near-complete* "Tara" MAGs from Parks *et al*, Nature Microbiology 2017; Tara Oceans samples

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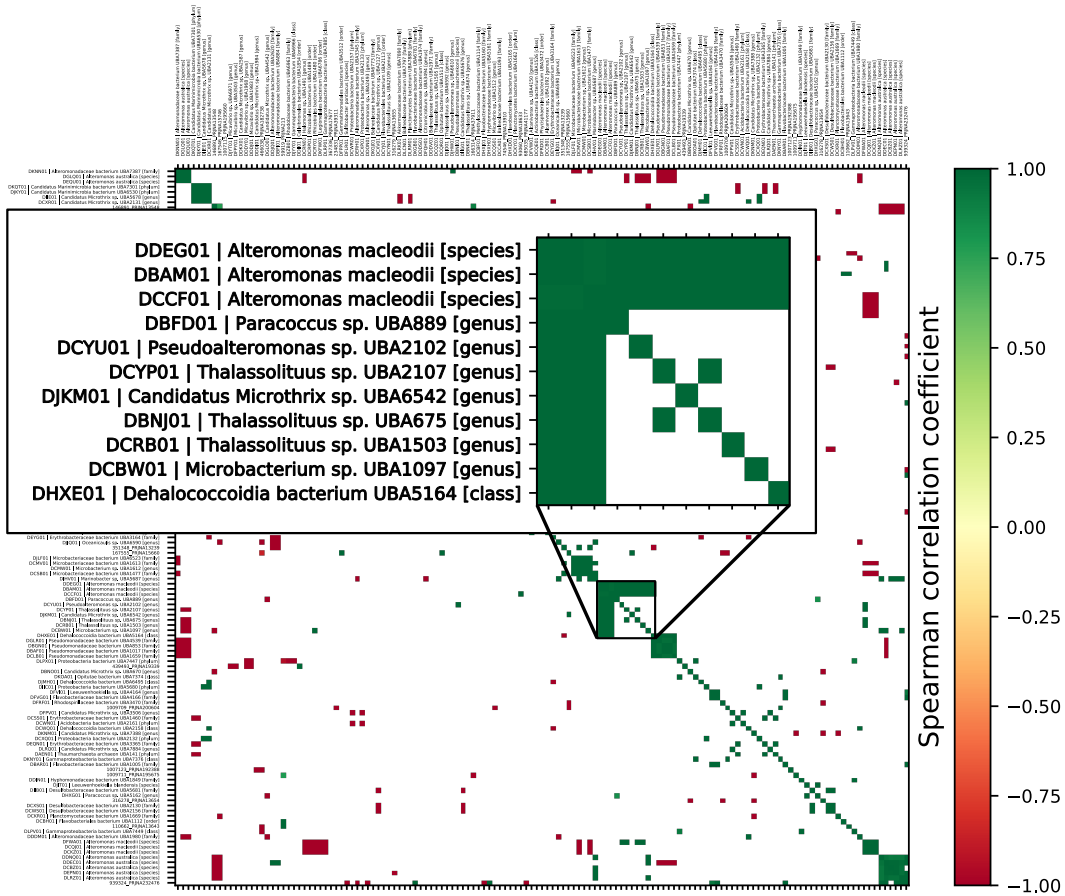
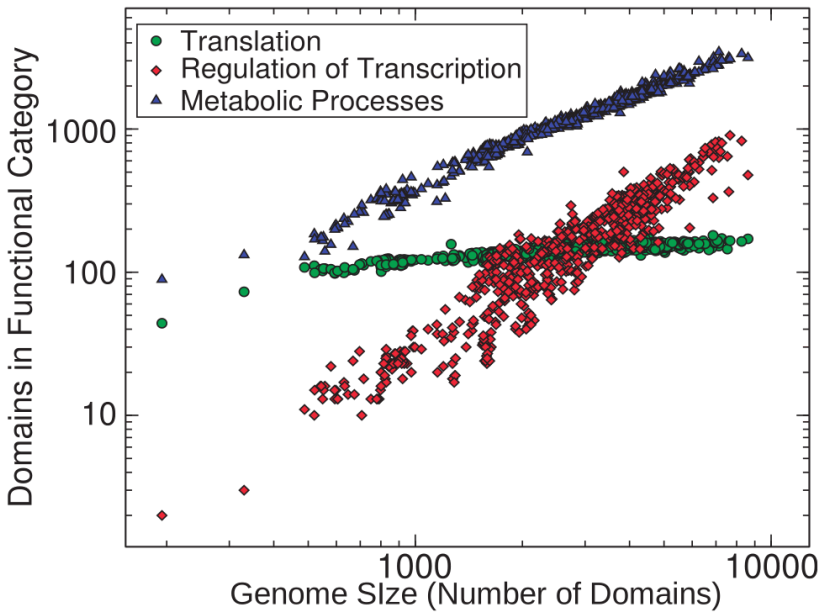



Data: *near-complete* "Tara" MAGs from Parks *et al*, Nature Microbiology 2017; Tara Oceans samples

# FUNCTIONAL CONTENT OF PROKARYOTIC GENOMES: SCALING LAWS OF LAB-CULTIVATED STRAINS




**Scaling laws**

$$n_c = \beta_c \times n^{\alpha_c}$$

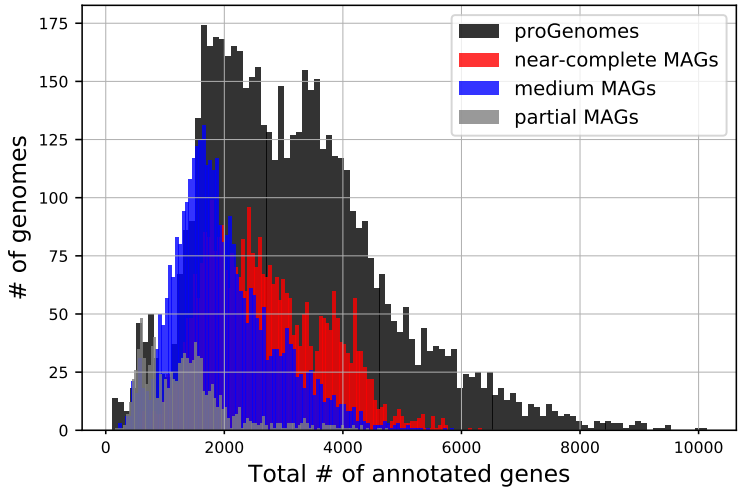
$n_c$: number of gene in cat c
$n$: total number of genes

- Uncovered from ∼700 (lab-cultivated) prokaryotes
- What about environmental genomes?

Grilli *et al*, Nucleic Acid Research 2012

# Functional annotation of environmental genomes

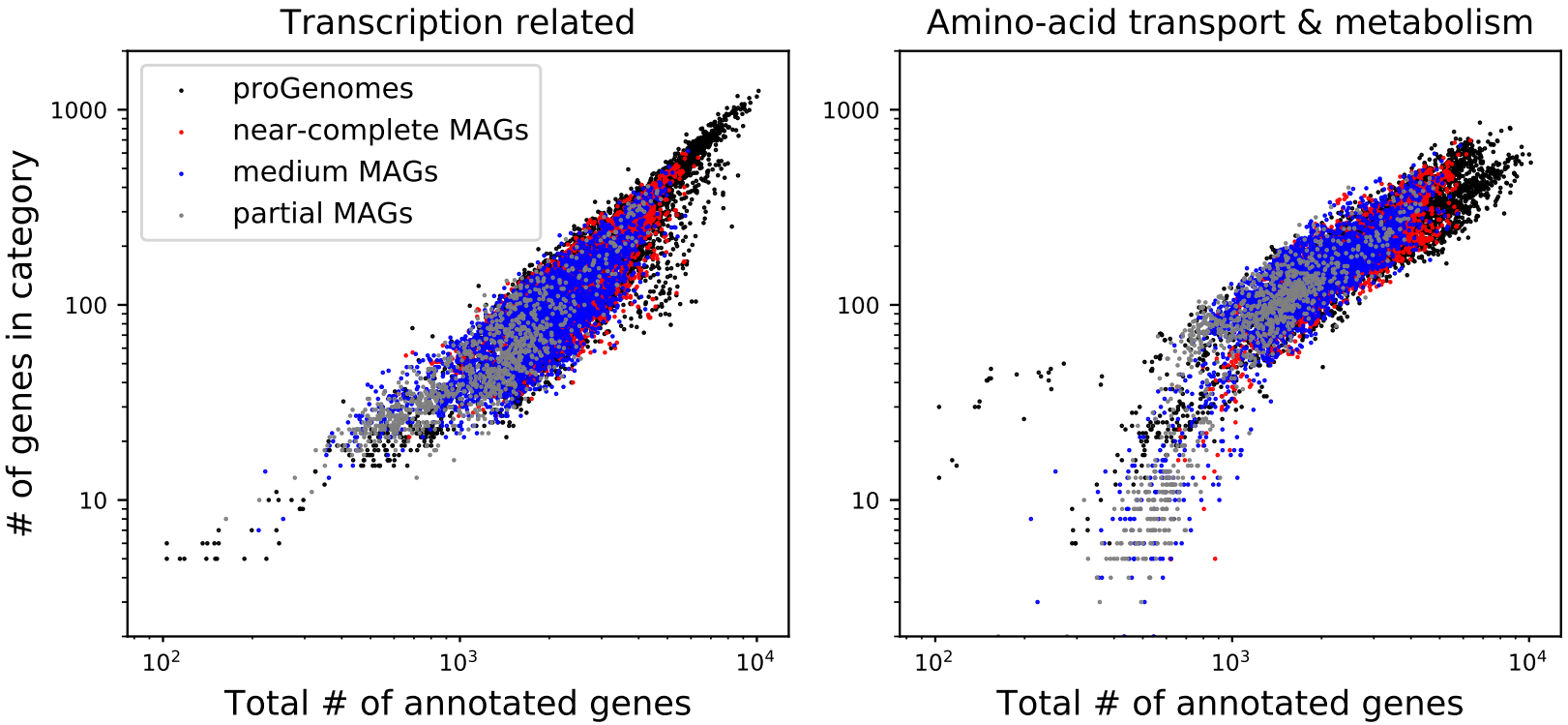
- Annotation pipeline (Prodigal/eggNOGmapper)
- 8000 MAGs annotated along ~25k complete genomes




## Functional annotation databases

- Strategies: Orthologous groups (eggNOG) VS protein domains (pfam)
- Annotations: eggNOG (50%), KEGG (30%), Gene Ontology terms

# Scaling laws in MAGs




Could "social" prokaryotes be functional outliers in such laws?

*Work in progress...*

# Wrapping up

## In summary...

- Microbial diversity largely unknown
- Intensive experimental (sampling and sequencing) and theoretical (genome prediction) research efforts to uncover new *environmental genomes*
- We try to accumulate clues to predict associations

## Perspective

- Revisit scaling laws at the ecosystem level
- Add more clues of associations (metaT?)
- Next step: reconstruct metabolic models of consortia to explain microbe social interactions

# 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

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