

Microbial communities through the lens of high throughput sequencing, data integration and metabolic networks analysis

developing computational approaches to better understand microbial assemblages

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PhD candidate



1. My short story
2. Bioinformatics methods for microbial diversity assessment
 - 2.1 pema: a metabarcoding pipeline
 - 2.2 darn: known unknowns in COI amplicon data
3. PREGO: a knowledge-base for organisms - environments - processes associations
4. dingo: a Python library for metabolic flux sampling
5. Os & 1s in molecular biology
6. microbetag: enhancing microbial interactions inference from co-occurrence networks
7. Publications

My story starts at a small but quite a nice place

Ancient Olympia



Great times with a lot of basketball and even more *hows* and *whys*

.. moves in Athens

Biology Department, National & Kapodestrian University



Thesis on the morphology,
morphometry and anatomy of
species of the genus
Pseudamnicola in Greece

.. and then to a "horrible" place called Crete

Medical School (MSc), Biology department (PhD) of UoC,
Hellenic Centre for Marine Research



MSc thesis on eDNA metabarcoding for biodiversity assessment:
Algorithm design and bioinformatics analysis pipeline implementation

Microbial ecology & biogeochemical cycles

a corner-stone for life on earth

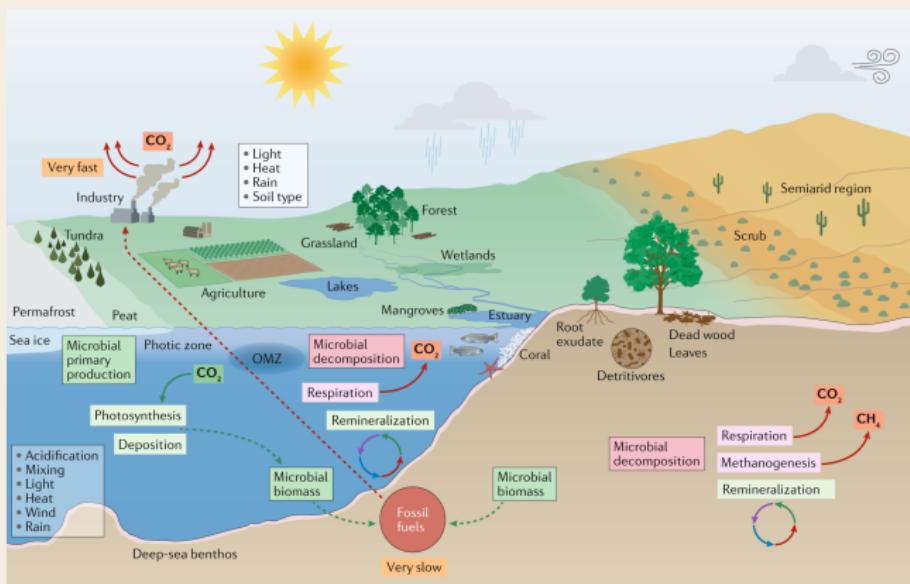


Figure from: Cavicchioli et al. Nature Reviews Microbiology 17.9 (2019): 569-586.

Questions to address

for a deeper understanding of microbial assemblages

Community
structure

who

everyone is everywhere

Functional
potential

what

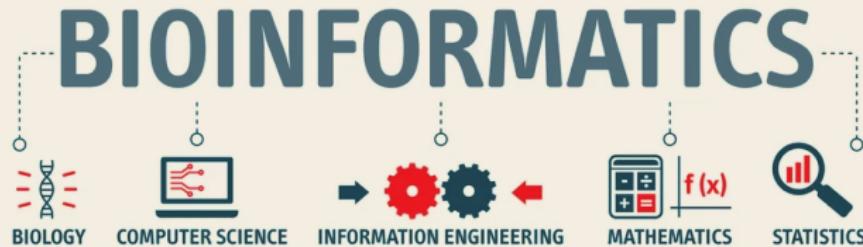
zero-sum game

Microbial
interactions

why

the entangled bank

We are living in a computational era
both a challenge & an opportunity



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eDNA metabarcoding for biodiversity assessment

Marker genes

1. **16S rRNA:** Bacteria, Archaea
2. **12S rRNA:** Vertebrates
3. **18S rRNA:** Small eukaryotes, Metazoa
4. **ITS:** Fungi
5. **COI:** Eukaryotes
6. ***rbcl:*** Plants
7. ***dsrb:*** Bacteria, Archaea
8. ...

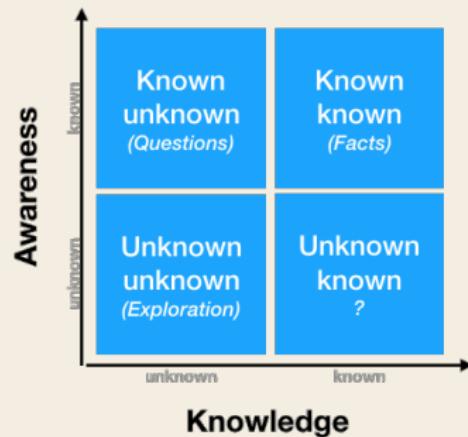
Methodology



- Sampling
- Extraction
- Bioinformatics
- Biodiversity analysis

Bioinformatics challenges

for the analysis and the interpretation of amplicon data





PEMA

a pipeline for eDNA metabarcoding analysis

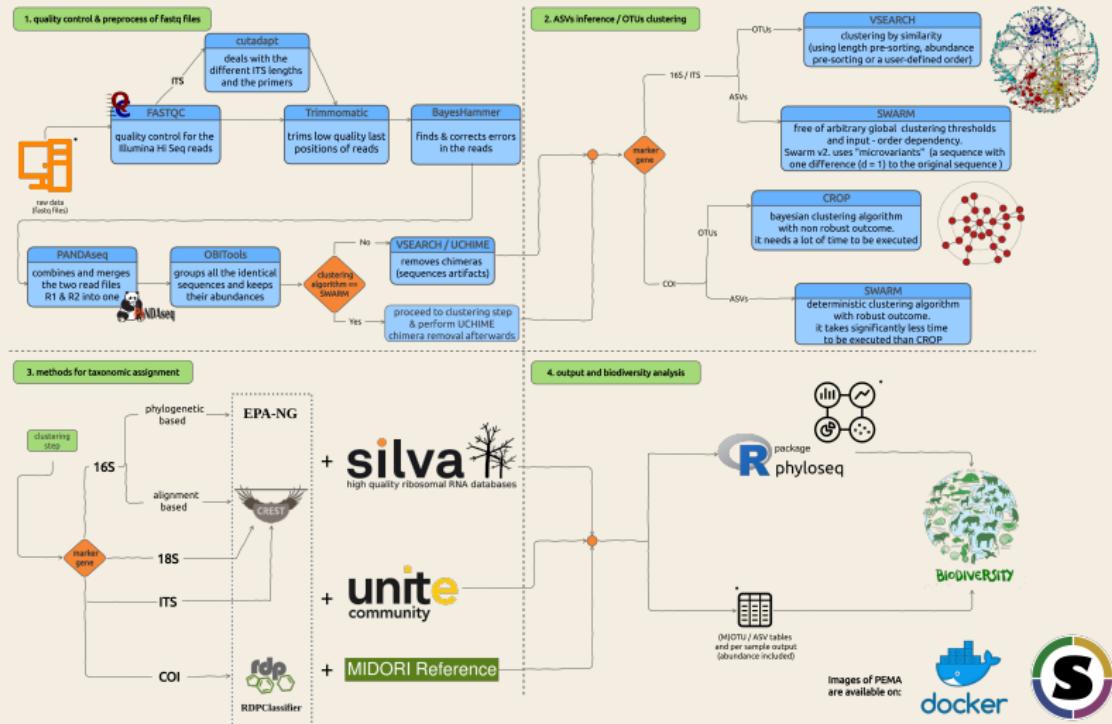
<https://github.com/hariszaf/pema>

pema.hcmr.gr

PEMA features

one step at a time!

PEMA in a nutshell

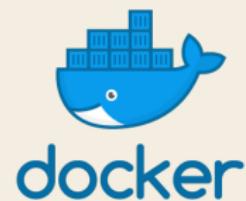


PEMA coding insights

Being a geek just for a bit !

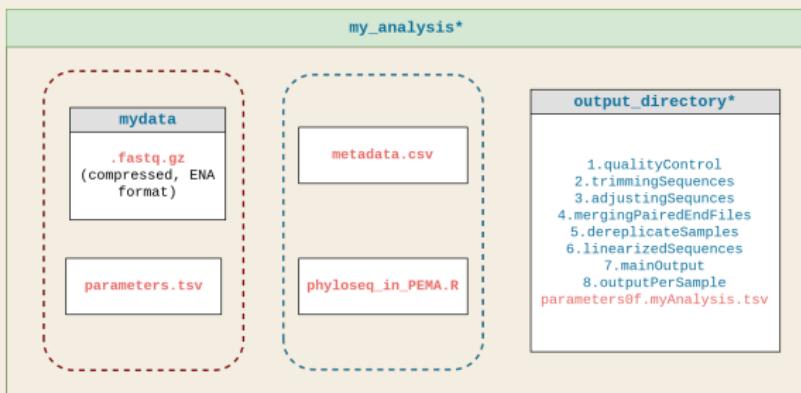
```
for(int i : range(1,  
    in := "in_$i.tx  
    sys date > $in  
  
    out := "out_$i.t  
    taskC out <- in  
        sys echo Tas  
    }  
}
```

BigDataScript
programming language



Containerization

Mount your I/O give & take



text file
directory

***user can edit the name**

(the rest **need** or will have the exact names shown)

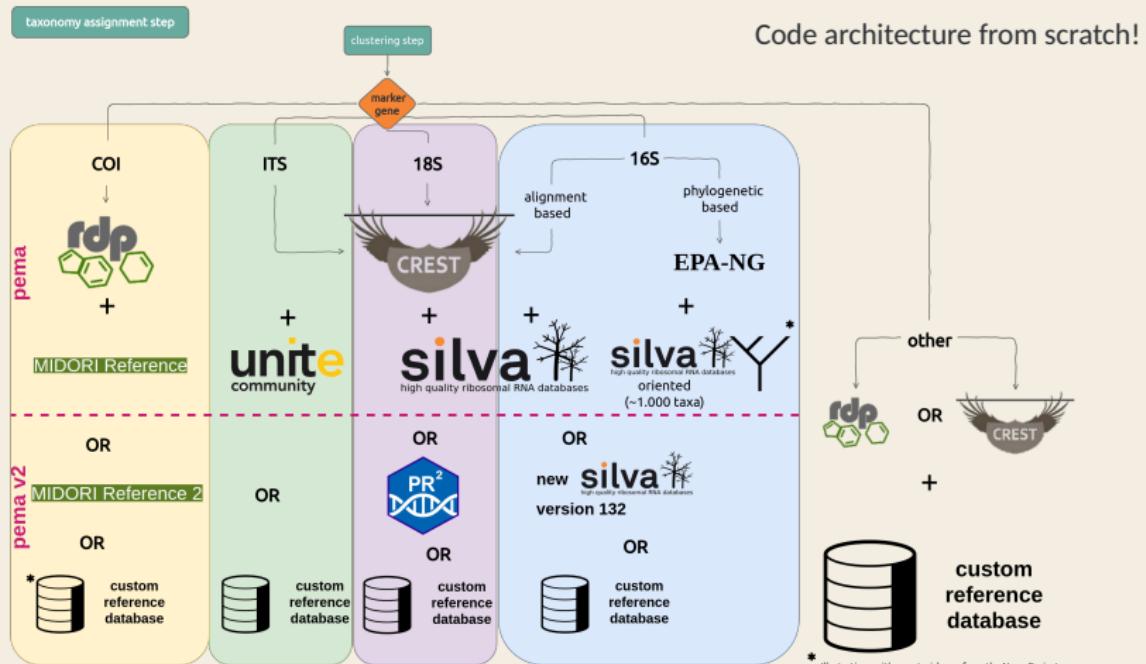
— mandatory input files
- - - optional input files

	Sample 1	Sample 2	Sample 3	Sample 4
Taxon 1	1	0	1	2
Taxon 2	0	1	0	2
Taxon 3	1	1	0	4



PEMA v.2

addressing some of the challenges



* Illustrations with an asterisk are from the Noun Project



darn

<https://github.com/hariszaf/darn>

Dark mAtteR iNvesigator

investigating known unknown
in COI amplicon data

What is all these unassigned
OTUs / ASVs?

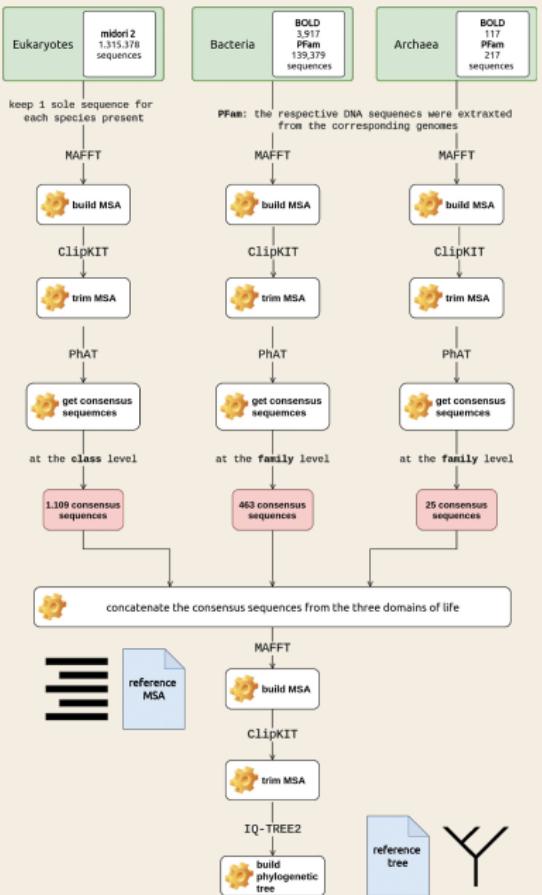
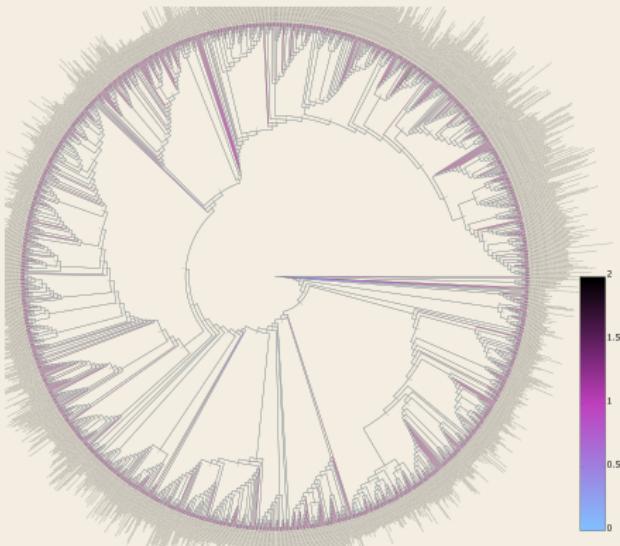


Figure from: [10.3897/mbmg.5.69657](https://doi.org/10.3897/mbmg.5.69657)

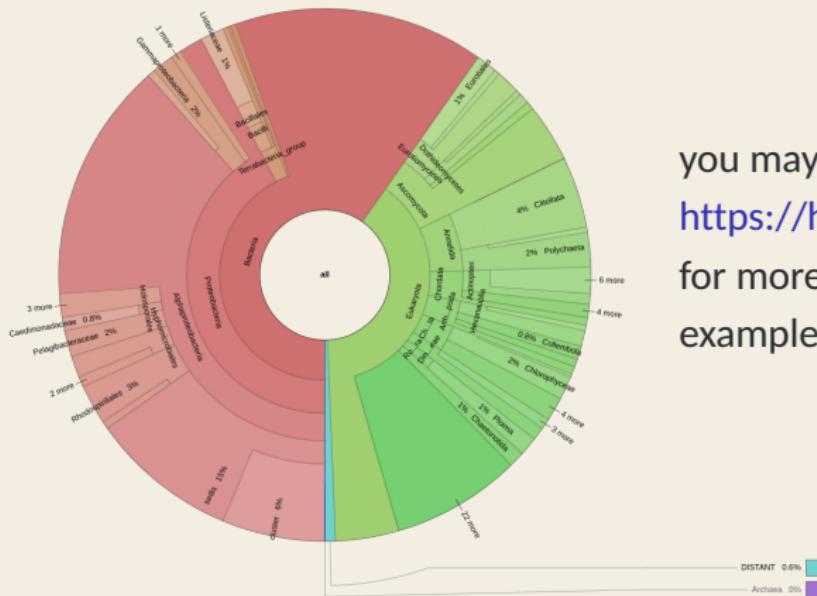
Phylogeny of the COI consensus sequences retrieved *the tree that DARN makes use of*



the consensus sequences have been placed in their corresponding taxonomic branches, proving the tree valid

Bacteria are everywhere!

... Archaea too!



you may have a look at

<https://hariszaf.github.io/darn/>
for more DARN output
example cases

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PROCESS ENVIRONMENT ORGANISM

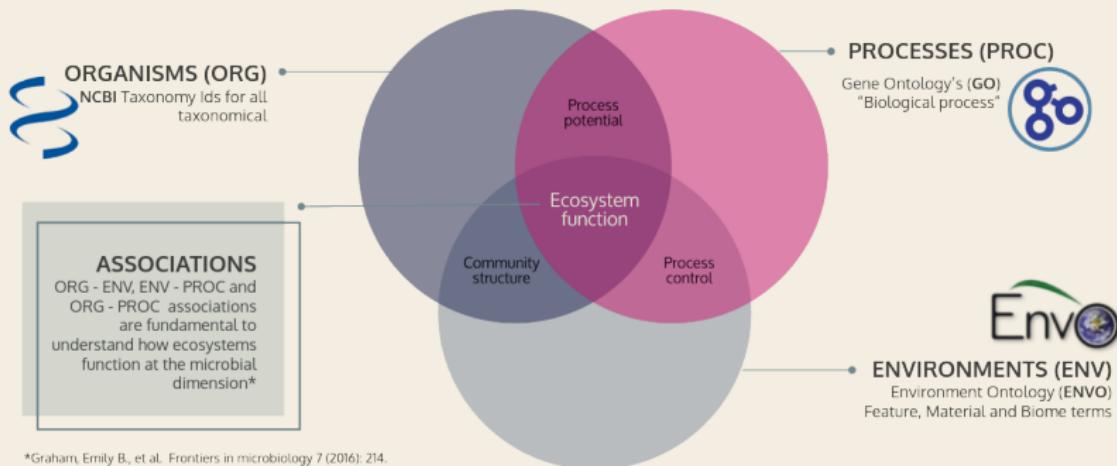
related repositories under

<https://github.com/orgs/lab42open-team>

web-app under

<http://prego.hcmr.gr/>

PREGO as processes - environments - organisms and how to link them



Metadata example

from various metagenome repositories

Sample metadata [-]



Collection date:	11/1/11
Elevation:	200
Environment (biome):	soil
Environment (feature):	nosZ
Environment (material):	soil DNA
Environmental package:	MIGS/MIMS/MIMARKS.soil
Geographic location (depth):	15-20cm
Instrument model:	454 GS FLX Titanium
Investigation type:	metres-survey
NCBI sample classification:	410658
Project name:	EcoFINDERS



Project Information

Cultured	No
Ecosystem	Environmental
Ecosystem Category	Aquatic
Ecosystem Subtype	Oceanic
Ecosystem Type	Marine

MG-RAST ID	name	biome	feature	material	sample	library	location	country	coordinates	download	
mgm4702467.3	06032015b_S2_L001_R2_001	Large lake biome	lake	water	mgs485560	mg485562	Cincinnati	USA	39.11, -84.5		
mgm4702469.3	06052015a_S3_L001_R2_001	Large lake biome	lake	water	mgs485566	mg485568	Cincinnati	USA	39.11, -84.5		
mgm4702471.3	06032015a_S1_L001_R2_001	Large lake biome	lake	water	mgs485554	mg485556	Cincinnati	USA	39.11, -84.5		

MG-RAST
metagenomics analysis server

Named Entity Recognition

tagging the literature

Identification of potentially important pathways missing from the model

EXTRACT	X
Protein	
Chemical compound	
Organism	
Environment	
Tissue	
Disease/phenotype	
Gene Ontology term	

From the metagenomic bins, we were able to identify two **metabolic processes** that were not previously included in the model. A number of MAGs (bin.59, bin.15, bin.73) clustered to the KEGG genomes of **freshwater sulfur**-oxidizing autotrophs capable of denitrification, *Sulfuritalea hydrogentivorans* [41], and *Sulfuricella denitrificans* [42]. These MAGs contained the diagnostic genes for **carbon fixation** (*rbcLS*), **sulfur** cycling (*dsrAB*), and denitrification (*nosZ*). One MAG (bin.59) also clustered with **iron** oxidizing autotroph *Sideroxydans lithotrophicus* **ES-1**. Bin.59 is the most relatively abundant bin from 17 to 21 m depth. Thus, if this MAG is associated with **iron** oxidation, it also contains **sulfur**-cycling genes that add to metabolic flexibility, which was previously observed [40]. The model did not include **sulfide oxidation** with **nitrate**, so it is unclear from the current model predictions where this process is expected to occur within the water column to compare to the MAG distributions.

Example text from Arora-Williams et al. Microbiome 6.1 (2018): 1-16.

PREGO methodology

co-occurrence again!

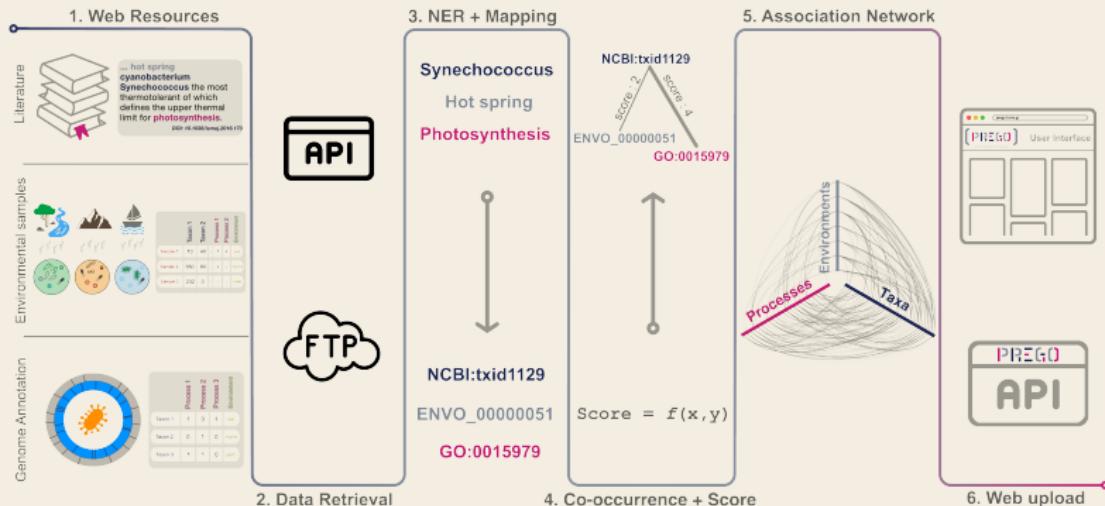


Figure from the PREGO publication that is now under review.

PREGO in action

looking for environments a taxon is present

Desulfatiglans anilini DSM 4660 [1121399]

Synonyms: Desulfatiglans anilini DSM 4660, D. anilini DSM 4660, D anilini DSM 4660, Desulfatiglans DSM 4660, Desulfatiglans str. DSM 4660 ...

Environments Biological Processes Molecular Function Documents Downloads

Literature

Search:

Name	Z-score	Confidence
Oil seep	3.0	★★★★★
Marine mud	3.0	★★★★★
Marine sediment	2.8	★★★★★
Brackish water	2.4	★★★★★
Oil reservoir	2.2	★★★★★
Anaerobic sediment	2.0	★★★★★
Cold seep	1.8	★★★★★
Contaminated sediment	1.7	★★★★★
Neritic sub-litoral zone	1.4	★★★★★
Oil spill	1.4	★★★★★
Petroleum	1.1	★★★★★
Sea floor	1.1	★★★★★

Showing 1 to 12 of 12 entries

Environments Biological Processes Molecular Function Documents Downloads

Literature

Search:

Name	Z-score	Confidence
benzoyl-CoA catabolic process	4.3	★★★★★
Benzene catabolic process	3.6	★★★★★
Acetone metabolic process	3.5	★★★★★
Phenanthrene catabolic process	3.5	★★★★★
Sulfate reduction	3.3	★★★★★
Ketone body catabolic process	3.2	★★★★★
Naphthalene catabolic process	3.2	★★★★★
Alkane catabolic process	3.1	★★★★★
Benzoate catabolic process	3.0	★★★★★
Denitrification pathway	2.8	★★★★★
Sulfide ion homeostasis	2.6	★★★★★
Ketone catabolic process	2.6	★★★★★
Methanogenesis	1.8	★★★★★
Electron transport chain	1.0	★★★★★

Showing 1 to 14 of 14 entries

The PREGO knowledge-base is already available under <http://prego.hcmr.gr/>.

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<https://github.com/GeomScale/dingo>

From a stoichiometric matrix to a constraint-based model

Metabolites	Reactions				
	R_1	R_2	R_3	R_4	R_5
	-1	0	0	0	0
	1	-1	0	0	0
	0	1	-1	0	0
	0	1	0	0	-1
	0	0	1	0	0
	0	0	0	-1	0
	0	0	0	1	-1
	0	0	0	0	1

(S-matrix) \times (Flux vector) = (0)

Flux Balance Analysis

Maximize minimize an objective function:

$$\psi = c_1 v_1 + c_2 v_2 + \dots + c_5 v_5$$

such that:

$$S * v = 0$$

and for each reaction i :

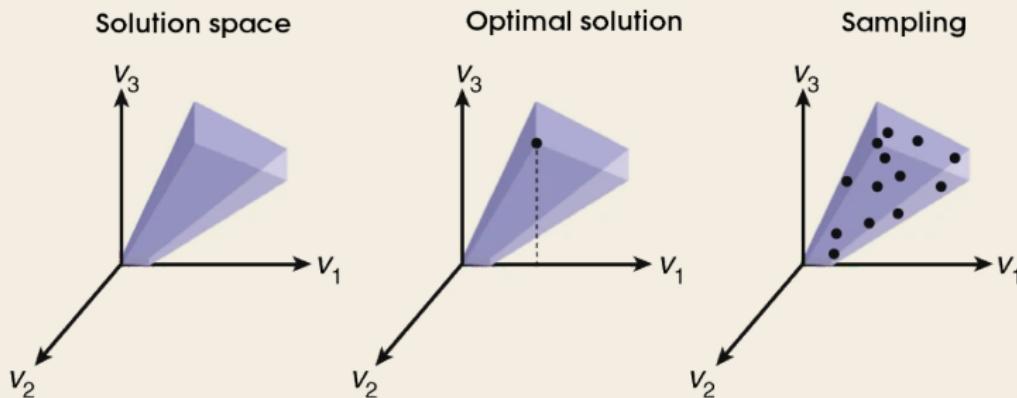
$$lb_i \leq v_i \leq ub_i$$

where lb : lower bound,
 ub : upper bound and

S : the stoichiometric matrix

Flux sampling

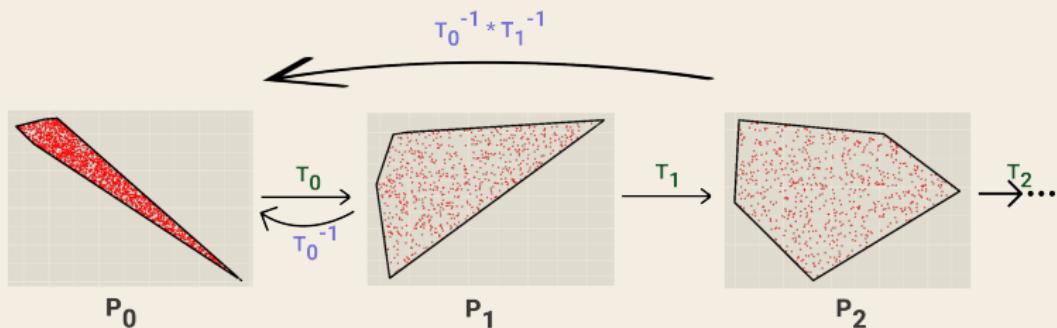
an alternative approach



- enables the analysis of GEMs without the need of an objective function
- determines the feasible solution spaces for fluxes in a network based on a set of conditions as well as the probability of obtaining a solution

Figure from: Heirendt et al. Nature protocols 14.3 (2019): 639-702.

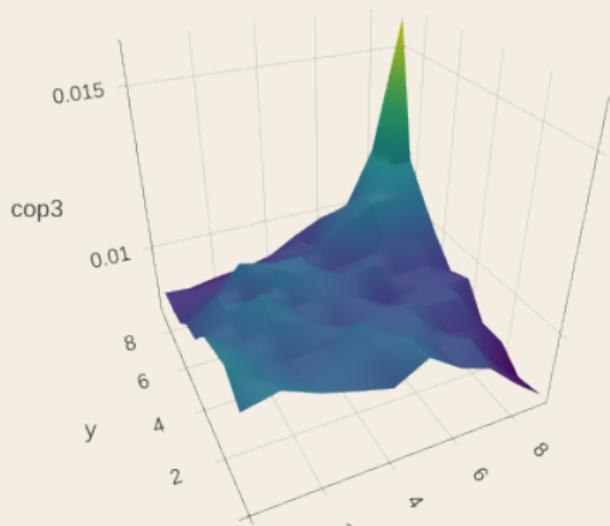
Our Markov Chain Monte Carlo (MCMC) algorithm for flux sampling



Steps of an MMCS phase

- **sampling step:** using a variant of the **Billiard walk**
- **rounding step:** calculate a linear transformation T_i that puts the sample into isotropic position and then apply it on P_i to obtain the polytope of the next phase
- check several statistic tests

What is the probability of a flux value of a reaction
with respect to the flux value of another reaction

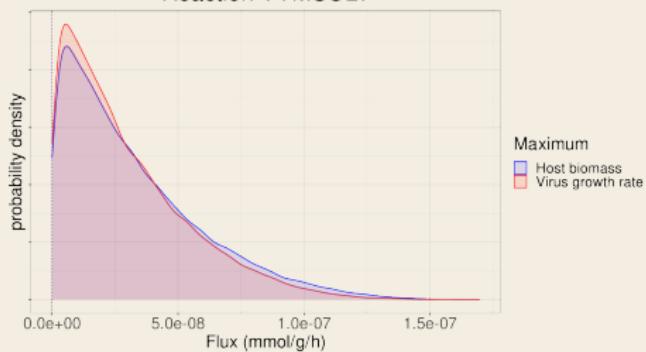


Find possible targets against SARS-CoV-2

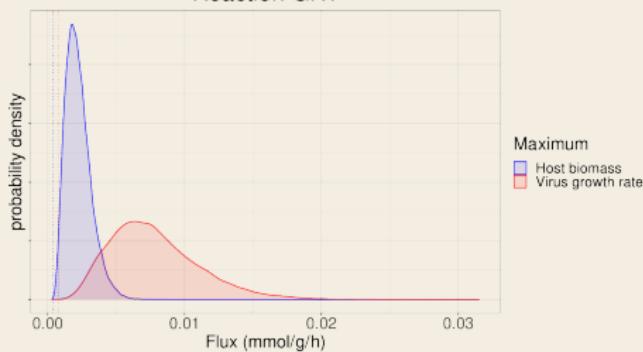
a flux sampling application



Reaction TYMSULT



Reaction GK1

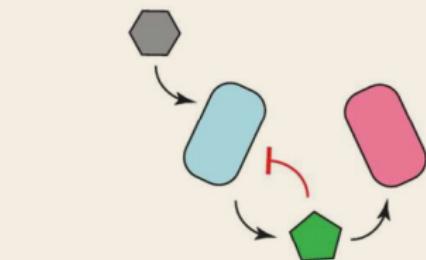


- Check if the flux distribution of a reaction changes.
- Find possible anti-viral targets and study further.

Further applications of metabolic flux sampling



Scott, William T., et al. "Metabolic flux sampling predicts strain-dependent differences related to aroma production among commercial wine yeasts." Microbial cell factories 20.1 (2021): 1-15.

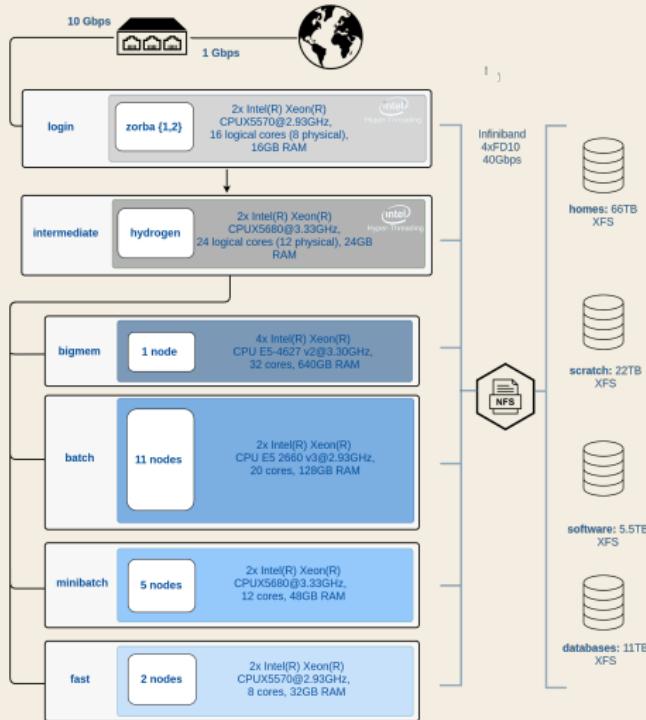


What about microbial interactions ?

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Zorbas: the HPC facility of IMBBC

a Tier 2 (regional) HPC facility



Block diagram of the
Zorba architecture

Computing infrastructures an alternative for the most!



We will develop a workflow for the analysis of Genomic Observatories (GOs) data that will allow researchers to deal better with the increasing amount of data



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microbetag: annotating co-occurrence networks and a trip to KU Leuven

We will try building 3 modules:

- pathway complementarity
- environmental conditions and phenotypic data integration
- flux sampling on pairs of metabolic models (if possible)

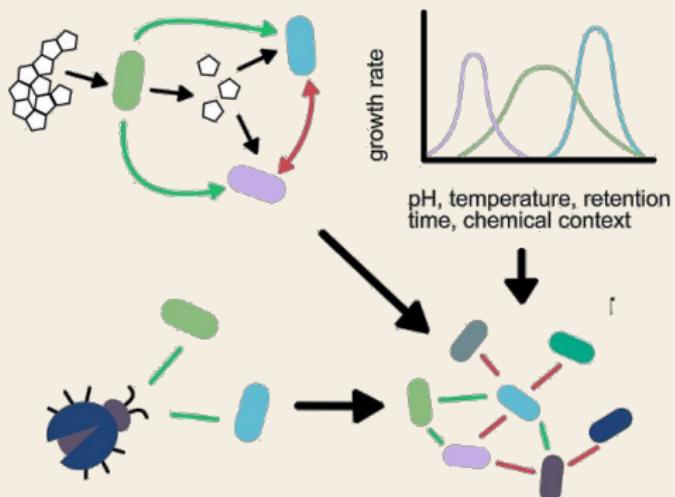


Figure from Röttjers & Faust (2018). FEMS microbiology reviews. 42. 10.1093/femsre/fuy030.

First steps (1/3)

pathway complementarity module

1. use abundance & metadata table to run FlashWeave
2. get the NCBI Taxon id of each taxon present in the edge file
3. search for available reference genomes for these ids
4. use KEGG modules to get major metabolic pathways of interest
5. search for pathway complementarity in each module of interest

Relative work

- Levy & Borenstein. Proceedings of the National Academy of Sciences 110.31 (2013): 12804-12809.
- Zelezniak et al. Proceedings of the National Academy of Sciences 112.20 (2015): 6449-6454.

First steps (2/3)

phenotypical annotation module

1. BugBase to get:

- Gram Positive & Negative
- Biofilm Forming
- Pathogenic Potential
- Mobile Element Containing
- Oxygen Utilizing
- Oxidative Stress Tolerant

Further annotation sources to be considered:

- SigMol
- BacDive

2. FAPROTAX database:

to map taxa to established metabolic or other ecologically relevant functions,
using the current literature on cultured strains

First steps (3/3)

ecoEFMs

Nutrition or nature: disentangling the complex forces shaping prokaryote pan-genomes

Daniel R. Garza^{1,5}, F. A. Bastiaan von Meijenfeldt², Bram van Dijk⁴, Annemarie Boleij³, Martijn A. Huynen¹, Bas E. Dutilh^{1,2}

- (1) Centre for Molecular and Biomolecular Informatics, Radboud Institute for Molecular Life Sciences, Radboud University Medical Centre, Geert Grootplein 28, 6525 GA Nijmegen, The Netherlands
- (2) Theoretical Biology and Bioinformatics, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands
- (3) Department of Pathology, Radboud Institute for Molecular Life Sciences (RIMLS), Radboud University Medical Center, Nijmegen, The Netherlands.
- (4) Department of Microbial Population Biology, Max Planck Institute for Evolutionary Biology, Plön 24306, Germany
- (5) Microbial Systems Biology, Laboratory of Molecular Bacteriology, Department of Microbiology, Immunology and Transplantation, Rega institute, KU Leuven, Leuven, Belgium.

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Publications

- [1] Zafeiropoulos, H., Paragkamian, S., Ninidakis, S., Pavlopoulos, G.A., Jensen, L.J. & Pafilis, E. PREGO: a literature- and data-mining resource to associate microorganisms, biological processes, and environment types. - *under revision at Microorganisms journal*
- [2] Zafeiropoulos, H., Gargan, L., Hintikka, S., Pavloudi, C., & Carlsson, J. (2021). The Dark mAtteR iNvestigator (DARN) tool: getting to know the known unknowns in COI amplicon data. *Metabarcoding and Metagenomics*, 5, e69657.
- [3] Chalkis, A., Fisikopoulos, V., Tsigaridas, E., & Zafeiropoulos, H. (2021). Geometric algorithms for sampling the flux space of metabolic networks, *37th International Symposium on Computational Geometry (SoCG 2021)*.
- [4] Zafeiropoulos, H., Gioti, A., Ninidakis, S., Potirakis, A., Paragkamian, S., ... & Pafilis, E. (2021). Os and 1s in marine molecular research: a regional HPC perspective. *GigaScience*, 10(8), giab053.
- [5] Zafeiropoulos, H., Viet, H. Q., Vasileiadou, K., Potirakis, A., Arvanitidis, C., Topalis, P., ... & Pafilis, E. (2020). PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes. *GigaScience*, 9(3), giaa022.

Thank you for your attention
and your patience ;)

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Dr. Pafilis E.

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Dr. Chalkis A.

Prof. Tsigaridas E.

Dr. Fisikopoulos V.

