



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

on the road to a PhD
Haris Zafeiropoulos

1. Bioinformatics methods for microbial diversity assessment
 - 1.1 pema: a metabarcoding pipeline
 - 1.2 darn: known unknowns in COI amplicon data
2. PREG0: a knowledge-base for organisms - environments - processes associations
3. dingo: a Python library for metabolic flux sampling
 - 3.1 Flux sampling
4. Tristomo swamp: a hybrid amplicon & shotgun metagenomics analysis
5. Publications

eDNA metabarcoding

Marker genes

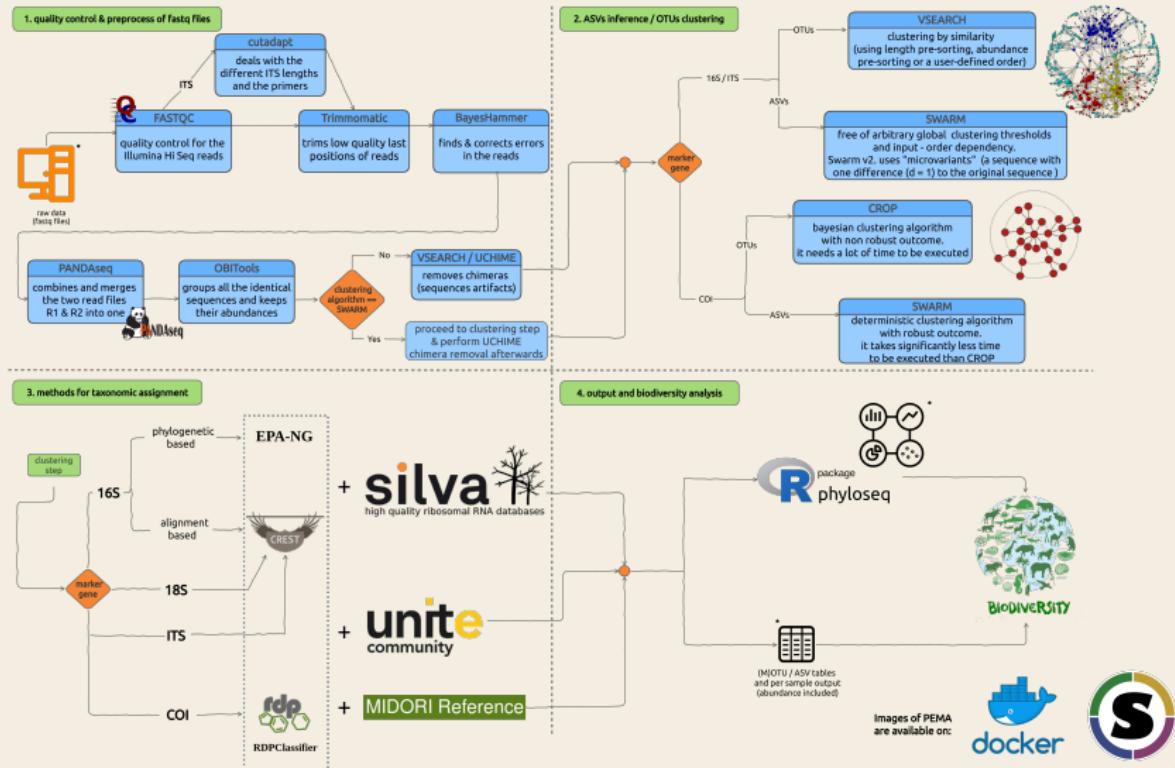
1. **16S rRNA:** Bacteria, Archaea
2. **12S rRNA:** Vertebrates
3. **18S rRNA:** Small eukaryotes, Metazoa
4. **ITS:** Fungi
5. **COI:** Eukaryotes
6. ***rbcl:*** Plants
7. ***dsrb:*** Bacteria, Archaea
8. ...

Bioinformatics analysis steps

1. Sequence pre-processing
2. OTUs clustering / ASVs inference
3. Taxonomic assignment
4. Biodiversity analysis

PEMA architecture

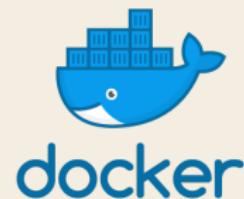
PEMA in a nutshell



Being a geek just for a bit !

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

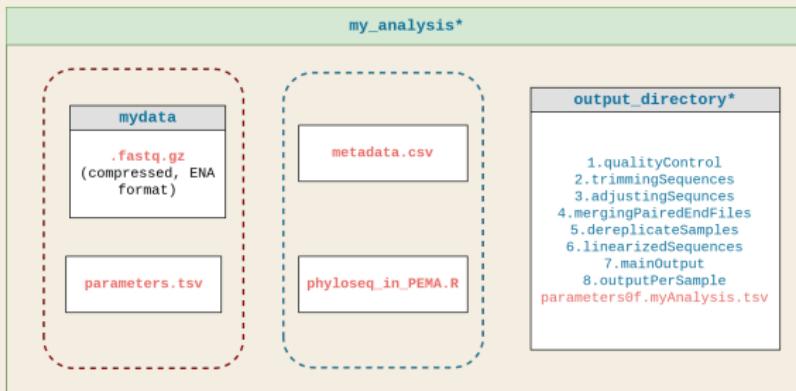
BigDataScript
programming language



Containerization

Mount your I/O

you give something - you take something



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

1st version published in 2020

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Volume 9, Issue 3

March 2020

Article Contents

Abstract

Background

PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes 

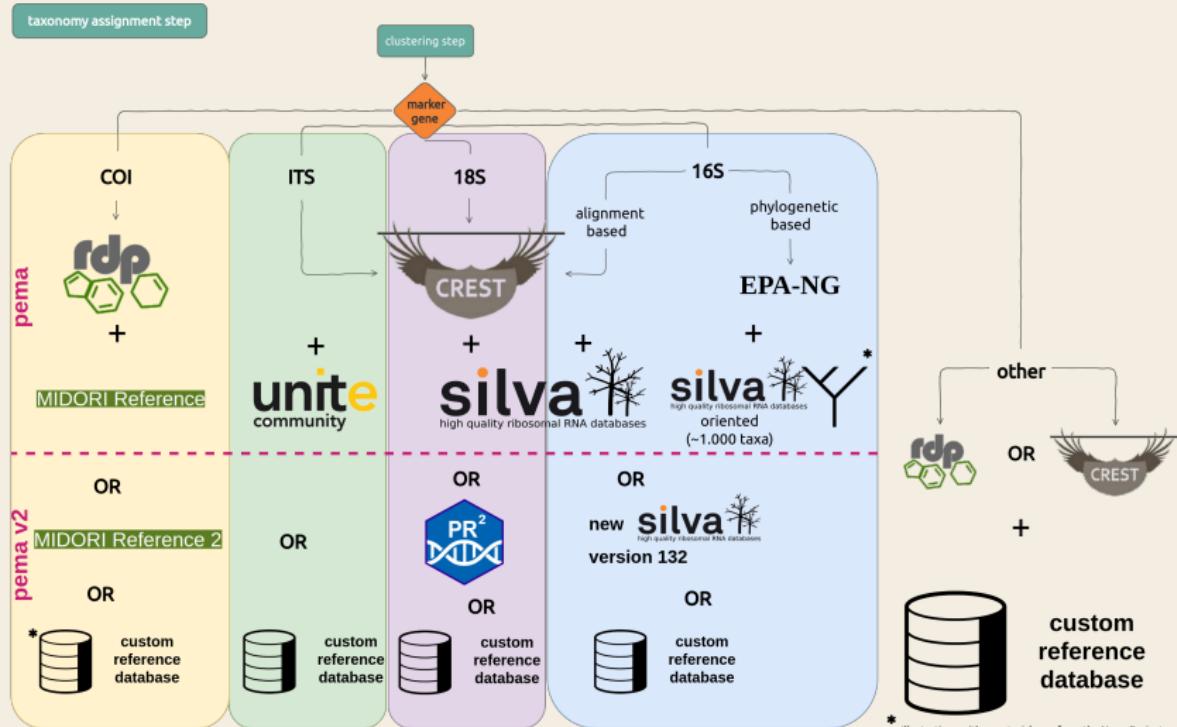
Haris Zafeiropoulos , Ha Quoc Viet, Katerina Vasileiadou, Antonis Potirakis, Christos Arvanitidis, Pantelis Topalis, Christina Pavloudi, Evangelos Pafilis

GigaScience, Volume 9, Issue 3, March 2020, gja022,
<https://doi.org/10.1093/gigascience/gja022>

Published: 12 March 2020 Article history ▾

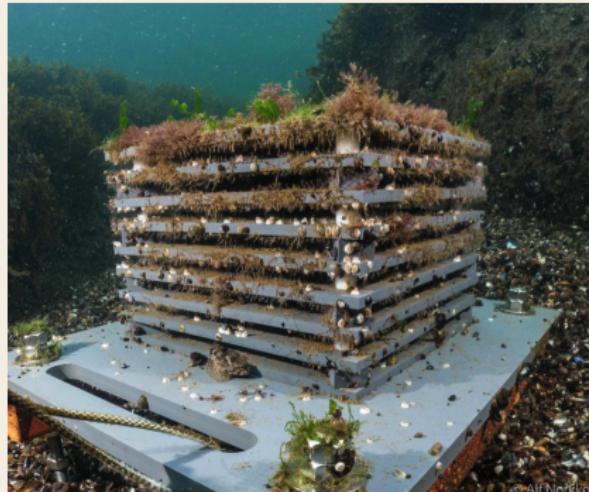
A correction has been published: *GigaScience*, Volume 9, Issue 12, December 2020, gja150, <https://doi.org/10.1093/gigascience/gja150>

PEMA v.2



Latest PEMa version

addressing the challenges of the community



ASSEMBLE 
ASSOCIATION OF EUROPEAN MARINE BIOLOGICAL LABORATORIES EXPANDED

MBON
Marine Biodiversity
Observation Network

pema:v.2.1.4 includes:

1. analysis of 12S rRNA data now supported ([12S Vertebrate Classifier v2.0.0-ref database](#))
2. PR2 as an alternative reference database for the case of 18S rRNA
3. the ncbi-taxonomist tool was added to return the NCBI Taxonomy Id of the taxonomies found

open source is cool

interacting with the community

The screenshot shows a GitHub repository page for 'hariszaf / pema'. The repository is public and has 1 master branch. The 'Code' tab is selected, showing the 'CONTRIBUTING.md' file. The file content is as follows:

```
master → pema / CONTRIBUTING.md

hariszaf Revert "Develop"
Latest commit 1a4f725 on Dec 11, 2020 History

A 2 contributors

184 lines (103 sloc) 6.57 KB

Contribute to the PEMA repo!

Thank you all for taking the time to contribute! 🎉

The following is a set of guidelines for contributing, in terms of guidelines, not rules. Feel free to contribute to this document as in the rest of the repo! 😊

Table of Contents

• Dependencies
• Fork PEMA repository to build your own repo
• Prepare to contribute!
  • GitFlow workflow
    • Create new branch for your work
• Make your contributions on your branch
• Pull request (PR) and the job is done
• Review
• Acknowledgements
```

PEMA aims at building a community to discuss challenges on metabarcoding come up with solutions and why not develop some of them!

How to and further documentation at pema.hcmr.gr

A place for sharing news as well as thoughts and remarks on how to run metabarcoding analyses using the PEMA containers or other software. Made by Haris Zafeiropoulos.

- Home
- Get PEMA
- Basics for running PEMA
- PEMA output
- Running on HPC
- Running on personal computer
- 16/18S analysis
- COI analysis
- ITS analysis
- Training the CREST classifier
- Training the RDPClassifier
- Tuning tuning tuning!
- GitHub repo
- Blog

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PEMA investigating metabarcoding

Welcome

Hey there!

This is the PEMA main site for *how to use* and further metabarcoding tips and hints!

You may find PEMA as a Docker and as a Singularity container.

Here is the [PEMA GitHub repository](#) if you want to have a look on the source code and why not, to contribute to!

For any running issues you may have, or for any further features you would like to see included on PEMA, you can reach us through the [PEMA Gitter community](#) or at pema@hcmr.gr.

Thanks for your interest on PEMA! Keep metabarcoding!

The PEMA team



PEMA
a pipeline for eDNA metabarcoding analysis

DARN: investigating known unknown in COI amplicon data

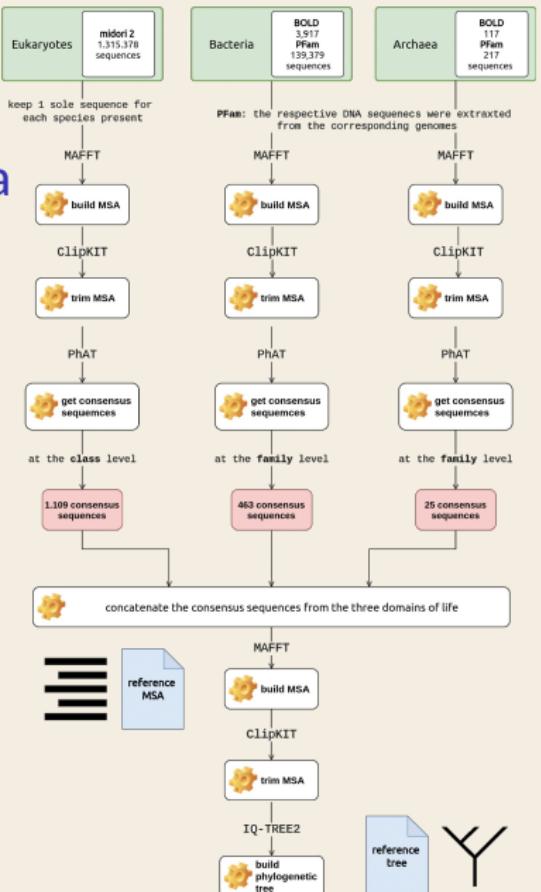


Figure from: Heirendt, Laurent, et al. Nature protocols 14.3 (2019): 639-702.

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PREGO methodology

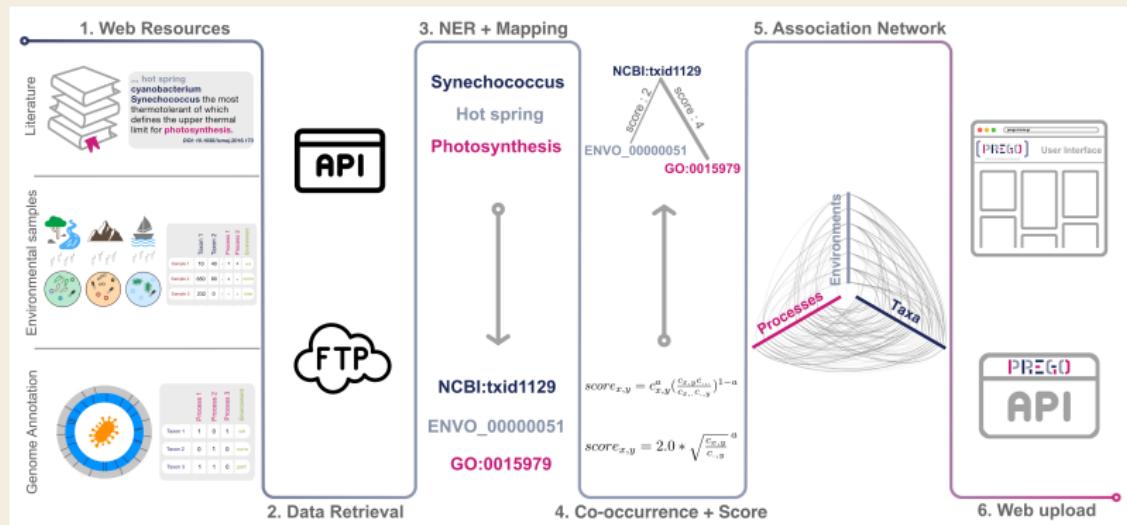


Figure from: Heirendt, Laurent, et al. Nature protocols 14.3 (2019): 639-702.

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Genome-scale metabolic reconstruction

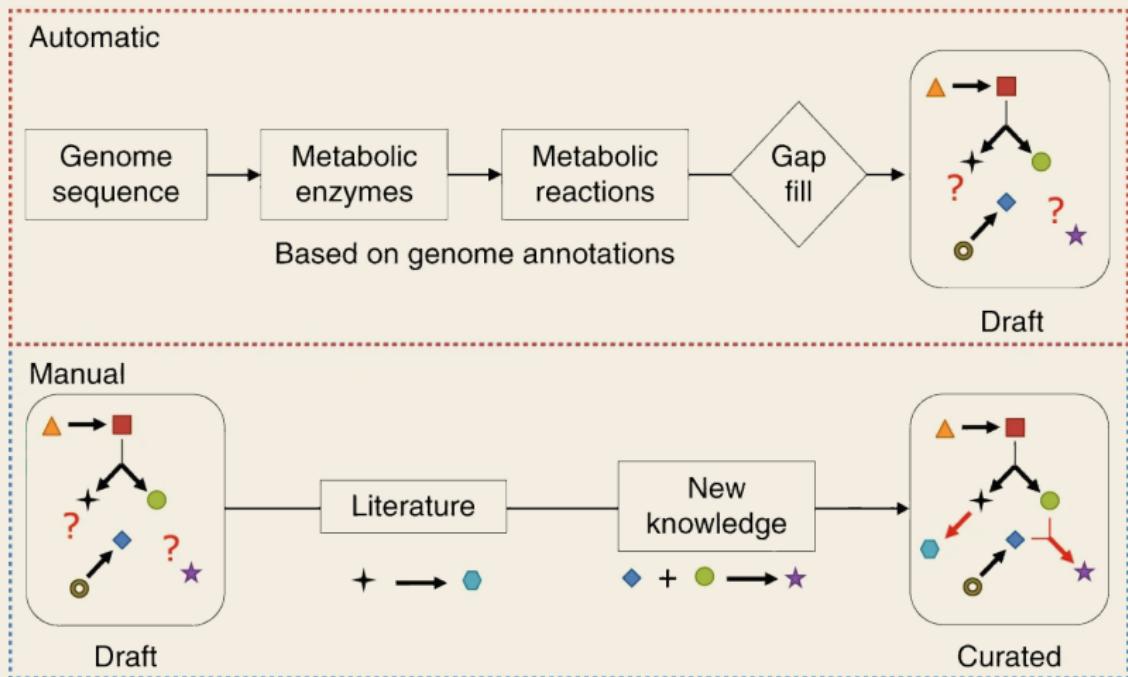


Figure from: Heirendt, Laurent, et al. Nature protocols 14.3 (2019): 639-702.

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 :

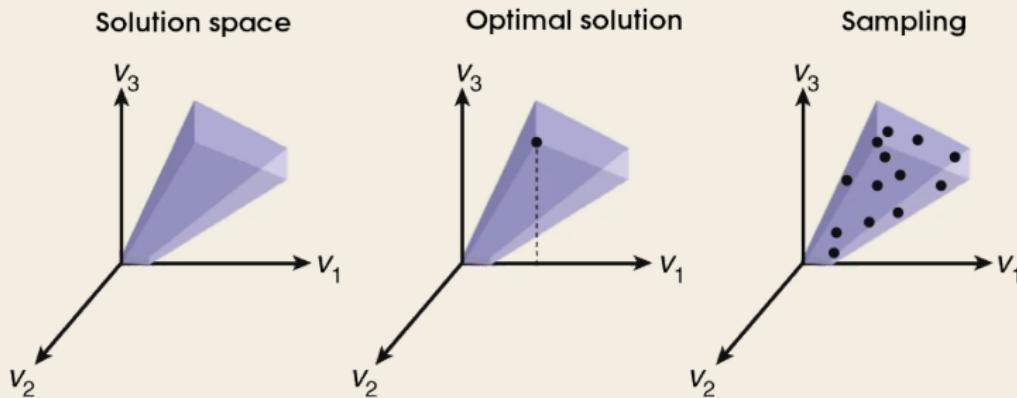
$$lb_i \leq v_i \leq ub_i$$

where lb : lower bound,
 ub : upper bound and

S: the stoichiometric matrix

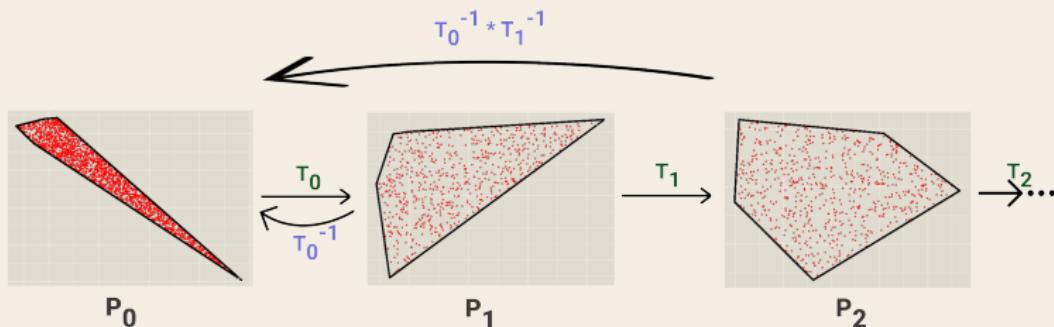
Flux sampling

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

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

Find possible targets against SARS-CoV-2

a flux sampling application

Bioinformatics, 36(26), 2020, i813–i821

doi: 10.1093/bioinformatics/btaa813

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Systems

FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2

Alina Renz^{1,2,*}, Lina Widerspick¹ and Andreas Dräger^{1,2,3,*}

¹Computational Systems Biology of Infections and Antimicrobial-Resistant Pathogens, Institute for Bioinformatics and Medical Informatics (IBMI) and ²Department of Computer Science, University of Tübingen, Tübingen 72076, Germany and ³German Center for Infection Research (DZIF), partner site Tübingen, Germany

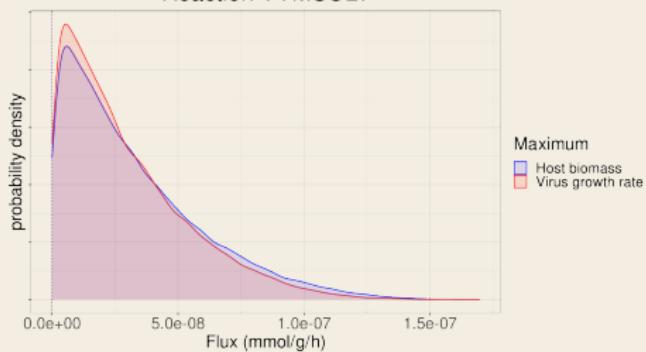
- Renz et al. '20 built the biomass function of Sars-Cov-2 to build a host - virus network
- Using FBA they computed an optimal steady state using
 - (i) human biomass maintenance,
 - (ii) virus growth rate
- They found reaction GK1 as a possible anti-viral target.

Find possible targets against SARS-CoV-2

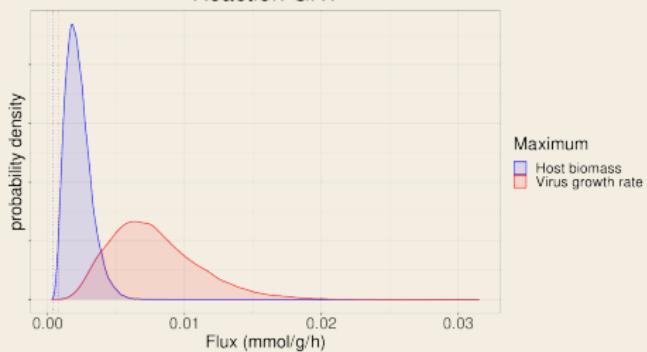
a flux sampling application



Reaction TYMSULT



Reaction GK1

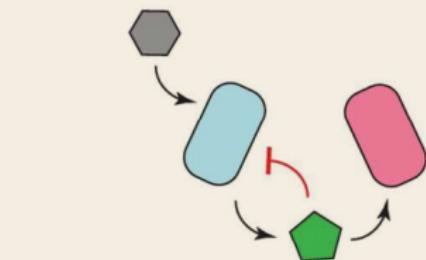


- Check if the flux distribution of a reaction changes.
- Find possible anti-viral targets and study further.

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 ?

dingo: a Python library for flux sampling



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

how to GColab notebook



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Publications

TeX, L^AT_EX, and Beamer

- [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 submission*
- [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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