

Zafeiropoulos Haris

Bioinformatics, Systems Biology, Microbial Ecology

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About Me

I am developing bioinformatics approaches to enhance the study of microbial communities and their backbone: microbial interactions. As a bioinformatician, I have developed tools covering a range of fields: from metagenomics sequencing analysis to random flux sampling. My main scientific interests focus on microbial interactions and especially metabolic ones. I am keen on the ways microbial communities are instructed from their environment and the effect that this structure has back to the environment. In my endeavors, metabolic modeling has been a rather useful arsenal!

Social Network

-  Github Profile
-  [haris.zaf2](#)
-  [@haris_zaf](#)

Languages

-  English ● ● ● ● ●
-  French ● ● ● ● ●

Research projects - working Experience

- 2022 - currently **3D'omics** Post-doc
Generate 3D omics landscapes, achieving reconstructions of intestinal host microbiota ecosystems.
- 2022 - 2022 **A workflow for marine Genomic Observatories data analysis** Research associate
Making the large volumes of data produced by genomic observatories more easily interpretable by providing the taxonomic inventories of each sample in a timely manner and in a non-technical format.
- 2018 - 2021 **PREGO: Process, environment, organism (PREGO)** PhD
PREGO is a systems-biology approach to elucidate ecosystem function at the microbial dimension.
- 2019 - present **ELIXIR-GR** technical support
ELIXIR-GR is the Greek National Node of the ESFRI European RI ELIXIR, a distributed e-Infrastructure aiming at the construction of a sustainable European infrastructure for biological information.
- 2018 - 2020 **RECONNECT** PhD
RECONNECT is an Interreg V-B "Balkan-Mediterranean 2014-2020" project. It aims to develop strategies for sustainable management of Marine Protected Areas (MPAs) and Natura 2000 sites.

Education

Graduate studies

- 2018 - 2022 **PhD in Bioinformatics** University of Crete, Biology department
Dissertation IMBBC - HCMR
Microbial communities through the lens of high throughput sequencing, data integration and metabolic networks analysis
- 2016 - 2018 **M.Sc. in Bioinformatics** University of Crete, School of Medicine
grade: 9.1/10.0
Master Thesis IMBBC - HCMR
eDNA metabarcoding for biodiversity assessment: Algorithm design and bioinformatics analysis pipeline implementation

Undergraduate studies

- 2011 - 2016 **B.Sc. in Biology** National & Kapodistrian University of Athens
grade: 6.2 / 10.0
Bachelor Thesis School of Science, department of Biology
Morphology, morphometry and anatomy of species of the genus *Pseudamnicola* in Greece

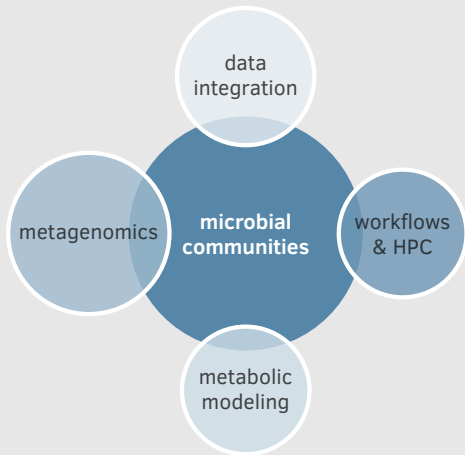
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Software

pema prego darn dingo
microbetag

Research fields



Memberships




Publications


- 2024 **dingo: a Python package for metabolic flux sampling**
Chalkis, A., Fisikopoulos, V., Tsigaridas, E. and Zafeiropoulos, H.
Bioinformatics Advances, DOI: 10.1093/bioadv/vbae037
- 2024 **Predicting microbial interactions with approaches based on flux balance analysis: an evaluation.**
Joseph, C., Zafeiropoulos, H., Bernaerts, K. and Faust, K.
BMC Bioinformatics, DOI: 10.1186/s12859-024-05651-7
- 2024 **Establishing the ELIXIR Microbiome Community**
Finn, R.D., Balech, B., Burgin, J., Zafeiropoulos, H., Willassen N.P., Pelletier E., Batut B and 18 more
F1000Research, DOI: 10.12688/f1000research.144515.1
- 2023 **metaGOflow: a workflow for the analysis of marine Genomic Observatories shotgun metagenomics data**
Zafeiropoulos, H., Beracochea, M., Ninidakis, S., Exter, K., Potirakis, A., De Moro, G., Richardson, L., Corre, E., Machado, J., Pafilis, E. and Kotoulas, G.
GigaScience, DOI: 10.1093/gigascience/giad078
- 2023 **A pile of pipelines: An overview of the bioinformatics software for metabarcoding data analyses.**
Hakimzadeh, A., Abdala Asbun, A., Zafeiropoulos, H., Anslan S. and 22 more
Molecular Ecology Resources, DOI: 10.1111/1755-0998.13847
- 2023 **Metabolic models of human gut microbiota: Advances and challenges.**
Garza, D.R., Gonze, D., Zafeiropoulos, H., Liu, B. and Faust, K.
Cell Systems, DOI: 10.1016/j.cels.2022.11.002
- 2022 **Deciphering the community structure and the functional potential of a hypersaline marsh microbial mat community.**
Pavloudi, C. and Zafeiropoulos, H.
FEMS Microbiology Ecology, DOI: 10.1093/femsec/fiac141
- 2022 **Automating the Curation Process of Historical Literature on Marine Biodiversity Using Text Mining: The DECO Workflow.**
Paragkamian, S., Sarafidou, G., Mavraki, D., Pavloudi, C., Beja, J., Eliezer, M., Lipizer, M., Boicenco, L., Vandepitte, L., Perez-Perez, R., Zafeiropoulos, H. and others
Frontiers in Marine Science, DOI: 10.3389/fmars.2022.940844
- 2022 **PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types**
Zafeiropoulos, H., Paragkamian, S., Ninidakis, S., Pavlopoulos, G., A., Jensen, L., J., Pafilis, E.
Microorganisms DOI: 10.3390/microorganisms10020293
- 2021 **The Dark mAtteR iNvestigator (DARN) tool: getting to know the known unknowns in COI amplicon data.**
Zafeiropoulos, H., Gargan, L., Hintikka, S., Pavloudi, C. & Carlsson, J.
Metabarcoding and Metagenomics, DOI:10.3897/mbmg.5.69657
- 2021 **0s & 1s in marine molecular research: a regional HPC perspective**
Zafeiropoulos, H., Gioti A., Ninidakis S., Potirakis A., ..., & Pafilis E.
GigaScience, DOI: 10.1093/gigascience/giab053


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Coding Skills


 Unix / Linux / AWK


 Python 3.0


 Matlab

 R


 C++


 HTML / CSS / JS

 Docker & Singularity


 REST API


Math and Stats


 Linear Algebra


 Constraint-based modelling

Barskills

 Microbial ecology

 Metabolic modeling

 Coding/programming

 Scientific writing

2021

Geometric Algorithms for Sampling the Flux Space of Metabolic Networks
Chalkis, A., Fisikopoulos, V., Tsigaridas, E. & Zafeiropoulos, H.
37th International Symposium on Computational Geometry (SoCG 2021), DOI: 10.4230/LIPIcs.SocG.2021.21

2021

The Santorini Volcanic Complex as a Valuable Source of Enzymes for Bioenergy
Polymenakou, P.N., Nomikou, P., Zafeiropoulos, H., Mandalakis, M., Anastasiou, T.I., Kiliass, S., Kyrpides, N.C., Kotoulas, G. & Magoulas, A.
Energies, DOI: 10.3390/en14051414

2020

PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS & COI marker genes
Zafeiropoulos, H., Viet, H.Q., Vasileiadou, K., Potirakis, A., Arvanitidis, C., Topalis, P., Pavloudi, C. & Pafilis, E
GigaScience, DOI:10.1093/gigascience/giaa022

2024

Improving genome-scale metabolic models of incomplete genomes with deep learning
Boer, M.D., Melkonian, C., Zafeiropoulos, H., Haas, A.F., Garza, D. and Dutilh, B.E.
under revision in *iScience*, *bioRxiv*

2024

microbetag: simplifying microbial network interpretation through annotation, enrichment tests & metabolic complementarity analysis
Zafeiropoulos, H., Delopoulos, E.I.M., Erega, A., Geirnaert, A., Morris, J. and Faust, K.
under review in *Microbiome*

2024

A long-term ecological research data set from the marine genetic monitoring programme ARMS-MBON 2018-2020
Daraghme, N., .. Zafeiropoulos, H... Pavloudi, C., and Matthias O.
under review in *Molecular Ecology Resources*

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Conferences

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|------|---|-------------|
| 2024 | Belgian Society for Microbiology: Annual Symposium @ Brussels, Belgium
<i>Poster presentation:</i> microbetag: simplifying microbial network interpretation through annotation, enrichment and metabolic complementarity analysis | BSM2024 |
| 2022 | 1st Applied HoloGenomics conference @ Bilbao, Spain
<i>Poster presentation:</i> microbetag: a microbial co-occurrence network annotator | AHC2022 |
| 2022 | 18th International Symposium on Microbial Ecology @ Laussane, Switzerland
<i>Poster presentation:</i> Reverse ecology and systems biology approaches to identify key processes ensuring life in extreme environments | ISME18 |
| 2021 | Bioinformatics Open Source Conference (BOSC) - online
<i>Flash talk:</i> dingo: A python library for metabolic networks sampling & analysis.) | BOSC2021 |
| 2021 | 1st DNAQUA International Conference - online
<i>Flash talk:</i> PEMA v2: addressing metabarcoding bioinformatics analysis challenges | DNAQUA |
| 2020 | Federation of European Microbiological Societies (FEMS) - online
<i>Flash talk:</i> Mining literature and -omics (meta)data to associate microorganisms, biological processes and environment types | FEMS2020 |
| 2020 | PyData Global - online
<i>Oral presentation:</i> Geometric and statistical methods in systems biology: the case of metabolic networks | PyData2020 |
| 2019 | network2019: 4th Symposium on Ecological Networks @ Paris, France
Participation. | network2019 |
| 2019 | 8th International Barcode of Life Conference @ Trondheim, Norway
<i>ePoster presentation:</i> P.E.M.A.: a Pipeline for Environmental DNA Metabarcoding Analysis | iBOL |
| 2018 | European Conference on Computational Biology (ECCB) 2018 @ Athens, Greece
<i>Poster presentation:</i> P.E.M.A.: a Pipeline for Environmental DNA Metabarcoding Analysis | ECCB18 |

Workshops & Summer schools

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|------|---|----------|
| 2023 | Economic Principles in Cell Physiology @ Paris, France
Mathematical modeling of cellular systems and “resource allocation thinking”. <i>Poster presentation:</i> “sampl’em all”: exploring potential flux sampling applications | EPCP2023 |
| 2022 | Microbial communities: current approaches and open challenges
Interdisciplinary exchanges in microbial communities’ research and the emerging challenge areas. | UMCW06 |
| 2022 | ELIXIR Fluxomics Training School 2021
An introduction to the field of fluxomics and the experimental and computational methods used to estimate and predict metabolic fluxes | ELIXFLUX |
| 2020 | Metagenomics, Metatranscript- omics and multi 'omics for microbial community studies
A Physalia Course from Prof. Dr. Curtis Huttenhower | material |

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Supervision

ongoing	Andrey Radev, MSc student @ Bioinformatics KU Leuven Visualisation and analysis of microbial growth data to facilitate interactions investigation and interactions' strength assessment	
ongoing	Anna Voukouna, MSc student @ Bioinformatics DUTH, Greece Investigation of microbial metabolic interactions potential across the Genome Taxonomy Database representative genomes	
ongoing	Sotiris Touloupoulos, Google Summer of Code 2024 with GeomScale org. Pre- and post-sampling features to leverage flux sampling at both the strain and the community level	post
2023-2024	Sofia Monsalve Duarte, MSc student @ Bioinformatics KU Leuven "Creation and implementation of a database interface for the collection and analysis of microbial growth data"	
2023	Ermis Ioannis Michail Delopoulos, Google Summer of Code 2023 with NRNB org. Development of a Cytoscape App for microbe-microbe association networks	post
2022-2024	Ermis Ioannis Michail Delopoulos, MSc student @ Bioinformatics KU Leuven "Development of a graphical user interface for microbetag"	
2022-2023	Julia Casado Gómez-Pallete, MSc student @ Bioinformatics KU Leuven "Development of a database for human gut bacterial growth curves"	thesis

Teaching

2024	Exploring the microbiome with high-throughput sequencing technologies: a bioinformatics perspective (part II) Lecture on MSc "Applied Bioinformatics & Data Analysis" in Democritus University of Thrace, Greece	slides
2024	Exploring the microbiome with high-throughput sequencing technologies: a bioinformatics perspective Lecture on MSc "Applied Bioinformatics & Data Analysis" in Democritus University of Thrace, Greece	slides
2023	eDNA metabarcoding, pipeline development & high performance computing Lecture on MSc "Applied Bioinformatics & Data Analysis" in Democritus University of Thrace, Greece	slides
2023	eDNA metabarcoding, pipeline development & high performance computing Lecture on MSc "Applied Bioinformatics & Data Analysis" in Democritus University of Thrace, Greece	slides
2022	Genome-scale model reconstruction Lectures on "Master en bioinformatique et modélisation" of the Université Libre de Bruxelles.	GColab notebook
2021	Microbiome Data Analyses Workshop Online Tutorial: PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S rRNA, ITS and COI marker genes.	MDAWO
2020	Environmental DNA & DNA metabarcoding Lecture on MSc "Environmental Biology" in University of Crete.	slides

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Awards

2021	Google Summer of Code Project title: <i>From DNA sequences to metabolic interactions: building a pipeline to extract key metabolic processes</i>	GSoC
2021	European Molecular Biology Organization Short-Term Fellowship Project title: <i>"Exploiting data integration, text-mining and computational geometry to enhance microbial interactions inference from co-occurrence networks"</i>	EMBO
2020	Federation of European Microbiological Societies Meeting Attendance Grant for joining the <i>"Metagenomics, Metatranscript- omics and multi 'omics for microbial community studies"</i> Physalia course	FEMS
2019	Short Term Scientific Mission (STSM) @ DNAqua-net COST action Project title <i>A comparison of bioinformatic pipelines and sampling techniques to enable benchmarking of DNA metabarcoding</i> . Report.	DNAqua-net
2018	Best Poster Award @ Hellenic Bioinformatics conference for <i>PEMA: a Pipeline for Environmental DNA Metabarcoding Analysis</i>	HBIO

References

Karoline Faust	Department of Microbiology, Immunology and Transplantation, Rega Institute for Medical Research, Laboratory of Molecular Bacteriology, KU Leuven Leuven, 3000, Leuven, Belgium ☎: +3216322698 ✉: karoline.faust@kuleuven.be
Pafilis Evangelos	Institute of Marine Biology, Biotechnology & Aquaculture, Hellenic Centre for Marine Research, (IMBBC - HCMR), Gournes, Pediados, P.O. Box 2214, Heraklion Crete 71003, Greece ☎: +30 2810 337740 ✉: pafilis@hcmr.gr
Elias Tsigaridas	Institut de Mathématiques de Jussieu - Paris Rive Gauche, Sorbonne Université - Campus Pierre et Marie Curie, Case courrier 247, 4, place Jussieu, 75252, Paris Cedex 05, France ☎: +33 014427 8539 ✉: elias.tsigaridas@inria.fr
Georgios Kotoulas	Institute of Marine Biology, Biotechnology & Aquaculture, Hellenic Centre for Marine Research, (IMBBC - HCMR) Gournes, Pediados, P.O. Box 2214, Heraklion Crete 71003, Greece ☎: +30 2810 337740 ✉: kotoulas@hcmr.gr