



U. PORTO
FC
FACULDADE DE CIÊNCIAS
UNIVERSIDADE DO PORTO

Sponsorship



BIOPORTUGAL S.A.
Químico, Farmacêutica

Meta_Microbial Workshop

Metagenomic and bioinformatic insights into
microbial communities

Main Goal

*Provide an **overview** of current tools to analyse next-generation sequence data and to make **insightful interpretation** towards the fields of microbial ecology and environmental microbiology.*

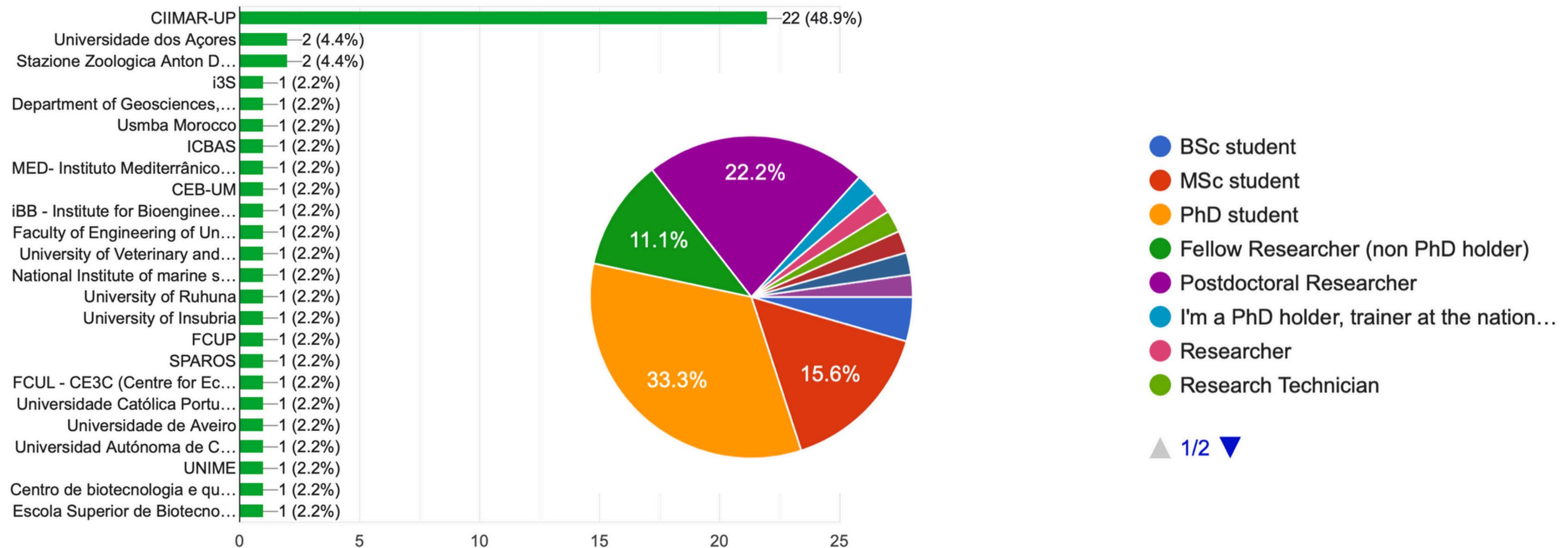
- **Overview of different tools**, not super in-depth of a single tool
- Theoretical with a bit of “hands-on”, mostly in the 3rd day
- Targeted (Metabarcoding) and Untargeted Metagenomics (DNA, not RNA)
- Concept-focused (not immediately applicable) - not “recipe-based” - as always, critical thinking needed for further analyses. And TIME! Dedicated time has a 2-fold outcome: 1 - learning, and 2 - getting to know your data.
- Applicable to a wide-range of research questions (even though intrinsically biased)
- Motivation: increased need from “non-microbial” fields

Practical Info

- Second Edition (apologies for uncertainties, program adjustments, etc.)
- Wi-fi networks
 - **eduroam** (your own credentials)
 - **wifi_eventos** (**username:** sc.wifi.3@fc.up.pt, **password:** [METAbio2024](#)).
- Lunch provided at the Multirest restaurant (building next to this one)
- Breaks during the day and coffee-breaks in the end of each day (with coffee, water, juice, and cookies provided)
- Please feel free to ask questions during presentations (interrupt and discuss)
- Survey will be sent at the end of the workshop (please respond so that we can improve future workshops)

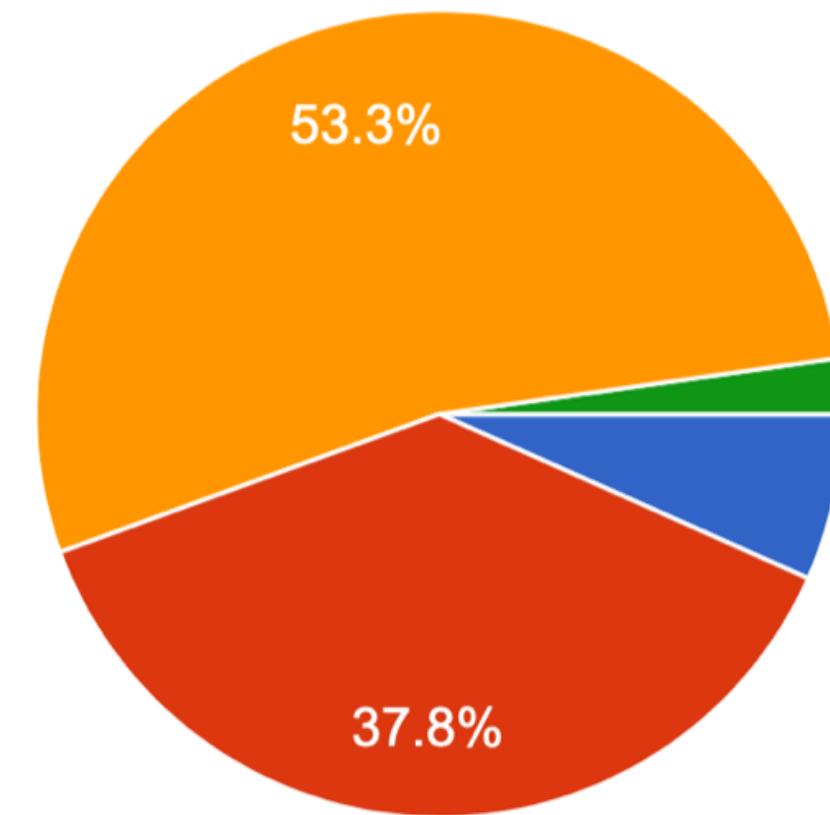
Introductory notes

45 participants registered
(24 institutions, 5 international)



Introductory notes

45 participants registered
(90% without or only some experience with bioinformatic tools to investigate microbial communities)



- Yes. I'm a proficient user of bioinformatic tools to analyse microbial communities.
- Yes. I occasionally use bioinformatic tools to analyse microbial communities.
- No. I have no previous experience with next-gen sequencing analysis of microbial communities.
- I have used it once for 16S amplicon sequencing analysis only

Intros/Theory and amplicon-based

Time	Agenda item
09:15 - 09:30h	Participants registration
09:30 - 09:45h	Welcome session and program overview - All instructors
09:45 - 10:15h	Next-generation sequencing technologies and data generation (MS) - Short Lecture
10:15 – 10:45h	Sampling protocols and standardization (CM + FP) - Short Lecture
10:45 - 11:00h	Break
11:00 - 12:00h	R tools for microbial ecology studies (FP) - Lecture and brief practical examples
12:00 - 13:00h	Python in microbial ecology studies (NG) - Lecture and brief practical examples
13:00 - 14:00h	Lunch
14:00 - 16:00h	Metabarcoding (amplicon sequencing) analysis workflow (FP + MS) - Lecture and brief practical examples (<i>dada2</i> , <i>phyloseq</i> , <i>vegan</i> , <i>picrust2</i> , ...) - 16S rRNA gene reads processing (short and long reads) - Ecological analysis (alpha- and beta- diversity)
16:00 – 17:00h	Coffee and Posters Session

- ← The working object and historical context
- ← Obtaining the working object
- ← Programming tools
- ← Metabarcoding: theoretical concepts, foundations, workflow description, potential outputs and interpretations

Intros/Theory and shotgun-based

Time	Agenda item	
09:30 – 10:15h	Exploring Online Resources and Repositories I (CM) - Practical example (<i>Silva NGS</i>)	User-friendly resources (metabarcoding)
10:15 – 11:00h	Insights on data visualization and analysis (FP) - Lecture and brief practical examples	Good-practice recommendations and discussions about data visualisation and analysis.
11:00 - 11:15h	Break	
11:15 - 13:00h	Metagenomics (shotgun sequencing) analysis workflow (AR + MS) - Lecture and brief practical examples - Raw reads processing (<i>trimmomatic</i> , <i>megahit</i> , <i>concoct</i> , ...) - Taxa and functional annotation (<i>bowtie2</i> , <i>prokka</i> , <i>GTDB</i> , ...)	Metagenomics: theoretical concepts, foundations, workflow description, potential outputs and interpretations
13:00 - 14:00h	Lunch	
14:00 - 14:45h	Phylogenetic trees from high-throughput sequence data (AR) - Lecture and practical example (<i>iTOL</i>)	Phylogenetic trees from hundreds/thousands of sequences - computation and visualisation
14:45 – 15:30	Exploring Online Resources and Repositories II (MS) - Lecture and practical examples (<i>IMG</i> , <i>MG-RAST</i> , <i>KBase</i> , <i>MGNify</i>)	User-friendly resources (metagenomics)
15:30 - 16:15h	Alternative statistical and data analyses (MS) - Lecture and practical examples (AIC, Networks, etc.)	Examples of analyses that won't be performed in the hands-on sessions but may be useful for your research.
16:15 - 17:00h	Coffee and Posters Session	

Hands-on

Two parallel sessions (Metabarcoding and Metagenomics)

Pick your poison

Day 3 - September 6th, 2024

Time	Agenda item
Two parallel “hands-on” sessions (metabarcoding and metagenomics)	
Metabarcoding (09:30 - 17:00h, Room 011)	From raw data to community structure insights (FP + MS) - Raw read processing in R. Data cleaning and normalization. Ecological and compositional analysis. Questions, discussions, etc.
Metagenomics (09:30 - 17:00h, Room 012)	From raw data to taxonomic and functional insights (AR + NG) - Raw read processing in Python. Data cleaning and normalization. Taxonomic and functional annotation. Questions, discussions, etc.
17:00h	Farewell with Port Wine (Cheers!)

R + RStudio
(virtual machine)

Python
(remote server +
terminal)

Catarina Magalhães



I teach at the Faculty of Sciences, University of Porto, in the Biology undergraduate and master's programs. I am also a researcher at CIIMAR, working within the Microbiome Ecology and Biogeochemistry research team.

My research focuses on Microbial Ecology and Biogeochemistry, with an emphasis on understanding how climate change and human disturbances influence microbiome diversity and its essential functions.

I am currently a member of the coordination committee of PROPOLAR and a delegate of the IASC Marine Working Group. Through these roles, we are actively engaged in Polar research and international microbiome monitoring efforts using metabarcoding and metagenomic approaches.

Within the Meta-Microbial WS, I will share my experience and data on marine microbiome sampling protocols. I will also demonstrate how to use the SILVA-NGS platform to quickly analyze and share metabarcoding datasets generated from NGS technology.

Miguel Semedo



Education

- PhD in Marine Sciences (2019) from Virginia Institute of Marine Science (VIMS)
- BSc and MSc in Biochemistry (2009) from FCUP

Research

- Junior Researcher at CIIMAR since 2020
 - Microbial Ecology
 - Nitrogen Cycle
 - Environmental Toxicology
 - Anthropogenic Microbial World (impacts of human activities on the microbial realm - currently in the deep-sea)

Adriana Rego



Education

- PhD in Biomedical Sciences (2023), ICBAS, University of Porto
- BSc in Biology (2015) and MSc in Cellular and Molecular Biology (2017) from FCUP, University of Porto

Research

- Junior Researcher at CIIMAR since 2023
 - Microbial and chemical ecology
 - Bioprospection - diversity and distribution of biosynthetic gene clusters across the environment
 - Microbiome composition of environmental cyanobacterial biofilms

Francisco Pascoal



Education

- PhD candidate in Biology at Faculdade de Ciências and CIIMAR, Universidade do Porto.
- Masters degree in Microbiology at Instituto Superior Técnico;
- Bachelor in Cell and Molecular Biology at NOVA University.

Research

- Microbial Rare Biosphere;
- Data science applications to microbial ecology;
- Author of ulrb R package.



Nicola Gambardella



- **Bachelor's degree** in Molecular Biology, University of Padova
- **Master's degree** in Molecular Biology and Bioinformatics, University of Padova.
- Master's **thesis** on comparing different computational methods for the study of microbial community in the arctic.
- Currently **research assistant** at CIIMAR
 - studying microbial communities in permafrost environments, with a focus on microorganisms involved in mercury.
- Starting soon a **PhD** funded by "LaCaixa" INPhINIT fellowship program about the *identification and characterization of prokaryotic players involved in N and Hg cycling in permafrost*.

Leandro de Mattos Pereira



Currently, Junior Researcher on the BBF4 project in the Cyanobacterial Natural Products team (Leão Laboratory), CIIMAR

Education

- PhD in Computational and Systems Biology (2014), Oswaldo Cruz Institute, Fiocruz RJ. Concentration Area: Functional Genomics, Evolution and Phylogenomics.
- MSc in Biosciences and Biotechnology (2009) from Fluminense State University (UENF), Rio de Janeiro, Brazil.
- Bachelor in Biological Science - Biotechnology - UENF.

Research

- AI Applied in the Analysis of Proteins Sequences.
- Functional annotation, Comparative Genomics and Phylogenomics.
- Microbiome, Metabarcoding and Environmental Metagenomics.
- Functional genomics.

CIIMAR's PhD Students Committee



**Leonor
Pizarro**



**Rúben
Pereira**



- The PhD Students Committee was established in 2019 to serve as a representative body for all PhD students affiliated with CIIMAR
- The Committee organizes regularly a diverse range of activities, from which the annual Blue Think Conference stands out as the committee's flagship and largest event

Participants introduction