

XIII EDITION BIOINFORMATICS OPEN DAYS

CONFERENCE BOOK

UNIVERSITY OF MINHO

GUALTAR CAMPUS

MARCH 14, 15 AND 16TH,

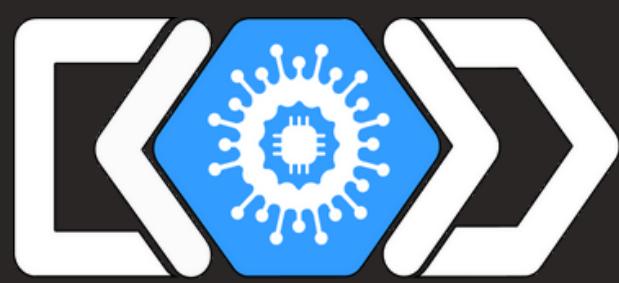
2024



Bioinformatics Open Days



[/bioinformaticsopendays](http://bioinformaticsopendays)



Bioinformatics Open Days 2024

WELCOME MESSAGE

Greetings,

It is with great pleasure that we welcome you all to the XIII Edition of the Bioinformatics Open Days! This student-led initiative has been promoting knowledge exchange among students, teachers, and researchers in the Bioinformatics and Computational Biology fields since 2012, and this year's event promises to be as exciting as ever. The scope of the main scientific sessions and keynote lectures cover a range of topics that include Cell Level Simulations and Digital Twins, The Role of Knowledge in Artificial Intelligence for Scientific Discovery, Understanding the functional potential of microbial communities, and Computational design of tailor-made of antiviral biopharmaceuticals.

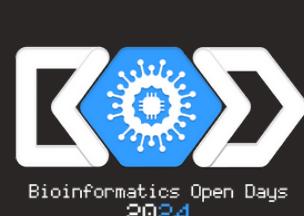
In addition to these stimulating talks, we have planned three workshops with different applications and backgrounds, as well as innovative oral and poster communications. Furthermore, we are also including a discussion on the reality of the corporate world, which will provide participants with valuable insights and guidance on starting their professional life in Bioinformatics.

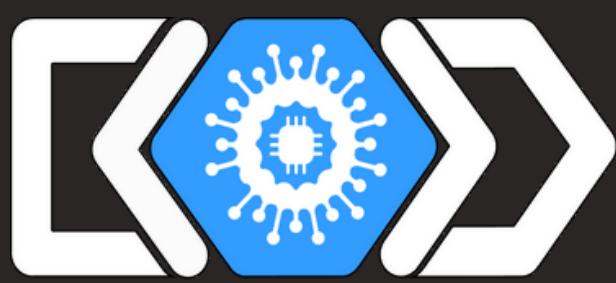
We are thrilled to be a platform for knowledge sharing and community building within the Bioinformatics field. We hope that this year's event will provide a great experience for everyone and help advance the future of Bioinformatics, both nationally and internationally.

Thank you for your participation and enthusiasm, and we look forward to seeing you at the XIII Edition of the Bioinformatics Open Days.

Kind regards,

The Organizing Committee of BOD 2024.





Bioinformatics Open Days 2024

THE ORGANIZING COMMITTEE



MIGUEL ROCHA
General Chair



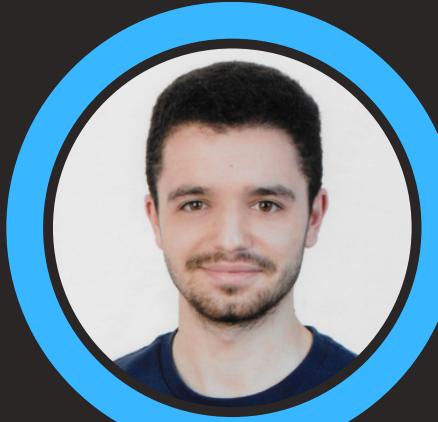
GONÇALO APOLINÁRIO
President



BRUNO SÁ
Vice-President
Students meeting



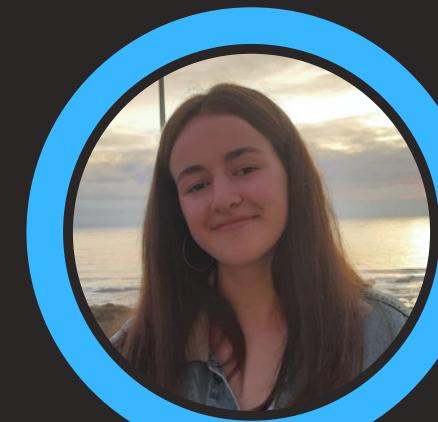
TIAGO SILVA
Finances



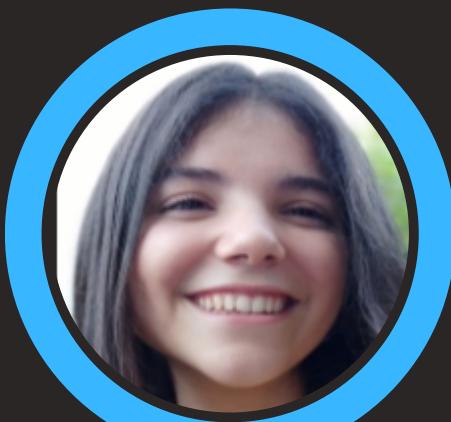
PAULO SEIXAL
Scientific Program



RUBEN FERNANDES
Scientific Program



JOANA ARAÚJO
Logistics



MARIANA BRAGA
Logistics



JOANA GONÇALVES
Logistics



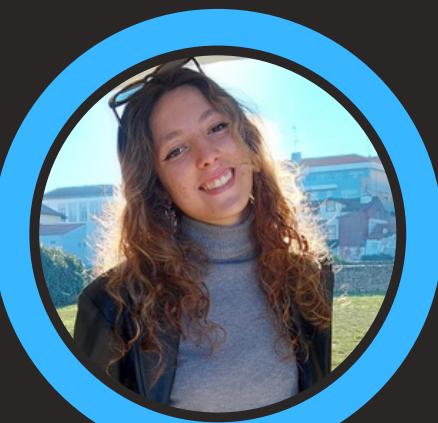
GUILHERME SOUSA
Students meeting



LUÍS FERREIRA
Students meeting



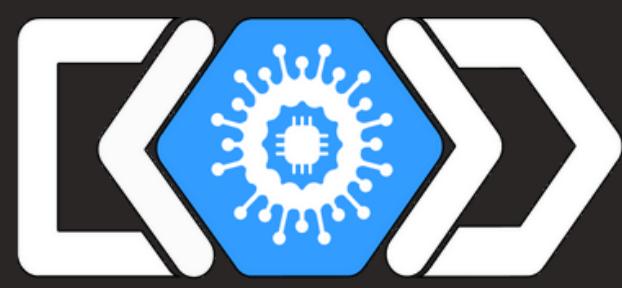
BRUNA ALMEIDA
Event Promotion



ANA LISBOA
Event Promotion



JOSÉ LEMOS
Event Promotion



Bioinformatics Open Days 2024

THE ORGANIZING COMMITTEE



DUARTE VELHO



SAMUEL BAPTISTA



DIOGO ESTEVES

Logistics

Logistics

Logistics



RICARDO OLIVEIRA



BEATRIZ SANTOS



CARLOS GOMES

Logistics

Logistics

Logistics



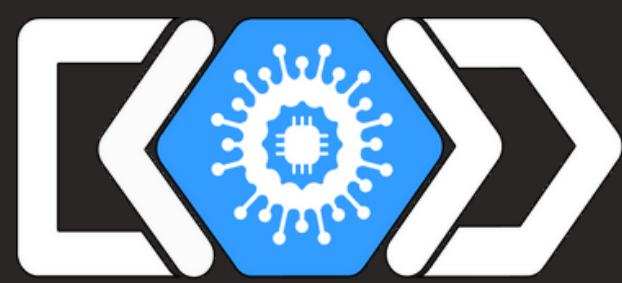
JOÃO FERREIRA

Logistics



IAN ALVES

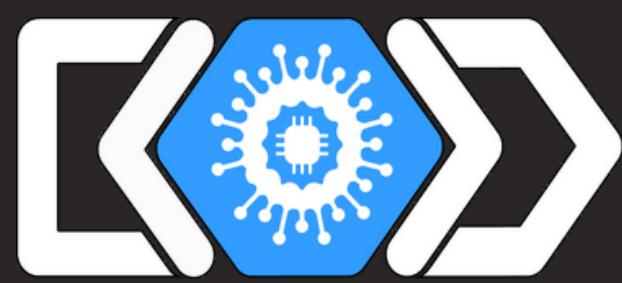
Logistics



Bioinformatics Open Days 2024

CONTENTS

Program	1
Scientific Sessions and Keynote Lectures	6
Scientific Submissions	11
Network Session	13
Workshops	14
Sponsors and Collaborators	17



Bioinformatics Open Days 2024

PROGRAM

MARCH 14TH - THURSDAY

09:30 H **Opening session**

Keynote Lecture

- Cell Level Simulations and Digital Twins

10:00 H **Alfonso Valencia**

10:45 H **Coffee Break**

Keynote Lecture

- The Role of Knowledge in Artificial Intelligence for Scientific Discovery

11:00 H **Cátia Pesquita**

Round Table

Bioinformatics in Portugal and Spain - the present and future perspectives

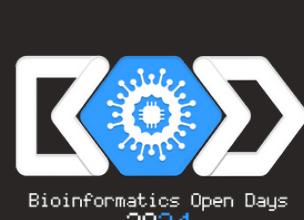
12:00 H **Chaired by Inês Chaves**
Alfonso Valencia, Cátia Pesquita

12:45 H **Lunch**

Keynote Lecture

- Understanding the functional potential of microbial communities

14:00 H **Robert Finn**



/bioinformaticsopendays



Bioinformatics Open Days 2024

PROGRAM

MARCH 14TH - THURSDAY

Oral Communications [Session 1]

Get to know MIMt! A new, smaller and curated 16S rRNA reference database with less redundancy and higher accuracy at species-level identification - **M. Pilar Cabezas**

14:45 H Prediction of novel small RNAs from *Pseudomonas aeruginosa* - **Vânia Pobre**

Finding novel genes coding for eco-friendly surfactants from hypersaline Iberian locations using metagenomic approaches - **Cátia Santos Pereira**

Individual-based modelling elucidates about the role of nanomaterials on methane production - **João Sequeira**

Poster Highlights [Session 1]

15:45 H

Submission n°. 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 and 24.
*The respective submissions can be checked in the Annex "Scientific Submissions".

16:00 H

Poster Session 1 & Coffee Break

Oral Communications [Session 2]

An Automated Structure-Based Platform for Gene Discovery and Enzyme Engineering - **João Correia**

16:45 H

Computationally-designed miniproteins showing neutralization activity against SARS-CoV-2 - **Pedro Moreira**

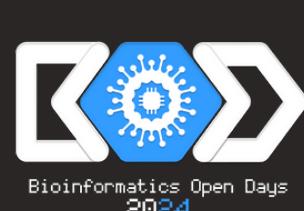
Deep Learning on Chaos Game Representation for Resistome - **Javier Montoya**

Modeling deep neural network architectures to improve schizophrenia predictability using genotype data - **Daniel Martins**

20:00 H

Social Dinner and post-dinner activities

@ Taberna do Migaitas, Braga



Bioinformatics Open Days
2024



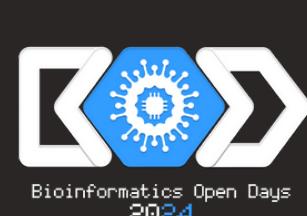


Bioinformatics Open Days 2024

PROGRAM

MARCH 15TH - FRIDAY

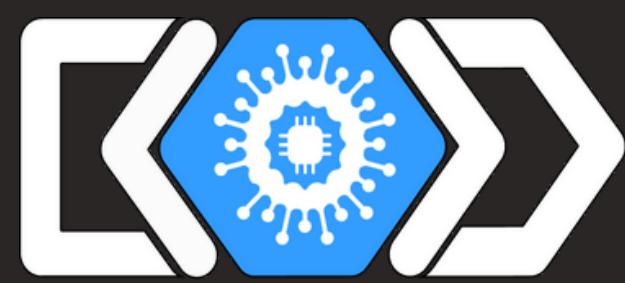
09:30 H	Keynote Lecture • Computational design of tailor-made of antiviral biopharmaceuticals Diana Lousa
10:15 H	Poster Highlights [Session 2 - software] Submission nº. 25, 26, 27, 28, 29 ,30, 31. *The respective submissions can be checked in the Annex "Scientific Submissions"
10:30 H	Poster Session 2 (software) & coffee break
	Oral Communications [Session 3] A network science approach to interpret multidimensional associations between human transcriptome, tissues and traits - Darmit Kumar
11:15 H	The Portuguese Variome from over 12,000 Exomes: Streamlining Clinical Diagnostics and Translational Research - Mariana Ribeiro Runs of homozygosity: bioinformatic approaches for diagnostic purposes and population analysis in 12,000 exomes - Susana Valente
	Sequence to graph alignment based copy number calling using a flow network formulation - Hugo Magalhães
	Plugging the holes: an intuitive software tool for reproducibility in Molecular Biology - Patrícia Fernandes
12:30 H	Lunch
	Session with companies
14:00 H	Silico Life, OmnimAI, Accenture and iLoF



Bioinformatics Open Days
2024



/bioinformaticsopendays



Bioinformatics
Open Days 2024

PROGRAM

MARCH 15TH - FRIDAY

15:00 H Job fair and coffee break

16:00 H Closing Session

17:00 H Social Activities: Quizz
@ Carpe Noctem, Braga

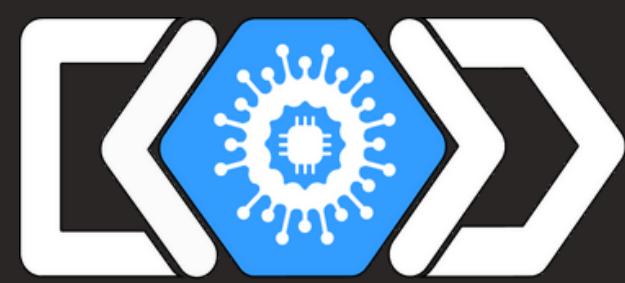
19:00 H Social Activities: BBQ
@ Carpe Noctem, Braga



Bioinformatics Open Days
2024



/bioinformaticsopendays



Bioinformatics
Open Days 2024

PROGRAM

MARCH 16TH - SATURDAY

Workshops

Introduction to RNA-Seq data analysis

- Vânia Pobre

09:30 H

Tools and computational resources for the life sciences

- Gil Poiares-Oliveira

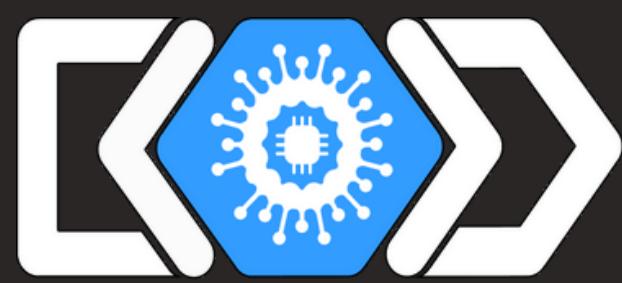
Introduction to Computational Protein Design Tools

- Pedro Moreira
-



Bioinformatics Open Days
2024





SCIENTIFIC SESSIONS AND KEYNOTE LECTURES

Cell Level Simulations and Digital Twins

In this presentation, I will address the area of simulations of cell behaviour that include molecular networks, pathways and cellular interactions, covering the space between atomistic simulations, based on Molecular Dynamics and system level simulations of organs, based on fluid dynamics equations.

PerMedCoE (HPC/Exascale Centre of Excellence in Personalised Medicine, has developed a framework (PhysiBoSS) that combines agent based simulations of cell interactions in the context of a given environment (PhysiCell) with Boolean simulations of biological pathways (MaBoSS, probabilistic Boolean framework) implemented in each cell.

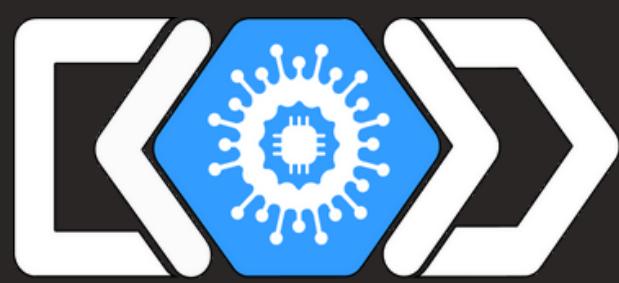
We have tested the capacity of these models to use as input genomic information, from bulk to single cell data, to provide mechanistic molecular models and testable hypothesis on different biomedical scenarios. Use cases include simulations of COVID infection on layers of epithelial cells or the simulations of temporal evolution of tumours and their micro-environments in response to genomic alterations or drug treatments.

In the final part, I will discuss the possible avenues for the integration of cell level simulations in the context of larger systems including digital twins of human organs and the potential application in areas of personalised medicine and preclinical trials.



Alfonso Valencia

Computational biologist, pioneer scientist applying computer science to solve biological problems, recognized as leader in his field. Focused on the analysis of large collections of genomic data, especially protein interaction networks applied to (epi)Genomics, Cancer Biology and Precision Medicine, his group train the application of Natural Language technology to the biomedical domain. He earned a PhD in Biochemistry and Molecular Biology (UAM) plus a PostDoctoral researcher in Bioinformatics (EMBL Heid). Prof. at ICREA, Scientific Director and Director's of Life Sciences in BSC-CNS. Head of the Spanish node of the European Infrastructure for Life-Science Information, ELIXIR. Founding member and former President of the ISCB. Elected member of the European Molecular Biology Organization (EMBO). Executive Editor of "Bioinformatics" OUP, Section Editor of Mol Oncol. Editor FEBS Letters, Prof. Honoris Causa by the Danish Technical University.



SCIENTIFIC SESSIONS AND KEYNOTE LECTURES

The Role of Knowledge in Artificial Intelligence for Scientific Discovery

Artificial intelligence (AI) is increasingly pervasive in scientific research, creating the need for a deeper understanding of the broader implications of its use, both in terms of scientific validity, utility and societal impact.

In recent years, deep learning and generative AI techniques have been game-changers in many high-impact scientific challenges, exploring the large volumes of data produced in the last decades by high-throughput techniques. These data-hungry models ignore centuries of accumulated scientific knowledge and open the question: do we really need to stand on the shoulders of giants to see farther?

In this talk, I will discuss how incorporating scientific knowledge into AI for scientific discovery can tackle challenges along the scientific pipeline, from data collection to explainability as an epistemic tool, based on examples from our work in AI for the life sciences.



Cátia Pesquita

Cátia Pesquita is an Associate Professor in Computer Science at the Department of Informatics of the Faculty of Sciences of the University of Lisbon and a senior researcher at LASIGE where she leads the Health and Biomedical Informatics Research Line.

She has a multidisciplinary background in Biology and Computer Science, and together with her research group, LiSeDa Lab, she does research at the intersection between Artificial Intelligence and Data Science, focusing on applications in the life and health sciences. She is also vice-president of the Biodata.pt association devoted to the valorisation of the biological data generated by Portuguese Science, and is involved in activities to promote computer science career paths to young women.

Her research areas include Semantic Web, Biomedical Ontologies, Knowledge Graphs, Ontology Matching, Semantic Similarity, Explainable Artificial Intelligence.



Bioinformatics Open Days 2024

SCIENTIFIC SESSIONS AND KEYNOTE LECTURES

Bioinformatics in Portugal and Spain - the present and future perspectives

Join us for a discussion on the current status and future outlook of bioinformatics in Portugal and Spain. Featuring experts Cátia Pesquita from Portugal and Alfonso Valencia from Spain, moderated by Inês Chaves. Gain insights into the cutting-edge advancements and collaborative initiatives shaping the bioinformatics landscape in these two countries.



Cátia Pesquita

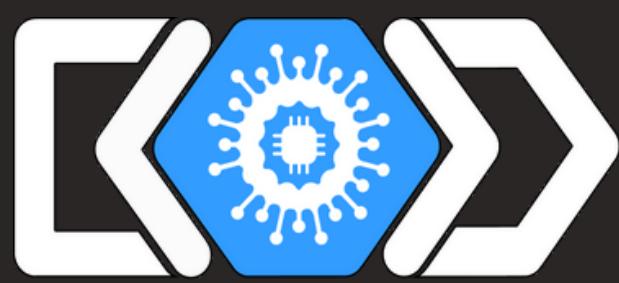


Alfonso Valencia



Inês Chaves

Inês is a Researcher in Plant Biochemistry area. She is studying the ability of plants to adapt and resist and she wants to unveil the molecular processes behind this. She is working in the genome of cork oak tree, and in the plant microorganism interactions. To her the thematic of data sharing and knowledge exchange has become more and more important and so she is working in the development of the National and European Bioinformatics Infrastructure envisioning the open data and science. Moreover, she is collaborating in the development of controlled vocabulary (e.g. Crop Ontology) and standards (MIAPPE).



Bioinformatics Open Days 2024

SCIENTIFIC SESSIONS AND KEYNOTE LECTURES

Understanding the functional potential of microbial communities

The field of metagenomics has expanded rapidly over the past decade, both in terms of the number and diversity of different datasets, and the volume of biological insight that can be gleaned from the sequence data. One area of significant growth has been the assembly of data sets, and the subsequent elucidation of genomes, so called metagenome assembled genomes (MAGs). Here, I will present the methods we have developed to start to understand all parts of the microbial kingdom, from virus to prokaryotes to eukaryotes. This has provided unprecedented insights into the coding potential of microbiomes from a diverse range of environments. Of particular note, the metagenomic assemblies facilitate deeper insights into the metabolic functions encoded, and which microbes are producing them. For example, biosynthetic gene clusters (BGCs) encode the genes necessary for natural products such as antimicrobials and signalling molecules that can play major roles in various ecological processes. Many of these natural products have also been exploited for industrial biotechnology or pharmaceutical applications. I will present our efforts on the accurate identification of BGCs in (meta)genomic data, which has unveiled a large treasure trove of new BGCs in metagenomic assemblies. I will also cover some of the technologies we have used to ensure the reproducibility of our pipelines and lessons learned.

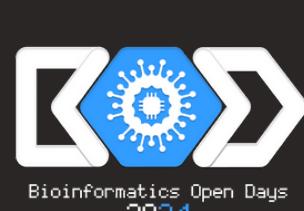


Robert Finn

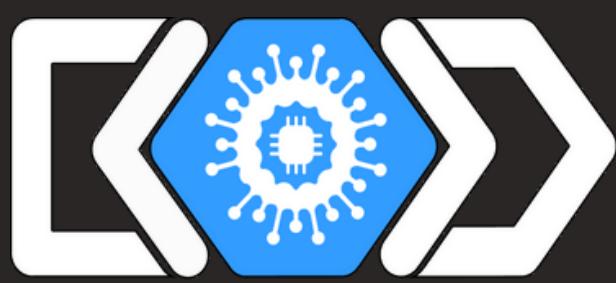
Dr Rob Finn leads EMBL-EBI's Sequence Families team, which is responsible for the InterPro, Pfam, Rfam and RNACentral data resources. The team also looks after EMBL-EBI's fast-growing Metagenomics data service.

Rob joined EMBL-EBI from the Janelia Research Campus in the US, where he led a group that designed fast, web-based, interactive protein-sequence searches and annotations. Between 2001 and 2010, he was the project leader for Pfam at the Wellcome Trust Sanger Institute in the UK.

Rob's academic background is in microbiology and he holds a PhD in biochemistry from Imperial College, London.



Bioinformatics Open Days
2024



SCIENTIFIC SESSIONS AND KEYNOTE LECTURES

Computational design of tailor-made antiviral biopharmaceuticals

The recent COVID-19 pandemic has highlighted the devastating consequences of unpreparedness for such events, not only on public health but also on social and economic levels. As it is not possible to accurately predict which virus(es) will cause the next pandemic(s), it is of utmost importance to find new solutions that allow the effective targeting of a broad range of viruses and have easy and cost-effective discovery, development, production and validation process trajectories.

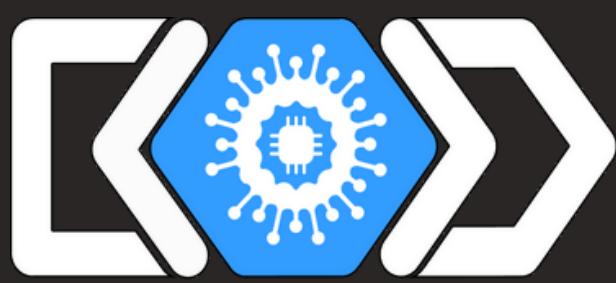
Within the scope of the BioPlaTTAR project, we have built an integrated platform for biopharmaceutical development, to quickly and efficiently respond to viral threats in a streamlined pipeline, ranging from rational design to in vivo validation. This pipeline starts from the computational design of a diverse set of protein leads that block targets on the viral surface; then takes these designs, produces them in a high-throughput expression platform, and selects top leads after several rounds of physical-chemical characterization and in vitro and in vivo validation of activity. This pipeline has been validated in three consecutive rounds of design and experimental evaluation leading to the development of several miniproteins that bind to the SARS-CoV-2 receptor binding domain with high affinity (in the low nm range) and were shown to neutralize this virus in high-throughput neutralization assays using ACE2-expressing cells. The combination of artificial intelligence and physics based modelling methods, as well as the close integration of computational and experimental data have been key factors for the consecutive improvement of this platform.



Diana Lousa

Diana Lousa [F] is currently a Researcher at the Protein Modelling Lab, ITQB NOVA. She obtained her PhD in Biochemistry, with a specialization in Computational Biology in 2013. The main goal of her current research focuses on the application of computational biophysics to develop tailor-made biopharmaceuticals against viral pathogens, such as influenza, zika, HIV and SARS-CoV-2. She is the co-coordinator of the projects EvaMobs funded by Horizon Europe (HORIZON-HLTH-2023-DISEASE-03-04) and BioPlaTTAR funded by the La Caixa Foundation (HR22-00722).

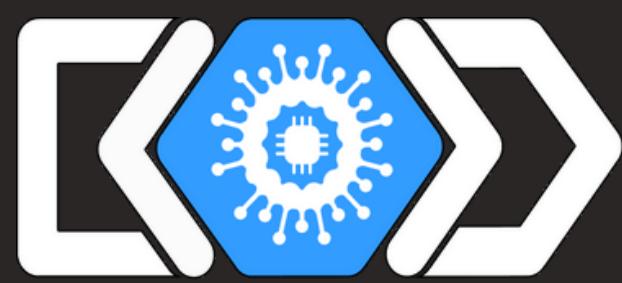
She has been a member of the executive committee of the ITQB NOVA Postdoctoral Association and has organized/is organizing several scientific meetings, including the 2022 FEBS Young Scientists Forum. She is the assistant-coordinator of the Master in Computational Biology and Bioinformatics of the NOVA University.



Bioinformatics Open Days 2024

SCIENTIFIC SUBMISSIONS

Nº	Authors	Title	Accept as
1	M. Pilar Cabezas et al.	Get to know MiMt! A new, smaller and curated 16S rRNA reference database with less redundancy and higher accuracy at species-level identification	Oral
2	Joana Silva et al.	Prediction of novel small RNAs from <i>Pseudomonas aeruginosa</i>	Oral
3	Cátia Santos-Pereira et al.	Finding novel genes coding for eco-friendly surfactants from hypersaline Iberian locations using metagenomic approaches	Oral
4	João C. Sequeira et al.	Individual-based modelling elucidates about the role of nanomaterials on methane production	Oral
5	João Correia et al.	An Automated Structure-Based Platform for Gene Discovery and Enzyme Engineering	Oral
6	Pedro Moreira et al.	Computationally-designed miniproteins showing neutralization activity against SARS-CoV-2	Oral
7	Javier Montoya et al.	Deep Learning on Chaos Game Representation for Resistome	Oral
8	Daniel Martins et al.	Modeling deep neural network architectures to improve schizophrenia predictability using genotype data	Oral
9	Darmit Kumar et al.	A network science approach to interpret multidimensional associations between human transcriptome, tissues and traits	Oral
10	Mariana Ribeiro et al.	The Portuguese Variome from over 12,000 Exomes: Streamlining Clinical Diagnostics and Translational Research	Oral
11	Susana Valente et al.	Runs of homozygosity: bioinformatic approaches for diagnostic purposes and population analysis in 12,000 exomes	Oral
12	Hugo Magalhães et al.	Sequence to graph alignment based copy number calling using a flow network formulation	Oral
13	Patrícia Ataíde et al.	Plugging the holes: an intuitive software tool for reproducibility in Molecular Biology	Oral
14	Sónia Silva et al.	Exploring bioinformatics tools to characterize a new regulator of <i>Candida glabrata</i> biofilm matrix	Poster
15	Ríos-Castro, R et al.	A preliminary metabarcoding study of the diversity of Eukaryotic and Prokaryotic communities in the socio-ecological system from Rias Baixas (NW Spain)	Poster
16	Maria Benedita Pereira et al.	Computational design of antiviral biologics targeting Zika virus envelope protein	Poster
17	Madalena C. Marques et al.	Antiviral proteins targeting Influenza A hemagglutinin: design, production and characterization	Poster
18	André R. F. Salgueiro et al.	Artificial Intelligence-Based Design of Antibody-like Engineered Protein Scaffolds	Poster
19	Diogo Silva et al.	Addressing the challenge of oligomerization in computational protein design	Poster
20	Margarida Cardeano Pinheiro et al.	Exploring the Genomic Diversity of Hepatitis E Virus in European Rabbits: A Search for Optimal Primers	Poster
21	Rafaela Lopes et al.	Medical Procedure Recognition and Entity Linking in Spanish	Poster
22	Jéssica Rodrigues et al.	Discovery of new Ligands for Biopharmaceuticals Purification	Poster
23	Rigoberto Rincón Ballesteros et al.	Characterization of metabolic phenotypes in Genome-scale models of complex diseases through Machine Learning	Poster



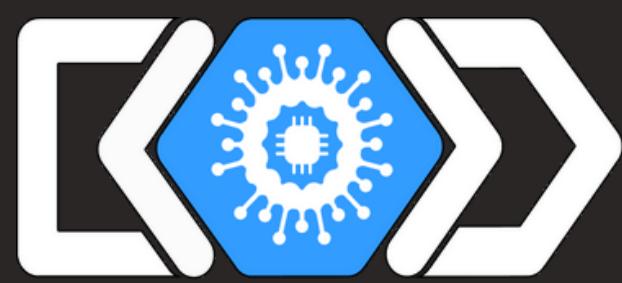
Bioinformatics Open Days 2024

SCIENTIFIC SUBMISSIONS

24	Gonçalo Apolinário et al.	Exploring methane mitigation strategies in photosynthetic microorganisms through genome-scale metabolic models	Poster
25	Jorge Miguel Silva et al.	An Efficient Toolkit for Large-Scale Genomic Analysis and Its Application to Multi-Resistant Bacteria	Software
26	Miguel Santos et al.	Development and deployment of an infrastructure for genomic health data	Software
27	Clara Cerqueira et al.	Creating a Comprehensive Database of Plastic Degrading Enzymes for Machine Learning Applications	Software
28	Rafael Vieira et al.	Bridging Aptamer Information: Standardization and Curation of Diverse Databases	Software
29	Mariana Fernandes et al.	Unifying Information on Plastic Degrading Enzymes Across Different Databases	Software
30	Rafaela Andrade et al.	A metagenomics pipeline for the characterization of human gut microbiome in colorectal cancer	Software
31	Marta Ferreira et al.	Precision Genome Analysis: Unraveling SNVs and CNVs with a Multi-Variant Caller WGS Workflow	Software

If you want to know more about the content of the each poster/oral presentation, check out our Abstract Book, available below:





Bioinformatics Open Days 2024

NETWORK SESSION

Session with companies

In the Networking Session participants will have the opportunity to interact with each company representative, incentivizing follow-up questions and general discussion about starting their professional career. The aim is to expose successful and growing technological-based companies, whilst closing the gap between company representatives and all those interested.



SilicoLife



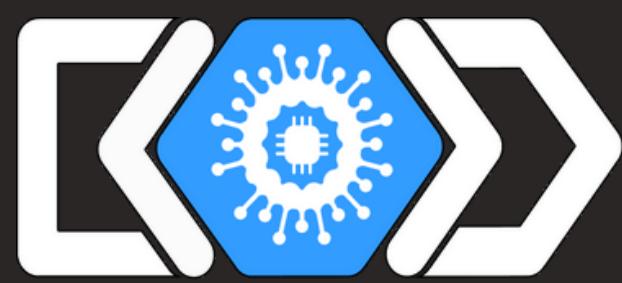
iLoF



Accenture



OmniumAI



Bioinformatics Open Days 2024

WORKSHOPS

Introduction to RNA-Seq data analysis

In this hands-on workshop we will cover the basis for RNA-Seq data analysis using open access tools.

The first part of the workshop will be a quality control assessment using FastQC and how we can use the QC report to clean RNA-Seq data.

The second part will be the mapping of the reads with the Bowtie2 tool and how to interpret the resulting mapping statistics. Finally, we will cover the visualization and quantification of the data using the ARTEMIS genome browser.



Vânia Pobre

Pos-doc Researcher na ITQB-UNL

Tools and computational resources for the life sciences

Discover the resources that ELIXIR, the European bioinformatics infrastructure, has at your disposal to help you through all the phases of biological data gathering, analysis and publication.

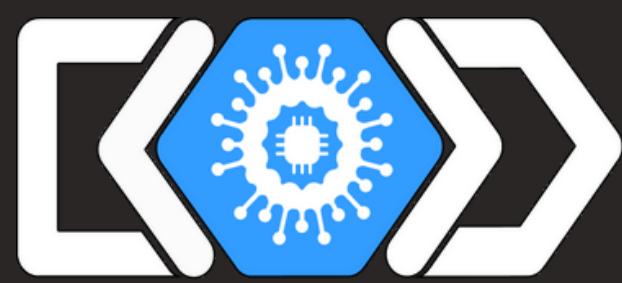
Gil Poiares-Oliveira

Currently, works at INESC-ID as a Bioinformatics Technician providing support to BioData.pt training programmes.



Bioinformatics Open Days
2024





Bioinformatics
Open Days 2024

WORKSHOPS

Introduction to Computational Protein Design Tools

Using structure-based computational design tools, this workshop will walk you through a pipeline focused on improving protein attributes, such as binding affinity to specific protein targets.

Initially, we'll examine the 3D structure of our starting proteins using molecular visualization tools like PyMOL to gain insights crucial for the design process. Next, we'll utilize cutting-edge deep-learning protein design tools like RFDiffusion and ProteinMPNN to craft your proteins. Subsequently, we will leverage AlphaFold2, a powerful protein secondary structure prediction, to select the most promising results.



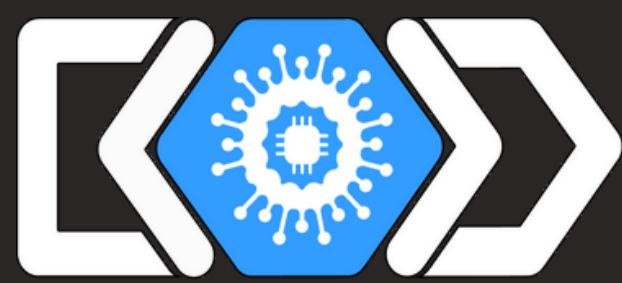
Pedro Moreira

PhD Candidate at ITQB



Bioinformatics Open Days
2024





Bioinformatics Open Days 2024

SPONSORS AND COLLABORATORS

Thank you note

Dear Sponsors, Collaborators, Volunteers, and Members of the Organizing Committee,

On behalf of the XIII Edition of the Bioinformatics Open Days, we would like to express our most sincere appreciation for your support and contributions to the event. Your hard work and dedication are key in making the conference a success.

We extend our deepest thanks to our sponsors and collaborators, whose generosity and partnership made it possible to create a program of keynote talks, workshops, and networking opportunities that will be both informative and enjoyable. Your contributions ensured that our event remains an accurate representation of the present and future of the Bioinformatics field, and we are grateful for your commitment to our cause.

We also want to express our gratitude to the volunteers and members of the organizing committee, whose efforts were essential in the planning and execution of the event. Your dedication and commitment to the conference are critical to its success, and we appreciate the time and effort you put into organizing the various aspects of the event.

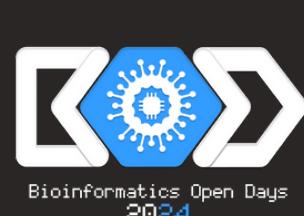
We would like to express a special thank you to the Student Association for the Bioinformatics students of the University of Minho (NEBIUM, Núcleo de Estudantes de Bioinformática da Universidade do Minho). We are grateful for the time, effort, and dedication you put into organizing various aspects of the conference. Your expertise and advice were essential in shaping the program and ensuring that it met the needs of all attendees.

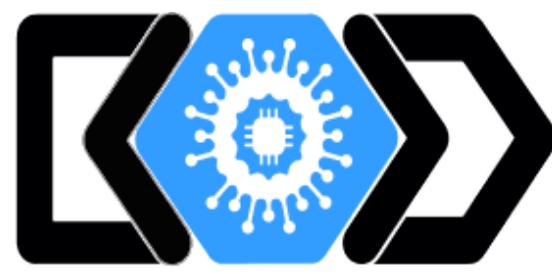
Finally, we would also like to extend our appreciation to the general chair, Professor Miguel Rocha, for his insightful opinions and experience. His guidance and leadership were instrumental in ensuring the success of the event.

In conclusion, the success of the XIII Edition of the Bioinformatics Open Days was a result of the collective efforts of all of you. We are deeply grateful for your support and look forward to continuing our partnership in future editions.

Sincerely,

Gonçalo Apolinário
President of the Bioinformatics Open Days 2024





Bioinformatics
Open Days 2024

SPONSORS AND COLLABORATORS



BioData.pt



SILICOLIFE

accenture

iLAF

TUB
TRANSPORTES
URBANOS DE BRAGA

Thank You



LICOR
BEIRÃO

Saborosa

Nicola
DESEN 1779



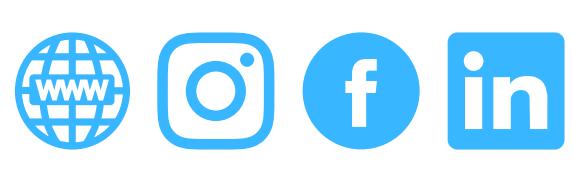
BRAGA
Cidade autêntica



 aauminho



Bioinformatics Open Days
2024


[/bioinformaticsopendays](#)

XIII EDITION BIOINFORMATICS OPEN DAYS

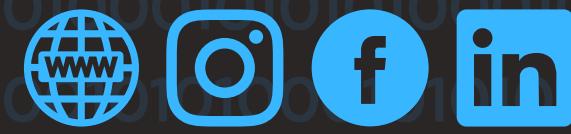
Thank you for joining us at XIII BOD!

Your participation and support are greatly appreciated. We look forward to seeing you at future events and continuing to grow our Bioinformatics community.



Bioinformatics Open Days

2024



/bioinformaticsopendays



Bioinformatics Open Days
2024



/bioinformaticsopendays