



PhD Advanced Course

Pathogen Multiomics and Bioinformatics

Date: 11/07/2022- 15/07/2022

ECTS: 6

Classes:22,5 hours

Course Coordinator:

João Perdigão, Faculdade de Farmácia da Universidade de Lisboa

Teaching staff:

João Perdigão, Faculdade de Farmácia da Universidade de Lisboa

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Short Introduction

The Pathogen Multiomics and Bioinformatics advanced course is structured around six distinct modules that spans the entire spectrum from the introduction to NGS data and quality control to genome-wide association studies applied to different pathogens. While the course comprehends a solid theoretical component that underpins the learning and execution of the different analytical stages in the practical sessions which comprise most of the course. It is intended that the participants apprehend the concepts and fundamentals of the analytical procedures that are necessary to translate the large data volumes generated by NGS platforms while systematically consolidating the theoretical basis of this knowledge.

The course is open to PhD students from the FFUL doctoral program, but also to PhD students from other institutions or professionals coming from different areas such as pharmaceutical sciences, medicine, biology or other related areas including post-doctoral researchers aiming to develop work that involves NGS data.

Goals and Learning Outcomes

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The course program intends to provide the participants with a broader and deeper understanding with diverse omics technologies, bioinformatic terminology and the available tools to carry out different analytical stages. In the end, the course participants should be able to:

1. Understand, interpret and assess the different types and formats of data generated by NGS platforms as well as to perform quality-control steps;
2. Map sequence data to a reference genome, identify variants on a genome-wide scale as well as performing its functional annotation;
3. Carry out de novo assembly steps, including comparative analysis and genomic annotation;
4. Integrate the previous analytical steps to genome-wide phylodynamic approaches aiming to study the evolution and dissemination of pathogens of public health importance;
5. Perform transcriptomic analysis, evaluation and identification of differentially expressed genes;
6. Characterize polymicrobial samples envisaging the assessment of its microbial composition and metagenome;
7. Understand, interpret and perform Genome-Wide Association Studies (GWAS);

Assessment

Assessment is optional, however, for accreditation of the 6 ECTS, assessment will be done via submission of two reports focused on the relevance of the methodologies presented and analytical tools towards the individual PhD project and, a second report, consisting of a research or implementation project that encompasses the studied methodologies (group project).

Programme

The course comprehends a solid theoretical component that underpins the learning and development of the different analytical stages through practical sessions which comprise most of the course. The course also includes theoretical sessions and a strong practical computer-based approach to the analysis of genomic, transcriptomic or metagenomic data.

1. *Introduction to NGS data and Quality Control;*
2. *Reference Assembly (mapping): mapping, data visualization, variant calling and functional annotation;*
3. *De novo genome Assembly: concepts and optimization, contig ordering and scaffolding, annotation;*
4. *Introduction to Phylogenetics and Phylodynamics;*
5. *Pathogen profiling toolbox: from NGS to phenotype;*
6. *Transcriptomics and RNA-Seq;*
7. *Introduction to Microbiome Analysis and Metagenomics;*
8. *Genome-Wide Association Studies (GWAS).*

The course also includes an Invited Guest Seminar day, covering some of the technologies and approaches covered in the practical sessions.

Registration and Fees

The registration is through the FenixEdu Platform until **July 4, 2022**.

Registration Guide ([Portuguese](#) or [English](#))

Tuition Fee:

This course is free for 1st year PhD students of FFUL.

PhD Students from others institutions:

- Registration with evaluation: 125€
- Registration without evaluation: 100€

Other attendees should consult the [webpage](#)

The course will run with a minimum of 6 participants to a maximum of 30 participants. When the maximum number of registrations is reached, a total of 10 vacancies will be available for PhD students of the FFUL Doctoral Program.

Preliminary timetable

	Day 1	Day 2	Day 3	Day 5	Day 6
9:30	<u>Module 1</u>	<u>Module 3</u>	<u>Module 5</u>	<u>Module 6</u>	
.	Mapping,	Transcriptomics	Phylogenetics	Metagenomic	Invited Guest
.	Visualization	and RNA-Seq	and Public	Analysis of	Seminars
.	and Variant		Health	Bacterial	
13:00	Calling			Populations	
Lunch Break					
14:00	<u>Module 2</u>	<u>Module 4</u>	<u>Module 5</u>	<u>Module 7</u>	
.	De novo	Pathogen	Phylogenetics	Genome-Wide	Invited Guest
.	Assembly	Analytical	and Public	Association	Seminars
.		Toolbox	Health	Studies (GWAS)	
18:00					