

Short Course in Bioinformatics

 17^{th} – 19^{th} March 2025

AGENDA

March 17th 2025

Time	Duration	Торіс	Speaker	
10h00	15'	Welcoming session	Pedro Leão	
10h15	45 '	Introduction to Bioinformatics in Natural Products Discovery	Adriana Rego	
11h00	30'	NLP/AI for Functional Annotation of Enzymes: A Case Study with FAALPred	Leandro Pereira	
11h30	30'	Coffee-break		
12h00	30'	Introduction to antiSMASH and BiG-SCAPE workflows	Catarina Loureiro	
12h30 Lunch break				
14h00	60'+30'	Hands- on session antiSMASH and BiG-SCAPE	Catarina Loureiro	
15h30	30'	Coffee-break		
16h00	30' + 60	Introduction to GNPs and MicrobeMASST	Mauricio Caraballo	
		Hands-on session – MicrobeMASST		







March 18th 2025

Time	Duration	Торіс	Speaker		
9h00	60'+30'	Phylogenetic approaches to natural product discovery	Hans Singh		
		(short) Hands-on session NaPDos2			
10h30	30'	Coffee-break			
11h00 30 '+45' 12h15		Genomic context of target biosynthetic genes	Adriana Rego		
		(short) Hands-on session genomic context	Adriana Rego and Catarina Loureiro		
		genomic context			
Lunch break					
13h45	45+60'	Introduction to computational protein structure prediction			
		Hands-on session to computational protein structure prediction, molecular docking	Arménio Barbosa		
15h30 Coffee-break					
15h45	30′	EFI-SSN and Sequence-Based Functional Prediction in Enzyme Discovery	Raquel Castelo Branco		









March19th 2025

Tin	ne	Duration	Торіс	Speaker
10	h	15'	Welcoming session - Presentation of the speakers	
10	h15	30'	<i>Open-science-driven development of genome mining tools and their application on microbiomes</i>	Catarina Loureiro
10	h45	15'	Q&A	
11h	100	30'	Coffee-break	
11h	130	45 '	Advancing Biotechnology with Molecular Modeling: Applications in Drug Discovery, Protein Purification and Self-Assembly	Arménio Barbosa
121	า15	15'	Q&A	
12ł	า30		Lunch break	
14	h30	45 '	Targeted gene cluster mining with GATOR-GC	Marc G. Chevrette
15ł	H15	15'	Q&A	
15ł	า30	30'	Coffee-break	
161	h00	45'	A journey for the discovery of microbial molecules, the need of reference datasets, and using small molecules to understand symbiotic relationships in ants' ecosystems	Mauricio Caraballo
16	H45	15'	Q&A	
17ł	h00	10'	Final remarks	





