

Mathematical Foundations in Bioinformatics 2021 (MatBio 2021)

Programme

15 September 2021

09:00 – 09:15	Welcome Speech by Prof. Luca Viganó	
SESSION 1 (09:15 – 11:00)		
Chair: Dr Fatima Vayani		
09:15 – 10:00	Dr Katherina Huber <i>(University of East Anglia (UEA))</i>	Invited Talk: Phylogenetic networks, a way to cope with complex evolutionary processes
10:00 – 10:15	Katerina Pierouli <i>(Agricultural University of Athens)</i>	Genome regulation by long non-coding RNAs
10:15 – 10:30	Maria Georga & Ariadni Papadaki <i>(University of Montpellier)</i>	5' untranslated region and identification of regulatory elements that control transcriptional activity in immunoglobulins
10:30 – 10:45	Md. Shariful Islam Bhuyan <i>(Bangladesh University of Engineering and Technology)</i>	Indel Call Filtering using Gradient Boosting
10:45 – 11:00	Eleni Papakonstantinou <i>(Agricultural University of Athens)</i>	A novel approach on pharmacophore elucidation for transmembrane proteins
11:00 – 11:15	BREAK	

SESSION 2 (11:15 – 13:00)		
Chair: Dr Mai Alzamel		
11:15 – 12:00	Dr Leena Salmela <i>(University of Helsinki)</i>	Invited Talk: Improving genome assembly with long range data
12:00 – 12:15	Sara Moussadeq <i>(University of Clermont l’Auvergne)</i>	Analysis of the immune response to Sars-CoV-2 using IMGT immunoinformatics tools and clonotype research
12:15 – 12:30	Thanasis Mitsis <i>(Agricultural University of Athens)</i>	A bioinformatic analysis on the glucocorticoid receptor in an effort to provide new insights on nuclear receptors’ role in homeostasis maintenance
12:30 – 12:45	Dr Md Shamsuzzoha Bayzid <i>(Bangladesh University of Engineering and Technology)</i>	Inferring Optimal Species Trees in the Presence of Gene Duplication and Loss: Beyond Rooted Gene Trees
12:45 – 13:00	Chahrazed Debbagh <i>(Université de Montpellier)</i>	In silico characterization of the gene repertoire of immunoglobulins of Gorilla gorilla gorilla
13:00 – 13:30	LUNCH BREAK	

SESSION 3: (13:30 – 15:15)		
Chair: Dr Christopher Hampson		
13:30 – 14:15	Prof. Sofia Kossida <i>(Université de Montpellier)</i>	Invited Talk: IMGT®[®], the international ImMunoGeneTics information system®[®], an overview
14:15 – 14:30	Io Diakou <i>(Agricultural University of Athens)</i>	A computational pipeline for the research of anti-virals against Ebola virus
14:30 – 14:45	Frederik Wieder <i>(FU Berlin)</i>	Flux cones of metabolic networks
14:45 – 15:00	Muhammad Ali Nayeem <i>(Bangladesh University of Engineering and Technology)</i>	PASTA with many application-aware optimization criteria for alignment based phylogeny inference
15:00 – 15:15	Youcef Barkat & Djaib Brahim <i>(University Of Science And Technology Houari Boumediene)</i>	Explainable AI: Application in Gene Finding
15:15 – 15:30	BREAK	

SESSION 4 (15:30 – 17:45)		
Chair: Dr Simon Puglisi		
15:30 – 16:30	Prof. Srinivas Aluru <i>(Georgia Institute of Technology)</i>	Invited Talk: Genome graphs: Models, Algorithms, and Applications
16:30 – 16:45	Dr Jamie Alnasir <i>(Imperial College London)</i>	Encoding information into DNA
16:45 – 17:00	Dr Daniel Gibney <i>(Georgia Institute of Technology)</i>	On the Complexity of Approximate Pattern Matching on De Bruijn Graphs
17:00 – 17:15	Jessica Mitchell & Justin Noland <i>(North Carolina A&T State University)</i>	Efficient Algorithm for the Maximal Strip Recovery Problem
15:00 – 17:30	Holly Koponen <i>(McMaster University)</i>	Computing Maximal Covers for Protein Sequences
17:30 – 17:45	Nabil Ibtehaz <i>(Bangladesh University of Engineering and Technology)</i>	NORTH: A Naive Bayes based ORTHologous cluster prediction tool
17:45 – 18:00	Closing Remarks	