
MCEB 2026
Heraklion, Crete
04-08 May

PROGRAM

Monday, 04/05

18:00	Check-in and registration. Astir Beach hotel
20:00	Dinner. Astir Beach hotel

Tuesday, 05/05

08:30-09:00	Registration
09:00-10:00	Keynote: Dimitrios Paraskevis Chairperson: Alexis Stamatakis
10:00-10:40	*Talks*
	1. Marino Gabriele. Unsupervised Bayesian neural networks enable inference of complex phylodynamic processes
	2. Noah Wahl. Highways of horizontal gene transfer for modeling large gene flow events under the UndatedDTL model
10:40-11:30	Coffee break
11:30-12:10	*Talks*
	3. Pablo Gutiérrez De La Peña. Deep learning skylines in diversification studies
	4. Annabel Large. TKF-based models with latent and hierarchical structure are competitive with parameter-heavy neural networks as models of protein sequence evolution
12:10-12:40	Short break, discussions
12:40-13:20	5. Menno De Jong. How long does gene flow persist? A comparative genomic analysis across mammals.
	6. Gonché Danesh. Pooling or splitting genomic clusters for birth–death inference under heterogeneous sampling: a simulation study
13:30-15:00	Lunch at Cretaquarium
15:30-16:30	Keynote: Rosa Fernández Chairperson: Stephane Guindon
16:30-17:30	Software session
17:30-19:30	Poster session 1, apéritif
20:00	Dinner at Astir Beach hotel

Wednesday, 06/05

09:00-10:00	Keynote: David Posada Chairperson: Cilia Antoniou
10:00-10:40	*Talks*
	7. Vidhi Vidhi. Phylogenetic tree reconstruction using Bayesian statistics in Chronic Lymphocytic Leukemia (CLL).
	8. Tobias Dieselhorst. Coupling mutation and branching processes and its implications on parameter identifiability
10:40-11:30	Enhanced Coffee break
11:30-12:10	*Talks*
	9. John Rhodes. Inferring the Tree of Blobs of a Species Network
	10. Maria Vasilarou. Independent hybridization events, followed by genomic rearrangements, shape genome evolution of polyploid *A. kamchatica*
12:30-14:00	Bus trip to Rouvas Gorge
14:00-20:00	Rouvas Gorge hike
20:00-22:00	Dinner at Votomos tavern in Zaros village
22:00-23:30	Bus trip to Astir Beach hotel

Thursday, 07/05

09:00-10:00	Keynote: Nick Goldman Chairperson: Fabio Pardi
10:00-10:40	*Talks*
	11. Rui Borges. Phylogenetic inference with not-so-rare mutations and wee tiny organisms
	12. Frédéric Lemoine. Phylogenetic Instability: A Set of Indices for Rogue Taxa Identification
10:40-11:30	Coffee break
11:30-12:10	*Talks*
	13. Xia Feifei. High-resolution population structure inference using genome-wide short tandem repeat variations.
	14. Carina Mugal. A simulation framework for the study of population-level processes in phylogenetics
12:10-12:40	Short break, discussions
12:40-13:20	15.Anzhelika Koldaeva. Phenotype prediction across deep evolutionary distances.
	16. Anders Poulsen Charmouh. Estimating Gene Conversion Tract Length and Rate From PacBio HiFi Data.
13:30-15:00	Lunch at Cretaquarium
16:30-17:30	Keynote: Laura Kubatko Chairperson: Olivier Gascuel
17:30-19:30	Poster session 2, apéritif
20:00	Dinner at Astir Beach hotel

Friday, 08/05

09:00-10:00	*Talks* CHAIRPERSON: ALEXIS STAMATAKIS
	17. DAMIEN M DE VIENNE. Revealing ghost lineages with phylogenomics.
	18. STEVEN MAERE. The rise of polyploids during environmental upheaval.
	19. DARREN OVERMAN. Arboreal Networks .
10:00-10:30	Coffee break
10:30-11:30	*Talks*
	20. BANU CETINKAYA. Drawing Gene Trees Inside a PhyloFusion Network
	21. CLESSIN AUGUSTIN. Phylogeography of avian influenza H5N1 in the sub-Antarctic amid undersampled diversity.
	22. ALEXANDROS STAMATAKIS. RAxML meets Machine Learning in RAxML-NG v2.0
11:40-12:00	Discussion, closing remarks

Software session

1. DANIEL HUSON: Displacement optimized (DO) layout of phylogenetic networks and tanglegrams
2. TOBIA OCHSNER: PhyloSpec: a phylogenetic modeling language
3. SAMUEL HONG: Posterior tree topology summarization in Bayesian phylogenetics using TreeTracer

Poster sessions

Session 1

1. FLORENCE PAUTET: Temporal decay of shared haplotypes between populations
2. MARIO CAPOBIANCO: Automatic detection of fitness shifts in pathogen phylogenies using contrastive learning
3. ANNA ZHUKOVA: Rapid tests for epidemic aspect detection from pathogen transmission trees
4. YARI CERRUTI: Modeling varying demography along phylogenies from large-scale genomic data
5. KLEOPATRA VENETSIANOU NEFELI: Genomic Diversity and Evolutionary History in the Mediterranean Monk Seal
6. SOPHIE HEIDIG: Exploring Temperature-Dependent Protein Diversity in Achromatium
7. SAMUEL ALEXANDER: A formalization of Hennig's no-splitting species criterion
8. DIOGO DA SILVA RIBEIRO: Inferring gene flow from phylogenies with too many genomes
9. MARIUS BRUSSELMANS: An adaptive time-tree transition kernel for Bayesian phylogenetic inference
10. IGHOR ARANTES: Phylodynamic Analysis of the Spread of the Oropouche Virus in Brazil During the 2023-2025 Outbreak
11. NIKITA KULIKOV: PhyloAI: Fast and accurate machine-learning-based inference of quartet topologies
12. IOANNA KOTARI: Merging evolutionary timescales to quantify adaptation
13. BEN BETTISWORTH: Statistical Verification of Simulation Software for Biogeography
14. LUCIA MARTIN FERNANDEZ: Quantifying and Predicting Multiple Sequence Alignment Difficulty

Session 2

15. Yongkuk Kim: Prevalence-Scan Signatures of Frequency-Dependent Selection via Cytoplasmic Incompatibility: Threshold Bands in Post-Release Dengue Control
16. Wakinyan Benhamou: Infectious agent transmission from carcasses can select for increased virulence
17. Mena Khalaf: Computational Detection of Antimicrobial Peptide Candidates from Brown Algae via Integrated AI and Bioinformatics Approaches
18. Georges Hanna: Targeted Sampling Strategies for National-Scale Viral Phylogeography
19. Alexandros Kourtidis: The changing water flea: gene flow and local adaptation in a Daphnia magna metapopulation
20. Alexandre Barroso: From Genomes to Venoms: Evolutionary and Comparative Analysis of Toxin Families in Stony Corals (Cnidaria)
21. Marcus Overwater: The Calibrated Coalescent Point Process for Bayesian Molecular Clock Dating
22. Cristina Montoya: Variation Barcodes: a tool to preserve biodiversity through monitoring genetic diversity
23. Nicola Mulberry: Age-Dependent Phylodynamics with application to single-cell lineage trees
24. Ufuk Topalan: Thousands of Wasps, Hundreds of BINs: Are Barcode Clusters Real Species?
25. Melissa Viveiros Moniz: A DNA Time Machine: Using Herbarium Genomics to Track Genetic Diversity Trends Across Time
26. Jeon Huiyong: Bridging Spectral Decomposition and Neural Operator Learning for Periodic and Climate Dynamics
27. Edyta Mazur: Flavonora: a new genus of lecanoroid lichens (Ascomycota, lichenized fungi)
28. Daniel Wright: TreeSpotter: A software tool for assessing tree-basedness in phylogenetic networks