PROGRAM

Monday, May 12

12h00 – 13h00	Check-in, Carmen de la Victoria or Corrala de Santiago
13h00 – 15h00	Lunch, Carmen de la Victoria
15h00 – 20h00	Check-in, Carmen de la Victoria or Corrala de Santiago
20h00 – 22h00	Welcome cocktail and Dinner, Carmen de la Victoria

Tuesday, May 13

9h15	Start of the conference, Carmen de la Victoria
9h30 – 10h30	**Keynote** - Lisa Pokorny Montero *Genomic approaches to the study of plant evolution*
10h30 – 11h00	Coffee Break
11h00 – 12h00	**Talks**
	Chloe Shiff *Enumeration of labeled binary trees compatible with a multifurcating perfect phylogeny*
	Sebastian Ramos-Onsins *Exploring the variability through the relative Site Frequency Spectrum (rSFS)*
	Pavel Flegontov *Genetic landscapes are manifolds obscured by poor sampling and data pruning: towards an optimal protocol for visualization of population structure*
12h00 – 12h10	Short Break
12h10 – 12h50	**Talks**
	Yexuan Song *Sampling Aware Ancestral State Inference*
	Rayan Chikhi *Planetary-Scale Sequencing Data Analysis Surveys Evolution*
13h00 – 15h00	Lunch, Carmen de la Victoria
15h00 – 17h00	Free afternoon
17h00 – 17h30	Coffee & Tea
17h30 – 18h30	**Keynote** - Harald Ringbauer *Advanced Ancient DNA Analysis - Investigating Long Shared Haplotypes*
18h30 – 20h00	**Posters** & Wine – No. 1 to No. 15
20h00 – 21h30	Dinner, Carmen de la Victoria

Wednesday, May 14

9h30 – 10h30	**Keynote** – Kristina Wicke *Inference of phylogenetic networks*
10h30 – 11h00	Coffee Break
11h00 – 12h00	**Talks**
	Sophie Kersting *Tree balance in phylogenetic models*
	Sishuo Wang *New Methods for Dating Deep-Time Bacterial Evolution Based on Ancient Symbiosis and Complex Substitution Models*
	Manolo Perez *PhyloCNN: Improving tree representation and neural network architecture for deep learning from trees in phylodynamics and diversification studies*
12h00 – 12h10	Short Break
12h10 – 12h50	**Talks**
	Carina Mugal *Applications of stochastic reproduction-selection models for the study of non-equilibrium dynamics in molecular evolution*
	Moritz Otto *Inferring the history of gene copy number evolution*
13h00 – 15h00	Lunch, Carmen de la Victoria
15h00 – 15h40	**Talks**
	Camille Steux *Inferring a demographic history for common chimpanzees using models of structured populations with changes in connectivity*
	John Rhodes *Identifiability of phylogenetic networks*
15h40 – 16h00	Coffee & Tea
16h00 - 17h30	Free time
17h30 – 20h00	Visit of Alhambra
20h00 – 21h30	Free Dinner in the Old City or Dinner, Carmen de la Victoria

Thursday, May 15

9h30 – 10h30	**Keynote** – Sophie Abby *Evolution of biosynthetic pathways in Bacteria*
10h30 – 11h00	Coffee Break
11h00 – 12h00	**Talks**
	Roser Homs Pons *Phylogenetic invariants for time-reversible evolutionary models*

	Anastasis Togkousidis *Investigating Overfitting in Maximum* Likelihood *Phylogenetic Inference: A Systematic Approach*
	Hector Banos *Misspecification Strikes: How ASTRAL and other quartet-based methods can Mislead in the Presence of Hybridization, even for Non-Anomalous Scenarios*
12h00 – 12h10	Short Break
12h10 – 12h50	**Talks**
	Anna Zhukova *Is simpler better? Effects of phylodynamic model misspecification on epidemiological estimates*
	Daniel Huson *New algorithms for layout and capture of phylogenetic trees and networks*
13h00 – 15h00	Lunch, Carmen de la Victoria
15h00 – 17h00	Free afternoon
17h00 – 17h30	Coffee & Tea
17h30 – 18h30	**Keynote** - Jaime Huerta-Cepas *Functional and evolutionary significance of the unknown microbial biosphere*
18h30 – 20h00	**Posters** & Wine – No. 16 to No. 29
20h00 – 21h30	Dinner, Carmen de la Victoria

Friday, May 16

9h30 – 10h30	**Keynote** – Richard Durbin *Population genome variation – going beyond SNPs*
10h30 – 11h00	Coffee Break
11h00 – 12h00	**Talks**
	Mareike Fischer *On the reliability of Maximum Parsimony for encoding and reconstructing phylogenetic trees*
	Niels Holtgrefe – Squirrel *Reconstructing semi-directed phylogenetic level-1 networks from four-leaved networks or sequence alignments*
	Sebastian Höhna *Testing new approaches in population genomics and phylogenomics on fireflies*
12h00 – 13h00	End of the conference, luggage…,
13h00	Farewell Lunch (not included), Carmen de la Victoria

POSTERS

(*between A0 and A1 in vertical orientation*)

Tuesday, May 13, 18h30-20h

1. Rachita Srivastava
   Comparative demographic analysis of Cardamine hirsuta and Arabidopsis thaliana

2. Menno De Jong
   Distance-based Inference of Species Trees

3. Miguel Álvarez-Herrera
   Expanding the scope of evolution reporting and analysis: from intra-patient dynamics to outbreaks

4. Jaime Iranzo
   Gene clustering methods for comparative pangenomics

5. Elizabeth Allman
   Inferring a Tree of Blobs under the Network Multispecies Coalescent model

6. Nicole Huber
   mitoTree: A Modern Open-Source Framework for Advancing Mitochondrial DNA Phylogenetics

7. Martin Frohn
   On properties driving diversity index selection

8. Charles-Elie Rabier
   Phylogenetic network inference with ABC Random Forest : application to rice domestication

9. Haoyu Chen
   Testing SNP data under overdispersion

10. Eva Pardo Otero
    Artificial Intelligence for Assessing Genetic Load in Population Genetics in Trees

11 Carlota Medrano
   Assessing Simulator Bias in Phylogenetic Data with an AI-based Approach

12. Esther Funes-Ligero
    Impact of ploidy variation on the female allocation strategy throughout the plant's life stages

13. Cristina Montoya De Haro
    Variation barcodes for species conservation using mitochondrial genome

14. Teresa Garnica Gonzalez
    Comparative analysis of coffee genomes

15. Kate Truman
    Inference using the Skyline Stratigraphic Range Fossilized Birth-Death model

Thursday, May 15, 18h30-20h

16. Carlos Olmedo-Castellanos
Using bioinformatics to identify molecular self-incompatibility systems in Erysimum incanum and Erysimum wilczekianum: hints about their evolution and phylogeny

17. Camilo Ferrón
Neighbourhood effects on male and female fitness in a natural population of Moricandia moricandiodies

18. Emma Bouvet
Exploring the diversity and evolution of ubiquinone biosynthesis across bacteria and eukaryotes

19. Ghislain Camarata
Inference of dispersal and density parameters from spatial genomics data, using simulation-based machine learning methods

20. Lea Palao
Reference Genome Choice: How Non-Conspecific Genomes Distort Population Genetic Diversity

21. Melissa Viveiros Moniz
Genomic Insights into the Dispersal, Speciation, and Adaptation of Erysimum in Macaronesia

22. Pablo Arino Fernandez
TreeLSTM and Transformer Models in Phylogenetic Analysis: Advancing from Tree-Level to Node-Level Evolutionary Inference

23. Etheimer Paul
Expanding a time divergence estimation method for bacteria by expliciting an evolutionary model

24. Pablo Gutierrez De La Pena
Node-based Split-Tree Encoding in Deep Neural Networks Captures Rate Heterogeneity in Large Phylogenetic Trees

25. Andras Barea Marquez
Refining phylogeography of Olea europaea L. through mitochondrial & cytoplasmic phylogenomics

26. Theo Brunet
Modeling of the metabolism of bacterial predation

27. Timothée Salzat-Hervouette
Investigating the evolution of phototrophy in Pseudomonadota

28. Yannick Schaefer
Modeling the evolution of tandemly arrayed gene families affected by interlocus gene conversion, selection and recombination

29. Angela Aguado-Lara
On the Brink of Extinction: Integrating Phylogenomics and Evolutionary Heritage to Refine the EDGE Concept in Afrotropical Euphorbiaceae