Monday

9h45-10h Welcome, introduction

10h-11h Keynote (chair: Franz Baumdicker)

Harnessing AI in phylogenomics
Tal Pupko

11h-11:30h Simulating realistic data (1/2, chair: Franz Baumdicker)

Assessing usefulness of artificial genomes via local ancestry inference
Maïwen Demeulle, Titouan Chambe, Antoine Szatkownik, Léo Planche, Burak Yelmen, Flora Jay

11h30-12h coffee break

12h-13h Simulating realistic data (2/2, chair: Franz Baumdicker)

Simulations of Sequence Evolution: How (Un)realistic They Are and Why
Johanna Trost, Julia Haag, Dimitri Höhler, Laurent Jacob, Alexandros Stamatakis, Bastien Boussau

Fitting Indel Evolution Model Parameters to PFam Protein Alignments with a GPU-accelerated Framework
Annabel Large, Ian Holmes

13h-14h30 lunch break

14h30-15h30 Keynote (chair: Alexandros Stamatakis)

Deep learning for the phylogenetic inference of species diversification
Hélène Morlon

15h30-16h30 Phylogenetics (1/2, chair: Alexandros Stamatakis)

Phyloformer: Towards fast and accurate phylogeny reconstruction with self-attention networks
Luca Nesterenko, Luc Blassel, Bastien Boussau, Laurent Jacob

Learning from an Artificial Neural Network in Phylogenetics
Alina Leuchtenberger

16h30-17h coffee break

17h-18h Phylogenetics (2/2, chair: Alexandros Stamatakis)

Neural networks can predict ghost species diversity from gene transfers
Enzo Marsot, Théo Tricou, Laurent Jacob, Bastien Boussau, Damien De Vienne

Predicting Phylogenetic Bootstrap Values via Machine Learning
Julius Wiegert, Julia Haag, Dimitri Hoehler, Alexandros Stamatakis

18h-19h poster session (posters can hang for the rest of the conference)

Tuesday

9h-10h Keynote (chair: Laurent Jacob)

Generative adversarial networks, transfer learning, and interpretability for evolutionary inference
Sara Mathieson

10h-11h Predictions on a single sequence (1/2) : Protein Language Models (chair: Laurent Jacob)

Illuminating the functional landscape of the dark proteome across the Animal Tree of Life through natural language processing models
Gemma I. Martínez-Redondo, Israel Barrios, Marçal Vázquez-Valls, Ana M. Rojas, Rosa Fernández

Deciphering Deep Phylogeny and Evolution of Protein Families through Protein Language Models
Ivan Koludarov

11h-11h30 break

11h30-13h30 Predictions on a single sequence (2/2) (chair: Laurent Jacob)

Classification of the evolutionary origin of orphan genes using machine learning approaches
Nikolaos Vakirlis, Anne Kupczok, Jori De Leuw, Leonardos Mageiros, Christoforos Nikolaou

Unsupervised learning as a tool to retrieve genomes from undersampled taxa: Fast and slow evolution in myxozoans
Claudia Weber

Long context windows improve deep learning methods for predicting genomic regulation
Ian Holmes

Interpreting artificial neural networks for detecting genome-wide association signals for complex traits
Burak Yelmen, Maris Alver, Silva Kasela, Lili Milani

13h30-14h30 lunch break

Afternoon: time for exchange/networking, optional short hike (bus + hike at Sroumpoulas
https://blog.fodelebeach.gr/uncategorized/mount-stroumboulas/

Wednesday

9h-10h Keynote (chair: Nikolaos Alachiotis)

Inference of Coalescence Times and Variant Ages Using Convolutional Neural Networks
Pier Palamara

10h-11h Population genetics (chair: Nikolaos Alachiotis)

Using supervised machine learning methods to infer demographic history from genomic data
Arnaud Quelin, Flora Jay, Frédéric Austerlitz

Unifying Ideas from the Sequentially Markovian Coalescence with Deep Learning for Population Genomic Inference
Kevin Korfmann, Aurélien Tellier

11h-11h30 break

11h30-13h Detecting positive selection (chair: Flora Jay)

Scalable CNN-based classification of selective sweeps using derived allele frequencies
Sjoerd Van den Belt, Nikolaos Alachiotis

Detecting selective sweeps using FPGA-accelerated spiking convolutional neural networks Hanqing Zhao, Federico Corradi, Zhanbo Shen, Nikolaos Alachiotis

Detecting Positive Selection using Convolutional Neural Networks
Charlotte West, Conor Walker, Nicola DeMaio, Nick Goldman

13h-14h30 lunch break

14h30-16h Phylodynamics (chair: Flora Jay)

Improving tree representation and neural network architecture for deep learning from phylogenies in phylodynamics and diversification studies
Manolo Perez, Olivier Gascuel

Transformers for EpiDemiological DYnamics: from genomic data to epidemiological parameters
Vincent Garot, Luca Nesterenko, Luc Blassel, Anna Zhukova, Samuel Alizon, Laurent Jacob

Assessing the power of artificial intelligence approaches for birth-death model classification Pablo Gutiérrez de la Peña, Guillermo Iglesias Hernández, Andrea Sánchez Meseguer, Isabel Sanmartín

16h-16h15 closing comments

16h15-18h after conference chill out (posters can still hang until 18h)

Poster Session:

01	Hierarchical ancestry inference with tangletrees and Simulation-Based Inference of demographic histories	Baumdicker Franz
02	OliveTrees: A suite of computational tools for effective phylogenetic analysis, manipulation and visualization	Charamis Jason
03	Disentangling the genomic basis of terrestrialization across animals through a transcriptomics spyglass	Eleftheriadi Klara
04	Quantum simulation and estimation of processes and branch lengths in phylogenetic trees: the tools of Quantum Walks and ML Variational Quantum Algorithms	Ellinas Demosthenes
05	Ancestral reconstruction of CRISPR arrays and probabilistic models for their evolutionary dynamics reveal selective effects along their length	Fehrenbach Axel
06	Good-Wines: Integrative Analysis of Vitis Next-Generation Sequencing Data to Optimize Cultivar Identification.	Matzavras Panayiotis
07	Distilling Protein Embedding Information into Phylogenetic Trees	Olenyi Tobias
08	Topological comparison of coalescent tree inference tools.	Pouyet Fanny
09	Uncovering the architecture of selection from experimentally evolved populations with Machine Learning	Ribeiro Diogo
10	Machine Learning for Predicting Antibiotic Resistance in Escherichia coli	Teimouri Melika
11	Identifying the multiple drivers of cactus diversification	Thompson Jamie
12	Domain based prediction of human Protein-Protein Interactions	Tsaglioti Electra
13	Statistical framework to determine indel-length distribution	Wygoda Elya
14	Mapping Nanopore Squiggles to Graphs Enables Accurate Taxonomic Assignment and Captures Evolutionary Relationships Between Organisms	Zeng Wenhuan
15	Identifying the multiple drivers of cactus diversification	Thompson Jamie