

## Monday

8h45-9h Welcome, introduction

9h-10h Keynote

*Harnessing AI in phylogenomics*

Tal Pupko

10h-11h Phylogenetics (1/2)

*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

11h-11h30 coffee break

11h30-13h Simulating realistic data

*Assessing usefulness of artificial genomes via local ancestry inference*

Maiwen Demeulle, Titouan Chambe, Antoine Szatkownik, Léo Planche, Burak Yelmen, Flora Jay

*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

*Deep learning for the phylogenetic inference of species diversification*

Hélène Morlon

15h30-16h30 Phylogenetics (2/2)

*Neural networks can predict ghost species diversity from gene transfers*

Enzo Marso, Théo Tricou, Laurent Jacob, Bastien Boussau, Damien De Vienne

*Predicting Phylogenetic Bootstrap Values via Machine Learning*

Julius Wiegert, Julia Haag, Dimitri Hoehler, Alexandros Stamatakis

16h30-17h coffee break

17h-19h poster session [posters could hang for the rest of the conference?]

## Tuesday

9h-10h Keynote

*Generative adversarial networks, transfer learning, and interpretability for evolutionary inference*

Sara Mathieson

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

*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)

*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 [1 keynote, 8 contributed, poster session]

9h-10h Keynote

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

10h-11h Population genetics (1/2)

*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 Population genetics (2/2): selective sweep detection

*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

*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 poster session