Introduction 9h00-9h10 : Pierre Paoletti 9h10-9h40 : Auguste Genovesio (IBENS)

ML as an advanced tool for extracting experimental data 9h40-10h20: Keynote: Thomas Walter (Mines-Paris, Institut Curie) TBA

10h20-10h45 : Alan Tourancheau & Diletta Ciardo (IBENS, Hyrien team) Uncovering DNA replication footprints with Nanopore sequencing

Coffee break (25')

11h10-11h35 : Anthony Lourdiane (IBENS, Bourdieu team) Inferring neural data sequences using Restricted Boltzmann Machines

<u>ML to build statistical models of biological data</u> 11h35-12h15 : Keynote: Simona Cocco (LPENS) *From sequence data to fitness predictions and design in proteins and nucleic acids* 

12h15-12h40 : David Stroebel (IBENS, Paoletti team, Protein platform) Alphafold, a game changer in protein biology: Uses, limits and perspectives

Lunch break (Espace Curie, 1h20')

14h-14h25 : Ethan Cohen (IBENS, Genovesio team) Integrating Cell Painting and AI: A Novel Approach for Early-Stage Compound Pre-Selection

14h25-14h50 : Roy Elhourany (IBENS, Bowler team; current affiliation: Univ. Littoral Côte d'Opale, Univ. Lille & CNRS) Observing Phytoplankton Community Structure from Space Using Machine Learning Methods

From ML to theory

14h50-15h30 : Keynote: James Whittington (Stanford University & Oxford University) How artificial and biological neural networks build schemas of sequences

Coffee break (20')

15h50-16h15 : Jorge Cossio Diaz (JRC, PSL LPENS) Designing molecular RNA switches with Restricted Boltzmann machines

16h15-16h40 : Sophia Lambert (IBENS, Morlon team; current affiliation: University of Oregon, Eugene, USA) Deep Learning from Phylogenies for Diversification Analyses

16h40-17h20 : Keynote: Srdjan Ostojic (DEC ENS) Linking structure and function in recurrent neural network models of cognitive tasks

17h20-17h30: Concluding remarks