

# MCEB 2024

(<https://mceb2024.sciencesconf.org/?lang=en>)

Le Hameau de l'Etoile<sup>1</sup>  
17-21 June

## Monday, June 17

18:00 Welcoming of participants. Apéritif

20:00 Dinner

## Tuesday, June 18

09:00-10:00 (Plenary address) **Tal Pupko**

10:00-10:30 Break

10:30-10:50

Kate Truman *"Identifiability of the Fossilised Birth-Death model"*

10:50-11:10

François Rousset. *"Better confidence intervals in simulation-based inference"*

11:10-11:30

Miguel De Navascués. *"Demographic inference from radiocarbon data"*

11:40-12:00

Andreas Futschik. *"Detecting selection using signature kernels: A novel*

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<sup>1</sup> <https://maps.app.goo.gl/gMAnSEfvF2boZt1Q6>

method for multi-locus Wright-Fisher models with recombination"

12:00-12:20

Anna Zhukova *"Epidemiological birth-death models with partner notification"*

12:15-14:00 Lunch break

14:00-17:30 Discussions

17:30-18:30 (Plenary address) **Claire Guinat**

18:30-20:00 Poster session 1

20:00 Dinner

## Wednesday, June 19

09:00-10:00 (Plenary address) **Claudia Solis-Lemus**

10:00-10:30 Break

10:30-10:50

Scott Edwards *"New Bayesian methods for linking genomic and phenotypic variation"*

10:50-11:10

Isabel San Martín. *"Assessing the power of artificial intelligence approaches for birth-death models"*

11:10-11:30

Cécile Ané *"Identifying circular orders for blobs in phylogenetic networks"*

11:40-12:00

Wakinyan Benhamou *"Inferring the life-history traits of new viral variants from epidemiological and evolutionary dynamics"*

11:00-12:20

Antoine Aragon *"Learning evolutionary parameters from allelic trees"*

12:20-14:00 Lunch break

Free afternoon

## Thursday, June 20

09:00-10:00 (Plenary address) **Jean-Michel Marin**

10:00-10:30 Break

10:30-10:50

Marius Brusselmans *"On the importance of assessing topological convergence in Bayesian phylogenetic inference"*

10:50-11:10

Luc Blassel *"Phyloformer: towards fast and accurate phylogeny estimation with self-attention networks"*

11:10-11:30

Katharina Huber *"Ploidy profiles and phylogenetic networks with horizontal arcs"*

11:40-12:00

Carlos Albors *"Substitution rate prediction as a pretraining task for models of human genomes"*

12:00-12:20

Marta Pelizzola *"Robust learning of mutational signatures using non-negative matrix factorization"*

12:20-14:00 Lunch break

14:00-17:30 Discussions

17:30-18:30 (Plenary talk) **Yun S. Song**

18:30-20:00 Poster session 2

## Friday, June 21

09:00-10:00 (Plenary address) **Caroline Colijn**

10:00-10:30 Break

10:30-10:50

Simon Boitard "*SelNeTime : a new method inferring demography and selection from genomic time series data*"

10:50-11:10

Lars Berling "*Statistics in the space of ranked time trees*"

11:10-11:30

Frédéric Lemoine "*The Bayesian phylogenetic bootstrap and its application to short branches and trees*"

11:30-11:50

Hector Banos "*Topics in profile mixture models: Overparameterization and a Linked general-time reversible model*"

12:50-12:10

Carolin Kosiol "*Polymorphism-aware models in RevBayes: Species trees, disentangling Balancing Selection and CG-biased gene conversion*"

12:10-13:30 Lunch break

13:30 Departure to Montpellier (arrival scheduled at 14:30 at Gare Routière)

#### Poster session 1

- Jordan Moutet "*Algorithms to reconstruct past indels: a parsimony approach*"
- Amélie Ngo "*Applying mathematical models to unravel pathogen evolution: identifying severe phenotype association through computational phylogenetics*"
- Valentino Giulio Dalla Riva "*Are evolutionary unique species ecologically unique?*"
- Yuki Takasawa "*Beyond the majority rule consensus tree*"
- Mael Guivarch "*Comparing clustering methods to highlight fine-scale genetic structure using simulations and POPGEN data*"

- Bastien Boussau *"Detection of site-specific selection regimes in protein alignments using transformers"*

## Poster session 2

- Anastasis Togkousidis *"Early stopping in Maximum Likelihood Phylogenetic Inference"*
- Askar Gafurov *"Efficient analysis of annotation colocalization accounting for genomic contexts"*
- Nikita Kulikov *"Machine learning phylogenetics empowered by dimensionality reduction techniques"*
- Harry Gordon *"Simulation based inference of the evolutionary history of wildcats (Felis silvestris): Machine learning for population genomics"*
- Vincent Moulton *"The space of equidistant cactuses"*
- Daniel Hudson *"Trees, networks, QR codes and the SplitsTree App"*