MCEB 2022
Château d’Oex, Suisse
June 26-30, 2022
MATHEMATICAL AND COMPUTATIONAL EVOLUTIONARY BIOLOGY

Program

LIRMM
CNRS
Université de Montpellier
UNIL | Université de Lausanne
Swiss National Science Foundation
BiM
INRAE
Labex NUMEV
SIB
Swiss Institute of Bioinformatics
**Meeting Point**

Directly at the Hotel Roc & Neige on Sunday, May 26th.

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=> inside France use 0 to start (06 48...), outside france use +33 without the 0 (336 48...)

**Location**

The conference will be held in the village of Chateau d’Oex, The municipality is located in the Vaud part of the Sarine valley between the Saanenland in the canton of Bern (in French: Gessenay) upstream and the Intyamon in the canton of Fribourg downstream, at an altitude of approximately 1,000 m. Château-d’Œx is the largest municipality in the canton of Vaud, with an area of 11,374 ha, of which 2% is residential and infrastructure land, 44.6% is agricultural land, 35.9% is woodland and 16.6% is unproductive land.

The minimum altitude of the municipality is 870 m at the level of the Sarine, the average altitude is 1,489 m and the highest point is at 2,548 m on the summit of Tarent on the Pic Chaussy - Cape au Moine ridge. The municipality comprises several villages and hamlets. Apart from Château-d’Œx, the main town, the most important are Les Moulins and Les Granges, at the bottom of the valley, as well as L’Étivaz and La Lécherette, on the road to the Col des Mosses.
Hôtel Roc et Neige

Route des Monnaires 46, 1660 Château-d’Oex
Telephone +41 (0)26 924 33 50
info@rocetneige.ch
https://www.roc-et-neige.ch/contact

Train:
To get there by train, you have to go through Geneva, then Lausanne, Montreux and finally Chateau d’Oex. It takes 2h30 from Geneva. To reach the hotel from the station, you have to walk a distance of 800m. The map below explains the itinerary.

Tickets and information
Montreux-Oberland Bernois - Buy tickets - 00 41 21 989 81 90
SNCF - 01 84 94 36 35
Chemins de fer fédéraux suisses - Buy tickets - 00 41 900 300 300
Sunday, June 26th

19h00    Welcome drink
20h00    Dinner

Monday, June 27th

09h00    Keynote – Niko Beerenwinkel

*Inferring tumor evolution from single-cell data*

10h00    Coffee break

10h40    Scholz Guillaume

*Fast detection of recombinant sequences in viruses using phylo-k-mers*

11h00    Latrille Thibault

*Empirical evidence for positive selection that is not adaptive evolution*

11h20    Break

11h40    Mashayekhi Somayeh

*Fractional coalescent*

12h00    Otto Moritz

*Recombination, selection and the evolution of tandem gene arrays*

12h30    Lunch

Afternoon: social activities and discussions

17h30    De Sousa Mota Bárbara

*Imputation of ancient genomes*

17h50    Anchieri Lucas

*Benchmarking methods using time-series data to infer selection*

18h10    Break

18h40    Nesterenko Luca

*Phyloformer: Fast and accurate phylogeny estimation with self-attention networks*

19h00    De Vienne Damien M.

*The overlooked effect of ghost lineages for the study of gene flow*

19h30    Dinner
**Tuesday, June 28th**

09h00  **Keynote – Denise Kühnert**  
*Archaeogenetics meets phylodynamics: tracking the evolution of pathogens over millennia*

10h00  Coffee break

10h40  **Cornuault Josselin**  
*Do genes’ coalescence times carry information on demography?*

11h00  **Catanzaro Daniele**  
*Balanced Minimum Evolution: Theoretical and Computational Advances*

11h20  Break

11h40  **Bollen Nena**  
*Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020*

12h00  **Huson Daniel**  
*SplitsTree6 - integrating phylogenetic trees and networks*

12h30  Lunch  
**Afternoon: social activities and discussions**

17h  **Keynote - Carolin Kosiol**  
*Polymorphism-aware phylogenetics models*

18h  Poster session (1 to 12) + aperitif

19h30  Dinner

**Wednesday, June 29th**

09h00  **Keynote – David Bryant**  
*The Concatenation Question*

10h00  Coffee break

10h40  **Szollosi Gergely**  
*Trade-off between reducing mutational accumulation and increasing commitment to differentiation determines tissue organization*
11h00  featherstone leo  
assessing the effects of date and sequence data in phylodynamics

11h20: break

11h40  zhukova anna  
fast and accurate resolution of the birth-death exposed-infectious (bdei) model

12h00  bastide paul  
a cauchy process to model trait evolution on a phylogeny

12h30  lunch
afternoon: social activities and discussions

17h  keynote – maria anisimova  
phylogenetics with indels

18h  poster session (13 to 23) + aperitif

19h30  dinner

Thursday June 30th

09h00  keynote – cécile ané  
estimating species networks to model reticulate evolution: challenges and identifiability

10h00  coffee break

10h40  dalla riva giulio valentino  
phylogenetics and ecological networks: old challenges and new opportunities

11h00  urban lara  
the ghost of past selection in the critically endangered kākāpō

11h20  break

11h40  layan maylis  
impact and mitigation of sampling bias to determine viral spread: evaluating discrete phylogeography through ctmc models and structured coalescent model approximations

12h00  vaughan timothy - bayesian phylodynamic inference of multi-type population trajectories using genomic data

12h30  lunch
14h00  departure
Keynote speakers

> Cecile ANE
*Professor of Botany and Statistics*
University of Wisconsin–Madison

> Maria ANISIMOVA
*Head of Applied Computational Genomics and Lecturer, SIB group leader*
ZHAW School of Life Sciences and Facility Management
Fachstelle Computational Genomics

> Niko BEERENWINKEL
*Professor Dep. of Biosystems Science and Eng*
ETH Zürich Computational Biology Group

> David BRYANT
*Professor University of Otago*
University of Otago, New Zealand

> Carolin KOSIOL
*Lecturer in Bioinformatics*
University of St Andrews

> Denise KÜHNERT
*Transmission, Infection, Diversification & Evolution Group - Research Group Leader*
Max Planck Institute for the Science of Human History
1 - **Jowkar Gholamhossein**  
ARPIP: Ancestral sequence Reconstruction with insertions and deletions under the Poisson Indel Process

2 - **Gamblin Jasmine**  
Beyond one-gain models for pangenome evolution

3 - **Rocu Pauline**  
Sampling consistency of diffusion statistics in bayesian phylogeography

4 - **Talibart Hugo**  
PPalign: Optimal alignment of Potts models representing proteins with direct coupling information

5 - **Linard Benjamin**  
Improving gene classification into gene families via phylo-k-mers

6 - **Romashchenko Nikolai**  
Mutual Information-based Feature Selection of Informative Phylo-k-mers

7 - **Li Yimin**  
Preprocessing Strategies for Bayesian Phylogeographic Analysis Using Large-Scale Genomic Sequence Data

8 - **Wirtz Johannes**  
Combinatorics of multiple-merger coalescent genealogies

9 - **Potter Barney**  
Leveraging tools from Nextstrain for bespoke phylogenetic analysis of viral pathogen epidemics

10 - **Tuffet Rémi**  
Modeling the dynamics of antibiotic resistance genes: towards an ecology of the bacterial pangenome

11 - **Zarebski Alexander**  
Estimation of reproductive number and prevalence using genomic and time series data

12 - **Bastian Mélodie**  
Bridging the gap between population genomic and phylogenetic approaches

13 - **Moi David**  
Convolutional graph networks for Coevolution detection in COVID19

14 - **Nahata Kanika**  
Bayesian model comparison of molecular clock models - a phylogenetic simulation study

15 - **Carpentier Mathilde**  
Protein folds as synapomorphies of the tree of life

16 - **Boussau Bastien**  
Evaluation of methods to detect shifts in directional selection at the genome scale
17 - Verbiest Max
Uncovering the Diverse Roles of Short Tandem Repeat Variation in Colorectal Cancer

18 - Genestier Alice
The influence of genetic dosage on PRDM9-dependent evolutionary dynamics of meiotic recombination

19 - Pourhasanzade Fateme
An Individual-based model to study the importance of trade-offs in the evolution and diversification of traits in host-phage population dynamics

20 - Hong Samuel
GPU-accelerated online phylodynamic inference using BEAST

21 - Koubinova Darina
Intergeneric relationships within Ophioglossaceae untangled with organelle phylogenomics

22 - Paul Zaharias
The robustness of bootstrap branch supports with respect to taxon sampling

23 - David Swofford
Likelihood Via Decomposition: A fast, highly parallelizable alternative to Felsenstein pruning for computing likelihoods of phylogenetic trees