MCEB 2022

Château d'Oex, Suisse
June 26-30, 2022

MATHEMATICAL AND COMPUTATIONAL EVOLUTIONARY BIOLOGY

Program

INFORMATION

Meeting Point

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

In case of problems :
Olivier Gascuel : +33 (0) 06 48 12 14 82
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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 ha5 , 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.
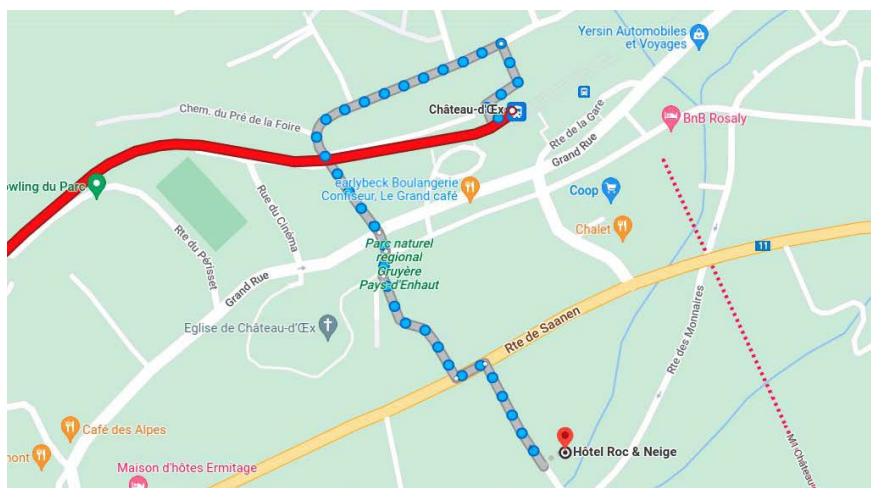To reach the hotel from the station, you have to walk a distance of 800m.
The map below explains the itinerary.

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

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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

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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

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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

Posters

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

Notes

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