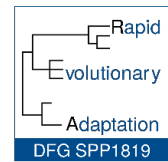


SPP1819
Summer Workshop 12th - 14th Mai 2020
Technical University of Munich, Freising, Germany



Title: "Inference of past demographic history using full genome data"

Objectives:

- 1) Learn and practice the inference of demography from full genome data using various methods.
- 2) Participate to a joint work to assess the power of these methods and writing of a research paper summarizing the findings.

Summary of the concept:

With the advances in sequencing technology, it is feasible to scan genomes for genes under selection to pinpoint the bases of rapid adaptation in various species. This is made possible by the theoretical prediction (which has been tested on many species since) that selection acts locally while demographic and stochastic effects of genetic drift occurs affect the whole genome. Furthermore, it may be interesting in its own right to study the demographic history of a population or species, especially in link to changes/colonization of new habitats, new ecological niches or as a consequence of climate change. In this workshop we want to assess different methods that use full genome polymorphism data to draw statistical inference of the past demography of a population. We want specifically learn how to use and parametrize them, assess their advantages, pitfalls and limitations. Two main classes of methods will be studied with guest instructors who developed them: 1) the Sequential Markov Coalescent (SMC) based methods such as PSMC, MSMC and SMC++, and 2) methods partitioning the genome in many smaller units and using summary statistics of the polymorphism data such as ABLE and Approximate Bayesian Computation (ABC). As most methods are based and tested on human datasets with long scaffolds and large genomes and large sample size, it is important to assess the quality of the inference based on the required number of individuals and length of sequences. We will divide the participants into two groups. One group will analyze a set of small datasets typical for the groups of the SPP1819 (non-model species, genomes may be incomplete, high number of transposable elements,...), while the second will be designing simulation scenarios to be evaluated (using msprime or other coalescent simulators).

On day one and two we will provide with the instructors a summary of the theory of coalescence, summary statistics, bases of demographic signatures as well as introduction to ABC, SMC and Hidden Markov Model statistical tools. On day two, the participants will be divided into groups based on a short informal presentation of their research projects.

On day two and three the inferences will be run and the first meta-analyses performed. Participants will leave at lunch time on day three. We will further set up a common virtual working place to exchange results and build up material for a publication.

Location: Technical University of Munich (TUM), Campus Weihenstephan, Freising, Germany.

Practical informations: The workshop will start on Tuesday 12th Mai at 9.00 and finish at lunch time on Thursday 14th of Mai 2020. The participants are asked to arrive on Monday 11th in the evening.

Organizers: Prof Aurelien Tellier, TUM, Prof Karl Schmid Uni. Hohenheim.
Silke Bauer (TUM), B. Dößelmann (Uni Hohenheim)

Instructors:

Simon Boitard (INRA – Toulouse, France): ABC methods for full genome data

Konrad Lohse (Uni. Edinburgh, UK): Inference methods of population divergence using full genome data

T. Sellinger (TUM), K. Boendel (Uni. Hohenheim), F. Freund (Uni Hohenheim).