ForBio course: Phylogenomics,

Marine Biological Station Tollboden,
Drøbak, UiO June 03 – 15, 2018

Tentative schedule

Each day will end with a discussion of the results before dinner and after the dinner with a discussion about general problems about the methods as well as specifically associated ones with students' projects. There is also the possibility for students to present their research projects. All sessions will include several coffee breaks to relax and recharge the mind. Each day we will have a lunch break from 12-13 and a dinner break from 18-20.

Sunday, 3rd

15-18

Refresher on working on the command line.

Monday, 4th

9-12:

Set-up of lab & upload of material

Introduction into the general topic & review of sequencing technologies

13-17:

Sequence data formats, quality control measurement, assembly of genomes & transcriptomes

Tuesday, 5th

9-12:

Assessment of assembly quality & orthology assignment

13-17:

Assessment of orthology assignment, compilation of sequences into datasets, sequence alignment, masking of data

Wednesday, 6th

9-12:

Concatenation of individual gene datasets, matrix reduction, visualization of missing data in the dataset

13-17:

Model selection and tree reconstruction approaches

Thursday, 7th

9-12:

Introduction into rogue taxa in the datasets

13-17:

Base composition heterogeneity between taxa and across genes

Friday, 8th

9-12:

Introduction into Branch length heterogeneity and its visualization

13-17:

Measuring branch length heterogeneity using metric approaches

Saturday, 9th

9-12 & 13-17:

Buffer for the first week, if schedule should get delayed

In the evening:

Course dinner & party – social event

Sunday, 10th

Free day; for interested participants Tour to Oslo in the afternoon (based on interest expressed during the first week)

Monday, 11th

9-12:

Evolutionary rate, saturation and models of substitution

13-17:

Incongruencies between single gene trees and their causes (model misspecification, paralogy, incomplete lineage sorting, horizontal gene transfer, ancestral hybridisation) & detecting partitions in large scale datasets

Monday, 11th

9-12:

Evolutionary rate, saturation and models of substitution

13-17:

Incongruencies between single gene trees and their causes (model misspecification, paralogy, incomplete lineage sorting, horizontal gene transfer, ancestral hybridisation) & detecting partitions in large scale datasets

Tuesday, 12th

9-12:

Detecting incongruencies between partitions using Paralogy detection

13-17:

Detecting incongruencies between partitions using Partition approaches

Wednesday, 13th

9-12 & 13-17:

BLAST at the command line and contamination screening using metabarcode-based approaches (development of a pipeline as the case problem for the course assessment)

Thursday, 14th

9-12:

Network reconstructions

13-17:

Supertree & coalescence tree methods

Friday, 15th

9-12:

Novel approaches to analyze phylogenomic data using the quartet-based PINGUIN method

13-14:

Summary & wrap-up