

Workshop on molecular phylogenetics

Centre for Marine Living Resources & Ecology, Kochi,
October 8-10, 2018

Day 1 (October 8, Monday)

9:30 -11:00

Origin of tree building

Introduction, Taxonomy vs. Systematics

11:00-12:30

Methods of tree building using DNA sequence data-I

Distance approach: UPGMA, NJ

Estimating pairwise genetic distance and nucleotide substitution models

12:30-1:30

Lunch

1:30-2:30

Methods of tree building using DNA sequence data-II

Character state approach (discrete methods): Parsimony

2:30-6:00

Computer lab: Installation of programs, working with the program MEGA and PAUP

Day 2 (October 9, Tuesday)

9:30 -11:30

Methods of tree building using DNA sequence data-II

Character state approach (discrete methods): Maximum likelihood and Bayesian approaches

11:30-12:30

Comparing different methods of tree building

Clustering (algorithmic) vs. search (optimality criteria) methods, character state approach (discrete methods) vs. distance approach, heuristic searches

Statistical tests

Bootstrap (BT), Likelihood ratio test and applications, test for monophyly (parametric BT, S-H test)

12:30-1:30

Lunch

1:30-2:30

Phylogenetic approach to species delimitation

2:30-6:00

Computer lab: Working with the programs PAUP, Partition finder, RAxML and MrBayes

Day 3 (October 10, Wednesday)

9:30-11:00

Applications of molecular phylogenetics

Molecular phylogenetics: frequently asked questions

11:00-12:30

Introduction to biogeography

Unraveling historical biogeographic patterns of the Indian subcontinent using skinks as a model system

12:30-1:30

Lunch

1:30-2:30

Molecular Dating

Molecular clock hypothesis, strict molecular clock, relaxed molecular clocks

Species trees

Multispecies coalescent models

2:30-6:00 Computer lab: Working with the programs S-DIVA, BEAST and SVDquartet
Extra time for discussing topics covered thus far (if needed); discussion on individual projects