Course name: Phylogenetics with R

Credits: 6 ECTS

Class type: On-line lectures + individual practice

Type of the exam: questionaire

Prerequisites (if exist):
Courses:
- Biological data analysis with R

Course description: Phylogenetics is the taxonomical classification of organisms based on how closely they are related in terms of evolutionary differences. The course will familiarize students with different phylogenetics algorithms and practical software applications for biological problems.
- Introduction to phylogenetics, and essentials of evolution as background
- Data types for phylogenetic analysis and parsimony
- Distance based methods, distance matrices, nucleotide substitution models
- Model based methods: maximum likelihood and Bayesian phylogenetics
- Auxiliary methods: bootstrapping, consensus trees, tree comparison
- Visualization of phylogenetic trees

Required reading:


Lecturer (name, position, degree): Zoltán Gáspári, associate professor, PhD

Additional lecturers, if exist: 