

Course name: Phylogenetics with R	Credits: 6 ECTS
Class type: On-line lectures + individual practice	Hours per week:
Type of the exam: questionnaire	
Prerequisites (if exist): Courses: <ul style="list-style-type: none"> • 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. <ul style="list-style-type: none"> • 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:	
Recommended reading: Wiley, E.O. & Lieberman, B.S. (2011) Phylogenetics: Theory and Practice of Phylogenetic Systematics, 2nd. ed. Wiley-Blackwell	
Lecturer (<i>name, position, degree</i>): Zoltán Gáspári, associate professor, PhD	
Additional lecturers , if exist:	