

## **MOLEKULARNÍ PHYLOGENETICS AND TAXONOMY**

### **MB160P21 (HAMPL, NOVOTNÝ) 2021**

Lectures will be held on Mondays 9:00-10:30 am

- 4. 10. - Introduction, taxonomy, molecular characters, sekvencing of DNA (Hampl)
- 11. 10. - Alignment of sequences (Novotný)
- 18. 10. – Sequence databases and searches in them (Novotný)
- 25. 10. – Other methods of obtaining of molecular data – multilocus methods (RAPD, RFPL etc.), microsatellites, minisatellites, SINE elements, protein mass fingerprint (Hampl)
- 1. 11. - SNP, sequence evolution, calculation of genetic distances (Hampl)
- 8. 11. – Phylogenetic trees I. - Protein distances, reconstruction of phylogenetic trees from the distance matrix, anatomy of trees (Hampl)
- 15. 11. - Phylogenetic trees II. Rate heterogeneity, search through the tree space, maximum parsimony (Hampl)
- 22. 11. - Phylogenetic trees III. - Maximum likelihood, Bayesian metod (Hampl)
- 29. 11. - Phylogenetic trees IV. - Multigene analyses, robustness of branching, rooting of trees, topology tests, molecular dating (Hampl)
- 6. 12. – Forensic genetics, DNA barcoding (Hampl)
- 13. 12. 2020 – Intraspecific phylogeny, population structure and gene flow, phylogeography, examples (Hampl)
- 20. 12. 2020 – Metabarcoding – methods of diversity analyses from environmental sequencing data (Hampl)
- 10. 1. – Presentation of student essays

## **PRACTICALS OF MOLECULAR PHYLOGENETICS**

### **MB160C21 (FÚSSY AND TREITLI) 2020**

Lectures will be held online on Zoom on Fridays at 10:40-13:40 am.

- 27. 11. – Database searches, sequence formats, alignment
- 4. 12. – Trees from the DNA sequences
- 11. 12. – Trees from amino acid sequences
- 18. 12. – Bayesian methods, molecular dating
- 8. 1. 2021 – Metabarcoding