

Georg-August-Universität Göttingen Module M.Biodiv.479: Phylogenomics	6 C 6 WLH
<p>Learning outcome, core skills:</p> <p>The research field of phylogenomics comprises the utilization of genome and transcriptome data for the inference of phylogenetic trees. In this modul students will be introduced to the theoretical and practical knowledge of how to assemble genomes and transcriptomes and their annotation. Moreover, techniques to search for genes in such data will be presented (e.g., BLAST, hidden markov models). Additionally, the students will work with different alignment- and read mapping methods. Based on the assembled datasets different tree reconstruction methods will be conducted (Neighbor Joining, Maximum Parsimony, Maximum Likelihood, Bayesian Inference) and critically discussed. Within an accompanying seminar actual studies in the field of evolutionary genomics are presented and discussed.</p> <p>Students get an introduction into the Linux environment and the installation of all programs will be done independently. The command line will be mainly used for all analyses. Students will learn to perform genome-scale analyses for the reconstruction of phylogenetic trees. Within a seminar students will present recently published genomic studies in English language. In the last week, datasets will be analysed independently and results will be summarized as poster, which will be presented within a short talk.</p>	<p>Workload:</p> <p>Attendance time: 84 h</p> <p>Self-study time: 96 h</p>
<p>Course: M.Biodiv.479.VL Introduction to phylogenomics (Lecture)</p>	1 WLH
<p>Course: M.Biodiv.479.Sem Introduction to phylogenomics (Seminar)</p> <p>This course is open for students of the double degree programme at the partner universities. The sessions of this course might be conducted in a remote format like online video conference.</p>	1 WLH
<p>Course: M.Biodiv.479.Ue Introduction to phylogenomics (Exercise)</p>	4 WLH
<p>Examination: Oral Presentation (approx. 15 minutes)</p> <p>M.Biodiv.479.Mp: Introduction to phylogenomics</p> <p>Examination requirements:</p> <p>Short talk (ca. 12-15 minutes) and poster presentation</p>	6 C
<p>Examination requirements:</p> <p>Knowledge of how to reconstruct phylogenetic trees using genomic and transcriptomics data. Critical discussion of phylogenetic analyses and overview of actual controversies.</p>	
<p>Admission requirements:</p> <p>none</p>	<p>Recommended previous knowledge:</p> <p>none</p>
<p>Language:</p> <p>English</p>	<p>Person responsible for module:</p> <p>Dr. Sarah Bank-Aubin</p>
<p>Course frequency:</p> <p>each summer semester</p>	<p>Duration:</p> <p>1 semester[s]</p>
<p>Number of repeat examinations permitted:</p> <p>twice</p>	<p>Recommended semester:</p> <p>1</p>

Maximum number of students:	
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15	
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