Georg-August-Universität Göttingen	6 C
Module M.Biodiv.479: Phylogenomics	6 WLH
Learning outcome, core skills:	Workload:
The research field of phylogenomics comprises the utilization of genome and	Attendance time:
transcriptome data for the inference of phylogenetic trees. In this modul students will	84 h
be introduced to the theoretical and practical knowledge of how to assemble genomes	Self-study time:
and transcriptomes and their annotation. Moreover, techniques to search for genes in	96 h
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.	
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.	
Course: M.Biodiv.479.VL Introduction to phylogenomics (Lecture)	1 WLH
Course: M.Biodiv.479.Sem Introduction to phylogenomics (Seminar)	1 WLH
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.	
Course: M.Biodiv.479.Ue Introduction to phylogenomics (Exercise)	4 WLH
Examination: Short talk (ca. 12-15 minutes) and poster presentation	6 C
M.Biodiv.479.Mp: Introduction to phylogenomics	
Examination requirements:	
Knowledge of how to reconstruct phylogenetic trees using genomic and transcriptomics	
data. Critical discussion of phylogenetic analyses and overview of actual controversies.	

Admission requirements:	Recommended previous knowledge:
none	none
Language:	Person responsible for module:
English	Dr. Sarah Bank-Aubin
Course frequency:	Duration:
each summer semester	1 semester[s]
Number of repeat examinations permitted:	Recommended semester:
twice	1
Maximum number of students: 15	