

WiSe20_Molecular Phylogenetics (Theorie)

Modulvariante zu: Aktuelle Themen der Biodiversität, Evolution und Ökologie

Titel: Molecular Phylogenetics (Theorie)			
Hochschule/Fachbereich/Institut: Freie Universität Berlin/Fachbereich BCP/Institut für Biologie			
Modulverantwortliche/r: Prof. Thomas Borsch			
Zugangsvoraussetzungen: Keine			
<p>Qualifikationsziele: Understanding phylogenetic relationships is of fundamental importance in biology. Today phylogenetic hypotheses open up a wide field of further questions such as character and trait evolution, tempo and mode of species diversification, taxonomic classification, and historical biogeography. This course provides an introduction to phylogenetic theory and methods for generating molecular phylogenetic trees. After the course, the students should (1) be familiar with the basic concepts of phylogenetics and be able to critically reflect on the phylogenetic aspects in relevant biological literature; and should (2) know protocols and methods (wet lab and bioinformatics analysis) that are widely applied in phylogeny reconstruction. The student will learn methods and protocols, from material collection to sequence generation, by implementing them in the lab. Furthermore, students will acquire knowledge on how to analyze sequence data with the goal of reconstructing phylogenetic trees, and get familiar with the most important computer programs.</p>			
<p>Inhalte: The course will use selected groups of flowering plants as exemplars to reconstruct phylogenetic trees based on DNA sequence data. It starts with the collection and documentation of plant material (living collection and herbarium of the BGBM) and the isolation of genomic DNA. Subsequently, laboratory steps including PCR amplification and sequencing will be carried out. The primary data (such as pherograms) will be analyzed, assembled and processed into a matrix of sequence characters. Data matrices will then be analyzed with a spectrum of methods and computer programs to reconstruct phylogenetic trees, The trees will be digitally visualized and discussed in relation to the knowledge gained on the respective study group. The course employs a mini-project approach with which participants can, to a large extent, generate and analyze their own data. The lecture and seminar part will address the theory of phylogenetics (cladistics), homology and definition of characters comparing DNA and morphology, sources of molecular characters from the different genomic compartments (plastid, mitochondrial, nuclear), study design, multiple sequence alignment, models of sequence evolution, phylogenetic tree reconstruction using parsimony, Maximum Likelihood and Bayesian Interference, evaluation of node confidence, the use of phylogenetic trees to understand character and trait evolution and to inform classification, as well as current trends in molecular phylogenetics and our understanding of the evolutionary diversification of plants. While the course works with plants, the basic concepts and methods are also applicable to other groups of organisms.</p>			
Lehr- und Lernformen	Präsenzstudium (Semesterwochen-stunden = SWS)	Formen aktiver Teilnahme	Arbeitsaufwand (Stunden)
Vorlesung	2	–	Präsenzzeit V 30 Vor- und Nachbereitung V 15 Präsenzzeit S 15 Vor- und Nachbereitung S 60
Seminar	1	Vortrag und Diskussion	Prüfungsvorbereitung und Prüfung
Modulprüfung		Klausur (60 Minuten), ggf. ganz oder teilweise im Antwort-Wahl-Verfahren; kann auch in Form einer elektronischen Prüfungsleistung durchgeführt werden, oder schriftliche Dokumentation der Forschungsergebnisse (ca. 10 Seiten) oder Prüfungskolloquium (ca. 20 Minuten)	
Veranstaltungssprache	Deutsch und Englisch		
Pflicht zur regelmäßigen Teilnahme	Seminar: ja, Vorlesung: Teilnahme wird empfohlen		
Arbeitsaufwand insgesamt	150 Stunden		5 LP