

Curriculum and course program of ZGS

Obligatory topics need confirmation letter of successful participation in ZGS or comparable course program

| | Module number | Responsible | Length of course (in days) | Participati on latest in year | Internal Remarks |
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| Obligatory courses | | | | | |
| <i>In total maximum 14 days</i> | | | | | |
| Introduction to epistemology and ethics in science | ZGS-O1 | Wolfgang Wägele | 3 x 90 min | 1 | <i>also can be taken in year 2 (why not?)</i> |
| Principles of Systematics, Taxonomy and Nomenclature | ZGS-O2 | Dirk Ahrens | 2 | 1 | <i>could be shortened?</i> |
| General introduction in cladistics - morphology | ZGS-O3 | Wolfgang Wägele | 1 | 2 | |
| General introduction to molecular phylogenetic systematics | ZGS-O4 | Christoph Mayer Bernhard Misof | 2 | 2 | |
| Overview Imaging morphology | ZGS-O5 | Benjamin Wipfler | 1/2 | 2 | |
| Scientific collecting, field logistics, data management | ZGS-O6 | Matthias Geiger | 1 | 1 | |
| Presentation for scientific and public audience | ZGS-O7 | Eva Bärmann, Sabine Heine | 1 | 1 | |
| Scientific writing | ZGS-O8 | Heike Wägele, Fabian Herder | 2 | 1 | <i>Better outsourced in the beginning, e.g., www.science-craft.com</i> |
| Writing a scientific grant application | ZGS-O9 | Heike Wägele | 2 | 2 | <i>Better outsourced in the beginning, e.g., www.science-craft.com</i> |
| Monday Colloquium | ZGS-O10 | | 45 min | 1-3 | <i>At least 15 per year</i> |
| Talk within the Monday Colloquium | ZGS-O11 | supervisor | 30 min | 2 | |
| Biological Colloquium at university of Bonn | ZGS-O12 | | 45 min | 1-3 | <i>At least 10 per year</i> |
| Participation in students' retreat and presentation of a talk | ZGS-O13 | Supervisor/coor dinator? | 2 | 1-3 | <i>(at least one time)</i> |

| Facultative courses | Module number | Responsible | Duration (in days) | Remarks |
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| A Computational skills | | | | |
| HPC@ZFMK and introduction to Linux Obligatory | ZGS-FA1 | Alex Donath | 2 | Fakultativ or obligate? Prerequisite for many programs and cluster work |
| B Collection related methods | | | | |
| Collection and Extraction of Soil Arthropods Wesener | ZGS-FB1 | Thomas Wesener | 2 | |
| Preserving samples for molecular and morphological work | ZGS-FB2 | Jonas Astrin, Benjamin Wipfler | ½ | |
| Morphological Data Bases (MorphDBase) | ZGS-FB | Peter Grobe | | fehlt |
| Datenbanken (e.g., Diversity Workbench) | ZGS-FB | Peter Grobe | | Fehlt |
| C Research and methods Morphology | | | | |
| Basics in histology | ZGS-FC1 | Heike Wägele | 2 | |
| Geometric morphometrics | ZGS-FC2 | Eva Bärmann | 2 | |
| MicroCT scanning | ZGS-FC3 | Benjamin Wipfler | 1 | |
| 3D reconstruction | ZGS-FC4 | Benjamin Wipfler | 2 | |
| Phylogenetic tree reconstruction programs (morphological), PAUP, TNT | ZGS-FC5 | Ximo Mengual Marianne Espeland, Heike Wägele | 2 | |
| Introduction in ecomorphology | ZGS-FC6 | Till Töpfer | 1/2 | |
| D Research and methods Molecular | | | | |
| Programs and databases relevant to start molecular work | ZGS-FD1 | Lars Podsiadlowski, Matthias Geiger | 1 | |
| Metabarcoding (Theory and practical applications) | ZGS-FD2 | Sarah Bourlat | 2 | |
| BLAST – searching for sequences in data bases | ZGS-FD3 | Alex Donath, Christoph Mayer | 1 | |
| Alignment programs | ZGS-FD4 | Patrick Kück | 2 | |
| Alignment evaluation programs in molecular analyses | ZGS-FD5 | Patrick Kück | 2 | |
| Measure of phylogenetic support | ZGS-FD6 | Bernhard Misof, Christoph Mayer | 1 | |
| Genetree based phylogenetic methods (multispecies | ZGS-FD7 | Christoph Mayer, | 2 | |

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| coalescent methods) | | Marianne Espeland | | |
| Species delimitation tests | ZGS-FD8 | Marianne Espeland, Lars Podsiadlowski | 2 | |
| Analysis and visualisation of data from population genetics/genomics approaches | ZGS-FD9 | Lars Podsiadlowski Dirk Ahrens? | 2 | |
| Evolutionary models, maximum likelihood and model selection | ZGS-FD10 | Christoph Mayer, Bernhard Misof | 2 | |
| Evolutionary models and distance methods used for phylogenetic tree reconstruction | ZGS-FD11 | Christoph Mayer | 2 | |
| E Species, habitat and evolution modelling related methods | | | | |
| Phylogenetic comparative methods | ZGS-FE1 | Ralph Peters | 2 | |
| Introduction into Geographic Information System GIS | ZGS-FE2 | Dennis Rödder | 5 | |
| Introduction to scientific programming in R | ZGS-FE3 | Dennis Rödder | 5 | |
| F Further communication skills | | | | |
| Working with reference databases (Endnote, etc.) | ZGS-FF1 | Björn Quast | 1 | fehlt |
| Using libraries and retrieving information from online platforms | ZGS-FF2 | Katharina Schmidt- loske, Jonas Astrin, Mareike Krupka | 1 | |
| Offenes Trainings- und Coachingprogramm | ZGS-FF | | | https://www.gleichstellung.uni-bonn.de/de/foerderung/offenes-trainings-und-coachingprogramm |
| Kursprogramm Promotion plus | ZGS-FF | | 1 to several | https://www.uni-bonn.de/forschung/promotion/fuer-promovierende/qualifizierung/kurse-sole18 |
| Participation on the Leibniz PhD Network | ZGS-FF | | 1 to several | https://www.leibniz-gemeinschaft.de/karriere/wissenschaftlicher-nachwuchs/leibniz-phd-network/ |
| Participation in Doctoral workshops of the Leibniz Association | ZGS-FF | | 1 to several | https://www.leibniz-gemeinschaft.de/transfer/service/doktoranden-workshops/ |

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| Introduction to epistemology and ethics in science | |  |
| Modulnummer ZGS-O1, | obligatory | Duration of module: 3 x 90 minutes |
| responsible | Wolfgang Wägele | |
| Section | ZFMK | |
| lecturers | Wolfgang Wägele Jan Decher | |
| Goal of course | | |
| This course is recommended for following subjects | Not applicable | |
| Details or course program | Foundations of scientific thinking are rarely taught, but should be familiar to any researcher. We will discuss the distinction of different levels of ontology, the role of logics, what is a truth in science, and the disclosure of unethical behavior using real examples from published literature..... | |
| Recommended reading | Foundations of Biophilosophy, Martin Mahner & Mario Bunge, Springer: 1997. | |
| This course is exclusively for the ZGS | | |

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| Principles of Systematics, Taxonomy and Nomenclature | |  |
| Modulnummer ZGS-O2, | obligatory | Duration of module: 2 days |
| responsible | Dirk Ahrens | |
| Section | ZFMK | |
| lecturers | Dirk Ahrens, Thomas Wesener, Matthias Geiger | |
| Goal of course | General introduction to Principles of Systematics, Taxonomy and Nomenclature including methods of species delimitation | |
| This course is recommended for following subjects | Not applicable | |
| Details or course program | <p>This seminar focuses on general principles of taxonomy and classification including the zoological nomenclature and scientific theory, procedures and methods related to taxonomy. It provides not only the basic skills for a taxonomist but also introduces into newest and cutting edge methods of species delimitation where classical "Old School" knowledge is linked with modern hypothesis-based science. Lectures will provide an overview on the history of taxonomy, species concepts, zoological nomenclature, classification and species delimitation based on morphological and molecular traits as well as on integrative taxonomy.</p> | |
| Recommended reading | will be announced | |
| This course is exclusively for the ZGS | | |

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| General introduction to cladistics | |  |
| Modulnummer ZGS-O3, | obligatory | Duration of module: 1 day |
| responsible | Wolfgang Wägele | |
| Section | ZFMK | |
| lecturers | Wolfgang Wägele | |
| Goal of course | Introduction to theory and practice of cladistic analyses based on morphological data to better understand pitfalls in application | |
| This course is recommended for following subjects | Not applicable | |
| Details or course program | Epistemological foundations of cladistics will be presented, together with best practice rules of character analysis and character coding. Participants will learn the basics of distance and maximum parsimony clustering of morphological data. Practical exercises with error analyses complete the course. | |
| Recommended reading | Pages 155-163, 181-224, 305-308 in: Foundations of Phylogenetic Systematics, J. W. Wägele, Verlag Dr. F. Pfeil, München (available here: https://www.researchgate.net/publication/263277681_Foundation_of_Phylogenetic_Systematics) | |
| This course is exclusively for the ZGS | | |

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| Introduction to molecular phylogenetic systematics | |  |
| Modulnummer ZGS-04, | obligatory | Duration of module: 2 days |
| responsible | Christoph Mayer and Bernhard Misof | |
| Section | ZFMK | |
| lecturers | Christoph Mayer | |
| Goal of course | <p>The module provides a very general overview of molecular phylogenetic systematics. In the course, the most important methods will be introduced, from data set generation, sequence alignment, to tree reconstruction. In particular, we will focus on potential problems and sources of errors in tree reconstructions.</p> <p>After the course, students shall be equipped with fundamental knowledge in this subject, such that they can understand publications and problems in this field. The discussion on sources of error and biases is of particular importance, since a critical evaluation of the own results is essential in all steps in a phylogenetic tree reconstruction.</p> | |
| This course is recommended for following subjects | Not applicable | |
| Details or course program | <p>The course introduces the following main topics: (i) alignments as hypotheses. Bad alignments can lead to wrong trees, (ii) distances among sequences and distance based methods, tree reconstruction methods based on optimality criteria, such as maximum likelihood (iii) Bayesian methods, (iv) sources of error and biases in phylogenetic tree reconstruction, (v) measures of branch support, (vi) phylogenetic dating. All these topics can only be introduced in brief.</p> | |
| Recommended reading | <ul style="list-style-type: none"> - Knoop & Müller 2006: Gene und Stammbäume, Elsevier - Wägele, Wolfgang 2005: Foundations of Phylogenetic systematics, Pfeil Verlag - Lemey, Salemy et al. 2009: The phylogenetic handbook, Cambridge Univ. Press - Felsenstein, Inferring Phylogenies, Sinauer Associates, Inc. | |
| This course is exclusively for the ZGS | | |

| Overview of morphological imaging techniques | |  |
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| Modulnummer ZGS-O | obligate | Duration of module: ½ day |
| responsible | Dr. Benjamin Wipfler | |
| Section | ZTE | |
| lecturers | Dr. Benjamin Wipfler | |
| Goal of course | The aim of the course is to give students an overview over the different imaging methods including their potential applications, advantages and disadvantages. Additionally examples will be provided for potential applications. | |
| This course is recommended for following subjects | All fields related to evolutionary biology or morphology. | |
| Details or course program | <p>The following techniques including their application, sample preparation and advantages and disadvantages will be discussed during the course:</p> <p>Methods to study external morphology:</p> <ul style="list-style-type: none"> • Digital microscopy • Scanning electron microscopy • Line drawings <p>Methods to study anatomy:</p> <ul style="list-style-type: none"> • Histology • μ- computed tomography (μ-CT) • Positron emission tomography (PET) • Confocal laser scanning microscopy (CLSM) • Light-sheet-fluorescence microscopy (LSFM) • Serial-block-face scanning electron microscopy (SBF-SEM) & focused ion beam scanning electron microscopy (FIB-SEM) • Nuclear magnetic resonance imaging (NMRI) | |
| Recommended reading | Wipfler B, Pohl H, Yavorskaya MI, Beutel RG. (2016). A review of methods for analysing insect structures – the role of morphology in the age of phylogenomics. <i>Current Opinions in Insect Science</i> , 18: 60-68. | |
| This course is exclusively for the ZGS | | |

Scientific collecting, field logistics, data management

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| Modulnummer ZGS-06, | obligatory | Duration of module: 1 day |
| responsible | Dr. Matthias Geiger | |
| Section | ZMB | |
| lecturers | Matthias Geiger, Björn Rulik, NN | |
| Goal of course | The students will get an overview on the importance of correct collecting methods starting from planning an expedition, over acquiring necessary permits and how to know whether this is necessary (Nagoya!), to practically preparing field equipment and gold standard documentation approaches. They learn how to collect morphology & DNA-friendly and efficient in terms of data management and sustainability. | |
| This course is recommended for following subjects | Not applicable | |
| Details or course program | Based on a jointly developed, fictive expedition the students will actively develop their own system and checklists for conducting biodiversity inventories. | |
| Recommended reading | Eymann, J., Degreef, J., Häuser, C., Monje, J. C., Samyn, Y., & VandenSpiegel, D. (2010). Manual on field recording techniques and protocols for All Taxa Biodiversity Inventories and Monitoring. Abc Taxa. | |
| This course is exclusively for the ZGS | | |

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| Presentation for scientific and public audience | |  |
| Modulnummer ZGS-07, | obligatory | Duration of module: 2 days |
| responsible | Dr. Eva Bärmann Sabine Heine | |
| Section | ZTE, ZMB, public Relations | |
| lecturers | Eva Bärmann Matthias Geiger Sabine Heine | |
| Goal of course | Students will get an overview of pitfalls when giving talks or poster presentations and of the importance of addressing the audience properly. After the module students will be able to convincingly present their study topic in a short time (“elevator talk”) and are familiar with the basics for creating entertaining yet informative presentations. The students will then achieve knowledge in managing and executing the steps of print media production (print and or electronic media, including radio, video and internet contents). Additionally the students will learn why it is necessary and reasonable to provide access to press releases, interim reports and annual reports to all target groups | |
| This course is recommended for following subjects | | |
| Details or course program | The course will provide a theoretical introduction on oral presentation techniques and poster design, using lots of illustrating examples. It will also address related issues such as dealing with nervousness, talking confidently, and copyright issues. Based on each student’s PhD topic they will design a poster and develop their own “elevator talk” using group feedback for improvement. Students develop advertising strategies by analyzing advertising styles used in different media. They determine target groups and decide what information can be used when informing the public or stake holder by using exciting information without making false promises. Using specific scientific information, students create press releases, newsletters or ads to communicate effectively with the public. | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

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| Scientific writing | |  |
| Modulnummer ZGS-08, | obligate | Duration of module: 2 days |
| responsible | Prof. Heike Wägele | |
| Section | all | |
| lecturers | Outsourced in the beginning, e.g., www.science-craft.com Prof. Heike PD Dr. Fabian Herder | |
| Goal of course | Publishing your results in scientific journals | |
| This course is recommended for following subjects | All subjects | |
| Details or course program | <p>The course is about</p> <ul style="list-style-type: none"> • How to plan your publication • how to find the right journal (avoid piracy journals) • practical techniques to develop scientific writing skills • guidelines to write an article in an efficient way • understanding publishing processes | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

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| Writing a scientific grant application | |  |
| Modulnummer ZGS-09 | obligate | Duration of module: 2 days |
| responsible | Prof. Heike Wägele | |
| Section | all | |
| lecturers | Outsourced in the beginning, e.g., www.science-craft.com Prof. Heike PD Dr. Fabian Herder | |
| Goal of course | How to apply and write an application for funding research | |
| This course is recommended for following subjects | All subjects | |
| Details or course program | <p>The course is about</p> <ul style="list-style-type: none"> • How to write hypothesis driven project proposals • how to “sell” and convince reviewers about the importance of your work • developing time schedules, milestones deliverables • how to manage deadlines • reviewing processes | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

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| HPC@ZFMK and introduction to Linux | |  |
| Modulnummer ZGS-O10, | facultative | Duration of module: 2 days |
| responsible | Dr. Alexander Donath | |
| Section | ZMB | |
| lecturers | Awa Rumler-Somé Dr. Alexander Donath | |
| Goal of course | The course aims to introduce the Linux command-line and how to run computing jobs on the HPC resources of the ZFMK. | |
| This course is recommended for following subjects | This course is for students who plan to use the HPC clusters of the ZFMK in their own PhD projects. | |
| Details or course program | The participants will learn how to use the Linux command-line (bash) and various GNU programs. Following this, they will learn the theoretical background of high-performance computing. They will learn how to access the various HPC clusters of the ZFMK, how to transfer data to and from the clusters, and how to submit computing jobs. | |
| Recommended reading | - | |
| This course is exclusively for the ZFMK. | | |

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| Soil Arthropods – collection, extraction and determination | |  |
| Modulnummer ZGS FB1, | facultative | Duration of module: 2 days |
| responsible | Dr. Thomas Wesener | |
| Section | ZTE | |
| lecturers | T. Wesener | |
| Goal of course | The students will achieve practical knowledge in the collection, extraction and determination of soil arthropods and other soil taxa. | |
| This course is recommended for following subjects | Anyone studying arthropods, soil ecology or being generally interested in the hidden world beneath our feet. | |
| Details or course program | Various extraction techniques are explained. A soil sample will then be actively taken and extracted utilizing different techniques. Outputs are compared. Material will then be sorted, determined, preserved, labelled and stored for future usage. | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

Preserving samples for molecular and morphological work



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| Modulnummer ZGS-FB2, | obligatory only for empirical studies | Duration of module: 1/2 day |
| responsible | Jonas Astrin & Benjamin Wipfler | |
| Sections | Biobank & Morphology lab | |
| lecturers | Jonas Astrin, Benjamin Wipfler | |
| Goal of course | This module will explain the necessity for preserving samples for morphological and molecular work, will point out factors that compromise sample quality and will familiarize the students with the more common techniques used to preserve samples for molecular and morphological collections. | |
| This course is recommended for following subjects | Any study including empirical work with biological samples (beyond observational data), i.e. with natural history collection samples. | |
| Details or course program | <ul style="list-style-type: none"> - Rationale for vouchersing / preserving natural history objects, role of natural history collections - Factors that deteriorate sample quality for molecular and for morphological use - Introduction to preservation techniques and fluids - Advantages and disadvantages of the respective techniques and chemicals - Brief primer on curation of natural history objects | |
| Recommended reading | <p>Nagy, Z. T. (2010) A hands-on overview of tissue preservation methods for molecular genetic analyses. <i>Organisms Diversity and Evolution</i> 10, 91-105.</p> <p>Zimkus, B. M. & Ford, L. S. (2014) Best practices for genetic resources associated with natural history collections: Recommendations for practical implementation. <i>Collection Forum</i> 28, 77-112.</p> <p>[es kommen noch 1-2 Artikel von Beny]</p> | |
| This course is exclusively for the ZGS | | |

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| Morphological Databases, Biodiversity workbench, etc... Evtl 2 Module??? | |  |
| Modulnummer ZGS-FBx, | facultative | Duration of module: nicht mehr als 2 days |
| responsible | Dr. Peter Grobe | |
| Section | | |
| lecturers | Dr. Peter Grobe Birgit Klasen? NN | |
| Goal of course | | |
| This course is recommended for following subjects | | |
| Details or course program | MorphDBase? | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

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| Basics in Histology | |  |
| Modulnummer ZGS-FC1, | facultative | Duration of module: 2 days |
| responsible | Prof. Dr. Heike Wägele | |
| Section | ZMB | |
| lecturers | H. Wägele | |
| Goal of course | The students will achieve practical knowledge in dehydration, embedding in methacrylate, slicing and staining of biological material. Additionally they learn basics of terminology used in interpretation of histological results. | |
| This course is recommended for following subjects | Morphological analyses (3 D reconstruction is possible afterwards) and to understand morphological structures on cellular level. | |
| Details or course program | Various histological techniques are explained. Material will then actively be worked on, starting with dehydration and preparation for embedding. In parallel already embedded material will then be sliced with a microtome, stained and covered for long term storage. Introduction in terminology of structures on cellular level is provided. | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

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| Geometric morphometrics | |  |
| Modulnummer ZGS-FC2, | facultative | Duration of module: 2 days |
| responsible | Dr. Eva Bärmann | |
| Section | ZTE | |
| lecturers | E. Bärmann | |
| Goal of course | The students will get a theoretical and practical introduction in morphometric methods, including analysis of linear measurements, as well as landmark analysis. | |
| This course is recommended for following subjects | This course is for students who plan to use morphometric methods in their own PhD projects. | |
| Details or course program | After a short theoretical introduction on the aims and applications of geometric morphometrics, students will develop their own training data set of linear measurements from small mammal skulls. These will be used for learning various analysis methods, such as Principal Component Analysis (PCA) and Discriminant Analysis (DA). Photos of the same specimens will be used for practical training in 2D landmark analysis. 3D landmark analysis will be covered in theory only. | |
| Recommended reading | Webster, M. and Sheets, H.D., 2010. A practical introduction to landmark-based geometric morphometrics. In: Quantitative Methods in Paleobiology, pp. 163-188, Paleontological Society Short Course, October 30th, 2010. The Paleontological Society Papers, Volume 16, John Alroy and Gene Hunt (eds.). | |
| This course is exclusively for the ZGS | | |

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| μ-CT – theory and practice | |  |
| Modulnummer ZGS-FC3, | facultative | Duration of module: 1 day |
| responsible | Dr. Benjamin Wipfler | |
| Section | ZTE | |
| lecturers | Dr. Benjamin Wipfler | |
| Goal of course | The aim of the course is to provide a basic introduction into the theory and practice of μ-CT scanning. Differences and particularities in the scanning between different groups of animals such as arthropods (exoskeleton) and vertebrates (endoskeleton) as well as strengths and weaknesses of μ-Ct compared to other 3-dimensional imaging techniques will be discussed. At the end, students should be able to conduct their own μ-Ct scans. | |
| This course is recommended for following subjects | Any subject associated to morphology, anatomy or morphometrics. It is recommended that participants of this module also participate in ZGS-FC4 3D-reconstructions. | |
| Details or course program | <ul style="list-style-type: none"> - Theory of μ-Ct scanning - Introduction into staining techniques - Sample preparation & mounting - Scanning parameters and the handling of the scanning software - Reconstruction of the projections - Security procedures and μ-CT lab rules / ethics - Advantages / disadvantages of μ-CT compared to other imaging methods | |
| Recommended reading | <p>Metscher BD (2009). MicroCT for comparative morphology: simple staining methods allow high-contrast 3D imaging of diverse non-mineralized animal tissues. BMC Physiology, 9: 11.</p> <p>Wipfler B, Pohl H, Yavorskaya MI, Beutel RG. (2016). A review of methods for analysing insect structures – the role of morphology in the age of phylogenomics. Current Opinions in Insect Science, 18: 60-68.</p> | |
| This course is exclusively for the ZGS | | |

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| 3D Reconstructions | |  |
| Modulnummer ZGS-FC4, | facultative | Duration of module: 2 days |
| responsible | Dr. Benjamin Wipfler | |
| Section | ZTE | |
| lecturers | Dr. Benjamin Wipfler | |
| Goal of course | The aim of the course is to provide a basic introduction into 3-dimensional reconstructions with the software packages Amira, VG Studiomax and Maya. The import and handling of μ -Ct scans, histological sections or other imaging techniques will be shown in theory and practical exercises. Students are welcome to bring their own data. | |
| This course is recommended for following subjects | Any subject associated to morphology, anatomy or morphometrics. It is recommended that all participants of ZGS-FC3 (μ -CT – theory and practice) and ZGS-FC1 also take part in this module. | |
| Details or course program | <ul style="list-style-type: none"> - Theory of 3D reconstructions: volume vs surface rendering. - Data import and processing - Introduction into segmentation with Amira - Surface rendering with Maya - Volume rendering with VG Studiomax - Morphometrics - Handling the virtual machines | |
| Recommended reading | - | |
| This course is exclusively for the ZGS | | |

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| Phylogenetic tree reconstruction software using morphological characters (e.g., PAUP*, TNT) | |  |
| Modulnummer ZGS-FC5, | Facultative | Duration of module: 2 days |
| Responsible | Dr. Ximo Mengual | |
| Section | ZTE | |
| Lecturers | Dr. Ximo Mengual Dr. Marianne Espeland Prof. Dr. Heike Wägele | |
| Goal of course | This module will explain the use of software to carry out phylogenetic analyses using morphological characters, and will reinforce the basic knowledge of cladistics. | |
| This course is recommended for following subjects | Any study including morphological data sets to infer phylogenetic relationships among taxa. | |
| Details or course program | <ul style="list-style-type: none"> - Importance of morphological data in the genomic era. - How to code morphological characters: e.g., continuous vs discrete characters. - How to combine morphological and molecular data. - Use of software: e.g., PAUP*, TNT, MrBayes. | |
| Recommended reading | <p>Giribet, G. (2015) Morphology should not be forgotten in the era of genomics—a phylogenetic perspective. <i>Zoologischer Anzeiger - A Journal of Comparative Zoology</i>, 256: 96-103.</p> <p>Hall, B.G. (2017) <i>Phylogenetic Trees Made Easy: A How-To Manual</i> (5th Edition). Sinauer Associates Press.</p> <p>Swofford, D.L., Sullivan, J. (2009) Phylogeny inference based on parsimony and other methods using PAUP*. In: Lemey et al. (Eds) <i>The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing</i>, pp. 267-312.</p> <p>Kitching, I.J., Forey, P.L., Humphries, C.J., Williams, D.M. (1998) <i>Cladistics: The Theory and Practice of Parsimony Analysis</i>. 2nd edition. Oxford University Press.</p> <p>Lipscomb, D. (1998) <i>Basics of Cladistic Analysis</i>. George Washington University. https://www2.gwu.edu/~clade/faculty/lipscomb/Cladistics.pdf</p> <p>Skelton, P., Smith, A., Monks, N. (2002) <i>Cladistics: A Practical Primer on CD-ROM</i>. Cambridge University Press.</p> <p>Goloboff, P.A., Farris, J.S., Nixon, K. (2003) TNT: Tree analysis using New Technology. Program and documentation available at http://www.zmuc.dk/public/phylogeny/TNT/</p> <p>Goloboff, P.A., Farris, J.S., Nixon, K. (2008) TNT, a free program for phylogenetic analysis. <i>Cladistics</i>, 24: 774–786.</p> <p>Lewis, P.O. (2001) A Likelihood Approach to Estimating Phylogeny from Discrete Morphological Character Data. <i>Systematic Biology</i>, 50(6): 913-925.</p> | |
| This course is exclusively for the ZGS | | |

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| Programs and databases relevant to start molecular work | |  |
| Modulnummer ZGS-FD1 | Obligatory | Duration of module: 2 days |
| responsible | Dr. Lars Podsiadlowski | |
| Section | ZMB | |
| lecturers | Dr. Lars Podsiadlowski Dr. Matthias Geiger | |
| Goal of course | The students will get basic knowledge in working with molecular data, including sequences produced in our lab and sequences from databases. | |
| Key competences | Handling & transformation of molecular data from raw sequences and from external sources. Searching databases effectively. The ability to estimate the quality of sequence data. | |
| Details or course program | <p>A short theoretical overview about current sequencing techniques, their pros and cons, and their costs will start the course. As well sequence data formats will be presented. In the first practical part raw data from Sanger sequencing and NGS approaches will be analysed, using a set of software tools (Geneious, fastQC, trimmomatic). Quality check, trimming and contamination issues will be discussed in detail and with examples from real datasets.</p> <p>A second practical part will be on working with databases and best strategies to explore the available datasets. NCBI nucleotide, protein databases, as well as the short read archive (SRA) will be presented with deep detail in searching strategies. Comparing new data with databases (e.g. with blast and hmmer; on websites and on local computers) is another topic, and a crucial next step in analysing molecular data.</p> <p>Manual and automatic retrieval of molecular sequences will be practiced. Special databases for barcodes and species identification (e.g. BOLD) will also be a topic of the course. Finally the last part will focus on how to maintain sequence quality for publishing own molecular datasets in databases.</p> | |
| Recommended reading | | |
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| Evolutionary models, maximum likelihood and model selection | |  |
| Modulnummer ZGS-FD10, | facultative | Duration of module: 4 day |
| responsible | Christoph Mayer and Bernhard Misof | |
| Section | ZFMK | |
| lecturers | Christoph Mayer and Bernhard Misof | |
| Goal of course | The students will get a good working knowledge for using the maximum likelihood method and for selecting appropriate models of sequence evolution. | |
| This course is recommended for following subjects | Phylogenetic tree reconstructions. | |
| Details or course program | In this course, we first introduce models of sequence evolution. This includes several models from the Jukes Cantor model to the general time reversible model. Variants of these models, such as models with invariant sites, heterogeneous site rates modelled by a gamma distribution and free rate models are introduced and discussed. Second, the likelihood function is introduced that is used to compute the likelihood for a given phylogenetic tree. Heuristic tree search methods, which explore the tree space with the aim of finding the tree with the highest likelihood, are discussed briefly. Finally, methods for determining the best evolutionary model among a set of given models are introduced. All methods are introduced on a theoretical basis and applied to real data sets in computer exercises. | |
| Recommended reading | Will be announced later. | |
| This course is a selected part of a master course at the university and is also offered to students of the ZGS. | | |

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| Evolutionary models and distance methods used for phylogenetic tree reconstruction | |  |
| Modulnummer ZGS-FD11 | facultative | Duration of module: 4 day |
| responsible | Christoph Mayer | |
| Section | ZFMK | |
| lecturers | Christoph Mayer | |
| Goal of course | This module introduces distance based methods for phylogenetic tree reconstruction | |
| This course is recommended for following subjects | Phylogenetic tree reconstructions. | |
| Details or course program | In this course, we first introduce models of sequence evolution. This included several models from the Jukes Cantor model to the general time reversible model. Variants of these models, such as models with invariant sites, heterogeneous site rates modelled by a gamma distribution and free rate models are introduced and discussed. Second the students get to know how to measure distances among sequences and how to correct sequences for multiple substitutions using evolutionary models. Furthermore, characteristics of distances are discussed from which one can determine whether a clock like tree exists for these distances and whether a tree exists that represents these distances. Finally distance based methods of tree reconstruction are introduced, namely, UPGMA, Neighbourjoining, Minimum Evolution. | |
| Recommended reading | Will be announced later. | |
| This course is a selected part of a master course at the university and is also offered to students of the ZGS. | | |

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| Metabarcoding: Theory and practical applications | |  |
| Modulnummer ZGS FD2, | facultative | Duration of module: 2 days |
| responsible | Dr. Sarah Bourlat Dr. Vera Fonseca | |
| Section | ZMB | |
| lecturers | Dr. Sarah Bourlat Dr. Vera Fonseca | |
| Goal of course | To teach the theoretical framework behind metabarcoding, how metabarcoding data are produced and analyzed as well as the potential applications in research. | |
| This course is recommended for following subjects | This course is for students who plan to use metabarcoding in their own PhD projects. | |
| Details or course program | <ul style="list-style-type: none"> - Theoretical framework behind metabarcoding and barcoding. - Metabarcoding in practice: Experimental design, environmental sampling, amplicon library preparation, sequencing, software for analysis of metabarcoding data, clustering and taxonomic assignment, reference databases. - Metabarcoding outputs: species lists, OTU tables and diversity indices, putting results in a biological context. - Applications of metabarcoding to research with examples such as food webs and trophic chains, host parasite interactions, species detection, biomonitoring and biodiversity assessment, macroecology and ecosystem dynamics, conservation and ecosystem management. | |
| Recommended reading | Taberlet, P., Bonin, A., Zinger, L., Coissac, E. Environmental DNA: For Biodiversity Research and Monitoring. Oxford University Press (2018). | |
| This course is exclusively for the ZGS | | |

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| BLAST – searching for sequences in data bases | |  |
| Modulnummer ZGS-FD3 | facultative | Duration of module: 1 day |
| responsible | Christoph Mayer | |
| Section | ZFMK | |
| lecturers | Christoph Mayer, Lars Podsiadlowski and Alexander Donath | |
| Goal of course | The course provides a theoretical introduction to the blast algorithm. Its application is demonstrated in computer exercises. After the course the students should be in the position to use blast searches for their research. They should be able to choose an appropriate word size for their application and to interpret their results using the E-value. | |
| This course is recommended for following subjects | Phylogenetic analyses. | |
| Details or course program | In this course the theoretical background of the blast algorithm is introduced. In computer exercises the students will learn how to use the online NCBI blast search and stand alone blast. They will get to know the different blast version such as blastn, megablast, blastp, blastx, tblastx, and psiblast. The students will learn how to choose a suitable word size and how to interpret so called E-values. | |
| Recommended reading | Will be announced later. | |
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Alignment programs in molecular analyses



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| Modulnummer ZGS-FD4, | facultative | Duration of module: 2 days |
| responsible | Patrick Kück | |
| Section | ZMB | |
| lecturers | Patrick Kück | |
| Goal of course | Deeper knowledge of the meaning and purpose of alignment applications in molecular phylogenetics | |
| This course is recommended for following subjects | This course is for all students using molecular data for their analyses | |
| Details or course program | Introduction into the theory and practical application of multiple sequence alignment tools, comprising different ideas of greedy, progressive, or consistency based algorithms and their realization in recent alignment software like MAFFT, MUSCLE, T-COFFEE, or DialignTX. | |
| Recommended reading | David A. Morrison, Multiple Sequence Alignments for Phylogenetic Purposes, Australian Systematic Botany, 19, 479-539 Michael S. Rosenberg, Sequence Alignment (Methods, Models, and Strategies), University of California Press 2009 | |
| This course is exclusively for the ZGS | | |

Alignment evaluation programs in molecular analyses



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| Modulnummer ZGS-FD5, | facultative | Duration of module: 2 days |
| responsible | Patrick Kück | |
| Section | ZMB | |
| lecturers | Patrick Kück | |
| Goal of course | Homology assessment of multiple sequence alignments a priori tree reconstruction | |
| This course is recommended for following subjects | This course is for all students using molecular data for their analyses | |
| Details or course program | Introduction into the theory and practical application of alignment evaluation tools for the identification of potentially randomized sequence similarity, heterogeneous sequence divergence, and compositional bias. | |
| Recommended reading | <p>Misof & Misof, 2009, A Monte Carlo approach successfully identifies randomness in multiple sequence alignments: A more objective means of data exclusion, <i>Sys Biol</i>, 58:21-34</p> <p>Kück et al., 2012, AliGROOVE - visualization of heterogeneous sequence divergence within multiple sequence alignments and detection of inflated branch support, <i>BMC Bioinformatics</i>, 15:294</p> <p>Kück & Struck, 2014, BaCoCa - a heuristic software tool for the parallel assessment of sequence biases in hundreds of gene and taxon partitions, <i>MPE</i>, 70:94-98</p> | |
| This course is exclusively for the ZGS | | |

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| Measures of phylogenetic support | |  FORSCHUNGS museum KOENIG |
| Modulnummer ZGS-FD6, | fakultative | Duration of module: 1 day |
| responsible | Bernhard Misof and Christoph Mayer | |
| Section | ZMB | |
| lecturers | Bernhard Misof and Christoph Mayer | |
| Goal of course | This course provides an overview on measures of phylogenetic branch support and introduces the theoretical concepts behind these measures. | |
| This course is recommended for following subjects | Phylogenetic analyses. | |
| Details or course program | This course introduces measures of phylogenetic branch support from bootstrap, jackknife, Bayesian posterior probabilities, to quartet distances, four cluster likelihood mapping, and partition log likelihood scores. | |
| Recommended reading | Will be announced later. | |
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| Gene tree based phylogenetic methods (multispecies coalescent methods) | |  |
| Modulnummer ZGS-FD7 | facultative | Duration of module: 2 day |
| responsible | Christoph Mayer and Marianne Espeland | |
| Section | ZFMK | |
| lecturers | Christoph Mayer and Marianne Espeland | |
| Goal of course | Introduction to gene tree based phylogenetic methods such as the multispecies coalescent methods. | |
| This course is recommended for following subjects | | |
| Details or course program | This course discusses methods that use gene trees to compute species (phylogenetic) trees. The course introduces the theoretical concepts of several of these methods as well as their advantages and disadvantages. The “Astral method”, which is currently the most efficient of these methods, is introduced in computer exercises. Its performance is compared to maximum likelihood based methods. | |
| Recommended reading | Will be announced later. | |
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| Species delimitation | |  |
| Modulnummer ZGS-FD8, | facultative | Duration of module: 2 days |
| responsible | Marianne Espeland | |
| Section | ZTE | |
| lecturers | Marianne Espeland Lars Podsiadlowski | |
| Goal of course | Introduction to state of the art species delimitation software | |
| This course is recommended for following subjects | Phylogenetics, systematics, speciation, taxonomy | |
| Details or course program | The aim of this course is to provide students with an introduction to species delimitation methods used for molecular taxonomy, their strengths and limitations. These include methods based on a single locus (e.g. GMYC, PTP, ABGD), multi-locus coalescent methods (DISSECT/STACEY, BPP etc, Structure), and a method combining the multi-locus approach with morphological data (iBPP) | |
| Recommended reading | Leavitt et al. (2015). The dynamic discipline of species delimitation: progress toward effectively recognizing species boundaries in natural populations https://bit.ly/2qsjWix Rannala (2015). The art and science of species delimitation. Current Zoology https://bit.ly/2AImPBL | |
| This course is exclusively for the ZGS | | |

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| Analysis and visualisation of data from population genetics/genomics approaches | |  |
| Modulnummer ZGS FD9 | Facultative | Duration of module: 2 days |
| responsible | Dr. Lars Podsiadlowski | |
| Section | ZMB | |
| lecturers | Dr. Lars Podsiadlowski | |
| Goal of course | The students will achieve practical knowledge in working with population level sequence and SNP data, using computer based methods. They will also learn about how to plan a population genetics study (sample size, marker selection). | |
| Key competences | Theory and practice of population genetics analysis. Handling, transformation, analysis and visualization of molecular datasets. Accurate planning of population genetics experiments. | |
| Details or course program | <p>In a theoretical part basic concepts and underlying models of population genetics will briefly be explained (e.g. genetic drift, selection, linkage disequilibrium, selective sweep, coalescent). As well the current set of molecular marker systems (sequences, SNP data, microsatellites) will be compared, discussing the pros and cons in relation to the scientific question under study.</p> <p>Example datasets consisting of sequences from mitochondrial DNA samples, as well as genome wide SNP data will be used for demonstrating the power of population genetics approaches. Stand-alone software tools, as well as python and R-based approaches will be used to describe geographic variation, demographic history and population structure, and to analyze recombination rate and selection processes.</p> <p>Data visualization in form of haplotype networks, principal component analysis and structure plots will complete the module.</p> | |
| Recommended reading | Hahn, Matthew 2018: Molecular population genetics, Oxford Univ. Press | |
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| From phylogenetic trees to evolutionary histories | |  |
| Modulnummer ZGS-FE1, | facultative | Duration of module: 2 days |
| responsible | Dr. Ralph Peters | |
| Section | ZTE | |
| lecturers | Dr. Ralph Peters | |
| Goal of course | Understanding what is needed to get from phylogenetic trees to evolutionary inferences, which methods can be applied, and which data can be incorporated | |
| This course is recommended for following subjects | Any study involving phylogenetic trees. | |
| Details or course program | We will exemplarily outline and discuss the workflow in studies addressing evolutionary histories. This spreads from formulating research questions and designing a study to answering these based on inferred (or adopted) phylogenetic trees. The course will not target any cladistic or phylogenetic methods, but merely all other aspects of an evolutionary history study, with a focus on so-called phylogenetic comparative methods, on implementing fossil data and on incorporating taxonomic expertise. | |
| Recommended reading | To be announced | |
| This course is exclusively for the ZGS | | |

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| Introduction into Geographic Information System GIS | |  |
| Modulnummer ZGS-FE2 | facultative | Duration of module: 5 days |
| responsible | Dr. Dennis Rödder | |
| Section | ZTE | |
| lecturers | Dr. Dennis Rödder | |
| Goal of course | To teach the theoretical framework of basic GIS analyses, species distribution modelling (SDM) techniques and spatial conservation planning. | |
| This course is recommended for following subjects | Students interested in spatial analyses in conservation science, biogeography and evolutionary biology | |
| Details or course program | <ul style="list-style-type: none"> - Introduction to GIS and basics of spatial explicit ecological modelling - Talks will be presented by each participant on various topics (theory, methods, examples) - Exercises and tutorials on basic GIS functionality and its applications in biodiversity studies | |
| Recommended reading | <p>Elith, J., & J. R. Leathwick (2009): Species distribution models: ecological explanation and prediction across space and time. <i>Annu. Rev. Ecol. Evol. Syst.</i> 40: 677-697.</p> <p>Guisan, A, W. Thuiller, & N. E. Zimmermann (2017): <i>Habitat suitability and distribution models – with applications in R.</i> Cambridge University Press.</p> | |
| This course is exclusively for the ZGS | | |

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| Introduction to scientific programming in R | |  |
| Modulnummer ZGS-FE3 | facultative | Duration of module: 5 days |
| responsible | Dr. Dennis Rödder | |
| Section | ZTE | |
| lecturers | Dr. Dennis Rödder | |
| Goal of course | Introduction to scientific programming in R | |
| This course is recommended for following subjects | All subjects | |
| Details or course program | <ul style="list-style-type: none"> - Basic syntax of the R programming language - Syntax of R functions and objects - Examples of various R packages - Automatization of work flows in R - Creating and effectively applying own scripts in R | |
| Recommended reading | R short reference card available from: https://cran.r-project.org/doc/contrib/Short-refcard.pdf | |
| This course is exclusively for the ZGS | | |

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| Working with reference databases (Endnote, etc.) | |  |
| Modulnummer ZGS-FE1, | facultative | Duration of module: 1/2 days |
| responsible | NN | |
| Section | | |
| lecturers | NN | |
| Goal of course | | |
| This course is recommended for following subjects | | |
| Details or course program | | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |

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| Using libraries and retrieving information from online platforms | |  |
| Modulnummer ZGS-FF2, | facultative | Duration of module: 1 day |
| responsible | Dr. Katharina Schmidt-Loske | |
| Section | Biohistoricum | |
| lecturers | Dr. Katharina Schmidt-Loske Thomas Bader Mareike Kruppa Jonas Astrin | |
| Goal of course | <ul style="list-style-type: none"> - Learn how to use the ZFMK libraries and online literature search tools - how to get in touch with research archives - how to find specific documents, e.g. autographs? | |
| This course is recommended for following subjects | This course is relevant to all students who want to search for literature either physically in the ZFMK libraries or the Biohistoricum archive, or online | |
| Details or course program | Traditional search engines are a suboptimal tool for targeted retrieval of scientific publications or documents. Several search options for scientific literature and archived documents will be presented. Furthermore, a tour will guide future users through the central library, the Biohistoricum and some of the taxonomically specialized ZFMK libraries. | |
| Recommended reading | https://www.zfmk.de/de/forschung/bibliothek https://www.zfmk.de/dateien/atoms/files/leitfaden_infoversorgung_zfmk_2015-03.pdf Both sources are in German, but these are not mandatory readings and students will be walked through the described resources in English during the course. That said, an online translator transmits a pretty good picture of most of the content on these pages | |
| This course is exclusively for the ZGS | | |

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| Media and Presentation | |  |
| Modulnummer ZGS-FF3, | facultative | Duration of module: 1 day |
| responsible | Sabine Heine | |
| Section | Public Relations | |
| lecturers | Sabine Heine | |
| Goal of course | The students will achieve knowledge in managing and executing the steps of print media production (print and or electronic media, including radio, video and internet contents). Additionally the students will learn why it is necessary and reasonable to provide access to press releases, interim reports and annual reports to all target groups. | |
| This course is recommended for following subjects | Individual active press work for scientists in the scope of public relation and marketing | |
| Details or course program | Students develop advertising strategies by analyzing advertising styles used in different media. They determine target groups and decide what information can be used when informing the public or stake holder by using exciting information without making false promises. Using specific scientific information, students create press releases, newsletters or ads to communicate effectively with the public. | |
| Recommended reading | | |
| This course is exclusively for the ZGS | | |