



Module syllabus: Advanced methods in animal diversity

1. Overall information

Module coordinator	dr Łukasz Depa
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ECTS	2
Method for the verification of learning outcomes	<p>The final grade for the module is weighted on the average of the following student activities:</p> <ul style="list-style-type: none">- Active participation in the practical classes (continuous evaluation of practical skills, tests and reports) (0.4)- Preparation of a final report from the methods used (0.6) <p>To be awarded a final grade, the student must have passed each activity of the module.</p> <p>Grades: below 51% – fail (F); 51-60% – with minimum academic criteria (E); 61-65% – satisfactory (D); 66-75% – good (C); 76-85% – very good (B), ≥ 85% – excellent (A)</p>

2. Description of student activity and work

Lecture/discussion sessions	
Responsible instructor	dr Łukasz Depa
Content	<p>The main objective of this module is to acquaint students with the basic methods for determining animal biodiversity, species identity and phylogenetic relationships based on molecular markers.</p> <p>Lectures/discussion sessions consist of presenting the role of molecular markers in zoology with a special emphasis on the phylogenetic studies of insects. Phylogenetic problems will be introduced and some basic concepts related to them will be explained. The possibilities of using proper molecular markers, such as EF1-α, COI, COII, 16S rRNA, 18S rRNA, cytochrome b, to reconstruct the ancestral relationships of trees on different taxonomic levels (species, genus, tribe, subfamily and higher) will be discussed. Molecular analysis results will be compared with the classic classification, which is based on morphological characters</p> <p>Lecture/discussion session content: Becoming familiar with molecular databases. Processing the DNA sequences obtained after their isolation using programs, such as Chromas, ClustalX, BioEdit. Reconstructing phylogenetic trees based on different methods (UPGMA, Neighbour-Joining, Maximum Likelihood, Maximum Parsimony) and evaluating their reliability. Visualising (TreeView) and interpreting the results obtained.</p>
Number of didactic hours (contact hours)	5
Literature	1. AVISE J. C. (2004). Molecular markers, natural history, and evolution. Sinauer Associates, 684 pp.





	2. Hall B. G. (2004). Phylogenetic Trees Made Easy: a How-to Manual, Second Edition (With Cd-Rom). Sinauer Associates, Inc 221pp. 3. Nei M., Kumar S. (2000). Molecular Evolution and Phylogenetics ,Oxford University Press, USA, 333pp
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Laboratory	
Responsible instructor	Dr Łukasz Depa
Laboratory projects	1. Phylogeny and taxonomic status of representatives of various groups of Hemiptera based on the sequences of mitochondrial and molecular markers that are available in GenBank
Methodology of laboratory classes	Practical exercises that are performed in small groups under the supervision of the instructor, which will include: <ul style="list-style-type: none">• Designing and accomplishing the procedure• Downloading the data and checking it using the proper programs for phylogenetic studies• Preparing a report of the obtained results
Number of didactic hours (contact hours)	10
Literature	Online manuals and guides are available on different websites, such as: http://www.ncbi.nlm.nih.gov/ http://evolution.genetics.washington.edu/phylip/software.html http://www.technelysium.com.au/chromas.html http://www.clustal.org/ http://www.mbio.ncsu.edu/BioEdit/BioEdit.html http://taxonomy.zoology.gla.ac.uk/rod/treeview/treeview_manual.html http://www.megasoftware.net/mega61.html

3. Forms of verification

Continuous evaluation of knowledge, activity and practical skills	
Grades	Grades are awarded on a scale of A-F, where A is the best and F is a fail. <u>An excellent performance (A)</u> – the student actively participates in the laboratory work, demonstrates an excellent understanding of the analytical procedures (their aims, sequence and outcomes), is engaged and creative in solving current problems and in assessing and presenting the results. <u>A good performance (C)</u> – the student demonstrates good judgment and knowledge, correctly performs an experiment, correctly exhibits a sense of procedure, properly provides an assessment and presentation of the experimental results. <u>A satisfactory performance (E)</u> – the student demonstrates satisfactory judgment and knowledge, is poorly engaged and needs additional help to finish the analysis and final assessment of the results correctly, presents a satisfactory presentation of the experimental results.





	A performance that does not meet the minimum academic criteria (F) – the student is not engaged in the experiment, does not exhibit a sense of the procedures, interprets and presents the results poorly.
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Reports from realised laboratory projects

Evaluation	<p>Evaluation is comprised of the judgment and knowledge related to the practical project sense and methods, engagement in the realisation, the quality of the assessment and presentation of the experimental results, use of reference materials.</p> <p>Grades for reports are awarded on a scale of A-F, where A is the best and F is a fail.</p> <p>An excellent report (A) – without any essential errors</p> <p>Fail (F) – no report</p>
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Final exam

Grades	<p>Grades are awarded on a scale of A -F, where A is the highest and F is a fail.</p> <p>Excellent (A) – the student presents a fluent knowledge of phylogenetic methods and other aspects of using molecular markers, has minimal errors that do not affect the quality of the presentation.</p> <p>Good (C) – the student presents a good knowledge of phylogenetic methods and other aspects of using molecular markers, makes rare but subtle errors.</p> <p>Satisfactory (E) – the student exhibits a satisfactory knowledge, but with a poor understanding of phylogenetic analysis and other aspects of molecular markers and makes subtle errors.</p> <p>Fail (F) – the student does not present a satisfactory knowledge of phylogenetic methods and other aspects of molecular markers and makes many substantial errors, which disqualify their presentation.</p>
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