

## Course plan ZOL412ME2

Course title	<b>Advanced Evolutionary Biology and Molecular Systematics</b>
Course code	<b>ZOL 412 ME2</b>
Credit value	2 (22 hours Lectures & 23 hours P )
objectives	This course aims to: Outline and explain the concepts in evolutionary biology; evolutionary process, mechanisms and types;
Intended Learning Outcome	Upon the completion of this course , the student should be able to; <ul style="list-style-type: none"> <li>• Construct ideas about the process of evolution</li> <li>• Interpret the theories in detail and discriminate them</li> <li>• Distinguish bio molecules as tools for taxonomy</li> <li>• Investigate different techniques and models to evaluate the evolution of different groups of organisms</li> </ul>
<b>Course content</b>	Mechanism of most accepted and plausible evolutionary theories. Processes other than natural selection. Developing phylogenetic trees using morphological and molecular data- parsimony, maximum likelihood, Neighbour joining and Bayesian approaches. Recent advances in molecular taxonomy and its use in biological systems.
Teaching and learning methods	Lecture presentation , tutorial discussion, field based studies, laboratory based experiments, take-home assignments, problem based student presentations
Course plan Theory	<p><b>L1-11-</b> Introducing and recalling the evolutionary principles and theories. Discussion on different papers describing discrepancies in those theories with special focusing on natural selection- Group discussion on given papers and articles; Student presentations describing the papers; each student will have a session to describe their findings and critique with questions and feedback (<b>ICA1</b>)</p> <p><b>L12-15-</b> Morphology based taxonomy; introducing the creation of phylogeny and cladogram using morphometry- Lectures and hands on work in computer</p> <p>L16 – Assignment – Students will prepare a cladogram for a given set of data – <b>ICA 2</b></p> <p><b>L17-20-</b> Introducing molecular taxonomy and uses – lectures</p> <p><b>L21-22-</b> tutorial</p> <p><b>Session 1-3-</b> Students will be asked to visit the University premises to identify a group of flora/ fauna to describe their relationship based on their observation. They will work individually and then their work will be presented and the feedback will be given – ICA1</p>

	<p><b>Session4 and 5-</b> Molecular based data will be processed and the deduction of phylogeny based on different models will be discussed – hands on <i>in-silico</i> work and discussion</p> <p><b>Session6</b> – recalling</p> <p><b>Session 7-</b> ECE exam</p>
Evaluation Methods	<p>Theory: In-Course Assessments (30%) End of Course Examination (70%)</p> <p>Practical: In-Course Assessments (30%) End of Course Examination (70%)</p> <p><b>Marks obtained in theory component (MT) and practical component (MP) will be computed into Overall Marks as (6MT+4MP)/10</b></p>
Exam blue print	<p>The ECE (Theory) will have four questions from any of the following sections;</p> <ul style="list-style-type: none"> <li>• Criticising different theories describing evolution based on given example</li> <li>• Natural selection and the principles</li> <li>• Taxonomy- Molecular and morphology based</li> </ul> <p>Practical ECE will be with 4-5 questions with different mark weightage covering all the sessions with questions may include identification, spotting, comment and critique.</p>
References	<ul style="list-style-type: none"> <li>• Gajapathy,K. (2015).Beginners Guide to Sandfly Taxonomy. Lambert Academy press, Germany.</li> <li>• Darwin’s Ghost (2000); the origin of species updated. Steve Jones. Ballantine Publishing Group. New York..</li> <li>• Gajapathy et al. (2016) Use of Bioinformatics in Revealing the Identity of Nature’s Products with Minimum Genetic Variation: The Sibling Species. In (edited by Sumiko Anno): Gene environment Interaction Analysis; methods in Bio Informatics and Computational Biology. Pan Stanford press. Singapore.</li> </ul>
Resource person	Dr. K. Gajapathy

Sgd

Gajapathy K