Biology 4289b – Biosystematics and Phylogenetics - Course Outline – 2017

Systematics unifies all of biology by providing a framework for understanding the diversity of species and their inter-relatedness. The integration of molecular approaches has propelled systematics to the forefront of biological research and phylogenetic analysis of DNA sequences has eliminated any remaining doubt that earthly species are related by common ancestry. From Woese's proposal that the living world consists of three, monophyletic primary kingdoms, the admission of DNA fingerprints as court evidence, the global Tree of Life Project, to Hebert's Barcoding Project, the use of molecular biology and bioinformatics has literally transfigured our understanding of evolutionary history. Biology 4289b will introduce the fundamental principles involved in biosystematics and phylogenetics. Students will learn about the three operations of systematics, namely description, classification, and identification, and acquire the skills required to analyze DNA sequences in a phylogenetic context. The course consists of formal lectures as well as student presentations based on library research assignments and computer-based projects.

Prerequisites: Biology 2581b and completion of 1.5 courses from Biology at the 300 level or above. Biology 3466b is recommended.

Instructor

MA Lachance, Professor of Biology, 2036 BGS, 519 661 3752, lachance@uwo.ca

Timetable

Lectures: Tuesday, Wednesday, and Friday, 9:30 – Physics and Astronomy 106
Practicals: Tuesday and Friday, 10:30 – North Campus Building 105

Evaluation

Midterm	25%	Friday February 17, 9:30, in class
Final	45%	Final exam period (TBA)
Labs and pop quizzes	30%	Allocation of lab marks will be discussed in class

Required texts

Course notes for 2017 by MA Lachance – available for a nominal fee at the Bookstore

Dawkins R and Wong Y - 2016 The Ancestor's Tale. A Pilgrimage to the Dawn of Life. 2nd Edition, Weidenfeld and Nicolson.

Optional texts

Hall BG 2011 Phylogenetic Trees Made Easy - A How-To Manual. Fourth Edition. Sinauer, Sunderland MA. A simplified introduction to the use of free software, specially MEGA, to align sequences and construct various types of phylogenetic trees.

Baum D & Smith S 2013 Tree Thinking: an Introduction to Phylogenetic Biology. Roberts, Greenwood Village, CO. A conceptual overview of the principles of phylogenetics. A highly recommended introduction.

Hillis et al. (eds) 1996 Molecular Systematics, 2nd edition, Sinauer, Sunderland Ma. An excellent, varied overview of the different approaches available in 1996. Detailed laboratory protocols

are given at the end of many chapters. Excellent glossary of technical terms. Unfortunately, the field has changed a lot since that time, and the book is in the need of a major revision.

Nei M & Kumar S 2000 Molecular Evolution and Phylogenetics. Oxford University Press. An excellent text for those who wish to explore the biological and mathematical theory and principles of phylogenetic reconstruction.

Page RDM & Holmes EC 1998 Molecular Evolution - A Phylogenetic Approach. Blackwell, Oxford. Probably the most lucid text available on various methods of phylogenetic analysis. Quite up-to-date considering the date of publication.

The assignments will consist of small research projects focussed on some of the fundamental concepts explored in the course. See course website: http://instruct.uwo.ca/biology/489a/

1. Students will choose a taxon at the level of genus or above, that they will use as a case study to explore the various concepts introduced in the course. These will include the various species concepts that have been applied to that taxon, a character analysis of some of the most frequently studied phenotypic traits, and examples of applications of molecular phylogenetics to the taxon. The results of these explorations will be presented with PowerPoint in the practicals. See course website
2. The practicals will be a blend of progress reports on the assignments plus an exploration of library and internet resources relevant to systematics or phylogenetics. In particular, we shall learn the basics of the NCBI Taxonomy database and *BLAST* search algorithms.
3. Students are encouraged to engage in discussion during presentations.
4. An overall performance mark will be assigned by the instructor based on criteria such as attendance, quality of presentations, timeliness, response to comments and suggestions, etc.

The midterm will consist of short answer or multiple choice questions (25 marks) and will serve as practice for the final, which will follow a similar format. In preparation for the examinations, it is recommended that each student draw an extensive list of concepts introduced in each lecture and periodically ascertain that the concepts are well understood.

The use of portable electronic devices of any sort is prohibited during the midterm and the final. All practicals must be completed except as discussed with instructor. The use of electronic devices in the classroom must meet with instructor approval.

Accommodation for absences from the midterm or the final must be in accordance to university policy: https://studentservices.uwo.ca/secure/index.cfm

Scholastic offences are taken seriously and students are directed to read the policy at http://www.uwo.ca/univsec/handbook/appeals/scholastic_discipline_undergrad.pdf

Please contact the course instructor if you require material in an alternate format or if you require any other arrangements to make this course more accessible to you. You may also wish to contact Services for Students with Disabilities (SSD) at 661-2111 x 82147 for any specific question regarding an accommodation.

See the course website for information of mental health and relevant services offered by the university.

Topics

Introduction to biosystematics
Taxonomy versus systematics
Operations of taxonomy
Types of taxonomy
Taxa and related concepts
Characters in general: data types
Epistemology
Nominalism versus realism
Typology versus population thinking
Nomenclature
Codes
The nomenclatural type
The species
Schools of thought in systematics
Taxon structure
Qualities of Taxonomic Characters
Different Ways of Being Similar
Character similarity
Reductionism and holism
More definitions
Processes
Classifications
Character states
The importance of defining objectives clearly
DNA studies in molecular systematics
DNA base compostion
DNA/DNA reassociation
From relational to descriptive approaches
Catalogs
RFLP and related approaches
DNA sequencing
PCR – The polymerase chain reaction
DNA polymerase
Denaturation time and temperature
Extension time and temperature
Annealing conditions and primer design
Magnesium
Sequence editing
Alignment
Phylogenetic reconstruction
The number of possible trees
Cladistic methods
Phenetic methods
Optimality versus algorithmic approaches
Distance corrections
Examples of tree building methods
Maximum parsimony analysis
Minimum evolution/Neighbour-joining trees
The Neighbour-Joining algorithm
Maximum likelihood phylogenies
Markov Chain Monte Carlo Bayesian analysis
Confidence levels
Parsimony haplotype networks
Split decomposition networks
Roots
Newick trees
Some of the things to watch for in trees
Applications of sequencing to identification
3-Primer PCR
DGGE
SSCP
SWAPP PCR
DNA heteroduplex assay
DNA sequence management and analysis software