Biology 9289b – Biosystematics and Phylogenetics - Course Outline – 2015

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 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/9289b 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 – University Community Centre 53
Tutorials: Wednesday 10:30-12:30. Somerville 1310 Jan 7 and 14. HSB 13 Jan 21 onwards.

Required text

Dawkins R 2004 The Ancestor's Tale. A Pilgrimage to the Dawn of Life. Weidenfeld and Nicolson. ISBN-10: 0297825038.

Optional texts

See Biology 4289b course outline.

Evaluation

Assignments and Presentations 30%
Midterm 25% - Friday, February 13, in class
Final examination 45% - TBA

The assignments will consist of research projects focussed on some of the fundamental concepts explored in the course and relevant to the students' graduate research projects. Unlike students registed in Biology 4289b, graduate students are not bound to five species. The assignments should explore deeper, innovative aspects of systematics and/or phylogenetics. You may be asked to assign a mark for your colleagues' presentations.

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.
Peer evaluations will be expected to be fair and dispassionate. Sources of the information presented in class must be attributed in accordance to common practice in the scientific community. Scholastic offences are taken seriously and students are directed to read the appropriate policy, specifically, the definition of what constitutes a Scholastic Offence, at the following Web site:
http://www.uwo.ca/univsec/pdf/academic_policies/appeals/scholastic_discipline_grad.pdf

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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
