PH8010: COMPUTATIONAL MOLECULAR EVOLUTION

Effective Term

Summer Term 2026

Part I Course Overview

Course Title

Computational Molecular Evolution

Subject Code

PH - Infectious Diseases and Public Health

Course Number

8010

Academic Unit

Infectious Diseases and Public Health (PH)

College/School

Jockey Club College of Veterinary Medicine and Life Sciences (VM)

Course Duration

One Semester

Credit Units

3

Level

R8 - Research Degree

Medium of Instruction

English

Medium of Assessment

English

Prerequisites

Nil

Precursors

Nil

Equivalent Courses

Nil

Exclusive Courses

Nil

Part II Course Details

Abstract

This course introduces students to molecular evolution and phylogenetics through a blend of concept-driven lectures and practice-based workshops. Students will develop hands-on proficiency with model-based methods for analyzing the evolution of DNA, RNA and proteins, including substitution models, maximum-likelihood and Bayesian tree inference, molecular clocks, and hypothesis testing. Practical sessions will guide students in building, evaluating and interpreting phylogenetic trees using widely adopted tools (e.g., IQ-TREE for ML inference and model selection, BEAST 2 for time-calibrated Bayesian analyses), with opportunities to apply workflows to real research datasets; students are encouraged to bring their own data. Designed for a diverse cohort, the course scaffolds the necessary mathematics and coding through step-by-step labs, equipping students to apply rigorous evolutionary models in contemporary research.

Course Intended Learning Outcomes (CILOs)

	CILOs	Weighting (if app.)	DEC-A1	DEC-A2	DEC-A3
1	Explain and compare core theories and models in molecular evolution. Solve simple population-genetic problems while describing key properties of phylogenetic trees.	40	x	x	
2	Apply and troubleshoot end-to-end phylogenetic workflows on DNA/RNA/protein datasets.	30		x	x
3	Design, justify, and communicate a reproducible evolutionary analysis and hypothesis test (e.g., molecular clocks, selection, diversification), interpret uncertainty and limitations, and present findings to a professional standard.	30	x	x	x

A1: Attitude
Develop an attitude of discovery/innovation/creativity, as demonstrated by students possessing a strong sense of curiosity, asking questions actively, challenging assumptions or engaging in inquiry together with teachers.

A2: Ability
Develop the ability/skill needed to discover/innovate/create, as demonstrated by students possessing critical thinking skills to assess ideas, acquiring research skills, synthesizing knowledge across disciplines or applying academic knowledge to real-life problems.

A3: Accomplishments
Demonstrate accomplishment of discovery/innovation/creativity through producing /constructing creative works/new artefacts, effective solutions to real-life problems or new processes.

Learning and Teaching Activities (LTAs)

	LTAs	Brief Description	CILO No.	Hours/week (if applicable)
1	Lectures	Concept-driven lectures covering principles and applications of molecular evolution; guidance on study design and interpretation; and the modern methods used in current research.	1, 2, 3	
2	Computer-based practical sessions	Hands-on labs that scaffold full workflows on real datasets. Emphasis on troubleshooting, convergence diagnostics, and reproducible reports.	1, 2, 3	

3	Research seminar & project clinic	Short discussion sessions and live clinics where students present progress, critique recent phylogenetics papers, and get targeted feedback on their analysis plans, assumptions, and uncertainty reporting; students are encouraged to bring their own data.	2, 3	

Assessment Tasks / Activities (ATs)

	ATs	CILO No.	Weighting (%)	Remarks ("-" for nil entry)	Allow Use of GenAI?
1	Exercises: Computer exercises and handout exercises	1, 2, 3	60	-	No
2	Project: Written report based on individual mini project	1, 2, 3	40	Small group case write-up and presentation	No

Continuous Assessment (%)

100

Assessment Rubrics (AR)

Assessment Task

Exercises

Criterion

What is accessed: Application of core concepts; correct execution of workflows; basic tree handling and plots; clarity and reproducibility of write-ups.

Excellent

(A+, A, A-)
Consistently correct and efficient analyses; models and parameters are well-justified; code run reproducibly with documented steps; figures are publication-quality; mini-reports are well-structured with insightful conclusions and clear limitations.

Good

(B+, B, B-)
Demonstrates a solid understanding of laboratory concepts; Submits a structured report with minor errors and reasonable conclusions.

Fair

(C+, C, C-)
Demonstrates a partial understanding of core concepts; workflows mostly complete but error prone; code/plots inconsistently documented; conclusions limited.

Marginal

(D)

Basic understanding evident but uneven execution; frequent assistance needed for calculations or software; model choice weakly justified; code run inconsistently; figures/reports are poorly structured with vague or unsupported conclusions.

Failure

(F)
Conceptual misunderstandings; incorrect or missing hand-calculations; inappropriate or non-running analyses; no reproducible record; figures/reports are disorganized, error-prone, and lack valid conclusions.

Assessment Task

Project

Criterion

What is accessed: Study design & justification; end-to-end workflow (data curation, tree making, model testing; calibration/clock where relevant); biological interpretation; presentation delivery; reproducible artifact.

Excellent

(A+, A, A-)
Innovative, well-designed study tightly aligned to a clear question; methods expertly chosen and justified; strong support metrics; uncertainties and assumptions critically evaluated; conclusions are biologically insightful and defensible; presentation polished and engaging; fully reproducible materials.

Good

(B+, B, B-)
Solid study addressing the question; appropriate methods with reasonable justification; support and diagnostics mostly adequate; limitations noted; conclusions are coherent; presentation is organized; reproducible materials largely complete with minor gaps.

Fair

(C+, C, C-)
Addresses the question but unevenly; methods acceptable yet thinly justified; support/diagnostics have gaps; conclusions tentative; presentation adequate; reproducible materials present but need fixes to run reliably.

Marginal

(D)
Limited or generic design; methods applied but weakly integrated with the question; support/diagnostics incomplete; interpretation superficial or partly inconsistent; presentation somewhat disorganized; reproducibility materials incomplete or difficult to run.

Failure

(F)
Incoherent or incorrect design; methods misapplied or missing; no valid support/diagnostics; interpretation unsupported; presentation unclear; no usable reproducible artifact.

Part III Other Information

Keyword Syllabus

Phylogenetics analysis; natural selection; molecular clock; sequencing; tree-building methods; Bayesian phylogenetics & MCMC

Reading List

Compulsory Readings

	Title
1	Online user manuals for different software and pipeline (to be provided during the course).

Additional Readings

	Title
1	Yang, Ziheng. Molecular evolution: a statistical approach. Oxford University Press, 2014.
2	Scornavacca, Celine, Frédéric Delsuc, and Nicolas Galtier. "Phylogenetics in the genomic era." (2020).
3	Letunic, Ivica, and Peer Bork. "Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy." Nucleic acids research 39.suppl_2 (2011): W475-W478.
4	Yang, Ziheng. "PAML 4: phylogenetic analysis by maximum likelihood." Molecular biology and evolution 24.8 (2007): 1586-1591.