

BIOL 4356/5370 Bioinformatics

Spring 2026 (3 Credits)

Contact Information

Instructor: Dr. Ashley Teufel

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Office Hours: Thursday 12-2:00PM, 3:30-5:00PM, or by appointment

Class Time: Tuesday/Thursday 2:00 PM - 3:15 PM

Location: Science & Technology Room 279

Course Description

Unlike a traditional bioinformatics course with exams and problem sets, this course simulates a research lab environment. Students will learn bioinformatics skills (Python, R, sequence analysis, phylogenetics) in the context of applying them to a real research question with unknown answers.

This course is modeled as a Course-Based Undergraduate Research Experience (CURE) where students will conduct original research. Students will work as a collaborative research team to collect and analyze data, with the goal of producing a collaborative manuscript and presenting individually at the undergraduate research symposium.

Research Project

Our central research question: Do computationally predicted protein features of influenza correlate with environmental variables (temperature, precipitation, etc.) or host species, after accounting for phylogenetic relationships?

We focus on hemagglutinin (HA) because it mediates host cell attachment and is directly involved in transmission. Each student will own one prediction type (e.g., intrinsic disorder, glycosylation sites, stability, aggregation propensity) while sharing a common HA sequence dataset and phylogenetic tree.

Each student will:

1. Contribute to shared data infrastructure (sequence database, phylogenetic tree, climate data)
2. Own one computational prediction type (e.g., intrinsic disorder, glycosylation sites, stability)
3. Conduct statistical analysis on their prediction data
4. Write their sections of the collaborative paper
5. Present an individual poster at the undergraduate research symposium

Learning Outcomes

By the end of this course, students will be able to:

1. Retrieve and curate biological sequence data from public databases
2. Construct and interpret multiple sequence alignments and phylogenetic trees
3. Use Python to batch process biological data and parse output files
4. Apply appropriate statistical methods including phylogenetic comparative methods
5. Create publication-quality figures in R

6. Communicate research through scientific writing and poster presentation
7. Collaborate effectively on a research project including peer review
8. Practice reproducible research through documentation and organized workflows

Course Structure

Tuesdays - Collaborative Work: Progress check-ins, troubleshooting, code comparisons, peer review, and group decisions. Student-driven with instructor facilitating.

Thursdays - Skill Workshops: Instructor-led sessions introducing new tools and techniques. Hands-on tutorials.

"Try It Then Converge" Model: Students attempt new skills independently before class discussion. This builds problem-solving confidence and reveals common stumbling blocks.

Course Schedule

Week	Dates	Tuesday	Thursday	Checkpoint
1	1/20, 1/22	Intro, syllabus, project overview	Setup: Python, R, terminal basics	
2	1/27, 1/29	Research design discussion	NCBI databases, sequence retrieval	Setup complete
3	2/3, 2/5	Sequence curation decisions	FASTA parsing with Python	
4	2/10, 2/12	Code troubleshooting	Multiple sequence alignment	Dataset curated
5	2/17, 2/19	Alignment review & trimming	Phylogenetics intro: tree building	
6	2/24, 2/26	Tree interpretation	Environmental data collection	Alignment done
7	3/3, 3/5	Prediction tool assignments	Batch processing predictions	Tree complete
8	3/10, 3/12	SPRING BREAK	SPRING BREAK	
9	3/17, 3/19	Progress check: predictions	R data visualization	Predictions run
10	3/24, 3/26	Figure critique session	PGLS intro: phylo comparative methods	
11	3/31, 4/2	Statistical troubleshooting	LaTeX/Overleaf workshop	Stats complete
12	4/7, 4/9	Methods section peer review	Results writing workshop	Figures done
13	4/14, 4/16	Results peer review	Discussion writing; poster design	Methods/Results draft
14	4/21, 4/23	Discussion peer review	Poster work session	Discussion draft
15	4/28, 4/30	Poster presentations	Manuscript assembly	Poster complete
16	5/5, 5/7	Final revisions	Submission & reflection	Final paper

Grading

There are no exams. Grades are based on participation in the research process and the quality of your contributions.

A = 90-100%, B = 80-89%, C = 70-79%, D = 60-69%, F < 60%

Weekly Checkpoints (150 points)

Due each Tuesday by class time. Quick demonstration that you attempted the week's task. Graded complete/incomplete.

10 checkpoints × 15 points = 150 points

Major Deliverables (600 points)

Deliverable	Description	Points
Analysis & Figures	Your prediction analysis complete with publication-quality figures	150
Methods & Results	Your sections of the collaborative paper	150
Individual Poster	Presented at undergraduate research symposium	100

Deliverable	Description	Points
Peer Review Quality	Quality of feedback given during peer review sessions	100
Collaborative Contributions	Participation in shared infrastructure and group decisions	100
TOTAL		600

Undergraduate Total: 150 (checkpoints) + 600 (deliverables) = 750 points

Graduate Student Additional Deliverable (+150 points)

Deliverable	Description	Points
Introduction Section	Lead writing of background/literature review for collaborative paper	100
Mentorship	Documented peer mentoring of undergraduate student(s)	50
TOTAL		150

Graduate Total: 150 + 600 + 150 = 900 points

What Goes Where

Individual (your own GitHub/files):

- Your prediction scripts and output
- Your methods and results sections
- Your poster

Collaborative (shared Overleaf):

- Background/introduction (grad student leads)
- Discussion
- Abstract

Course Policies

Attendance: This is collaborative research - attendance matters.

Late Checkpoints: Can be made up within one week for full credit. After that, no credit.

Late Deliverables: 10% penalty per day late. Communicate early if struggling.

Broader Use of Generative AI Permitted Within Guidelines

Use of artificial intelligence (AI) tools, including ChatGPT, is permitted in this course for students who wish to use them. To adhere to our scholarly values, students must cite any AI-generated material that informed their work (this includes in-text citations and/or use of quotations, and in your reference list). Using an AI tool to generate content without proper attribution qualifies as academic dishonesty and violates Texas A&M-San Antonio's standards of academic integrity.

A Note on Research

This is real research with unknown outcomes. We may find exciting correlations, or we may find nothing. Both are valid scientific results. The skills you learn and the process you experience are the primary goals.

Research rarely goes according to plan. If we collectively hit a wall - a tool doesn't work, data is messier than expected, our approach needs rethinking - we'll adapt together. Due dates exist to keep us moving, but they're not more important than doing the work right.

Welcome to the lab.

University Policies

FOR UNIVERSITY POLICIES SEE DOCUMENT ON BLACKBOARD