

Department of Biological Sciences
BISC 4171
Undergraduate Research (1 credit)
NeuroGene Explorer Syllabus - Spring 2026

Instructor: Dr. Damien O'Halloran (he/him/his)

Email: damienoh@gwu.edu

Office: SEH 6530

Office hours: By appointment (Zoom or in person).

Course format: Asynchronous/independent research. There is no scheduled meeting time. Students complete work independently and communicate with the instructor by email and/or appointment as needed.

Course materials + starter code: The course GitHub repository (download as a ZIP; no Git required) contains the starter scripts, README instructions (including quick commands), and PDFs. Repository name: dohalloran/BISC-4171-NeuroGene-Explorer (link posted on Blackboard).

Course Description

BISC 4171 is a 1-credit undergraduate research course. Students will conduct an independent, guided bioinformatics research project with a neural focus. Students will download a public gene-expression count table (no raw FASTQ processing required) and build a small Python pipeline to perform quality checks, rank genes by differences between groups, and interpret findings in the context of brain biology.

Learning Objectives and Outcomes

- Set up a reproducible Python environment for data analysis (pandas, numpy, matplotlib).
- Explain what a gene count matrix is and how metadata defines experimental groups.
- Perform basic QC checks and visualization for gene-count data.
- Compute and interpret simple gene-ranking results for two required comparisons: (1) WT SD5 vs WT HC5 and (2) Shank3 vs WT (matched condition).
- Communicate results clearly in a midterm progress report, final report, and lightning talk slide.
- Use AI tools responsibly for code debugging when helpful (optional), and be able to explain your final code and results in your own words.

Prerequisites

No formal programming prerequisite is required. Students should be willing to follow step-by-step Python instructions and ask questions when stuck.

Minimum Technology Requirements and Skills

- Regular access to a reliable computer (Mac/Windows/Linux) with internet.
- Ability to install software (Miniconda recommended) and run Python scripts from a terminal.
- Use of GW Blackboard and GW email for course communications.

Course Structure and Credit Hour Expectations

This 1-credit course is designed for light but consistent progress across the semester. Students should expect approximately 2-3 hours per week of independent work on average. Work will vary by week depending on your progress and debugging needs.

Required Materials

- Course materials, project packet, and starter scripts are provided via the course GitHub repository (download as ZIP; no Git required) and Blackboard.
- Software: Python 3.11+, pandas, numpy, matplotlib, scipy, statsmodels.
- Public dataset: NCBI GEO GSE113754 (processed counts tables).

Communication

We will communicate primarily via GW email and Blackboard announcements. Because the course has no scheduled meeting time, students are encouraged to email brief status updates or questions as needed and to request an appointment when additional support is helpful. Course materials and starter scripts are distributed via Blackboard and the course GitHub repository (ZIP download).

Assessment and Grading

Graded components:

- Midterm Progress Report (Aim 1: WT SD5 vs WT HC5): 35%
- Final Report (Aim 1 + Aim 2 genotype required): 45%
- Lightning talk (one-slide PDF + optional 2-3 min recording): 10%
- Code + reproducibility package: 10%

Deadlines

The Midterm Progress Report is due by noon on the Friday before Spring break. The Final Report and Lightning Talk are due by noon on the last day of class.

Late Work

I expect work to be submitted on time. Because there are only a few major deliverables, late submissions are generally not accepted unless you contact me at least 48 hours before the deadline and we agree on an alternate plan.

Academic Integrity and Generative AI

By submitting work for evaluation in this course, you represent it as your own intellectual product. You must not fabricate data or results, and you must properly cite any external sources you use.

Generative AI tools are permitted in a limited way: students may use AI to debug code (e.g., interpret error messages, suggest fixes, or refactor code for clarity). There is no AI log requirement. However, you must (1) be able to explain your final code and analysis in your own words and (2) include a brief disclosure in your report (1-2 sentences) describing any AI assistance you used and for what purpose. Using AI to generate large portions of your written reports without attribution, to fabricate results, or to submit work you do not understand is not permitted and may be treated as an academic integrity violation.

Netiquette and Professionalism

Remain professional, respectful, and courteous in all communications (email, Blackboard, Zoom). If you are upset, wait before sending messages. The instructor reserves the right to address inappropriate communication consistent with university policy.

Student Support and Accessibility

If you have a disability or other condition that may affect your participation, please contact Disability Support Services (DSS) and notify me as early as possible so we can work together to provide appropriate accommodations.

If you need technology help, contact GW Information Technology support. For additional student support resources, consult the university links posted on Blackboard.

Project Summary

Students will complete two required analyses using the NeuroGene Explorer pipeline:

- Aim 1: WT SD5 vs WT HC5 (sleep deprivation effect).
- Aim 2: Shank3 vs WT under matched condition (genotype comparison required).

