

Problem: Make a pretty website, but only spend time on content

Solution: Mark down

Course description

Programming skills and software tools for building automated bioinformatics pipelines and computational biology analyses. Emphasis on UNIX tools and R libraries for distilling raw sequencing data into interpretable results. This course is aimed at students familiar with UNIX and with some programming experience in python, R, or C/C++.

Instructional staff

- * [Cole Trapnell](<http://cole-trapnell-lab.github.io/>)
- * Teaching assistant: April Lo

Please click on the links above for email addresses and office locations.

Meeting times and locations

Classes:

Monday and Wednesday, 10:30 – 12:20 am, [zoom](<http://www.washington.edu/home/maps/southcentral.html?gnom>).

Class Slack:

We will use Slack during class and outside of class to communicate, share code snippets, ask and answer questions. The class slack is here:

- * [gs-bioinf-workflows.slack.com](<https://gs-bioinf-workflows.slack.com>)

You will receive an invitation to join prior to the first class.

Office hours:

- * No official office hours. Post questions on Slack as needed.

Prerequisites

- * Substantial background in molecular and cellular biology, genetics, biochemistry, or related disciplines.
- * Familiarity with UNIX.
- * Some programming experience in python, R, or C/C++.
- * Students are encouraged to have taken GENOME559 and/or GENOME560.

genome569

[View on GitHub](#)

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Markdown file structure

```
---  
title: "genome569"  
output: html_document  
---
```

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