# 09-18-24_weekly-update

## Cappy Pugliese

## 2024-09-18

**Last Week**

**9/9 – 9/13**

- finished reading most of the Forsythe 2021 paper
- finished my individual development plan
- practiced more with using github
- learned about the cluster and started the sign up process
- dropped one of my classes (conservation bio) since my courseload was too much

**This Week**

**9/16 – 9/17**

- checked out whitenose.org
- finished skimming through the rest of the Forsythe 2021 paper
- skimmed through the other 2 WNS papers
- tried to finish setting up cluster account
  - wasn't letting me reset my password for some reason
  - but I might just have to wait a week or so

**9/18**

- downloaded fastQC to laptop
- downloaded a random *P. destructans* fastq file
  - had some trouble downloading the right file format, but then I figured it out
  - tried to run it through fastQC
  - there was a file format error
- decided it was a great time to start up my lab notebook
  - set up a repository in github
  - figured out how to add r files to my repository
  - figured out how to create r markdown files
  - wrote this r markdown file

**9/19**

- tried to re-run the fastq file through fastQC
  - once again there was a file format error
  - I tried downloading a different fastq file to see if it was just that particular file
  - still recieved the same file format error
  - downloaded it a different way again and still recieved the same file format error

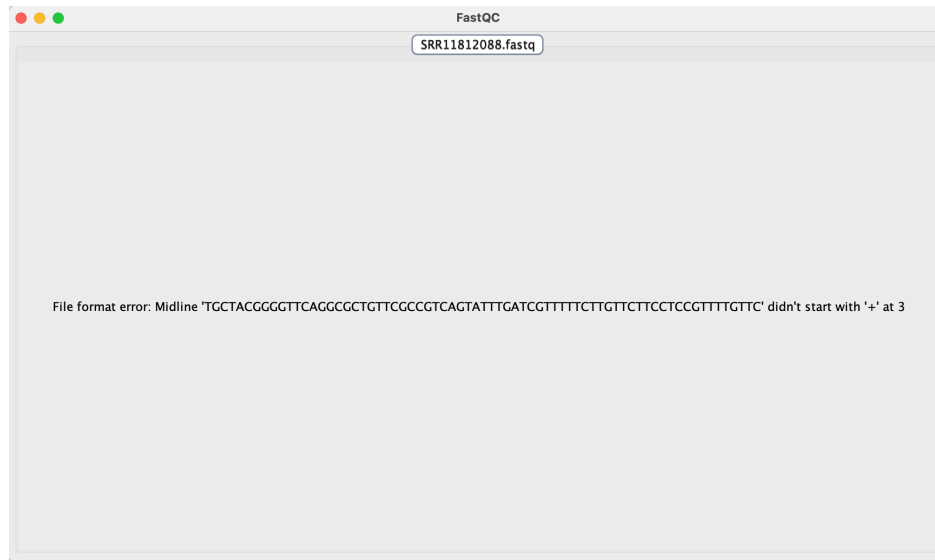– unsure of what I am doing wrong or if I need to go in and change the file format?



Figure 1: file error message

- watched some xanadu intro videos
  – learned how to use the terminal to sign into the head computer
  – was able to successfully sign in and out of the cluster using the command line