

Weekly Update

Cappy Pugliese

10/28 - 11/1

This Week

10/28

- led evolution lunch
- everyone worked on their lab website page during lab meeting

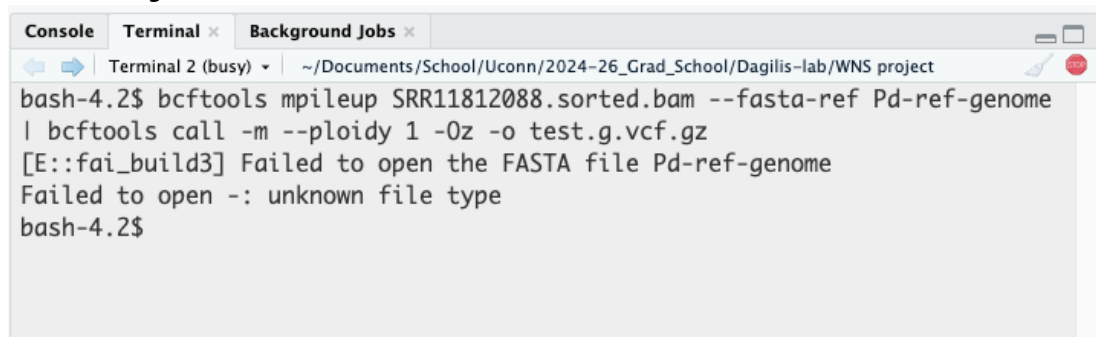
10/29

- began revising preproposal topic
- started looking at some more WNS papers

10/30

- created an excel sheet to better organize the WNS papers I was looking at
- met with Andrius
 - need to start thinking about members for my advisory committee
- tried to work more on the WNS analysis file
 - struggled a bit to get the picard command to work (got a bit of help from Andrius)
 - was able to successfully edit the BAM file
 - was not able to call the genotype
 - * the command was unable to open up the reference genome file I had downloaded
 - * it is very possible I downloaded the ref genome incorrectly

- * I did try redownloading it (the same way as before) and renaming it to have .fasta at the end of it, but nothing changed

A screenshot of a terminal window with three tabs: 'Console', 'Terminal', and 'Background Jobs'. The 'Terminal' tab is active, showing a command prompt 'bash-4.2\$'. The user has entered the command 'bcftools mpileup SRR11812088.sorted.bam --fasta-ref Pd-ref-genome | bcftools call -m --ploidy 1 -Oz -o test.g.vcf.gz'. The terminal output shows an error: '[E::fai_build3] Failed to open the FASTA file Pd-ref-genome' followed by 'Failed to open -: unknown file type' and the prompt 'bash-4.2\$'. The window title bar indicates the path '~/Documents/School/Uconn/2024-26_Grad_School/Dagilis-lab/WNS project'.

- also edited my lab member page a little
- added a bioinformatics resources post on the blog portion of the lab website