

# Weekly Update

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5/05 - 5/09

## **Finals Week**

### **Monday 5/5**

- spent basically the entire day finalizing my final group project's gitlab

### **Tuesday 5/6**

- looked back again at the haplotypcaller output
- sorted out all of the samples that ran out of memory and did not finish creating an index file alongside the g.vcf file
- made a new script to re-run just these samples with more memory
- put the new script running and hopefully everything works out
  - otherwise there might be something else going on or I still didn't give it enough memory
- also did some file tidying up in my own directory

#### **future todos:**

- check to make sure script ran properly and all samples generated an indexed file (.tbi - I'm assuming this is an index file, although I'm not actually sure)
- trouble shoot if any of the samples didn't run properly
- merge everything back into one folder if things do run properly

- can delete the test Pd\_03 run from my own directory if run2 works out
- make the script for the next GVCF process