Once the BAM files are ready, the information in them will be used to call variants. Essentially, records will be created of all sites across the reference genome where the query data had different bases/sequences. The tool for this step is still being decided on. Known tools require the data to resemble the reference genome to a certain extent. The fact that the input DNA is that of multiple individuals, means that there might be more discrepancies than these programs can account for. This will likely take more time, estimating two weeks of hands-on analysis with about a week after to run. If DNA of a single individual is used, this will take a week of run time and about two hours of hands-on analytical time.

Finally, the results of the variant calling will need to compared between