**Mapping reads with BWA**

1. Prepare HPC environment:
   1. rclone, BWA, samtools installed in your bubble
2. Move into your scratch directory (/scratch/alpine/$USER), activate your bio bubble
   1. cd /scratch/alpine/$USER
   2. conda activate bio
3. Download reads from Google Drive:
   1. rclone copy bioinfo:2023/Reads/readFile\_F.fastq.gz . -P
   2. rclone copy bioinfo:2023/Reads/readFile\_R.fastq.gz . -P
4. Download the reference genome from Google Drive:
   1. rclone copy bioinfo:2023/Pant.hap.fasta . -P
5. Index the reference genome for mapping (will take ~10-30 minutes!):
   1. bwa index Pant.hap.fasta
6. Edit your job submission script:
   1. bwa command
   2. samtools command
   3. resource request
7. Submit job
8. Once job completes, check output, make sure job completed successfully
   1. samtools flagstat bamFile
   2. ls -l \*.bam
9. Upload bam file to Google Drive:
   1. rclone copy bamFile bioinfo:2023/Bams/ -P