Midterm work

100 credit

- Input: EcoTestRead2.fq
- Output: VCF files
- Your program should be able to read .fq file and output to a .vcf file
- Integrate BWT in the alignment
- Allow one mismatch in the alignment
- Successfully call most mismatch
- No open source software is allowed to use

120 credit (optional)

- Input: HomoExonReads.fq
- Output: VCF files
- Your program should be able to read .fq file and output to a .vcf file
- Integrate BWT in the alignment
- Allow one mismatch in the alignment
- Be capable to handle the human genome data, all analysis done in 12 hours.
- Successfully call most mismatches
- No open source software is allowed to use

Due date

- First check: April 23;
- Second check: April 30;
  - 5% credit off