**POST SEQUENCING ANALYSES EXERCISES**

1. Using FastQC, carry out quality checks on the seven (7) pairs of sample fastq files provided in the “Exercise\_files” folder on the shared google drive (<https://drive.google.com/drive/folders/1Lay00lIavQjOPzohroBRxCx9wvPQTWX3?usp=sharing>).
2. From your analysis above, group the samples into “good”, “bad” and “moderate” quality.
3. Tabulate the indices used for your groupings above and indicate your reason for placing fastq files into these groups.
4. Aggregate the fastqc report files using MultiQC **(Optional)**
5. Assemble all “good” and “moderate” quality fastqs using CGI assembler