

Exercise 1: If you do not have an account on Galaxy (<https://usegalaxy.org/>), please go visit the website and create an account.

Exercise 2: Reconstruct the sequence from the gel electrophoresis

Exercise 3: Align the following reads to the reference genome and highlight the variation site/sites. For simplicity, you can use “.” to represent the nucleotide if it is the same as the reference genome.

Read1: ATGGCATTGCAATTTGACAT

Read2: TGGCATTGCAATTTG

Read3: AGATGGTATTG

Read4: GATGGCATTGCAA

Reference genome: AGATGGTATTGCAATTTGACAT

Exercise 4: The instruction and demo are on the slides. Answer following questions:

a. How many reads were in each FASTQ file?

b. What is the read length for each file

c. Which FASTQ file has better quality?