Lab3

Bioinformatics

Due September 9, 2020

1) In a text editor, write a \*.sam file corresponding to the alignment found in Lab3\_Alignment3.fasta. Load your file into Geneious to make sure it is correct. Use any quality scores you like. You might find the following sites helpful:

<https://samtools.github.io/hts-specs/SAMv1.pdf>

https://bioinformatics.uconn.edu/resources-and-events/tutorials-2/file-formats-tutorial/#fileformats\_sam

<https://broadinstitute.github.io/picard/explain-flags.html>

<https://en.wikipedia.org/wiki/SAM_(file_format)>

2) Convert the following fastq quality scores into phred scores and error probabilities. Assume Phred+33 format:

Qual PHRED prob

! \_\_\_\_\_\_ \_\_\_\_\_\_

A \_\_\_\_\_\_ \_\_\_\_\_\_

4 \_\_\_\_\_\_ \_\_\_\_\_\_

3) Convert the following error probability into phred scores and error probabilities. Assume Phred+33 format:

Prob PHRED Qual

0.0001 \_\_\_\_\_\_ \_\_\_\_\_\_

0.001 \_\_\_\_\_\_ \_\_\_\_\_\_

0.01 \_\_\_\_\_\_ \_\_\_\_\_\_