1) Consider a reference genome with genes as follows:

AGAGAGAG|AACAACAACAAC|GGGAAAGGGAAA

gene 1 | gene 2 | gene 3

Suppose that mRNA is extracted from a sample, and during sequencing is

broken into the following fragments: GGG, AAC, ACA, GAA, and GAG

(Note: the nucleotide ‘T’ appears in DNA while ‘U’ appears in mRNA. If there was a ‘U’ in one of the reads, we could replace it with a ‘T’ during this mapping step).

What are the read counts for each of the 3 genes?

Gene 1:

Gene 2:

Gene 3: