Exercise/Assignment

Case study: There are 7 reported positive cases of SARS-CoV-2 in location **X** which needed urgent sequencing to ascertain the potential threat. You have been provided with the raw sequencing data for all 7 samples, generated via Illumina NextSeq using the ARTIC protocol (FastQ Format). For all 7 samples you need to:

1. Assemble the full genome using Galaxy and Exatype
2. Assess the quality of each sample and flag those that might be poor quality
3. Assign lineage (pangolin) and clades (nextclade) for each sample and also assess quality based on pangolin and nextclade outputs
4. Compare the quality assignments between Galaxy and Exatype
5. Compare the lineage and clade assignments between Galaxy and Exatype
6. Identify any mutations or variants of concern/interest
7. Create a report that outlines this information and your recommendations to your Department of Health.

Find raw sequencing data and additional data files here:
Onlime – [9_10E] Galaxy pipeline