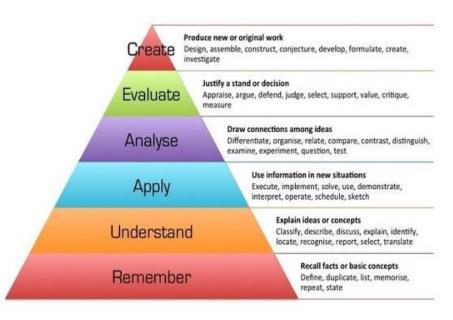
Viral Genomics and Bioinformatics Learning Outcomes

After completing this course, participants should be able to:

- Apply Unix/Linux command-line and write basic shell scripts for automating bioinformatics tasks
- <u>Recognise the different</u> file formats related to genome sequencing data (Illumina, Minion, and ARCTIC protocol outputs)
- <u>Select</u> an appropriate strategy for quality control of NGS data
- <u>Perform</u> reference mapping using different software (e.g. BWA, Bowtie, Novoalign, Tanoti).
- <u>Evaluate</u> genome assemblies using statistics and visualisations
- <u>Use</u> multiple de-novo assemblers for viral genome reconstruction (e.g. SPAdes, ABYSS, IDBA-UD)
- <u>Use</u> metagenomics tools such as KRAKEN and Centrifuge to detect and identify viral pathogens
- <u>Select</u> appropriate software tools to call variants from a genome assembly.
- <u>Compute</u> multiple sequence alignments and <u>construct</u> phylogenetic trees to understand viral evolution and transmission dynamics
- Build a pipeline for analysis, interpretation and identification of viral pathogens.
- Identify effective methods for disseminating knowledge and skills in viral bioinformatics.



COVID-19