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
- **Recognise the different** file formats related to genome sequencing data (Illumina, Minion, and ARCTIC protocol outputs)
- **Select** an appropriate strategy for quality control of NGS data
- **Perform** reference mapping using different software (e.g. BWA, Bowtie, Novoalign, Tanoti).
- **Evaluate** genome assemblies using statistics and visualisations
- **Use** multiple de-novo assemblers for viral genome reconstruction (e.g. SPAdes, ABYSS, IDBA-UD)
- **Use** metagenomics tools such as KRAKEN and Centrifuge to detect and identify viral pathogens
- **Select** appropriate software tools to call variants from a genome assembly.
- **Compute** multiple sequence alignments and **construct** 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.