

Overview – Bioinformatics for Flu and RSV

Clyde Dapat



WHO Collaborating Centre
for Reference and
Research on Influenza
VIDRL



A joint venture between The University of Melbourne and The Royal Melbourne Hospital

Motivation

- RSV and influenza virus pose significant public health threats
- Timely detection and monitoring are important in mitigating the spread of pathogens
- Capacity for bioinformatics analysis of influenza and other respiratory viruses at national and regional laboratories remains limited.
- Pressing need for training and capacity building for NGS data analysis

Learning outcomes

Upon completion of the course, participants will be able to:

- Perform whole-genome assembly
- Evaluate the quality control of NGS data and consensus sequences
- Identify variants and detect mutations
- Perform phylogenetic analysis
- Submit sequence to genetic database

Course content

- Bioinformatics for RSV and influenza
- Quality control of NGS data and consensus sequences
- Principles of genome assembly
- Identify variants and detect mutations
- Phylogenetic analysis
- Data sharing to genetic databases

Course structure

- Course is organized in modules
- Each module includes introductory lecture, step-by-step tutorial
- Analysis of assigned datasets

Thank you !

clyde.dapat@influenzacentre.org



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