WHO Collaborating Centre for Reference and Research on Influenza
VIDRL

World Health Organization
Philippines

KDCA
Korea Disease Control and Prevention Agency

Course Overview

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CENTRE FOR PATHOGEN GENOMICS

Doherty Institute

THE UNIVERSITY OF MELBOURNE

The Royal Melbourne Hospital

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

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Motivation

- SARS-CoV-2 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

- SARS-CoV-2 and influenza overview
- Introduction to NGS data analysis
- Quality control of NGS data and consensus sequences
- Principles of genome assembly
- Identify variants and detect mutations
- Phylogenetic analysis
- Data sharing to genetic databases

Case study

- Participants will receive 10 sequence data of flu viruses collected from the Philippines
- Analyze and interpret results

Extra assignment

- Pipeline development

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THANK YOU

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