Bioinformatics Analysis of Whole Genome Sequencing Workshop (*Mycobacterium tuberculosis*)

Organized by

Faculty of Medicine and Health Sciences

UMS
UNIVERSITI MALAYSIA SABAH

in collaboration with

NUS
National University of Singapore

Saw Swee Hock
School of Public Health

Date: **8th - 9th October 2018**

Time: **9.00 am to 5.00 pm**

Venue: **Bioinformatic Lab, Biotechnology Research Institute, Universiti Malaysia Sabah**

Seat Limit: **30 participants**

Registration fee:

RM 100 (UMS student or staff)

RM150 (Non-UMS)

For more information:
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For registration:
https://docs.google.com/forms/d/e/1FAIpQ
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2mdWnG9DuOICoKiworvGN5uZwJm-
Ew/viewform?usp=sf_link

	8th October 2018 (Day 1)		**9th October 2018 (Day 2)**
Session 1 **0900 – 1030**	Opening Ceremony Introduction to whole-genome sequencing for infectious disease surveillance • Review of sequencing technologies and its applications especially for public health microbiology and surveillance		Mapping and Variant(s) Detection (Lab Practical) • Use of command line software programs to map sequence reads to a reference and identifying genetic variants.
Break			
Session 2 **1100 – 1230**	Sequence data processing for quality control and species identification • Overview of sequence data processing for quality control		Identification and annotation of SNPs for prediction of bacteria drug resistance • Overview of genetic markers associated with bacteria drug resistance
Lunch			
Session 3 **1330 – 1500**	Sequence data processing for quality control and species identification (Lab Practical) • Use of command line software programs to assess quality of data generated, removal of poor quality bases/sequences, and rapid identification of species sequenced.		SNP Phylogenetic tree for inference of bacteria epidemiological clustering • Overview of SNP phylogenetic tree for inference of bacteria epidemiological clustering
Break			
Session 4 **1530 – 1700**	Mapping and Variant(s) Detection • Overview of sequence data processing for mapping reads to bacteria reference genome to identify genetic variants such as single nucleotide polymorphisms (SNPs)		Annotation/Interpretation of SNPs and SNP phylogenetic tree • Use of software programs to infer resistance profile of bacteria isolates sequenced, and epidemiological clustering