



## **Whole Genome sequencing and Bioinformatics Training**

4-7 March 2025

Lilongwe, Malawi

### **Day 1 – Introduction to WGS and Online Bioinformatics Basics**

*Focus: Setting the stage, understanding sequencing technologies, performing BLAST and exploring different online tools.*

#### **Morning Session 10:00-12:30: Welcome and Overview**

- **Introductions & Goals:**
  - o Welcome and participant introductions.
  - o Outline training goals.
- **WGS Overview:**
  - o Overview of whole genome sequencing (WGS) technologies and their laboratory roles.
  - o Basic bioinformatics concepts: file formats and sequence data types
  - o Basic bioinformatics operations: assembly, mapping, alignment, variant calling

#### **Lunch 12:30-13:30**

#### **Afternoon Session 13:30-16:00: Introduction to Online Tools**

- **Demonstrations**
  - o Overview of browser-based platforms such as BLAST, Galaxy, Epi2me, PathogenWatch, CGE, Assembly Server, Illumina Dragen, Terra Bio, etc.
  - o Walk-through of each platform's interface and navigation tips.
  - o Optional: brief demo of command-line workflow (e.g., BAP)
- **Hands-On Exercise:**
  - o BLAST Mystery Species Identification, and troubleshoot what went wrong between wet and dry lab
  - o Identify bacterial species using on-line platforms (BLAST, KmerFinder, Pathogen Watch) and learn to detect a common quality issue

## Day 2 – Quality Control (QC) and Assembly

*Focus: Understanding data quality, performing QC on raw reads, and exploring assembly theory and practice.*

### Morning Session 9:30-12:30: Quality Control (QC) of Raw Reads

- **Presentation:**
  - o Concepts of data quality and its impact on downstream analysis.
  - o Common issues: adapter contamination and low-quality reads.
  - o Illumina Reads QC (and 3 puzzles)
- **Demonstration:**
  - o Review examples of good and poor run reports from Oxford Nanopore Technologies (ONT)
- **Hands-On Exercises:**
  - o (Optional) install WSL and Ubuntu command-line environment
  - o Use off-line FastQC and on-line ONT QC tool to assess sample data.
  - o Review pre-loaded sample datasets and interpret QC reports.

### Lunch 12:30-13:30

### Afternoon Session 13:30-16:00: Assembly Theory, Exercises, and QC

- **Presentation:**
  - o Assembly Approaches:
    - Reference-based vs. de-novo assembly (including de Bruijn graphs)
    - Issues such as contamination and high contig counts.
  - o Assembly Types:
    - Long, short, and hybrid assemblies.
  - o Tools like BV-BRC for assembly.
  - o Quality Assessment:
    - QC tools such as QUAST, MultiQC, CheckM, and BUCO.
- **Hands-On Exercises:**
  - o Generate assemblies (ideally using participants' own data) via the BV-BRC Assembly Service.
  - o Evaluate assembly quality using QC reports (QC reports from NICD as examples?).

## Day 3 – Typing and AMR Analysis Using Online Platforms

*Focus: Understanding antimicrobial resistance (AMR) fundamentals and using online tools for bacterial typing and AMR gene detection.*

### Morning Session 9:30-12:30: Typing & AMR Fundamentals

- **Presentation:**
  - Compare traditional lab-based typing methods with bioinformatics approaches.
- **Demonstration:**
  - KmerFinder, MLST, serotyping.
  - ResFinder, PlasmidFinder, VirulenceFinder
- **Hands-On Exercise:**
  - Recap on how ResFinder/PlasmidFinder/etc work.
  - Build your own AnythingFinder with MyDBFinder, MyKmerFinder

### Lunch 12:30-13:30

### Afternoon Session 13:30-16:00: Hands-On AMR Exercise

- **Review & Discussion:**
  - Revisit CGE results and discuss findings.
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- **Hands-On Exercises:**
  - Use web-based tools for AMR gene detection (e.g., ResFinder, CARD, PathogenWatch, MEFinder, PlasmidFinder).
  - Demo / Integrate data with hAMRonization (if possible)
  - Discuss interpretation of results and the importance of consensus among tools (e.g., comparing ResFinder, AMRFinderPlus, CARD)

## Day 4 – Bacterial Typing and Phylogenetic Analysis via Online Tools

*Focus: Leveraging online platforms for bacterial typing and exploring phylogenetic relationships.*

### Morning Session 9:30-12:30: Bacterial Typing Overview

- **Presentation - Overview of Typing Methods:**
  - Introduction to methods such as MLST and cgMLST and their applications in tracking AMR epidemiologically.
  - Discussion on SNP and cgMLST analysis (kmer distance vs. SNPs vs genes/alles).
- **Additional Topics:**
  - Use of multiple sequence alignment (MSA) and tree-building tools.
  - Overview of tools such as CSI Phylogeny, MinTyper, and BEAST (including rooted trees, bootstrapping, and clock/time analysis).
- **Demonstration:**
  - Live demo using Enterobase.

### Lunch 12:30-13:30

### Afternoon Session 13:30-16:00 Hands-On Phylogenetic Analysis & Simulated Outbreak Scenario

- **Hands-On Exercise:**
  - Participants work with sample datasets to generate and visualize phylogenetic trees using off-line GrapeTree and online tools such as Microreact, and iTOL.
- **Theory & Discussion:**
  - Interpreting tree topology and understanding outbreak clusters.
  - Discuss practical implications for AMR surveillance.
- **Simulated Outbreak Scenario**
  - **Tasks:**
    - Identify AMR genes using a web-based tool.
    - Perform bacterial typing and generate a phylogenetic tree.
    - Interpret the integrated results to propose potential clinical and epidemiological actions.
- **Wrap-Up:**
  - Q&A session and final discussion.