# Bioinformatics for One Health Pathogen Genomics

## A Training Workshop
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# CURRICULUM

## Goal

To build capacity among researchers for the analysis and interpretation of bacterial genomic data to support antimicrobial resistance surveillance within One Health frameworks.

## Objectives

- Deliver hands-on bioinformatics modules tailored to bacterial AMR genomic surveillance.
- Equip participants with practical skills in web-based and introductory coding-based tools for bacterial genome analysis.
- Facilitate collaboration and knowledge exchange among researchers engaged in genomic surveillance of AMR.

## Course Prerequisites

- Basic knowledge of microbiology, molecular biology, or related life sciences.
- Interest in antimicrobial resistance and bacterial genomics.
- **No prior programming experience required.**

## Learning Outcomes

By the end of this training, participants will be able to:

- Describe key steps in the bacterial genome analysis and bioinformatics workflow.
- Recognize and manipulate standard NGS data file formats (e.g., FASTQ, FASTA, GenBank).
- Access and extract genomic data from public biological databases.
- Use web-based tools for AMR gene prediction, bacterial typing, and annotation.
- Build and interpret phylogenetic trees for bacterial pathogens.
- Execute basic Linux terminal commands and run pre-written scripts to automate analyses.

## Course Schedule

| Day | Focus | Modules / Activities | Topics / Tools |
|---|---|---|---|
| Day 1 | Foundations of Genomics & AMR Bioinformatics | • Pre-course assessment of participant expectations<br>• Interactive discussion on pre-course video materials<br>• Biological Databases and Resources<br>• NGS Technologies and NGS Data Formats<br>• Sequence Alignments | • NCBI, EMBL, UniProt-<br>• FASTQ, FASTA, GenBank formats<br>• BLAST (n/x)<br>• Resistance gene detection |
| Day 2 | Bacterial Genome Analysis & Phylogeny | • Bacterial Genome Analysis-Bacterial Typing<br>• Phylogeny Construction and Visualization<br>• Quality Check & Genome Assembly<br>• Group presentations | • CARD, RGI, AMRFinderPlus, ResFinder<br>• MLST (CGE), PathogenWatch<br>• MicroReact, Patric, Figtree<br>• FastQC, SPAdes |
| Day 3 | Applied Genomics: *Lactococcus* & Case-Based Work | • Lactococcus garvieae outbreak investigation - Vietnam Fish Farm Dataset<br>• Case Work: Outbreak Investigation<br>• Nanopore Sequencing & Hybrid Assembly for MGE Analysis<br>• Group presentations | • Hybrid assembly (Illumina + Nanopore)<br>• Mobile genetic element (MGE) profiling<br>• Contextual AMR interpretation |
| Day 4 | Linux & Scripting for Genomic Workflows | • Introduction to Linux and Terminal Navigation<br>• Command Line–Based Sequence Analyses<br>• Course Evaluation & Feedback | • Linux basics (mkdir, cd, ls, grep, nano)<br>• Running pre-written shell scripts<br>• Bioinformatics workflows in bash |

## Tools & Platforms Used

- **Web-Based Tools:**
  NCBI, BLAST (n/x), CARD, RGI, ResFinder, AMRFinderPlus, PathogenWatch, MLST (CGE)
- **Software & Command Line Utilities:**
  FastQC, MultiQC, SPAdes, Figtree, Nano, grep, bash scripting, Linux terminal (Mac/Linux VM), Jyputer lab in Google Collab

- **Databases & Resources:**
  GenBank, UniProt, AMR gene databases (CARD, Resfinder, ARG-ANNOT), mobile genetic element databases
- **Visualization & Analysis Platforms:**
  MicroReact, BV-BRC, CSIPhylogeny, Galaxy, iTOL, RStudio

## Topics Covered

- Next-generation sequencing (NGS) technologies and data formats
- Biological databases and genomic data retrieval
- Sequence alignment, annotation, and resistance gene detection
- Quality control and genome assembly workflows
- Bacterial genotyping, subtyping, and phylogenetic analysis
- Hybrid assembly and mobile genetic element (MGE) investigations
- Command-line tools and Linux scripting for genomics workflows
- Interactive computing environments (Jupyter, Colab)
- Case-based learning with *Lactococcus garvieae* from aquaculture outbreaks
- One Health applications in AMR surveillance and outbreak response