

SAGeSA Workshop: Evaluating Tools for AMR Detection and the Role of AI in Data Analysis

Date: 25 April

Time: 08:30 – 10:30 GMT (10:30 – 12:30 CAT)

Workshop Objective

This session aims to equip participants with the skills to critically evaluate antimicrobial resistance (AMR) predictions using **Pathogenwatch** and **ResFinder**, while integrating AI tools like **ChatGPT** for data analysis.

Through practical exercises with real **Staphylococcus aureus** genomic data, participants will:

- ✓ Compare results from multiple bioinformatics tools
- ✓ Identify discrepancies in AMR predictions
- ✓ Assess the strengths and limitations of AI-driven methods

By the end of the session, attendees will have a deeper understanding of how to use AI **efficiently and responsibly** in bioinformatics workflows, ensuring careful interpretation of results **without over-reliance on automated outputs**.

Workshop Overview

This session guides participants through evaluating AMR predictions while critically assessing the role of AI in data analysis. Using real **S. aureus** genomic data, participants will explore how AI tools like **ChatGPT** can support—but not replace—careful interpretation. They will compare outputs from different tools, identify discrepancies, and discuss why results may differ.

Emphasis will be placed on:

- ◆ Using AI **efficiently and responsibly** in bioinformatics workflows
- ◆ Understanding AI's limitations in AMR research
- ◆ Avoiding over-reliance on automated outputs

Key Activities

- 1 **Tool Comparison:** Analyse bacterial WGS data using different bioinformatics tools. Examine genes and variants predicted to confer AMR
- 2 **Data Processing Approaches:** Compare outputs from various software tools with manual analysis, spreadsheets, and scripting
- 3 **AI Integration:** Apply AI-driven methods to process data and compare software outputs

4 **Discussion & Assessment:** Conclude with a discussion on AI's accuracy in data analysis—**can it be trusted for critical decision-making?**

Learning Outcomes

At the end of this session, participants will be able to:


- ✓ Use **Pathogenwatch** and **ResFinder** to analyze AMR genes
- ✓ Compare AMR predictions from different tools
- ✓ Use **Python (Google Colab notebook)** to automate AMR result comparisons
- ✓ Apply **AI (ChatGPT)** to facilitate data analysis and interpretation
- ✓ Critique the suitability of AI for bioinformatics research

Target Audience

- ◆ Researchers with a **solid understanding of bacterial genomics and antimicrobial resistance (AMR)**
- ◆ Familiarity with **Python scripting** or any other programming language is recommended but **not required**

Prerequisites


 Web browser: **Google Chrome** or **Mozilla Firefox**

 Create an account with:

- [Pathogenwatch](#)
- [ChatGPT](#)

Trainers

 **Monica Abrudan** – Wellcome Connecting Science, United Kingdom

 **Stanford Kwenda** – National Institute for Communicable Diseases, South Africa

Apply Now!

 **Application Form:** <https://forms.gle/wf8BYEcUxdrptmZn6>
