

Digital One Health Nanopore AMR Bioinformatics workshop: Pre-workshop preparation

Date: Tuesday, 27 August 2024. 9.30am – 4.30pm

Venue: Central Public Health Laboratories, Old Butabika Road, Kampala

The workshop will mainly be performed on the 3 Nanopore Dell analyses laptops. You may also bring your own laptop if you have one. Most of the workshop will use the Galaxy platform that can be accessed on the internet with any web browser such as Chrome or Firefox.

What is Galaxy?

Galaxy is a widely-used scientific analysis platform that aims to make bioinformatics accessible to researchers that do not have computer programming experience. Galaxy is hosted on computer centres in multiple locations around the world and is free to use. Galaxy is a shared resource, and therefore during peak hours you may experience slower analyses. You may only create 1 account per person in each Galaxy location.

During the workshop we will use a Workflow (combination of analyses) in Galaxy that takes in as input basecalled Nanopore reads (FASTQ format) and identifies the presences of AMR genes. Basecalling cannot be done in Galaxy and will be done on the EPI2ME platform. EPI2ME will also be covered briefly during the workshop.

To ensure that we make the most of our workshop on the 27th of August, please do at least Step 1 and as much of Step 2 as possible. Step 3 is optional but recommended if you would like to familiarise yourself with what Galaxy can do.

Step 1: Create an account on the European (EU) Galaxy instance usegalaxy.eu – [Please follow instructions here](#) (Please do this at a minimum)

Step 2: [Short introduction](#) to the Galaxy interface (Please do as much as possible)

Step 3: More material to familiarise yourself with Galaxy (You are encouraged to explore and try some of these)

[Long introduction](#) (use arrow keys to navigate)

[More tutorials and training material](#)