Chapter 6 Finding AMRs

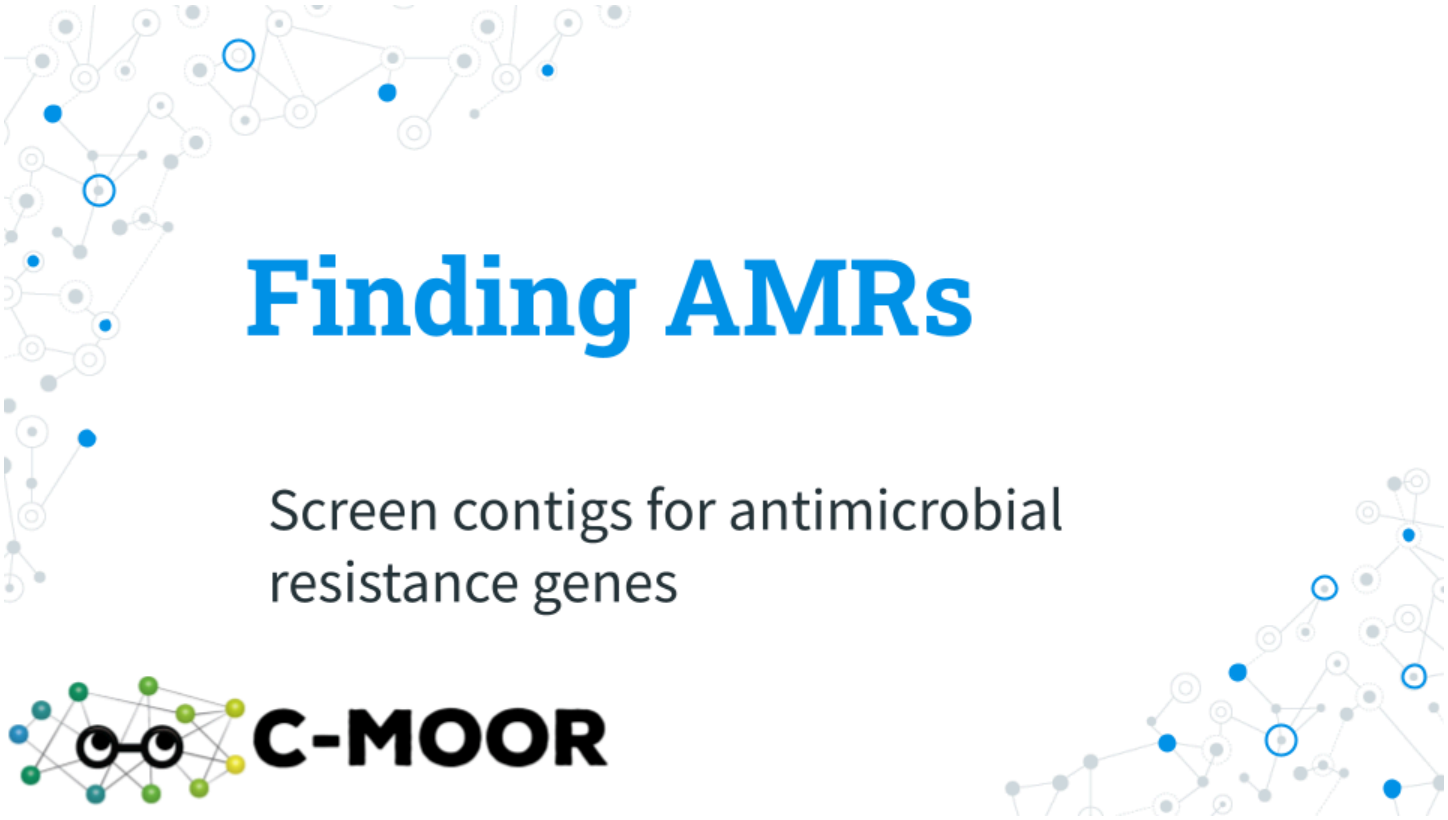
Overview

Purpose

Learning Objectives

Introduction

Antimicrobial resistance genes (AMR genes) allow microbes to counteract the effects of antimicrobial drugs used to treat infections. Databases such as the NCBI Pathogen Detection Reference Gene Catalog and the Comprehensive Antibiotic Resistance Database contain thousands of curated resistance genes and help make AMR-related data more widely available. Here we use the ABRicate tool which can mass screen contigs for antimicrobial genes using a variety of databases including the NCBI database. A similar strategy can be used to screen for virulence factors using databases such as the Virulence Factor Database (VFDB).



[slides] [video]

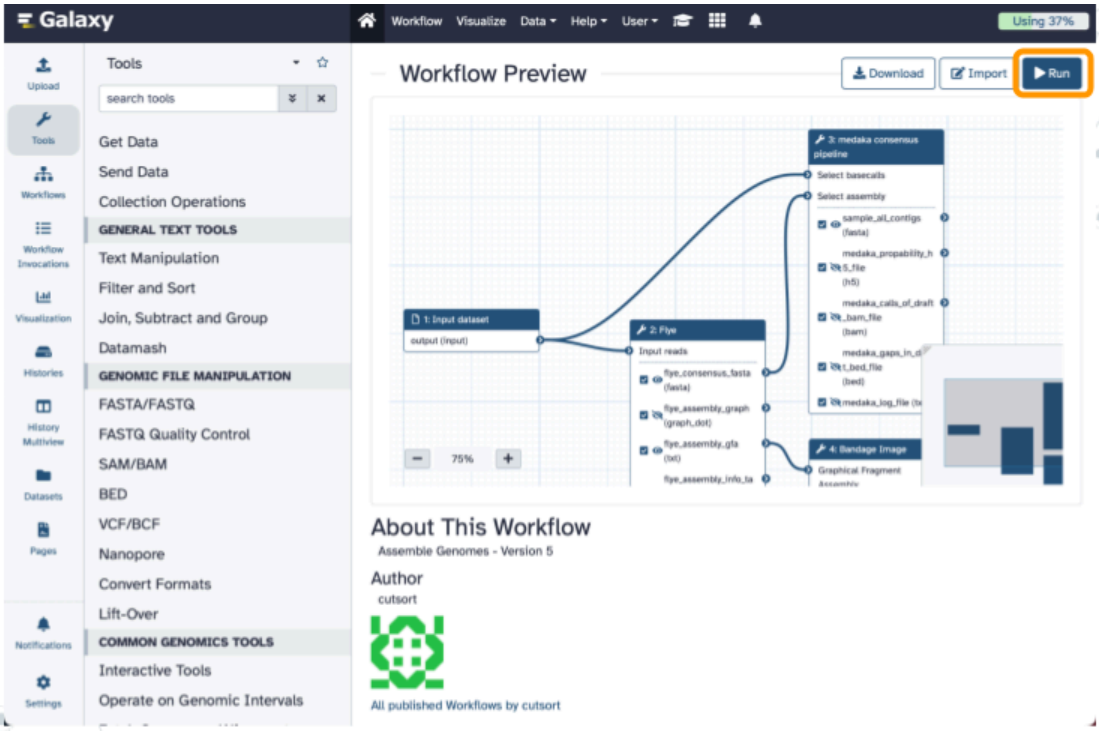
Activity 1 – Assemble Genomes

Estimated time: 45 min (~30 min computing)

Instructions

1. Run workflow

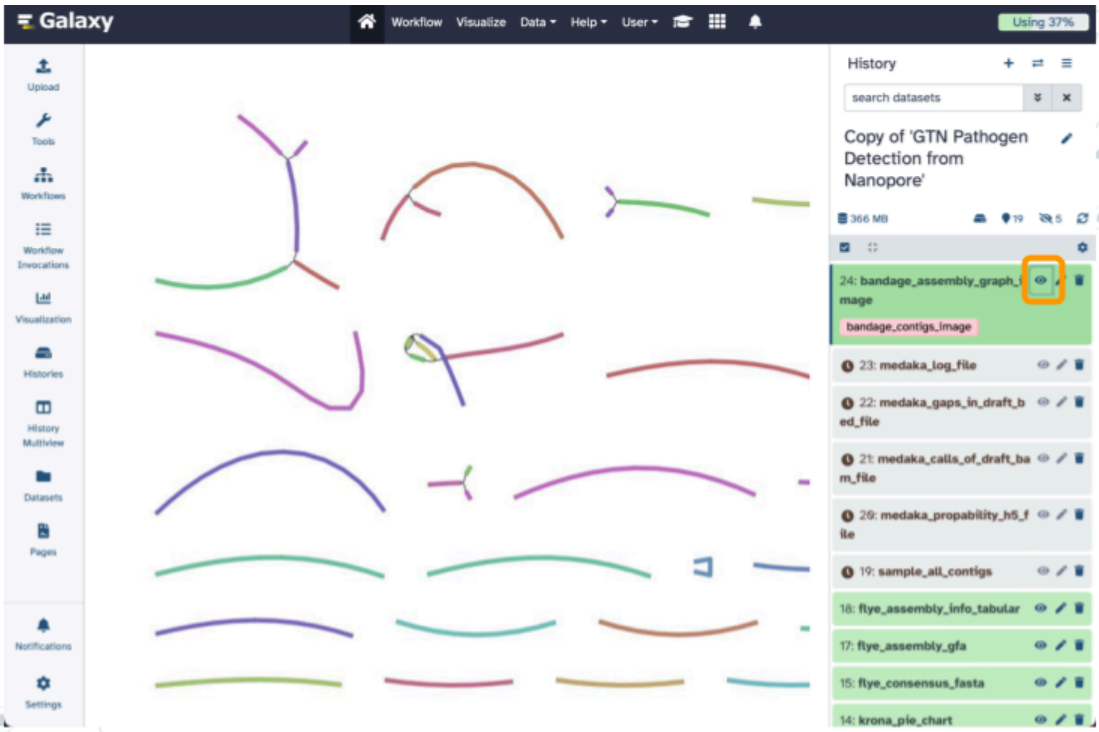
- Open the Assemble Genomes public workflow
- Click on `Run` and then `Run Workflow` on the `fastp on data 5: Read 1 output` dataset
- Wait ~30 minutes as the Flye, Bandage, and medaka jobs are scheduled, run, and complete



usegalaxy.org/u/cutsort/w/assemble-genomes

2. View results

- Click on the Display icon (eyeball) next to the dataset tagged `bandage_contigs_image`
- Examine how many contigs are large vs small, linear vs branched



Questions

You can refer to this completed history to answer these questions while you wait for your jobs to complete.

1A. How many contigs were assembled?

1B. Why did flye separate these in this way? How does flye decide to group them into this numbers of contigs?

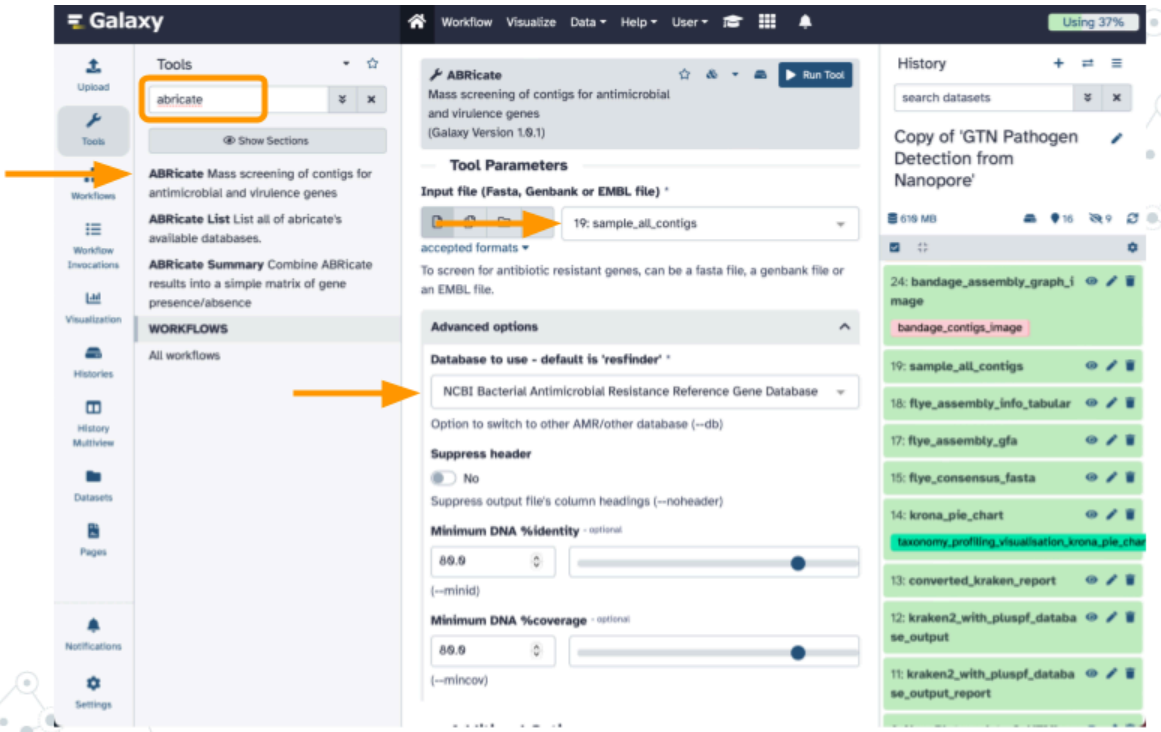
Activity 2 – Finding AMRs

Estimated time: 15 min

Instructions

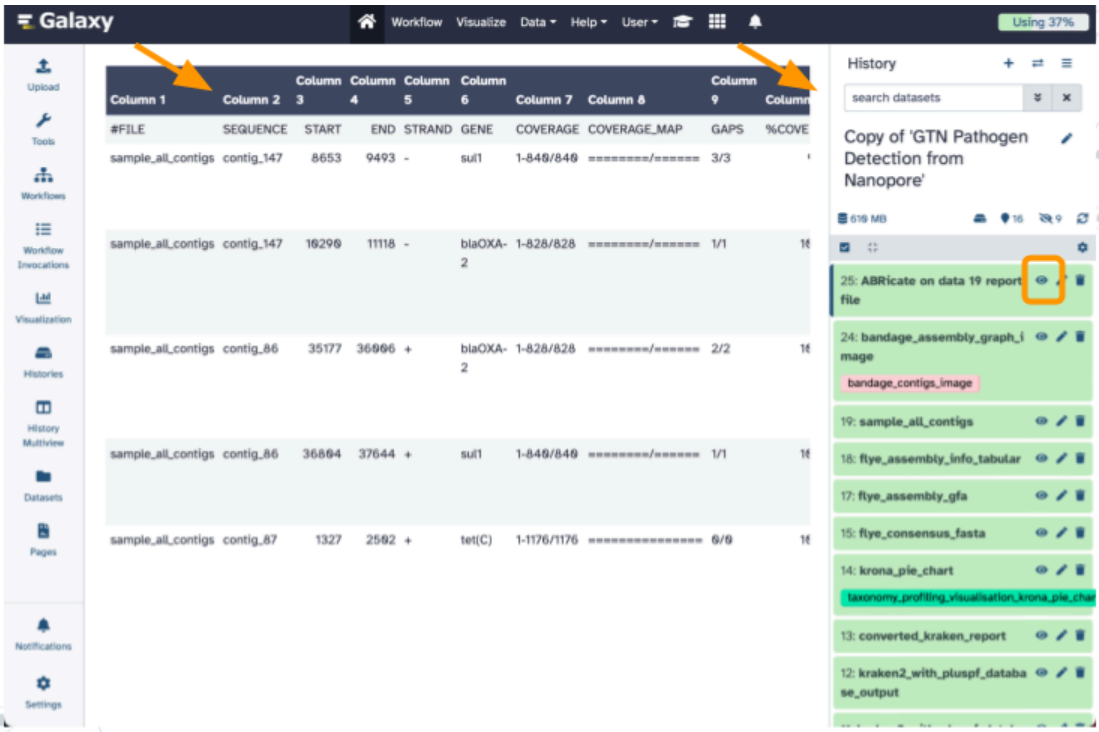
1. Run ABRicate

- Select “Tools” in the left menu, search for `abr`, and click on the `ABRicate` tool
- Configure with the following parameters before clicking “Run Tool”
    - Input file: `sample_all_contigs`
    - Advanced options > Database to use: `NCBI Bacterial Antimicrobial Resistance Reference Gene Database`



2. View results

- Click on the Display icon (eyeball) next to the `ABRicate report file` dataset
- Examine how many contigs contain an antimicrobial gene (Column 2) and how many categories of resistance genes are found (Column 15)



Questions

2A. How many antibiotic resistance genes were found in the sample?

2B. Which antibiotic genes were found on which contigs?

2C. What antibiotics are associated with the identified antibiotic genes? What is the target of the antibiotic(s) and mechanism of action?

Footnotes

Resources

- Google Doc

Contributions and Affiliations

- Jennifer Kerr, Notre Dame of Maryland University
- Rosa Alcazar, Clovis Community College
- Frederick Tan, Johns Hopkins University
- Based on “Pathogen detection from (direct Nanopore) sequencing data using Galaxy - Foodborne Edition” (GTN)

Last Revised: September 2024
