



## 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).



# Finding AMRs

Screen contigs for antimicrobial resistance genes



[\[slides\]](#) [\[video\]](#)

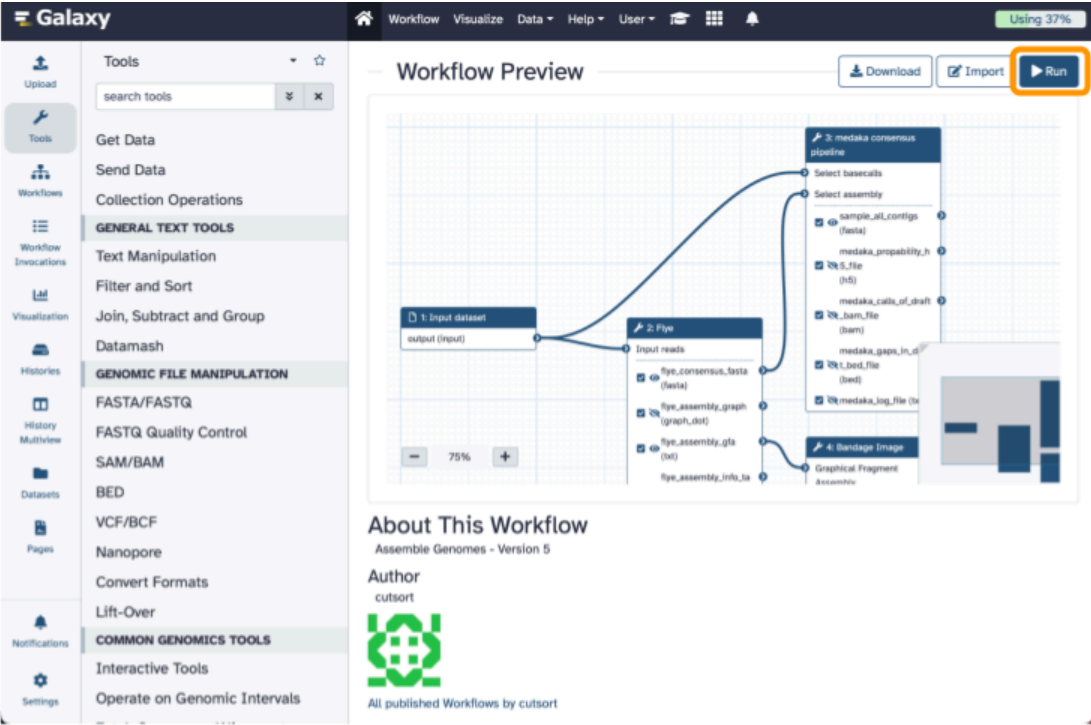
### Activity 1 – Assemble Genomes

*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



**Workflow Preview**

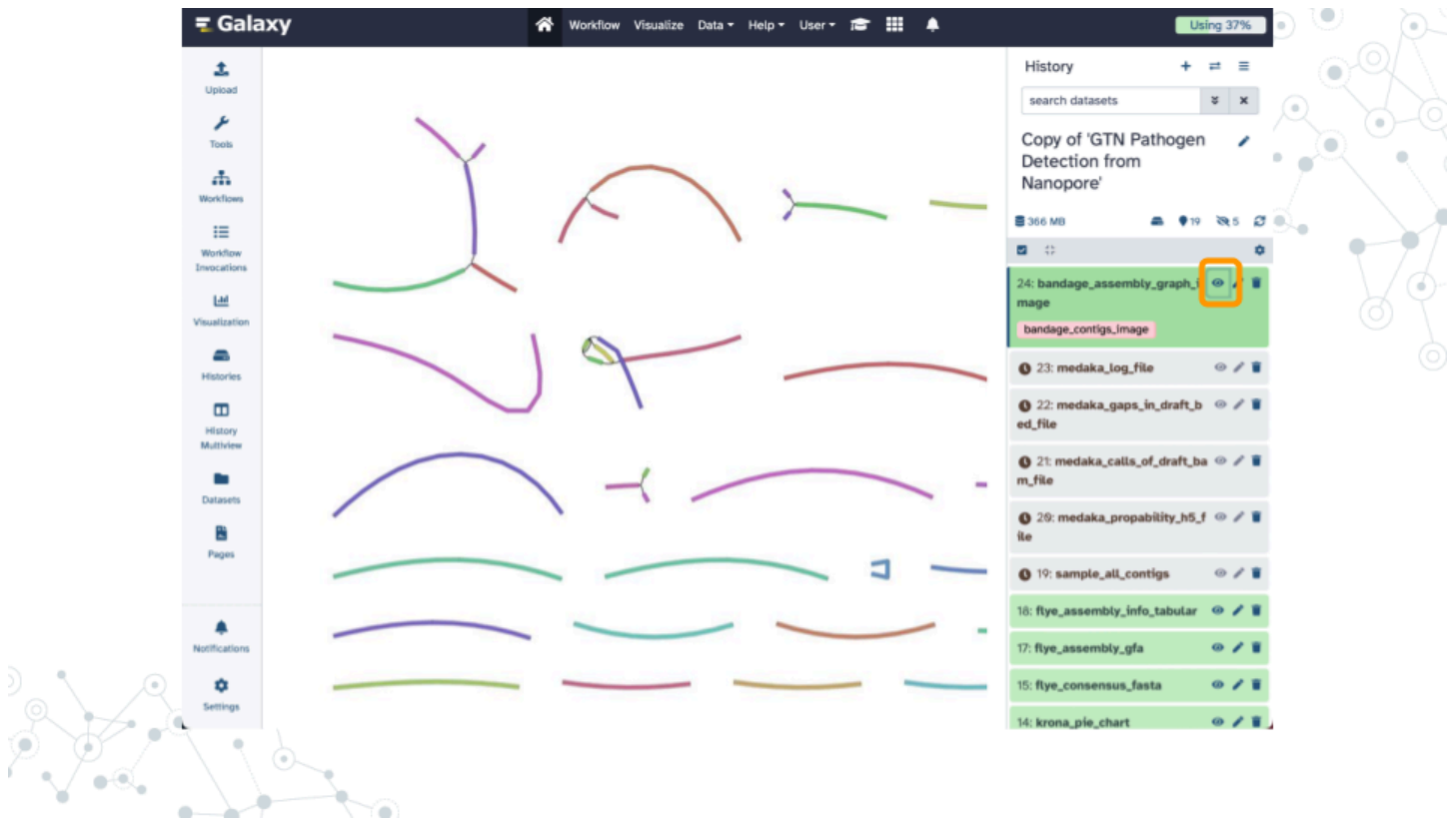
Download Import **Run**

**About This Workflow**  
Assemble Genomes - Version 5  
Author: cutsort  
All published Workflows by cutsort

[usegalaxy.org/u/cutsort/w/assemble-genomes](https://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?

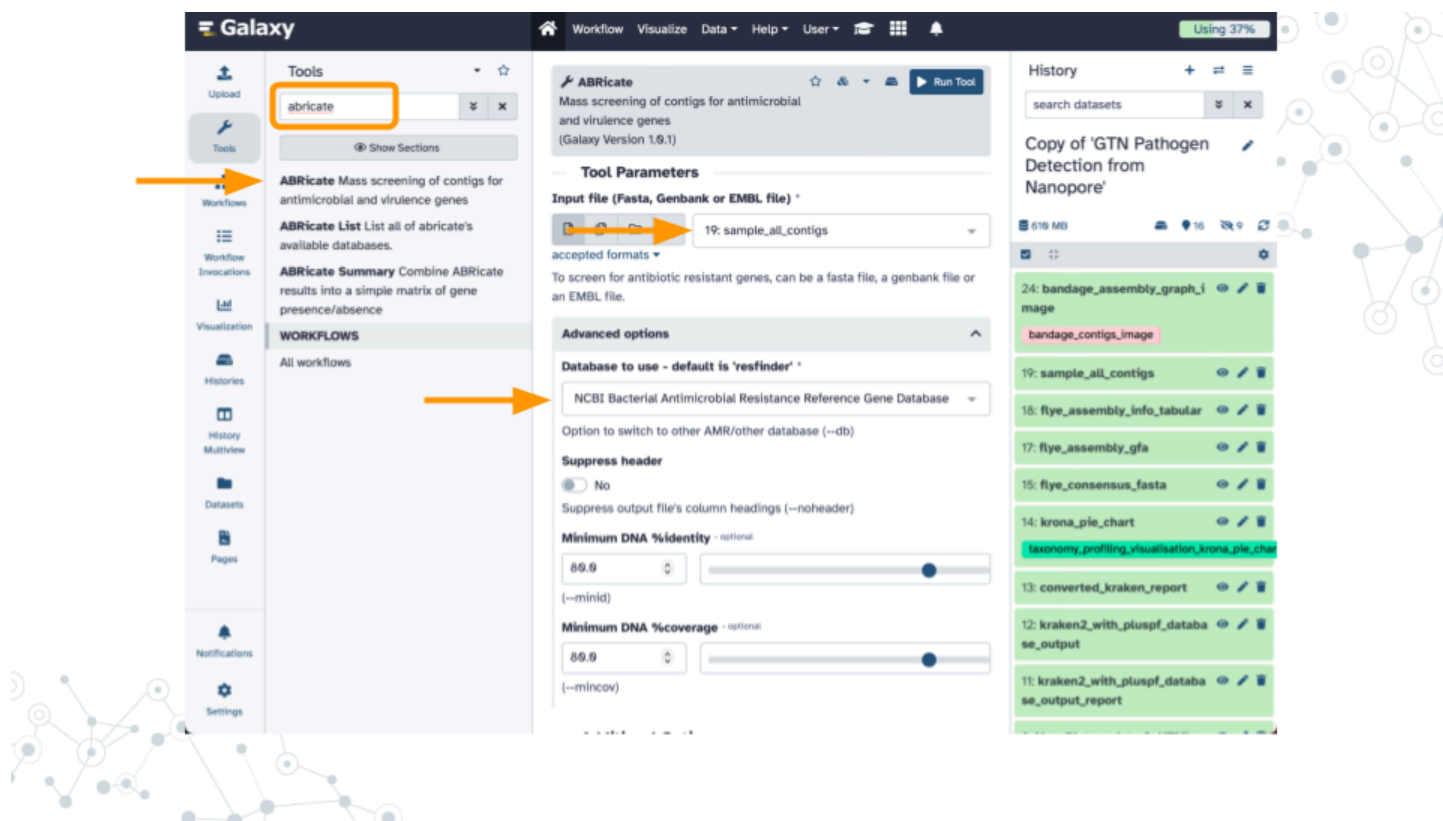
### Activity 2 – Finding AMRs

Estimated time: 15 min

### Instructions

#### 1. Run ABRicate

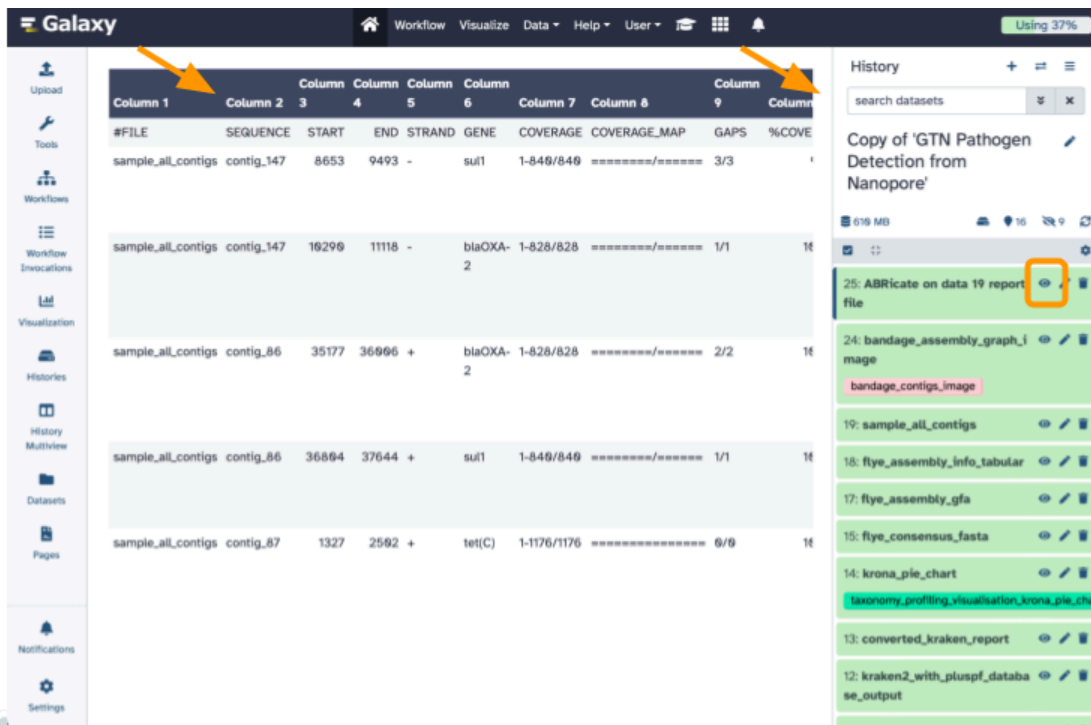
- Select “Tools” in the left menu, search for abr, and click on the ABRicate tool
- Configure with the following parameters before clicking “Run Tool”
  - Input file: sample\_all\_contigs
  - Advanced options > Database to use: NCBI Bacterial Antimicrobial Resistance Reference Gene Database



The screenshot displays the Galaxy web interface. On the left, the 'Tools' menu is open, and 'abricate' is selected. The main panel shows the ABRicate tool configuration. The 'Input file' is set to '19: sample\_all\_contigs'. Under 'Advanced options', the 'Database to use' is set to 'NCBI Bacterial Antimicrobial Resistance Reference Gene Database'. The 'Minimum DNA %identity' and 'Minimum DNA %coverage' are both set to 89.9. The right sidebar shows the 'History' panel with a list of datasets, including 'sample\_all\_contigs' and 'bandage\_contigs\_image'.

#### 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)



The screenshot shows the Galaxy web interface. The main panel displays a table of antibiotic resistance genes. The table has columns for #FILE, SEQUENCE, START, END, STRAND, GENE, COVERAGE, COVERAGE\_MAP, GAPS, and %COVE. The table contains several rows of data, including sample\_all\_contigs, contig\_147, contig\_86, and contig\_87. The right panel shows the workflow history, with a list of steps including 'Copy of GTN Pathogen Detection from Nanopore', 'ABRicate on data 19 report file', 'bandage\_assembly\_graph\_image', 'bandage\_contigs\_image', 'sample\_all\_contigs', 'flye\_assembly\_info\_tabular', 'flye\_assembly\_gfa', 'flye\_consensus\_fasta', 'krona\_pie\_chart', 'taxonomy\_profiling\_visualisation\_krona\_pie\_chart', 'converted\_kraken\_report', and 'kraken2\_with\_pluspf\_database\_output'.

Column 1	Column 2	Column 3	Column 4	Column 5	Column 6	Column 7	Column 8	Column 9	Column 10
#FILE	SEQUENCE	START	END	STRAND	GENE	COVERAGE	COVERAGE_MAP	GAPS	%COVE
sample_all_contigs	contig_147	8653	9493	-	su1	1-848/848	*****	3/3	
sample_all_contigs	contig_147	16296	11118	-	blaOXA-2	1-828/828	*****	1/1	
sample_all_contigs	contig_86	35177	36996	+	blaOXA-2	1-828/828	*****	2/2	
sample_all_contigs	contig_86	36864	37644	+	su1	1-848/848	*****	1/1	
sample_all_contigs	contig_87	1327	2562	+	tet(C)	1-1176/1176	*****	6/6	

### 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](#))

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