

# Using Bactopia for highly scalable, portable and customizable bacterial genome analyses

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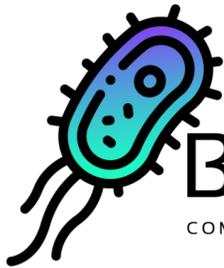
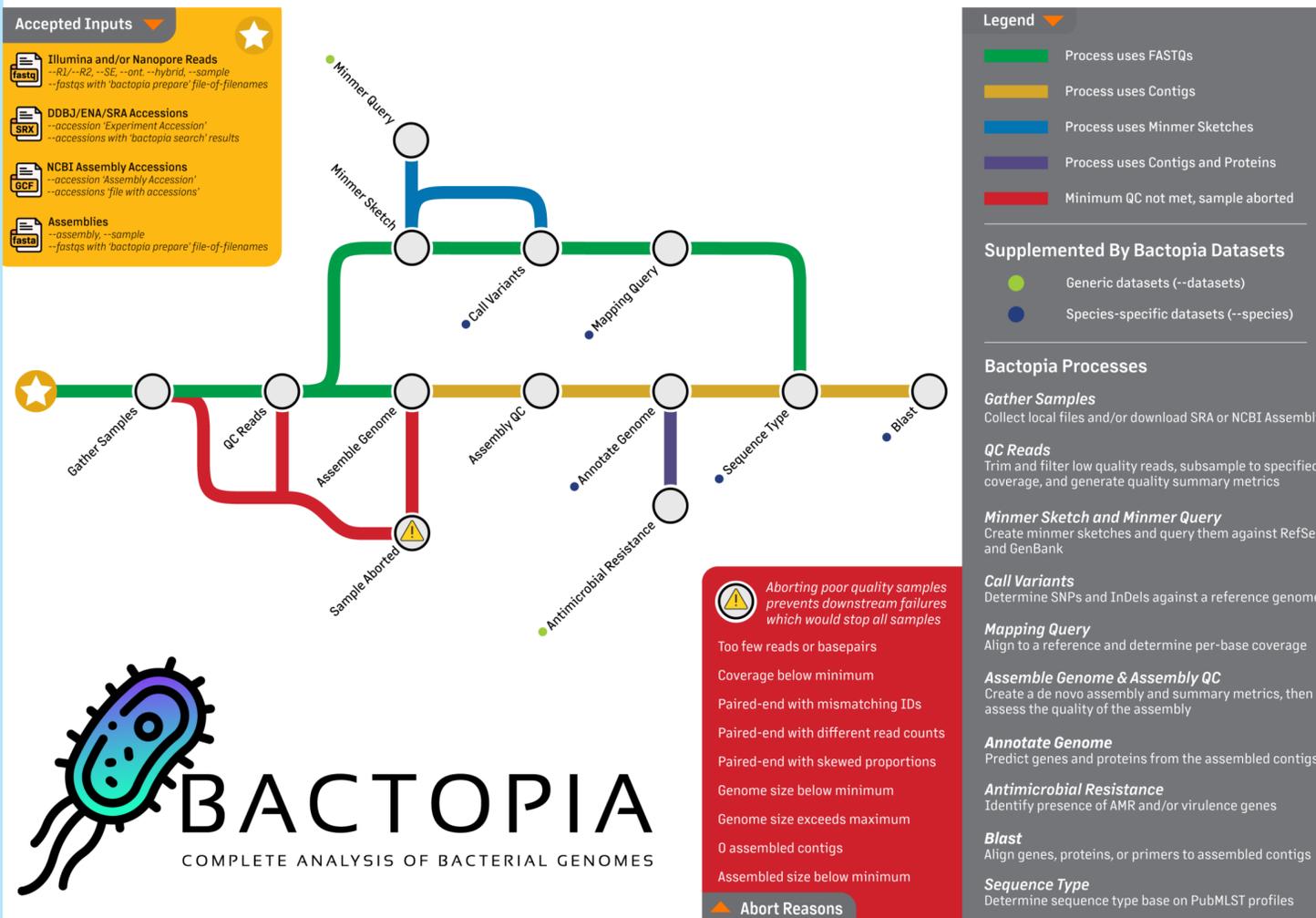
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Learn more about Bactopia!



# BACTOPIA

COMPLETE ANALYSIS OF BACTERIAL GENOMES

## Highlights

- Complete analysis of bacterial genomes
- Built with [Nextflow DSL2](#) following [nf-core practices](#)
- Supports Illumina and Oxford Nanopore reads
- Process genomes from NCBI's Sequence Read Archive and Assembly databases
- Includes more than [130 bioinformatics tools](#)
- [33 Bactopia Tools](#) allow for more science
- Easily supplement analyses with [public datasets](#)
- Extensive documentation of [tool outputs](#)
- [Highly customizable](#) to fit your specific needs
- Available on Bioconda, Docker, and Singularity

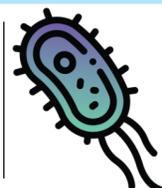
## Bactopia is platform Independent

By using Nextflow, Bactopia can run on multiple platforms, including:



# BACTOPIA TOOLS

More workflows for more science



## ANTIMICROBIAL RESISTANCE

- Abricate**  
Mass screening of contigs for antimicrobial and virulence genes
- AMRFinder+**  
Identify antimicrobial resistance in genes or proteins
- Resistance Gene Identifier**  
Predict antibiotic resistance from assemblies

## ANNOTATION

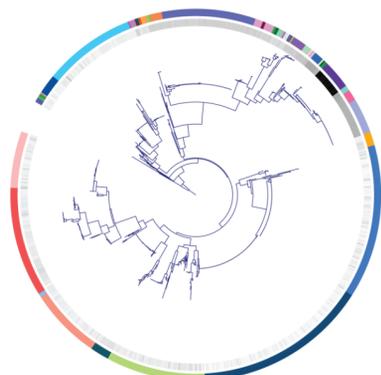
- Bakta**  
Rapid annotation of bacterial genomes and plasmids
- eggNOG-Mapper**  
Functional annotation of proteins using orthologous groups and phylogenies

## DISTANCE

- FastANI**  
Fast alignment-free computation of Average Nucleotide Identity (ANI)
- mash dist**  
Calculate Mash distances between sequences
- mashtree**  
Quickly create a tree using Mash distances

## SEQUENCE SURVEY

- CheckM**  
Assess the assembly quality of your samples
- mlst**  
Automatic MLST calling from assembled contigs



## PANGENOME

Create a pan-genome and core-genome phylogeny of your samples. Additionally, supplement your samples by including publicly available assemblies.

## TAXONOMIC CLASSIFICATION

- GTDB**  
Identify marker genes and assign taxonomic classifications
- Kraken2**  
Taxonomic classifications of sequence reads

## MOBILE GENETIC ELEMENTS

- ISMMapper**  
Identify insertion site positions in bacterial genomes
- MOB-suite**  
Reconstruct and annotate plasmids in bacterial assemblies

## MERLIN

Use Merlin to automatically run species-specific tools for the following organisms.

Escherichia	Mycobacterium
Haemophilus	Neisseria
Klebsiella	Salmonella
Legionella	Staphylococcus
Listeria	Streptococcus

## SPECIES SPECIFIC

- AgrVATE**  
Rapid identification of *Staphylococcus aureus* agr locus type
- ECTyper**  
In-silico prediction of *Escherichia coli* serotype
- emmtypier**  
emm-typing of *Streptococcus pyogenes* assemblies
- hicap**  
cap locus serotype and structure in *Haemophilus influenzae* assemblies
- HpsuisSero**  
Serotype prediction of *Haemophilus parasuis* assemblies
- Kleborate**  
Screen *Klebsiella* assemblies for MLST, sub-species, and genes of interest
- legsta**  
Typing of *Legionella pneumophila* assemblies
- LisSero**  
Serogroup typing prediction for *Listeria monocytogenes*
- meningotype**  
Serotyping of *Neisseria meningitidis* assemblies
- ngmaster**  
Multi-antigen sequence typing for *Neisseria gonorrhoeae*
- SeqSero2**  
Salmonella serotype prediction from reads or assemblies
- SISTR**  
Serovar prediction of *Salmonella* assemblies
- spaTyper**  
Computational method for finding spa types in *Staphylococcus aureus*
- SsuisSero**  
Serotype prediction of *Streptococcus suis* assemblies
- staphylococcus-secmec**  
Primer based SCCmec typing of *Staphylococcus aureus* genomes
- TBProfiler**  
Detect resistance and lineages of *Mycobacterium tuberculosis*

# Bactopia Step-By-Step

