# Bactopia v2: Highly scalable, portable and customizable bacterial genome analyses

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#### Legend

	Process uses FASTQs
	Process uses Contigs
	Process uses Minmer Sketches
_	Process uses Contigs and Proteins
	Minimum QC not met, sample aborted

#### Supplemented By Bactopia Datasets



Species-specific datasets (--species)

#### **Bactopia Processes**

Gather Samples Collect local files and/or download SRA or NCBI Assembly

**QC** Reads Trim and filter low quality reads, subsample to specified coverage, and generate quality summary metrics

Minmer Sketch and Minmer Query Create minmer sketches and query them against RefSeq and GenBank

**Call Variants** Determine SNPs and InDels against a reference genome

**Ariba Analysis** Query FASTQs against Ariba datasets

**Mapping Query** Align to a reference and determine per-base coverage

Assemble Genome & Assembly QC Create a de novo assembly and summary metrics, then assess the quality of the assembly

Annotate Genome Predict genes and proteins from the assembled contigs Antimicrobial Resistance

Identify presence of AMR and/or virulence genes Blast

Align genes, proteins, or primers to assembled contigs

Sequence Type Determine sequence type base on PubMLST profiles

# Highlights

- Written in Nextflow DSL2, greatly increases Bactopia's ability to fit your needs
- Supports Illumina, Oxford Nanopore technologies as well as NCBI's Sequence Read Archive and Assembly databases
- Includes more than <u>130 bioinformatics tools</u> into a single pipeline
- <u>33 Bactopia Tools</u> allow easy comparative analyses of Bactopia outputs
- Available on Bioconda, Docker, and Singularity

## Bactopia v2, written in Nextflow DSL2, supports Nanopore reads and includes more than 130 Bioinformatic tools!



## More Bactopia Tools!

Bactopia Tools are a set of additional Nextflow workflows you can conveniently run on your Bactopia outputs. Currently there are <u>33</u> Bactopia Tools for analyses like pan-genome construction and serotyping. A framework was created to make the addition of new Bactopia Tools easier than ever.



## **Custom Workflows**

With DSL2, custom workflows can now be easily created and shared with others.To demonstrate this, we have implemented <u>Staphopia</u>, as a named Bactopia workflow. Staphopia is the combination of the Bactopia and staphtyper, a Bactopia Tool for analysis of *Staphylococcus* aureus genomes.

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### **Test Everything**

Bactopia v2 features per-module tests using real bacterial sequences as inputs available from <u>bactopia-tests</u>. Currently 100+ tests have been created to verify that more than 10,000 output files. We have integrated these tests into <u>GitHub Actions</u> to ensure the stability of Bactopia over time.



### **Curated Datasets**

Bactopia includes automated methods to create species-specific datasets, but these methods remain fairly broad. In order to address this we have created the bactopia datasets organization, for community members to curate species- specific datasets, such as *Staphylococcus aureus*. Users can then integrate these curated datasets in their own analyses.



### Merlin has arrived!

"MinmER assisted species-specific bactopia tool seLectIoN", or *Merlin*, uses distances based on the RefSeq sketch downloaded by "bactopia datasets" to automatically run tools for members of *Escherichia*, *Haemophilus*, Klebsiella, Legionella, Listeria, Mycobacterium, Neisseria, Salmonella, Staphylococcus, and Streptococcus.

You can use Merlin in Bactopia with the "--ask\_merlin" parameter, or alternatively you can run Merlin as a Bactopia Tool!

## nf-core/ 👚 influences

<u>nf-core</u> is a community effort to curate analysis pipelines built using Nextflow. This effort has created a powerful design framework for developing Nextflow pipelines. Bactopia v2 has followed their lead by implementing modules from <u>nf-core/modules</u> for Bactopia Tools, per-module tests (<u>nf-core/modules</u>), and an argument parser (<u>nf-core/tools</u>).