# Expanding Bactopia as a framework for bacterial, fungal, and metagenomic analysis

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Legend 🗸	
	Process uses FASTQs
	Process uses Contigs
	Process uses Contigs and Proteins
	Minimum QC not met, sample aborted

# **Bactopia Processes**

#### Gather

Collect local files and/or download sequences from SRA/ENA/DDBJ or NCBI Assembly accessions

QC

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

Assembler

Create a de novo assembly (standard, hydbrid, or short read polished) and summary metrics

Sketcher Create minmer sketches and query them against GTDB and RefSeq

Annotator Predict genes and proteins from the assembled contigs

Antimicrobial Resistance Identify presence of AMR and/or virulence genes

Sequence Type Determine sequence type base on PubMLST profiles

# Bactopia Tools

60+ additional workflows for seamless downstream analyses such as pan-genome contruction, serotyping, AMR, and phylogenies

# **Shape Your Science**

Each process in Bactopia functions as an independent module, enabling straightforward reshaping to develop custom workflows tailored to your specific needs







fastq

fasta

clean-yer-reads is a simple reshaping of Bactopia that enables you to QC sequences across any organism, including metagenomic samples.

With clean-yer-reads you still have full access to all available Bactopia Tools.









Illumina and/or Nanopore Reads

Assemblies --assembly, --sample



# clean-yer-reads



# teton

teton reshapes Bactopia with a focus on human read scrubbing and taxonomic classification, by utilizing the existing Scrubber and the Bracken modules.

teton makes for a useful first step for all sequence analysis.









# mycotopia

mycotopia represents a specialized adaptation of Bactopia, specifically for the analysis of non-bacterial samples. It has been reshaped for haploid fungal organisms, including the notable fungal pathogen Candida auris. It serves as a prime example of Bactopia's flexibility in meetings its users' needs



# PUBLIC HEALTH

# **Bactopia Highlights**

## **Broad Sequencing Support**

Compatible with both Illumina and Nanopore sequencing technologies

## **Modular Pipeline**

A comprehensive, end-to-end modular pipeline for flexible genomic analysis

# **Extensive Toolset**

Incorporates over 150 bioinformatic tools for diverse research needs

# **Reliable Updates**

Actively supported and consistently maintained for over 5 years

# Widespread Adoption

Achieved over 1,000,000 downloads, reflecting global trust and utility

## **Community-Driven**

Contributed over 180 enhancements back to the open-source community

# **AllTheBacteria Support**

Supports further analysis of the 2,000,000 assemblies from the AllTheBacteria project



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