Designing mechanisms into Bactopia to support its users and contribute back to the community

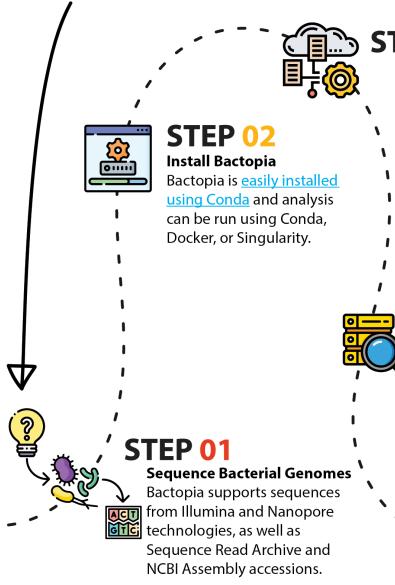
Nextflow Summit 2022 Robert A. Petit III, PhD. Wyoming Public Health Laboratory





What is Bactopia?

Bactopia is an extensive Nextflow pipeline for the complete analysis of bacterial genomes. To learn more, follow the step-by-step guide below.



STEP 03

Search Public Databases

'bactopia search' can supplement your analysis with publicly available genome sequences.

STEP 04

Build Datasets

'bactopia datasets'

downloads publicly

available datasets to

further supplement

your analysis.

STEP 06

Analysis with Bactopia

Bactopia processes
genomes with more than
150 bioinformatic tools
and is easily adapted to
fit your needs.

STEP 05

Create a Sample Sheet

<u>'bactopia prepare'</u> is used to create a sample sheet allowing you to efficiently process a single sample or thousands.

STEP 08 Investigate Results Once completed,

numerous output files are available for your genomic investigations.

STEP 07

Further Analysis with Bactopia Tools

After Bactopia is finished, more than 30 additional workflows, called Bactopia Tools, are available to take your analysis even further.

How can I minimize maintenance burdens for Bactopia, but also contribute back to the community?



I set some ground rules for design



Tools must be free and open-source



Tools must be available from Bioconda or Conda-Forge



Bactopia Tools must be available from nf-core/modules

What are the outcomes of these rules?



Bactopia Tools must be available from nf-core/modules

From nf-core Bactopia has implemented:

- CI modeled after nf-core/modules
- Dynamic configs/schema via nf-core lib
- Many more features...

In return contributions to nf-core/modules

- 45 new modules
- 19 updates to existing modules



Tools must be available from Bioconda or Conda-Forge

- Contributed 25 recipes, 65 updated recipes, and 1,750+ PR reviews
- Addition to the Bioconda core-team



Tools must be free and open-source

- Many tools originally written for Bactopia made available as stand-alone
- PRs submitted with fixes from User/CI identified bugs
 - Ariba, Bowtie2, Kleborate, Seroba, Shovill, Shigatyper





Final Remarks

- Becoming more important for pipeline developers to work closely with tool developers
- Join inclusive bioinformatic communities, ask questions, make contributions
- Starting a new Nextflow pipeline? Start with nf-core
 - Check out #new-pipelines, you're probably not alone!
 - Don't have to be "nf-core" to use nf-core practices

Acknowledgements

The developers of open-source tools that make their tools freely available to the community —



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- Ashley Norberg





• Tim Read, PhD





Questions? (with some scenes from Wyoming, USA)

