



BACTOPIA

COMPLETE ANALYSIS OF BACTERIAL GENOMES

Enhancing and Expanding the Bactopia Framework

Robert A. Petit III, PhD

Wyoming Public Health Laboratory

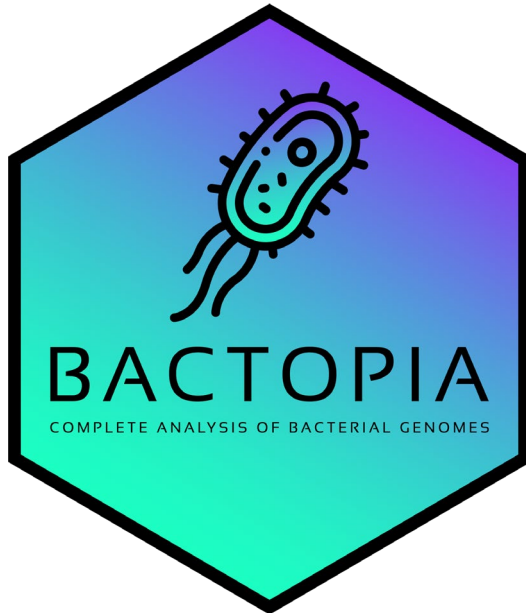
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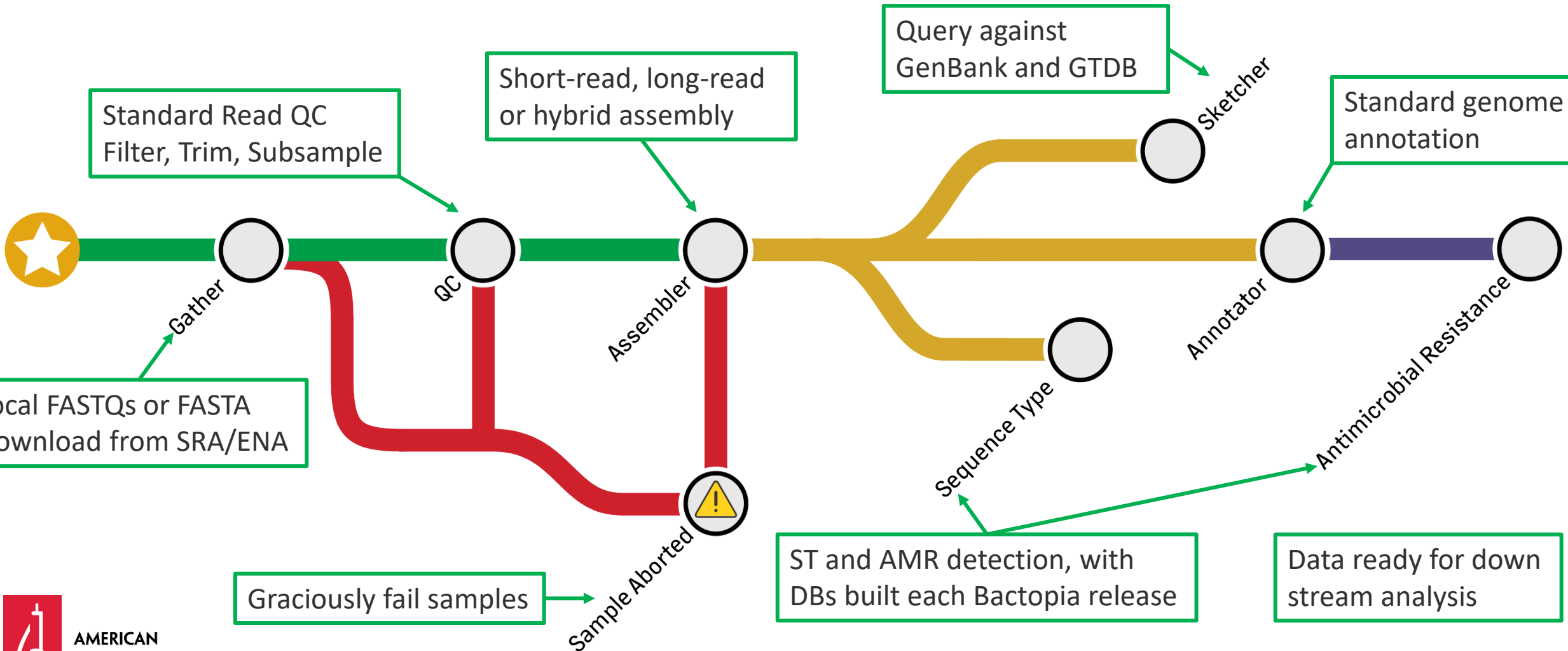


Bactopia - A pipeline for bacterial genomics



- End-to-end pipeline for bacterial genome analysis
 - Written in Nextflow, following nf-core standards
 - Available from Conda, Docker, or Singularity
 - Supports numerous compute infrastructures
- Active user-base providing regular feedback
 - Global users from academia, government, commercial
- Consistently maintained for 5+ years

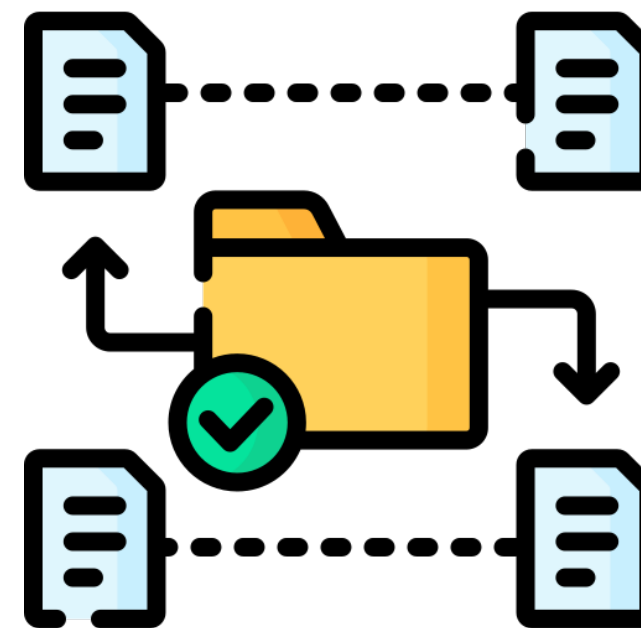
Bactopia – Shaping Data for Next-Step Analyses



Bactopia organizes your project for you

The "sample" is the organizational unit

- Tool specific directories
 - Outputs, logs and version info
- Timestamped run specific directories
 - Resource usage and automatic merging of delimited outputs
- Programmatic access to all outputs for automatic import into Bactopia Tools



Bactopia Tools – Simplifying comparative genomics

- 65+ workflows for more science
 - Uses standardized output structure
 - Single parameter change (`--wf`)

Example Bactopia Tool Usage

```
# Process Staphylococcus aureus samples  
bactopia --samples saureus.txt
```

- Categories
 - Organism-specific
 - Mobile elements
 - Antimicrobial resistance & virulence
 - Pan-genome
 - SNP/InDel
 - Taxon Classification
 - Phylogeny

```
# Run Bactopia Tools
```

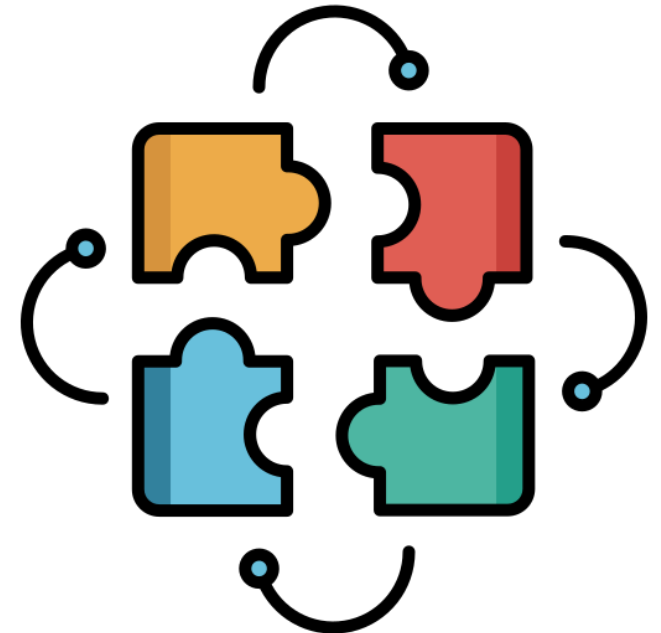
```
# Staph-specific tools (agr, sccmec, spa)  
bactopia --wf staphtyper
```

```
# Call SNPs, build core-snp tree  
bactopia --wf snippy --accession GCF_000009645
```



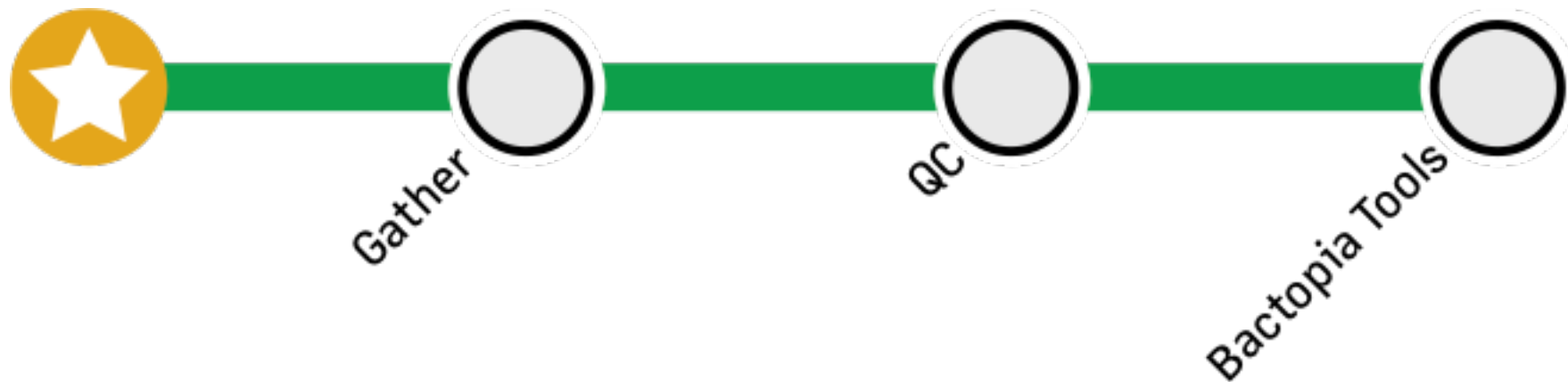
Think about Bactopia as a framework of interchangeable modules

- Every step in Bactopia is an *independent* plug and play module
 - Defined input, outputs, and parameters
 - Compatible modules are easily linked
- Allows for easy reshaping of Bactopia to meet user needs
 - *I just want to call SNPs, not all the other stuff*
 - *I just want to see what's in my metagenomic sample*
 - *I just want the species and genome size automatically determined*



clean-yr-reads - Reshaping for QCing reads

Reshaping of Bactopia that enables you to QC sequences across any organism, including metagenomic samples, while maintaining access to Bactopia Tools



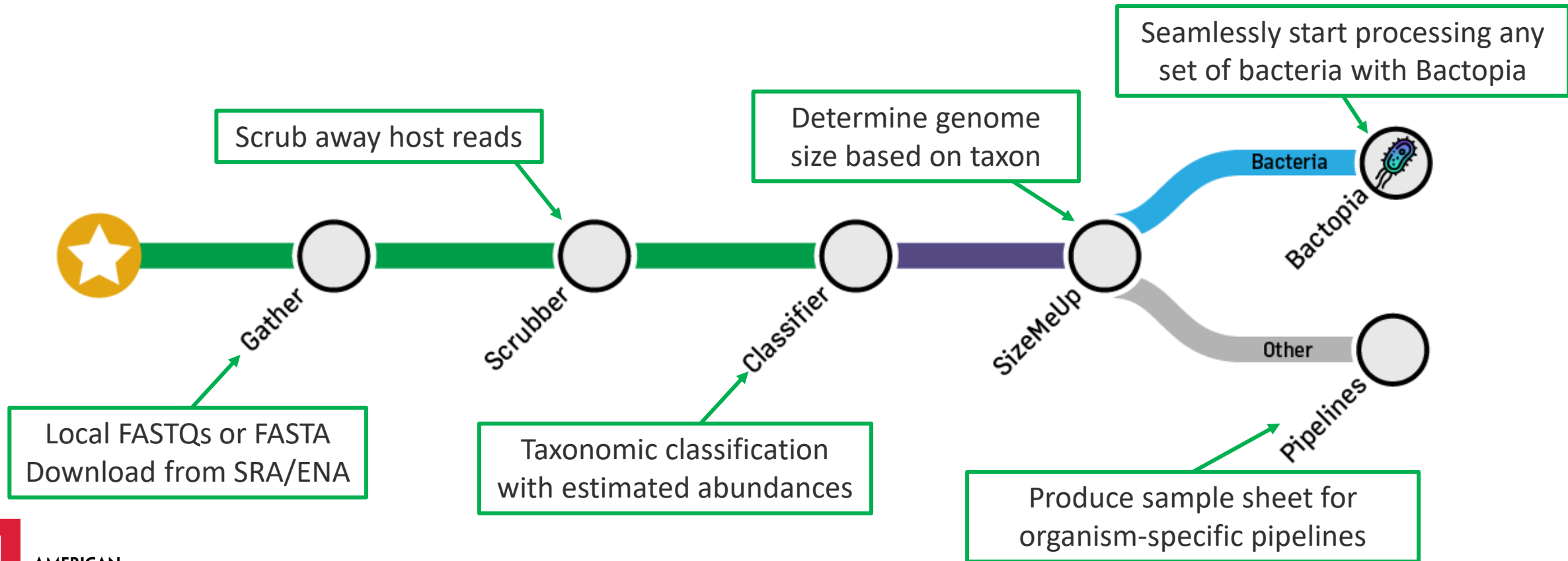
I just want to call SNPs, not all the other stuff (CYR -> Snippy)

I just want to see what's in my metagenomic sample (CYR -> Bracken)



teton – Reshaping for all types of sample

Named after the Grand Teton Range in Wyoming



Bactopia supports AllTheBacteria (ATB)

- 2,500,000 bacterial assemblies
 - allthebacteria.readthedocs.io
- **bactopia atb-downloader**
 - *Download ATB assemblies by BioSample, TaxID, or Species*
- **bactopia atb-formatter**
 - *Arrange ATB assemblies for Bactopia Tool usage*

Example ATB Usage

```
# Download Staphylococcus aureus samples  
bactopia atb-downloader --query 1280
```

```
# Format for Bactopia Tool usage  
bactopia atb-formatter --path atb-assemblies
```

```
# Staph tools, plasmid, and core-genome tree  
bactopia --wf sccmec  
bactopia --wf mobsuite  
bactopia --wf pangenome
```



Bactopia is more than wrapper, it's a contributor

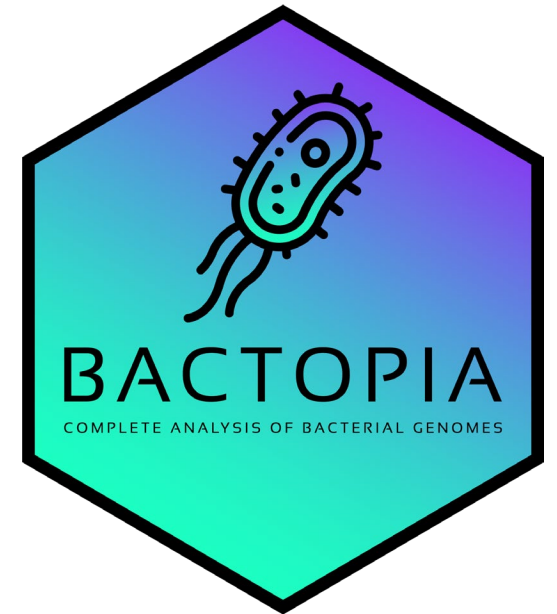
- Hundreds of contributions back to the bioinformatics community
 - New or fixed Bioconda recipes (*and lots of PR reviews*)
 - New modules for nf-core/modules
 - Bug fixes and features to upstream tools
- Tools originally developed for Bactopia made standalone
 - camlhmp - Classification through yAML Heuristic Mapping Protocol
 - sccmec - A tool for typing SCCmec cassettes in assemblies
 - dragonflye - Assemble bacterial genomes from Nanopore reads
 - fastq-dl - Download FASTQ files from SRA or ENA repositories
 - Many more!



Poster PIP-TUES-145

Wrap Up and What's Next

- Bactopia has evolved from an end-to-end pipeline into a highly flexible framework for bacterial genome analysis
- What's Next?
 - More Bactopia Tools and these “reshapings” of Bactopia
 - Visualizations and standardized reports!
 - E.g. How to use Bactopia with MicrobeTrace & Microreact
 - Tutorials, use-cases to help improve docs for non-binfiles



Acknowledgements

The many developers of open-source software and the users of Bactopia that are regularly providing feedback.



Chayse Rowley & Taylor Fearing

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EMERGENT Group

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Shannon Petit



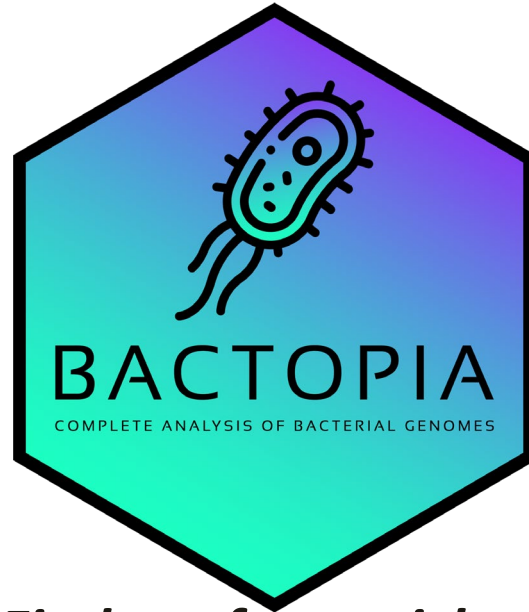
Find me for a sticker!



Thank You and Questions?

Contact Information

- Robert Petit
- robert.petit@wyo.gov
- GitHub: @rpetit3
- Twitter: @rpetit3



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