

Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes

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Centre for Pathogen Genomics Bioinformatics Seminar
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Yo! 🖐️

I AM ROBERT

WPHL's bioinformatician and developer of Bactopia

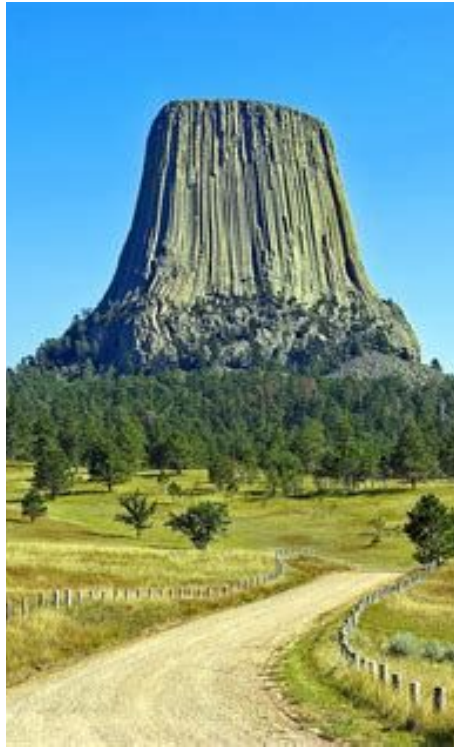


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What's Wyoming like?

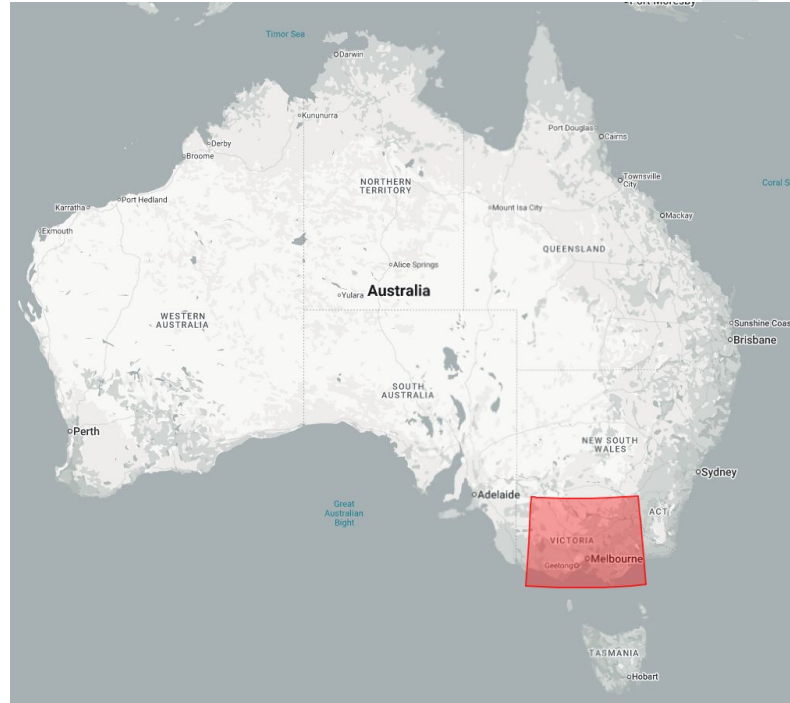


Wyoming is home to a rural PHL

Wyoming, USA

Area: 253,335 km²

Population: 581,381



Melbourne, Australia

Area: 9,993 km²

Population: 5,435,590

Wyoming Public Health Laboratory

- 15-25 people at WPHL
- Genomic and wastewater surveillance
- Domestic and international trainings
- Strong relationship with Vet Lab and Ag Lab

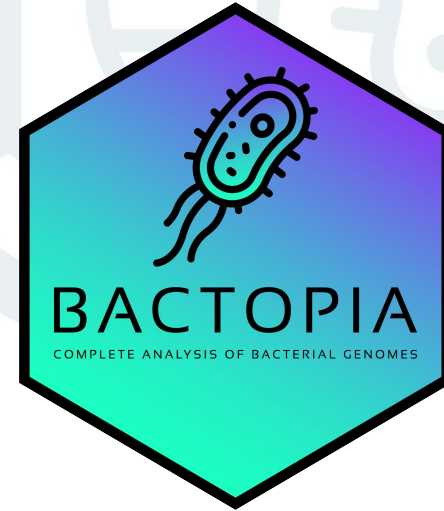


What is “Bactopia”?



Bactopia streamlines bioinformatics analysis

- ***End-to-end pipeline for bacterial genome analysis***
 - Written in Nextflow, following latest standards
 - Available from Conda, Docker, or Singularity
 - Supports numerous compute infrastructures
- ***Wraps 150+ bioinformatic tools into stand-alone modules***
- ***Active user-base providing regular feedback***
 - Includes folks at WPHL, as well as global users from academia, government, and commercial
- ***Consistently maintained for 7+ years***



bactopia.io

Bactopia includes routine yet essential steps in bacterial genome analysis.



Gather

QC

Assembler

Annotator

Sketcher

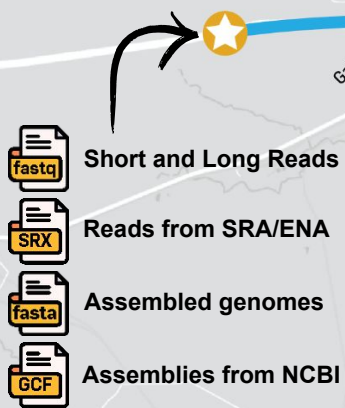
AMR

MLST



BACTOPIA
COMPLETE ANALYSIS OF BACTERIAL GENOMES

From the start, Bactopia is flexible, supporting short reads, long reads, and assembled genomes.



BACTOPIA
COMPLETE ANALYSIS OF BACTERIAL GENOMES

Sequences are automatically assessed and cleaned to ensure reliable downstream results.



BACTOPIA
COMPLETE ANALYSIS OF BACTERIAL GENOMES

Bactopia adapts to your data, by utilizing multiple assembly strategies out of the box.



Short-read, long-read, hybrid, and short-read polished assemblies are supported



BACTOPIA
COMPLETE ANALYSIS OF BACTERIAL GENOMES

Bactopia's final steps deliver annotations, AMR predictions, MLST typing, and genome sketches



BACTOPIA
COMPLETE ANALYSIS OF BACTERIAL GENOMES

Bactopia's core steps structure your data for smooth integration into downstream workflows.



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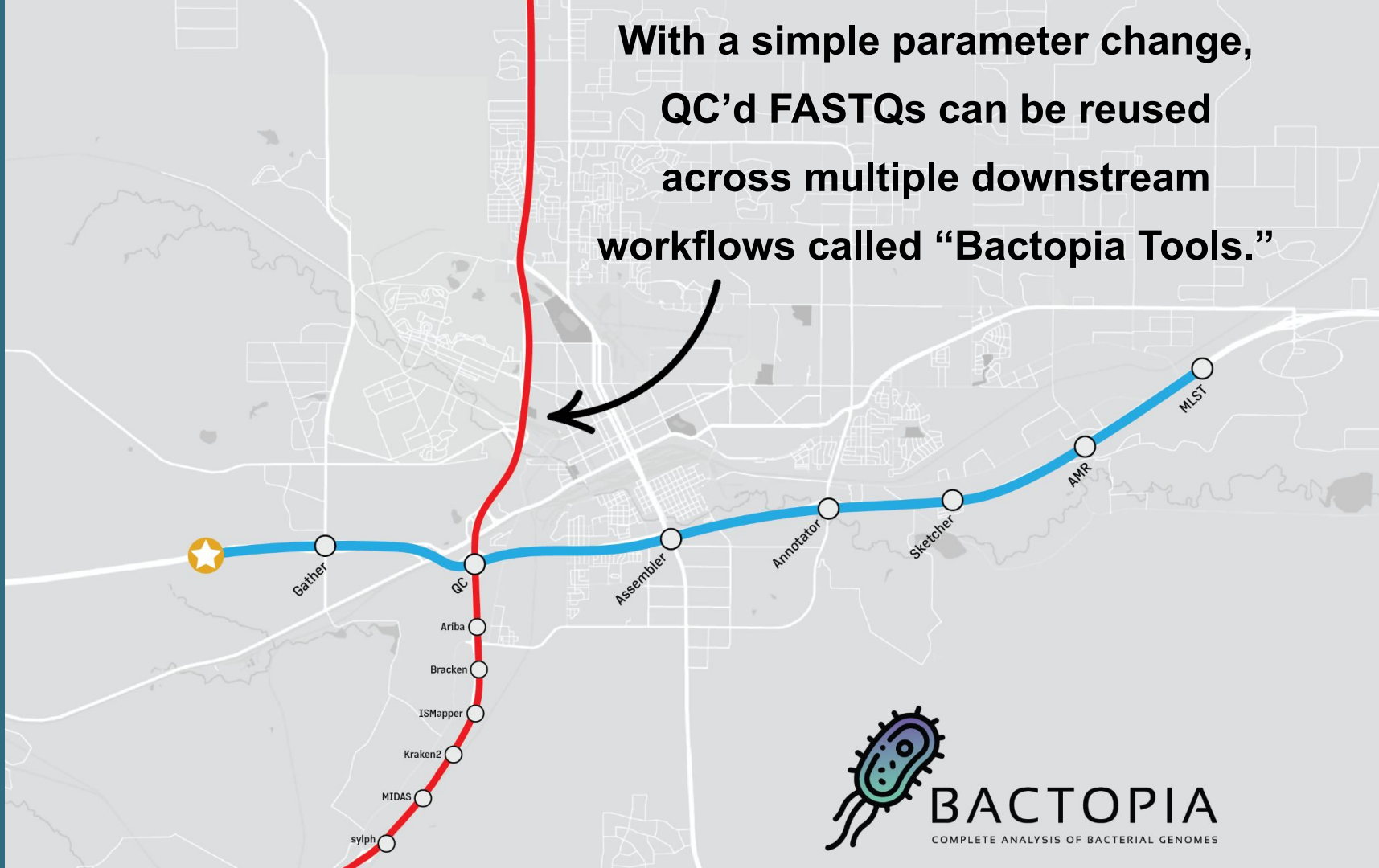
AMR

MLST



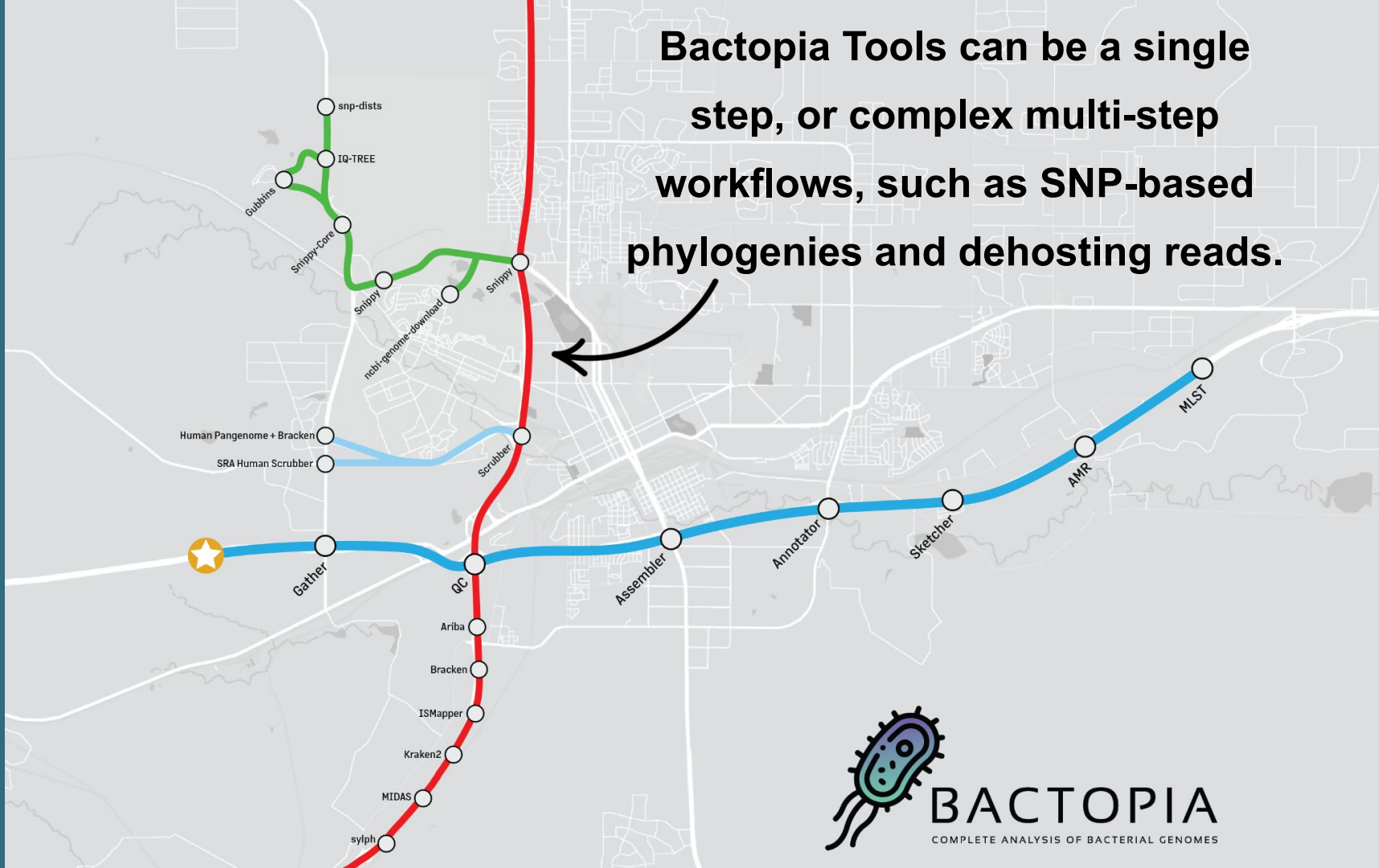
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COMPLETE ANALYSIS OF BACTERIAL GENOMES

With a simple parameter change,
QC'd FASTQs can be reused
across multiple downstream
workflows called "Bactopia Tools."



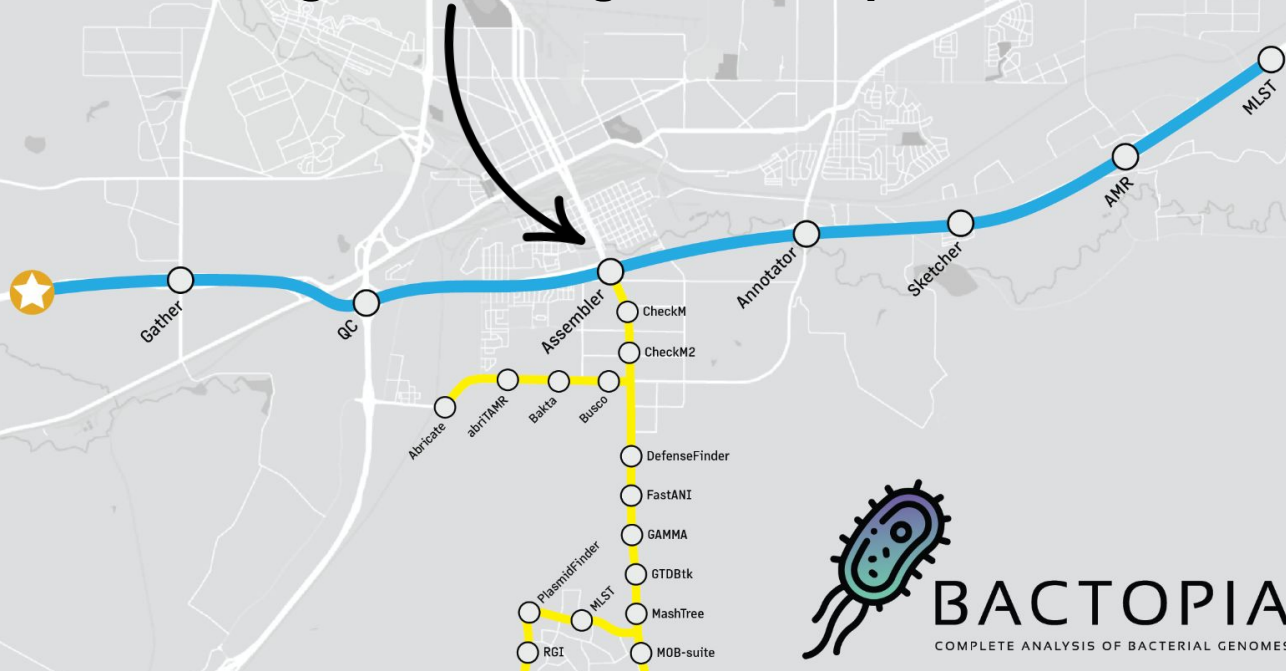
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Bactopia Tools can be a single step, or complex multi-step workflows, such as SNP-based phylogenies and dehosting reads.



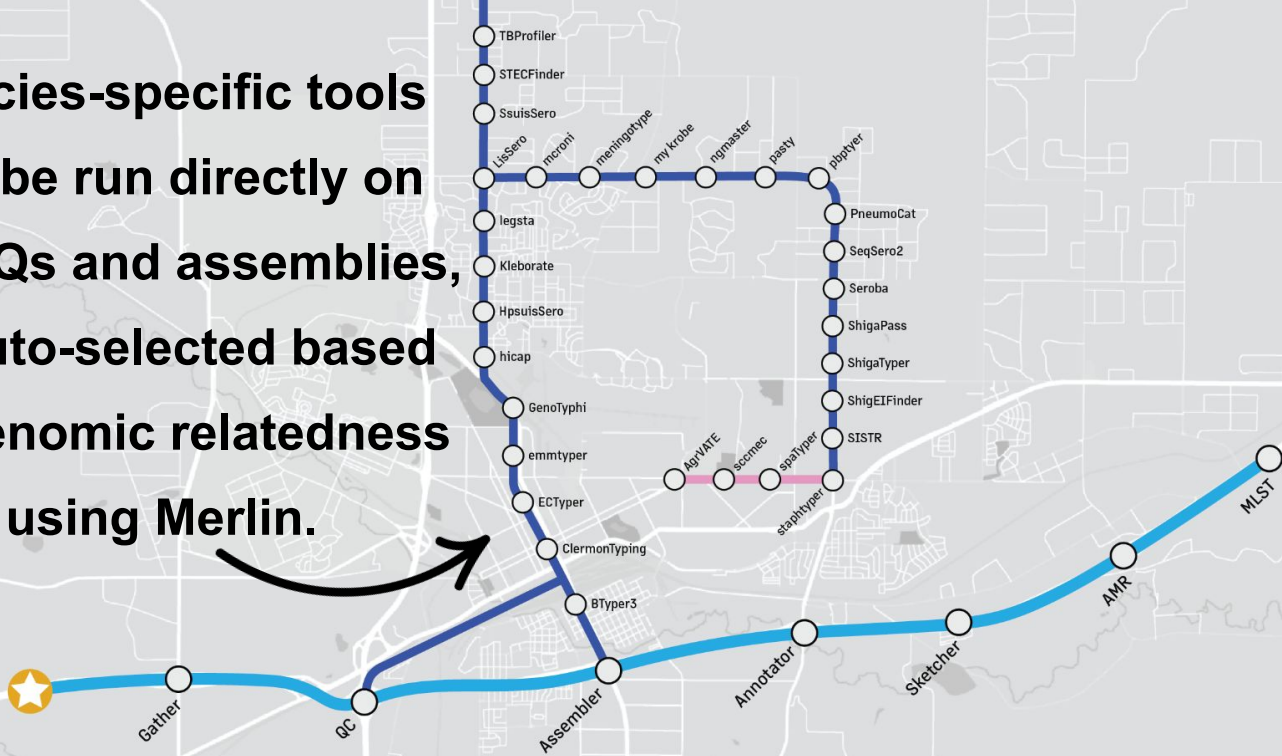
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COMPLETE ANALYSIS OF BACTERIAL GENOMES

As with QC'd FASTQs, assembled genomes can be processed using a wide range of Bactopia Tools.



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COMPLETE ANALYSIS OF BACTERIAL GENOMES

**Species-specific tools
can be run directly on
FASTQs and assemblies,
or auto-selected based
on genomic relatedness
using Merlin.**



BACTOPIA
COMPLETE ANALYSIS OF BACTERIAL GENOMES

After annotation, there are more Bactopia Tools available for you to make use of.



Gather

QC

Assembler

Annotator

BLAST+

Sketcher

AMR

MLST

PhisSP

EggNOG-Mapper

AMRFinder+

blastn

blastp

blastx

tblastn

tblastx



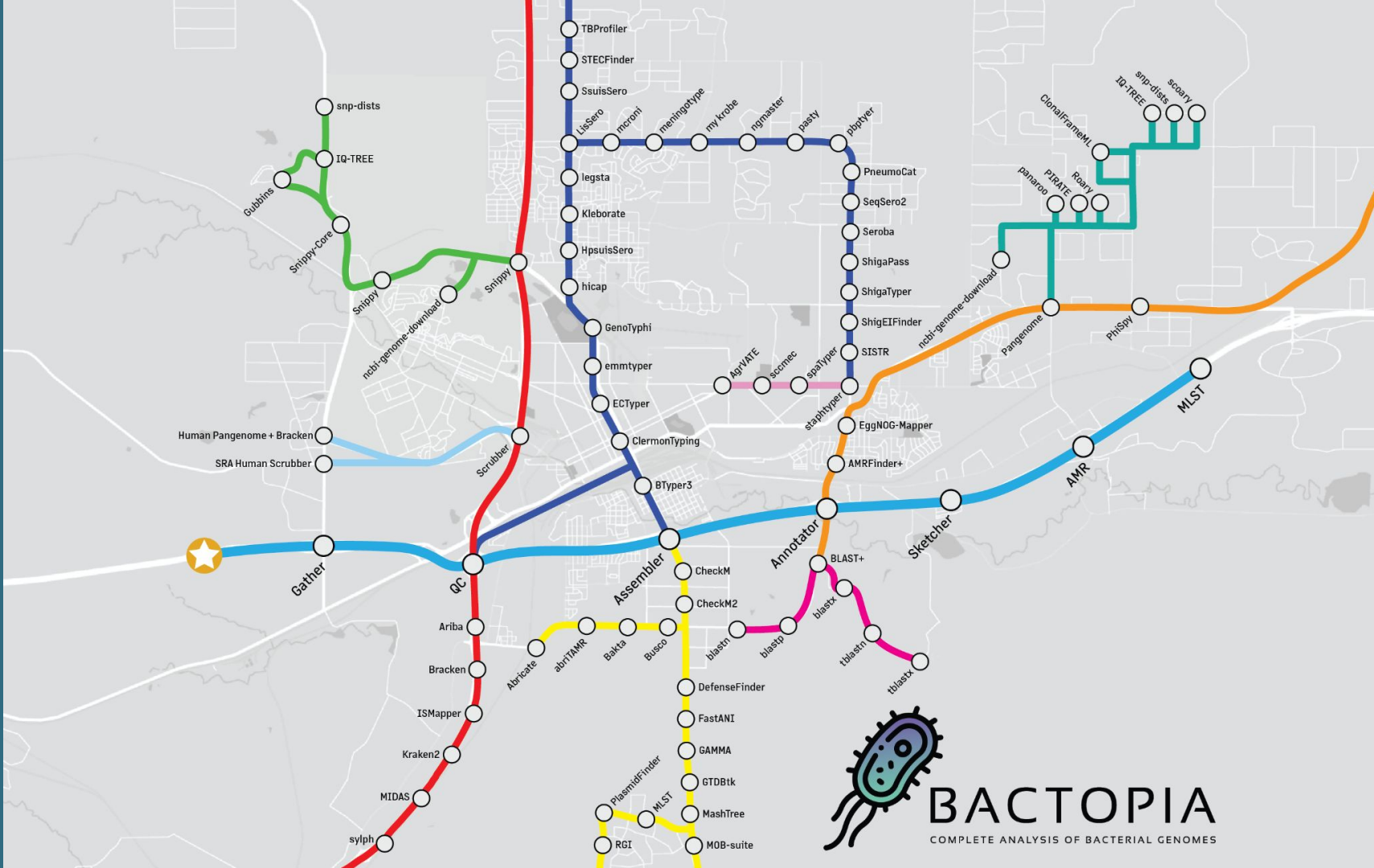
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COMPLETE ANALYSIS OF BACTERIAL GENOMES

Including one for building pangenomes and core-genome phylogenies from your samples.



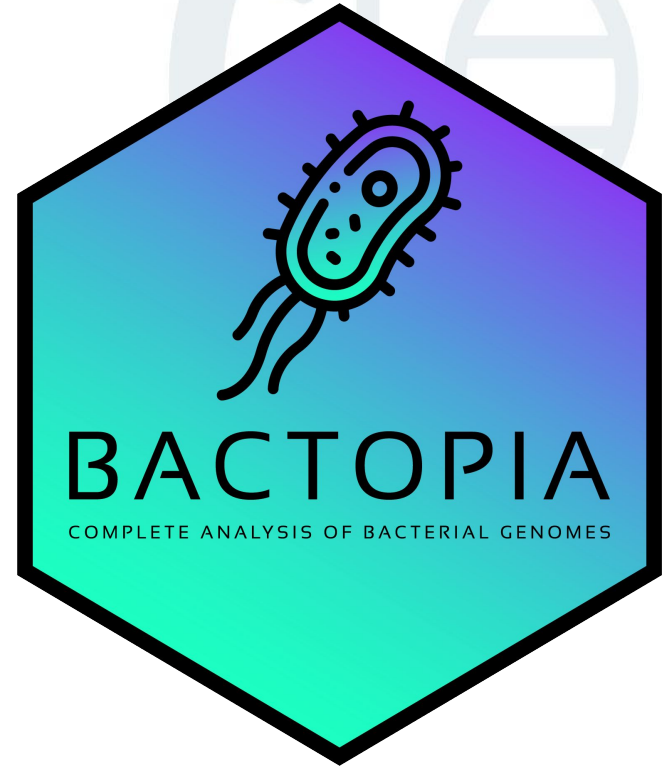
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COMPLETE ANALYSIS OF BACTERIAL GENOMES

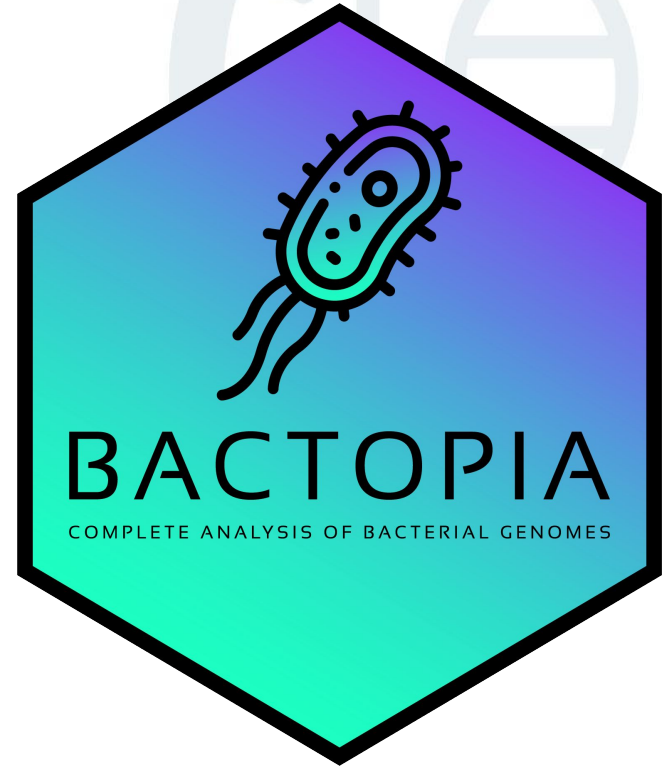
Support system outside the Bactopia pipeline

- bactopia.io - documentation site
- bactopia-py
 - 27 CLI commands to help users and devs
- nf-bactopia
 - Bactopia specific Nextflow plugin
- bactopia-tests
 - Real samples used by Bactopia testing



Bactopia v4 was recently released

- Completely rewritten for 26.04+
 - Static types, record type, strict syntax
- nf-test implemented for all steps
- Expanded ecosystem
 - Revamped bactopia-py
 - Created nf-bactopia Plugin
 - Docs built from inline GroovyDocs
- Improved AI/LLM experience



Improving AI/LLM experience



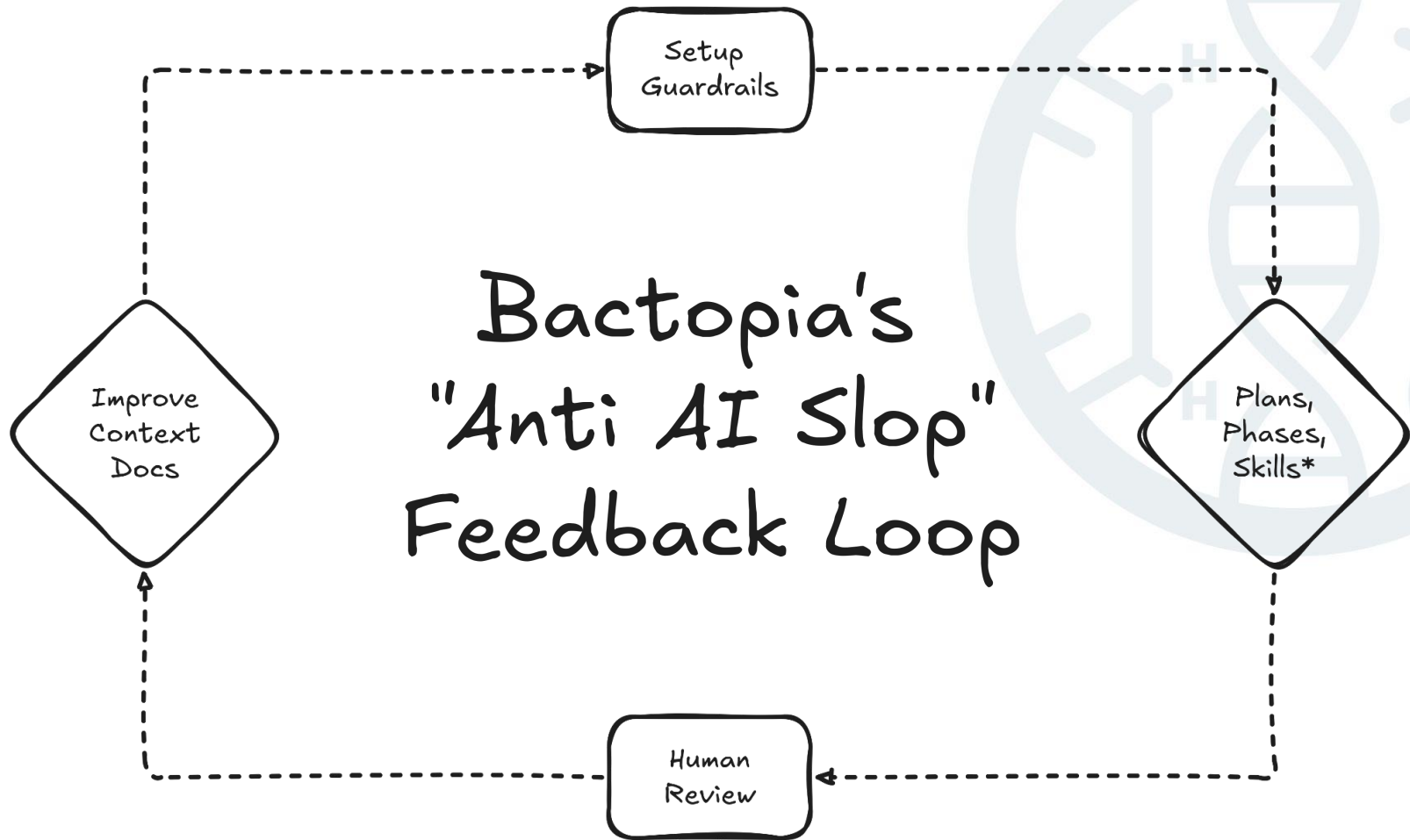
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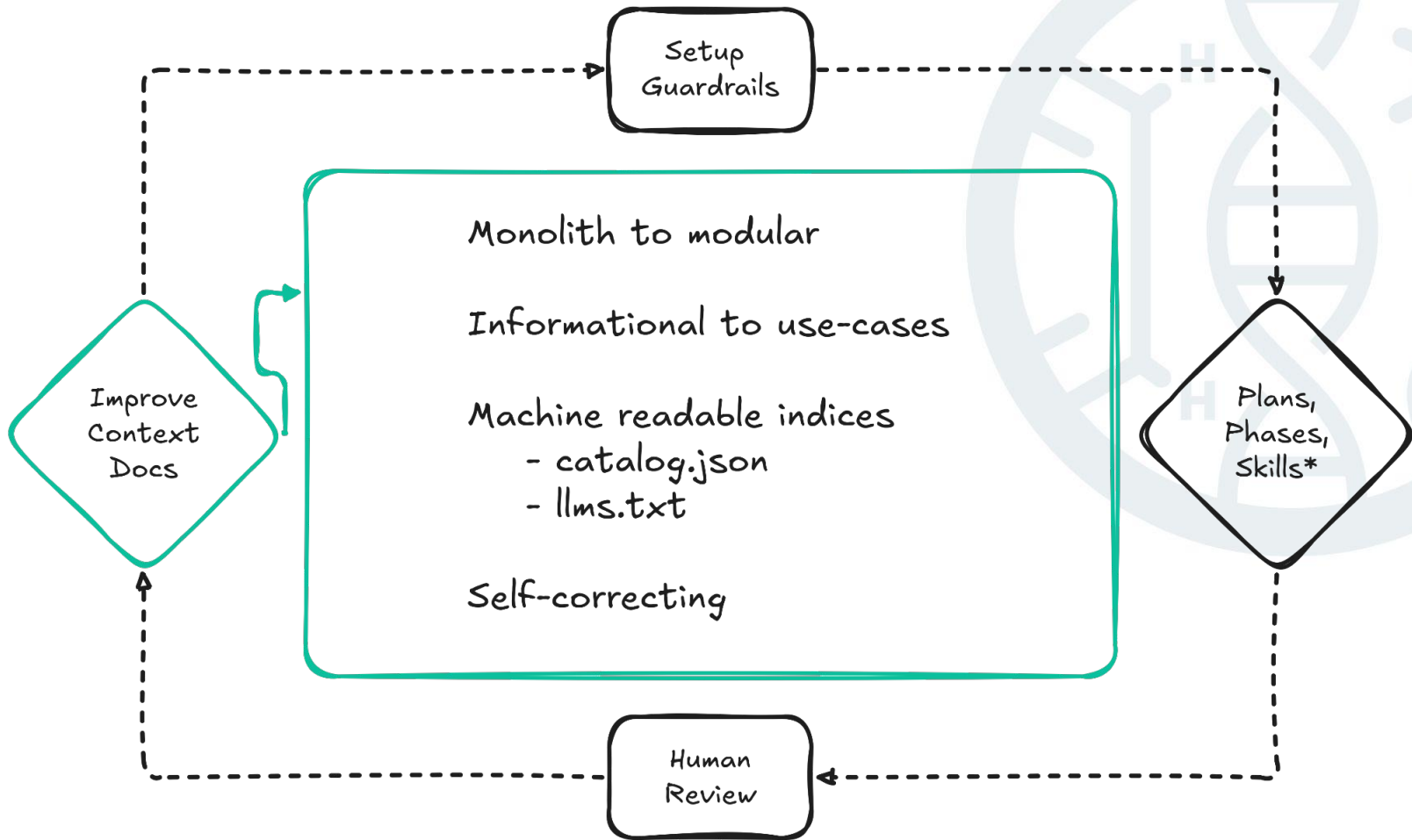


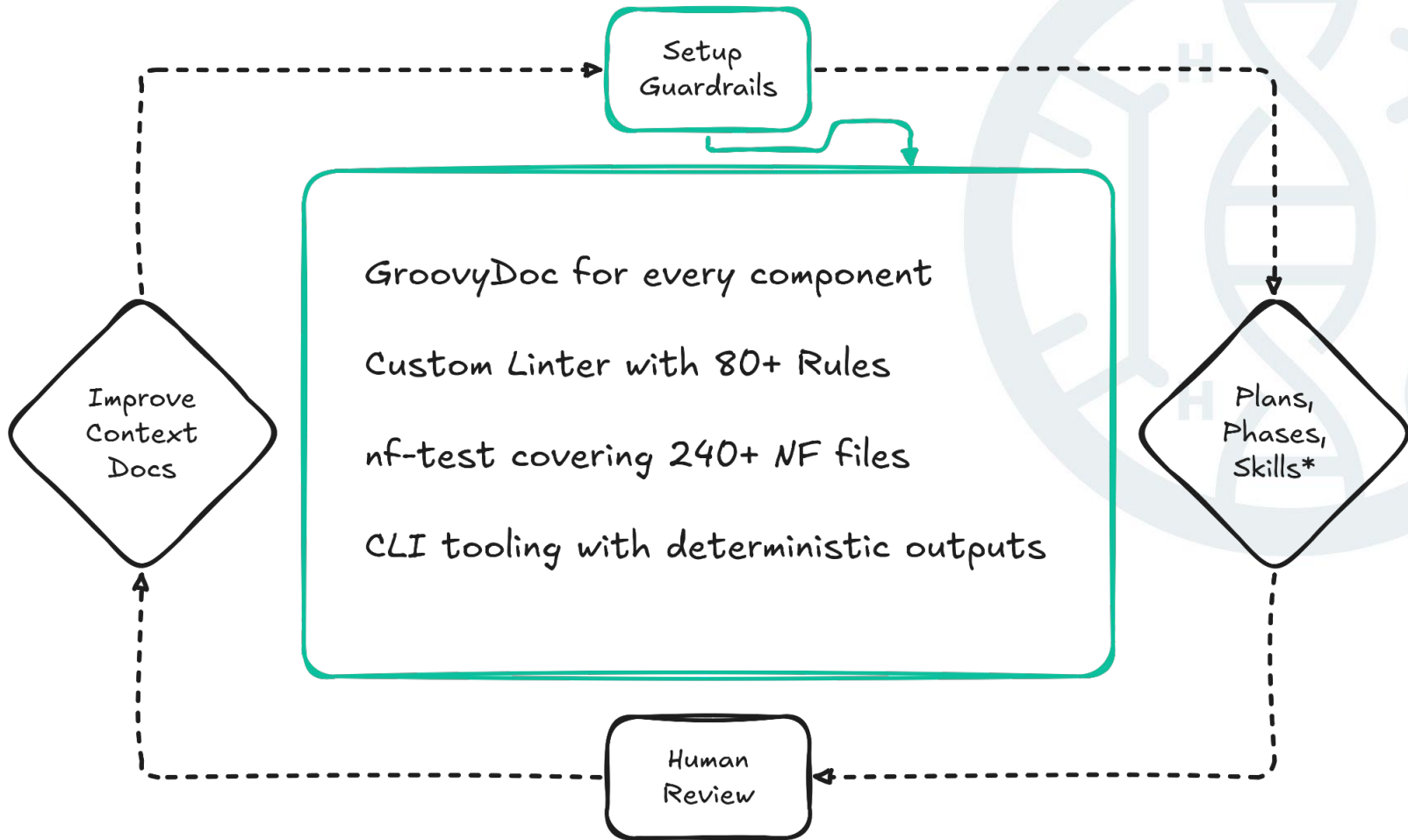
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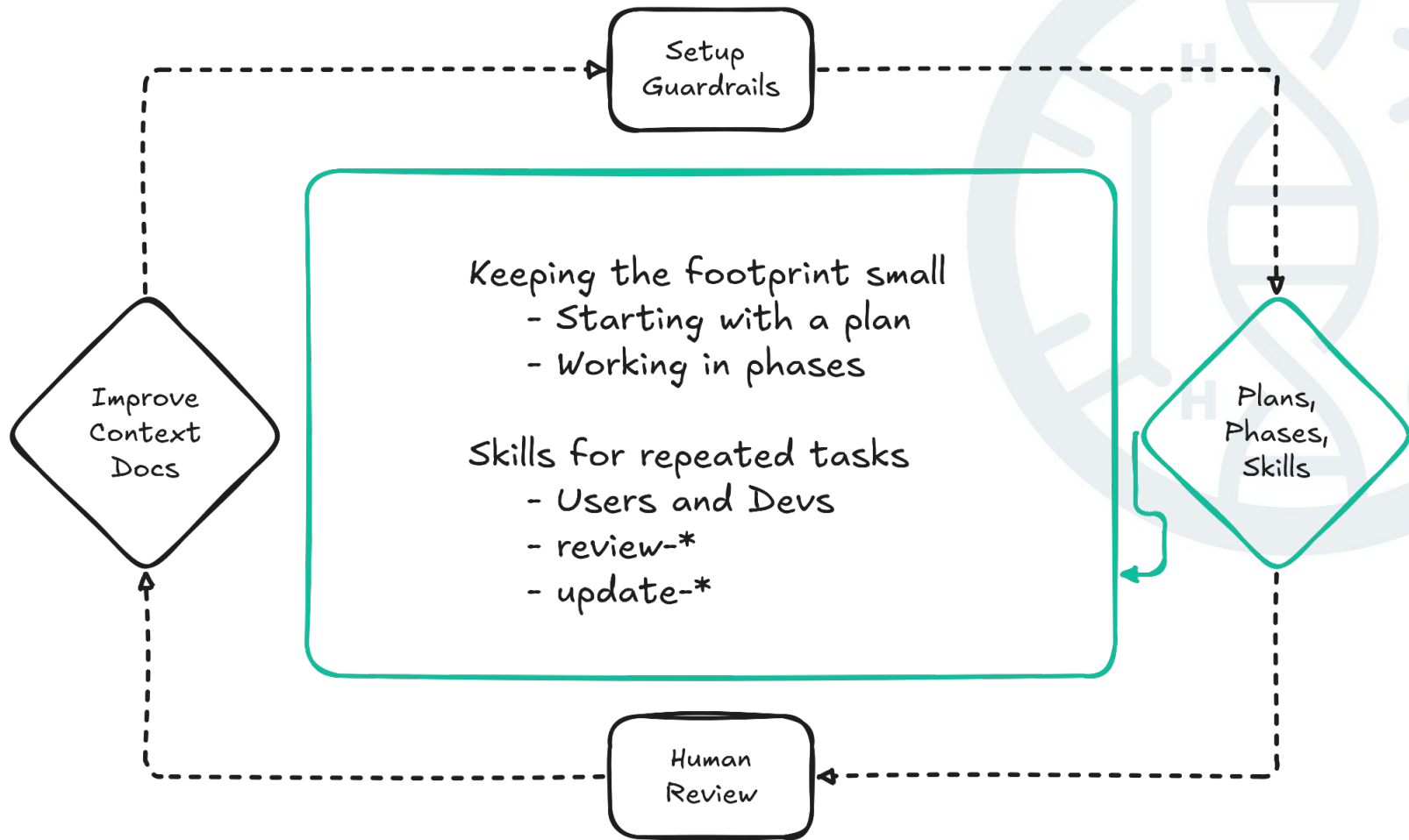


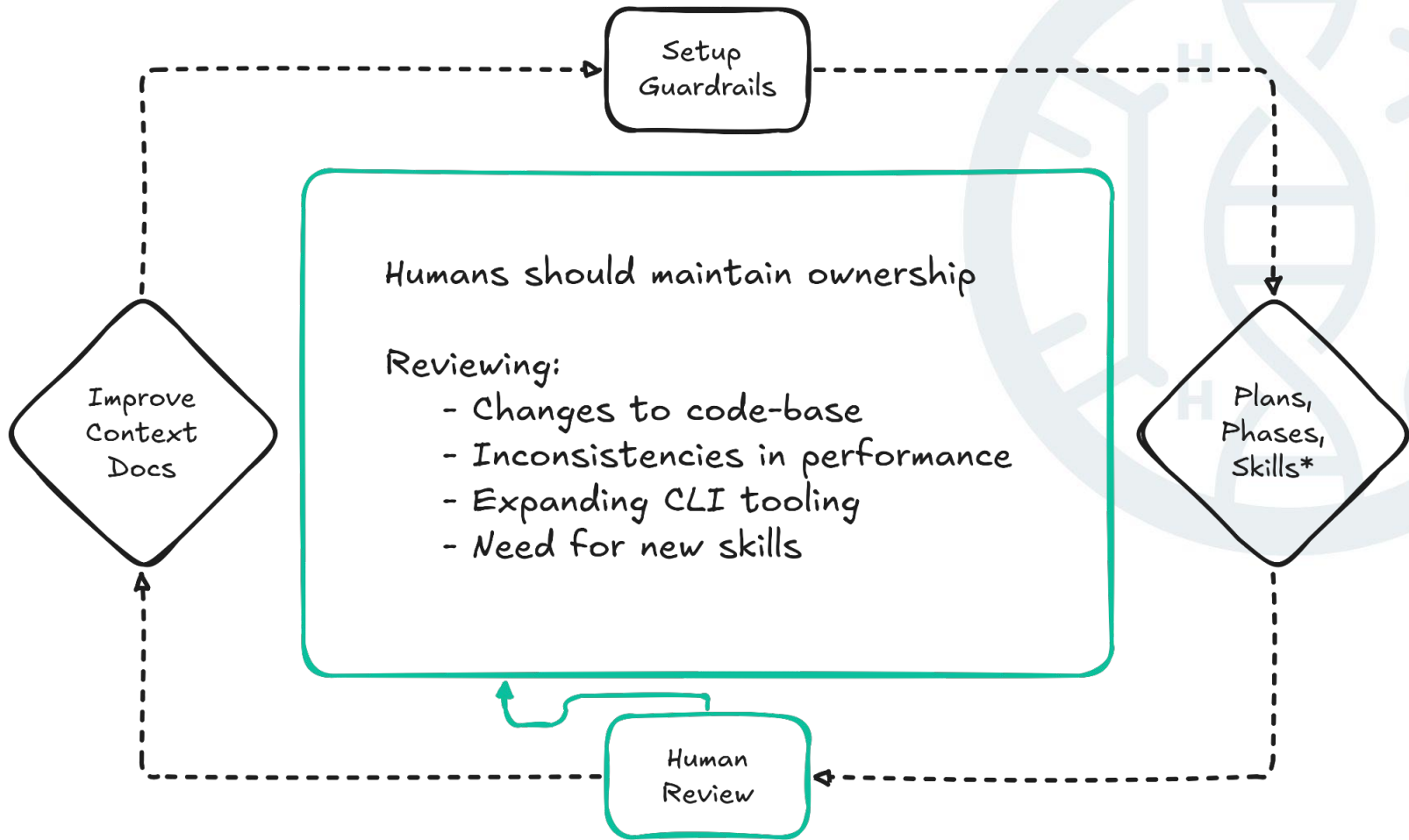
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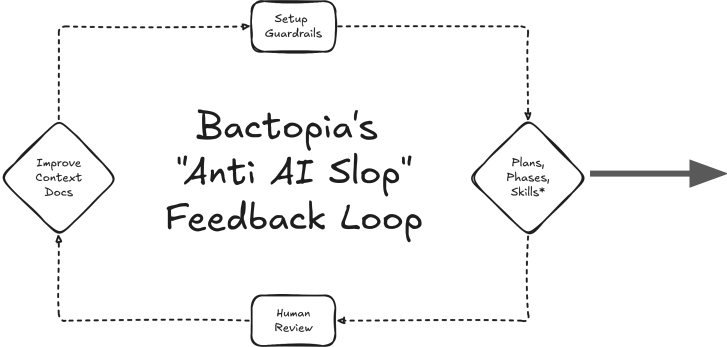


Example: add-bactopia-tool Skill

- Could we create a skill to add a new Bactopia Tool?
 - E.g. “add a bactopia tool for gigatyper”
- How the skill works:
 - Asks users questions
 - Checks requirements
 - Reads tool docs
 - Compares it to existing Bactopia Tools
 - Generates all the files and tests
 - Runs all the tests



Example: add-bactopia-tool Skill



Document tabs +

- setup 1
- Round 1
- Round 2
- Round 3
- Round 4
- Round 5
- Round 6
- Round 7
- Round 8
- Cleanup
- StaphSCAN
- traitar3
- ncbi-stxtyper

Prompt:
/add-bactopia-tool stxtyper which is available from bioconda under "ncbi-stxtyper"

It just worked

Let's Wrap This Up

What's next and all that fun stuff



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Many things are still brewing

- Bactopia v4 made the code-base more machine readable... *what about the outputs?*
 - Standardizing outputs
 - Adding context
 - Bactopia MCP server?
 - Query outputs through natural language
- More:
 - Bactopia Tools
 - AI assisted translations
 - Better tutorials / use case examples



Bactopia streamlines bacterial genome analysis

Bactopia is a flexible pipeline that allows its users to focus more on the science behind their samples.

It will continue to be sustained for 7+ years through support from WPHL, Emory University, CAPE, and CZI.

There are many around the world utilizing Bactopia, and we are still only scratching the surface of where we plan to take it.



EMORY
UNIVERSITY
SCHOOL OF
MEDICINE

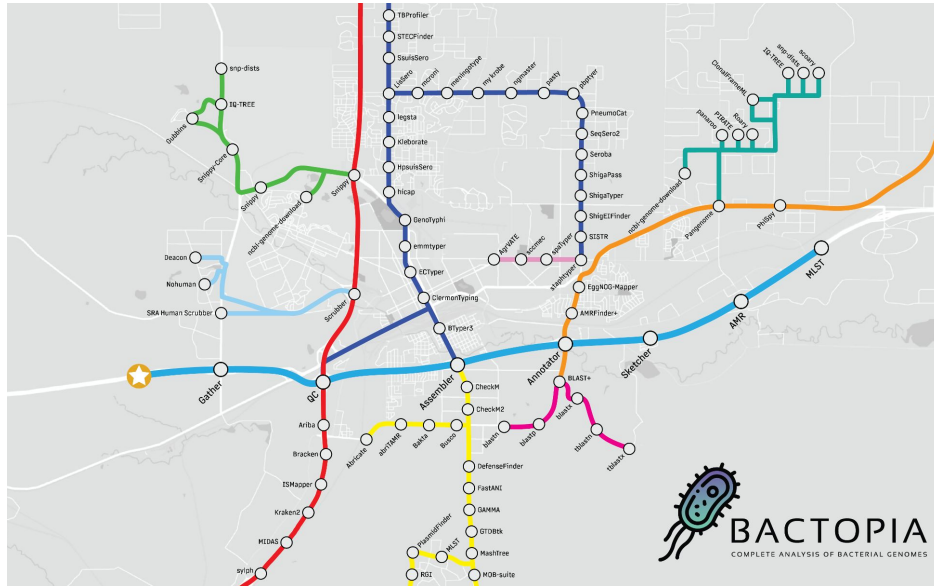


OPEN SCIENCE PROGRAM



Acknowledgements

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



WPHL

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Emory

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EMERGENT Group

RUSH

Ahmed Babiker

Funders

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EMORY UNIVERSITY SCHOOL OF MEDICINE

CAPE Center for Applied Pathogen Epidemiology and Outbreak Control

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Thank you! Happy to take any questions

Learn more about Bactopia at
bactopia.io

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