

Pangenome analysis

Date etc

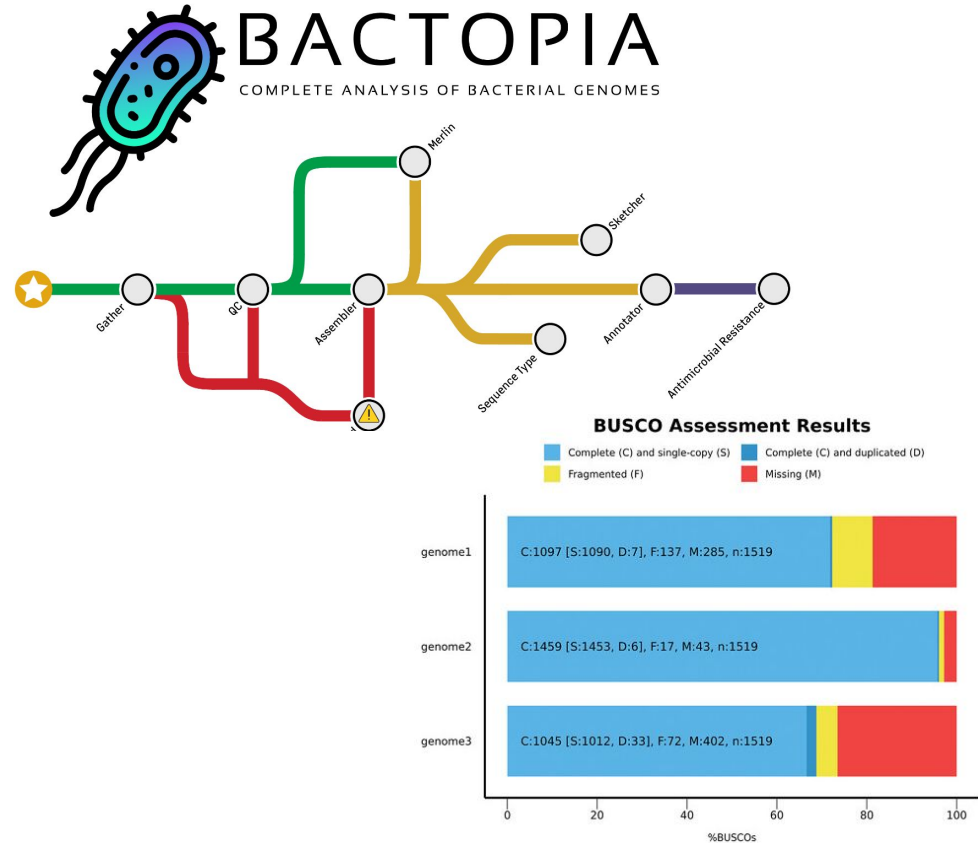
NC STATE UNIVERSITY



Infectious disease dynamics lab

- Assemblies
- Annotations
- Variant calling

- Bactopia pipeline
- BUSCO



- Identify and classify antimicrobial resistance (AMR), virulence and stress genes from whole genome sequences.
- Produce visualizations of bacterial pangenome and understand the biological significance of the different types.

Resistome

Set of genes that provide resistance to antimicrobial agents.



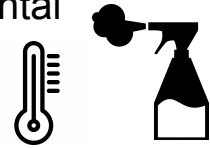
Virulome

Set of genes that are responsible for a pathogen's virulence.



Stress

Set of genes that allow pathogens to survive to environmental stressors.



Understanding the **interplay** of these elements is crucial to control the spread and impact of pathogens.

Holistic approaches that consider the **interconnected** nature of these elements is essential for developing successful interventions.

- Known AMR, Virulence and Stress genes on a genome.
 - Comprehensive database integration.
 - High sensitivity and specificity.
 - User-Friendly.
 - Customizable.
 - Integration into workflows → Bactopia



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AMRFinderPlus and the Reference Gene Catalog facilitate examination of the genomic links among antimicrobial resistance, stress response, and virulence

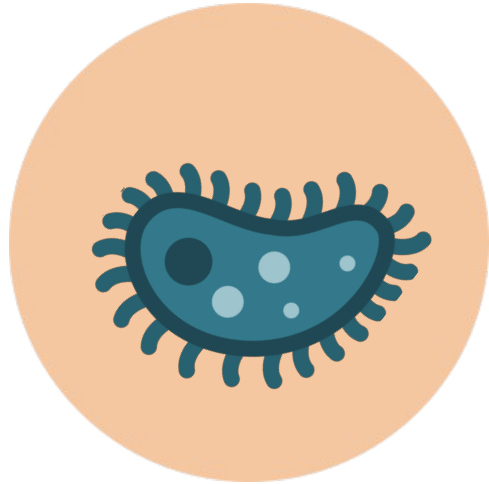
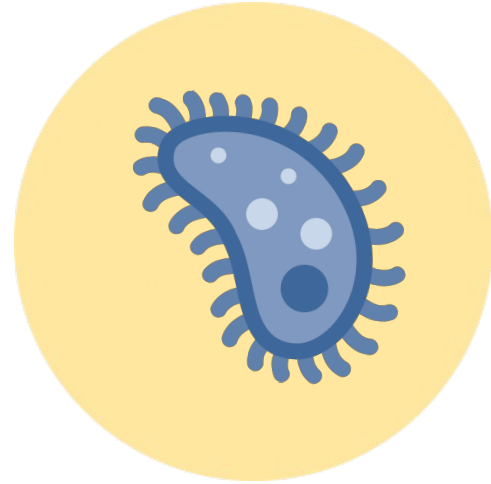
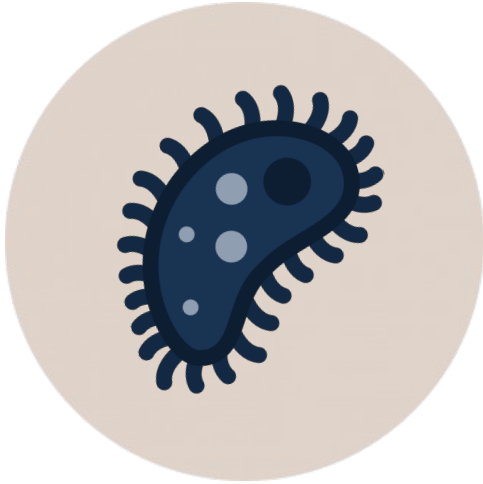
[Michael Feldgarden](#) , [Vyacheslav Brover](#), [Narjol Gonzalez-Escalona](#), [Jonathan G. Frye](#), [Julie Haendiges](#), [Daniel H. Haft](#), [Maria Hoffmann](#), [James B. Pettengill](#), [Arjun B. Prasad](#), [Glenn E. Tillman](#), [Gregory H. Tyson](#) & [William Klimke](#)

[Scientific Reports](#) **11**, Article number: 12728 (2021) | [Cite this article](#)

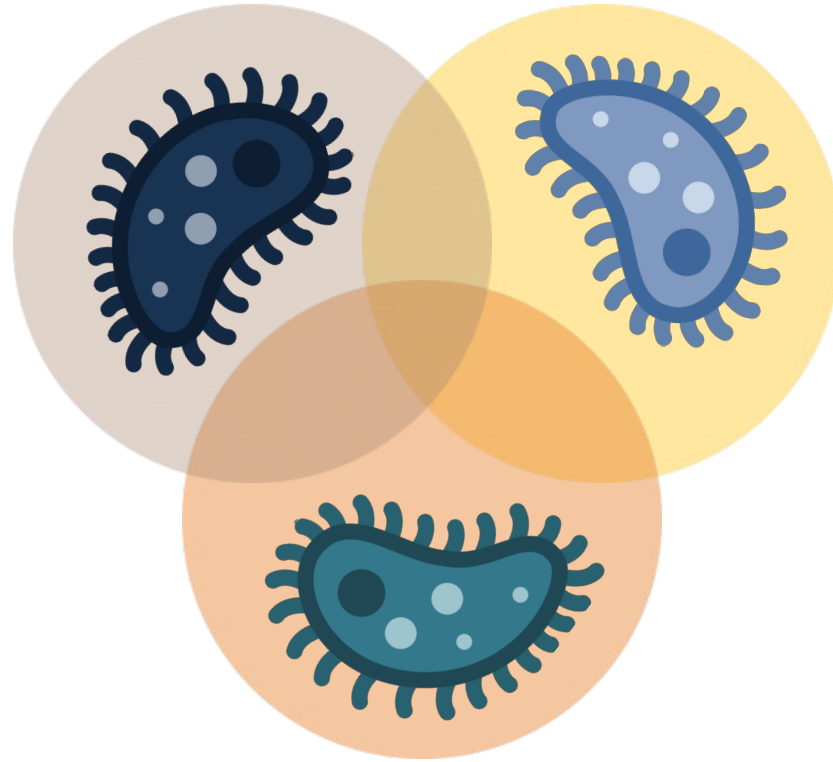
- Entire set of genes found in a taxonomic group of organisms.
- Understanding the genomic diversity within bacterial species.
- Reflect the dynamic nature of their genomes and adaptive potential of a species, providing insights into its ecological versatility, pathogenicity, and evolution.
- Comprehensive view of the entire gene repertoire within a taxonomic group,

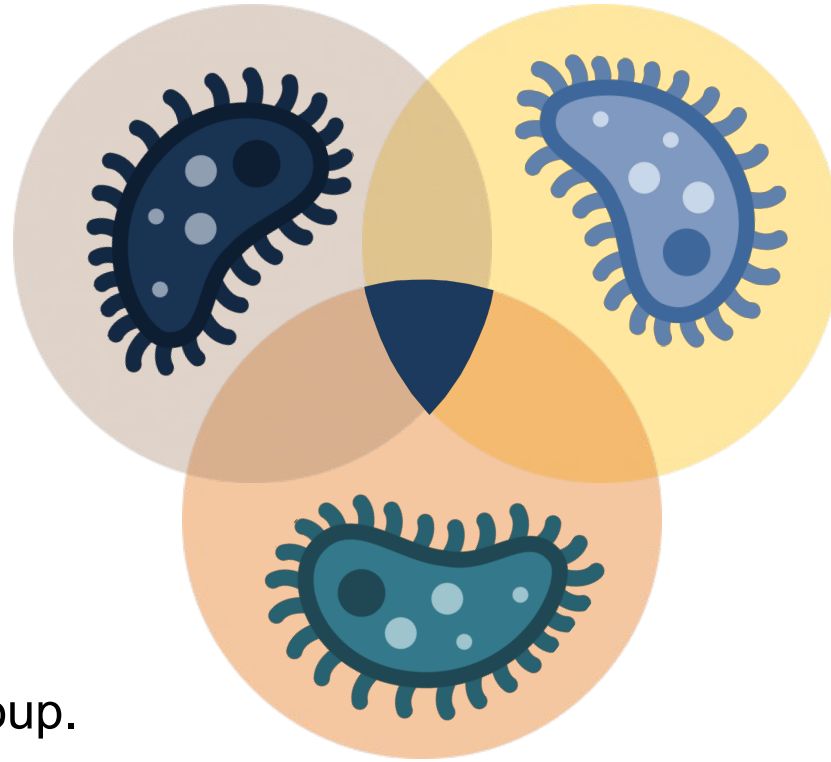


Pangenome

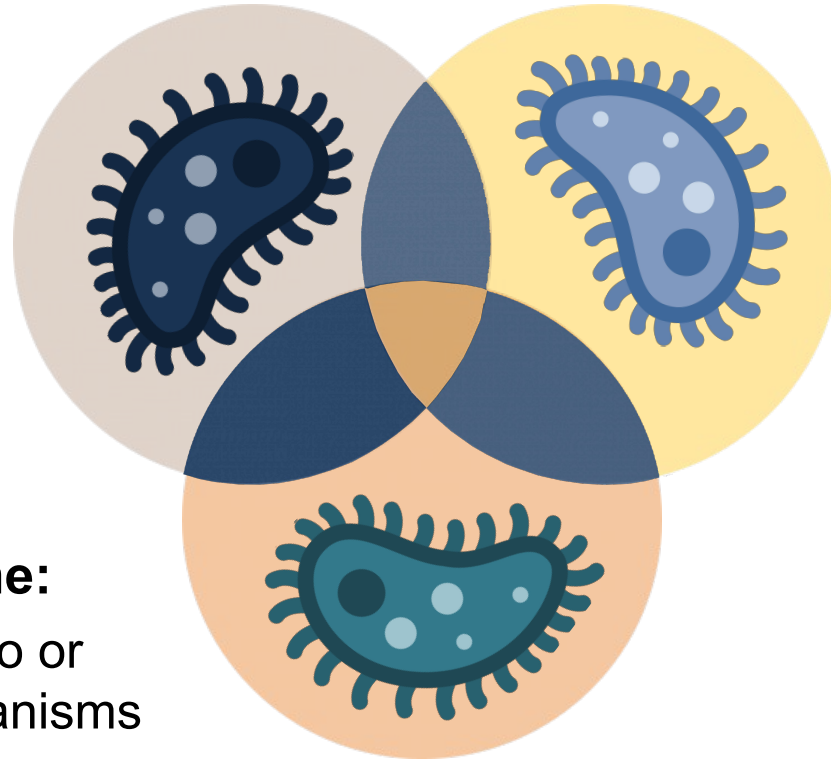


Pangenome

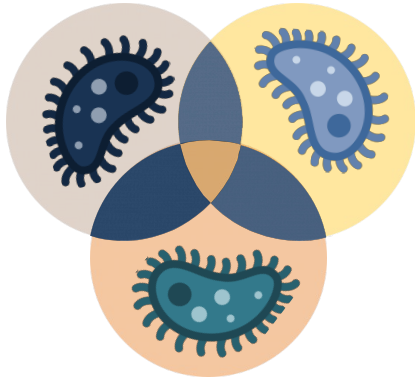


**Core genome:**

Genes shared by all organisms of the group.

**Accessory genome:**

Genes shared by two or more but not all organisms of the group.

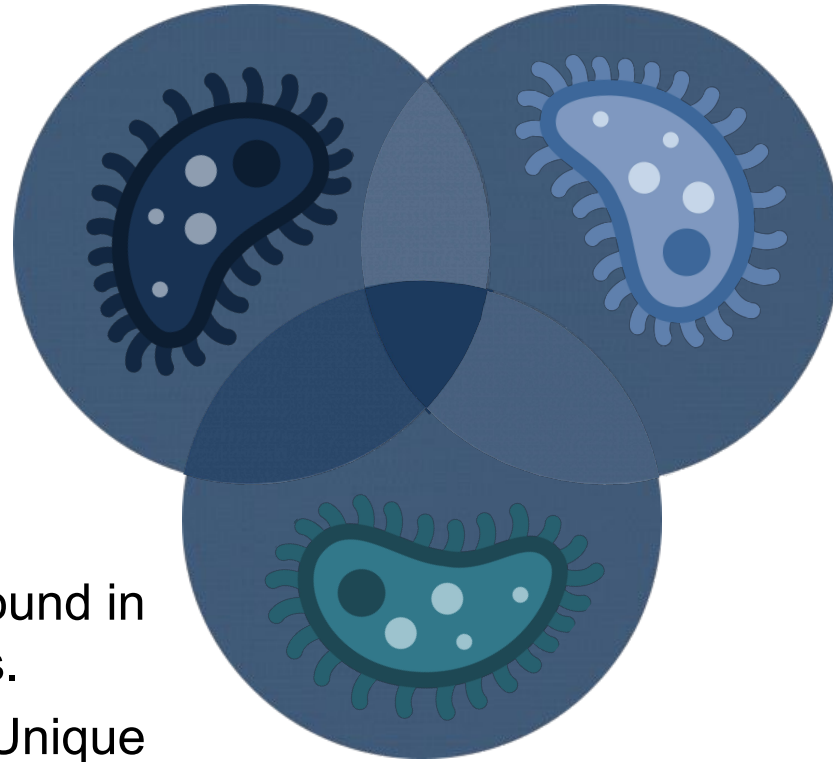


Accessory genome AKA dispensable genome:

- Horizontal gene transfer
- Mutations in pre-existing genes
- Environmental adaptations (AMR, virulence...)

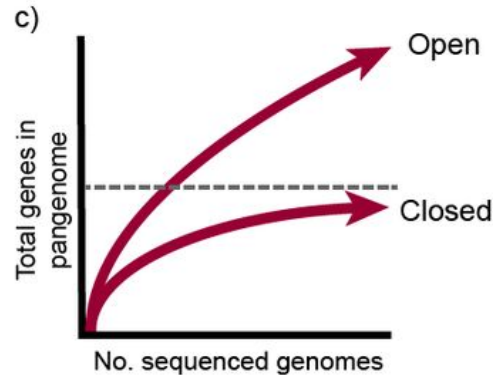
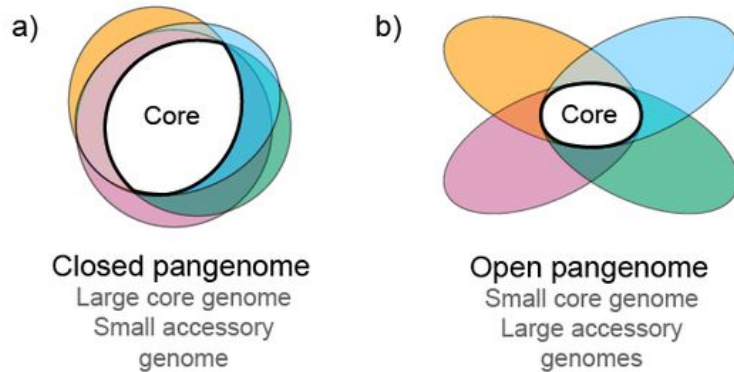
Genomic plasticity?

- Mobile genetic elements and hypervariable regions.
- Variations in one or more genomes within a bacterial population.

**Pangenome:**

Entire set of genes found in a group of organisms.

Core + Accessory + Unique genes

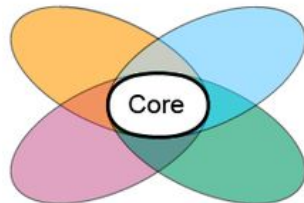


“In an open pangenome its size increases indefinitely when adding new genomes; thus sequencing additional strains will likely yield novel genes. Conversely, in a closed pangenome, adding new genomes will not lead to the discovery of new coding capabilities.”

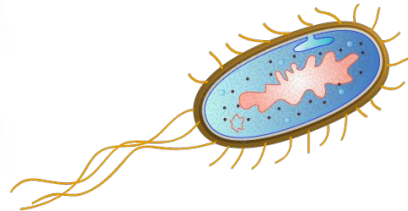
Bosi E, Fani R, Fondi M. Defining orthologs and pangenome size metrics. *Methods Mol Biol.* 2015; 1231:191-202. doi: 10.1007/978-1-4939-1720-4_13. PMID: 25343867.

Open Genome:

- Capacity to acquire genetic material from its environment (HGT).
- Ability to rapidly adapt to changing environmental conditions, enhancing survival by incorporating beneficial genes.
- Can lead to the evolution of new traits, promoting diversity within bacterial populations.



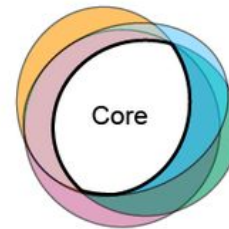
Open pangenome
Small core genome
Large accessory
genomes



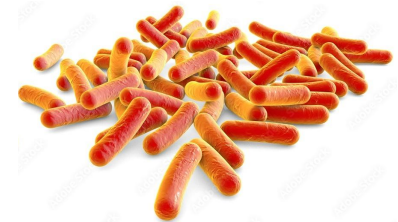
Escherichia coli

Closed Genome:

- Limited capacity for acquiring exogenous DNA, may have mechanisms that restrict the uptake of foreign genetic material.
- Stability and conservation of specific genetic traits leading to a more clonal population structure.
- Limit the ability of bacteria to adapt to new challenges. This can be advantageous in stable environments but not in dynamic or hostile conditions.



Closed pangenome
Large core genome
Small accessory
genome



*Mycobacterium
tuberculosis*

Kim, Y., Gu, C., Kim, H. U., & Lee, S. Y. (2020). Current status of pan-genome analysis for pathogenic bacteria. *Current opinion in biotechnology*, 63, 54-62. <https://doi.org/10.1016/j.copbio.2019.12.001>

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Questions

