

Introduction to Bacterial Bioinformatics

Date, Location





Dr. Cristina Lanzas
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Professor in Infectious Disease.

Specialist in mathematical and computational epidemiology.

Epidemiological models to address a variety of pathogen-host systems including health-care associated pathogens, zoonotic, and enteric pathogens in projects funded by NIH, FDA, CDC, and USDA.

Understand the principles and mechanisms of transmission and its drivers, and to leverage new data streams, including movement and sequence data, and data integration techniques to inform disease transmission and control.

Genomic epidemiology of infectious diseases



Dr. Manuel Jara



Dr. Alba
Frias-De-Diego



Infectious disease dynamics lab



Dr. Manuel Jara, an evolutionary biologist, excels in eco-evolutionary analysis of pathogen transmission. His interdisciplinary approach, blending bioinformatics and ecological models, addresses global health challenges. With expertise in numerous model organisms, his experience on antibiotic resistance and pathogen outbreak prediction, Manuel's research showcases a commitment to impactful science.

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Dr. Manuel Jara



Dr. Alba Frias-De-Diego, specializes in genomic epidemiology of antimicrobial resistance. Her expertise spans genetics, infectious diseases, and evolution. Her commitment to a one-health perspective is evident in research aiming to understand the evolutionary patterns of pathogen and antimicrobial resistance evolution.

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Frias-De-Diego

- Learning to identify and download genomic data from NCBI.
- Use of the Bactopia pipeline to download sequence metadata, assess sequence QC and determine sequence completeness using 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.
- Identify and detect plasmid material and specific point mutations from whole genome sequences.
- Use pangenome GWAS to measure the association between gene presence and phenotypic traits of interest.

- Lectures and explanations
- Hands-on activities

Day 1

1. Introductions and course overview.
2. Downloading genomic data.

Day 2

1. Quality Control.
2. Assemblies and annotations.
3. Bactopia
4. BUSCO

Day 3

1. AMR, Virulence, Stress genes.
2. Pangenome.
3. Gene identification.
4. Pangenome visualization.

Day 4

1. Genotype vs Phenotype - PanGWAS
2. Pan-GWAS analysis
3. Plasmid detection.
4. Point mutations

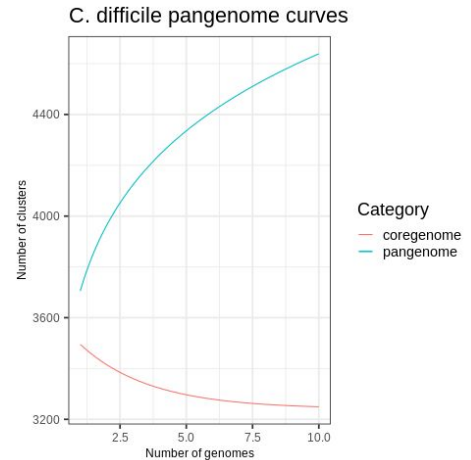
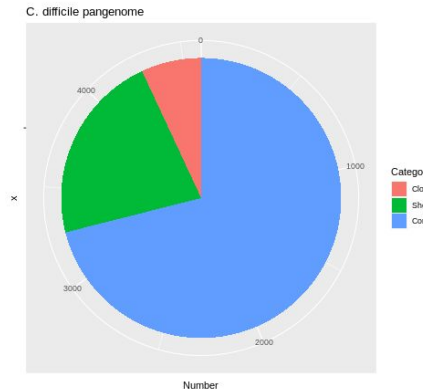
Final Project

1. Choose a bacteria from the list (or talk to us). **One per student.**
2. Run the learned analysis.
3. Organize your results in **up to** three slides. You will have only **three minutes** to present your results on day 4.

Day 3 part 1: Indicate the number of AMR, virulence and stress genes found.
(Average the 5 sequences).



Day 3 part 3: Pangenome visualization.



Does your bacteria have an open or closed pangenome? What could be the biological reason for it?

- Allows users to write and execute code through the browser.
- Linked to Google Drive.
- Independent of your operative System.
- Same speed.
- Same capacity.



Questions

