MILRD Virtual Training Projects

Research Staff · Postdocs · Graduate Students

VTP OVERVIEW

Metagenomics + Microbial Surveillance
(Collaboration with David Danko, Mason Lab, Cornell Medical Center)

Aim

Characterize mass-transit environmental microbiome samples using metagenomic analysis.

Learning Goals

| Discussion Topics	Bioinformatics Tasks + Methods
● Next Generation Sequencing methods and data structures ● Principles and Methods of microbiome analysis ● Comparison: 16S vs. metagenomic analysis ● Principles and methods of data QC, alignment, microbial characterization, sample comparison	● Data QC ● Human read removal ● Taxonomic characterization ● Microbial taxonomic characterization and quantification ● PCA ● Visualization ● Comparison to Human Microbiome Project samples

Suggested Preparation

Linux/Unix command-line & R fundamentals

Summary

Mass-transit systems, and other components of the built environment, have unique microbiomes. MetaSUB is an international consortium that aims to characterize the microbiome of the urban built environment. The consortium has established a global "DNA map" of microbiomes in mass transit systems, which has implications for public health—including disease epidemiology and the rise of antibiotic-resistant pathogens.

In this VTP—created with and supported by the Mason Lab at Cornell Medical Center—you'll analyze your own assigned dataset with help from your mentor and in collaboration with your cohort, which can include PhD students, postdocs, and staff researchers from industry.
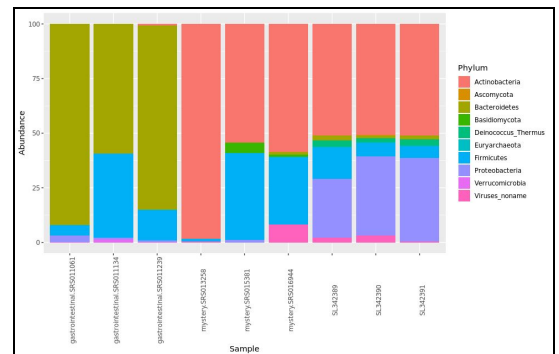
Throughout the week, you'll characterize, quantify and visualize microbial genome data from sequenced swabs of public urban environments. In the Linux terminal on your own high-performance compute instance, you'll perform genomic data quality control, genome alignment, taxonomic characterization, and in R, you'll conduct a principal component analysis and visualizations. To conclude, you'll compare your results to those from the Human Microbiome Project to elucidate the source of your assigned sample and brainstorm compelling new downstream questions you could ask of the data.
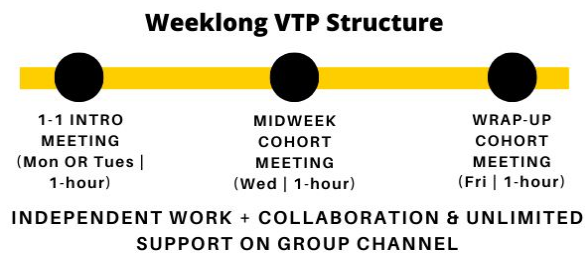
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Source Data
Danko, D., Bezdan, D. et al. *Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance*. Preprint on bioRxiv. New York Times Coverage.

Schedule

Weeklong VTP Structure

1-1 INTRO MEETING (Mon OR Tues | 1-hour)

MIDWEEK COHORT MEETING (Wed | 1-hour)

WRAP-UP COHORT MEETING (Fri | 1-hour)

INDEPENDENT WORK + COLLABORATION & UNLIMITED SUPPORT ON GROUP CHANNEL

Total Effort: ~10 hours

MILRD Provides
- ❖ Unlimited support from expert mentors
- ❖ Access to all required high-performance cloud-compute resources (AWS), analysis tools and software
- ❖ Access to all source data required to complete your project
- ❖ Optional Pre-VTP Preparation

Participants Provide
- ❖ A computer running Windows or MacOS
- ❖ Google Chrome, Safari, Firefox, or Edge
- ❖ A stable Internet connection

Sign Up
Review VTP dates and enrollment instructions on our Enrollment & Contact page.

info@milrd.org