

MILRD Virtual Training Projects

Undergraduates · High School Students

VTP OVERVIEW

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

Who should enroll

Undergraduates and high school students who are interested to:

Learn about how metagenomic analysis is being used by practitioners in academia, industry, and government. VTPs can help inform: undergraduate/graduate study & program selection, applications for internships and first jobs.

Work alongside professionals and trainees from academia, industry and government. Each participant is assigned their own dataset and works in a small group with other participants. Our personalized platform mixes professionals, trainees, & graduate students with college & high school students to enable peer-learning and networking opportunities—without leaving beginners behind or holding back folks with more expertise.

Develop mentorship and leadership skills. Participants who complete a VTP can apply to serve as an assistant mentor to future cohorts of the project.

Domains

Data science, Metagenomics, Infectious Diseases, Microbiology, Cellular/Molecular Biology, Genomics, Bioinformatics

Aim

Characterize mass-transit environmental microbiome samples using metagenomic analysis.

Learning Goals

<i>Discussion Topics</i>	<i>Bioinformatics Tasks + Methods</i>
<ul style="list-style-type: none">● 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● Applications of metagenomics analysis in research and biotech sectors● Programming languages and data science methods used in bioinformatics analysis	<ul style="list-style-type: none">● Utilize the Linux and R programming languages for statistical analysis and visualization● 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 (optional)

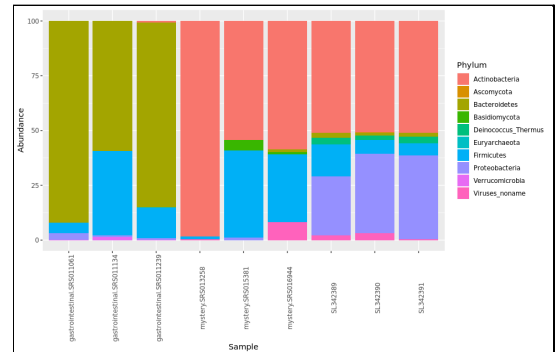
Summary

Mass-transit systems, and other components of the built environment, have

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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.

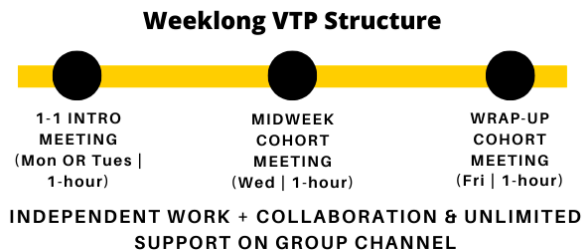


Throughout the week, you'll characterize, quantify and visualize microbial genome data from sequenced swabs of public urban environments. In the Linux terminal on your own high-performance compute instance, you'll perform genomic data quality control, genome alignment, taxonomic characterization, and 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.

Source Data

Danko, D., Bezdán, D. et al. *Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance*. [Preprint on bioRxiv](#). [New York Times Coverage](#).

Schedule



Total Effort: ~15-20 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.