

MILRD Virtual Training Projects

Undergraduates · High School Students

VTP OVERVIEW

Variant Calling + COVID-19

Collaboration with Dr. Adriana Heguy, NYU Medical Center

Who should enroll

Undergraduates and high school students who are interested to:

Learn about how variant 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, Variant Calling, Infectious Diseases, Microbiology, Cellular/Molecular Biology, Genomics, Bioinformatics

Aim

Characterize nucleotide and amino acid variants from SARS-CoV-2+ patient samples

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 resequencing analysis and variant detection● Principles and methods of data QC, alignment, variant calling● Next Generation Sequencing methods and data structures● Principles and methods of data QC, alignment, microbial characterization, sample comparison● Applications of variant 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 for statistical analysis and visualization● Data QC● Human read removal● Alignment● Variant Calling● Variant Filtering● Visualization● Nucleotide and Amino Acid variant characterization● Evaluation in GisAID

Suggested Preparation

Linux/Unix command-line fundamentals (optional)

Summary

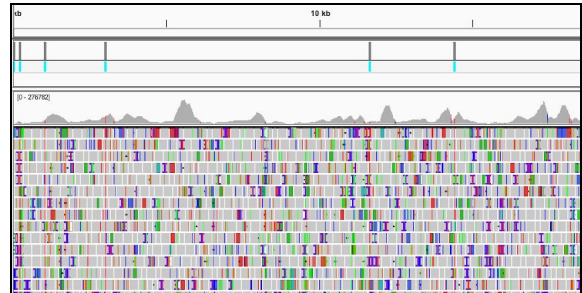
The Covid-19 Pandemic—caused by Severe Acute Respiratory Syndrome

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Coronavirus 2 (SARS-CoV-2)—has infected over 6.9 million people and claimed over 400,000 lives in the past six months. This pandemic underscores the pressing need to interrogate the cellular, molecular, and physiological aspects of SARS-CoV-2 to help expand diagnostic and clinical treatments for Covid-19.

In this VTP—created with the help of Adriana Heguy's Research Group at NYU Med—you'll analyze your own assigned dataset with help from your mentor and in collaboration with your cohort.

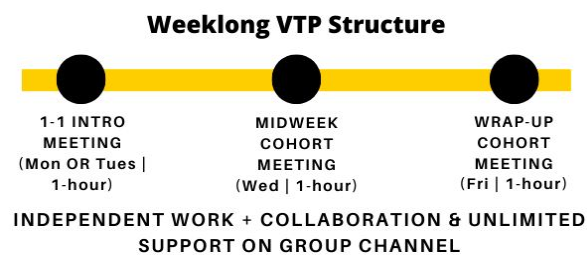


Throughout the week, participants will characterize clinical SARS-Cov2+ genomic data. In the Linux terminal, you will perform genomic data quality control, genome alignment, variant calling and visualization on SARS-Cov2+ samples.

Source Data

Maurano et al. *Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City Region*. [Genome Research 2020](#). [Preprint on MedRxiv](#). [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.