## **VTPs**

Microbial Surveil...

#### instructions

Collaborate
Cohort Results

- ▶ Drosophila + sc...
- ▶ Variant Calling +...
- ▶ Single-cell Trans...
- ▶ Economics + So...

## VTPs / Microbial Surveillance + Metagenomics Analysis / Instructions

#### Contents

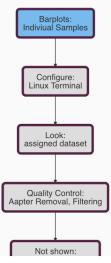
- 1. Getting Started
- 2. Introduction to the project
- 3. Rationale: MetaSub Project
- 4. Overview: Bioinformatics Analysis
- 5. Bioinformatics Tasks
- 6. Beyond this Training
- 7. Post-VTP Survey

# М

# 4 Overview: bioinformatics analyses

This guide is intended to teach you how to teach you one component of metagenomic analysis: how to plot abundances at the "phylum" level for each metagenomics sample.

Throughout the VTP, each participant characterizes, quantifies and visualize microbial metagenomics data from sequenced swabs of public urban environments on their own AWS High Performance Compute instance. In the Linux terminal, they perform genomic data quality control, genome alignment, taxonomic characterization & abundance quantification, and in R, they viaualize results, conduct a principal component analysis. To conclude, they investigate their most abundant species and use the Patric database to consider how they would determine the strains of these species.



Text

# Option 1: Preferred QA UI

## **VTPs**

▼ Microbial Surveil...

#### instructions

Collaborate
Cohort Results

- Drosophila + sc...
- ▶ Variant Calling +...
- ▶ Single-cell Trans...
- ► Economics + So...

## VTPs / Microbial Surveillance + Metagenomics Analysis / Instructions

#### Contents

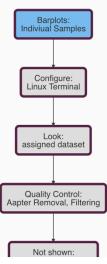
- 1. Getting Started
- 2. Introduction to the project
- 3. Rationale: MetaSub Project
- 4. Overview: Bioinformatics Analysis
- 5. Bioinformatics Tasks
- 6. Beyond this Training
- 7. Post-VTP Survey

# Μ

# 4 Overview: bioinformatics analyses

This guide is intended to teach you how to teach you one component of metagenomic analysis: how to plot abundances at the "phylum" level for each metagenomics sample.

Throughout the VTP, each participant characterizes, quantifies and visualize microbial metagenomics data from sequenced swabs of public urban environments on their own AWS High Performance Compute instance. In the Linux terminal, they perform genomic data quality control, genome alignment, taxonomic characterization & abundance quantification, and in R, they viaualize results, conduct a principal component analysis. To conclude, they investigate their most abundant species and use the Patric database to consider how they would determine the strains of these species.



Interesting. What's AWS?

# VTPs / Microbial Surveillance + Metagenomics Analysis / Instructions MILRD ~ alignment, taxonomic characterization & abundance quantification, and in R, they viaualize results, conduct a principal component analysis. To Contents conclude, they investigate their most abundant species and use the Patric database to consider how they would determine the strains of these 1. Getting Started species. 2. Introduction to the project VTPs 3. Rationale: MetaSub Project Barplots: Indiviual Samples 4. Overview: Bioinformatics Analysis ▼ Microbial Surveil... 5. Bioinformatics Tasks 6. Beyond this Training instructions 7. Post-VTP Survey Configure: Linux Terminal Collaborate **Cohort Results** Look: ▶ Drosophila + sc... assigned dataset ▶ Variant Calling +... Quality Control: Aapter Removal, Filtering ► Single-cell Trans... Interesting. What's AWS? ► Economics + So... М What is R?

#### MILRD ~ VTPs / Microbial Surveillance + Metagenomics Analysis / Instructions alignment, taxonomic characterization & abundance quantification, and in R, they viaualize results, conduct a principal component analysis. To Contents conclude, they investigate their most abundant species and use the Patric database to consider how they would determine the strains of these 1. Getting Started species. 2. Introduction to the project **VTPs** 3. Rationale: MetaSub Project Barplots: Indiviual Samples 4. Overview: Bioinformatics Analysis Microbial Surveil... 5. Bioinformatics Tasks 6. Beyond this Training instructions 7. Post-VTP Survey Configure: Linux Terminal Collaborate **Cohort Results** Look: ▶ Drosophila + sc... assigned dataset ▶ Variant Calling +... Quality Control: Aapter Removal, Filtering ▶ Single-cell Trans... Interesting. What's AWS? ▶ Economics + So... Dots should emerge Cursor blinks and prints text to screen word by word one by one as Al generates the User can type new query response and it's into chatbox while Al printed to the screen response is being generated, but they cannot submit it (i.e. `return`/`enter > What is R? key is disabled) suuntil the Al's response to the previous query is posted

# **VTPs**

▼ Microbial Surveil...

#### instructions

Collaborate
Cohort Results

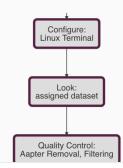
- Drosophila + sc...
- ▶ Variant Calling +...
- ▶ Single-cell Trans...
- ▶ Economics + So...

## VTPs / Microbial Surveillance + Metagenomics Analysis / Instructions

 $\times$ 

#### Contents

- 1. Getting Started
- 2. Introduction to the project
- 3. Rationale: MetaSub Project
- 4. Overview: Bioinformatics Analysis
- 5. Bioinformatics Tasks
- 6. Beyond this Training
- 7. Post-VTP Survey



Interesting. What's AWS?

Amazon Web Services (AWS) is a collection of remote computing services (also called web services) that make up a cloud computing platform, offered by Amazon.com. These services operate from 12 geographical regions across the world. It provides a variety of services such as computing power, storage, and databases to name a few. It allows customers to rent virtual computers on which to run their own computer applications. AWS is one of the most widely used cloud computing platforms and is particularly popular among startups and enterprises for its scalability and flexibility.

What is R?

# Option 2: Alternate QA UI (Not preffered)

Microbial Surveil...

instructions

Collaborate

Cohort Results

Drosophila + sc...

▶ Variant Calling +...

► Single-cell Trans...

► Economics + So...

**VTPs** 

VTPs / Microbial Surveillance + Metagenomics Analysis / Instructions

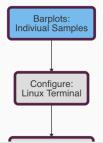


# М

# 4 Overview: bioinformatics analyses

This guide is intended to teach you how to teach you one component of metagenomic analysis: how to plot abundances at the "phylum" level for each metagenomics sample.

Throughout the VTP, each participant characterizes, quantifies and visualize microbial metagenomics data from sequenced swabs of public urban environments on their own AWS High Performance Compute instance. In the Linux terminal, they perform genomic data quality control, genome alignment, taxonomic characterization & abundance quantification, and in R, they viaualize results, conduct a principal component analysis. To conclude, they investigate their most abundant species and use the Patric database to consider how they would determine the strains of these species.



#### **Thread**



Interesting. What's AWS?





Thanks.



You're welcome! Let me know if you have any other questions.

I

-