labibi Documentation

Release 1.0

C. Titus Brown

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Contents

Lead Instructors: Harriet Alexander and C. Titus Brown

Co-Instructors: Jessica Blanton, Adelaide Rhodes, Shawn Higdon, Jessica Mizzi, Phillip Brooks, Veronika Kivenson

These are the online materials for the environmental metagenomics workshop run as part of the Data Intensive Biology Summer Institute at UC Davis (DIBSI).

We will be using HackMD to take collective notes throughout the course: HackMD.

CHAPTER 1

Monday, Day 1:

11am: Meet in Valley Hall (room TBA), setup, and introductions.

- Logging into the cloud (XSEDE Jetstream)

Noon - 1:15: Lunch

1:15 - 2pm: Group meeting with all of DIBSI

2pm - 4pm:

- Working on Command Line
- Command Line Blast

Homework: *Skim* the Critical Assessment of Metagenome Interpretation (CAMI) Paper

CHAPTER 2

Tuesday, Day 2:

9am - Noon:

- Introduction to dataset we will be using
- Evaluating your short-read data set quality Noon - 1:15: Lunch

1:15 - 4pm:

- Lecture about assembly from Titus Brown
- Trying quality trimming and assembly with your own data!

CHAPTER 3

Wednesday, Day 3:

9am - Noon:

- Assembling your short read data set with MEGAHIT
- Quickly searching and comparing your samples with sourmash

Noon - 1:15: Lunch

1:15 - 4pm:

- Mapping short reads to the assembly *time permitting*
- Binning genomes out of your metagenome

CHAPTER 4

Thursday, Day 4:

9am - Noon:

- Annotating your dataset with Prokka
- Quantifying abundance across samples with Salmon

Noon - 1:15: Lunch

1:15 - 4pm:

- Anvi'o
- A brief discussion of workflows & repeatability

CHAPTER 5

Friday, Optional Day 5: TBD (plotting, visualization, jupyter notebooks...)

What next?

Resources:

SEQ Answers

Biostars

Data Carpentry

DIB Summer Institute

CHAPTER 6

Undone

See the complete table of contents

CHAPTER 7

Technical information

The github repository for this workshop is public at https://github.com/ngs-docs/2017-ucsc-metagenomics