16s rDNA sequencing analysis workshop agenda

Lectures:

- Sequencing and information theory
    - DNA extraction
    - Library preparation
    - Sequencing & output files
    - 16S defined
- QIIME2 (Q2) software
    - What is Q2
    - How to use Q2 files/commands
- Basic command line
    - Terminal
    - Common commands
- Importing data into Q2
- QC & ASV assignment
    - QC thresholds
    - Chimeras
    - ASV assignment
    - Sequencing depth
- Ecology
    - Alpha & beta diversity
    - Differential abundance testing
- Statistics
    - Types of tests
    - Differential abundance testing
- How to ask a bioinformatician a question

Practical

- Ecology – run alpha/beta for yourself
- Work on your own!
    - Choose a different diet/age/probiotic condition to look at and start with filtering the feature table and work through to differential abundance
    - If you have your own data bring that to work on!

Metagenomics sequencing analysis workshop agenda

Lectures:

- Sequencing and information theory
  - DNA extraction
  - Library preparation
  - Sequencing & output files
- MCW's RCC
  - What is it?
  - How it works & how to get an account?
- Basic command line
  - Terminal
  - Common commands
- Taxonomic & functional profiling
  - QC
  - Profile reads directly
  - Profile using MAGs
- Anvi'o
  - What is anvi'o?
  - Sample dataset
  - Anvi'o databases
- How to ask a bioinformatician a question

Practical

- Run through anvi-interactive and manual binning