

## 1. Unix crash course

- Getting a Unix environment
- Working with files and directories
- Six incredible commands / Redirectors and wildcards
- Some Powerful everyday examples
  - Renaming 1,000 files
  - Making a barcode fasta file to demultiplex samples
  - Converting NCBI taxon IDs to organism lineages
- Variables and For loops
- Version control (github)
- Accessing data from NCBI at the command line
- Help installing tools / An introduction to Conda
- The amazing power of EMACS / org-mode

## 3. Marker Gene Sequencing overview

- Background of sequencing technology

## 4. Intro to FASTA/FASTQ file formats

- Compression formats and tools (zip, gzip, pbzip, bzip2, pigz)
- Demultiplexing example (Sabre / QIIME demux)
- Trimming / QA/QC (Trimmomatic, cutadapt, FASTQC/MultiQC)

## 5. Microbiome Sequencing Processing Pipelines

- Introduction to R
  - Installing R packages
  - R- DADA2 Processing pipeline
  - Going deeper with indexing
- Processing with DADA2 using the QIIME2-cli / R 3.6.1 environments
  - Setting up our working environment
  - Quality trimming/filtering
  - Generating an error model of our data
  - Dereplication
  - a conversation about OTUs vs ASVs
  - read pair merging
  - Generating a count table
  - Chimera identification (chimeraslayer)
  - Overview of counts throughout
    - Assigning taxonomy (silva132, rdp, greengenes)
    - Extracting the standard goods from DADA2
    - Removing likely contaminants (decontam)

## 6. Microbiome Analysis in R

- Taxonomic summaries
- Diversity Indexes (Alpha and Beta)
- Betadisper and permutational ANOVA
- Differential abundance analysis with DESeq2

## 7. Other Analysis / Visualization tools

- Galaxy
- LEFSE
- Metacoder
- Docker for Bioinformatics

## 8. Pipeline containerization using nextflow/nf-core

## 9. A brief overview of shotgun metagenomic sequencing

