

- Basic Unix
 - Getting started
 - Files & directories
 - Redirects & wildcards
 - Six glorious commands
 - Bash variables and for loops

- Basic GitHub
 - Underdevelopment

- Python
 - What is Python?
 - Introduction to tech used in lessons
 - Syntax & print statements
 - Data types
 - Setting up loops
 - User input/output
sys.argv vs argparse
 - Sorting
 - Modularization via functions
 - Writing & running scripts
 - Defensive programming
 - Invoking libraries
 - Biopython

- R
 - Introduction & RStudio Cloud
 - Basics in R
 - Import data and summarizing data
 - Data wrangling -basics
 - Intro to ggplot2
 - Data wrangling +ggplot2
 - Advance ggplot2
 - Introduction to functions
 - R tutorials -Amplicon analysis with phyloseq
 - R tutorial -Estimating diversity and statistical analysis
 - R tutorials -microbiome time-series

- Functional Annotation
 - Predicting ORFs
 - Orthology annotation
 - HMM annotation
 - Pipeline options for annotating microbial genomes
 - KEGG
 - CAZy
 - MEROPS
 - anitSMASH
 - OrthoMCL & inParanoid
 - Confirming functional orthologs
 - NCyc
 - FeGenie
 - Subcellular localization
 - Prophage & Mobile elements

- Amplicons/eDNA
 - Introduction
 - Preprocessing data
 - Using count tables -phyloseq
 - Advanced -Test selection
 - Advanced -Vegan
 - Advanced -Ordination & Hierarchical clusterings
 - Advanced -Differential abundance analysis

- Metagenomics
 - Introduction
 - Taxonomic classification -kmers
 - Taxonomic classification -sketches
 - Taxonomic classification -mapping
 - Assembly
 - Assembly Visualization
 - Binning
 - Evaluating bins
 - Phylogenomics
 - Workflows
 - Workflow demos
 - Leveraging an HPC
 - Publication
 - Funding!

- Transcriptomics
 - Introduction
 - Caveats
 - Mapping reads
 - Differential expression
 - Assembly
 - Assembly quality assessment

- Networks
 - Building a network from abundance data P1
 - Building a network from abundance data P2
 - Looking at your network in a GUI
 - Analyzing your network in a GUI
 - Basic network analysis
 - Visualization in R

- Pop gen & comparative genomics

- Data Viz

