

Online Bioinformatics Training Workshop Schedule and Assignments

Note: Some of the reading assignments refer to a section in the guide with multiple pages. Participants should read all of the pages in the assigned section.

*Annotation Outline is an outline of much of the rest of the guide and is intended to be a quick reference. You are not responsible for reading all of the linked pages in this section; merely should note the organization.

Day	Live Sessions	Pre-session Readings	Short Videos	Computer
1	<ul style="list-style-type: none"> Welcome and Overview 	<ul style="list-style-type: none"> Introduction Annotation Outline* Genome annotation Overview Decision Trees Mechanics: DNA Master part I (through "Generating a rough draft...") 	<ul style="list-style-type: none"> Setting DNA Master Preferences Autoannotation BLASTing your genome in DNA Master Saving your DNA Master file 	<ul style="list-style-type: none"> Auto-annotate and BLAST Ellie in DNA Master Save File
2	<ul style="list-style-type: none"> Genome Overview Compare genomes using Phamerator Compare using BLASTN on phagesdb.org 	<ul style="list-style-type: none"> Guiding principles Interpreting Phamerator maps Mechanics: Phamerator Mechanics: Other 	<ul style="list-style-type: none"> Phagesdb tour Phamerator overview GeneMark output Aragorn output tRNAscanSE output 	<ul style="list-style-type: none"> Generate GeneMarkS and GeneMark host files. Generate Aragorn and tRNAscanSE outputs. Phamerator map of Ellie and others
3	<ul style="list-style-type: none"> Call genes 5-10 Choosing starts 	<ul style="list-style-type: none"> Evaluating gene predictions Evaluating gene starts Mechanics: DNA Master part 2 	<ul style="list-style-type: none"> Using Starterator GeneMark Overview Other DNA Master videos 	<ul style="list-style-type: none"> Call genes 11-25 in DNA Master.
4	<ul style="list-style-type: none"> Functions Review first 10 genes 	<ul style="list-style-type: none"> Bacteriophage Biology Predicting Phage Gene Functions Cluster specific forums Official Function List Databases 	<ul style="list-style-type: none"> Using HHPred SEA-PHAGES Forums tour 	<ul style="list-style-type: none"> As many genes as you can call
5	<ul style="list-style-type: none"> Office hours 	<ul style="list-style-type: none"> Predicting tRNAs Documenting your annotation Case Studies 	<ul style="list-style-type: none"> Frameshift tRNAs 	<ul style="list-style-type: none"> As many genes as you can call

6	<ul style="list-style-type: none"> Sequencing Black Box/What's in a name? Review of genes (participant choice) 	<ul style="list-style-type: none"> Reviewing Gaps Quality control Bioinformatics Basics Programs 	<ul style="list-style-type: none"> Checking the Gaps and Functions Genome profile 	<ul style="list-style-type: none"> Finish genome
7	<ul style="list-style-type: none"> Graham Hatfull Difficult genes/features Revisit notes 	<ul style="list-style-type: none"> Last Call Submitting your files to phagesdb How to pass preliminary QC 		<ul style="list-style-type: none"> Finish genome
8	<ul style="list-style-type: none"> File submissions Investigating clusters PECAAN 	<ul style="list-style-type: none"> PECAAN Review to Improve 	<ul style="list-style-type: none"> Making your submission files Submitting your annotation 	<ul style="list-style-type: none"> Generate the files for file submission
9	<ul style="list-style-type: none"> Annotation QC— behind the scenes Review to Improve Where and when to ask questions 	<ul style="list-style-type: none"> SEA-PHAGES DLP forums 	<ul style="list-style-type: none"> Review to Improve 	<ul style="list-style-type: none"> Review to improve Brainstorm DLP delivery
10	<ul style="list-style-type: none"> Pedagogy and DLP Wrap UP 			