Online Bioinformatics Training Workshop Schedule and Assignments
December 6 – 17, 2021, 11:00AM – 1:00PM

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 note the organization.

Week 1

Day December	Live Sessions	Pre-live Session Readings	Short Videos	Tasks
6th	• Welcome and Overview	• Introduction • Annotation Outline* • Genome annotation Overview • Decision Trees • Mechanics: Part 1(through "Generating a rough draft…)	• Auto-annotation • BLASTing your genome in DNA Master • Saving your DNA Master file	• Auto-annotate and then BLAST Madiba in DNA Master • Save File
7th	• Genome Overview • Compare genomes using Phamerator • Compare using BLASTN on phagesdb.org	• Guiding principles • Mechanics: Phamerator • Mechanics: Other	• Phagesdb tour • Phamerator overview • GeneMark output • Aragorn output • tRNAscanSE output	• Generate GeneMark S and GeneMark host files • Generate Aragorn and tRNAscanSE outputs. • Phamerator map of Madiba and others
8th	• Call genes 6-12 • Choosing starts • Record keeping	• Evaluating gene predictions • Evaluating gene starts • Mechanics: DNA Master	• Using Starterator • GeneMark output overview • Other how-to DNA Master videos	• Call genes 13-30 in DNA Master.
9th	• tRNAs • Programmed frameshift • 30 genes (participant's choice) • Call some reverse genes	• Predicting tRNAs • Frameshift	• Frameshift • tRNAs	• As many genes as you can call

10th	• Bacteriophage Biology (what genes to expect) • Functions • Documenting gene calls	• Bacteriophage Biology • Predicting Phage Gene Functions • Case Studies • Cluster specific forums • Official Function List • Databases	• Using HHPred	• As many genes as you can call • Assign functions

Week 2

13th	• Sequencing Black Box/What's in a name? • Check your work!	• Reviewing Gaps • Quality control • Bioinformatics Basics • Programs	• Make genome profile	• Make genome profile & map
14th	• Check gaps • Difficult genes/features	• Checking gaps	• Checking the gaps	• Keeping working on the genome, review the first genes that you called
15th	• Calling more genes • Graham			• Finish genome
16th	• File submissions • Annotation QC—behind the scenes • Review to Improve • Where and when to ask questions	• Submitting your files to phagesdb • SEA-PHAGES forums • Review to Improve	• Making your submission files • Submitting your annotation • Review to Improve	• Generate the files for file submission • Review to Improve
17th	• Investigating clusters • PECAAN • Pedagogy	• PECAAN		•