

SEA-PHAGES
Bioinformatics
Workshop
December 5, 2016
OVERVIEW

WORKSHOP OBJECTIVES

Participants will be able to:

- **Characterize and investigate mycobacteriophage genomes.** This includes the details of gene calling evaluation, functional assignments, preparing a final product of a submission file **that meets QC requirements.** This year's genome is Mycobacteriophage CrystalP.
- **Install and use the software** for annotation / analyses of mycobacteriophages. The software includes DNA Master, Phamerator, and other web-based tools.
- **Identify the basic concepts** that underpin the bioinformatics of phage biology.
- **Explore classroom implementation strategies**

Primary learning method is:

- Learn by doing
 - Gather the data.
 - Do the work: annotate & analyze the genome.
 - Do science like scientists do it.
[Translation: new technology changes at a moment's notice]

Focus of the week's work:

- Annotate Mycobacteriophage CrystalP's genome
 - Learn to manipulate the tools we use:
 - DNA Master
 - GeneMark
 - BLAST
 - Phamerator
 - Hhpred
 - Starterator
- Produce a **quality** genome annotation
 - Sequence quality control
 - Annotation quality control

Further analyses:

- Sequencing & Finishing of the genomes
 - Consed & Assembly
- Gene functions
- Bioinformatic comparative analyses

Final Product of the week:

- Submit the genome to GenBank

Logistics

- Name badges must be worn at all times
- Restrooms
- No roaming through the building
- Questions? – Ask Pitt or SEA staff
- Refreshments (keep to the schedule)
- Technology
 - Live Streaming
 - The microphones
 - ClickShare