**Introduction to Actinobacteriophage Bioinformatics** Performing Preliminary Functional Assignments Using Phams

**Objectives**

Participants will be able to:

* access and search the on-line Bioinformatics Guide.
* use PhagesDB to assign preliminary functions to actinobacteriophage genome features.
* use Phamerator to contextualize the ‘draft functions’ of a genome.
* describe overall architecture of an actinobacteriophage genome.
* recognize that supporting evidence is needed to make a scientific claim for each gene’s function.

**Goals**

To assign preliminary functions to the auto-annotated genes of Microbacterium phages [Gershwin](http://phagesdb.org/phages/Gershwin/) and [Efeko](http://phagesdb.org/phages/Efeko/).

**Guiding Questions**

What genes does a phage need to be a phage?

How are functions assigned?

How can comparative genomics help to assign functions?

What is the supporting evidence for your claim?

**Background**

SEA-PHAGES is a two-semester course that can simply be divided into two tasks:

1. Find a phage and send DNA to be sequenced.
2. Upon receipt of a sequenced genome, annotate the genome.

Annotating a genome consists of identifying the features that are found in that genome, including protein coding genes, tRNAs, tmRNAs, and other special features.

For each open reading frame or region of nucleotide sequence, you must answer three questions.

* 1. Is it a gene?
  2. What is its start?
  3. Does it have a function?

For tonight’s activity, we are going to focus on “Does each gene have a function?”

**Task**

Using PhagesDB and Phamerator, *preliminarily* assign as many functions as you can to the genes in the phage genomes Gershwin and/or Efeko.

**Procedure**

1. Using the [Bioinformatics Guide](https://seaphagesbioinformatics.helpdocsonline.com/home), locate “[Preliminary Function Assignment Using Phams](https://seaphagesbioinformatics.helpdocsonline.com/article-29)”. Follow the procedure outlined, and add as many functions as you can to the genome maps provided. Take note of conflicts or uncertainties for future discussion.
2. Once you have found as many functions as you can, look at the genomes at [Phamerator.org](http://phamerator.org/). Find an overview of Phamerator [here](https://seaphagesbioinformatics.helpdocsonline.com/article-15). Search the guide to find the “How do I make a Phamerator Map” article, and then compare your genomes to close relatives.