**Initial Genome Investigation**

During this workshop, we will be working with the genome of Schubert, which was found at the University of Pittsburgh. The goal of this investigation is to learn about the context of your genome of interest, and to be introduced to PhagesDB and Phamerator.

Go to PhagesDB. (<http://phagesdb.org/>)

1. How long is the genome of Schubert?
2. What is the cluster and subcluster assignment of Schubert?
3. What are the two phages most closely-related to Schubert? (Hint: BLAST)

Go to Phamerator. (<http://phamerator.org>)

1. If you don’t have a Phamerator account, create one.
2. Go to **Genome Maps**. Select the genomes of Schubert and its two closest relatives. Click **View Map**.

On Phamerator maps, each gene is represented by a box either above (rightwards-transcribed) or below (leftwards-transcribed) the genome. Boxes are colored according to the gene Phamily (Pham) to which they belong.

1. What are your overall impressions of these genomes in terms of number of genes, amount of coding vs non-coding space, variation in length of genes or genomes, transcription directions, similarity to one another, etc.?
2. In Schubert, approximately what percentage of genes are transcribed leftwards?
3. Find a gene that is absent from Schubert but present in at least one of its two most-closely related genomes.
4. Which gene in Schubert likely codes for its “major capsid protein”?
5. What is the longest gene in the Schubert genome and what does it do? What is the second longest gene and what does it do?
6. Are there any Schubert virion structure and assembly genes (i.e. capsid, tail etc) that are transcribed leftwards?

Above or below each gene’s box are two numbers. The first number identifies the gene phamily (pham) to which that gene belongs. The second number (in parentheses) tells how many members of that pham exist in this entire database. A gene is considered an orpham (and colored white) if it is the only member of its phamily. Any pham can be further investigated at <http://phagesdb.org/phams/>

1. What pham does Schubert gene *55* belong to? Find that pham on PhagesDB. What are the functional assignments of some of that pham’s members?
2. Does Schubert have any orphams? If so, which gene(s)?
3. In Phamerator, return to the Select Genomes tab. Select Schubert as well as one phage from each EA subcluster, then View Map. Do genomes in the same cluster have the same overall organization? How do the EA subclusters differ?