**Initial Genome Investigation**

During this workshop, we will be working with the genome of RagingRooster, which was found during the 2017 workshops. 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 RagingRooster?
2. What is the cluster and subcluster assignment of RagingRooster?
3. What are the two phages most closely-related to RagingRooster? (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 RagingRooster, its two closest relatives, and phage Phaedrus. 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 RagingRooster, approximately what percentage of genes are transcribed leftwards?
3. Find a gene that is absent from RagingRooster but present in at least one of its two most-closely related genomes.
4. Why is Phaedrus shorter than the other genomes?

In Phamerator, if a gene has been assigned a function, that function will be written above that gene’s box (for forward genes) or below that gene’s box (for reverse genes). Genomes whose name includes “\_Draft” have only been auto-annotated, and will not have any functions called. Genomes without the “\_Draft” suffix are final annotations with functions.

1. Which gene in RagingRooster likely codes for its Major Capsid Protein?
2. What is the longest gene in the RagingRooster genome and what does it do?
3. Are there any RagingRooster 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 RagingRooster gene *55* belong to? Find that pham on PhagesDB. What are the functional assignments of some of that pham’s members?
2. Does RagingRooster have any orphams? If so, which gene(s)?
3. In Phamerator, return to the Select Genomes tab. Select all Cluster B3 phages, as well as one phage from each of B1, B2, B4, B5, B6, and B7, then View Map. Do genomes in the same cluster have the same overall organization?