**Bioinformatics Workshop Learning Objectives and Resources**

**Workshop Day 3: Wednesday December 11th**

Data obtained and analyzed today will answer the questions:

* What is the gene’s function?

| **Category** | **Topic** | **Learning Objective** | **Resources** |
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| **Phage Biology** | Review of Protein Structure | Describe the structure and function of proteins and amino acids in bacteriophages | [Protein structure and function basics](https://seaphagesbioinformatics.helpdocsonline.com/article-92) |
| Phage-Specific Functions and Genome Organization | List functions present in almost all bacteriophage genomes | [Functions present in (almost) all bacteriophage genomes](https://seaphagesbioinformatics.helpdocsonline.com/article-91) |
| Describe the basic architecture of the bacteriophage genome | [Bacteriophage Gene Functions](https://seaphagesbioinformatics.helpdocsonline.com/article-5) |
| Explain structural gene synteny in bacteriophage genomes | [Using synteny to assign gene function](https://seaphagesbioinformatics.helpdocsonline.com/article-90) |
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| **Mechanics** | Acquiring Data | Perform a preliminary function assignment of the genes in a phage genome  | [Preliminary function assignment using phams](https://seaphagesbioinformatics.helpdocsonline.com/article-29)[Predicting phage gene functions](https://seaphagesbioinformatics.helpdocsonline.com/article-39) |
| Perform database searches (BlastP-PhagesDB, BlastP-NCBI, BlastP-DNA Master, Conserved Domain Database, and HHPred) for matches to a phage protein sequence | [BLASTP at NCBI (GenBank)](https://seaphagesbioinformatics.helpdocsonline.com/article-59)[BLASTing (or re-BLASTING) a single gene on DNA Master](https://seaphagesbioinformatics.helpdocsonline.com/article-57)[Using Conserved Domain Database BLAST matches to assign functions](https://seaphagesbioinformatics.helpdocsonline.com/article-32)[Aligning your protein sequence using HHPred](https://seaphagesbioinformatics.helpdocsonline.com/article-71) |
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| **Data Analysis** | Proposing a Function for a Gene | Synthesize a proposed functional assignment for a gene using:* BlastP results from PhagesDB, NCBI, and DNA Master
* The Conserved Domain Database
* HHPred
 | [Using BLASTP to assign/refine/support functions](https://seaphagesbioinformatics.helpdocsonline.com/article-30)[Using Conserved Domain Database BLAST matches to assign functions](https://seaphagesbioinformatics.helpdocsonline.com/article-32)[Using HHPred to assign functions](https://seaphagesbioinformatics.helpdocsonline.com/article-43) |
| Refining Functional Assignments | Refine a proposed gene functional assignment by weighting the quality of database entries and results from BlastP (PhagesDB, NCBI, and DNA Master), the Conserved Domain Database, and HHPred | [Evaluating the quality of the database entry](https://seaphagesbioinformatics.helpdocsonline.com/article-87) |
| Evaluate a proposed functional assignment in the context of genome organization (synteny) | [Using synteny to assign gene function](https://seaphagesbioinformatics.helpdocsonline.com/article-90) |
| Determine if a proposed functional assignment is phage-appropriate and on the SEA-PHAGES approved functions list | [Official SEA-PHAGES function list](https://seaphagesbioinformatics.helpdocsonline.com/article-96) |
| Evaluate a proposed functional assignment for a gene in the context of the entire bacteriophage genome, the hierarchy for assigning gene functions using alignment, and the guiding principles of annotation | [Guiding principles of annotation](https://seaphagesbioinformatics.helpdocsonline.com/article-27)[Hierarchy for assigning gene functions via alignment](https://seaphagesbioinformatics.helpdocsonline.com/article-35) |
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| **Annotating Special Cases** |  | Locate and use information in the Online Bioinformatics Guide to annotate special cases, including programmed translational frameshifts, genes with introns, and genes that cross the first base pair of the genome | [Annotating Programmed Translational Frameshifts](https://seaphagesbioinformatics.helpdocsonline.com/article-54)[Annotating Genes with Introns](https://seaphagesbioinformatics.helpdocsonline.com/article-53)[Annotating Genes that Cross bp1 of the Genome](https://seaphagesbioinformatics.helpdocsonline.com/article-55) |