**Bioinformatics Workshop Learning Objectives and Resources**

**Workshop Day 2: Tuesday December 10th**

Data obtained and analyzed today will answer the questions:

* Is it a gene?
* Where does it start?

| **Category** | **Topic** | **Learning Objective** | **Resources** |
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| **Phage Biology** | Exploring Phage Genomes | Identify the cluster and sub-cluster of a phage  | [Actinobacteriophage Database](https://seaphagesbioinformatics.helpdocsonline.com/article-9) |
| List some common characteristics of all phage genomes | [The Guiding Principles of Bacteriophage Annotation](https://seaphagesbioinformatics.helpdocsonline.com/article-27)[The Basics: Functions Present in Almost All Genomes](https://seaphagesbioinformatics.helpdocsonline.com/article-91) |
| List some ways in which phage genomes differ both within a cluster and between clusters | [Phage Cluster List at PhagesDB](https://phagesdb.org/clusters/) |
| Biological Information Flow in Phages | Identify one potential hypothesis explaining why a phage genome may contain tRNA genes  | Refer to posted slides from the “Biological Flow of Information” presentation |
| Outline the flow of biological information in a bacteriophage |
| Diagram the structure of a typical prokaryotic single gene and an operon  |
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| **Mechanics** | Acquiring Data | Draw a genome map of related phage genomes using Phamerator | [Making Phamerator maps](https://seaphagesbioinformatics.helpdocsonline.com/phameratormaps) |
| Generate a GeneMark coding potential graph for your phage genome | [Running GeneMarkS on PhagesDB.org](https://seaphagesbioinformatics.helpdocsonline.com/untitled-17)[Running the online versions of GeneMark](https://seaphagesbioinformatics.helpdocsonline.com/article-68) |
| **Mechanics** | Acquiring Data | Run tRNAScan-SE and Aragorn to identify potential tRNA genes in your genome | [Predicting tRNA and tmRNA genes](https://seaphagesbioinformatics.helpdocsonline.com/article-40)[Running the online version of Aragorn](https://seaphagesbioinformatics.helpdocsonline.com/article-56)[Running tRNAScan-SE online](https://seaphagesbioinformatics.helpdocsonline.com/article-83) |
| Obtain the Starterator report for a pham | [Starterator](https://seaphagesbioinformatics.helpdocsonline.com/article-23)[Starterator Pham Reports](https://seaphagesbioinformatics.helpdocsonline.com/article-95) |
| Locate information in the Online Bioinformatics Guide on adding/deleting/changing the start site of genes | [Changing the Start Site of a Gene](https://seaphagesbioinformatics.helpdocsonline.com/article-61)[Adding a Gene](https://seaphagesbioinformatics.helpdocsonline.com/article-52)[Deleting a Gene](https://seaphagesbioinformatics.helpdocsonline.com/article-65) |
| Identify phages related to a genome by using BLASTn on PhagesDB and NCBI | [BLASTing your phage genome sequence against the Actinobacteriophage database](https://seaphagesbioinformatics.helpdocsonline.com/article-58) |
|  |  |
| **Data Analysis** | Annotation Refinement and Enhancement | Correctly evaluate a GeneMark coding potential graph to determine if a gene contains coding potential | [Interpreting the GeneMark output](https://seaphagesbioinformatics.helpdocsonline.com/article-38) |
| Evaluate a proposed start site using BLASTp alignments | [Using BLASTp to Inform Your Start Coordinate Choice](https://seaphagesbioinformatics.helpdocsonline.com/article-88) |
| Evaluate whether a given start site is conserved within a pham | [Interpreting Starterator Reports](https://seaphagesbioinformatics.helpdocsonline.com/article-37) |
| Examine a potential start site in the context of ribosome binding sites | [Evaluating Ribosome Binding Sites](https://seaphagesbioinformatics.helpdocsonline.com/article-33) |
| **Data Analysis** | Annotation Refinement and Enhancement | Determine if a gene call is well-supported within the context of the entire bacteriophage genome  | [Evaluating protein coding gene predictions](https://seaphagesbioinformatics.helpdocsonline.com/article-28)[Evaluating Start Codons in Protein Coding Genes](https://seaphagesbioinformatics.helpdocsonline.com/article-34)[The Guiding Principles of Bacteriophage Annotation](https://seaphagesbioinformatics.helpdocsonline.com/article-27) |
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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) |