

What's New for School Year 2015-16 in Phage Genome Annotation

Created by DJS November 2015.

The purpose of this document is to target the most prominent changes and/or updates to DNA Master Annotation Guide. Happy Annotating!

We have purposefully chosen to make no major changes to the annotation guide this year. DNA Master has been updated since our last revision (November 2014). DNA Master is now at version 5.22.21 Build 2466 1 Sept 2015. You can find your current version by going to **Help -> About**. Instead, we ask that you focus on producing better annotations because you are familiar with the process and requirements.

Merge

Changes in DNA Master are minimal. The build used for the current annotation guide was Version 5.22.19 Build 2448, dated 13 June 2014. The only change that I can point to is the location of the **Merge** function. The **Merge** function is now located **File -> Process -> Merge**.

Formal cover sheet

Annotation submissions now require a formal cover sheet that includes information like the submitter's name and email address, etc. Please use the formal cover sheet with all annotation submissions from now on. The cover sheet is available on seaphages.org under Faculty Documents.

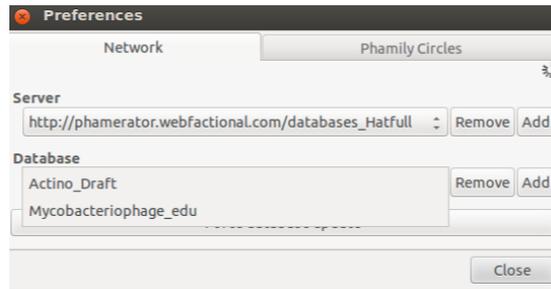
Additional Hosts

If you are annotating additional hosts, you will find the heuristic model for GeneMark most helpful (GeneMarkS, trained on self). GeneMark may not have the sequence files of the species or strain that you are using in the lab. Still look at the outputs of related hosts. They may prove helpful. Know that PhagesDB does not provide the one button approach to the additional hosts analyses. You will need to follow the protocols in Section of the manual Do not overcall genes. Please make sure you have evidence to call a gene rather than filling a space. You may not want to limit your exploration to a single host. Know that if you use the GeneMark graphic output, you are looking at the same piece of data that is imported into the DNA Master file.

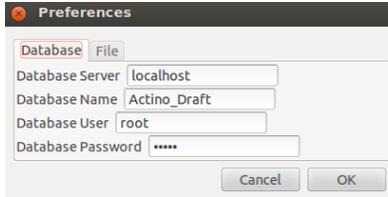
Phamerator

We have consolidated all Actinobacteria phages into one Phamerator database, Actino_Draft. In addition to the Actino_Draft Database, we will continue to add 'fixed' datasets as we publish. In any given paper that uses a Phamerator data, a fixed database (with a unique name) is identified in the methods section of a paper. In addition, if you are using Etude as a teaching tool, you will find it in a separate database, Mycobacteriophage_edu*.

*To change databases in Phamerator, go to Preference :



If using Starterator, make sure that you have it pointed at the correct database. Go to Edit -> Preferences:



The remainder of this document is the What's New information since 2012 provided as a handy reference.