**IT22700 Biotechnology Lab II**

**Final Paper**

**Final Draft Due: Wednesday, May 3, 2017**

Each student should submit their own unique paper.

Prepare a final scientific paper communicating your research findings from the semester.

Your final paper should look like a journal article, including 2 columns and figures integrated throughout with appropriate titles. The following research paper describing the genomic analysis of a mycobacteriophage uses similar techniques and can be used as an example. You can access this paper from any Purdue computer.

Pham, T., Sera-Jacobs, D., Pedulla, M., Hendrix, R., and Hatfull, G. (2007) **Comparative genomic analysis of mycobacteriophage Tweety: evolutionary insights and construction of compatible site-specific integration vectors for mycobacteria**. 153: 2711-2723.

Accessed at: <http://www.microbiologyresearch.org/docserver/fulltext/micro/153/8/2711.pdf?expires=1461163560&id=id&accname=guest&checksum=B2A82559C1DE457FD69586288D0C1135>

Points for the final paper will be assigned as follows:

|  |  |
| --- | --- |
| Introduction | 20 |
| Materials and Methods | 20 |
| Results | 30 |
| Discussion | 20 |
| Literature Cited | 10 |
| **Total** | **100** |

**In addition to the format from the sample journal article, the following briefly address important topics to consider for each section:**

**Introduction**

* What are mycobacteriophage?
* Why is it important to study mycobacteriophages?
  + Why is our research significant?
* What is known about mycobacteriophages and specifically genomic analysis?
  + What research has already been done in comparative genomic analysis?
  + How are mycobacteriophage genomes characterized?
* What is known specifically about the mycobacteriophage you worked on this semester?
* What is known about the cluster that your mycobacteriophage is assigned to?
* What are you doing and why? How will your efforts contribute to the existing gap in knowledge, or what we know about mycobacteriophages?
* At least 5 primary sources (peer-reviewed journal articles) are required to support your statements

**Methods**

What have you done this semester? Your methods should have enough detail so that someone could repeat your experiment but you should not copy the protocols directly from your lab book. You should cite resources for your protocols and the software that you used to conduct the genome annotation, in silico experiments and bioinformatics analysis. Follow the appropriate format for a scientific article.

* Phage isolation and genome sequencing, including the bacteria strain
* Bioinformatics analysis----describe the different databases and software that you used
* Include appropriate references to support your methods

**Results**

What data did you collect this semester? Your data should correspond to your methods section and should be presented as figures with titles and legends. You should be able to provide evidence of:

* + Auto-annotation in DNA Master and Phamerator
  + Annotation of genes, including start sites
  + Functional annotation with BLAST, PhagesDB, HHPRED, Phamerator
  + Additional characterization to predict function
  + Quality control with genome annotation using PECAAN

**Discussion**

In addition to providing data, you should also discuss and provide an analysis of your results. Tell the story of the work you have done this semester.

Your discussion should mirror your introduction and provide a conclusion to the story you began in the beginning as you presented what is known and unknown in the field. What is the impact of your results on the field? What are the future directions for your research? If you had more time, what do you think would be the most interesting and/or most productive next step, based upon your findings and the existing gaps in knowledge?