**IT227 Biotechnology Lab 2**

**Spring 2017**

**Reflection 2**

**Due Wednesday, March 1 2017**

Kathryn Atherton

**Call for Participation in the Howard Hughes Medical Institute Science Education Alliance Phage Symposium**

The 2016 8th Annual SEA-PHAGES Symposium will be held on **June 9-11, 2017, Janelia Research Campus** in Reston, VA. The primary focus will be on the scientific developments during the past year. We need two students to represent the research conducted at Purdue University this year.

* Are you interested in attending and available from June 9-11 to travel to the HHMI SEA Symposium and willing to help prepare the presentation?
  + No, I am unavailable.
* If you are interested in attending, please write a brief paragraph explaining why you want to represent Purdue at the HHMI symposium and also what you hope to gain from attending the conference and how it will impact your professional development. Depending upon the number of interested participants, you may be asked to present a research summary from the past year to the class. Participants will be selected based upon their written rationale, their presentation and feedback from their fellow classmates, peer leaders and instructional faculty.

Each school participating in the 2017 Symposium is also expected to submit one scientific abstract about bacteriophage work accomplished this year to be considered for a student-delivered scientific talk; all student(s) will present a poster on this work at the Symposium. **The abstract is due on April 25, 2017**. We will work together to prepare an abstract.

Decisions for the conference must be made quickly since space is very limited and registration will close in mid-March. We will need to select the participants by Thursday, March 16.

**Questions for Individual Reflection:**

Please reflect on your genome annotation work thus far and the group presentations from last week, using the following questions as a guide:

* What section of genome were you assigned? How many genes were auto-annotated? How many genes did you call in your final draft?
  + My group was assigned the last section of the genome: 40900-50341 bp.
  + 24 genes were originally called.
  + We called 23 genes in the final annotation.
* What were the general characteristics of your section of genome? Interesting findings? What phages seemed most similar based upon recurrence in BLAST homology searches?
  + All of the features called in the final annotation were in the backward direction in the complementary strand.
  + The start codon frequency was similar to the Annotation Guide’s recommendations (8.7% TTG, 37.1% ATG, 52.2% GTG).
  + Most of the BLASTp results were hypothetical proteins, unfortunately. More wet-lab data will be required to confirm the decisions made for the annotation.
  + The phages most closely related to JewelBug were VohminGhazi, Isiphiwo, McFly, Kazan, CloudWang9, and Artemis2UCLA.
* Provide an overview of major changes that you made to the auto-annotation.
  + The biggest changes made were adding a feature (72.5) and deleting two forward-running features (87 and 89).
  + Feature 72.5 was added as there was a large gap (119 bp) between features 72 and 73 and coding potential was found in the area in GeneMark.
  + Features 87 and 89 were deleted due to a lack of evidence supporting their existence. Between the two features, there was one poor BLASTp result, there were not analogous genes in similar phamerator maps to allow for a comparison between the genes, and there was little to no coding potential in the areas where the genes were suggested to be called by DNAMaster. Additionally, there was not enough space surrounding the genes to merit a reversal of direction and the three features surrounding the genes (86, 88, and 90) had much stronger evidence supporting their existence.
* What issues or challenges did you face? Are there genes that you encountered where the evidence was not clear or there are multiple options for the final gene call?
  + One major issue faced was that of Feature 75. The original call left a large gap following the gene (161 bp), had mediocre BLASTp results and Shine Dalgarno scores, and had plenty of room to extend the ORF in order to cover more coding potential. Longer ORFs were tested and better BLASTp results and Shine Dalgarno scores were found, but the best option found had too large an overlap with Feature 76, so the original call was kept.
  + It was recommended that we continue looking into the longer call, as it has better evidence. The guiding principles can be ignored if there is enough evidence to overrule it.
* Based upon the feedback from the class, do you think you need to further review the changes?
  + I don’t think so. I think we looked at a lot of evidence and really supported all of our decisions in order to make the best annotation we could.
* Are there any additional issues or challenges you faced?
  + We had some issues with large gaps between genes due to deletions that could not be filled by extending genes.
  + We may look into adding more features, if at all possible.
* What additional thoughts do you have about your section of the genome in context of the rest of the genome, in light of the findings presented by others?
  + I found our section of the genome to have a lot more genes than other sections, despite having quite a few large gaps. This is probably due to having shorter genes than most other groups. Some other groups had a lot more cut and dry decisions to make. Most of the DNAMaster calls were accurate, whereas our group had to make more changes than most.
* Provide an overview of the functions you have annotated thus far for your section of genome.
  + Most of the functions are unknown at this time, unfortunately.
  + For the known functions, we had a couple of helix-turn-helix domains, an antirepressor, a resuscitation-promoting factor RpfA, an exonuclease/helicase, a DNA Methyltransferase, a DNA Methylase,
* What do you think would be an interesting project to explore further through advanced bioinformatics analysis? Is there a research paper and/or additional bioinformatics resources beyond those that we have used thus far in class that could help guide you and provide a rationale for your project?
  + I think that annotating the genome of the phage that I discovered would be very interesting! I really enjoyed isolating it in the wet lab, so characterizing it further would really be amazing, because I would be able to see the phage through the entire research process.
  + We talked about Starterator towards the beginning of the semester, but have not used it yet to help us determine our starts. Yi recommended making a few changes to our annotation, so maybe with Starterator data we could see why he feels that his recommendations are more viable.
* Do you think that the work you have done thus far in the semester is research? Why or why not?
  + Yes, I do think that this is research! We have been running tests and coming up with new conclusions that will help other scientists draw conclusions in the future. This is new The annotation we have made as a class will be evidence for future annotations of similar phages.