IT227 Biotechnology Lab II

Spring 2017

Reflection 1

Due Friday, February 10

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Now that you have been immersed in the research project for this semester and become familiar with the software and technology we will be using as our research tools this semester, consider the following questions and answer as if you were providing an explanation to a fellow classmate that is not enrolled in this course:

* What is a gene?
  + A gene is a section of DNA that codes for a certain protein that an organism needs to produce for a certain function of life.
* What does it mean to “call a gene?”
  + “Calling a gene” means that one determines whether or not a certain section of DNA is a viable gene, as well as exactly where in the DNA the start and stop positions are most likely placed so that the organism can use that code for the protein production.
* How do you annotate a genome?
  + One annotates a genome by analyzing the sequence of DNA and finding start and stop codons which could potentially be the endpoints of a gene. After that, the potential genes are compared to a database of sequenced genes from other organisms to determine if related organisms have similar features, which would verify its presence, as well as the many potential start positions for the gene (there can be more than one possible start site, but not more than one possible stop site). This information is then compared with a map of the coding potential and the genome map of other organisms that are closely related. One uses all of these sources to determine which potential start site is most likely to be used by the organism. The coding potential map shows which sections of DNA are most likely to have genes. One tries to incorporate as much of the coding potential as possible in the genes. The genome map is used to see how similar the genome is to related genomes. If multiple organisms have very similar features, this strengthens the probability that the features are genes in the organism being studied.

Reflect on your experience thus far and consider the following questions:

* What do you think is going well?
  + I think the group works together very well to debate and discuss the possibilities of each gene. We can depend on each other to work diligently and answer questions we have about confusing or difficult decisions we have to make about our section of the genome
* What suggestions do you have for improvement?
  + I think it would be nice if we got a little bit of feedback on a few of the more difficult decisions we have made about our section in order to ensure that we are fully understanding everything that we are doing and are on the right track for the future. I think we can also think more about the genome has a whole and how each of our genome sections fit together.
* What are you learning that you can apply to your current major/career interests?
  + I really want to do research in genetics as a career, so learning about the study of genetics with an organism that has a relatively small and basic genome is a good starting point.
* What is your greatest take away or “aha” moment?
  + I think once we talked about the order in which we should look to various data sources and the order of precedence of various data points that we should look at when making decisions, I understood the process of decision making much more fully.
* What remaining questions do you have?
  + Is it possible that neither Glimmer nor GeneMark will call a gene used by the organism? There are some spots of our section of the genome that have large gaps with some coding potential in them, but do not have features called by either program.

The guidelines for your research paper will be posted next week and two of the sections you will need to prepare include both an introduction and conclusion.

It is important to find primary sources and references that provide background and rationale for addressing:

* why is this an important research problem,
* what is the current knowledge in the field,
* what are the existing gaps in knowledge and understanding,
* how do your results help address this gap and
* what are your ideas for future research based upon your results from the semester.

This week, we will begin to work together and collaborate to develop a list of annotated primary literature for the course that can help you begin thinking about the literature foundation of evidence you will provide for your introduction and conclusion in your research paper.

* Find a reference that you think is interesting and relevant to the phage research project.
* Next, post the Purdue libraries link with the citation in APA format to the Blackboard discussion board (you can access the Discussion Board from the link in the Blackboard course in the left-hand panel) so that others enrolled in the course can read it too.
* Then provide details in your post to answer the following questions:
  + Provide a brief summary of the paper.
  + Why did you select this paper?
  + What did you find interesting and how does it relate to the phage research project?

**Please copy the details that you posted in the discussion board and share in this reflection assignment for grading.**

Link: http://purdue-primo-prod.hosted.exlibrisgroup.com/primo\_library/libweb/action/openurl?date=2014&aulast=Hatfull&issue=3&isSerivcesPage=true&spage=e1003953&title=PLOS+pathogens+%3A&dscnt=2&auinit=GF&atitle=Mycobacteriophages%3A+windows+into+tuberculosis&url\_ctx\_fmt=null&sid=google&vid=purdue\_services\_page&volume=10&institution=PURDUE&issn=1553-7366&id=doi%3A10.1371%2Fjournal.ppat.1003953&dstmp=1486590435135&fromLogin=true

Summary: This review paper discusses a lot of the basics about Mycobacteriophages and how their discovery promotes furthering the field of genetics, especially surrounding tuberculosis. It also discusses potential applications of mycobacteriophages and the genetic information being analyzed.

Why I selected the paper: I selected this paper because it gave me a big-picture review of what the SEA-PHAGES project does for science. It is easy to get lost in the little details of the project as we look at individual genes, and this paper helped me to realized how what we do in class every Wednesday and Friday will provide key information for future research.

What I found interesting: I found the section on possible therapeutic applications of mycobacteriophage to be very interesting. I hope to one day do research in the field of medicine, so knowing that my research now could one day help scientists develop a new treatment for tuberculosis is amazing!

How it relates to our project: The paper directly describes how SEA-PHAGES has helped to develop knowledge about the huge diversity of mycobacteriophage and the possible applications of this knowledge.

This activity will help us build a cumulative bibliography among the class.

To begin thinking about the impact of your results and ideas for future research, here are some helpful resources to consider:

* iBioseminar from Professor Graham Hatfull entitled, “II. Bacteriophages: Genomic insights (<http://www.ibiology.org/ibioseminars/microbiology/graham-hatfull-part-2.html> )” and “III. Mycobacteriophage Genomics (<https://www.ibiology.org/ibioseminars/microbiology/graham-hatfull-part-3.html> )
* TedTalk “We can edit our DNA but lets do it wisely, (<http://www.ted.com/talks/jennifer_doudna_we_can_now_edit_our_dna_but_let_s_do_it_wisely?utm_source=newsletter_weekly_2015-10-24&utm_campaign=newsletter_weekly&utm_medium=email&utm_content=talk_of_the_week_button#t-93489> )by Jennifer Doudna, co-inventor of a groundbreaking new technology for editing genes. The tool, referred to as CRISPR-Cas9, allows scientists to make precise edits to DNA strands. It could lead to treatments for genetic diseases but there are also ethical considerations for this new tool.
* The following article was recently published and provides a great example for the potential impact of your research project this semester and the power of comparative genomics:
  + Watch the YouTube video: [Hatfull Nature Microbiology Paper Presentation](https://www.youtube.com/watch?v=KpLA6RkVRnc)
  + Read the paper: [Hatfull, et al Nature Microbiology Jan 2017: Prophage-mediated defense against viral attack and viral counter-defense](https://mycourses.purdue.edu/bbcswebdav/pid-8516755-dt-content-rid-34742215_1/xid-34742215_1)

If you are interested in exploring either of these topics in more detail, there are many recent publications on both phage genomics and the CRISPR system that can be accessed online through the Purdue Libraries.

There are also many resources at both the SEA PHAGES website and the Phages Database website that can help guide you as you work on your phage research project. In addition to the software links and annotation guide that you have been using, both sites also have a collection of primary research papers. These papers can help you begin thinking about the broader impact of your findings and how your work on this project fits into the bigger scientific community of phage researchers.

You can go to the SEA PHAGES website (<http://seaphages.org/> ) and select the “News/Pubs” tab to explore “publications”. Alternatively, you can go to phagesdb.org (<http://phagesdb.org/> ) and select “Publications” to explore the phage papers posted for reference on this website.