Kevin Wyllie's Reflection

Statement of Work

The goal of this project was to create a gene database for *Burkholderia cenocepacia* and to use this database for the purpose of conducting an analysis on microarray data generated by Van Acker et al (2013). This data measured the transcriptomic effects of tobramycin (an antibiotic) on the bacterium. The database was constructed using data from Burkholderia Genome Database, UniProt and Gene Ontology Consortium. The microarray data was taken from the paper, Biofilm-Grown *Burkholderia cepacia* Complex Cells Survive Antibiotic Treatment by Avoiding Production of Reactive Oxygen Species. Once the gene database (found here) was created, the processed microarray data (found here) were fed through a software called GenMAPP, which analyzed the data and returned significantly changed cellular processes (gene ontology terms - see above for files and results). We then compared the biological implications of our analysis to that of Van Acker et al (2013).

Assessment of Project

This project, I think, was a success. I can't speak for the QA and Coder (though the process seemed to go smoothly for them as well), but Veronica and I faced a healthy difficulty curve (substantial, yet reasonable) in processing and analyzing the microarray data. The only thing that "didn't" work for us was initially proceeding further than we should've with statistical analysis, which ended up being a waste of time as we had not properly accounted for the multitude of technical replicates within our data. But retracing our steps wasn't horribly difficult. To be quite honest, if I were to do this project again, the only thing I would change is that I would stress out about it less, because it was much easier than I had expected!

I believe the quality of our work was high. We got slightly ahead of schedule, and thus had more time afterward to carefully examine our methods and verify that we had processed the data correctly. The organization may have been the most difficult part at first, managing between my individual page and the group page. The requirements for the group page initially seemed overwhelming, but it wasn't a problem in the end. We certainly completed all of the "milestones" in this project. Again, this was not an issue because we overestimated the difficult of this project and thus spent ample time on it.

Reflection on the Process

- What did you learn?
    - With your head?
        - I learned a lot about the microbial response to certain antibiotics! But more broadly, this project gave me a deeper understanding of the importance of deeply comprehending the scientific reasons for carrying out each step in the process of analyzing results.

- With your heart?
  - I think this project taught me a lot about how to communicate with people of different skillsets. Although every student in the class did the same assignments before this project, upon beginning this project we each re-familiarized ourselves with the appropriate processes to carry out our specific roles (and, being busy college students, *only* those necessary processes). Thus, when communicating with Anu and Brandon, I had to find ways to explain my part of the project to someone who didn't know as much about the data processing protocols (and that's totally ok; it wasn't their responsibility to know these things, and this is mirrored in real workplace settings). Of course, when they communicated with Veronica and I, they had to water down their protocols as well.
- With your hands (technical skills)?
  - Every time I do microarray analysis-related tasks in Excel (whether in this class or with the Dahlquist Lab), it feels like I get a little better at it. And this project was no different. Excel, in general, is a skill that develops through repeated use, so that's certainly a technical skill I developed further. However, in this project we faced the added difficulty of knowing that nobody more experienced than Veronica and I would be checking our work as closely. So there was more pressure, but it just meant that we scrutinized our work more closely, which only added to the learning experience.
- What lesson will you take away from this project that you will still use a year from now?
  - A deeper understanding of the scientific principles behind microarray analysis, particularly with respect to how it is processed. While I may not be *carrying out* microarray analyses upon graduating from LMU (and thus graduating from the Dahlquist Lab), it seems like this technology will become even more pervasive within the field of biology, so and understanding of its inner-workings will be useful. Who knows? It may even become a standard method in medicinal science!