

Lab 3 – Part 2 Report

This report is worth 50 points. It is due on May 5 at 11:59 PM.

It should have two sections.

Section 1:

From the KEGG data results, what kind of functions does this bacteria perform? Does it have any unusual metabolic pathways? Are there any pathways that are populated in the KEGG pathways that seem surprising? Why are they surprising? Why do you think they are showing up in the annotation of the bacterial genome?

Section 2:

We also looked at antibiotic resistance genes in 6 different bacterial genomes. IN general, you should discuss the spread of antibiotic resistance genes across these genomes. Be sure to include answers to the following:

1. For each bacterial genome or assembly, what is the most common antibiotic resistance gene?
2. From the data, are there resistance genes that are commonly found in multiple bacterial species? Are there ones that you only see in one species of bacteria?
3. Do you think the *Staphylococcus aureus* that we used for assembly last week is methicillin-resistant? What evidence did you use to make that decision?

References

You should cite all the resources you used.