Genome Assembly and Annotation assignment

Using abyss to annotate the same gene, there were some key differences to note. Abyss covers regular GC content while SPAdes covered scaffold gc content. Spades has a coverage histogram in addition to misassemblies graph. Spades included cumulative number of genomic features, curve of genomic features, number of complete genomic figures. Overall, it seems SPAdes provided more data compared to Abyss.

QUAST is a useful tool to assess the quality of genome assemblies. Its metrics provide an insight into the quality, reliability, and accuracy of data. Some important metrics in QUAST include, but are not limited to:

* + 1. The total length of the genome
    2. Number of contigs
    3. Assembly continuity (contained in contigs)
    4. GC content
    5. Missassemblies
    6. Genome fraction (% aligned)

RAST - still downloading

A screenshot of a computer

Description automatically generated

A screenshot of your file organization showing that you generated all appropriate files and folders on your computer.

A screenshot of a computer

Description automatically generated

A screenshot of a computer

Description automatically generated