GitHub Link: <https://github.com/jmande1/bioinformatics>

Comparing SPAdes versus ABySS

There are a multitude of differences across the output between SPAdes and ABySS. Similarities though, are few, and thus would be easier to list them versus the latter. The following parameters are similar between SPAdes and ABySS: Reference GC (%), # scaffold gap ext. mis., # unaligned mis. contigs, complete and partial BUSCO (%), # c. translocations, # c. inversions, # scaffold misassemblies, # s. relocations, # s. translocations, # s. inversions, # unaligned mis. contigs, # fully unaligned contigs, fully unaligned length, and # partially unaligned contigs.

The important output metrics are the # contigs, the total sequence length, the contig N50, L50, GC content, total aligned length, and BUSCO results. For the # contigs, the output metrics are 191 and 150, respectively from Spades and Abyss. For the total sequence length (>= 0 bp), the output metrics are 4813654 and 4871123, respectively from Spades and Abyss. For the contig N50, the output metrics are 193475 and 272520 from Spades and Abyss respectively. For the L50, the output metrics are 8 and 6 from Spades and Abyss respectively. For the GC content (%), the output metrics are 52.13 and 52.19 from Spades and Abyss respectively. For the total aligned length, the output metrics are 4710913 and 4769483, from Spades and Abyss respectively. Interestingly, the results were identical with the complete BUSCO at 98.65% and the partial BUSCO at 0.00%.

A pie chart with many colors

Description automatically generated



A screenshot of a computer

Description automatically generated