BV-BRC Test Report

A1. Service – Genome Assembly - Bacteria

Item to test	Genome Assembly Service using bacterial read files and SRA accessions
URL	
Prerequisites	Bacterial Fasta contig files in Workspace
References	
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Test date	21-Apr-2022 (follow-up from original test)
Test result	**Passed**

Overview

- Test the Genome Assembly Service using exemplar reads sets for bacterial genomes.
- Test input options, i.e., single-end and paired-end read sets using files uploaded to the workspace and using an SRA run accession as input.
- Test the assembly strategies, i.e., Auto, Unicycler, SPAdes, Canu, MetaSPAdes, PlasmidSPAdes, and MDA.
- For each job submitted, verify successful completion of the job, presence of output files, and quality of the assembled contigs by comparing them with the same or closely related public genome.

Test Data

Dataset	Rational	Input Format	Input

- All test datasets and corresponding job results are available in the following public workspace:

Test Results

- All assembly jobs completed successfully, without any errors.
- All jobs resulted in expected output files in corresponding job output directory, providing assembly report in HTML format and assembled contigs in fasta format.
- The assembly report was informative and provided a concise summary of the input reads, assembly process and parameters used, iterative refining steps, filtering of the contigs based on minimum length and coverage, Quast report, and the reads used in the assembly. It also provided an assembly graph.
- For each of the genomes, the total length of the assembled contigs were as expected when compared to those in corresponding public genomes in PATRIC.

- All test datasets and corresponding job results are available in the following public workspace: https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/Genome%20Assembly/Bacteria
- Below are a series of screenshots showing successful completion of the jobs, availability of the result files in the workspace, excerpts of the assembly report and summary of assembled contigs and total length for each of the jobs.

Sceenshots

References

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