Benchmarking eight software tools for de novo genome assembly, including for SARS-CoV-2

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A new study compares and assesses eight de novo genome assembly software tools on actual viral next-generation sequencing data. The study, which includes the whole genome sequence data of SARS-CoV-2, the virus that causes COVID-19, is published in *OMICS: A Journal of Integrative Biology*.

Genome assembly is one of the crucial steps in whole genome sequencing data analyses and understanding viral genomics. A variety of different genome assembly software tools have been developed. In the present study, coauthors Amit Kumar Gupta and Manoj Kumar, from the Institute of Microbial Technology, Council of Scientific and Industrial Research, and the Academy of Scientific and Innovative Research, in India, performed a comparative evaluation and benchmarking of eight assemblers on viral next-generation sequencing data.

The investigators concluded that "overall, three assemblers, i.e., SPAdes, IDBA, and ABySS, performed consistently well, including for genome assembly of SARS-CoV-2." They also suggest that using two or more assembly approaches should be considered in viral next-generation sequencing studies, especially in clinical settings.

"Genome assembly is vital to molecular epidemiology and clinical management of COVID-19 and other infectious outbreaks. Comparative evaluation of the genome assembly tools has been lacking on data from viral origin. The new study fills this knowledge gap, building on sequencing data of SARS-CoV-2, dengue virus 3, human

immunodeficiency virus 1, hepatitis B virus, West Nile virus, amongst others. This benchmarking is a fine example of genomic applications in planetary health and opens up new possibilities to accelerate innovation in clinical diagnostics, drug and vaccine development. I welcome new manuscripts dealing with large-scale biology and multi-omics ecology research for peer-review in the journal," says Vural Özdemir, MD, Ph.D., DABCP, Editor-in-Chief of *OMICS*.

More information: Amit Kumar Gupta et al, Benchmarking and Assessment of Eight De Novo Genome Assemblers on Viral Next-Generation Sequencing Data, Including the SARS-CoV-2, *OMICS: A Journal of Integrative Biology* (2022). DOI: 10.1089/omi.2022.0042

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