Resource Summary Report

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Installation and Getting Started

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Proper Citation

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Protocol Information

URL: https://dx.doi.org/10.17504/protocols.io.d5k84v

Authors: Afiahayati, Sato K, Namiki T, Hachiya T, Tanaka H, Sakakibara Y.

Group: VERVE Net, Hurwitz Lab

Summary: Motivation: An important step of "metagenomics" analysis is the assembly of multiple genomes from mixed sequence reads of multiple species in a microbial community. Most conventional pipelines employ a single-genome assembler with carefully optimized parameters and post-process the resulting scaffolds to correct assembly errors. Limitations of the use of a single-genome assembler for de novo metagenome assembly are that highly conserved sequences shared between different species often causes chimera contigs, and sequences of highly abundant species are likely mis-identified as repeats in a single genome.Methods:We modified and extended a single-genome and de Bruijn-graph based assembler, Velvet, for de novo metagenome assembly. Our fundamental ideas are first decomposing de Bruijn graph constructed from mixed short reads into individual sub-graphs and second building scaffolds based on every decomposed de Bruijn sub-graph as isolate species genome.

Affiliations: Sakakibara Lab, Sakakibara Lab, Sakakibara Lab, Sakakibara Lab, Sakakibara Lab, Sakakibara Lab

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