MetaVelvet : An extension of Velvet assembler to de novo metagenome assembly from short sequence reads

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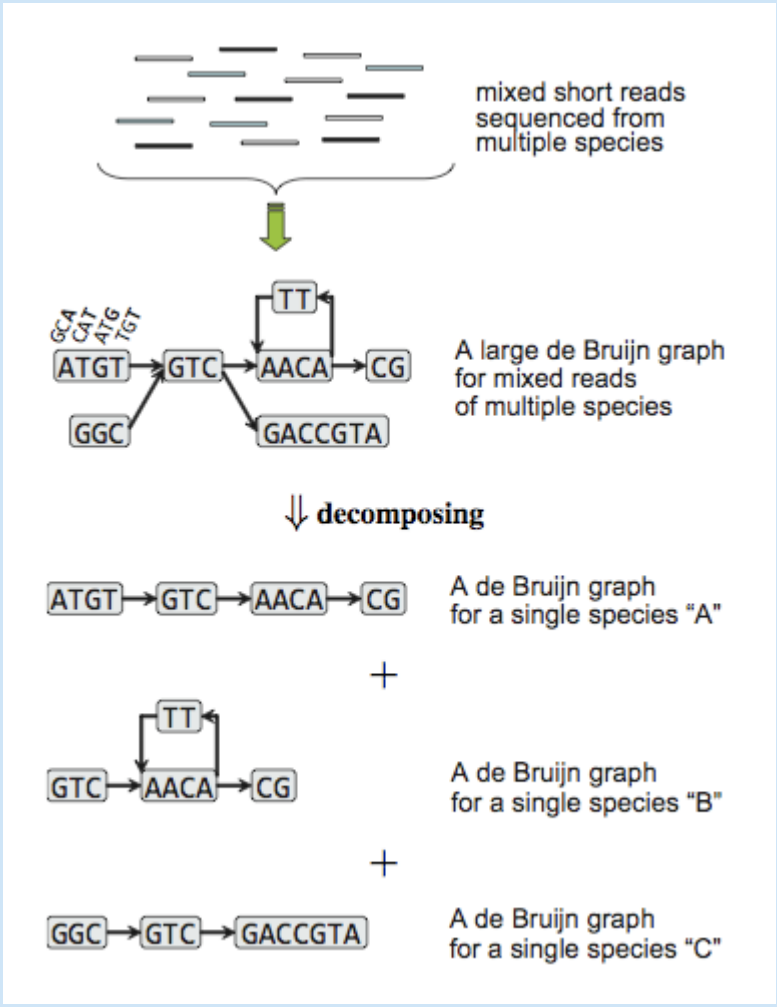
Abstract

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.



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PROTOCOLS

1. Installation and Getting Started

CONTACT: Bonnie Hurwitz

2. Manual setting of k-mer coverage peaks

CONTACT: Bonnie Hurwitz

3. Use Bambus2 scaffolding module

CONTACT: Bonnie Hurwitz

4. How to use paired-end information for graph decomposition

CONTACT: Bonnie Hurwitz