Assembling complete microbial genomes with Iterative Hybrid Assembly

Lei Liu

Yulin Wang

You Che

Yiqiang Chen

Yu Xia

Ruibang Luo

Suk Hang Cheng

Chunmiao Zheng

Tong Zhang

Video Byte

Keywords: microbes, microbial community, metagenomes, genomes, metagenomics, nanopore, long reads, short reads, hybrid assembly, microbial dark matter, genome assembly, metagenome assembly, Iterative Hybrid Assembly, anammox, *Ca. Brocadia*, hydrazine synthase, enriched microbial community, bacterial genomes, bacteria, low coverage, high contiguity, one-stage partial-nitrification anammox, anammox system, Microbiome

Posted Date: February 25th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-275906/v1>

License: This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Abstract

Microbial metagenomes are like a blueprint of all the functions performed by a microbial community. Some microbes can't be grown in the lab, so metagenomics is important for investigating otherwise-unknown microbial "dark matter". Short-read sequencing provides large amounts of data, but it's hard to assemble into complete genomes. A recent study combined short-read data with nanopore long-read data using Iterative Hybrid Assembly (IHA). The researchers reconstructed 49 metagenome-assembled genomes (MAGs), including some with very low coverage. In total, 34 MAGs did not belong to any known genus, representing unknown microbe groups. The IHA method revealed more of the genes present than a short-read-only approach and showed that the anammox genome of genus *Ca. Brocadia* contains two identical hydrazine synthase genes. The current method is best for enriched microbial communities and will be extended to high-complexity samples in the future.