



07
DÉC.
2021

🕒 de 12h30 à 14h

📍 Salle de formation du PRABI

SÉMINAIRE

Automated strain-level metagenome assembly using long reads

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High-throughput short-read metagenomics has enabled large-scale species-level analysis and functional characterization of microbial communities. Microbiomes often contain multiple strains of the same species, and different strains have been shown to have important differences in their functional roles. Despite this, strain-level resolution from metagenomic sequencing remains challenging. Recent advances on long-read based methods enabled accurate assembly of bacterial genomes from complex microbiomes and an as-yet-unrealized opportunity to resolve strains. Here we present Strainberry, a metagenome assembly method that performs strain separation in single-sample low-complexity metagenomes and that relies uniquely on long-read data. We benchmarked Strainberry on mock communities and real datasets. It provided high-quality strain-resolved assemblies in low-complexity metagenomes, but was also able to unravel a more fine-grained microbial diversity in samples of higher complexity.