

REVIEW ARTICLE

Strategies and tools in illumina and nanopore-integrated metagenomic analysis of microbiome data

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Abstract

Metagenomic strategy serves as the foundation for the ecological exploration of novel bioresources (e.g., industrial enzymes and bioactive molecules) and biohazards (e.g., pathogens and antibiotic resistance genes) in natural and engineered microbial systems across multiple disciplines. Recent advancements in sequencing technology have fostered rapid development in the field of microbiome research where an increasing number of studies have applied both illumina short reads (SRs) and nanopore long reads (LRs) sequencing in their metagenomic workflow. However, given the high complexity of an environmental microbiome data set and the bioinformatic challenges caused by the unique features of these sequencing technologies, integrating SRs and LR is not as straightforward as one might assume. The fast renewal of existing tools and growing diversity of new algorithms make access to this field even more difficult. Therefore, here we systematically summarized the complete workflow from DNA extraction to data processing strategies for applying illumina and nanopore-integrated metagenomics in the investigation in environmental microbiomes. Overall, this review aims to provide a timely knowledge framework for researchers that are interested in or are struggling with the SRs and LR integration in their metagenomic analysis. The discussions presented will facilitate improved ecological understanding of community functionalities and assembly of natural, engineered, and human microbiomes, benefiting researchers from multiple disciplines.

KEYWORDS

gene-centric metagenomics, genome-centric metagenomics, hybrid sequencing, illumina and nanopore-integrated metagenomics, microbiome, metagenomics, nanopore sequencing

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