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Sensitive Identification and Quantification of Microbial Species in Metagenomes

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Abstract

Shotgun Metagenomics has emerged as a popular approach for understanding the underlying microbial community composition and metabolic potential in the recent years. Many computational methods have been developed in order decipher the taxonomic composition based on de novo assembly, marker genes, read assignment and a combination of approaches. However, the performance of some of the methods in terms of time and memory requirement hinders their usage. This work presents a method developed to deduce the taxonomic composition of the underlying community with an emphasis on the time reduction. The quality checked reads are initially subjected to Human DNA contamination removal by mapping it to HG19 reference genome. The unaligned reads are then mapped to bacterial reference genomes followed by viral and fungal genomes using bowtie2. The remaining reads are then subjected to 3 cycles of de novo assembly, contigs gap closure and ORF prediction followed by the annotation. The mapped reads and the contigs are used to infer the taxonomic profile of the metagenome. The method is validated by comparing these taxonomic profiles with ones generated using simulated reads. The method has been broadly tested on a set of 36 oral samples. The metagenomics analysis approach taken by us typically gives a taxonomic profile covering 60 -70% of the data including bacteria and viruses with a short runtime (6 hrs).

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