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Comparative metagenomics analysis of palm oil mill effluent (Pome) using three different bioinformatics pipelines (Article) (Open Access)

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Abstract

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The substantial cost reduction and massive production of next-generation sequencing (NGS) data have contributed to the progress in the rapid growth of metagenomics. However, production of the massive amount of data by NGS has revealed the challenges in handling the existing bioinformatics tools related to metagenomics. Therefore, in this research we have investigated an equal set of DNA metagenomics data from palm oil mill effluent (POME) sample using three different freeware bioinformatics pipelines' websites of metagenomics RAST server (MG-RAST), Integrated Microbial Genomes with Microbiome Samples (IMG/M) and European Bioinformatics Institute (EBI) Metagenomics, in term of the taxonomic assignment and functional analysis. We found that MG-RAST is the quickest among these three pipelines. However, in term of analysis of results, IMG/M provides more variety of phylum with wider percent identities for taxonomical assignment and IMG/M provides the highest carbohydrates, amino acids, lipids, and coenzymes transport and metabolism functional annotation beside the highest in total number of glycoside hydrolase enzymes. Next, in identifying the conserved domain and family involved, EBI Metagenomics would be much more appropriate. All the three bioinformatics pipelines have their own specialties and can be used alternately or at the same time based on the user's functional preference. © 2019, International Islamic University Malaysia-IIUM.

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