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TITLE

Meta-analysis of gut microbiome from HIV infected individuals

ABSTRACT

Recent advance and popularization of genomic sequencing enable us to obtain a massive number of short read sequences from samples. Short read sequencing data of a microbial community, referred to as microbiome data, often represent a symptom of disease progression. In fact, analysis of metagenomic sequencing of fecal samples from HIV infected individuals indicated a significant compositional change of the gut microbiota characterized by enrichment of a particular bacterial species. Despite increasing related works in number, comprehensive evaluation of existing HIV microbiome studies have not been performed yet. In this presentation, we would like to introduce our ongoing research progress on a meta-analysis of gut microbiome from HIV infected individuals. Microbiome datasets associated with HIV infection in public databases are collected and analyzed. For the collected datasets, we apply a pseudo-time reconstruction method to estimate a possible trajectory that imitates disease progression of HIV infected individuals. Based on these analyses, we discuss a property of marker bacterial species that well represent a time-course progression of HIV infection.