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Trajectory inference of HIV progression with microbiome data

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Information analysis of amplicon sequencing of fecal samples from HIV positive individuals suggested an enrichment of a particular bacterial species in the gut microbiota, as referred to dysbiosis. Although a sufficient number of samples has already accumulated for both HIV positive and negative subjects, time-series datasets are rarely available. Hence difficulty remains in tracing the compositional change of the gut microbiota during HIV infection.

In this presentation, we would like to introduce our ongoing research progress on the application of trajectory inference methods to construct a pseudo-trajectory that may imitate disease progression of HIV infection. Our computational analysis suggested that enrichment of the *enterobacteriaceae* family may occur at the initial phase of HIV infection during which inflammatory responses would be facilitated in the gut. This finding is consistent with known observations for the enrichment of the *enterobacteriaceae* family in several inflammatory diseases.

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