MICROBIAL SOCIAL NETWORK DEMYSTIFIED IN THE ERA OF GENOMICS

Microbes (nodes in different shapes) form a complex community by interacting (links connecting the nodes) with each other. Understanding such interactions is a key step towards understanding how the community functions.

A team of researchers from the Genome Institute of Singapore (GIS) has developed a novel method, BEEM-Static, that can predict ecological interactions from microbial profiling data generated from high-throughput sequencing. They developed the novel machine-learning approach to learn models depicting ecological relationship between microbes. The research was published in *PLoS* on 8 September 2021.

Microbial communities represent complex ecosystems that impact various aspects related to human health, eg. agriculture, food processing, disease biology, and healthcare. Microbial interaction network is similar to a social network between people. Some species are friends and they help each other grow better, some species compete for resources, while some species are enemies and harm the growth of other species. Unravelling the interactions between members of a microbial community is a key step towards understanding how the community functions, forecasting its dynamics, and rationally designing interventions which alter the community's structure and function.

Computational prediction of microbial interactions is becoming a popular approach thanks to the growing amount of high-throughput sequencing data. However, existing methods either cannot provide biologically meaningful predictions or require additional experimental data, which is inaccessible for most of the datasets generated using high-throughput sequencing.

> "BEEM-Static solves an important technical challenge by eliminating the need for additional experimental data to quantify total microbial population sizes, making it possible to utilise the large collection of public datasets, where such measurement is inaccessible."
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> *Dr Niranjan Nagarajan, Associate Director,*
> *Laboratory of Metagenomic Technologies & Microbial Systems,*
> *GIS*

BEEM-Static outperformed 10 state-of-the-art methods based on statistical models in prediction accuracy. The team applied BEEM-Static to over 4,000 human gut microbial profiling samples and identified multiple stable configurations characterised by distinct microbial population sizes and ecological interactions.

> "We hope that BEEM-Static will become a useful tool for studying the ecology of microbes. We also believe that its core algorithm will motivate the application of using mathematical models to study large microbial systems."
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> *Prof Patrick Tan, Executive Director, GIS*

To date, the team has developed two algorithms, BEEM (published in Microbiome in 2019) and BEEM-Static, which leverages data collected through different sampling strategies (longitudinal and cross-sectional, respectively).