



## Channing Microbiome Seminar

March 4, 2016, 11am @ 5th floor conference room



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### Global metabolic interaction network of the human gut microbiota with community-level disease implications

**Abstract:** The role of our gut microbiota in health and disease is largely attributed to the collective metabolic activities of the inhabitant microbes. A global mechanistic framework of the microbial community structure, mediated through metabolite transport, would provide important insights into the complex dynamics governing host-associated microbial ecology. Here, we constructed the first literature-curated network of the human gut microbiota (NJS16), with metabolic interactions between microbial species coupled with the host system. The network encompasses ~600 microbial species and 3 human cell types, interlinked by chemical compounds via >5,000 annotated small-molecule transport and macromolecule degradation events. We demonstrated the utility of our network in the analysis of disease-related microbiota by computing metabolic influence in the gut ecosystems of type 2 diabetes (T2D) patients. These microbial communities were found to harbor core microbial groups, which exert distinctively large metabolic influence and may thereby modulate the global dynamics of the gut ecosystem. Moreover, the T2D microbial communities, distinguished solely by socio-demographic traits, show commonalities in metabolic functional properties, but not in taxonomic profiles. In addition to particular toxic metabolites robustly produced across different microbial communities in T2D, we found an interesting possibility that some microbial products, seemingly nontoxic or even beneficial to the host, may in fact help maintain the structural integrity of T2D-specific microbial communities. This suggests that, at the community-level, supposedly benign microbes secreting those nontoxic or beneficial products may contribute indirectly towards disease. Our network framework shows promise for investigating complex microbe-microbe and host-microbe chemical cross-talk, and identifying disease-associated features.

*Bio:* Jaeyun Sung is a postdoctoral research fellow in Ramnik Xavier's laboratory at Harvard Medical School and the Broad Institute. His current research interests are using systems biology approaches towards understanding the biomolecular mechanisms underlying host-microbe relationships, particularly between the human gut microbiota and host immune system. He received his PhD in Chemical Engineering at the University of Illinois at Urbana-Champaign, where he worked on constructing statistical inference algorithms to discover transcriptomic biomarkers of brain-specific cancers.

Hosted by Travis Gibson and Yang-Yu Liu