Metagenomics: From algorithms to microbiome investigations

Dr. Tarini Shankar Ghosh
Computational and Systems Biology Lab, Genome Institute of Singapore, 60 Biopolis St, #02-01, Singapore

Summary:

The recent emergence of next generation sequencing technologies has led to the advent of the metagenomics approach. Metagenomic sequencing help us to understand the role and impact of the microbiome in health and disease. Several genomic signatures including homology analysis of 16S rRNA encoding gene, whole genome sequencing, metagenomic wide association studies, metagenomic single-nucleotide polymorphism detection, *oriC* to *ter* ratio of metagenomic sequences have demonstrated associations of microbiome richness, eveness, dynamics, functional repertoire and metabolic state with susceptibility to several diseases, including malnourishment, type 2 diabetes, auto-inflammatory disorders, cancer, cardiovascular disease, rheumatoid arthritis, and metabolic disorders.

By enabling the direct extraction and sequencing of the genomic content of all resident microbes in an environment, metagenomics facilitates a comprehensive characterization of the taxonomic and functional diversity, by extending the purview of these investigations to even those microbial species that are not amenable to currently available laboratory based culturing techniques. However, given the sheer volume and taxonomic complexity, efficient and accurate bioinformatic/statistical analysis of metagenomic sequence data requires the development of specialized algorithms/analysis protocols.

The current talk is divided into two parts. The first part of the talk will mention our recent findings on methodology development for computational analysis of metagenomes. The major focus will be on the research idea(s) underlying a couple of these methods, specifically explaining how subtle improvements in classification and profiling strategies can result in dramatic improvements in accuracy, as well as in identifying sequences from hitherto uncharacterized microbial lineages that are differentially abundant in specific environments.

The second part of the talk will focus on human microbiome investigations. This will involve my work probing (i) the role of gut microbes in the onset and progression of malnourishment of Indian children (ii) Fecal carriage of antibiotic resistance genes and carbohydrate active enzymes in gut microbiota across individuals from diverse nationalities using statistical and network based analysis (iii) the microbial basis for inflammatory bowel diseases in the Indian population and (iv) identification of specific bacterial species facilitating gut microbiome recovery during/post antibiotic treatment.