As DNA sequencing technologies continue to improve, sequencing of microbial genomes can now be done routinely. We have gone from a group of researchers spending years to generated and study one bacterial genome to an individual researcher comparing tens or hundreds of similar genomes at a time with the help of bioinformatic applications.

Pangenomic analysis allows us to decipher how a bacterium evolves and how certain small mutations could have a large impact on disease outcome. In recent years, we have also started to sequence the genetic material directly isolated from a microbial community (microbiota) in order to bypass culturing. The International Human Microbiome Consortium and associated efforts are trying to decipher the interactions between our bodies and our microbiotas. The metagenomics approach allows researchers to study an entire microbial community in relation to health and diseases but new challenges arise on how to assign taxonomic and functional information to incomplete and sometimes novel sequences. With the increased scale of sequencing, new bioinformatics and statistical tools are needed to facilitate data process and interpretation. In this talk, I’ll discuss the progress and challenges of microbial genomic analysis with examples drawn from my own research and from literature. Through this talk, I wish to demonstrate that microbial genomics has benefit greatly from the technological improvements over the years and there is a bright future in applying microbial genomics to improve human health.