THEO PORTLOCK: Abstract for Cell Symposia: Metabolites in Signalling and Disease

The role of gut microbiota in humans is of great interest, and metagenomics provides key opportunities for extensively analysing bacterial diversity in health and disease. Despite increasing efforts to expand microbial gene catalogues and an increasing number of metagenomes assembled genomes, there has been few investigations in pan-metagenomics and in-depth functional analysis across different geographies and diseases. Here, we explored 5,708 human gut metagenome samples across 19 countries and 23 diseases, performing compositional, functional cluster, and integrative analysis. We identified *Fusobacterium nucleatum* and *Anaerostipes hadrus* with the highest frequencies, enriched and depleted respectively, across different disease cohorts. Distinct functional distributions were observed in the gut microbiome of westernized and non-westernized populations. Additionally, a random forest machine learning model explained by SHapley Additive exPlanations (SHAP) identified key species as disease biomarkers. This compositional and functional analysis are presented in an open-access Human Gut Microbiome Atlas (www.microbiomeatlas.org), allowing for exploration of the richness, diseases, and regional signatures of the gut microbiota across different cohorts.