

Functional Redundancy of the Human Gut Microbiome During Colorectal Cancer

Specific Aims

Aim 1. Assess the importance of functional gene redundancy of the gut microbiome in CRC.

Hypothesis: Using functional gene profiles instead of only taxonomic profiles improves the classification modeling of samples as CRC or non-cancerous because of functional redundancy in the gut microbiome.

- A. Build taxonomic profiles with OTUs from 16S rRNA gene sequences and build profiles of functional gene potential from metagenomes.
- B. Compare taxonomic composition to functional gene potential of microbiomes within and between disease states to determine presence and degree of functional redundancy.
- C. Build machine learning models to classify samples as CRC or non-cancerous with taxonomic composition, functional gene potential profiles, or both as model features and compare performance.

Aim 2. Assess the importance of integrating functional gene potential with active metabolites to characterize function of the gut microbiome in CRC.

Hypothesis: Using active metabolic pathways confirmed with mass spectrometry instead of all potential metabolic pathways from metagenomes improves the classification modeling of samples as CRC or non-cancerous.

- A. Annotate compounds from untargeted mass spectrometry with the GNPS database and select those known to be products of bacterial metabolic pathways with the MetaCyc database.
- B. Calculate the intersection of pathways associated with active metabolites and the pathways from functional potential profiles.
- C. Build machine learning models to classify samples as CRC or non-cancerous with all potential metabolic pathways or only confirmed active metabolic pathways as model features and compare performance.