



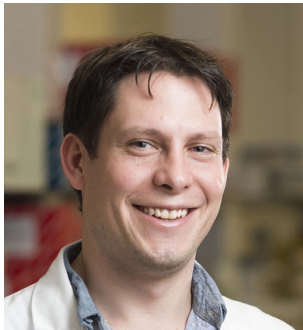
Channing Microbiome Seminar

May 3 (Friday), 2024, 9AM (ET)

MCP 5th-floor large conference room & Zoom:

<https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZnJiYVZzQ3NEQT09>

Meeting ID: 810 7095 9105; Passcode: 984617



Samuel Forster

Hudson Institute of Medical Research, Australia

Combining culturing and clades to understand site specificity in Inflammatory Bowel Disease

The opportunities for therapeutic interventions targeting the gastrointestinal microbiota are now clear. From inflammatory bowel disease to chronic infections such as infection, microbiome-based medicines have demonstrated remarkable efficacy. Despite these opportunities, fundamental microbiological understanding and knowledge of bacterial roles within the gastrointestinal tract remains limited. To address this gap we have developed high-resolution, culture-based shotgun metagenomic sequencing, phylogeny-based clade-specific analysis methodologies and genome scale modelling approaches for application to inflammatory bowel disease. Performing detailed bacterial culturing with matched metagenomics and host transcriptomics across up to three intestinal sites (terminal ileum, cecum and rectum; n=386) from 200 patients, functionally distinct bacterial clades associated with either inflammatory bowel disease or health have been identified. These data demonstrate the importance of strain specific phenotypes and consideration of anatomical sites when developing and designing therapeutic interventions based on the microbiome.

Bio: A/Prof Sam Forster is a CSL Centenary Fellow who leads the Microbiota and Systems Biology laboratory at the Hudson Institute of Medical Research, Australia. His team's research brings together expertise in microbiology, immunology, and computational biology to understand the fundamental functions of the microbiome to develop rationally selected therapeutics. This work ranges from developing better methods to characterise the microbiome in diseases to understanding the impact of diet, antibiotics, phage and microbiome composition on community structure and resilience.

Hosted by Yang-Yu Liu