Bioinformatic Workflow for Metaproteomic Analysis of Host-Microbe Dynamics in Clinical Samples

Pratik Jagtap¹, Surbhi Bihani², Monica Kruk³, Subina Mehta¹, Aryan Gupta¹, Kevin Murray¹, Andrew Rajczewski¹, James Johnson³, Reid Wagner¹, Kristin Boylan¹, Amy Skubitz¹, Theresa Laguna¹, Sanjeeva Srivastava², Timothy Griffin¹

¹Biochemistry, Mol. Biology and Biophysics, University of Minnesota, Minneapolis, USA; ²Indian Institute of Technology Bombay, Mumbai, India; ³Minnesota Supercomputing Institute, University of Minnesota, Minneapolis, USA; ⁴Pulmonary and Sleep Medicine, Ann & Robert H. Lurie Children’s Hospital of Chicago, Chicago, USA

Clinical metaproteomics has the potential to offer insights into host-microbiome interactions. However, the field faces challenges in the detection of low-abundance microbial proteins. As a solution, we have developed an integrated workflow coupling mass spectrometry-based analysis with customized bioinformatic processing of microbial proteins. We have utilized this workflow in ongoing projects to identify microbial peptide panels for: A) co-infection status during COVID-19 pandemic waves, B) cystic fibrosis (CF) disease progression studies, and C) ovarian cancer biomarker discovery.