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Metaproteomics, the path to rapid microbiota diagnosis

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Short abstract:

The microbiota plays a major role in human health. To understand how microbial communities function, how they interact with the host and how dysbiosis can occur, we need to identify the diversity of microorganisms present and quantify the numerous molecular players at work. Proteins are the workhorses of biological systems. Metaproteomics is a key technology for such functional studies, as it can provide five types of answers for these highly complex samples: 1) identification of the taxa present, 2) quantification of the biomass of these organisms, 3) identification of the proteins of these taxa and their function, 4) identification of human biomarkers explaining the host response, and 5) overall functional representation of the biological system. Challenges in terms of mass spectrometry, interpretation and exploitation of results will be addressed using examples of fecal material from COVID19 patients and sputum from cystic fibrosis patients. Recent technologies such as the Astral tandem mass spectrometer will be presented to demonstrate the power of this approach for rapid medical diagnosis.