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PRESENTATION TITLE: Metabolomics: from raw LC-MS spectra to biological insights

ABSTRACT: Liquid-chromatography coupled with mass spectrometry (LC-MS) is the most popular platform for global metabolomics in biomedical studies, and is widely used for drug screening and monitoring. However, significant challenges remain in the downstream data analysis and interpretation. Over the past decade, my team has been actively developing a series of algorithms and tools to address the key computational challenges in metabolomics. In this talk, I will introduce our recent progress and application of global metabolomics, including 1) fast and sensitive spectra processing and compound annotation; 2) deep functional analysis from the annotated table; and 3) application to a microbiome multi-omics study.

BIOGRAPHY: Dr. Xia is an Associate Professor in McGill and a Canada Research Chair in Bioinformatics and Big data Analytics. His research explores transformative ways to address the current big data challenges arising from environmental and biomedical studies, with focus on metabolomics, transcriptomics, microbiomics and multi-omics integration. By leveraging cloud computing, visual analytics and novel algorithms, his team has developed several powerful computational platforms that are used by ~100,000s researchers worldwide each year.
