Machine Learning Methods for Proteomics

Abstract: Shotgun proteomics using mass spectrometry is enabling a revolution in the study of large-scale systems biology. Data-independent acquisition (DIA) is a mass spectrometry technique that regularly samples co-fragmented ions produced from multiple peptides falling within a specified mass range. While comprehensive, this approach results in highly complex mass spectra requiring the reconstruction of which fragment ions were produced from which peptides. Here we discuss machine learning methods to make those assignments and assess our confidence in that data.

About the Speaker: Brian Searle is an Assistant Professor at the Ohio State University Medical Center in the Department of Biomedical Informatics and a member of the Pelotonia Institute for Immuno-Oncology. Brian received his chemistry BA at Reed College in 2001. In 2004, he co-founded Proteome Software with Mark Turner and Dr. Ashley McCormack to produce and distribute cutting-edge data analysis software for proteomicists. In 2014, he returned to academia to earn his PhD with Dr. Michael MacCoss at University of Washington, where he developed methods to detect and quantify proteins and phosphosites using mass spectrometry. His lab spans the intersection of proteomics, mass spectrometry, bioinformatics, and technology development to study human genetic variation in the backdrop of cancer.

Brian C. Searle, PhD
Assistant Professor
Department for Biomedical Informatics, The Ohio State University
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Carmen Zoom