

Project: Identification and filtering of mass spectrometry peaks in complex mixtures

The use of mass spectrometry for selective reaction monitoring is a method to quantitate the expression of multiple proteins in a complex mixture. However, the outputs from the platform are variable, noisy and subject to batch, experimental and platform variations. Identifying the “true” peaks for any given peptide is a complicated task involving the identification of multiple transitions and recognition of which peaks remain consistent (in terms of overall shape and detection window). This project involves identifying “valid” peaks using time series analysis and Fuzzy logic to simplify the downstream tasks of peak selection and calling prior to final analysis.

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