

# CURRENT TRENDS IN MASS SPECTROMETRY AND CHROMATOGRAPHY

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## Group-DIA: A software tool for untargeted analysis of multiple data-independent acquisition (DIA) mass spectrometry files

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In recent years, DIA (Data-Independent Acquisition) has become an emerging strategy for analyzing complex peptides mixture. Compared with DDA (Data-dependent Acquisition), DIA selects mixtures of precursor ions for tandem mass spectrometry (MS/MS) analysis in an unbiased fashion. It is challenging to interpret the resulting MS/MS spectra from DIA using conventional searching tools, which is designed to identify one peptide per spectrum. Currently, targeted strategy is applied to analyze DIA data, such as OpenSWATH, which requires additional libraries build from DDA data. Here, we developed a software tool, Group-DIA, which is a library-free strategy for analyzing DIA data. We used group-DIA and DIA-Umpire, another library-free tool, to analyze SGS SWATH-MS data, and found Group-DIA can identify up to 50% more peptides than DIA-Umpire. We also compared the performance of Group-DIA and DIA-Umpire to analyze SWATH-MS data from immuno precipitation and mouse total cell samples, demonstrated that Group-DIA is an effective strategy of analyzing DIA data.

### Biography

Chuan-Qi Zhong has expertise in mass spectrometry and cell signaling pathway. His recent achievement is development of a novel DIA data analysis software tool, Group-DIA. SWATH-MS, one of DIA, has become a powerful tool for consistently quantifying thousands of proteins among multiple samples. His main research field focuses on development of DIA strategy and application of DIA strategy for investigation of signaling pathways.

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