Challenges of AP-MS data interpretation in biological relevance-driven studies

Investigating protein-protein interaction (PPI) networks helps determine the regulation underlying health and disease, hence it is crucial in successful therapy design. Most common approaches in elucidating PPIs encompass affinity-based techniques aimed at identifying proteins copurifying with the studied protein (AP or AE — affinity purification or enrichment). Due to its definability, mass spectrometry (MS) has been a method-of-choice for detection in such experiments, collectively termed AP-MS (or AE-MS). However, the biologically dynamic nature of PPIs, coupled to a kinetically dependent AP step makes AP-MS data highly variable, and its statistical quantitative interpretation challenging. This being explicit in studies employing biological relevance-driven design with no perturbance to protein expression level and/or absence of large fusion tags. In my talk I will try to emphasize the deemed sources of AP-MS variability from a biophysical perspective, and will be happy to discuss any suggestions for coping with them.