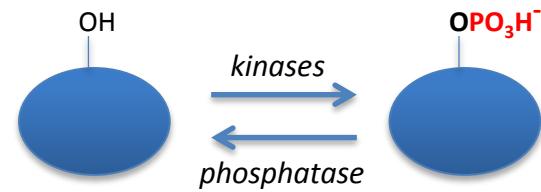
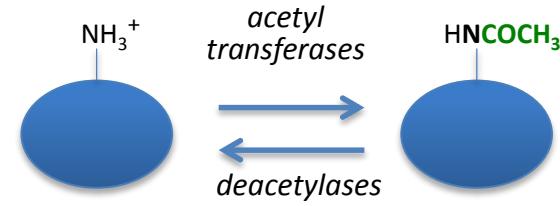


Skyline MS1 Filtering for label-free quantification targeting posttranslational modifications

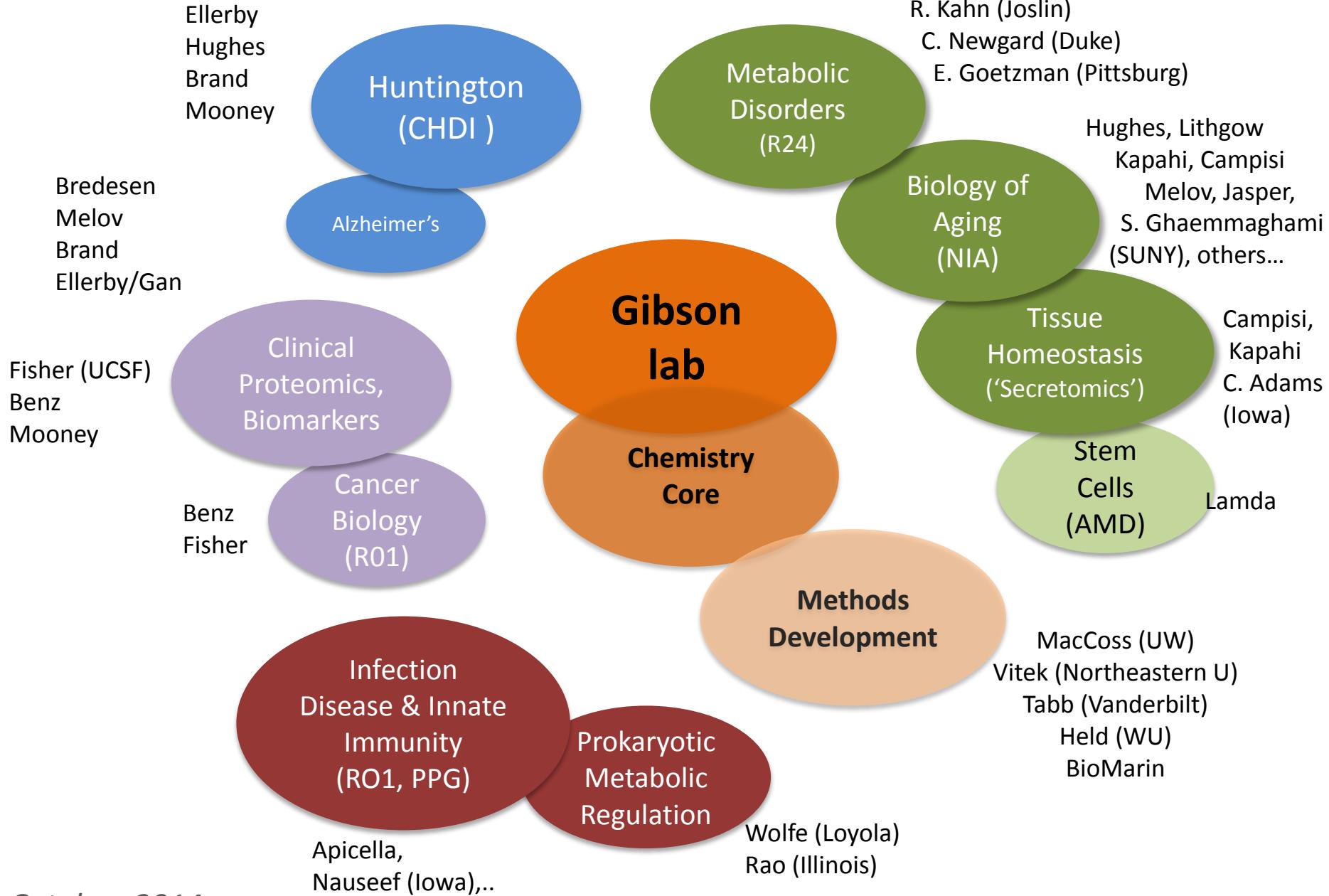


Birgit Schilling
Buck Institute for Research on Aging

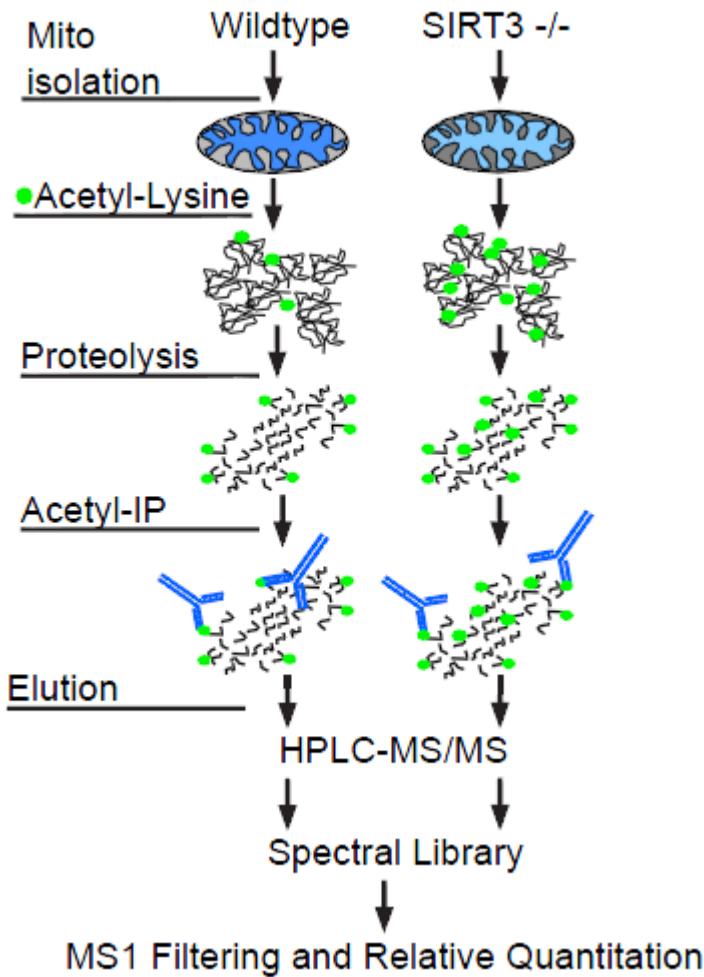


Webinar #1: Getting the Most Out of DDA Data with Skyline

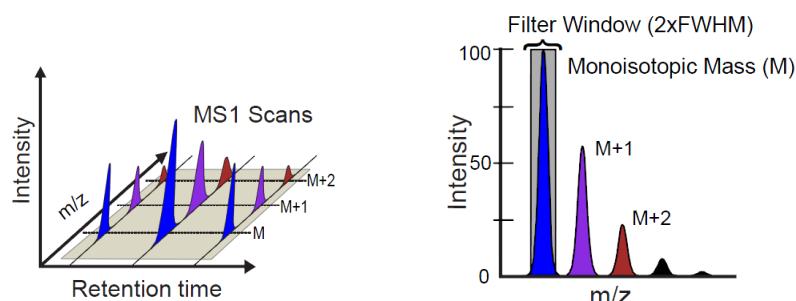
GIBSON LAB 2014



Development and Examples for MS1 Filtering Workflows



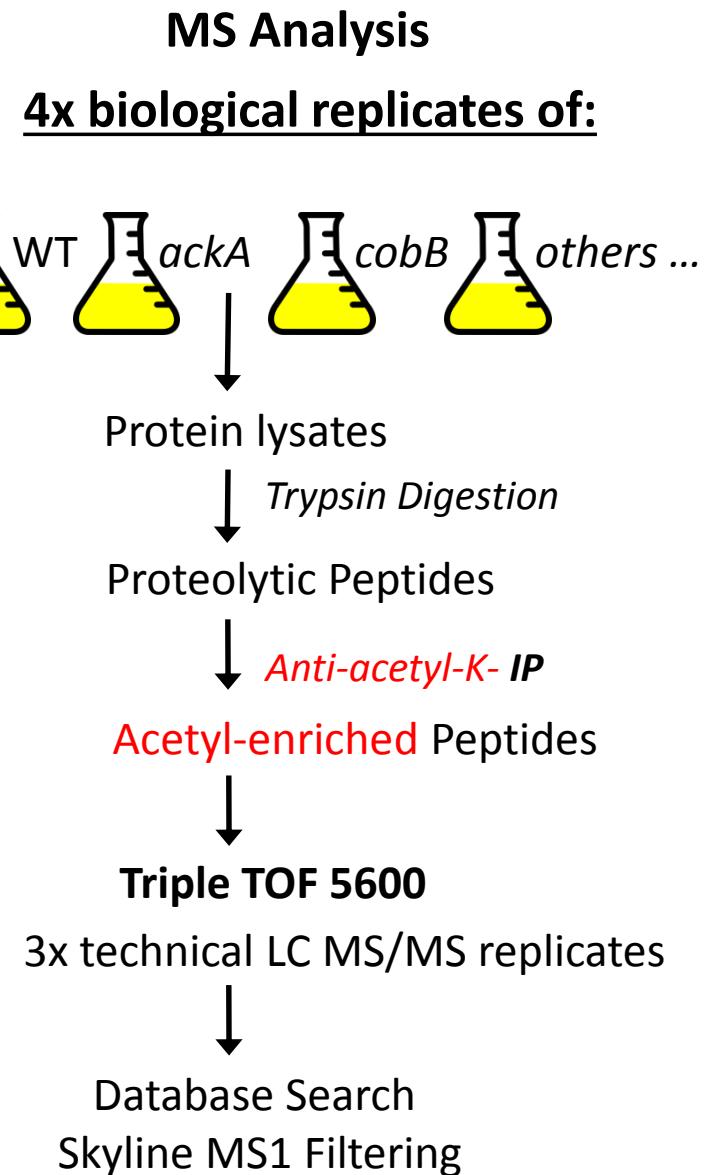
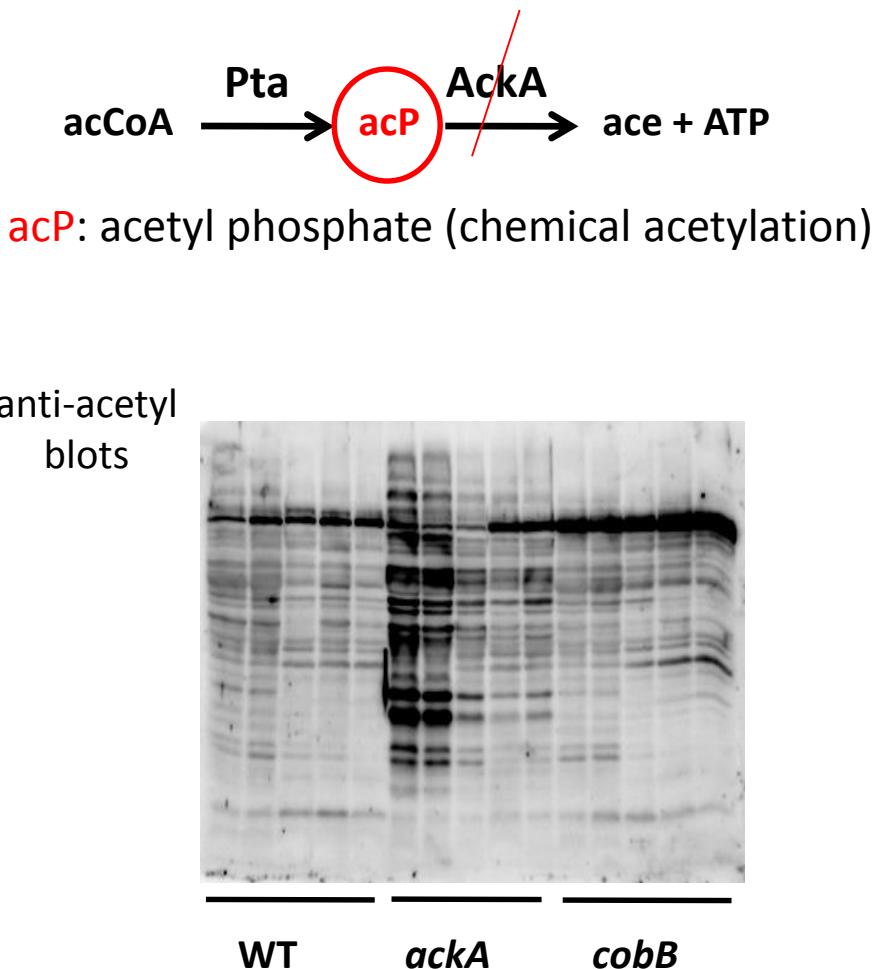
Schilling, Rardin, MacLean et al., *MCP*, 2012
Rardin et al., *PNAS*, 2013



- Data-dependent acquisitions (discovery workflows) depend on dynamic sampling of MS/MS spectra.
- **MS1 scans** are truly **data-independent** and can be used for relative quantification.
- MS1 Filtering uses ion extracted chromatograms of peptide precursor ions for relative quantification
- Easy **interfacing** in Skyline with other data independent, **targeted workflows**, i.e. MRM, MRM-HR (PRM), SWATH-MS2.
- Interface with Panorama

DATA examples

E. coli acetylation regulation - Background and Workflow



PHASE 1: Biomarker Discovery Using Conditioned Media from Cancer Cell Lines to predict cancer-specific plasma glycosites candidates

