From Missing Intensities to Uncertainty: A Conjugate Bayesian Framework for Differential Proteomics

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Abstract

Differential proteomics pipelines struggle with three recurring issues: missing intensities, correlation between peptides mapping to the same protein, and uncertainty quantification. In practice, many workflows reduce each analyte to point estimates and rely on p-values (often with a 5% threshold) to decide differential abundance. Even in widely used approaches such as limma-where variance is "moderated" through a hierarchical model-uncertainty is only partially propagated into the final decision. In this talk, we will present ProteoBayes, a fully Bayesian framework for differential proteomics designed to work naturally in multiple-imputation settings for missing values. Using a hierarchical model with conjugate priors on mean and variance parameters, we obtain closed-form posterior updates and can sample directly from posterior distributions-avoiding expensive MCMC. This yields interpretable outputs such as posterior distributions (and credible intervals) for effect sizes, and posterior evidence for differential abundance. Wewill also discuss an extension to multivariate differential analysis that accommodates inter-peptide correlations, enabling more coherent inference when peptides are not independent.

Keywords: Missing values and data generation

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