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Multiple-Platform Data Integration Method with Application to Combined Analysis of Microarray and Proteomic Data

It's desirable in genomic studies to select biomarkers that differentiate between normal and diseased populations based on related data sets from different platforms. Most recently developed integration methods focus on correlation analyses between gene and protein expression profiles. These methods select biomarkers with concordant behavior but do not directly select differentially expressed biomarkers. Other methods combine statistical evidence in terms of ranks and p-values, but they don't account for the dependency relationships among the data across platforms. We propose an integration method to perform hypothesis testing and biomarkers selection based on multi-platform data sets observed from normal and diseased populations.