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A Bayesian meta-analysis method to integrate multiple omics data

Much research effort has been devoted to the identification of enriched gene sets for omics experiments, however, these are often found to be inconsistent among independent studies. As progressively more data become available, statistical methods are needed to integrate information from multiple studies and improve the power of identifying enriched gene sets. In this lecture, a Bayesian partition model that provides a coherent framework for joint modelling of both gene set information and gene expression data from multiple studies will be introduced. The suggested methodology directly models omics data aiming to improve the detection of enriched gene sets by integrating information from different sources available. A generalized simulated annealing algorithm is employed to estimate the optimal partition of the data and accordingly summarize sets of data. The method has been successfully validated with simulated data, as well as cancer data and toxicity data. Additionally, the workflow has been integrated in a web application for toxicity prediction.