

Integrative analysis of multi-platform data

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Abstract: We propose a statistical framework of shared informative factor models that can jointly analyze multi-platform omic data and explore their associations with a disease phenotype. The common disease-associated sample characteristics across different data types can be captured through the shared structure space, while the corresponding weights of genetic variables directly index the strengths of their association with the phenotype. Extensive simulation studies and an application demonstrate the performance of the proposed method in terms of biomarker detection accuracy.