Integrative interaction analysis of multi-omics data

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Abstract: For the etiology, progression, and treatment of complex diseases, gene-environment (G-E) interactions have important implications beyond the main G and E effects. With the small sample sizes of omics profiling studies and noisy nature of omics data, the interaction analysis on a single dataset often leads to unsatisfactory results. In recent profiling studies, a prominent trend is to collect measurements on multi-omics data, including gene expressions as well as their regulators (copy number alteration, microRNA, methylation, etc.) on the same subjects. In our study, we propose a joint interaction analysis approach in an integrative perspective based on the biclustering and regularized estimation techniques, uniquely effectively accommodating the regulation relationships among multi-omics data. Simulations show that the proposed approach has significantly improved identification performance. In the analysis of cancer multi-omics data, biologically sensible findings different from the alternatives are made.