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Organized Quality Climate Collaboration Examination

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Editorial Note

For the etiology, progression, and treatment of complex diseases, Gene-Environment (G-E) interactions have important implications beyond the main G and E effects. G-E interaction analysis can be more challenging with higher dimensionality and need for accommodating the "main effects, interactions" hierarchy. In recent literature, an array of novel methods, many of which are based on the penalization technique, have been developed. In most of these studies, however, the structures of G measurements, for example, the adjacency structure of Single Nucleotide Polymorphisms (SNPs; attributable to their physical adjacency on the chromosomes) and the network structure of gene expressions (attributable to their coordinated biological functions and correlated measurements) have not been well accommodated. In this study, we develop structured G-E interaction analysis, where such structures are accommodated using penalization for both the main G effects and interactions. Penalization is also applied for regularized estimation and selection. The proposed structured interaction analysis can be effectively realized. It is shown to have consistency properties under high-dimensional settings. Simulations and analysis of GENEVA diabetes data with SNP measurements and TCGA melanoma data with gene expression measurements demonstrate its competitive practical performance. Colocalization aims at characterizing spatial associations between two fluorescently tagged biomolecules by quantifying the co-occurrence and correlation between the two channels acquired in fluorescence microscopy. Colocalization is presented either as the degree of overlap between the two channels or the overlays of the red and green images, with areas of yellow indicating colocalization of the molecules. This problem remains an open issue in diffraction-limited microscopy and raises new challenges with the emergence of super resolution imaging, a microscopic technique awarded by the 2014 nobel prize in chemistry. We propose GcoPS, for Geo-coPositioning System, an original method that exploits the random sets structure of the tagged molecules to provide an explicit testing procedure. Our simulation study shows that GcoPS unequivocally outperforms the best competitive methods in adverse situations (noise, irregularly shaped fluorescent patterns, and different optical resolutions). GcoPS is also much faster, a decisive advantage to face the huge amount of data in super resolution imaging. We demonstrate the performances of GcoPS on two biological real data sets, obtained by conventional diffraction-limited microscopy technique and by super resolution technique, respectively. Conditional screening approaches have emerged as a powerful alternative to the commonly used marginal screening, as they can identify marginally weak but conditionally important variables. However, most existing conditional screening methods need to fix the initial conditioning set, which may determine the ultimately selected variables. If the conditioning set is not properly chosen, the methods may produce false negatives and positives. Moreover, screening approaches typically need to involve tuning parameters and extra modeling steps in order to reach a final model. We propose a sequential conditioning approach by dynamically updating the conditioning set with an iterative selection process. We provide its theoretical properties under the framework of generalized linear models. Powered by an extended Bayesian information criterion as the stopping rule, the method will lead to a final model without the need to choose tuning parameters or threshold parameters. The practical utility of the proposed method is examined via extensive simulations and analysis of a real clinical study on predicting multiple myeloma patients' response to treatment based on their genomic profiles.

Bi-dimensionally Linked Matrices

Advances in molecular technologies have motivated new methodologies for the integration of multiple sources of high-content biomedical data. However, most statistical methods for integrating multiple data matrices only consider data shared vertically (one cohort on multiple platforms) or horizontally (different cohorts on a single platform). This is limiting for data that take the form of bi dimensionally linked matrices (eg, multiple cohorts measured on multiple platforms), which are increasingly common in large-scale biomedical studies. In this paper, we propose bi dimensional integrative factorization (BIDIFAC) for integrative dimension reduction and signal approximation of bi-dimensionally linked data matrices. Our method factorizes data into (a) Globally shared, (b) Row-shared, (c) Column-shared, and (d) Single-matrix structural components, facilitating the investigation of shared and unique patterns of variability.

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