基于重要性惩罚的联合图Lasso方法（IPJGL）：通过高斯图模型进行差异网络推断（吴凌云）

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Motivation: Differential network inference is a fundamental and challenging problem to reveal gene interactions and regulation relationships under different conditions. Many algorithms have been developed for this problem; however, they do not consider the differences between the importance of genes, which may not fit the real-world situation. Different genes have different mutation probabilities, and the vital genes associated with basic life activities have less fault tolerance to mutation. Equally treating all genes may bias the results of differential network inference. Thus, it is necessary to consider the importance of genes in the models of differential network inference.

Results: Based on the Gaussian graphical model with adaptive gene importance regularization, we develop a novel Importance-Penalized Joint Graphical Lasso method (IPJGL) for differential network inference. The presented method is validated by the simulation experiments as well as the real datasets. Furthermore, to precisely evaluate the results of differential network inference, we propose a new metric named APC2 for the differential levels of gene pairs. We apply IPJGL to analyze the TCGA colorectal and breast cancer datasets and find some candidate cancer genes with significant survival analysis results, including SOST for colorectal cancer and RBBP8 for breast cancer. We also conduct further analysis based on the interactions in the Reactome database and confirm the utility of our method.

Availability and implementation: R source code of Importance-Penalized Joint Graphical Lasso is freely available at https://github.com/Wu-Lab/IPJGL.

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Supplementary information: Supplementary data are available at Bioinformatics online.

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