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Dear Editor,

I am pleased to submit an original research article entitled "Consistent Multiple Nonnegative Matrix Factorization with Hierarchical Information for Gene Functional Modules Mining", for consideration for publication in BMC Bioinformatics.

Our work is highly related to gene module clustering, we believe that this manuscript is appropriate for publication by the Journal of BMC Bioinformatics. In this manuscript, our work proposes a new way to mining gene functional modules with the help of hierarchical structure information of phenotype ontology, by factorizing genome-phenome association data on mouse. Our proposed model CMNMF constrains the gene cluster matrix to remain consistent while it interacts with different phenotype ontology levels in decomposing the genome-phenome association matrix, meanwhile it restricts the similarity of adjacent phenotype ontology pairs to satisfy the hierarchical structure.

CMNMF and seven baseline methods are conducted on mouse gene-phenotype associations. The performance of clustering and GO enrichment analysis show the effectiveness of CMNMF. Additionally, a preliminary supervised CMNMF is proposed for showing its generalizing ability.

This manuscript describes original work and is not under consideration by any other journal. All authors have no conflicts of interest to disclose and approved the manuscript and this submission.

Thank you for receiving our manuscript and considering it for review. We appreciate your time and look forward to your response.

Sincerely yours,

MaoQiang Xie
