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—Title: Multi omics enrichment pathway score analysis

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## **Multi omics enrichment pathway score analysis**

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**Abstract.** With the advancement of biomedical technology, various types of omics data and details can be collected from living organisms. Omics refer to genetic information, which encompasses various biomaterials such as miRNA, mRNA, methylation level and metabolites. However, many studies have only explained biological mechanisms using one omics. Single omics makes it difficult to explain the rather complex biological mechanisms. To overcome this problem, we propose a new model that fuses multi omics through tensor decomposition. We created a multi omics pathway enrichment scoring scheme for each sample. For each group within a clinical feature, such as cancer subtypes or methylation signatures, the association of each omics for each pathway can be shown as a pie chart, which implies that strength, or contribution, of the each omics to the associated clinical feature. Through this, we would be able to visualize the overall landscape of the active omics in play. In order to evaluate the proposing enrichment score, clustering and classifying experiments were conducted using the multi-omics data of colon cancer patients collected from the TCGA-COAD cohort. We used the subtypes as target labels. Thus, the task is to classify the subtype groups using the quantified pathway scores. Pathways showing singularity in COAD patients were analysed using multi omics and proved association with new multi omics enrichment score.

**Keywords:** *Multi Omics; Tensor decomposition;*

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