iClusterPlus: integrative clustering analysis of multi-omics data

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1 Introduction

R package *iClusterPlus* was developed to identify integrative molecular subtypes of cancer and subtype-specific driving features using multi-omics data. Multi-omics data are typically generated from the experiments in which tumor samples are analyzed by multiple technologies, such as array comparative genomic hybridization (aCGH), gene expression microarrays, RNA sequencing (RNA-seq) and DNA sequencing (DNA-seq). Examples of these multi-omics datasets can be obtained from the Cancer Genome Atlas (TCGA) (`http://cancergenome.nih.gov/`).

The major functions in the package (Bioconductor version <= 3.22) include *iCluster2*, *tune.iCluster2*, *iClusterPlus*, *tune.iClusterPlus*, *iClusterBayes* and *tune.iClusterBayes*. Example usages of these functions can be found in the User's guide (**iManual.pdf**) on the iClusterPlus web page.

Starting from Bioconductor 3.23, updated functions including *iCluster2b*, *tune.iCluster2b*, *iClusterPlus2* and *iClusterBayes2* have been included in the package. The updated functions provide improved computational efficiency. For continuous multi-omics data, we recommend using *iCluster2b* and *tune.iCluster2b* to perform integrative clustering analysis. For multi-omics data with mixed data types, we recommend using *iClusterPlus2* and *iClusterBayes2* for integrative clustering analysis. Example usages of these functions can be found in the tutorials on the iClusterPlus web page.

References

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