iClusterPlus: integrative clustering of multiple genomic data sets

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1 Introduction

Programs iClusterPlus and iClusterBayes are developed for integrative clustering analysis of multi-type genomic data, which are significant extension of the iCluster program (Shen, Olshen and Ladanyi, 2009). Multi-type genomic data arise from the experiments where biological samples (e.g., tumor samples) are analyzed by multiple techniques, for instance, array comparative genomic hybridization (aCGH), gene expression microarray, RNA-seq and DNA-seq, and so on. Examples of these data can be obtained from the Cancer Genome Atlas (TCGA) (`http://cancergenome.nih.gov/`).

The iClusterPlus User's guide can be obtained from the Bioconductor web page. If you are using Unix/Linux, you can get the manual by typing the following code in R Console.

```
> if (!requireNamespace("BiocManager", quietly=TRUE))
    > install.packages("BiocManager")
> BiocManager::install("iClusterPlus")
> library(iClusterPlus)
> iManual()
```

In addition, a simulation was performed to test the package. For details, please see the R code in the `iClusterPlus/inst/unitTests/` folder.