iClusterPlus: integrative clustering of multiple genomic data sets

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1 Introduction

iClusterPlus is developed for integrative clustering analysis of multi-type genomic data and is an enhanced version of iCluster proposed and developed by 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.

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("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.