

# iClusterPlus: integrative clustering of multiple genomic data sets

Qianxing Mo<sup>1</sup> and Ronglai Shen<sup>2</sup>

April 7, 2020

<sup>1</sup>Department of Biostatistics & Bioinformatics  
H. Lee Moffitt Cancer Center & Research Institute  
[qianxing.mo@moffitt.org](mailto:qianxing.mo@moffitt.org)

<sup>2</sup>Department of Epidemiology and Biostatistics  
Memorial Sloan-Kettering Cancer Center  
[shenr@mskcc.org](mailto:shenr@mskcc.org)

## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
----------	---------------------	----------

## 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.