

# iClusterPlus: integrative clustering of multiple genomic data sets

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

October 13, 2014

<sup>1</sup>Division of Biostatistics  
Dan L. Duncan Cancer Center  
Baylor College of Medicine  
[qmo@bcm.edu](mailto:qmo@bcm.edu)

<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

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.