pumaclust User Guide

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1 Introduction

The pumaclust package is to cluster gene expression (1) given the estimated gene expression levels and uncertainties of these measurements from probe-level analysis models, like mgMOS (2) and multi-mgMOS (3) (available in R-package mmgmos). This package makes use of probe-level measurement error in clustering gene expression. The optimisation of parameters in pplr is done by donlp2 (4).

2 Case 1: Loading gene expression data from mmgmos results

If the expression data is stored in an instance of exprReslt class, eset, calculated from mmgmos, the following codes shows how to extract gene expression data from it and pass to pumaclust.

R> e<-exprs(eset) ##extract the mean of expression value into a matrix
R> se<-se.exprs(eset) ##extrac the standard deviation of expression value into a matrix
R> cl<-pumaclust(e,se,clusters=10) ## specify the number of clusters

3 Case 2: Loading gene expression data from csv files

If the results from mmgmos have already been saved in CSV files, data can be loaded directly from these files as the following,

R> cl<-pumaclust(efile="filename_of_exprs.csv", sefile="filename_of_se.csv",clusters=10)

Make sure that gene expression values should be in log2 scale.
References


