

# *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-pacakge *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

- [1] Liu,X., Lin,K.K., Andersen,B., and Rattray,M. (2006) Propagating probe-level uncertainty in model-based gene expression clustering. technical report available upon request.
- [2] Milo,M., Niranjana,M., Holley,M.C., Rattray,M. and Lawrence,N.D. (2004) A probabilistic approach for summarising oligonucleotide gene expression data. Technical report available upon request.
- [3] Liu,X., Milo,M., Lawrence,N.D. and Rattray,M. (2005) A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips. *Bioinformatics*, 21(18):3637-3644.
- [4] Peter Spellucci. DONLP2 code and accompanying documentation. Electronically available via <http://plato.la.asu.edu/donlp2.html>.