Package 'iClusterPlus'

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Title Integrative clustering of multi-type genomic data

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Suggests RUnit, BiocGenerics

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Description Integrative clustering of multiple genomic data using a joint latent variable model.

LazyData yes

License GPL (>= 2)

biocViews Microarray, Clustering

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R topics documented:

`breast.chr17` *Breast cancer data set DNA copy number and mRNA expression measure on chromosome 17*

Description

This is a subset of the breast cancer data from Pollack et al. (2002).

Usage

```
data(breast.chr17)
```

Format

A list object containing two data matrices: DNA and mRNA. They consist chromosome 17 data in 41 samples (4 cell lines and 37 primary tumors).

Source

This data can be downloaded at http://www.pnas.org/content/99/20/12963/suppl/DC1

References

Pollack, J.R. et al. (2002) Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors. Proc. Natl Acad. Sci. USA, 99, 12963-12968.

CNregions *A function to remove redundant copy number regions*

Description

This function is used to reduce copy number regions.

Usage

```
CNregions(seg, epsilon=0.005, adaptive=FALSE, rmCNV=FALSE, cnv=NULL,
       frac.overlap=0.5, rmSmallseg=TRUE, nProbes=15)
```

Arguments

seg	DNAcopy CBS segmentation output.
epsilon	the maximum Euclidean distance between adjacent probes tolerated for denying a nonredundant region. epsilon=0 is equivalent to taking the union of all unique break points across the n samples.
adaptive	Vector of length-m lasso penalty terms.
rmCNV	If TRUE, remove germline CNV.
cnv	A data frame containing germline CNV data.
frac.overlap	A parameter needed to be explain.
rmSmallseg	If TRUE, remove small segment.
nProbes	The segment length threshold below which the segment will be removed if rmSmallseq = TRUE.

Value

A matrix with reduced copy number regions.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References

Qianxing Mo, Sijian Wang, Venkatraman E. Seshan, Adam B. Olshen, Nikolaus Schultz, Chris Sander, R. Scott Powers, Marc Ladanyi, and Ronglai Shen. (2013). Pattern discovery and cancer gene identification in integrated cancer genomic data. Proc. Natl. Acad. Sci. USA.

See Also

breast.chr17,plotiCluster, compute.pod,iCluster,iClusterPlus

Examples

```
#data(gbm)
#library(GenomicRanges)
#library(cluster)
#reducedM=CNregions(seg,epsilon=0,adaptive=FALSE,rmCNV=TRUE,cnv=NULL,
#  frac.overlap=0.5, rmSmallseg=TRUE,nProbes=5)
```

`compute.pod` *A function to compute the proportion of deviation from perfect block diagonal matrix*

Description

A function to compute the proportion of deviation from perfect block diagonal matrix.

Usage

```
compute.pod(fit)
```

Arguments

`fit`	A iCluster object

Value

pod	proportion of deviation from perfect block diagonal matrix

Author(s)

Ronglai Shen <shenr@mskcc.org>

References

Ronglai Shen, Adam Olshen, Marc Ladanyi. (2009). Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. *Bioinformatics* 25, 2906-2912.

See Also

`iCluster`,`iCluster2`, `plotiCluster`

Examples

```
# library(iCluster)
# data(breast.chr17)
# fit=iCluster(breast.chr17, k=4, lambda=c(0.2,0.2))
# plotiCluster(fit=fit, label=rownames(breast.chr17[[2]]))
# compute.pod(fit)
```

coord *genomic coordinates*

Description

genomic coordinates for the copy number data in gbm

Usage

```
data(coord)
```

Format

A data matrix consists of chr number, start and end position for the genes included in the gbm copy number data.

References

Ronglai Shen, Qianxing Mo, Nikolaus Schultz, Venkatraman E. Seshan, Adam B. Olshen, Jason Huse, Marc Ladanyi, Chris Sander. (2012). Integrative Subtype Discovery in Glioblastoma Using iCluster. *PLoS ONE* 7, e35236

gbm *GBM data*

Description

This is a subset of the glioblastoma dataset from the cancer genome atlas (TCGA) GBM study (2009) used in Shen et al. (2012).

Usage

```
data(gbm)
```

Format

A list object containing three data matrices: copy number, methylation and mRNA expression in 84 samples.

Value

`gbm.seg`	GBM copy number segmentation results genereated by DNAcopy package.
`gbm.exp`	GBM gene expression data.
`gbm.mut`	GBM mutation data.

References

Ronglai Shen, Qianxing Mo, Nikolaus Schultz, Venkatraman E. Seshan, Adam B. Olshen, Jason Huse, Marc Ladanyi, Chris Sander. (2012). Integrative Subtype Discovery in Glioblastoma Using iCluster. *PLoS ONE* 7, e35236

`glp` *good lattice points using the uniform design*

Description

good lattice points using the uniform design (Fang and Wang 1995)

Usage

```
data(glp)
```

Format

A list object containing sampling design for s=2-5 where s is the number of tuning parameters.

References

Ronglai Shen, Qianxing Mo, Nikolaus Schultz, Venkatraman E. Seshan, Adam B. Olshen, Jason Huse, Marc Ladanyi, Chris Sander. (2012). Integrative Subtype Discovery in Glioblastoma Using iCluster. *PLoS ONE* 7, e35236

Fang K, Wang Y (1994) Number theoretic methods in statistics. London, UK: Chapman abd Hall.

`iCluster` *Integrative clustering of multiple genomic data types*

Description

Given multiple genomic data types (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, iCluster fits a regularized latent variable model based clustering that generates an integrated cluster assigment based on joint inference across data types

Usage

```
iCluster(datasets, k, lambda, scalar=FALSE, max.iter=50,epsilon=1e-3)
```

Arguments

datasets	A list object containing m data matrices representing m different genomic data types measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features.
k	Number of subtypes.
lambda	Vector of length-m lasso penalty terms.
scalar	If TRUE, assumes scalar covariance matrix Psi. Default is FALSE.
max.iter	Maximum iteration for the EM algorithm.
epsilon	EM algorithm convegence criterion.

Value

A list with the following elements.

meanZ	Relaxed cluster indicator matrix.
beta	Coefficient matrix.
clusters	Cluster assigment.
conv.rate	Convergence history.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References

Ronglai Shen, Adam Olshen, Marc Ladanyi. (2009). Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. *Bioinformatics* 25, 2906-2912.

See Also

breast.chr17,plotiCluster, compute.pod

Examples

```
data(breast.chr17)
fit=iCluster(breast.chr17, k=4, lambda=c(0.2,0.2))
plotiCluster(fit=fit, label=rownames(breast.chr17[[2]]))
compute.pod(fit)

#library(gplots)
#library(lattice)
#col.scheme = alist()
#col.scheme[[1]] = bluered(256)
#col.scheme[[2]] = greenred(256)
#cn.image=breast.chr17[[2]]
#cn.image[cn.image>1.5]=1.5
#cn.image[cn.image< -1.5]= -1.5
```

```
#exp.image=breast.chr17[[1]]
#exp.image[exp.image>3]=3
#exp.image[exp.image< -3]=3
#plotHeatmap(fit, datasets=list(cn.image,exp.image), type=c("gaussian","gaussian"),
#  row.order=c(FALSE,FALSE), width=5, col.scheme=col.scheme)
```

`iCluster2` *Integrative clustering of multiple genomic data types*

Description

Given multiple genomic data types (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, iCluster fits a regularized latent variable model based clustering that generates an integrated cluster assigment based on joint inference across data types

Usage

```
iCluster2(x, K, lambda, method=c("lasso","enet","flasso","glasso","gflasso"),
  chr=NULL, maxiter=50, eps=1e-4, eps2=1e-8)
```

Arguments

`x`	A list object containing m data matrices representing m different genomic data types measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features.
`K`	Number of subtypes.
`lambda`	A list with m elements; each element is a vector with one or two elements depending on the methods used.
`method`	Method used for clustering and variable selection.
`chr`	Chromosome labels
`maxiter`	Maximum iteration for the EM algorithm.
`eps`	EM algorithm convegence criterion 1.
`eps2`	EM algorithm convegence criterion 2.

Value

A list with the following elements.

`cluster`	Cluster assigment.
`centers`	cluster centers.
`Phivec`	parameter phi; a vector.
`beta`	parameter B; a matrix.
`meanZ`	meanZ
`EZZt`	EZZt
`dif`	difference
`iter`	iteration

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>,Ronglai Shen,Sijian Wang

References

Ronglai Shen, Sijian Wang, Qianxing Mo. (2013). Sparse Integrative Clustering of Multiple Omics Data Sets. *Annals of Applied Statistics.* 7(1):269-294

See Also

plotiCluster, compute.pod, iClusterPlus

Examples

```
## clustering
n1 = 20
n2 = 20
n3 = 20
n = n1+n2+n3
p = 5
q = 100

x = NULL
x1a = matrix(rnorm(n1*p), ncol=p)
x2a = matrix(rnorm(n1*p, -1.5,1), ncol=p)
x3a = matrix(rnorm(n1*p, 1.5, 1), ncol=p)
xa = rbind(x1a,x2a,x3a)
xb = matrix(rnorm(n*q), ncol=q)
x[[1]] = cbind(xa,xb)

x1a = matrix(rnorm(n1*p), ncol=p)
x2a = matrix(rnorm(n1*p, -1.5,1), ncol=p)
x3a = matrix(rnorm(n1*p, 1.5, 1), ncol=p)
xa = rbind(x1a,x2a,x3a)
xb = matrix(rnorm(n*q), ncol=q)
x[[2]] = cbind(xa,xb)

x1a = matrix(rnorm(n1*p), ncol=p)
x2a = matrix(rnorm(n1*p, -1.5,1), ncol=p)
x3a = matrix(rnorm(n1*p, 1.5, 1), ncol=p)
xa = rbind(x1a,x2a,x3a)
xb = matrix(rnorm(n*q), ncol=q)
x[[3]] = cbind(xa,xb)


x1a = matrix(rnorm(n1*p), ncol=p)
x2a = matrix(rnorm(n1*p, -1.5,1), ncol=p)
x3a = matrix(rnorm(n1*p, 1.5, 1), ncol=p)
xa = rbind(x1a,x2a,x3a)
xb = matrix(rnorm(n*q), ncol=q)
x[[4]] = cbind(xa,xb)
```

```
x1a = matrix(rnorm(n1*p), ncol=p)
x2a = matrix(rnorm(n1*p, -1.5,1), ncol=p)
x3a = matrix(rnorm(n1*p, 1.5, 1), ncol=p)
xa = rbind(x1a,x2a,x3a)
xb = matrix(rnorm(n*q), ncol=q)
x[[5]] = cbind(xa,xb)

method = c('lasso', 'enet', 'flasso', 'glasso', 'gflasso')
lambda=alist()
lambda[[1]] = 30
lambda[[2]] = c(20,1)
lambda[[3]] = c(20,20)
lambda[[4]] = 30
lambda[[5]] = c(30,20)

chr=c(rep(1,10),rep(2,(p+q)-10))
date()
fit2 = iCluster2(x, K=3, lambda, method=method, chr=chr, maxiter=20,eps=1e-4, eps2=1e-8)
date()

par(mfrow=c(5,1),mar=c(4,4,1,1))
for(i in 1:5){
barplot(fit2$beta[[i]][,1])
}

#library(gplots)
#library(lattice)

#plotHeatmap(fit2, datasets=x, type=rep("gaussian",length(x)),
   #row.order=c(TRUE,TRUE,FALSE,TRUE,FALSE),
   #sparse=rep(FALSE,length(x)), scale=rep("row",5), width=5,
   #col.scheme=rep(list(bluered(256)),length(x)))
```

`iClusterBayes` *Integrative clustering of multiple genomic data types*

Description

Given multiple genomic data types (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, iClusterBayes fits a Bayesian latent variable model that generates an integrated cluster assignment based on joint inference across data types and identifies genomic features that contribute to the clusters.

Usage

```
iClusterBayes(dt1,dt2=NULL,dt3=NULL,dt4=NULL,dt5=NULL,dt6=NULL,
type = c("gaussian","binomial","poisson"),K=2,n.burnin=1000,n.draw=1200,
prior.gamma=rep(0.1,6),sdev=0.5,beta.var.scale=1,thin=1,pp.cutoff=0.5)
```

Arguments

dt1	Data set 1 - a matrix with rows and columns representing samples and genomic features, respectively.
dt2	Data set 2 - a matrix with rows and columns representing samples and genomic features, respectively.
dt3	Data set 3 - a matrix with rows and columns representing samples and genomic features, respectively.
dt4	Data set 4 - a matrix with rows and columns representing samples and genomic features, respectively.
dt5	Data set 5 - a matrix with rows and columns representing samples and genomic features, respectively.
dt6	Data set 6 - a matrix with rows and columns representing samples and genomic features, respectively.
type	Data type corresponding to dt1-6, which can be gaussian, binomial, or poisson.
K	The number of eigen features. Given K, the number of cluster is K+1.
n.burnin	Number of MCMC burnin.
n.draw	Number of MCMC draw.
prior.gamma	Prior probability for the indicator variable gamma of each data set.
sdev	Standard deviation of random walk proposal for the latent variable.
beta.var.scale	A positive value to control the scale of covariance matrix of the proposed beta.
thin	A parameter to thin the MCMC chain in order to reduce autocorrelation. Discard all but every 'thin'th sampling values. When thin=1, all sampling values are kept.
pp.cutoff	Posterior probability cutoff for the indicator variable gamma. The BIC and deviance ratio will be calculated by setting parameter beta to zero when the posterior probability of gamma <= cutoff.

Value

A list with the following elements.

alpha	Intercept parameter.
beta	Information parameter.
beta.pp	Posterior probability of beta. The higher the beta.pp, the more likely the beta should be included in the model.
gamma.ar	Acceptance ratio for the parameter gamma.
beta.ar	Acceptance ratio for the parameter beta.
Z.ar	Acceptance ratio for the latent variable.
clusters	Cluster assignment.
centers	Cluster center.
meanZ	The latent variable.
BIC	Bayesian information criterion.
dev.ratio	see dev.ratio defined in glmnet package.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>

References

Mo Q, Shen R, Guo C, Vannucci M, Chan KS, Hilsenbeck SG. (2018). A fully Bayesian latent variable model for integrative clustering analysis of multi-type omics data. Biostatistics 19(1):71-86.

See Also

tune.iClusterBayes,plotHMBayes,iClusterPlus,tune.iClusterPlus,plotHeatmap

Examples

```
# see iManual.pdf
```

---

iClusterPlus *Integrative clustering of multiple genomic data types*

Description

Given multiple genomic data types (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, iClusterPlus fits a regularized latent variable model based clustering that generates an integrated cluster assignment based on joint inference across data types

Usage

```
iClusterPlus(dt1,dt2=NULL,dt3=NULL,dt4=NULL,
type=c("gaussian","binomial","poisson","multinomial"),
  K=2,alpha=c(1,1,1,1),lambda=c(0.03,0.03,0.03,0.03),
n.burnin=100,n.draw=200,maxiter=20,sdev=0.05,eps=1.0e-4)
```

Arguments

dt1	A data matrix. The rows represent samples, and the columns represent genomic features.
dt2	A data matrix. The rows represent samples, and the columns represent genomic features.
dt3	A data matrix. The rows represent samples, and the columns represent genomic features.
dt4	A data matrix. The rows represent samples, and the columns represent genomic features.
type	Data type, which can be gaussian, binomial, poisson, multinomial.
K	The number of eigen features. Given K, the number of cluster is K+1.

alpha	Vector of elasticnet penalty terms. At this version of iClusterPlus, elasticnet is not used. Therefore, all the elements of alpha are set to 1.
lambda	Vector of lasso penalty terms.
n.burnin	Number of MCMC burnin.
n.draw	Number of MCMC draw.
maxiter	Maximum iteration for the EM algorithm.
sdev	standard deviation of random walk proposal.
eps	Algorithm convergence criterion.

Value

A list with the following elements.

alpha	Intercept parameter.
beta	Information parameter.
clusters	Cluster assignment.
centers	Cluster center.
meanZ	Latent variable.
BIC	Bayesian information criterion.
dev.ratio	see dev.ratio defined in glmnet package.
dif	absolute difference for the parameters in the last and next-to-last iterations.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>,Ronglai Shen, Sijian Wang

References

Qianxing Mo, Sijian Wang, Venkatraman E. Seshan, Adam B. Olshen, Nikolaus Schultz, Chris Sander, R. Scott Powers, Marc Ladanyi, and Ronglai Shen. (2013). Pattern discovery and cancer gene identification in integrated cancer genomic data. *Proc. Natl. Acad. Sci. USA*. 110(11):4245-50.

See Also

plotiCluster,iCluster, compute.pod

Examples

```
# see iManual.pdf
```

plotHeatmap *A function to generate heatmap panels sorted by integrated cluster assignment.*

Description

A function to generate heatmap panels sorted by integrated cluster assignment.

Usage

```
plotHeatmap(fit,datasets,type=c("gaussian","binomial","poisson","multinomial"),
sample.order=NULL,row.order=NULL,sparse=NULL,threshold=rep(0.25,length(datasets)),
width=5,scale=rep("none",length(datasets)),col.scheme=rep(list(bluered(256)),
length(datasets)), chr=NULL, plot.chr=NULL, cap=NULL)
```

Arguments

fit	A iCluster object.
datasets	A list object of data matrices.
type	Types of data in the datasets.
sample.order	User supplied cluster assignment.
row.order	A vector of logical values each specificy whether the genomic features in the corresponding data matrix should be reordered by similarity. Default is TRUE.
sparse	A vector of logical values each specificy whether to plot the top cluster-discriminant features. Default is FALSE.
threshold	When sparse is TRUE, a vector of threshold values to include the genomic features for which the absolute value of the associated coefficient estimates fall in the top quantile. threshold=c(0.25,0.25) takes the top quartile most discriminant features in data type 1 and data type 2 for plot.
width	Width of the figure in inches
scale	A vector of logical values each specify whether data should be scaled. Default is FALSE.
col.scheme	Color scheme. Can use bluered(n) in gplots R package.
chr	A vector of chromosome number.
plot.chr	A vector of logical values each specificy whether to annotate chromosome number on the left of the panel. Typically used for copy number data type. Default is FALSE.
cap	Image color option

Details

The samples are ordered by the cluster assignment using the R code: order(fit$clusters). For each data set, the features are ordered by hierarchical clustering of the features using the complete method and 1-correlation coeffient as the distance.

Value

no value returned.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References

Ronglai Shen, Adam Olshen, Marc Ladanyi. (2009). Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. *Bioinformatics* 25, 2906-2912.

Ronglai Shen, Qianxing Mo, Nikolaus Schultz, Venkatraman E. Seshan, Adam B. Olshen, Jason Huse, Marc Ladanyi, Chris Sander. (2012). Integrative Subtype Discovery in Glioblastoma Using iCluster. *PLoS ONE* 7, e35236

See Also

iCluster,iCluster2

Examples

```
# see iManual.pdf
```

`plotHMBayes` *A function to generate heatmap panels sorted by integrated cluster assignment.*

Description

A function to generate heatmap panels sorted by integrated cluster assignment.

Usage

```
plotHMBayes(fit, datasets, type = c("gaussian", "binomial", "poisson"),
    sample.order = NULL, row.order = NULL, sparse = NULL,
    threshold = rep(0.5,length(datasets)), width = 5,
    scale = rep("none",length(datasets)),
    col.scheme = rep(list(bluered(256)),length(datasets)),
    chr=NULL, plot.chr=NULL, cap=NULL)
```

Arguments

fit	A iClusterBayes object.
datasets	A list object of data matrices.
type	Types of data in the datasets.
sample.order	User supplied cluster assignment.
row.order	A vector of logical values each specify whether the genomic features in the corresponding data matrix should be reordered by similarity. Default is TRUE.
sparse	A vector of logical values each specify whether to plot the top cluster-discriminant features. Default is FALSE.
threshold	When sparse is TRUE, a vector of threshold values to include the genomic features on the heatmap. Each data set should have a threshold. For each data set, a feature with posterior probability greater than the threshold will be included. Default value is 0.5 for each data set.
width	Width of the figure in inches
scale	A vector of logical values each specify whether data should be scaled. Default is FALSE.
col.scheme	Color scheme. Can use bluered(n) in gplots R package.
chr	A vector of chromosome number.
plot.chr	A vector of logical values each specify whether to annotate chromosome number on the left of the panel. Typically used for copy number data type. Default is FALSE.
cap	Image color option

Details

The samples are ordered by the cluster assignment by the R code: order(fit$clusters). For each data set, the features are ordered by hierarchical clustering of the features using the complete method and 1-correlation coefficient as the distance.

Value

no value returned.

Author(s)

Ronglai Shen <shenr@mskcc.org>,Qianxing Mo <qianxing.mo@moffitt.org>

References

Mo Q, Shen R, Guo C, Vannucci M, Chan KS, Hilsenbeck SG. (2018). A fully Bayesian latent variable model for integrative clustering analysis of multi-type omics data. Biostatistics 19(1):71-86.

See Also

iClusterBayes,plotHeatmap

Examples

```
# see iManual.pdf
```

`plotiCluster` *A function to generate cluster separability matrix plot.*

Description

A function to generate cluster separability matrix plot.

Usage

```
plotiCluster(fit,label=NULL)
```

Arguments

`fit`	A iCluster object
`label`	Sample labels

Value

no value returned.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References

Ronglai Shen, Adam Olshen, Marc Ladanyi. (2009). Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. *Bioinformatics* 25, 2906-2912.

See Also

`iCluster`, `compute.pod`

Examples

```
# library(iCluster)
# data(breast.chr17)
# fit=iCluster(datasets=breast.chr17, k=4, lambda=c(0.2,0.2))
# plotiCluster(fit=fit, label=rownames(breast.chr17[[2]]))
# compute.pod(fit)
```

plotRI *A function to generate reproducibility index plot.*

Description

A function to generate reproducibility index plot.

Usage

```
plotRI(cv.fit)
```

Arguments

cv.fit	A tune.iCluster2 object

Value

no value returned.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References

Ronglai Shen, Adam Olshen, Marc Ladanyi. (2009). Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. *Bioinformatics* 25, 2906-2912.

Ronglai Shen, Qianxing Mo, Nikolaus Schultz, Venkatraman E. Seshan, Adam B. Olshen, Jason Huse, Marc Ladanyi, Chris Sander. (2012). Integrative Subtype Discovery in Glioblastoma Using iCluster. *PLoS ONE* 7, e35236

See Also

iCluster

Examples

```
#data(simu.datasets)
#cv.fit=alist()
#for(k in 2:5){
#  cat(paste("K=",k,sep=""),'\n')
#  cv.fit[[k]]=tune.iCluster2(datasets=simu.datasets, k,nrep=2, n.lambda=8)
#}

##Reproducibility index (RI) plot
#plotRI(cv.fit)
```

simuResult — *The results for the analysis of the simulated data.*

Description

The simulation and analyis are described in iClusterPlus/inst/unitTests/test_iClusterPlus.R.

Usage

```
data(simuResult)
```

Format

list

Value

A list of objects returned by the iClusterPlus function.

References

iClusterPlus/inst/unitTests/test_iClusterPlus.R

tune.iCluster2 — *Integrative clustering of multiple genomic data types*

Description

Given multiple genomic data types (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, iCluster fits a regularized latent variable model based clustering that generates an integrated cluster assignment based on joint inference across data types

Usage

```
tune.iCluster2(x, K, method=c("lasso","enet","flasso","glasso","gflasso"),base=200,
 chr=NULL,true.class=NULL,lambda=NULL,n.lambda=NULL,save.nonsparse=F,nrep=10,eps=1e-4)
```

Arguments

x	A list object containing m data matrices representing m different genomic data types measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features.
K	Number of subtypes.
lambda	User supplied matrix of lambda to tune.
method	Method used for clustering and variable selection.

chr	Chromosome labels
n.lambda	Number of lambda to sample using uniform design.
nrep	Fold of cross-validation.
base	Base.
true.class	True class label if available.
save.nonsparse	Logic argument whether to save the nonsparse fit.
eps	EM algorithm convergence criterion

Value

A list with the following elements.

best.fit	Best fit.
best.lambda	Best lambda.
ps	Rand index
ps.adjusted	Adjusted Rand index.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>,Ronglai Shen,Sijian Wang

References

Ronglai Shen, Sijian Wang, Qianxing Mo. (2013). Sparse Integrative Clustering of Multiple Omics Data Sets. *Annals of Applied Statistics.* 7(1):269-294

See Also

iCluster2

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tune.iClusterBayes *Integrative clustering of multiple genomic data*

Description

In order to determining the appropriate number of clusters, tune.iClusterBayes calls iClusterBayes function and performs parallel computation for K=1,2,....

Usage

```
tune.iClusterBayes(cpus=6,dt1,dt2=NULL,dt3=NULL,dt4=NULL,dt5=NULL,dt6=NULL,
type=c("gaussian","binomial","poisson"),
    K=1:6,n.burnin=1000,n.draw=1200,prior.gamma=rep(0.1,6),
sdev=0.5,beta.var.scale=1,thin=1,pp.cutoff=0.5)
```

Arguments

cpus	Number of CPU used for parallel computation. If possible, let it be equal to the number of Ks.
dt1	Data set 1 - a matrix with rows and columns representing samples and genomic features, respectively.
dt2	Data set 2 - a matrix with rows and columns representing samples and genomic features, respectively.
dt3	Data set 3 - a matrix with rows and columns representing samples and genomic features, respectively.
dt4	Data set 4 - a matrix with rows and columns representing samples and genomic features, respectively.
dt5	Data set 5 - a matrix with rows and columns representing samples and genomic features, respectively.
dt6	Data set 6 - a matrix with rows and columns representing samples and genomic features, respectively.
type	Data type corresponding to dt1-6, which can be gaussian, binomial, poisson.
K	A vector. Each element is the number of eigen features. Given k, the number of cluster is k+1.
n.burnin	Number of MCMC burnin.
n.draw	Number of MCMC draw.
prior.gamma	Prior probability for the indicator variable gamma of each data set.
sdev	Standard deviation of random walk proposal for the latent variable.
beta.var.scale	A positive value to control the scale of covariance matrix of the proposed beta.
thin	A parameter to thin the MCMC chain in order to reduce autocorrelation. Discard all but every 'thin'th sampling values. When thin=1, all sampling values are kept.
pp.cutoff	Posterior probability cutoff for the indicator variable gamma. The BIC and deviance ratio will be calculated by setting parameter beta to zero when the posterior probability of gamma <= cutoff.

Value

A list named 'fit'. fit[[i]] is an object return by iClusterBayes, corresponding to the ith element in K. Each component of fit has the following elements.

alpha	Intercept parameter.
beta	Information parameter.
beta.pp	Posterior probability of beta. The higher the beta.pp, the more likely the beta should be included in the model.
gamma.ar	Acceptance ratio for parameter gamma.
beta.ar	Acceptance ratio for parameter beta.
Z.ar	Acceptance ratio for the latent variable.

clusters	Cluster assignment.
centers	Cluster center.
meanZ	Latent variable.
BIC	Bayesian information criterion.
dev.ratio	See dev.ratio defined in glmnet package.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>

References

Mo Q, Shen R, Guo C, Vannucci M, Chan KS, Hilsenbeck SG. (2018). A fully Bayesian latent variable model for integrative clustering analysis of multi-type omics data. Biostatistics 19(1):71-86.

See Also

iClusterBayes,plotHMBayes,iClusterPlus,tune.iClusterPlus,plotHeatmap

Examples

```
### see the users' guide iManul.pdf
```

---

tune.iClusterPlus *Integrative clustering of multiple genomic data*

Description

Given multiple genomic data (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, tune.iClusterPlus uses a series of lambda values to fit a regularized latent variable model based clustering that generates an integrated cluster assignment based on joint inference across data.

Usage

```
tune.iClusterPlus(cpus=8,dt1,dt2=NULL,dt3=NULL,dt4=NULL,
  type=c("gaussian","binomial","poisson","multinomial"),
  K=2,alpha=c(1,1,1,1),n.lambda=NULL,scale.lambda=c(1,1,1,1),
  n.burnin=200,n.draw=200,maxiter=20,sdev=0.05,eps=1.0e-4)
```

Arguments

cpus	Number of CPU used for parallel computation.
dt1	A data matrix. The rows represent samples, and the columns represent genomic features.
dt2	A data matrix. The rows represent samples, and the columns represent genomic features.
dt3	A data matrix. The rows represent samples, and the columns represent genomic features.
dt4	A data matrix. The rows represent samples, and the columns represent genomic features.
type	data type, which can be "gaussian","binomial","poisson", and"multinomial".
K	The number of eigen features. Given K, the number of cluster is K+1.
alpha	Vector of elasticnet penalty terms. At this version of iClusterPlus, elasticnet is not used. Therefore, all the elements of alpha are set to 1.
n.lambda	Number of lambda are tuned.
scale.lambda	A value between (0,1); the actual lambda values will be scale.lambda multiplying the lambda values of the uniform design.
n.burnin	Number of MCMC burnin.
n.draw	Number of MCMC draw.
maxiter	Maximum iteration for the EM algorithm.
sdev	standard deviation of random walk proposal.
eps	EM algorithm convergence criterion.

Value

A list with the two elements 'fit' and 'lambda', where fit itself is a list and lambda is a matrix. Each row of lambda is the lambda values used to fit iClusterPlus model. Each component of fit is an object return by iClusterPlus, one-to-one corresponding to the row of lambda. Each component of fit has the following objects.

alpha	Intercept parameter for the genomic features.
beta	Information parameter for the genomic features. The rows and the columns represent the genomic features and the coefficients for the latent variable, respectively.
clusters	Cluster assignment.
centers	Cluster centers.
meanZ	Latent variable.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>, Ronglai Shen <shenr$mskcc.org>

References

Qianxing Mo, Sijian Wang, Venkatraman E. Seshan, Adam B. Olshen, Nikolaus Schultz, Chris Sander, R. Scott Powers, Marc Ladanyi, and Ronglai Shen. (2012). Pattern discovery and cancer gene identification in integrated cancer genomic data. Proc. Natl. Acad. Sci. USA 110(11):4245-50.

See Also

plotiCluster,iClusterPlus,iCluster2,iCluster, compute.pod

Examples

```
### see the users' guide iManul.pdf
```

`utility` *Utility functions for iClusterPlus package*

Description

Some utility functions for processing the results produced by iClusterPlus methods.

Usage

```
getBIC(resultList)
getDevR(resultList)
getClusters(resultList)
iManual(view=TRUE)
```

Arguments

`resultList`	A list object as shown in the following example.
`view`	A logical value TRUE or FALSE

Value

`getBIC`	produce a matrix containing the BIC value for each lambda and K; the rows correspond to the lambda (vector) and the columns correspond to the K latent variables.
`getDevR`	produce a matrix containing the deviance ratio for each lambda and K; the rows correspond to the lambda (vector) and the columns correspond to the K latent variables.
`getClusters`	produce a matrix containing the cluster assigments for the samples under each K; the rows correspond to the samples; the columns correspond to the K latent variables.
`iManual`	Open the iClusterPlus User's Guide.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>

References

Qianxing Mo, Sijian Wang, Venkatraman E. Seshan, Adam B. Olshen, Nikolaus Schultz, Chris Sander, R. Scott Powers, Marc Ladanyi, and Ronglai Shen. (2012). Pattern discovery and cancer gene identification in integrated cancer genomic data. Proc. Natl. Acad. Sci. USA (invited revision).

See Also

tune.iClusterPlus, iClusterPlus, iCluster2

Examples

```
### see the users' guide iManual.pdf

#data(simuResult)
#BIC = getBIC(simuResult)
#devR = getDevR(simuResult)
#clusters = getClusters(simuResult)
```

---

variation.hg18.v10.nov.2010

Human genome variants of the NCBI 36 (hg18) assembly

Description

Human genome variants of the NCBI 36 (hg18) assembly

Usage

```
data(variation.hg18.v10.nov.2010)
```

Format

data frame

Value

variation.hg18.v10.nov.2010

Human genome variants of the NCBI 36 (hg18) assembly

References

http://projects.tcag.ca/variation/tableview.asp?table=DGV_Content_Summary.txt

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