Package ‘iClusterPlus’

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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

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.
known 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 rmSmallseg = 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

See Also

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

```r
# data(gbm)
# library(GenomicRanges)
# library(cluster)
# reducedM=CNregions(seg, epsilon=0, adaptive=FALSE, rmCNV=TRUE, cvn=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

```r
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


### See Also

`iCluster`, `iCluster2`, `plotiCluster`

### Examples

```r
# 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

<table>
<thead>
<tr>
<th>coord</th>
<th>genomic coordinates</th>
</tr>
</thead>
</table>

**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**


---

gbm

**GBM data**

<table>
<thead>
<tr>
<th>gbm</th>
<th>GBM data</th>
</tr>
</thead>
</table>

**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 generated by DNAcopy package. |
| gbm.exp | GBM gene expression data. |
| gbm.mut | GBM mutation data. |
References


---

**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**


---

**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 assignment 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 convergence criterion.

Value

A list with the following elements.

- **meanZ**: Relaxed cluster indicator matrix.
- **beta**: Coefficient matrix.
- **clusters**: Cluster assignment.
- **conv.rate**: Convergence history.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References


See Also

- `breast.chr17`, `plotiCluster`, `compute.pod`

Examples

```r
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)
```

```r
#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 assignment based on joint inference across data types.

**Usage**

```r
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 convergence criterion 1.
- `eps2`: EM algorithm convergence criterion 2.

**Value**

A list with the following elements.

- `cluster`: Cluster assignment.
- `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

See Also
plotiCluster, compute.pod, iClusterPlus

Examples
```r
## 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)
```
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

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


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 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 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.
- 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 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 coefficient as the distance.
Value

no value returned.

Author(s)

Ronglai Shen <shenr@mskcc.org>

References


See Also

iCluster.iCluster2

Examples

```r
# see iManual.pdf

plotHMBayes
```

---

**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**

```r
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)
```
plotHMBayes

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


See Also

iClusterBayes, plotHeatmap
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

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

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

```r
#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 analysis 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.
Description

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

Usage

```r
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

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,lambda=NULL,
    scale.lambda=c(1,1,1,1),maxiter=20,sdev=0.05,eps=1.0e-4)
**tune.iClusterPlus**

**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

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 assignments for the samples under each K; the rows correspond to the samples; the columns correspond to the K latent variables.

variation.hg18.v10.nov.2010

Author(s)
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References

See Also
tune.iClusterPlus, iClusterPlus, iCluster2

Examples
### see the users’ guide iManual.pdf

```r
#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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