

Package ‘iClusterPlus’

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

LazyData yes

LazyDataCompression bzip2

License GPL (>= 2)

biocViews Multi-omics, Clustering

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| | |
|--------------|--|
| breast.chr17 | <i>Breast cancer data set DNA copy number and mRNA expression measure on chromosome 17</i> |
|--------------|--|

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=5)
```

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 | Fraction of overlap between 2 segments. If rmCNV=TRUE, overlapped segments will be removed if the overlapped fraction \geq fra.overlap. |
| 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 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 | <i>genomic coordinates</i> |
|-------|----------------------------|

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 | <i>GBM data</i> |
|-----|-----------------|

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

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 and 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 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 Ψ . 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

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)
```

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

```
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

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)))

```

iCluster2b

Integrative clustering of multi-omics data

Description

Given multi-omics data (e.g., copy number, gene expression, DNA methylation) measured in the same set of samples, iCluster2b fits a regularized latent factor(variable) model that generates an latent factor matrix that can be used for integrative clustering of samples. In addition, the driver features of sample clustering can be identified by sparse coefficient matrices.

Usage

```

iCluster2b(xList,K=3, lambda, method=c("lasso","enet","flasso","glasso","gflasso"),
  chr=NULL, EM.iter=25, eps=1e-4, eps2=1e-6)

```

Arguments

| | |
|---------|---|
| xList | A list object containing m data matrices representing m multi-omics data measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features. |
| K | An integer representing the number of the latent factors used for modeling. |
| lambda | A list with m elements corresponding to the method argument. For lasso and glasso, each element is a positive value. For enet, flasso and gflasso, each element is a vector with two positive values. |
| method | Method used for variable selection. |
| chr | Chromosome labels |
| EM.iter | 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.

| | |
|-------|--|
| meanZ | A $n \times k$ matrix; the rows represent samples and the columns represent the K factors. |
| beta | A list object containing m coefficient matrices corresponding to the m data matrices. |
| iter | EM 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

[tune.iCluster2b](#), [iClusterPlus2](#), [iClusterBayes](#)

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 = iCluster2b(x, K=3, lambda, method=method, chr=chr, EM.iter=20,eps=1e-4, eps2=1e-6)
date()

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

```

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
```

| | |
|----------------|---|
| iClusterBayes2 | <i>Integrative clustering of multi-omics data</i> |
|----------------|---|

Description

Given multi-omics data (e.g., Somatic mutation, copy number, gene expression, DNA methylation) measured in the same set of samples, iClusterBayes2 fits a Bayesian latent factor model that generates an latent factor matrix that can be used for integrative clustering of samples. In addition, the driver features of sample clustering can be identified by the posterior probability of the model parameters.

Usage

```
iClusterBayes2(xList, type = c("gaussian", "binomial", "poisson"), K=3, 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

| | |
|----------------|---|
| xList | A list object containing m data matrices representing m multi-omics data measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features. The allowed maximum number of data matrices is 6 ($m < 7$). |
| type | Data type corresponding to the data matrices in xList, which can be gaussian, binomial, or poisson. |
| K | An integer representing the number of the latent factors used for modeling. |
| 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 \leq cutoff. |

Value

A list with the following elements.

| | |
|-----------|---|
| alpha | A list of object for the intercept parameters corresponding to the m data matrices. |
| beta | A list object containing m coefficient matrices corresponding to the m data matrices. |
| meanZ | A n x k matrix; the rows represent samples and the columns represent the K factors. |
| beta.pp | A list of posterior probability for the parameter beta. The higher the beta.pp, the more likely the beta should be included in the model. |
| gamma.ar | A list of acceptance ratio for the parameter gamma. |
| beta.ar | A list of acceptance ratio for the parameter beta. |
| Z.ar | Acceptance ratio for 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

[iClusterPlus2,plotHMBayes,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
```

| | |
|---------------|---|
| iClusterPlus2 | <i>Integrative clustering of multi-omics data</i> |
|---------------|---|

Description

Given multi-omics data (e.g., somatic mutation, copy number, gene expression, DNA methylation) measured in the same set of samples, iClusterPlus2 fits a regularized latent factor(variable) model that generates an latent factor matrix that can be used for integrative clustering of samples. In addition, the driver features of sample clustering can be identified by sparse coefficient matrices.

Usage

```
iClusterPlus2(xList, type=c("gaussian", "binomial", "poisson", "multinomial"), K=3,
              n.burnin=100, n.draw=200, maxiter=25, sdev=0.05, lambda.scale=1/3,
              BICrate.cutoff=rep(0.01, 4), min.shrinkage.rate=rep(0.05, 4))
```

Arguments

| | |
|---------------------------------|---|
| <code>xList</code> | A list object containing m data matrices representing m multi-omics data measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features. |
| <code>type</code> | Data type, which can be gaussian, binomial, poisson, multinomial. |
| <code>K</code> | An integer representing the number of the latent factors used for modeling. |
| <code>n.burnin</code> | Number of MCMC burnin. |
| <code>n.draw</code> | Number of MCMC draw. |
| <code>maxiter</code> | Maximum iteration for the EM algorithm. |
| <code>sdev</code> | standard deviation of random walk proposal. |
| <code>lambda.scale</code> | scaling factor for the lasso regularization parameter when the data type is binomial. Empirically, <code>lambda.scale</code> is within (0.1, 1). |
| <code>BICrate.cutoff</code> | BIC rate between iteration $i+1$ and i . If BIC rate $<$ BICrate.cutoff, the search for optimal lambda will stop. |
| <code>min.shrinkage.rate</code> | The minimum lasso shrinkage rates for multi-omics features. |

Value

A list with the following elements.

| | |
|------------------------|--|
| <code>alpha</code> | A list of object for the intercept parameters corresponding to the m data matrices. |
| <code>beta</code> | A list object containing m coefficient matrices corresponding to the m data matrices. |
| <code>meanZ</code> | A $n \times k$ matrix; the rows represent samples and the columns represent the K factors. |
| <code>BIC</code> | Bayesian information criterion. |
| <code>dev.ratio</code> | see <code>dev.ratio</code> defined in <code>glmnet</code> package. |
| <code>lambda</code> | Final lasso regularization parameters used for iCluster modeling. |

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. (2013). Pattern discovery and cancer gene identification in integrated cancer genomic data. *Proc. Natl. Acad. Sci. USA*. 110(11):4245-50.

See Also

[tune.iCluster2b](#), [iClusterPlus](#), [iClusterBayes](#)

Examples

```
# see iManual.pdf
```

pcaVarPlot

A function to make PCA variance plot of the combined matrix of multi-omics data matrices.

Description

Multi-omics data matrices are column-combined and then the PCA variance plot of the combined matrix is made.

Usage

```
pcaVarPlot(xList,K=10)
```

Arguments

| | |
|-------|---|
| xList | A list object containing m data matrices representing m multi-omics data measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features. |
| K | The number of principle components. |

Value

no value returned.

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>

References

TBD

See Also

[tune.iCluster2b](#), [iClusterPlus2](#), [iClusterBayes](#), [plotHeatmap](#)

Examples

```
# see tutorials
```

| | |
|-------------|---|
| plotHeatmap | <i>A function to generate heatmap panels sorted by integrated cluster assignment.</i> |
|-------------|---|

Description

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

Usage

```
plotHeatmap(fit, xList, type=c("gaussian", "binomial", "poisson", "multinomial"), sample.order=NULL,
            dist.method = "euclidean", hclust.method="ward.D", sparse=NULL, threshold=rep(0.25,length(
            feature.scale=rep(F,length(xList))), col.scheme=rep(list(bluered(256)),length(xList)), wi
            chr=NULL, plot.chr=NULL, cap=rep(0,length(xList)))
```

Arguments

| | |
|---------------|--|
| fit | A iCluster object. |
| xList | A list object of data matrices. |
| type | Types of data in the xList. |
| sample.order | User supplied cluster assignment. |
| feature.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. |
| dist.method | Method used to calculate distance (similarity) between features. Default method is "euclidean". Another choice is "correlation", which is Pearson correlation coefficient. |
| hclust.method | Method passed to hclust function. See hclust for details. |
| 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. |
| feature.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. |
| width | Width of the figure in inches. |
| 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 | A numeric vector used to control the heatmap colors. For example, cap=c(0,0.0.95,0.95) indicates that no truncation for the image data used to make heatmap 1 data, and the data used to make heatmaps 2 and 3 are truncated at 95% quantile. |

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 `hclust.method` and euclidean (or 1-correlation coefficient) as the distance.

Value

`feature.hclust` A list of objects returned by "hclust" that describes the tree produced by the clustering process. For a given data matrix, if `feature.order` is TRUE, the features of the data matrix are ordered by the tree generated by "hclust". Please see "hclust" for details.

`image.data` A list of data matrices used to make the heatmaps.

Author(s)

Ronglai Shen <shenr@mskcc.org>; Qianxing Mo <qianxing.mo@moffitt.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](#), [iCluster2b](#), [iClusterPlus2](#)

Examples

```
# see iManual.pdf
```

| | |
|-------------|---|
| plotHMBayes | <i>A function to generate heatmap panels sorted by integrated cluster assignment.</i> |
|-------------|---|

Description

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

Usage

```
plotHMBayes(fit, xList, type = c("gaussian", "binomial", "poisson"),
  sample.order = NULL, feature.order = NULL, dist.method="euclidean", hclust.method="ward.D",
  sparse = NULL, threshold = rep(0.5,length(xList)), feature.scale = rep(F,length(xList)),
  col.scheme = rep(list(bluered(256)),length(xList)), width=5, chr=NULL,
  plot.chr=NULL, cap=rep(0,length(xList)))
```

Arguments

| | |
|----------------------------|--|
| <code>fit</code> | A <code>iClusterBayes</code> object. |
| <code>xList</code> | A list object of data matrices. |
| <code>type</code> | Types of data in the <code>xList</code> . |
| <code>sample.order</code> | User supplied cluster assignment. |
| <code>feature.order</code> | A vector of logical values each specify whether the genomic features in the corresponding data matrix should be reordered by similarity. Default is <code>TRUE</code> . |
| <code>dist.method</code> | Method used to calculate distance (similarity) between features. Default method is "euclidean". Another choice is "correlation", which is Pearson correlation coefficient. |
| <code>hclust.method</code> | Method passed to <code>hclust</code> function. See <code>hclust</code> for details. |
| <code>sparse</code> | A vector of logical values each specify whether to plot the top cluster-discriminant features. Default is <code>FALSE</code> . |
| <code>threshold</code> | When <code>sparse</code> is <code>TRUE</code> , 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. |
| <code>feature.scale</code> | A vector of logical values each specify whether data should be scaled. Default is <code>FALSE</code> . |
| <code>col.scheme</code> | Color scheme. Can use <code>bluered(n)</code> in <code>gplots</code> R package. |
| <code>width</code> | Width of the figure in inches. |
| <code>chr</code> | A vector of chromosome number. |
| <code>plot.chr</code> | 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 <code>FALSE</code> . |
| <code>cap</code> | A numeric vector used to control the heatmap colors. For example, <code>cap=c(0,0.0.95,0.95)</code> indicates that no truncation for the image data used to make heatmap 1 data, and the data used to make heatmaps 2 and 3 are truncated at 95% quantile. |

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 `hclust.method` and euclidean (or 1-correlation coefficient) as the distance.

Value

| | |
|-----------------------------|--|
| <code>feature.hclust</code> | A list of objects returned by "hclust" that describes the tree produced by the clustering process. For a given data matrix, if <code>feature.order</code> is <code>TRUE</code> , the features of the data matrix are ordered by the tree generated by "hclust". Please see "hclust" for details. |
| <code>image.data</code> | A list of data matrices used to make the heatmaps. |
| | 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 | <i>A function to generate cluster separability matrix plot.</i> |
|--------------|---|

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)
```

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](#)

tune.iCluster2b *Integrative clustering of multi-omics data*

Description

This function finds optimal lasso regularization parameters for iCluster2b.

Usage

```
tune.iCluster2b(xList,K=3,method=c("lasso","enet"),min.lambda=10,max.lambda=500,
  lambda.iter=25,EM.iter=25,min.shrinkage.rate=rep(0.05,length(xList)), eps=1e-4, eps2=1e-6)
```

Arguments

| | |
|--------------------|---|
| xList | A list object containing m data matrices representing m multi-omics data measured in a set of n samples. For each matrix, the rows represent samples, and the columns represent genomic features. |
| K | An positive integer representing the number of the latent factors used for modeling. |
| method | Method used for the regularization of model parameters. |
| min.lambda | The minimum value of the lasso regularization parameter. |
| max.lambda | The maximum value of the lasso regularization parameter. |
| lambda.iter | the number of iteration to find an optimal lambda. |
| EM.iter | The number of iteration for the EM algorithm. |
| min.shrinkage.rate | The minimum lasso shrinkage rates for multi-omics features. |
| eps | EM algorithm convergence criterion 1. |
| eps2 | EM algorithm convergence criterion 2. |

Value

A list with the following elements.

| | |
|--------|---|
| meanZ | A n x k matrix; the rows represent samples and the columns represent the K factors. |
| beta | A list object containing m coefficient matrices corresponding to the m data matrices. |
| lambda | Final lasso regularization parameters used for iCluster modeling. |

Author(s)

Qianxing Mo <qianxing.mo@moffitt.org>

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

[iCluster2b](#), [iClusterPlus2](#), [iClusterBayes](#)

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 $K=1,2,\dots$

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 \leq 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 iManu1.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 iManu1.pdf
```

UM

Uveal Melanoma data

Description

This is a subset of the uveal melanoma (UM) multi-omics data from the cancer genome atlas (TCGA) study (2018), which were re-analyzed by Mo et al. (2021).

Usage

```
data(UM)
```

Format

Data matrices of somatic mutation, DNA copy number, methylation and mRNA expression for 80 UM primary samples.

Details

The TCGA UM multi-omics data (version 2016_01_28) were obtained from the Firebrowse portal (<http://firebrowse.org/>, accessed on 19 December 2018). The level 3 multi-omics data were processed for iCluster analysis, which were detailed in the Materials and Methods of Mo et al. (2021).

Value

| | |
|-------------|--|
| mut02 | Somatic mutation data matrix with 0 representing wild type and 1 representing somatic mutation. Genes with mutation rate $\geq 2\%$ in the 80 samples are kept in the data matrix. |
| cn | Copy number regions, which were generated by merging the log2 ratios of chromosome segments using the CNregions function. |
| methy25 | Methylation data matrix made of the top 25% most variable genes. |
| mrna25 | mRNA expression data matrix made of the top 25% most variable genes. |
| methy25Anno | Annotation for the genes in the methylation data matrix methy25. |
| clin4 | Clinical data of the 80 UM samples. |

References

Robertson, A.G.; Shih, J.; Yau, C.; Gibb, E.A.; Oba, J.; Mungall, K.L.; Hess, J.M.; Uzunangelov, V.; Walter, V.; Danilova, L.; et al. Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. 2018. *Cancer Cell* 33 (1), 151.

Mo, Q; Wan, L; Schell, MJ; Jim, H; Tworoger, SS; G Peng, G. Integrative analysis identifies multi-omics signatures that drive molecular classification of uveal melanoma. 2021. *Cancers* 13 (24), 6168

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. |
| 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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