Package ‘malani’

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Type Package

Title Machine Learning Assisted Network Inference

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Description Find dark genes. These genes are often disregarded due to no detected mutation or differential expression, but are important in coordinating the functionality in cancer networks.

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LazyData TRUE

Depends e1071, stats

RoxygenNote 5.0.1

NeedsCompilation no

Repository CRAN

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Contents

`dat` *A matrix of expression values.*

Description

A numeric matrix 100*20.

Usage

```
dat
```

Format

matrix.

`grp` *A vector of class labels for `dat`.*

Description

Vector length of 20.

Usage

```
grp
```

Format

vector

`Gsvmod` *G SVM models.*

Description

Returns accuracy performance of all genes. G support vector machine (SVM) classifiers trained using G different data matrixes, are used to predict labels in test data. Models are ranked based on prediction performances.

Usage

```
Gsvmod(dat.train, lab.train, dat.test, lab.test)
```

Arguments

`dat.train`	Train data with G features and (k-1)*S/k samples. Parameter k comes from cross-validation scheme and is specified by user (default is 2).
`lab.train`	Class labels for train data.
`dat.test`	Test data with G features and S/k samples.
`lab.test`	Class labels for test data.

Value

Accuracy scores for models. Each model represents one gene.

`intGenes` *Select initial gene list from original data matrix.*

Description

Train G-1 SVM models in `k-fold` cross validation scheme to select initial genes list.

Usage

```
intGenes(dat, grp, nfolds.out = 2, top.per = 0.05)
```

Arguments

`dat`	Original gene expression data matrix with G rows (number of genes) and S column (number of samples).
`grp`	Class labels.
`nfolds.out`	Outer cross validation number (default is 2).
`top.per`	All genes are ranked based on their models performance and `top.per%` of them are selected as initial genes.

Value

Selected initial genes.

Examples

```
data(malanidata)
int <- intGenes(dat,grp)
print(int$top.genes)
```

`malanidata` *Dataset for malani package*

Description

A numeric matrix G*S contains gene expressions data. G are the genes (rows) and S are the samples (columns).

Usage

```
malanidata
```

Format

A matrix of numeric values, 100 genes, 20 samples and class labels.

Examples

```
data(malanidata)
```

`pairmod` *Find best performing pairs*

Description

Combine each gene in initial set with all genes in the original set. Top `npair` pairs are selected to construct the `Q` matrix.

Usage

```
pairmod(X, LX, theta, npair = 10)
```

Arguments

`X`	Original gene expression data matrix. With G rows (number of genes) and S column (number of samples).
`LX`	Class labels.
`theta`	Initial gene set.
`npair`	Given a gene in initial set, top `npair` best performing pairs correspond to that gene are selected (Default is 10).

Value

Best (`npair*G/20`) performing pairs.

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