Package ‘JRF’

October 25, 2016

Version 0.1-4
Date 2015-11-17
Title Joint Random Forest (JRF) for the Simultaneous Estimation of Multiple Related Networks
Depends R (>= 3.0.0)
Suggests MASS
Description Simultaneous estimation of multiple related networks.
License GPL (>= 2)
URL https://www.r-project.org
NeedsCompilation yes
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Repository CRAN
Date/Publication 2016-10-25 20:31:57

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**Description**

Algorithm for the simultaneous estimation of multiple related networks. Some of the functions utilized are a modified version of functions contained in the R package randomForest (A. Liaw and M. Wiener, 2002).

**Usage**

\[ \text{JRF}(X, \text{ntree}, \text{mtry}, \text{genes.name}) \]

**Arguments**

- **X** List object containing expression data for each class, \( X = \text{list}(x_1, x_2, \ldots) \) where \( x_j \) is a \((p \times n_j)\) matrix with rows corresponding to genes and columns to samples. Missing values are not allowed.
- **ntree** numeric value: number of trees.
- **mtry** numeric value: number of predictors to be sampled at each node.
- **genes.name** vector containing genes name. The order needs to match the rows of \( x_j \).

**Value**

A matrix with \( i \) rows and \( c + R \) columns where \( i \) is the total number of gene-gene interactions and \( c \) is the number of classes. The first two columns contain gene names for each interaction while the remaining columns contain importance scores for different classes.

**References**


**Examples**

```r
# --- Derive weighted networks via JRF
nclasses=2 # number of data sets / classes
n1<n2<20 # sample size for each data sets
p<5 # number of variables (genes)
genese.name<-paste("G",seq(1,p),sep="") # genes name

# --- Generate data sets
```
data1 <- matrix(rnorm(p*n1), p, n1)  # generate data1
data2 <- matrix(rnorm(p*n2), p, n1)  # generate data2

# --- Standardize variables to mean 0 and variance 1

data1 <- t(apply(data1, 1, function(x) (x - mean(x)) / sd(x)))
data2 <- t(apply(data2, 1, function(x) (x - mean(x)) / sd(x)))

# --- Run JRF and obtain importance score of interactions for each class
out <- JRF(list(data1, data2), mtry=round(sqrt(p-1)), ntree=1000, genes.name)

---

**JRF_network**  
*Compute FDR of importance scores and return class-specific networks.*

**Description**

This function computes FDR of importance scores and returns class-specific networks.

**Usage**

JRF_network(out.jrf, out.perm, TH)

**Arguments**

- out.jrf: output object from function JRF.
- out.perm: output object from function Run_permutation.
- TH: Threshold for FDR.

**Value**

out list object containing the estimated gene-gene interactions for each class.

**References**


Examples

```r
# --- Derive weighted networks via JRF
nclasses=2                    # number of data sets / classes
n1<-n2<-20                   # sample size for each data sets
p<5                          # number of variables (genes)
genes.name<-paste("G",seq(1,p),sep="")  # genes name
M=5;                         # total number of permutations
fdr=.001;                     # fdr threshold

# --- Generate data sets
data1<-matrix(rnorm(p*n1),p,n1)  # generate data1
data2<-matrix(rnorm(p*n2),p,n1)  # generate data2
data1[1,]<-2*data1[2,]          # variable 1 and 2 interact under class 1

# --- Standardize variables to mean 0 and variance 1
data1 <- t(apply(data1, 1, function(x) { (x - mean(x)) / sd(x) } ))
data2 <- t(apply(data2, 1, function(x) { (x - mean(x)) / sd(x) } ))

# --- Run JRF and obtain importance score of interactions for each class
out<JRF(list(data1,data2),mtry=round(sqrt(p-1)),ntree=1000,genes.name)
out.perm<Run_permutation(list(data1,data2),mtry=round(sqrt(p-1)),ntree=1000,genes.name,M)
final.net<JRF_network(out,out.perm,fdr)
```

### JRF_permutation

#### Derive importance scores for permuted data.

**Description**

This function computes importance score for one permuted data set. Sample labels of target genes are randomly permuted and JRF is implemented. Resulting importance scores can be used to derive an estimate of FDR.

**Usage**

```r
JRF_permutation(X, ntree, mtry, genes.name, perm)
```

**Arguments**

- `X` List object containing expression data for each class, `X=list(x_1,x_2, ... )` where `x_j` is a `(p x n_j)` matrix with rows corresponding to genes and columns to samples. Missing values are not allowed.
**JRF_permutation**

- **ntree**: numeric value: number of trees.
- **mtry**: numeric value: number of predictors to be sampled at each node.
- **genes.name**: vector containing genes name. The order needs to match the rows of \( x_j \).
- **perm**: integer: seed for permutation.

**Value**

A matrix with \( i \) rows and \( c \) columns with \( i \) being the number of total interactions and \( c \) the number of classes. Element \((i,k)\) corresponds to the importance score for interaction \( i \) under class \( k \).

**References**


**Examples**

```r
# --- Derive weighted networks via JRF
nclasses=2  # number of data sets / classes
n1<n2<20    # sample size for each data sets
p<5        # number of variables (genes)
genes.name<-paste("G",seq(1,p),sep="")  # genes name
perm=1;    # set permutation seed

# --- Generate data sets
data1<-matrix(rnorm(p*n1),p,n1)  # generate data1
data2<-matrix(rnorm(p*n2),p,n1)  # generate data2

# --- Standardize variables to mean 0 and variance 1
data1 <- t(apply(data1, 1, function(x) ( (x - mean(x)) / sd(x) )))
data2 <- t(apply(data2, 1, function(x) ( (x - mean(x)) / sd(x) )))

# --- Run JRF and obtain importance score of interactions for each class
out<-JRF_permutation(list(data1,data2),mtry=round(sqrt(p-1)),ntree=1000,genes.name,perm)
```
Run_permutation

Derive importance scores for M permuted data sets.

Description
This function computes importance score for M permuted data sets. Sample labels of target genes are randomly permuted and JRF is implemented. Resulting importance scores can be used to derive an estimate of FDR.

Usage
Run_permutation(X, ntree, mtry, genes.name, M)

Arguments
X
List object containing expression data for each class, \( X = \text{list}(x_1, x_2, \ldots) \)
where \( x_j \) is a \( (p \times n_j) \) matrix with rows corresponding to genes and columns to samples. Rows need to be the same across objects, while samples can vary. Missing values are not allowed.

ntree
numeric value: number of trees.

mtry
numeric value: number of predictors to be sampled at each node.

genes.name
vector containing genes name. The order needs to match the rows of \( x_j \).

M
integer: total number of permutations.

Value
A three dimensional matrix \( (I \times M \times C) \) with \( I \) being the number of total interactions, \( M \) the number of permutations and \( C \) the number of classes. Element \( (i, j, k) \) corresponds to the importance score for interaction \( i \), permuted data \( j \) and class \( k \).

References


Examples

# --- Derive weighted networks via JRF
nclasses = 2  # number of data sets / classes
n1 < n2 < 20  # sample size for each data sets
p < 5  # number of variables (genes)
geness.name <- paste("G", seq(1, p), sep = "")  # genes name
perm = 1;  # set permutation seed
# --- Generate data sets

data1<-matrix(rnorm(p*n1),p,n1)  # generate data1
data2<-matrix(rnorm(p*n2),p,n1)  # generate data2

# --- Standardize variables to mean 0 and variance 1

data1 <- t(apply(data1, 1, function(x) (x - mean(x)) / sd(x) ))
data2 <- t(apply(data2, 1, function(x) (x - mean(x)) / sd(x) ))

# --- Run JRF and obtain importance score of interactions for each class

out<-Run_permutation(list(data1,data2),mtry=round(sqrt(p-1)),ntree=1000,genes.name,M)
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