Package ‘TFactSR’

January 20, 2025

Type Package

Title Enrichment Approach to Predict Which Transcription Factors are Regulated

Version 0.99.0

Description R implementation of 'TFactS' to predict which are the transcription factors (TFs), regulated in a biological condition based on lists of differentially expressed genes (DEGs) obtained from transcriptome experiments. This package is based on the 'TFactS' concept by Essaghir et al. (2010) <doi:10.1093/nar/gkq149> and expands it. It allows users to perform 'TFactS'-like enrichment approach. The package can import and use the original catalogue file from the 'TFactS' as well as users' defined catalogues of interest that are not supported by 'TFactS' (e.g., Arabidopsis).

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URL `https://afukushima.github.io/TFactSR/`

Depends R (>= 4.3.0)

Imports qvalue, stats

Suggests BiocStyle, knitr, rmarkdown, spelling, testthat

VignetteBuilder knitr

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Repository CRAN

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Contents

`AtCatalog` *A list of TF-target genes (TG) in Arabidopsis thaliana.*

Description

A catalogue of annotated target genes in Arabidopsis thaliana

Details

The original regulatory network datasets were downloaded from AtRegNet - AGRIS Arabidopsis (http://arabidopsis.med.ohio-state.edu/moreNetwork.html) and ATRM (http://atrm.cbi.pku.edu.cn/), respectively. Then we integrated them based on AGI code.

The catalogues version is 0.0.1.

Value

None

Author(s)

Atsushi Fukushima

References

Yilmaz A et al. NAR 39:D1118-1122 (2011)

`calculateEnrichmentTest`

performs enrichment analysis

Description

This function performs enrichment test (ET) based on Fisher's exact test

Usage

```
calculateEnrichmentTest(
  DEGs,
  catalog,
  TFs,
  TF.col = "TF..OFFICIAL_TF_CODING_GENE_NAME."
)
```

Arguments

`DEGs`	a character vector of DEGs (differentially expressed genes)
`catalog`	a data frame of TFactS catalog (ver. 2)
`TFs`	a character vector of transcription factor
`TF.col`	the name of the column that contains the TF names

Value

data.frame

Author(s)

Atsushi Fukushima Definition: m is the number of target genes annotated for the TF under consideration n is the number of query genes N is the number of regulations in the catalog k is the number of query genes that are annotated as regulated by TF (i.e., the intersection between the query and the TF signature)

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

Examples

```
data(DEGs)
data(catalog)

tftg <- extractTFTG(DEGs, catalog)
TFs <- tftg$TFs
```

```
res <- calculateEnrichmentTest(DEGs, catalog, TFs)
```

`calculateEvalue` *calculates E-value*

Description

This function calculates E-value based on .

Usage

```
calculateEvalue(df, TFs)
```

Arguments

`df`	a data frame containng p-values
`TFs`	a character vector of transcription factor

Value

data.frame

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

Examples

```
data(DEGs)
data(catalog)

tftg <- extractTFTG(DEGs, catalog)
TFs <- tftg$TFs

p.value <- runif(10)/(1:10)
df <- data.frame(p.value = p.value)
res <- calculateEvalue(df, TFs)
```

`calculateFDRBH` *calculates FDR by Benjamini and Hochberg method*

Description

This function calculates FDR based on BH.

Usage

```
calculateFDRBH(df)
```

Arguments

`df`	a data frame containg p-values

Value

data.frame

Author(s)

Atsushi Fukushima

References

Benjamini Y and Hochberg Y, J Roy Stat Soc B 57: 289?300 (1995)

Examples

```
p.value <- runif(10)/(1:10)
df <- data.frame(p.value = p.value)
res <- calculateFDRBH(df)
```

`calculateQvalue` *calculates Q-value*

Description

This function calculates Q-value based on Storey.

Usage

```
calculateQvalue(df, lambda = seq(0.05, 0.5, 0.01))
```

Arguments

`df`	a data frame containng p-values
`lambda`	a vector of the lambda values utilized to obtain pi0.lambda

Value

data.frame

Author(s)

Atsushi Fukushima

References

Storey JD, The Annals of Statistics 31:2013-2035 (2003)

Examples

```
data(example.df)
p.value <- example.df$p.value
df <- data.frame(p.value = p.value)
res <- calculateQvalue(df)
```

`calculateRC` *calculates Random Control (RC)*

Description

This function calculates Random Control (RC)

Usage

```
calculateRC(
  df,
  DEGs,
  catalog,
  TFs,
  all.targets,
  TF.col = "TF..OFFICIAL_TF_CODING_GENE_NAME.",
  lambda = 0.05,
  nRep = 100
)
```

Arguments

`df`	a data frame containg p-values
`DEGs`	a character vector of DEGs (differentially expressed genes)
`catalog`	a data frame of TFactS catalog (ver. 2)
`TFs`	a character vector of transcription factor
`all.targets`	a character vector of all target genes
`TF.col`	the name of the column that contains the TF names
`lambda`	a user-specified threshold of E-value (default: 0.05)
`nRep`	number of random selections (default: 100)

Value

data.frame

Author(s)

Atsushi Fukushima Definition: m is the number of target genes annotated for the TF under consideration n is the number of query genes N is the number of regulations in the catalog k is the number of query genes that are annotated as regulated by TF (i.e., the intersection between the query and the TF signature)

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

Examples

```
data(example.df)
data(catalog)
data(DEGs)

tftg <- extractTFTG(DEGs, catalog)
TFs <- tftg$TFs
all.targets <- tftg$all.targets

res <- calculateRC(example.df, DEGs, catalog, TFs, all.targets)
```

`calculateTFactS` *calculates TFactS*

Description

This function calculates TFactS

Usage

```
calculateTFactS(
  DEGs,
  catalog,
  TFs,
  all.targets,
  Q.value = FALSE,
  lambda1 = seq(0.05, 0.5, 0.01),
  lambda2 = 0.05,
  nRep = 100,
  TF.col = "TF..OFFICIAL_TF_CODING_GENE_NAME."
)
```

Arguments

`DEGs`	a character vector of DEGs (differentially expressed genes)
`catalog`	a data frame of TFactS catalog (ver. 2)
`TFs`	a character vector of transcription factor
`all.targets`	a character vector of all target genes
`Q.value`	logical. If it is TRUE, Q.value by Storey method.
`lambda1`	a vector of the lambda values utilized to obtain pi0.lambda
`lambda2`	a user-specified threshold of E-value (default: 0.05)
`nRep`	number of random selections (default: 100)
`TF.col`	the name of the column that contains the TF names

Value

data.frame

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

Examples

```
data(DEGs)
data(catalog)

tftg <- extractTFTG(DEGs, catalog)
TFs <- tftg$TFs
all.targets <- tftg$all.targets

res <- calculateTFactS(DEGs, catalog, TFs, all.targets)
```

`catalog` *A list of TF-target genes (TG) in TFactS.*

Description

A catalogue of annotated target genes based on TFactS.

Details

This was downloaded from TFactS (http://www.tfacts.org/).

The catalogues version is 2 (http://www.tfacts.org/TFactS-new/TFactS-v2/tfacts/data/Catalogues.xls).

Value

None

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

`DEGs` *An example list of DEGs from DEMO data in TFactS.*

Description

An example list of differentially expressed genes (DEGs).

Details

This was from DEMO data in TFactS (http://www.tfacts.org/). The list corresponds to 18 up-regulated genes.

Value

None

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

`DEGs39` *An example list of 39 DEGs from DEMO data in TFactS.*

Description

A list of 39 differentially expressed genes (DEGs).

Details

This was from DEMO data in TFactS (http://www.tfacts.org/). The list corresponds to 18 up-regulated genes and 21 down-regulated genes.

Value

None

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

`example.df` *An example result of enrichment analysis*

Description

An example result of enrichment analysis

Details

The size of data frame is 345 TFs and 6 columns.

Value

None

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

`example.list` *An example list of result of enrichment analysis*

Description

An example list of result of enrichment analysis

Details

The length of the list is 345 (TFs).

Value

None

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

`extractTFTG` *extracts transcription factor (TF) and target gene (TG) information*

Description

This function extracts information about transcription factor (TF) and target gene (TG) with TFactS Catalogue (v2).

Usage

```
extractTFTG(
  DEGs,
  catalog,
  TF.col = "TF..OFFICIAL_TF_CODING_GENE_NAME.",
  TG.col = "Target.gene..OFFICIAL_GENE_NAME."
)
```

Arguments

`DEGs`	a character vector of DEGs (differentially expressed genes)
`catalog`	a data frame of TFactS catalog (ver. 2)
`TF.col`	the name of the column that contains the TF names
`TG.col`	the name of the column that contains the TG names

Value

list

Author(s)

Atsushi Fukushima

Examples

```
data(DEGs)
data(catalog)

res <- extractTFTG(DEGs, catalog)
head(res$TFs)
```

`FASTcalculateRC` *calculates Random Control (RC) fastly?*

Description

This function calculates Random Control (RC)

Usage

```
FASTcalculateRC(
  df,
  DEGs,
  catalog,
  TFs,
  all.targets,
  TF.col = "TF..OFFICIAL_TF_CODING_GENE_NAME.",
  lambda = 0.05,
  nRep = 100
)
```

Arguments

`df`	a data frame containg p-values
`DEGs`	a character vector of DEGs (differentially expressed genes)
`catalog`	a data frame of TFactS catalog (ver. 2)
`TFs`	a character vector of transcription factor
`all.targets`	a character vector of all target genes
`TF.col`	the name of the column that contains the TF names
`lambda`	a user-specified threshold of E-value (default: 0.05)
`nRep`	number of random selections (default: 100)

Value

data.frame

Author(s)

Atsushi Fukushima

References

Essaghir A et al. Nucleic Acids Res. 2010 Jun;38(11):e120.

Examples

```
data(example.df)
data(catalog)
data(DEGs)

tftg <- extractTFTG(DEGs, catalog)
TFs <- tftg$TFs
all.targets <- tftg$all.targets

res <- FASTcalculateRC(example.df, DEGs, catalog, TFs, all.targets)
```

`formatET` *formats the result of enrichment test (ET)*

Description

This function formats the result of enrichment test (ET) based on Fisher's exact test

Usage

```
formatET(list)
```

Arguments

`list`	a list of the result of enrichment test (ncol = 6)

Value

data.frame

Author(s)

Atsushi Fukushima

Examples

```
data(example.list)
res <- formatET(example.list)
```

`formatRC` *formats the result of Random Control (RC)*

Description

This function formats the result of Random Control (RC) with random simulation based on Fisher's exact test

Usage

```
formatRC(df, list, nRep)
```

Arguments

`df`	a data frame of ET including E-values, FDR-BH, and Q-values
`list`	a list of the result of RC (ncol = 2)
`nRep`	the number of random selections (negative control)

Value

data.frame

Author(s)

Atsushi Fukushima

Examples

```
data(example.df)
data(example.list)
nRep <- 100
res <- formatRC(example.df, example.list, nRep)
```

`GenesUp_SH1H` *An example list of 74 DEGs from AtGenExpress stress dataset.*

Description

A list of 74 differentially expressed genes (DEGs) from AtGenExpress

Details

This was from DEMO data in the Supplemental data (Table S4. Genes regulated by UV-B light stress in roots and shoots; filename: TPJ_3052_sm_TabS4.xls) of the paper by Killian et al. TPJ (2008). The list corresponds to 74 genes up-regulated in roots and shoots 1 hour after onset of UV-B stress treatment.

Value

None

Author(s)

Atsushi Fukushima

References

Killian J et al. Plant J. 2007 Apr;50(2):347-363.

`TFactSR` *TFactSR: A package for identifying critical transcription factors.*

Description

TFactS is to predict which are the transcription factors (TFs), regulated in a biological condition based on lists of differentially expressed genes (DEGs) obtained from transcriptome experiments. This package is based on the TFactS concept and expands it. It allows users to performe TFactS-like enrichment approach. The package can import and use the original catalogue file from the TFactS website (http://www.tfacts.org/) as well as users' defined catalogues of interest that are not supported by TFactS (e.g., Arabidopsis).

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