

# Package: TFactSR (via r-universe)

August 26, 2024

**Type** Package

**Title** Enrichment Approach to Predict Which Transcription Factors are Regulated

**Version** 0.99.1

**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](https://doi.org/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).

**License** GPL-3

**URL** <https://afukushima.github.io/TFactSR/>

**Depends** R (>= 4.3.0)

**Imports** qvalue, stats

**Suggests** BiocStyle, knitr, rmarkdown, spelling, testthat

**VignetteBuilder** knitr

**biocViews** Network, Software, DifferentialExpression, GeneTarget, GeneExpression, Microarray, RNASeq, Transcription, NetworkEnrichment

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**Language** en-US

**Repository** <https://afukushima.r-universe.dev>

**RemoteUrl** <https://github.com/afukushima/tfactsr>

**RemoteRef** HEAD

**RemoteSha** a9773380be8d622d21a7595b64a1e8ae000706b3

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 ATRM

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


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### Description

A catalogue of annotated target genes in Arabidopsis thaliana based on ATRM

### Details

The original regulatory network datasets were downloaded from ATRM (<http://atrm.cbi.pku.edu.cn/>).

### Value

None

### References

Jin JP et al. Mol Bio Evol 32:1767-1773 (2015)

---

```
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.",  
  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)
TFs	a character vector of transcription factor
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

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	<i>calculates E-value</i>
-----------------	---------------------------

---

**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	<i>calculates FDR by Benjamini and Hochberg method</i>
----------------	--

---

**Description**

This function calculates FDR based on BH.

**Usage**

```
calculateFDRBH(df)
```

**Arguments**

df                    a data frame containng 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	<i>calculates Q-value</i>
-----------------	---------------------------

---

**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 containng 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.",
  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)
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
TG.col	the name of the column that contains the TG 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	<i>A list of TF-target genes (TG) in TFactS.</i>
---------	--

---

**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	<i>An example list of DEGs from DEMO data in TFactS.</i>
------	--

---

**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	<i>An example list of result of enrichment analysis</i>
--------------	---

---

**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	<i>extracts transcription factor (TF) and target gene (TG) information</i>
-------------	--

---

**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 containng 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**

<code>df</code>	a data frame of ET including E-values, FDR-BH, and Q-values
<code>list</code>	a list of the result of RC (ncol = 2)
<code>nRep</code>	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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