

# Package ‘TFutils’

December 27, 2024

**Title** TFutils

**Description** This package helps users to work with TF metadata from various sources. Significant catalogs of TFs and classifications thereof are made available. Tools for working with motif scans are also provided.

**Version** 1.26.0

**Depends** R (>= 4.1.0)

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**Suggests** knitr, data.table, testthat, AnnotationFilter, Biobase, GenomicFeatures, GenomicRanges, Gviz, IRanges, S4Vectors, EnsDb.Hsapiens.v75, BiocParallel, BiocStyle, GO.db, GenomicFiles, GenomeInfoDb, SummarizedExperiment, UpSetR, ggplot2, png, gwascat, MotifDb, motifStack, RColorBrewer, rmarkdown

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---

|              |   |
|--------------|---|
| anchor_pmids | <i>check columns of a dataframe for numerical tokens of 7 or 8 digits and create HTML anchors to pubmed.gov constituting a link to a PMID</i> |
|--------------|---|

---

**Description**

check columns of a dataframe for numerical tokens of 7 or 8 digits and create HTML anchors to pubmed.gov constituting a link to a PMID

**Usage**

```
anchor_pmids(dataframe)
```

**Arguments**

dataframe      a data.frame instance

**Value**

data.frame with HTML anchors to pubmed.gov inserted where 7- or 8-digit numbers are found

**Note**

The method of isolating putative PMIDs is peculiar to patterns found in the comment fields of annotated TF table (supplemental table S1 found in <https://www.cell.com/cms/10.1016/j.cell.2018.01.029/attachment/88c0eca1-66f9-4068-b02e-bd3d55144f79/mmc2.xlsx> of PMID 29425488). When DT::datatable is called on the output of this function with escape=FALSE the PMIDs will render as hyperlinks. Note that column 1 is assumed to be an ENSEMBL ID which could have 7 or 8 digits but is handled differently

**Examples**

```
litdf = data.frame(id="ENSG00000116819", a="Binds the same GCCTGAGGC sequence as the other AP-2s (PMID: 2478957)
  stringsAsFactors=FALSE)
anchor_pmids(litdf)
```

---

|                  |   |
|------------------|---|
| browse_gotf_main | <i>use DT::datatable to browse the Gotf table xxx</i> |
|------------------|---|

---

**Description**

use DT::datatable to browse the Gotf table xxx

**Usage**

```
browse_gotf_main(cache = BiocFileCache::BiocFileCache(ask = FALSE))
```

**Arguments**

cache            a BiocFileCache instance

**Value**

result of DT::datatable

**Note**

PMIDs are converted to HTML anchors and DT::datatable is run with escape=FALSE.

**Examples**

```
if (interactive()) browse_gotf_main()
```

---

browse\_humantfs\_main *use DT::datatable to browse the Lambert table S1*

---

**Description**

use DT::datatable to browse the Lambert table S1

**Usage**

```
browse_humantfs_main(cache = BiocFileCache::BiocFileCache(ask = FALSE))
```

**Arguments**

cache            a BiocFileCache instance

**Value**

result of DT::datatable

**Note**

PMIDs are converted to HTML anchors and DT::datatable is run with escape=FALSE.

**Examples**

```
if (interactive()) browse_lambert_main()
```

---

browse\_lambert\_gwaslinks

*browse several hundred disease-TF associations with hyperlinked PMIDs*

---

**Description**

browse several hundred disease-TF associations with hyperlinked PMIDs

**Usage**

```
browse_lambert_gwaslinks()
```

**Value**

DT::datatable

**Note**

Based on supplemental table S4 of PMID 29425488

**Examples**

```
if (interactive()) browse_lambert_gwaslinks()
```

---

browse\_lambert\_main    *use DT::datatable to browse the Lambert table S1*

---

**Description**

use DT::datatable to browse the Lambert table S1

**Usage**

```
browse_lambert_main(cache = BiocFileCache::BiocFileCache(ask = FALSE))
```

**Arguments**

cache                    a BiocFileCache instance

**Value**

result of DT::datatable

**Note**

PMIDs are converted to HTML anchors and DT::datatable is run with escape=FALSE.

**Examples**

```
if (interactive()) browse_lambert_main()
```

---

|            |   |
|------------|---|
| cisbpTFcat | <i>cisbpTFcat: data.frame with information on CISBP TFs for human, retained for reproducibility support; see cisbpTFcat_2.0 for a more recent catalog</i> |
|------------|---|

---

**Description**

cisbpTFcat: data.frame with information on CISBP TFs for human, retained for reproducibility support; see cisbpTFcat\_2.0 for a more recent catalog

**Usage**

```
cisbpTFcat
```

**Format**

```
data.frame
```

**Note**

Extracted March 2018, checked August 2018. The only changes observed are that genes ZUFSP and T are used has HGNC values in the March catalog; these symbols seem to be absent from the org.Hs.eg.db of August 2018. The records involved are 1356, 7412 and 7413. These symbols were left in the package image of CISBP in August 2018.

**Source**

<http://cisbp.cabr.utoronto.ca/bulk.php> select Homo\_sapiens

**Examples**

```
head(TFutils::cisbpTFcat)
```

---

|                |   |
|----------------|---|
| cisbpTFcat_2.0 | <i>cisbpTFcat_2.0: data.frame with information on CISBP TFs for human, described in PMID 31133749</i> |
|----------------|---|

---

**Description**

cisbpTFcat\_2.0: data.frame with information on CISBP TFs for human, described in PMID 31133749

**Usage**

```
cisbpTFcat_2.0
```

**Format**

```
data.frame
```

**Note**

Extracted August 2019.

**Source**

<http://cisbp.ccb.utoronto.ca/bulk.php> select Homo\_sapiens

**Examples**

```
head(TFutils::cisbpTFcat_2.0)
```

---

|                     |   |
|---------------------|---|
| defaultCircosParams | <i>basic layout parameters for circos</i> |
|---------------------|---|

---

**Description**

basic layout parameters for circos

**Usage**

```
defaultCircosParams()
```

**Value**

a list

**Examples**

```
head(defaultCircosParams())
```

---

|                   |   |
|-------------------|---|
| demo_fimo_granges | <i>a list of GRanges instances with TF FIMO scores returned by fimo_granges</i> |
|-------------------|---|

---

**Description**

a list of GRanges instances with TF FIMO scores returned by fimo\_granges

**Usage**

```
demo_fimo_granges
```

**Format**

a list of GRanges instances

**Examples**

```
names(S4Vectors::mcols(demo_fimo_granges$VDR[[1]]))
```

---

|                   |   |
|-------------------|---|
| directHitsInCISBP | <i>demonstrate interoperation of TF catalog with GWAS catalog</i> |
|-------------------|---|

---

**Description**

demonstrate interoperation of TF catalog with GWAS catalog

**Usage**

```
directHitsInCISBP(traitTag, gwascat)
```

**Arguments**

|          |  |
|----------|--|
| traitTag | character(1) string found in DISEASE/TRAIT field of gwascat instance |
| gwascat  | instance of <a href="#">gwaswloc-class</a>                           |

**Value**

data.frame

**Examples**

```
data(gwascat_hg19_chr17)
directHitsInCISBP("Prostate cancer" , gwascat_hg19_chr17)
```

---

|           |   |
|-----------|---|
| encode690 | <i>encode690: DataFrame extending AnnotationHub metadata about ENCODE cell line x TF ranges</i> |
|-----------|---|

---

**Description**

encode690: DataFrame extending AnnotationHub metadata about ENCODE cell line x TF ranges

**Usage**

```
encode690
```

**Format**

DataFrame

**Source**

see metadata(encode690)

**Examples**

```
names(TFutils::encode690)
TFutils::encode690[,1:5]
```



---

|        |   |
|--------|---|
| fimo16 | <i>fimo16: GenomicFiles instance to AWS S3-resident FIMO bed for 16 TFs</i> |
|--------|---|

---

**Description**

fimo16: GenomicFiles instance to AWS S3-resident FIMO bed for 16 TFs

**Usage**

```
fimo16
```

**Format**

GenomicFiles for a TabixFileList

**Source**

K. Glass FIMO runs, see <https://doi.org/10.1016/j.celrep.2017.10.001>

**Examples**

```
TFutils::fimo16
```

---

|         |  |
|---------|--|
| fimoMap | <i>fimoMap: table with Mnnnn (motif PWM tags) and HGNC symbols for TFs</i> |
|---------|--|

---

**Description**

fimoMap: table with Mnnnn (motif PWM tags) and HGNC symbols for TFs

**Usage**

```
fimoMap
```

**Format**

data.frame

**Source**

Kimberly Glass (rekr@channing.harvard.edu)

**Examples**

```
head(TFutils::fimoMap)
```

---

|              |  |
|--------------|--|
| fimo_granges | <i>create a list of GRanges for FIMO hits in a GenomicFiles instance, corresponding to a GRanges-based query</i> |
|--------------|--|

---

**Description**

create a list of GRanges for FIMO hits in a GenomicFiles instance, corresponding to a GRanges-based query

**Usage**

```
fimo_granges(gf, query)
```

**Arguments**

|       |  |
|-------|--|
| gf    | GenomicFiles instance, like fimo16 in TFutils              |
| query | a GRanges specifying ranges to check for TF binding scores |

**Value**

a list of GRanges, produced by GenomicFiles::reduceByRange

**Note**

Be sure to use register([BPPARAM]) appropriately.

**Examples**

```
if (interactive()) { # need internet
# setup -- annotate fimo16 object and create an informative
# query
colnames(fimo16) = fimo16$HGNC
si = GenomeInfoDb::Seqinfo(genome="hg19")["chr17"] # to fix query genome
myg = GRanges("chr17", IRanges(38.07e6,38.09e6), seqinfo=si)
requireNamespace("BiocParallel")
BiocParallel::register(BiocParallel::SerialParam())
f1 = fimo_granges(fimo16[, c("VDR", "POU2F1")], myg)
f1
}
```

---

|             |  |
|-------------|--|
| genemodelDF | <i>use EnsDb to generate an exon-level model of genes identified by symbol</i> |
|-------------|--|

---

**Description**

use EnsDb to generate an exon-level model of genes identified by symbol

**Usage**

```
genemodelDF(sym, resource, columnsKept = c("gene_id", "tx_id"), ...)
```

**Arguments**

|             |   |
|-------------|---|
| sym         | a character() vector of gene symbols  |
| resource    | should be or inherit from EnsDb, answering exons(), with AnnotationFilter::SymbolFilter as filter parameter |
| columnsKept | character vector used as columns param in exons()   |
| ...         | passed to exons()   |

**Value**

data.frame instance with exons in rows

**Note**

There are many approaches available to acquiring 'gene models' in Bioconductor; this one emphasizes the use of the exons method for Ensembl annotation.

**Examples**

```
if (requireNamespace("EnsDb.Hsapiens.v75")) {
  orm = genemodelDF("ORMDL3", EnsDb.Hsapiens.v75::EnsDb.Hsapiens.v75)
  dim(orm)
}
head(orm)
```

---

|                |   |
|----------------|---|
| genemodForGviz | <i>create a GeneRegionTrack instance for selected symbols</i> |
|----------------|---|

---

**Description**

create a GeneRegionTrack instance for selected symbols

**Usage**

```
genemodForGviz(
  sym = "ORMDL3",
  id_elem = c("symbol", "tx_id"),
  resource = EnsDb.Hsapiens.v75::EnsDb.Hsapiens.v75,
  ...
)
```

**Arguments**

|          |   |
|----------|---|
| sym      | character vector of gene symbols, should be neighboring genes   |
| id_elem  | vector of names of columns generated by genemodelDF to be used to label transcripts                         |
| resource | should be or inherit from EnsDb, answering exons(), with AnnotationFilter::SymbolFilter as filter parameter |
| ...      | passed to genemodelDF   |

**Value**

instance of Gviz GeneRegionTrack

**Note**

This function helps to display the locations of TF binding sites in the context of complex gene models. A complication is that we have nice visualization of quantitative affinity predictions for TFs in the vignette, based on ggplot2, but it is not clear how to use that specific code to work with Gviz.

**Examples**

```
if (requireNamespace("EnsDb.Hsapiens.v75") &
    requireNamespace("Gviz")) {
  orm = genomodForGviz("ORMDL3", resource= EnsDb.Hsapiens.v75::EnsDb.Hsapiens.v75)
  orm
  Gviz::plotTracks(orm, showId=TRUE) # change id_elem for shorter id string
}
```

---

get\_rslocs\_38

*utility to obtain location etc. for rsids of SNPs*

---

**Description**

utility to obtain location etc. for rsids of SNPs

**Usage**

```
get_rslocs_38(rsids = c("rs6060535", "rs56116432"))
```

**Arguments**

rsids                    character vector of dbSNP identifiers

**Value**

GRanges instance

**Note**

Uses rest.ensembl.org, posting to variant\_recorder/homo\_sapiens. Parses result minimally, using only the first SPDI to obtain location information, adding 1 as ensembl genomic coordinates are zero-based.

**Examples**

```
if (interactive()) get_rslocs_38() # see https://stat.ethz.ch/pipermail/bioc-devel/2020-October/017263.html
```

---

|         |  |
|---------|--|
| grabTab | <i>create table of TF targets and related metadata</i> |
|---------|--|

---

**Description**

create table of TF targets and related metadata

**Usage**

```
grabTab(
  tfstub = "STAT1",
  gscoll = TFutils::tftColl,
  orgdb = org.Hs.eg.db::org.Hs.eg.db,
  gwrngs = TFutils::gwascat_hg19_chr17
)
```

**Arguments**

|        |  |
|--------|--|
| tfstub | character(1) gene-like symbol for TF; will be grepped in names(gscoll)   |
| gscoll | a GSEABase GeneSetCollection   |
| orgdb  | an instance of OrgDb as defined in AnnotationDbi                         |
| gwrngs | a GRanges representing EBI gwascat, must have DISEASE/TRAIT, MAPPED_GENE |

**Value**

data.frame instance

**Note**

This function will link together information on targets of a given TF to the GWAS catalog.

**Examples**

```
gt = grabTab("VDR", gscoll=TFutils::tftColl,
  orgdb=org.Hs.eg.db::org.Hs.eg.db, gwrngs=TFutils::gwascat_hg19_chr17)
dim(gt)
head(gt)
```

---

|                    |   |
|--------------------|---|
| gwascat_hg19_chr17 | <i>gwascat_hg19: GRanges of march 21 2018 EBI gwascat, limit to chr17</i> |
|--------------------|---|

---

**Description**

gwascat\_hg19: GRanges of march 21 2018 EBI gwascat, limit to chr17

**Usage**

```
gwascat_hg19_chr17
```

**Format**

GenomicRanges GRanges instance

**Source**

gwascats::makeCurrentGwascats, with gwascats::lo38to19 applied

**Examples**

```
TFutils::gwascats_hg19_chr17[,1:5]
```

---

HGNCmap

*simple accessor for HGNCmap component of TFCatalog*

---

**Description**

simple accessor for HGNCmap component of TFCatalog

**Usage**

```
HGNCmap(x)
```

**Arguments**

x                    instance of TFCatalog

**Value**

dataframe instance

**Examples**

```
HGNCmap
```

---

hocomoco.mono

*hocomoco.mono: data.frame with information on HOCOMOCO TFs for human*

---

**Description**

hocomoco.mono: data.frame with information on HOCOMOCO TFs for human

**Usage**

```
hocomoco.mono
```

**Format**

data.frame

**Note**

Extracted March 2018

**Source**

<http://hocomoco11.autosome.ru/human/mono?full=true>

**Examples**

```
head(TFutils::hocomoco.mono)
```

---

`hocomoco.mono.sep2018` *hocomoco.mono.sep2018: data.frame with information on HOCO-MOCO TFs for human, Sept 2018 download*

---

**Description**

`hocomoco.mono.sep2018`: data.frame with information on HOCOMOCO TFs for human, Sept 2018 download

**Usage**

```
hocomoco.mono.sep2018
```

**Format**

data.frame

**Note**

Extracted September 2018

**Source**

<http://hocomoco11.autosome.ru/human/mono?full=true>

**Examples**

```
head(TFutils::hocomoco.mono.sep2018)
```

---

```
importFIMO,TabixFile,GRanges-method
      import a FIMO bed-like file@importFrom utils read.delim
```

---

**Description**

import a FIMO bed-like file@importFrom utils read.delim

**Usage**

```
## S4 method for signature 'TabixFile,GRanges'
importFIMO(src, parms, ...)

## S4 method for signature 'character,missing'
importFIMO(src, parms, ...)
```

**Arguments**

|       |  |
|-------|--|
| src   | TabixFile instance   |
| parms | a GRanges instance delimiting the import; multiple GRanges can be used |
| ...   | passed to GenomicRanges::GRanges                                       |

**Value**

instance of GRanges

**Examples**

```
if (requireNamespace("Rsamtools")) {
  tf = Rsamtools::TabixFile(system.file("M5946_1/chr1.bed.gz", package="TFutils"))
  importFIMO(tf, GenomicRanges::GRanges("chr1", IRanges::IRanges(1e6,11e6)))
}
```

---

```
importFIMO_local_split
```

*utility to read FIMO outputs from local resource(cluster), assuming bed text split by chromosome*

---

**Description**

utility to read FIMO outputs from local resource(cluster), assuming bed text split by chromosome

**Usage**

```
importFIMO_local_split(tf, chr)
```

**Arguments**

|     |                              |
|-----|------------------------------|
| tf  | character(1) file id         |
| chr | character(1) chromosome name |



**Value**

data.table instance

**Examples**

```
requireNamespace("GenomicRanges")
requireNamespace("IRanges")
importFIMO_local_split("M5946_1", "chr1")
dim(importFIMO_local_split("M5946_1", "chr17"))
```

---

|              |  |
|--------------|--|
| lambert_snps | <i>lambert_snps is Table S3 of Lambert et al PMID 29425488</i> |
|--------------|--|

---

**Description**

lambert\_snps is Table S3 of Lambert et al PMID 29425488

**Usage**

```
lambert_snps
```

**Format**

data.frame

**Examples**

```
head(lambert_snps)
```

---

|             |  |
|-------------|--|
| metadata_tf | <i>metadata_tf: list with metadata (motif_if and hgnc_symbol) about all the CISBP FIMO scan TF bed files</i> |
|-------------|--|

---

**Description**

metadata\_tf: list with metadata (motif\_if and hgnc\_symbol) about all the CISBP FIMO scan TF bed files

**Usage**

```
metadata_tf
```

**Format**

list

**Source**

K. Glass ran FIMO

**Examples**

```
TFutils::metadata_tf
```

---

|          |  |
|----------|--|
| named_tf | <i>named_tf: named list with the names being the hgnc_symbol of the motif_id</i> |
|----------|--|

---

**Description**

named\_tf: named list with the names being the hgnc\_symbol of the motif\_id

**Usage**

```
named_tf
```

**Format**

```
list
```

**Source**

K. Glass ran FIMO

**Examples**

```
TFutils::named_tf
named_tf[["VDR"]]
```

---

|                    |   |
|--------------------|---|
| retrieve_gotf_main | <i>acquire the CSV content for table S1 of Lambert et al. Cell 2018, "The Human Transcription Factors" from the Human TFS website</i> |
|--------------------|---|

---

**Description**

acquire the CSV content for table S1 of Lambert et al. Cell 2018, "The Human Transcription Factors" from the Human TFS website

**Usage**

```
retrieve_gotf_main(cache = BiocFileCache::BiocFileCache(ask = FALSE))
```

**Arguments**

cache            a BiocFileCache instance

**Value**

a tbl\_df

**Note**

This will download the spreadsheet if not found in cache.

**Examples**

```
if (interactive()) retrieve_gotf_main()
```

---

```
retrieve_humantfs_main
```

*acquire the CSV content for table S1 of Lambert et al. Cell 2018, "The Human Transcription Factors" from the Human TFS website*

---

**Description**

acquire the CSV content for table S1 of Lambert et al. Cell 2018, "The Human Transcription Factors" from the Human TFS website

**Usage**

```
retrieve_humantfs_main(cache = BiocFileCache::BiocFileCache(ask = FALSE))
```

**Arguments**

cache                    a BiocFileCache instance

**Value**

a tbl\_df

**Note**

This will download the spreadsheet if not found in cache.

**Examples**

```
if (interactive()) retrieve_lambert_main()
```

---

```
retrieve_lambert_main
```

*acquire the Excel spreadsheet content for table S1 of Lambert et al. Cell 2018, "The Human Transcription Factors"*

---

**Description**

acquire the Excel spreadsheet content for table S1 of Lambert et al. Cell 2018, "The Human Transcription Factors"

**Usage**

```
retrieve_lambert_main(cache = BiocFileCache::BiocFileCache(ask = FALSE))
```

**Arguments**

cache                    a BiocFileCache instance

**Value**

a tbl\_df

**Note**

This will download the spreadsheet if not found in cache.

**Examples**

```
if (interactive()) retrieve_lambert_main()
```

---

```
seqinfo_hg19_chr17    a Seqinfo instance for a chr17 in hg19
```

---

**Description**

a Seqinfo instance for a chr17 in hg19

**Usage**

```
seqinfo_hg19_chr17
```

**Format**

a Seqinfo instance

**Examples**

```
seqinfo_hg19_chr17
```

---

```
setupHIZE    process a gene_attribute_matrix.txt file from harmonizeome into a GeneSetCollection
```

---

**Description**

process a gene\_attribute\_matrix.txt file from harmonizeome into a GeneSetCollection

**Usage**

```
setupHIZE(txtfn = "gene_attribute_matrix.txt", tag)
```

**Arguments**

```
txtfn    character(1) path to gene_attribute_matrix.txt file from harmonizeome
tag      character(1) will be added to shortDescription field of each GeneSet instance
```

**Value**

GSEABase::GeneSetCollection

**Note**

After uncompressing content of [http://amp.pharm.mssm.edu/static/hdfs/harmonizome/data/cheappi/gene\\_attribute\\_matrix.txt.gz](http://amp.pharm.mssm.edu/static/hdfs/harmonizome/data/cheappi/gene_attribute_matrix.txt.gz) run this on gene\_attribute\_matrix.txt with tag="CHEA".

---

show,TFCatalog-method *produce a concise report on TFCatalog instance*

---

**Description**

produce a concise report on TFCatalog instance

**Usage**

```
## S4 method for signature 'TFCatalog'
show(object)
```

**Arguments**

object            instance of TFCatalog

**Value**

side effect

---

|           |                                  |
|-----------|----------------------------------|
| TFCatalog | <i>Constructor for TFCatalog</i> |
|-----------|----------------------------------|

---

**Description**

Constructor for TFCatalog

**Usage**

```
TFCatalog(name, nativeIds, HGNCmap, metadata)
```

**Arguments**

|           |  |
|-----------|--|
| name      | informative character(1) for collection  |
| nativeIds | character() vector of identifiers used by collection creators  |
| HGNCmap   | data.frame with column 1 nativeIds, column 2 HGNC or hgnc.heur for MSigDb and any other columns of use |
| metadata  | a list of metadata elements  |

**Value**

instance of TFCatalog

**Examples**

```
if (require("GSEABase")) {
  TFs_MSIG = TFCatalog(name="MsigDb.TFT",nativeIds=names(TFutils::tftColl),
  HGNCmap=data.frame(TFutils::tftCollMap,stringAsFactors=FALSE))
  TFs_MSIG
}
```

---

|                 |  |
|-----------------|--|
| TFCatalog-class | <i>define a structure to hold information about TFs from diverse reference sources</i> |
|-----------------|--|

---

**Description**

define a structure to hold information about TFs from diverse reference sources

**Slots**

name character

nativeIds character tokens used by the provider to enumerate transcription factors

HGNCmap data.frame with atleast two columns, native id as first column and HGNC symbol as second column

metadata ANY

**Note**

This class respects the notions that 1) a source of information about transcription factors should have a name, 2) each source has its own 'native' nomenclature for the factors themselves, 3) it is common to use the gene symbol to refer to the transcription factor, and 4) additional metadata will frequently be required to establish information about provenance of assertions about transcription factors.

---

|                |   |
|----------------|---|
| tffamCirc.plot | <i>use a radial plot (by default) for motif stack</i> |
|----------------|---|

---

**Description**

use a radial plot (by default) for motif stack

**Usage**

```
tffamCirc.plot(motiflist, circosParams = defaultCircosParams())
```

**Arguments**

motiflist a list of pfm instances from motifStack

circosParams a list of parameter settings for circos plot

**Value**

side effect to graphics device

**Examples**

```
p1 = tffamCirc.prep( )
tffamCirc.plot(p1[c(1:8, 10:17, 19)])
```

---

|                |   |
|----------------|---|
| tffamCirc.prep | <i>set up list of pfms in motifStack protocol</i> |
|----------------|---|

---

**Description**

set up list of pfms in motifStack protocol

**Usage**

```
tffamCirc.prep(tffam = "Paired-related HD factors{3.1.3}", trimfac = 0.4)
```

**Arguments**

|         |   |
|---------|---|
| tffam   | character(1) name of TF family as found in TFutils::hocomoco.mono field TF family |
| trimfac | fraction passed as parameter t to motifStack::trimMotif                           |

**Value**

a list of pfm instances as defined in motifStack

**Note**

Uses MotifDb, motifStack to create a list of pfms

**Examples**

```
n1 = tffamCirc.prep()
str(n1)
```

---

|         |  |
|---------|--|
| tffield | <i>tffield: data.frame with MSigDb TFs, TF targets as symbol or ENTREZ</i> |
|---------|--|

---

**Description**

tffield: data.frame with MSigDb TFs, TF targets as symbol or ENTREZ

**Usage**

```
tffield
```

**Format**

list

**Source**

MSigDb "c3" (motif gene sets) has been harvested for simple annotation of TFs and targets.

**Examples**

```
TFutils::tffield
tffield[1:3,]
```

---

TFtargs *gadget to help sort through tags naming TFs*

---

### Description

gadget to help sort through tags naming TFs

### Usage

```
TFtargs(
  gscoll = TFutils::tftColl,
  initTF = "VDR_Q3",
  gwcat = TFutils::gwascat_hg19_chr17,

  gadttitle = "Search for a TF; its targets will be checked for mapped status in GWAS catalog"
)
```

### Arguments

|           |  |
|-----------|--|
| gscoll    | a GSEABase GeneSetCollection                         |
| initTF    | character(1) initial TF string for app               |
| gwcat     | GRanges-like structure with GWAS catalog information |
| gadttitle | character(1) a title for the gadget panel            |

### Value

on app conclusion a data.frame is returned

### Note

Will use TFutils::gwascat\_hg19\_chr17 to look for 'MAPPED\_GENE' field entries matching targets, also hardcoded to use org.Hs.eg.db to map symbols

### Examples

```
if (interactive()) TFtargs()
```

---

tftColl *tftColl: GSEABase GeneSetCollection for transcription factor targets*

---

### Description

tftColl: GSEABase GeneSetCollection for transcription factor targets

### Usage

```
tftColl
```



**Format**

GSEABase GeneSetCollection instance

**Note**

run GSEABase::getGMT() on c3/TFT geneset collection from MSigDb

**Source**

broad institute

**Examples**

```
TFutils::tftColl
```

---

tftCollMap

*tftCollMap: data.frame with information on MSigDb TFs for human*

---

**Description**

tftCollMap: data.frame with information on MSigDb TFs for human

**Usage**

```
tftCollMap
```

**Format**

data.frame

**Note**

Annotation of TFs is ad-hoc. GeneSet names were tokenized, splitting by underscore, and then fragments were matched to SYMBOL and ALIAS elements of org.Hs.eg.db. Extracted March 2018

**Source**

<http://software.broadinstitute.org/gsea/msigdb/genesets.jsp?collection=TFT>

**Examples**

```
head(TFutils::tftCollMap)
```

---

|                    |   |
|--------------------|---|
| topTraitsOfTargets | <i>Use MSigDB TF targets resource to find targets of input TF and find traits to which these targets have been mapped</i> |
|--------------------|---|

---

### Description

Use MSigDB TF targets resource to find targets of input TF and find traits to which these targets have been mapped

### Usage

```
topTraitsOfTargets(TFsym, gsc, gwcat, ntraits = 6, force = FALSE, ...)
```

### Arguments

|         |   |
|---------|---|
| TFsym   | character(1) symbol for a TF must be present in tftCollMap[, "hgnc.heur"]   |
| gsc     | an instance of <a href="#">GeneSetCollection-class</a> , intended to enumerate targets of a single transcription factor in each GeneSet, as in TFutils::tftColl |
| gwcat   | instance of <a href="#">gwaswloc-class</a>  |
| ntraits | numeric(1) number of traits to report   |
| force   | logical see note, set to true if you want to skip mapping from TFsym to a specific motif or TF identifier used as name of a GeneSet in gsc                      |
| ...     | character() vector of fields in mcols(gwcat) to include   |

### Value

data.frame symbol, set force = TRUE to use a known 'motif' name among names(gsc)

### Note

If tftCollMap[, "hgnc.heur"] does not possess the necessary

### Examples

```
suppressPackageStartupMessages({
  library(GSEABase)
}) # more results if you substitute ebicat37 from gwascats below
topTraitsOfTargets("MTF1" , tftColl, gwascats_hg19_chr17)
```

---

|           |  |
|-----------|--|
| URL_s3_tf | <i>utility to generate link to biocfound bucket for FIMO TFBS scores</i> |
|-----------|--|

---

**Description**

utility to generate link to biocfound bucket for FIMO TFBS scores

**Usage**

```
URL_s3_tf(tag = "M3433")
```

**Arguments**

|     |  |
|-----|--|
| tag | character(1) token identifying TF, can be an HGNC gene name or Mnnnn PWM tag. It must be findable in TFutils::fimoMap table. |
|-----|--|

**Value**

character(1) URL

**Examples**

```
URL_s3_tf
```

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