Package ‘TFutils’

May 7, 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 1.25.0

Depends R (>= 4.1.0)

Imports methods, dplyr, magrittr, miniUI, shiny, Rsamtools, GSEABase, rjson, BiocFileCache, DT, httr, readxl, AnnotationDbi, org.Hs.eg.db, utils

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

License Artistic-2.0

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Contents

`anchor_pmids` *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*

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: 24789576)",
     stringsAsFactors=FALSE)
anchor_pmids(litdf)
```

browse_gotf_main *use DT::datatable to browse the Gotf table xxx*

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 — *cisbpTFcat: data.frame with information on CISBP TFs for human, retained for reproducibility support; see cisbpTFcat_2.0 for a more recent catalog*

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.ccbr.utoronto.ca/bulk.php select Homo_sapiens

Examples

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

cisbpTFcat_2.0 — *cisbpTFcat_2.0: data.frame with information on CISBP TFs for human, described in PMID 31133749*

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.ccbr.utoronto.ca/bulk.php select Homo_sapiens

Examples

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

defaultCircosParms — *basic layout parameters for circos*

Description

basic layout parameters for circos

Usage

```
defaultCircosParms()
```

Value

a list

Examples

```
head(defaultCircosParms())
```

demo_fimo_granges — *a list of GRanges instances with TF FIMO scores returned by* `fimo_granges`

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 — *demonstrate interoperation of TF catalog with GWAS catalog*

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 `gwaswloc-class`

Value

data.frame

Examples

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

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

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

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

Description

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

Usage

```
fimoMap
```

Format

data.frame

Source

Kimberly Glass (rekrg@channing.harvard.edu)

Examples

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

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

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

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 *create a GeneRegionTrack instance for selected symbols*

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 = genemodForGviz("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 *create table of TF targets and related metadata*

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 — *gwascat_hg19: GRanges of march 21 2018 EBI gwascat, limit to chr17*

Description

gwascat_hg19: GRanges of march 21 2018 EBI gwascat, limit to chr17

Usage

```
gwascat_hg19_chr17
```

Format

GenomicRanges GRanges instance

Source

gwascat::makeCurrentGwascat, with gwascat:::lo38to19 applied

Examples

```
TFutils::gwascat_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 HOCOMOCO 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

lambert_snps is Table S3 of Lambert et al PMID 29425488

Description

lambert_snps is Table S3 of Lambert et al PMID 29425488

Usage

```
lambert_snps
```

Format

data.frame

Examples

```
head(lambert_snps)
```

metadata_tf

metadata_tf: list with metadata (motif_if and hgnc_symbol) about all the CISBP FIMO scan TF bed files

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

named_tf: named list with the names being the hgnc_symbol of the motif_id

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

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_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 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 *Constructor for TFCatalog*

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

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 transctiption factor, and 4) additional metadata will frequently be required to establish information about provenance of assertions about transcription factors.

---

tffamCirc.plot — *use a radial plot (by default) for motif stack*

Description

use a radial plot (by default) for motif stack

Usage

```
tffamCirc.plot(motiflist, circosParms = defaultCircosParms())
```

Arguments

`motiflist`	a list of pfm instances from motifStack
`circosParms`	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 *set up list of pfms in motifStack protocol*

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)
```

tfhash — *tfhash: data.frame with MSigDb TFs, TF targets as symbol or ENTREZ*

Description

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

Usage

```
tfhash
```

Format

list

Source

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

Examples

```
TFutils::tfhash
tfhash[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,

   gadtitle = "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
`gadtitle`	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 — *Use MSigDB TF targets resource to find targets of input TF and find traits to which these targets have been mapped*

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 `GeneSetCollection-class`, intended to enumerate targets of a single transcription factor in each GeneSet, as in TFutils::tftColl
gwcat	instance of `gwaswloc-class`
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 gwascat below
topTraitsOfTargets("MTF1" , tftColl, gwascat_hg19_chr17)
```

URL_s3_tf — *utility to generate link to biocfound bucket for FIMO TFBS scores*

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

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URL_s3_tf
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