

# Package ‘TFutils’

October 16, 2019

**Title** TFutils

**Description** Package to work with TF data.

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EnsDb.Hsapiens.v75, BiocParallel, BiocStyle, GO.db,  
GenomicFiles, GenomeInfoDb, SummarizedExperiment, UpSetR,  
ggplot2, png, gwascat

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---

 cisbpTFcat

*cisbpTFcat: data.frame with information on CISBP TFs for human*


---

**Description**

cisbpTFcat: data.frame with information on CISBP TFs for human

**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.ccb.utoronto.ca/bulk.php> select Homo\_sapiens

**Examples**

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

---

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

---

**Description**

demonstrate interoperation of TF catalog with GWAS catalog

**Usage**

```
directHitsInCISBP(traitTag, gwascats)
```

**Arguments**

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

**Value**

data.frame

**Examples**

```
data(gwascats_hg19_chr17)
directHitsInCISBP("Prostate cancer" , gwascats_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)
```

---

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

---

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	<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**

gwascat::makeCurrentGwascat, with gwascat::lo38to19 applied

**Examples**

```
TFutils::gwascat_hg19_chr17[,1:5]
```

---

HGNCmap	<i>simple accessor for HGNCmap component of TFCatalog</i>
---------	---

---

**Description**

simple accessor for HGNCmap component of TFCatalog

**Usage**

```
HGNCmap(x)
```

**Arguments**

x                   instance of TFCatalog

**Value**

dataframe instance

**Examples**

HGNCmap

---

hocomoco.mono	<i>hocomoco.mono: data.frame with information on HOCOMOCO TFs for human</i>
---------------	---

---

**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	<i>hocomoco.mono.sep2018: data.frame with information on HOCOMOCO TFs for human, Sept 2018 download</i>
-----------------------	---

---

**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

<code>src</code>	TabixFile instance
<code>parms</code>	a GRanges instance delimiting the import; multiple GRanges can be used
<code>...</code>	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"))
```

---

```
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	<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"]]
```

---

setupHIZE	<i>process a gene_attribute_matrix.txt file from harmonizeome into a GeneSetCollection</i>
-----------	--

---

**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

**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

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

---

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::gwascap_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::gwascap\_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

**Note**

If tftCollMap[, "hgnc.heur"] does not possess the necessary symbol, set force = TRUE to use a known 'motif' name among names(gsc)

**Examples**

```
suppressPackageStartupMessages({
  library(GSEABase)
  library(TFutils)
}) # 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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