

Package ‘TFutils’

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Title TFutils

Description Package to work with TF data.

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Gviz, IRanges, Rsamtools, S4Vectors, org.Hs.eg.db,
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.cabr.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 gwaswloc-class

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"]]
```

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.

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

Description

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

Usage

```
tffhash
```

Format

```
list
```

Source

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

Examples

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

TFtargs	<i>gadget to help sort through tags naming TFs</i>
---------	--

Description

gadget to help sort through tags naming TFs

Usage

```
TFtargs(gscoll = TFutils::tftColl, initTF = "VDR_Q3",
        gwcat = TFutils::gwascats_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	<i>tftCollMap: data.frame with information on MSigDb TFs for human</i>
------------	--

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 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

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`*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

```
URL_s3_tf
```


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