

Package ‘rtfbsdb’

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Title Parse TF motifs from public databases, read into R, and scan using 'rtfbs'.

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Depends R (>= 2.6)

Imports rphast, rtfbs, bigWig, parallel, grid, cluster, methods, latticeExtra, lattice, apcluster

LinkingTo

Suggests RCurl, stringr

Description

Convenience functions to read and scan DNA sequences using Position Weight Matrices (PWMs)

License GPL version 3 or newer

biocViews Sequencing, Analysis

LazyLoad yes

R topics documented:

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CisBP.db-class	<i>Class "CisBP.db"</i>
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Description

The motif library from CisBP web site.
Link: <http://cisbp.ccbr.utoronto.ca/>

Objects from the Class

Objects can be created by calls of the form `CisBP.extdata`, `CisBP.zipload`, `CisBP.download`.

Slots

`species`: String indicating the species name defined in the CisBP dataset.
`zip.file`: String indicating the filename of temporary data file.
`zip.url`: String indicating the download source.
`zip.date`: String indicating the download date.
`file.tfinfo`: String indicating the TF filename, default is TF_Information.txt.

Extends

Class "`tfbs.db`", directly.

Methods

`tfbs.createFromCisBP` Build a `tfbs` object by querying the meta file of CisBP dataset and subsetting the results.
`CisBP.group` Get the statistical summary by grouping the field in the CisBP dataset.
`CisBP.getTFinformation` Get the TF Information stored in the CisBP dataset.

References

Weirauch, M. T., Yang, A., Albu, M., Cote, A. G., Montenegro-Montero, A., Drewe, P., ... & Hughes, T. R. (2014). Determination and inference of eukaryotic transcription factor sequence specificity. *Cell*, 158(6), 1431-1443.

See Also

[CisBP.getTFinformation](#), [CisBP.group](#), [tfbs.createFromCisBP](#)

Examples

```
showClass("CisBP.db")
```

CisBP.download	<i>Download CisBP dataset.</i>
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Description

Download TF data file from CisBP dataset and store it to temporary folder

Usage

```
CisBP.download(species = "Homo_sapiens",
               url = "http://cisbp.ccb.utoronto.ca/bulk_archive.php")
```

Arguments

species	String, indicating the species name in the CisBP dataset
url	String, the URL of bulk downloads from CisBP dataset, default is http://cisbp.ccb.utoronto.ca/bulk_archive.php

Details

The download function has been confirmed in the web site of cisbp.ccb.utoronto.ca o June, 2015.

Value

A CisBP object (class name: "[CisBP.db](#)") is returned with four items:

species	String indicating the species name
zip.file	String indicating the filename of temporary data file.
zip.url	String indicating the download source
file.tfinfo	String indicating the TF filename, default is TF_Information.txt.

References

Weirauch, M. T., Yang, A., Albu, M., Cote, A. G., Montenegro-Montero, A., Drewe, P., ... & Hughes, T. R. (2014). Determination and inference of eukaryotic transcription factor sequence specificity. *Cell*, 158(6), 1431-1443.

See Also

See Also as [CisBP.zipload](#), [CisBP.extdata](#).

Examples

```
#download zebra fish dataset
db1 <- CisBP.download("Danio_rerio");

#download Felis_catus dataset
db2 <- CisBP.download("Felis_catus");
```

CisBP.extdata	<i>Load internal CisBP dataset.</i>
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Description

Build a CisBP object from the internal zip file stored in this package

Usage

```
CisBP.extdata(species)
```

Arguments

species	String, only valid for human and mouse species, i.e. Homo_sapiens, Mus_musculus, or Drosophila_melanogaster
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Details

The CisBP data for Homo_sapiens and Mus_musculus are delivered by this package. When you use the newest dataset, you should download it from the website by [CisBP.download](#).

Value

A CisBP object (class name: "[CisBP.db](#)") is returned with four items:

species	String indicating the species name defined in the CisBP dataset.
zip.file	String indicating the filename of temporary data file.
zip.url	String indicating the download source
file.tfinfo	String indicating the TF filename, default is TF_Information.txt.

See Also

See Also as [CisBP.zipload](#), [CisBP.download](#).

Examples

```
#reading human data from extension data file in the package
db.human <- CisBP.extdata("Homo_sapiens")

#reading Drosophila_melanogaster from extension data file in the package
db.dm3 <- CisBP.extdata("dm3")
```

CisBP.getTFInformation

Get TF information with PWM status

Description

Get TF information with PWM status

Usage

```
CisBP.getTFInformation(cisbp.db, tf.information.type = NA)
```

Arguments

cisbp.db	A CisBP object (" CisBP.db ") including the TF_Information.txt.
tf.information.type	Number, indicating which TF meta file will be used. Available values are 1 for TF_Information.txt, 2 for TF_Information_all_motifs.txt and 3 for F_Information_all_motifs_plus.txt.

Details

Three TF information files in CisBP dataset.

- 1: TF_Information.txt : (direct motifs) or (no direct but inferred motifs with 90%)
- 2: TF_Information_all_motifs.txt: (direct motifs) and (inferred motifs above the threshold)
- 3: F_Information_all_motifs_plus.txt: All motifs

The following parts are copied from RAEDME.txt in zipped CisBP data file.

TF_Information.txt, TF_Information_all_motifs.txt, TF_Information_all_motifs_plus.txt - These files contain information on the TFs.

'TF_Information.txt' contains, for each TF, all directly determined motifs (see below). If a TF does not have a directly determined motif, this file will also include its best inferred motif. 'Best' is defined as the motif(s) obtained from the most similar TF (based on the

'TF_Information_all_motifs.txt' is a superset of 'TF_Information.txt'. It also includes any motif that can be inferred for a given TF, given the TF family-specific threshold. For example, if a TF has a directly determined motif, and two TFs with motifs with 90 TF_Information_all_motifs.txt will include all three motifs. Likewise, if a TF does not have a direct motif, but has two TFs with 90

'TF_Information_all_motifs_plus.txt' is a superset of the other two files. It contains all motifs for a given TF, which includes all direct motifs, and all inferred motifs above the threshold.

Value

A data frame returned with the status indicating PWM data is existing or not

TF_ID	Internal CisBP ID for the TF. Each gene has a unique TF_ID
-------	--

Family_ID	Internal CisBP ID for the TF family. A family is the unique set of DNA binding domains (DBDs) present in the protein.
TSource_ID	Internal CisBP ID for the source of the TF (i.e. where its genome sequence was obtained).
Motif_ID	Internal CisBP ID for the associated motif.
MSource_ID	Internal CisBP ID for the source of the motif (i.e. which database or study it came from)
DBID	External ID of the RBP (e.g., Ensembl ID)
TF_Name	Name of the TF
TF_Species	Species of the TF
TF_Status	Motif status of the TF. 'D' stands for directly determined motif. 'I' indicates that the motif is inferred from another TF, based on DBD similarity (see Weirauch et al. 2013 for details). 'N' means no motif is available.
Family_Name	Name of the TF's family
DBDs	The unique set of DBDs (Pfam names) present in the TF
DBD_Count	Number of unique DBDs in the TF
Cutoff	Cutoff used to infer motifs for the TF family
DBID	Motif ID from the associated database or study
Motif_Type	Experimental assay used to determine the motif
MSource_Identifier	ID for the source of the motif (i.e., its project name)
MSource_Type	Internal CisBP ID for the motif category
MSource_Author	First author for the source of the motif
MSource_Year	Year of publication of the motif source
PMID	Pubmed ID of the motif source
MSource_Version	Version of the source (i.e. database build)
TFSource_Name	Source of the TF (i.e. where did the genome build come from?)
TFSource_URL	URL of the TF source
TFSource_Year	Year the genome data was downloaded
TFSource_Month	Month the genome data was downloaded
TFSource_Day	Day the genome data was downloaded
<i>motif_existing</i>	Status indicating PWM data is existing or not

See Also

See Also as [CisBP.group](#), [CisBP.extdata](#), [CisBP.zipload](#), [CisBP.download](#)

Examples

```
# Load the internal CisBP dataset
db_human <- CisBP.extdata("Homo_sapiens");

df.tfinfo <- CisBP.getTFInformation( db_human, tf.information.type = 2)
show(head(df.tfinfo));
```

CisBP.group	<i>Summarize the motif number.</i>
-------------	------------------------------------

Description

Get the statistical summary by grouping the field in the CisBP dataset.

Usage

```
CisBP.group(cisbp.db,
            group.by=c("tf_name", "tf_species", "tf_status", "family_name",
                       "motif_type", "msource_id"),
            tf.information.type=NA )
```

Arguments

<code>cisbp.db</code>	A CisBP object (" CisBP.db ") including the TF_Information.txt.
<code>group.by</code>	String, indicating which field will be used to group values. Available values are <code>tf_name</code> , <code>tf_species</code> , <code>tf_status</code> , <code>family_name</code> , <code>motif_type</code> and <code>msource_id</code> .
<code>tf.information.type</code>	Number, indicating which TF meta file will be used. Available values are 1 for TF_Information.txt, 2 for TF_Information_all_motifs.txt and 3 for F_Information_all_motifs_plus.txt.

Details

Three TF information files in CisBP dataset.

- 1: TF_Information.txt : (direct motifs) or (no direct but inferred motifs with 90%)
- 2: TF_Information_all_motifs.txt: (direct motifs) and (inferred motifs above the threshold)
- 3: F_Information_all_motifs_plus.txt: All motifs

Value

A data frame returned includes two columns

<code>group_by</code>	Values of grouping field
<code>number</code>	Counts of group value

See Also

See Also as [tfbs.createFromCisBP](#)

Examples

```
# Load the internal CisBP dataset
db_human <- CisBP.extdata("Homo_sapiens");

# Group the motif count by the column of family_name in TF_Information.txt
gr1 <- CisBP.group(db_human, group.by="family_name", tf.information.type=1 );

# Group the motif count by the column of tf_status in TF_Information.txt
gr2 <- CisBP.group(db_human, group.by="tf_status", tf.information.type=1 );

# Group the motif count by the column of tf_status in TF_Information_all_motifs.txt
gr3 <- CisBP.group(db_human, group.by="tf_status", tf.information.type=2);

# Group the motif count by the column of tf_status in F_Information_all_motifs_plus.txt
gr4 <- CisBP.group(db_human, group.by="tf_status", tf.information.type=3);
```

CisBP.zipload	<i>Load the zipped CisBP file.</i>
---------------	------------------------------------

Description

Build a CisBP object from the zipped CisBP file.

Usage

```
CisBP.zipload(zip.file, species = "Homo_sapiens")
```

Arguments

zip.file	String, indicating the zipped file data
species	String, indicating the species name in the CisBP database

Details

The zip data canbe downloaded from the web site, please check [CisBP.download](#).

Value

A CisBP object (class name: "[CisBP.db](#)") is returned with four items:

species	String indicating the species name
zip.file	String indicating the filename of temporary data file.
zip.url	String indicating the download source
file.tfinfo	String indicating the TF filename, default is TF_Information.txt.

See Also

See Also as [CisBP.extdata](#), [CisBP.download](#).

Examples

```
# Download the dataset
db1 <- CisBP.download("Arabidopsis_thaliana");

# Loading the zip file, the db2 and db3 have same TF data.
# Here is an example to show how to use CisBP.zipload.
# We dont nee to download it by CisBP.download and then load it by CisBP.zipload
db2 <- CisBP.zipload(db1@zip.file, species="Arabidopsis thaliana");
```

```
print.tfbs.enrichment
```

Print the brief enrichment results

Description

Print the brief enrichment results.

Usage

```
## S3 method for class 'tfbs.enrichment'
print(x, ..., pv.threshold=0.05, pv.adj=NA )
```

Arguments

<code>x</code>	The result obtained by <code>tfbs.enrichmentTest</code> .
<code>...</code>	Additional arguments affecting the print produced.
<code>pv.threshold</code>	Numeric value, indicating whether the different cutoff of p-value is applied to select the significant motifs.
<code>pv.adj</code>	String, P-values correct method for <code>p.adjust</code> function. The available values are "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr" or "none". (default="bonferroni")

Details

This command shows the calling parameters and significant motifs from the result object. The significant motifs are selected by the corrected p-value cutoff(0.05) and at most 20 significant motifs are listed. The adjust method of p-value is defined in the calling function.

Value

No return values.

See Also

See also as `tfbs.enrichmentTest`.

Examples

```
#See example in tfbs.enrichmentTest
```

```
print.tfbs.finding Print scanning result of TF sites.
```

Description

Print scanning result of TF sites.

Usage

```
## S3 method for class 'tfbs.finding'  
print(x, ...)
```

Arguments

x	The result obtained by <code>tfbs.scanTFsite</code> .
...	Additional arguments affecting the print produced.

Details

This function shows a brief information including calling parameters and enriched motifs.

Value

No return values.

See Also

See Also as `tfbs.scanTFsite`

Examples

```
#See example in tfbs.scanTFsite
```

```
summary.tfbs.enrichment  
      Summarize the enrichment result
```

Description

Return the significant motifs based on the adjust p-values using multiple comparisons.

Usage

```
## S3 method for class 'tfbs.enrichment'  
summary(object, pv.threshold = 0.05, pv.adj = NA, ...)
```

Arguments

object	The result obtained by <code>tfbs.enrichmentTest</code> .
pv.threshold	The p-value threshold for significant motifs.
pv.adj	P-values adjust method for <code>p.adjust</code> function. The available values are "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr" or "none".
...	Additional arguments affecting the summary produced.

Details

A data frame with 6 columns is returned.

Value

The results is a data frame including 6 columns,

motif.id	Motif ID
tf.name	TF Name
Npos	Read count in positive loci.
expected	Read count in negative loci.
fe.ratio	The ratio of read counts between positive loci and negative loci.
starch	Cpmprocessed Bed filename
pvalue	p-value
pv.adj	adjusted p-value by multiple comparson method.

See Also

See also as `tfbs.enrichmentTest`.

```
summary.tfbs.finding
```

Summarize scanning results.

Description

Return a data frame with summarized TF sites for every motif if the calling parameter is "matches".

Usage

```
## S3 method for class 'tfbs.finding'
summary(object, ...)
```

Arguments

object	The result obtained by <code>tfbs.scanTFsite</code> .
...	Additional arguments affecting the summary produced.

Details

summary in class of `tfbs.finding` is returned.

Value

This function will return a data frame with summarized TF sites for every motif if the calling parameter is "matches", otherwise, NULL will be returned.

See Also

See Also as [tfbs.scanTFsite](#)

tfbs	<i>Create a tfbs object from the supplied PWM files.</i>
------	--

Description

Create a tfbs object from the supplied PWM files.

Usage

```
tfbs (filenames,
      names,
      species="Homo_sapiens",
      tf_info = NULL,
      tf_missing = NULL, ...)
```

Arguments

filenames	Vector of PWM files
names	Vector of unique gene symbols.
species	String indicating species name
tf_info	Data frame including meta information copied from CisBP data file for all existing motifs., Default: NULL
tf_missing	Data frame including meta information copied from CisBP data file for missing motifs., Default: NULL
...	Parameters, such as pseudocount, force_even, and the parameters used in read.table function.

Details

Load the PWM files to build a "[tfbs](#)" object.

Value

A tfbs object (class: "[tfbs](#)") including all PWM matrices. The all attributes are as follows:

TFID	Vector of non-unique ID for TF.
species	String indicating the species name
ntfs	Number of motifs in matrix.
pwm	A list including PWM matrices.
filename	Vector of PWM filename.

<code>mgisymbols</code>	Unique gene symbols for TF.
<code>tf_info</code>	Data frame, including extra information for all existing PWMs, it maybe different with motif dataset, default:NULL.
<code>tf_missing</code>	Data frame, including extra information for missing PWMs, it maybe different with motif dataset, default:NULL.
<code>distancematrix</code>	Distance matrix between motifs returned by <code>tfbs.clusterMotifs</code> , default:NULL.
<code>expressionlevel</code>	Data frame indicatig the result of expression level returned by <code>tfbs.getExpression</code> , default:NULL.
<code>cluster</code>	Matrix with 2 columns returned by <code>tfbs.clusterMotifs</code> , 1st column is the index of motifs and 2nd column is the group number of clustering, default:NULL.

The tfbs object can be created by the function of `tfbs`, `tfbs.dirs`, `tfbs.createFromCisBP`.

See Also

`tfbs`, `tfbs.dirs`, `tfbs.createFromCisBP`

Examples

```
# M3590_1.01 PAX5 ENSG00000196092
# M3590_1.01 PAX5 ENSG00000196092
fs1 <- system.file("extdata", "M3590_1.01.pwm", package="rtfbsdb")
fs2 <- system.file("extdata", "M3591_1.01.pwm", package="rtfbsdb")

cat(fs1, "\n");

tfs <- tfbs( c( fs1, fs2 ), names=c("M3590_1.01", "M3591_1.01"),
            header=TRUE, sep="\t" , row.names=1 );
str(tfs);
```

<code>tfbs-class</code>	<i>Class</i> "tfbs"
-------------------------	---------------------

Description

Tfbs object is a collection of motif PWM data. Some functions are provided based on the PWM and GENCODE data, such as clustering, search and compare.

Objects from the Class

Objects can be created by calls of the function of `tfbs.createFromCisBP`, `tfbs.dirs` and `tfbs`.

Slots

- species** String indicating the species name
- ntfs** Number of motifs in matrix.
- pwm** A list including PWM matics.
- filename** Vector of PWM filename.
- mgisymbols** Unique gene symbols for TF.
- tf_info** Data frame, including extra information for all existing PWMs, it maybe different with motif dataset, default:NULL.
- tf_missing** Data frame, including extra information for missing PWMs, it maybe different with motif dataset, default:NULL.
- distancematrix** Distance matrix between motifs returned by `tfbs.clusterMotifs`, default:NULL.
- expressionlevel** Data frame indicatig the result of expression level returned by `tfbs.selectExpressedMotifs` or `tfbs.getExpression`, default:NULL.
- cluster** Matrix with 2 columns returned by `tfbs.clusterMotifs`, 1st column is the index of motifs and 2nd column is the group number of clustering, default:NULL.

Methods

- tfbs.importMotifs** Import the licensed motifs or other missing motifs for tfbs object
- tfbs.getExpression** Estimate gene expression of target TF.
- tfbs.selectExpressedMotifs** Select the expressed motifs in GRO-seq, PRO-seq or RNA-seq experimental data.
- tfbs.clusterMotifs** Cluster the specified motifs and drawing the heatmap.
- tfbs.scanTFsite** Find TF sites from genome data within the BED ranges.
- tfbs.enrichmentTest** Comparative TFBS search with the BED ranges
- tfbs.selectByGeneExp** Select the motifs with minimum p-value from each group of clustering.
- tfbs.selectByRandom** Select the motifs randomly from each group of clustering.
- tfbs.drawLogosForClusters** Draw the motif logos by one group per page.
- tfbs.drawLogo** Draw the logo for a single TF motif.

See Also

The class definition of tfbs.

Examples

```
showClass("tfbs")
```

`tfbs.clusterMotifs` *Clustering the specified motifs and drawing the heatmap.*

Description

Clustering the specified motifs and drawing the heatmap.

Usage

```
tfbs.clusterMotifs(tfbs,
  method = c("agnes", "apcluster"),
  pdf.heatmap = NA,
  group.k = NA,
  apcluster.q = 0.99,
  ncores = 1,
  BG = log(c(0.25, 0.25, 0.25, 0.25)) )
```

Arguments

<code>tfbs</code>	A <code>tfbs</code> object (" <code>tfbs</code> ") returned by <code>tfbs.createFromCisBP</code> , <code>tfbs.dirs</code> or other functions.
<code>pdf.heatmap</code>	String, a PDF filename for heatmap.
<code>method</code>	String, available values are "agnes" and "apcluster".
<code>group.k</code>	Integer, if the method of agnes is used to do clustering, the parameter of k is optional to use as preset group number.
<code>apcluster.q</code>	Numeric value between 0 and 1, if the method of apcluster is used to do clustering, the parameter of q is optional to use as preset group number.
<code>ncores</code>	Number, the number of cores to use simultaneously.
<code>BG</code>	The log value of probabilities for nucleotide A, C, G and T as Background computing.

Details

This result of clustering will be used in the `tfbs.drawLogosForClusters`, `tfbs.selectByGeneExp`, `tfbs.enrichmentTest`.

`tfbs@cluster` will be updated by the clustering matrix which 1st column is the index of motifs and 2nd column is the group number of clustering.

Value

A matrix with 2 columns is returned, 1st column is the index of motifs and 2nd column is the group number of clustering.

See Also

See Also as `tfbs.selectByGeneExp` and `tfbs.selectByRandom`

Examples

```
# Load the internal CisBP data set
db <- CisBP.extdata("Homo_sapiens");

# Create a tfbs object by querying the meta file of CisBP dataset.
tfs <- tfbs.createFromCisBP(db, motif_type="ChIP-seq", tf.information.type=1 );

# Cluster the motifs using the "agnes" method
tfs <- tfbs.clusterMotifs(tfs, method="agnes", pdf.heatmap = "test-heatmap-agnes.pdf" );
show(tfs@cluster);

# Cluster the motifs using the "apcluster" method
tfs <- tfbs.clusterMotifs(tfs, method="apcluster", pdf.heatmap = "test-heatmap-apcluster.pdf" );
show(tfs@cluster);

# draw motif logos on one group per page.
tfbs.drawLogosForClusters(tfs, file.pdf = "test-cluster-logos.pdf");
```

```
tfbs.createFromCisBP
```

Create TF object by querying the CisBP dataset.

Description

Build a tfbs object by querying the meta file of CisBP dataset and subsetting the results.

Usage

```
tfbs.createFromCisBP(cisbp.db,
  tf_name = NULL,
  tf_status = NULL,
  family_name = NULL,
  motif_type = NULL,
  msource_id = NULL,
  tf.information.type = 1)
```

Arguments

<code>cisbp.db</code>	A CisBP object("CisBP.db"), including the file of TF_Information.txt.
<code>tf_name</code>	String, indicating the TF_name field will be used to select motifs.
<code>tf_status</code>	String, indicating the TF_Status field will be used to select motifs.
<code>family_name</code>	String, indicating the Family_Name field will be used to select motifs.
<code>motif_type</code>	String, indicating the Motif_Type field will be used to select motifs.
<code>msource_id</code>	String, indicating the MSource_Identifier field will be used to select motifs.
<code>tf.information.type</code>	Number, indicating which TF meta file will be used. Available values are 1 for TF_Information.txt, 2 for TF_Information_all_motifs.txt and 3 for TF_Information_all_motifs_plus.txt.

Details

The function includes three steps to build a tfbs object:

1) Searching the TF information and PWM files in the CisBP dataset according to the criteria specified by the parameters of *tf_name*, *tf_status*, *family_name*, *motif_type* and *msource_id*.

Value

A tfbs object is returned with PWM matrices, see Also as "[tfbs](#)"

See Also

See Also as [tfbs](#)

Examples

```
# Load the internal CisBP dataset
db_human <- CisBP.extdata("Homo_sapiens");

# Load all motifs and return a tfbs object.
tfs0 <- tfbs.createFromCisBP(db_human);

# Query the motifs by the conditions and return a tfbs object
tfs1 <- tfbs.createFromCisBP(db_human, family_name="Homeodomain", tf_status="D",
                             motif_type="ChIP-seq", msource_id= "MS01_1.01", tf.information.type=1 );

# Query the motifs by the conditions and return a tfbs object
tfs2 <- tfbs.createFromCisBP(db_human, family_name="Homeodomain", tf_status="D" );

# Query the motifs by the conditions and return a tfbs object
tfs3 <- tfbs.createFromCisBP(db_human, motif_type="ChIP-seq" );

# Query the motifs by the conditions and return a tfbs object
tfs4 <- tfbs.createFromCisBP(db_human, tf.information.type=2);
```

tfbs.db-class	Class "tfbs.db"
---------------	-----------------

Description

Abstract class for motif dataset. The CisBP class is a son class of tfbs.db.

Objects from the Class

Now code or function can be used to create this class.

Slots

species: Species name.

Methods

No methods defined with class "tfbs.db" in the signature.

See Also

"[CisBP.db](#)" inherits this class.

Examples

```
showClass("tfbs.db")
```

tfbs.dirs	Create a tfbs object from the folders.
-----------	--

Description

Create a tfbs object from all the PWM files found in the supplied folders.

Usage

```
tfbs.dirs(...,
  species = "Homo_sapiens",
  args.read.motif = NULL,
  pattern = glob2rx("*.pwm"),
  recursive = FALSE)
```

Arguments

...	Multiple strings, one or more folders can be used in this function.
species	String, including the species name.
args.read.motif	List, including <i>pseudocount</i> , <i>force_even</i> or other parameters used in <code>read.table</code> function.
pattern	String, a character vector specifying regular expression and wildcards.
recursive	Logical, indicating the loading recursively descends into subfolders or not, default: FALSE.

Details

Two parameters in the list of `args.read.motif` can be used:
pseudocount: log value for zero value in PWM matrix, default is -7.
force_even: whether the PWM matrix with odd size needs to be even.

Value

A tfbs object collecting all the PWM files in the specified folders. For the details of tfbs object, please see [tfbs](#)

See Also

The structure of tfbs object is described in "[tfbs](#)"

Examples

```
fs.dir <- system.file("extdata","", package="rtfbsdb")
tfs <- tfbs.dirs( fs.dir,
  args.read.motif = list(pseudocount=-7, header=TRUE, sep="\t" , row.names=1) );
str(tfs);
```

tfbs.drawLogo	<i>Draw single motif logo.</i>
---------------	--------------------------------

Description

Draw the motif logos in two models, 1 logo within a page or 1 group within one page.

Usage

```
tfbs.drawLogo(tfbs, file.pdf = NULL, index = NULL, tf_id = NULL,
  motif_id = NULL, tf_name = NULL, family_name = NULL,
  tf_status = NULL, groupby = NULL)
```

Arguments

tfbs	A tfbs object(" tfbs ")
file.pdf	String, the file name of PDF report.
index	Vector of number, indicating the motif index.
tf_id	Vector of string, indicating the TF_ID string, TF_ID is one motif attribute in TF_Information.txt. (Default=NULL).
motif_id	Vector of string, indicating the Motif_ID string, Motif_ID is one motif attribute in TF_Information.txt. (Default=NULL).
tf_name	Vector of string, indicating the TF_Name string, TF_Name is one motif attribute in TF_Information.txt. (Default=NULL).
family_name	Vector of string, indicating Family_Name string, Family_Name is one motif attribute in TF_Information.txt. (Default=NULL).
tf_status	String, indicating the TF_status value, TF_status is one motif attribute in TF_Information.txt. (Default=NULL).
groupby	String, indicating the group field is applied to print the motif, each group is printed in one page, the available values are NA, "Family_Name", "TF_Name", "TF_Status" or "Motif_Type". (Default=NA).

Details

Multiple selection is provided for outputting logos. The selected motifs by each criteria will be combined into one set.

Draw the motif logos in two models:

(1) 1 logo within a page (2) 1 group within one page. The motif logos are splitted if motif count is greater than 10.

Value

No return values.

See Also

See Also as `"tfbs"`

Examples

```
db <- CisBP.extdata("Homo_sapiens");

tfs <- tfbs.createFromCisBP(db);

motif_id <- c( "M5604_1.01", "M5441_1.01", "M5162_1.01", "M5352_1.01");
tf_id <- c( "T093250_1.01", "T093251_1.01", "T093252_1.01", "T093253_1.01");
family_name <- c( "p53", "Homeodomain", "Paired box", "Pipsqueak");

#Draw 10 motif logos from first one.
tfbs.drawLogo(tfs, file.pdf="test-drawLogo1.pdf", index=c(1:10) );

#Draw logos for specified Motif_ID, or TF_ID, or TF_Name, or Family_Name
tfbs.drawLogo(tfs, file.pdf="test-drawLogo2.pdf",
  motif_id = motif_id,
  tf_id = tf_id,
  tf_name = "AP-2",
  family_name = family_name,
  groupby = "TF_Status");

#Draw logos for specified TF_Status
tfbs.drawLogo(tfs, file.pdf="test-drawLogo3.pdf", tf_status="D", groupby="TF_Status");

#unlink("test-drawLogo1.pdf");
#unlink("test-drawLogo2.pdf");
#unlink("test-drawLogo3.pdf");
```

```
tfbs.drawLogosForClusters
```

Draw the motif logos by clustering.

Description

Draw the motif logos by one cluster per page.

Usage

```
tfbs.drawLogosForClusters(tfbs, file.pdf )
```

Arguments

tfbs	A tfbs object("tfbs").
file.pdf	String indicating a PDF filename.

Details

It is different with `tfbs.drawLogo` which is capable of printing out motif logos in group. This group is calculated by the `tfbs.clusterMotifs`, not is classified by any group filed.

Value

No return value.

See Also

See Also as `tfbs.clusterMotifs`

Examples

```
# Load the internal CisBP data set
db <- CisBP.extdata("Homo_sapiens");

# Create a tfbs object by querying the meta file of CisBP dataset.
tfs <- tfbs.createFromCisBP(db, motif_type="ChIP-seq", tf.information.type=1 );

# Cluster the motifs using the "cors" method
tfs <- tfbs.clusterMotifs(tfs, method="apcluster", pdf.heatmap = "test-heatmap1.pdf" );
show(tfs@cluster);

# draw motif logos on one group per page.
tfbs.drawLogosForClusters(tfs, "test-cluster1.pdf")
```

```
tfbs.enrichmentTest
```

Comparative TS sites between positive and negative TRE loci

Description

Comparative TS sites between positive and negative TRE loci for all motifs.

Usage

```
tfbs.enrichmentTest(tfbs,
  file.twoBit,
  positive.bed,
  negative.bed=NA,
  file.prefix=NA,
  use.cluster=FALSE,
  ncores=1,
  gc.correction=TRUE,
  gc.correction.pdf=NA,
  gc.robust.rep=NA,
  threshold = 6,
  threshold.type = c("score", "fdr"),
  gc.groups=1,
  background.order=2,
  background.length=100000,
  pv.adj = p.adjust.methods)
```

Arguments

<code>tfbs</code>	A <code>tfbs</code> object, see also " tfbs "
<code>file.twoBit</code>	String, the file name of genome data(e.g. hg19.2bit, mm10.2bit)
<code>positive.bed</code>	Data frame, bed-formatted TRE loci.
<code>negative.bed</code>	Data frame, bed-formatted background loci. If not specified, the genomic loci adjacent to positive one are randomly extracted as the negative bed.
<code>file.prefix</code>	String, the prefix for outputted BED file, no bed files output if NA
<code>use.cluster</code>	Clustering matrix with 2 columns, 1st column is the index of motifs and 2nd column is the group number of clustering. It can be obtained from tfbs.clusterMotifs . If no clustering matrix, all motifs are used to do the comparison. see <i>details</i>
<code>ncores</code>	Number, computing nodes in parallel environment.(default=1)
<code>gc.correction</code>	Logical value, if the difference between positive and negative TREs is significant, the resampling will be applied to the correction for the negative TREs. (default=TRUE)
<code>gc.correction.pdf</code>	String, indicating the pdf file name if the GC correction is checked. (default=NA)
<code>gc.robust.rep</code>	Number, indicating whether resampling background set multiple times is applied to get the median of binding sites. (default=NA)
<code>threshold</code>	Numeric value, if 'score' is specified in <code>threshold.type</code> , only binding sites with scores above this threshold are returned, if 'fdr' is specified in <code>threshold.type</code> , only binding sites with FDR (False Discovery Rate) less than this value can be selected. Default value is 6 for 'score' and 0.1 for 'fdr'.
<code>threshold.type</code>	String value, two options are available. only sites with scores above this threshold are returned, not be used if NA. (default = 'score')
<code>gc.groups</code>	Numeric value, indicating number of quantiles to group sequences into in <code>rtfbs</code> package. (default = 1)

<code>background.order</code>	Number, order of Markov model to build background.(default=2).
<code>background.length</code>	Number, length of the sequence to simulate background.(default=100000).
<code>pv.adj</code>	String, P-values correct method for <code>p.adjust</code> function. The available values are "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr" or "none". (default="bonferroni").

Details

The difference of GC contents between `positive.bed` and `negative.bed` is checked before the comparison. The p-value of Wilcoxon-Mann-Whitney test shows this difference and helps the user to determine whether the GC correction is necessary. If the difference is very significant, please set `gc.correction` to do GC content correction by resampling the TREs from negative bed data based on the frequency of TREs in negative bed data. Use the parameter of `gc.correction.pdf` to output vioplot figures in a pdf file if you want to check the visualized difference.

The clustering matrix indicates which motifs in the 1st column are selected to do comparison and which clustering group in the 2nd columns are applied to adjust p-values for multiple comparisons. The function applies the p-values adjust for each clustering group. If no clustering information, all motifs in the `tfbs` object will be selected and adjusted as one group, which is the most conservative method.

Value

A object with the class name of "tfbs.enrichment" will be returned in this comparison function. It includes one list of parameters `parm` and one data frame of results `result`.

`result` is a data frame with the following columns:

<code>motif.id</code>	Motif ID.
<code>tf.name</code>	TF name.
<code>Npos</code>	TF site count found in positive ranges.
<code>expected</code>	TF site count found in negative ranges.
<code>fe.ratio</code>	Ratio of fold enrichment.
<code>pvalue</code>	p-value calculated by fisher test.
<code>pv.adj</code>	p-value corrected by the multiple correction.
<code>starch</code>	Binary filename of detected TF sites.

The `result` can be outputted to a report by the function `tfbs.reportEnrichment`.

See Also

`print.tfbs.enrichment`, `summary.tfbs.enrichment`, `tfbs.reportEnrichment`.

Examples

```
library(rtfsdb);

file.twoBit <- system.file("extdata", "hg19.chr19.2bit", package="rtfsdb")
```

```

db <- CisBP.extdata("Homo_sapiens");
tfs <- tfbs.createFromCisBP(db, family_name="AP-2");

#make two dummy BED data frame for positive loci and negative loci
pos.bed <- data.frame(chr="chr19",
start=round(runif(1000,1000000, 2000000)),
stop=0,
name="",
score=0,
strand=".");
pos.bed$stop <- pos.bed$start + round(runif(1000, 20, 30));

neg.bed <- data.frame(chr="chr19",
start=round(runif(8000, 800000, 1800000)),
stop=0,
name="",
score=0,
strand=".");
neg.bed$stop <- neg.bed$start + round(runif(8000, 20, 30));

t1 <- tfbs.enrichmentTest( tfs,
file.twoBit,
pos.bed,
neg.bed,
gc.correction=TRUE,
ncores = 1); #ncores=3

#Show a brief result
t1;

#Show the comparison results of all motifs
show(t1$result);

summary(t1);

#Output the result to one pdf report.
tfbs.reportEnrichment(tfs, t1, file.pdf="test-tfbs-enrich-all.pdf", sig.only=FALSE);

file.ELF1 <- system.file("extdata","Chipseq-k562-chr19-ELF1.bed", package="rtfbsdb")
pos.bed<- read.table(file.ELF1)

tfs <- tfbs.createFromCisBP(db, family_name="Ets");

t2 <- tfbs.enrichmentTest( tfs,
file.twoBit,
pos.bed,
neg.bed,
gc.correction=TRUE,
gc.robust.rep=5,
ncores = 1); #ncores=3

show(t2)

#Output the result to one pdf report.
tfbs.reportEnrichment(tfs, t2, file.pdf="test-tfbs-enrich-both.pdf", sig.only=TRUE, enrich=TRUE)

```



```

t3 <- tfbs.enrichmentTest( tfs,
  file.twoBit,
  pos.bed,
  gc.correction=TRUE,
  gc.robust.rep=5,
  ncores = 1); #ncores=3

show(t3)

tfbs.reportEnrichment(tfs, t3, file.pdf="test-elf1-enrich-depleted.pdf", sig.only=TRUE, e

```

tfbs.getExpression *Estimate gene expression of target TF.*

Description

Gets expression level of target TF.
 USE extra_info\$DBID to find gene information encoded by GENCODE V21

Usage

```

tfbs.getExpression(tfbs,
  file.twoBit,
  file.gencode.gtf,
  file.bigwig.plus=NA,
  file.bigwig.minus=NA,
  file.bam=NA,
  seq.datatype = c("GRO-seq", "PRO-seq", "RNA-seq"),
  ncores =1 )

```

Arguments

tfbs	A tfbs object("tfbs").
file.twoBit	String, indicating the binary data of sequence. (e.g. hg19.2bit, mm10.2bit)
file.gencode.gtf	Gencode RDATA file encoded by ths package.
file.bigwig.plus	String, indicating bigwig file for strand plus(+) if seq.datatype is GRO-seq or PRO-seq.
file.bigwig.minus	String, indicating bigwig file for strand minus(-) if seq.datatype is GRO-seq or PRO-seq.
file.bam	String, indicating BAM file for rna reads if seq.datatype is RNA-seq.
seq.datatype	String, indicating which kind of seq data is applied to this function, three values are available: GRO-seq, PRO-seq and RNA-seq. (Default=GRO-seq)
ncores	Number, comupting nodes in parallel environment.

Details

For each motif, the occurrence ranges can be queried by the gene ID in the GENCODE database(for human, gencode.v21.annotation.gtf, for mouse: gencode.vM3.annotation.gtf). After the searching, one range obtained from the merge of the multiple ranges will be used to detect the reads count in the specified bigwig files(including plus and minus). The probability of each motif can be calculated by the reads count and lambda.

The lambda is determined by the following formulation:

```
r.lambda = 0.04 * sum(reads_in_all_chromosomes)/10751533/1000.
```

The dataset of GENCODE v21 (human) and vM3 (mouse) have been compiled into RDATA file and attached in this package.

The gencode_transcript_ext object can be accessed after the following command is executed successfully.

```
load( system.file("extdata", "gencode_human21_transcript_ext.rdata", package = "tfbs") )
```

Value

A tfbs object with new expression data frame including the following columns:

Motif_ID	Motif_ID from CisBP dataset or other data source.
DBID	DBID from CisBP dataset or other data source.
chr	String, chromosome name.
start	Integer, start position in which gene ID can be detected.
end	Integer, end position in which gene ID can be detected.
strand	String, + or -, indicating the strand direction.
bed_length	Integer, the length of range which gene ID can be detected.
reads	The reads number queried by BigWig function from the bigwig files(plus and minus)
lambda	The lambda parameter in poisson distribution.
prob	The probability calculated based on Poisson distribution.

See Also

See Also as "[tfbs](#)"

Examples

```
# Load the internal CisBP data set
db.human <- CisBP.extdata("Homo_sapiens");

# Create a tfbs object by querying the meta file of CisBP dataset.
tfs <- tfbs.createFromCisBP(db.human, motif_type="ChIP-seq", tf.information.type=1 );
```

```

file.bigwig.minus <- system.file("extdata", "GSM1480327_K562_PROseq_chr19_minus.bw", package="rtfbsdb")
file.bigwig.plus <- system.file("extdata", "GSM1480327_K562_PROseq_chr19_plus.bw", package="rtfbsdb")
hg19.twobit <- system.file("extdata", "hg19.chr19.2bit", package="rtfbsdb")
gencode.gtf <- system.file("extdata", "gencode.v21.annotation.chr19.gtf.gz", package="rtfbsdb")

tfs <- tfbs.getExpression(tfs, hg19.twobit, gencode.gtf, file.bigwig.plus, file.bigwig.minus)

```

`tfbs.importMotifs` *Import licensed motifs to tfbs object*

Description

Import licensed motifs to tfbs object

Usage

```
tfbs.importMotifs(tfbs, motif_ids, file.pwms)
```

Arguments

<code>tfbs</code>	A tfbs object (" <code>tfbs</code> ") returned by <code>tfbs.createFromCisBP</code> , <code>tfbs</code> , <code>tfbs.dirs</code> .
<code>motif_ids</code>	Vector of motif IDs, motif IDs are in accordance with the TF information which can be exported from <code>TF_information.txt</code> by <code>CisBP.getTFinformation</code> .
<code>file.pwms</code>	Vector of file names corresponding to the motif IDs specified in ' <code>motif_ids</code> '.

Details

The motif IDs will be checked according to the TF information in the Cis-BP database.

Value

A new tfbs object ("`tfbs`") merged with licensed motifs.

See Also

`tfbs.createFromCisBP`

Examples

```

library(rtfbsdb);

db <- CisBP.extdata("Homo_sapiens");
tfs <- tfbs.createFromCisBP(db, family_name="AP-2");
tfs;

motif_ids <- c( "M2938_1.02", "M2940_1.02", "M2940_2.02", "M4056_1.02" );

path <- system.file("extdata", package="rtfbsdb");
file_pwms <- paste(path, c("fake_M2938_1.02.pwm", "fake_M2940_1.02.pwm", "M2940_2.02.pwm"));

tfs <- tfbs.importMotifs(tfs, motif_ids, file_pwms );
show(tfs);

```

```
tfbs.reportEnrichment
```

Output report for enrichment results.

Description

Output enrichment results to a PDF report which includes motif names, counts of TF site, p-value, enrichment ratio and motif logos.

Usage

```
tfbs.reportEnrichment(tfbs, r.comp,
  file.pdf = NA,
  report.size = "letter",
  report.title = "",
  sig.only = TRUE,
  enrichment.type = c("both", "enriched", "depleted"),
  pv.threshold = 0.05,
  pv.adj = NA)
```

Arguments

tfbs	A tfbs object, see also " tfbs "
r.comp	A result object from the function of tfbs.enrichmentTest
file.pdf	String, the file name of PDF report.
report.size	String, the page size (default="letter")
report.title	String, the report title.
sig.only	String, indicating whether only significant motifs are outputted or not.(default=TRUE).
enrichment.type	String, three values are available for significant motifs to be printed out.(default="both").
pv.threshold	Numeric value,indicating whether the different threshold of p-value is applied to select the significant motifs.
pv.adj	String,indicating whether the different correction metod of p-value is applied to select the significant motifs.

Details

The table with 7 columns is outputted into a PDF report within letter size.

Two color bars are used to display p-values and enrichment ratios. Motif logos are shown visually in each row.

Value

No return values.

See Also

[tfbs.enrichmentTest](#), [summary.tfbs.enrichment](#).

Examples

```
# see examples in tfbs.enrichmentTest
```

```
tfbs.reportFinding Make report for scanning results.
```

Description

Output a PDF report includes motif names, counts of TF site and motif logos.

Usage

```
tfbs.reportFinding(tfbs,  
  r.scan,  
  file.pdf = NA,  
  report.size = "letter",  
  report.title = "")
```

Arguments

tfbs	A tfbs object, see also " tfbs "
r.scan	A result object from the function of tfbs.scanTFsite
file.pdf	String, the file name of PDF report.
report.size	String, the page size (default="letter")
report.title	String, the report title.

Details

The table with 4 columns is outputted into a PDF report within letter size.
Motif logos are shown visually in each row.

Value

No return values.

See Also

[tfbs.scanTFsite](#), [print.tfbs.finding](#)

Examples

```
#See example in tfbs.scanTFsite
```

tfbs.scanTFsite	<i>Find TF sites from genome data within the BED loci</i>
-----------------	---

Description

Find TF sites from genome data within the BED loci. Please notice that this package does not provided genome data such as hg19.2bit, mm10.2bit.

Usage

```
tfbs.scanTFsite(tfbs,
  file.twoBit,
  gen.bed,
  return.type=c("matches", "posteriors", "maxposterior", "writedb"),
  file.prefix=NA,
  usemotifs = NA,
  ncores = 1,
  threshold = 6,
  threshold.type = c("score", "fdr"),
  gc.groups = NA,
  background.order = 2,
  background.length = 100000)
```

Arguments

tfbs	A tfbs object (" tfbs ") returned by tfbs.createFromCisBP , tfbs , tfbs.dirs .
file.twoBit	String, the file name of genome data(e.g. hg19.2bit or mm10.2bit)
gen.bed	Data frame, bed-formatted loci information with 6 columns
return.type	String, four available values explained in th details(default = "matches")
file.prefix	String, the prefix for outputted file, only used when the return.type is <i>writedb</i>
usemotifs	Vector indicating indexes of motif to be used in scanning.
ncores	Number, computing nodes in parallel environment (default = 1).
threshold	Numeric value, if 'score' is specified in <code>threshold.type</code> , only binding sites with scores above this threshold are returned, if 'fdr' is specified in <code>threshold.type</code> , only binding sites with FDR (False Discovery Rate) less than this value can be selected. Default value is 6 for 'score' and 0.1 for 'fdr'.
threshold.type	String value, two options are available. only sites with scores above this threshold are returned, not be used if NA. (default = 'score')
gc.groups	Numeric value,indicating number of quantiles to group sequences into in <code>rtfbs</code> package (default = 1).
background.order	Numeric value,indicating the order of Markov model to build in <code>rtfbs</code> package (default = 2).
background.length	Numeric value, indicating length of the sequence to simulate in <code>rtfbs</code> package (default = 100000)

Details

(1) Four options are available for the function of `tfbs.scanTFsite` as follows.

- `matches`: returns all matching TF sites for all motifs.
- `writedb`: writes a bed file with matches sites. Assumes that `sort-bed` and `starch` tools are available in `$PATH`
- `posteriors`: returns the posteriors at each position in bed-formatted loci.
- `maxposterior`: returns the `max(posterior)` in each position in bed-formatted loci.

(2) In order to make the binary file with the parameter of `writedb`, make sure that `starchcat` and `sort-bed` command (in BEDOPS) can be accessed from R environment. If not, please put the folder in `$PATH`.

Value

A list object will be returned with the class name of `tfbs.finding`. The object wraps four sub-list as follows:

- 1) `parm`: Calling parameters(`fdr`, `threshold`, `gc.groups`...).
- 2) `bed`: Calling bed-formatted loci(`gen.bed`).
- 3) `summary`: A data frame including summarized information about matched TF sites for all motifs.
- 4) `result`: Scanning results which data type is depend on the parameter of `return.type`.

The option of `matches` returns a list including the result of every motif, which result is BED style data frame with the following columns.

<code>chrom</code>	chromosome
<code>chromStart</code>	start position
<code>chromEnd</code>	chromosome end position
<code>name</code>	
<code>score</code>	The score is given by the log likelihood ratio against the Marklov model(background).
<code>strand</code>	strand

The option of `writedb` will return a binary BED filename in which store all bed ranges.

The option of `posteriors` will return a list for each motif returned by `score.ms` function. Scores represent the motif 'match score', or the product of the probability of observing each base under the motif or background models. Scores are returned under the motif model for all positions in the sequence, on both forward and reverse strands, and under the background model.

The option of `maxposterior` will return a probability matrix which the row indicates the target loci and the column indicates the motif.

See Also

[print.tfbs.finding](#), [summary.tfbs.finding](#), [tfbs.reportFinding](#).

Examples

```

library(rtfbsdb);

file.twoBit <- system.file("extdata","hg19.chr19.2bit", package="rtfbsdb")

db <- CisBP.extdata("Homo_sapiens");
tfs <- tfbs.createFromCisBP(db, family_name="Ets");

gen.bed <- data.frame(chr="chr19",
  start=round(runif(10,1000000, 2000000)),
  stop=0,
  name="",
  score=0,
  strand=".");
gen.bed$stop <- gen.bed$start + 3000;

t1 <- tfbs.scanTFsite( tfs,
  file.twoBit,
  gen.bed,
  file.prefix="test.db",
  ncores = 1);

#show a brief information about the result
t1

#show the summary information in the result
show(t1$summary);

#show the matched TF sites for first motif
show(t1$result[[1]]);

#Output a PDF report for all motifs.
tfbs.reportFinding(tfs, t1, file.pdf="test-rtfbs-scan.pdf", report.title="ELF1");

file.ELF1 <- system.file("extdata","Chipseq-k562-chr19-ELF1.bed", package="rtfbsdb")
gen.bed<- read.table(file.ELF1)

t2 <- tfbs.scanTFsite( tfs,
  file.twoBit,
  gen.bed,
  file.prefix="test.db",
  return.type="writedb",
  ncores = 1);

t2

t3 <- tfbs.scanTFsite( tfs,
  file.twoBit,
  gen.bed,
  return.type="posteriors",
  ncores = 1);

t3

t4 <- tfbs.scanTFsite( tfs,

```



```

file.twoBit,
gen.bed,
return.type="maxposterior",
ncores = 1);

t4;

dim(t4$result);

```

```
tfbs.selectByGeneExp
```

Motif selection by gene expression level.

Description

Select the motifs with minimum p-value from each group of clustering.

Usage

```
tfbs.selectByGeneExp(tfbs)
```

Arguments

`tfbs` A tfbs object ("[tfbs](#)") with the data frame of gene expression level.

Details

The function of [tfbs.getExpression](#) should be successfully called and the results of gene expression should be returned before this function is called. The indexes of selected motifs will be used in the function of [tfbs.enrichmentTest](#) or [tfbs.scanTFsite](#).

Value

A vector of motif indices is returned.

See Also

See Also as [tfbs.selectByRandom](#), [tfbs.getExpression](#)

Examples

```

db <- CisBP.extdata("Homo_sapiens");

tfs <- tfbs.createFromCisBP(db, family_name="AP-2");

file.bigwig.minus <- system.file("extdata", "GSM1480327_K562_PROseq_chr19_minus.bw", package="rtfbsdb")
file.bigwig.plus <- system.file("extdata", "GSM1480327_K562_PROseq_chr19_plus.bw", package="rtfbsdb")
hg19.twobit <- system.file("extdata", "hg19.chr19.2bit", package="rtfbsdb")
gencode.gtf <- system.file("extdata", "gencode.v21.annotation.chr19.gtf.gz", package="rtfbsdb")

tfs <- tfbs.getExpression(tfs, hg19.twobit, gencode.gtf, file.bigwig.plus, file.bigwig.minus)

```

```
tfs <- tfbs.clusterMotifs(tfs, pdf.heatmap="test-AP2-heatmap.pdf" );  
usemotif <- tfbs.selectByGeneExp( tfs );
```

```
tfbs.selectByRandom
```

Random motif selection

Description

Select the motifs randomly from each group of clustering.

Usage

```
tfbs.selectByRandom(tfbs)
```

Arguments

`tfbs` A tfbs object("tfbs").

Details

The indexes of selected motifs can be used in the function of `tfbs.enrichmentTest` or `tfbs.scanTFsite`.

Value

A vector of motif indices is returned.

See Also

See Also as `tfbs.selectByGeneExp`, `tfbs.getExpression`

Examples

```
db <- CisBP.extdata("Homo_sapiens");  
tfs <- tfbs.createFromCisBP(db, family_name="AP-2");  
tfs <- tfbs.clusterMotifs(tfs, pdf.heatmap="test-AP2-heatmap.pdf" );  
usemotif <- tfbs.selectByRandom(tfs );  
show(usemotif);
```

```
tfbs.selectExpressedMotifs
```

Select expressed Motifs for GRO-seq, PRO-seq and RNA-seq data

Description

Select expressed Motifs for GRO-seq, PRO-seq and RNA-seq data

Usage

```
tfbs.selectExpressedMotifs(tfbs,
  file.twoBit,
  file.gencode.gtf,
  file.bigwig.plus=NA,
  file.bigwig.minus=NA,
  file.bam=NA,
  seq.datatype= c("GRO-seq", "PRO-seq", "RNA-seq"),
  pvalue.threshold = 0.05,
  include.DBID.missing=TRUE,
  ncores = 1 )
```

Arguments

tfbs	A tfbs object (" tfbs ") returned by <code>tfbs.createFromCisBP</code> , <code>tfbs</code> , <code>tfbs.dirs</code> .
file.bigwig.plus	String, indicating bigwig file for strand plus(+) if seq.datatype is GRO-seq or PRO-seq.
file.bigwig.minus	String, indicating bigwig file for strand minus(-) if seq.datatype is GRO-seq or PRO-seq.
file.bam	String, indicating BAM file for rna reads if seq.datatype is RNA-seq.
file.twoBit	String, indicating the binary data of sequence. (e.g. hg19.2bit, mm10.2bit)
file.gencode.gtf	String, indicating Gencode GTF file downloaded from the Gencode web site.
seq.datatype	String, indicating which kind of seq data is applied to this function, three values are available: GRO-seq, PRO-seq and RNA-seq. Default: GRO-seq
pvalue.threshold	Numeric, indicating .
include.DBID.missing	Logical, indicating whether the TFs without association with GENCODE through the DBID are selected.
ncores	Number, computing nodes in parallel environment for gencode data converting.

Details

1) If `seq.datatype` is GRO-seq or PRO-seq and the bigwig files are provided, the gene expression values are calculated through querying the TREs region from the GENCODE database(for human, `gencode.v21.annotation.gtf`, for mouse: `gencode.vM3.annotation.gtf`) and querying the reads count in the plus and minus bigWig files.

If `seq.datatype` is RNA-seq and the BAM file is provided, read counts for each TRE regions will be queried from the BAM file.

2) If the expressed TFs only is used in the `tfbs` object, the TFs with p-values corrected by Bonferroni less than 0.05 will be selected.

The following part explains how to calculate the gene expression.

For each motif, the occurrence ranges can be queried by the gene ID After the searching, one range obtained from the merge of the multiple ranges will be used to detect the reads count in the specified bigwig files(including plus and minus). The probability of each motif can be calculated by the reads count and lambda.

The lambda is determined by the following formulation:

For GRO-seq and PRO-seq data:

```
r.lambda = 0.04 * sum(reads_in_all_chromosomes)/10751533/1000.
```

For RNA-seq data:

```
r.lambda = mode( reads_in_1000_bp_windows_cross_all_gene_deserts )/1000.
```

This function will be failed to get the reads count if the BAM file is not indexed. Please use the command `samtools` to make the index file for the BAM file

```
samtools index your_bam_file
```

Value

A new `tfbs` object ("`tfbs`") with the matrix of gene expression level.

Examples

```
library(rtfsdb);

# Load the internal CisBP data set
db.human <- CisBP.extdata("Homo_sapiens");

# Create a tfbs object by querying the meta file of CisBP dataset.
tfs <- tfbs.createFromCisBP(db.human, motif_type="ChIP-seq", tf.information.type=1 );

file.bigwig.minus <- system.file("extdata","GSM1480327_K562_PROseq_chr19_minus.bw", packa
```

```
file.bigwig.plus <- system.file("extdata","GSM1480327_K562_PROseq_chr19_plus.bw", package="rtfbsdb")
hg19.twobit <- system.file("extdata","hg19.chr19.2bit", package="rtfbsdb")
gencode.gtf <- system.file("extdata","gencode.v21.annotation.chr19.gtf.gz", package="rtfbsdb")

tfs1 <- tfbs.selectExpressedMotifs(tfs,
  hg19.twobit,
  gencode.gtf,
  file.bigwig.plus,
  file.bigwig.minus,
  seq.datatype = "PRO-seq",
  pvalue.threshold=0.001,
  include.DBID.missing=TRUE,
  ncore=1);

show(tfs1)

file.bam <- "/local/storage/projects/NHP/AllData/bams/H3_U.fastq.gz.sort.bam"

tfs2 <- tfbs.selectExpressedMotifs(tfs,
  hg19.twobit,
  gencode.gtf,
  file.bam = file.bam,
  seq.datatype = "RNA-seq",
  pvalue.threshold=0.01,
  include.DBID.missing=TRUE,
  ncore=1);

show(tfs2)
```

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