

Package ‘Rcmonkey2’

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Title R interface to cMonkey2 (aka cmonkey-python)

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Description R package containing scripts and wrappers to interface with SQLite database returned by cMonkey2

Depends R (>= 3.1.1),RSQLite (>= 1.0.0),seqLogo (>= 1.10.0)

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LazyData true

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addTable	<i>Add table to existing SQLite database.</i>
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Description

addTable adds a table to an existing SQLite database from a tab-delimited file, e.g., Microbes Online genome annotation file

Usage

```
addTable(db_path = "", table_name = "", tab_file = "")
```

Arguments

db_path	Location of the SQLite database
table_name	Name for new table
tab_file	Tab-delimited file to add to database

Value

NULL (modified SQLite database)

getBiclustExpression	<i>Get biclust expression values from SQLite database.</i>
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Description

getBiclustExpression retrieves expression values (genes, conditions) from a user specified biclust and/or motif number at any iteration of cMonkey algorithm

Usage

```
getBiclustExpression(db_path = "", biclust = 1, iteration = "max",  
  ratios = "")
```

Arguments

db_path	Location of the SQLite database
biclust	Biclust number, integer
iteration	Iteration of biclust to retrieve, defaults to last (final) iteration
ratios	Path to tab-delimited file or variable containing gene expression data

Value

Matrix containing gene expression values for each gene and condition in the biclust

getConditions	<i>Get bicluster conditions from SQLite database.</i>
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Description

getConditions retrieves conditions from a user specified bicluster at any iteration of cMonkey algorithm

Usage

```
getConditions(db_path = "", bicluster = 1, iteration = "max")
```

Arguments

db_path	Location of the SQLite database
bicluster	Bicluster number, integer
iteration	Iteration of bicluster to retrieve, defaults to last (final) iteration

Value

Vector of conditions in the bicluster

getGenes	<i>Get bicluster genes from SQLite database.</i>
----------	--

Description

getGenes retrieves genes from a user specified bicluster at any iteration of cMonkey algorithm

Usage

```
getGenes(db_path = "", bicluster = 1, iteration = "max")
```

Arguments

db_path	Location of the SQLite database
bicluster	Bicluster number, integer
iteration	Iteration of bicluster to retrieve, defaults to last (final) iteration

Value

Vector of genes in the bicluster

getMastMotifs	<i>Get bicluster MAST motif info from SQLite database.</i>
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Description

getMastMotifs retrieves MAST output from a user specified bicluster and/or motif number at any iteration of cMonkey algorithm

Usage

```
getMastMotifs(db_path = "", bicluster = 1, iteration = "max",
  motif_num = seq(1, 10))
```

Arguments

db_path	Location of the SQLite database
bicluster	Bicluster number, integer
iteration	Iteration of bicluster to retrieve, defaults to last (final) iteration
motif_num	Number of the motif to return. Defaults to all motifs (assuming # motifs per bicluster < 10)

Value

data.frame containing information about the locations and properties of discovered motifs by MAST

getMemeMotifs	<i>Get bicluster MEME motif info from SQLite database.</i>
---------------	--

Description

getMemeMotifs retrieves MEME output from a user specified bicluster and/or motif number at any iteration of cMonkey algorithm

Usage

```
getMemeMotifs(db_path = "", bicluster = 1, iteration = "max",
  motif_num = seq(1, 10))
```

Arguments

db_path	Location of the SQLite database
bicluster	Bicluster number, integer
iteration	Iteration of bicluster to retrieve, defaults to last (final) iteration
motif_num	Number of the motif to return. Defaults to all motifs (assuming # motifs per bicluster < 10)

Value

data.frame containing information about the locations and properties of discovered motifs by MEME

getMotifPWM	<i>Get bicluster motif PWMs from SQLite database.</i>
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Description

getMotifPWM retrieves motif PWM(s) from a user specified bicluster and/or motif number at any iteration of cMonkey algorithm

Usage

```
getMotifPWM(db_path = "", bicluster = 1, iteration = "max",
            motif_num = seq(1, 10))
```

Arguments

db_path	Location of the SQLite database
bicluster	Bicluster number, integer
iteration	Iteration of bicluster to retrieve, defaults to last (final) iteration
motif_num	Number of the motif to return. Defaults to all motifs (assuming # motifs per bicluster < 10)

Value

List containing \$pwm and \$value for each motif requested

load_cMonkey	<i>Load cMonkey database.</i>
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Description

load_cMonkey Loads the SQLite databases produced from a cMonkey2 (aka python cMonkey) run

Usage

```
load_cMonkey(path = "", verbose = T)
```

Arguments

path	Location of the SQLite database
verbose	Should location of database be written to console

Value

Connection to SQLite database

plotMotif	<i>Plot cMonkey PSSM using seqLogo.</i>
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Description

plotMotif plots a PWM

Usage

```
plotMotif(pwm = NULL, db_path = "", bicluster = 1, iteration = "max",  
          motif_num = 1, ic.scale = TRUE, file = NULL)
```

Arguments

pwm	A PWM of the form:
pwm	A PWM of the form:

Value

Plot of the motif

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