Package ‘ggmotif’

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Type Package

Title Extract and Visualize Motif Information from MEME Software

Version 0.2.1

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Description Extract and visualize motif information from XML file from MEME software.
In biology, a motif is a nucleotide or amino acid sequence pattern that is widespread
and usually assumed to be related to specifical biological functions.
There exist many software was used to discover motif sequences from a set of nucleotide
or amino acid sequences. MEME is almost the most used software to detect motif.
It's difficult for biologists to extract and visualize the location of a motif
on sequences from the results from MEME software.

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Encoding UTF-8

Depends R (>= 3.5.0)

Imports tidyverse, dplyr, XML, magrittr, ggplot2, stringr, ggtree,
ape, patchwork, ggseqlogo, memes, universalmotif, treeio,
cowplot, ggsci, data.table

RoxygenNote 7.2.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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R topics documented:

`getMotifFromMEME` *Extract and Visualize Motif Information from MEME Software*

Description

`getMotifFromMEME` Extract motif information from the MEME software results.

Arguments

`data`	A txt file from MEME software.
`format`	The result format from MEME, txt or xml.

Value

Return a datafram

Author(s)

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Examples

```
filepath <- system.file("examples", "meme.txt", package = "ggmotif")
motif.info <- getMotifFromMEME(data = filepath, format = "txt")

filepath <- system.file("examples", "meme.xml", package = "ggmotif")
motif.info <- getMotifFromMEME(data = filepath, format = "xml")
```

`motifLocation` *Extract and Visualize Motif Information from MEME Software*

Description

`motifLocation` Visualize motif location in a specificial sequences..

Arguments

`data`	A data frame file from getMotifFromXML function.
`tree.path`	A file path of the correponding phylogenetic tree. The IDs of the phylogenetic tree must be same as the IDs of sequences used to identify motifs using MEME.

Value

Return a plot

Author(s)

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Examples

```
# without phylogenetic tree
filepath <- system.file("examples", "meme.xml", package = "ggmotif")
motif_extract <- getMotifFromMEME(data = filepath, format="xml")
motif_plot <- motifLocation(data = motif_extract)

# with phylogenetic tree
filepath <- system.file("examples", "meme.xml", package = "ggmotif")
treepath <- system.file("examples", "ara.nwk", package="ggmotif")
motif_extract <- getMotifFromMEME(data = filepath, format="xml")
motif_plot <- motifLocation(data = motif_extract, tree = treepath)
```

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