

# Package ‘ggmotif’

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**Type** Package

**Title** Extract and Visualize Motif Information from MEME Software

**Version** 0.1.3

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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 specific 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.

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 3.5.0)

**Imports** tidyverse,dplyr,XML,magrittr,ggplot2,stringr,ggtree,ape,patchwork

**RoxygenNote** 7.2.0

**NeedsCompilation** no

**Repository** CRAN

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getMotifFromMEME

*Extract and Visualize Motif Information from MEME Software*

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**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)**

Xiang LI <lixiang117423@foxmail.com>

**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*

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**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.

**Value**

Return a plot

**Author(s)**

Xiang LI <lixiang117423@foxmail.com>

**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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