

# Package ‘ggmotif’

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**Type** Package

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

**Version** 0.1.1

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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 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,aplot

**RoxygenNote** 7.1.1

**NeedsCompilation** no

**Repository** CRAN

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getMotifFromTxt      *Extract and Visualize Motif Information from MEME Software*

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**Description**

getMotifFromXML Extract motif information from the MEME software results, .txt file.

**Arguments**

data                  A txt file from MEME software.

**Value**

Return a vector or a dataframe

**Author(s)**

Xiang LI <lixiang117423@foxmail.com>

**Examples**

```
filepath <- system.file("examples", "meme.txt", package = "ggmotif")
motif_extract <- getMotifFromTxt(data = filepath)
```

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getMotifFromXML      *Extract and Visualize Motif Information from MEME Software*

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**Description**

getMotifFromXML Extract motif information from the MEME software results, XML file.

**Arguments**

XMLfile              A XML file from MEME software.

**Value**

Return a vector or a dataframe

**Author(s)**

Xiang LI <lixiang117423@foxmail.com>

**Examples**

```
filepath <- system.file("examples", "meme.xml", package="ggmotif")
motif_extract <- getMotifFromXML(XMLfile = filepath)
```

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ggmotif

*Extract and Visualize Motif Information from MEME Software*

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### **Description**

Extract and Visualize Motif Information from MEME Software

### **Author(s)**

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motif\_location

*Extract and Visualize Motif Information from MEME Software*

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### **Description**

getMotifFromXML Visualize motif location in a specific sequences..

### **Arguments**

data            A data frame file from getMotifFromXML function.

### **Value**

Return a datafram

### **Author(s)**

Xiang LI <lixiang117423@foxmail.com>

### **Examples**

```
filepath <- system.file("examples", "meme.xml", package="ggmotif")
motif_extract <- getMotifFromXML(XMLfile = filepath)
motif_plot <- motif_location(data = motif_extract)
```

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

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**Description**

`getMotifFromXML` Visualize motif location with a phylogenetic tree object..

**Arguments**

<code>data</code>	A data frame file from <code>getMotifFromXML</code> function.
<code>tree</code>	A tree file.

**Value**

Return a dataframe

**Author(s)**

Xiang LI <lixiang117423@foxmail.com>

**Examples**

```
filepath <- system.file("examples", "meme.xml", package="ggmotif")
treepath <- system.file("examples", "tree.nwk", package="ggmotif")
motif_extract <- getMotifFromXML(XMLfile = filepath)
motif_plot_with_tree <- motif_with_tree(data = motif_extract, tree = treepath)
```

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