

Package ‘JASPAR’

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Title R modules for JASPAR databases: a collection of transcription factor DNA-binding preferences, modeled as matrices.

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Description R modules for JASPAR data processing and visualization

Depends R (>= 2.9.0), gtools

Suggests

Enhances

License GPL (>= 2)

URL

Repository CRAN

Type Package

LazyLoad yes

Collate 'zzz.R' 'hello.R' 'JASPAR-package.R' 'JASPAR-internal.R'
'make_template.R'

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NeedsCompilation yes

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 JASPAR-package

The Package for R modules for JASPAR databases

Description

R modules for JASPAR databases

Details

Package: JASPAR
 Type: Package
 License: GPL (>= 2)

This package contains:
 modules and functions for JASPAR data processing and visualization.

An overview of functions

Function	Description
make_template	Make a template that feeds into JASPAR databases

```
## To install from online repositories (e.g. CRAN)
install.packages(pkgs="JASPAR", repos="http://cran.r-project.org")
```

```
## Sometimes the official repository might not be up to date,
## then you may install it from a downloaded source file;
## please replace '<current-version>' with actual version numbers:
install.packages(pkgs="JASPAR_<current-version>.tar.gz", repos=NULL)
```

```
## Load the package and get a complete list of functions, use
library(JASPAR)
ls("package:JASPAR")
```

```
## help documentation of the package
help(JASPAR) # this page
```

Value

NULL

Author(s)

Xiaobei Zhao

Maintainer: Xiaobei Zhao <xiaobei (at) binf.ku.dk>

References

Zhao et al (2013), "JASPAR 2013: An extensively expanded and updated open-access database of transcription factor binding profiles." (*In preparation*)

See `citation("JASPAR")` for BibTeX entries for LaTeX users.

See Also

[make_template](#)

Examples

```
require(JASPAR)      # load JASPAR
help(JASPAR)        # a help document of JASPAR
## data(package="JASPAR") # a list of datasets available in JASPAR (TBA)
ls("package:JASPAR") # a list of functions available in JASPAR
help(package="JASPAR") # help documentation on JASPAR
citation("JASPAR")   # citation for publications
demo("JASPAR-demo")  # run the demo

## view JASPAR Description
packageDescription("JASPAR")

## ## view JASPAR vignette (TBA)
## vignette("JASPAR-vignette",package="JASPAR")
```

make_template	<i>Make a template that feeds into JASPAR databases</i>
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Description

Make a template that feeds into JASPAR databases

Usage

```
make_template(x, PARAM = NA, TAG = NA, sep = "\t",
             outFpre = NULL)
```

Arguments

x	matrix, the pfm
PARAM	a list, the PARAM(s)
TAG	a list, the TAG(s)
sep	a string, the delimiter
outFpre	a string, a file path to save

Details

NA

Value

A string of the template, and save it in output format of '.template' and '.matrix' if 'outFpre' specified.

Author(s)

Xiaobei Zhao

Examples

```
x <-
  rbind(
    c(3, 0, 0, 0, 0, 0),
    c(8, 0, 23, 0, 0, 0),
    c(2, 23, 0, 23, 0, 24),
    c(11, 1, 1, 1, 24, 0)
  )

PARAM <-
  list(
    INT_ID=NULL,
    BASE_ID="MA0006",
    COLLECTION="CORE",
    VERSION=1,
    NAME="Arnt-Ahr",
    SPECIES="10090")

TAG <-
  list(
    class="bHLH",
    medline="7592839",
    tax_group="vertebrate",
    sysgroup="vertebrate",
    acc="P30561",
    acc="P53762",
    comment="dimer",
    type="SELEX",
    newest=1
  )

cat(make_template(x=x,PARAM=PARAM,TAG=TAG))
```

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*Topic **package**

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