

Package ‘sinew’

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Type Package

Title Create 'roxygen2' Skeleton with Information from Function Script

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Description

Create 'roxygen2' skeleton populated with information scraped from the within the function script. Also creates field entries for imports in the 'DESCRIPTION' and import in the 'NAMES-SPACE' files.

Can be run from the R console or through the 'RStudio' 'addin' menu.

Depends R (>= 2.3.0)

Imports rstudioapi,utils

Suggests roxygen2

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URL <https://github.com/metrumresearchgroup/sinew>

BugReports <https://github.com/metrumresearchgroup/sinew/issues>

LazyData true

NeedsCompilation no

RoxygenNote 6.0.1

Repository CRAN

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ls_param	<i>Return roxygen2 parameter calls from parameter dictionary</i>
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Description

Return roxygen2 parameter calls from the intersection of the parameters listed in the package dictionary and the formals of a function

Usage

```
ls_param(obj, dictionary = "man-roxygen/Dictionary-1.R", print = TRUE)
```

Arguments

obj	function or name of function
dictionary	character, path_to_dictionary, Default: 'roxygen-man/Dictionary-1.R'
print	boolean print output to console, Default: TRUE

Value

character vector

Examples

```
repo='https://raw.githubusercontent.com/metrumresearchgroup/sinew/master/'
dict_loc=file.path(repo,'man-roxygen/Dictionary-1.R')
ls_param(sinew::makeOxygen,dictionary=dict_loc)
```

makeDictionary	<i>Parse package R files to create dictionary of unique parameter definitions</i>
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Description

Given list of R files function returns roxygen2 template consisting of intersecting parameter definitions

Usage

```
makeDictionary(path, save_path = FALSE)
```

Arguments

path	character or character vector of paths to files to parse
save_path	boolean that allows for function to write template to man-roxygen subdirectory, Default: FALSE

Value

character/character vector of intersecting parameters

Examples

```
makeDictionary('./R')
```

```
makeImport
```

Scrape R script to create namespace calls for R documentation

Description

Scrape r script to create namespace calls for roxygen2, namespace or description files

Usage

```
makeImport(script, cut = NULL, print = TRUE, format = "oxygen")
```

Arguments

script	character connection to pass to readLines, can be file path, directory path, url path
cut	integer number of functions to write as importFrom until switches to import, Default: NULL
print	boolean print output to console, Default: TRUE
format	character the output format must be in c('oxygen','namespace','description'), Default: 'oxygen'

Examples

```
makeImport(list.files('R',full.names = TRUE),format = 'oxygen')
makeImport(list.files('R',full.names = TRUE),format = 'namespace')
makeImport(list.files('R',full.names = TRUE),format = 'description')
```

makeOxygen	<i>Creates skeleton roxygen2 with information from within function script</i>
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Description

Creates roxygen2 skeleton including title, description, import and other fields

Usage

```
makeOxygen(obj, add_default = TRUE, add_fields = c("details", "examples",
  "seealso", "rdname", "export"), use_dictionary = NULL, print = TRUE, ...)
```

Arguments

obj	function or name of function
add_default	boolean to add defaults values to the end of the PARAM fields, Default: TRUE
add_fields	character vector to add additional roxygen2 fields, Default: NULL
use_dictionary	character, path_to_dictionary, Default: NULL
print	boolean print output to console, Default: TRUE
...	arguments to be passed to makeImport

Details

add_fields can include any slot except for the defaults (title,description,param,return). The order in add_fields determines the order of printout. The roxygen2 fields to add are list below, for more information go to [Generating Rd files](#)

Field	Skeleton
author	AUTHOR [AUTHOR_2]
backref	src/filename.cpp
concept	CONCEPT_TERM_1 [CONCEPT_TERM_2]
describeIn	FUNCTION_NAME DESCRIPTION
details	DETAILS
example	path/relative/to/package/root
export	
family	FAMILY_TITLE
field	FIELD_IN_S4_RefClass DESCRIPTION
format	DATA_STRUCTURE
importClassesFrom	PKG CLASS_a [CLASS_b]
importMethodsFrom	PKG METHOD_a [METHOD_b]
include	FILENAME.R [FILENAME_b.R]
inherit	[PKG::]SOURCE_FUNCTION [FIELD_a FIELD_b]
inheritDotParams	[PKG::]SOURCE_FUNCTION
inheritSection	[PKG::]SOURCE_FUNCTION [SECTION_a SECTION_b]
keywords	KEYWORD_TERM
name	NAME

rdname	FUNCTION_NAME
references	BIB_CITATION
section	SECTION_NAME
source	\url{http://somewhere.important.com/}
slot	SLOTNAME DESCRIPTION
template	FILENAME
templateVar	NAME VALUE
useDynLib	PKG [routine_a routine_b]

Examples

```
makeOxygen(stats::lm,add_default = TRUE,add_fields = c('export','examples'))
```

tabular	<i>Tabular for roxygen2</i>
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Description

Convert data.frame to roxygen2 tabular format

Usage

```
tabular(df, header = TRUE, ...)
```

Arguments

df	data.frame to convert to table
header	boolean to control if header is created from names(df), Default: TRUE
...	arguments to pass to format

Value

character

Source

[roxygen2 formatting](#)

See Also

[format](#)

Examples

```
cat(tabular(mtcars[1:5, 1:5]))
cat(tabular(mtcars[1:5, 1:5],header=FALSE))
```

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