Package 'roxygen2'

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Title In-Line Documentation for R

Version 6.1.1

Description Generate your Rd documentation, 'NAMESPACE' file, and collation
field using specially formatted comments. Writing documentation in-line
with code makes it easier to keep your documentation up-to-date as your
requirements change. 'Roxygen2' is inspired by the 'Doxygen' system for C++.

License GPL (>= 2)

URL https://github.com/klutometis/roxygen

BugReports https://github.com/klutometis/roxygen/issues

Depends R (>= 3.1)

Imports brew, commonmark, desc (>= 1.2.0), digest, methods, pkgload
(>= 1.0.2), purrr, R6 (>= 2.1.2), Rcpp (>= 0.11.0), stringi,
stringr (>= 1.0.0), utils, xml2

Suggests covr, devtools, knitr, rmarkdown, testthat (>= 0.8.0)

LinkingTo Rcpp

VignetteBuilder knitr

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R topics documented:

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roxygen2-package   *roxygen2: In-Line Documentation for R*

Description

Generate your Rd documentation, 'NAMESPACE' file, and collation field using specially formatted comments. Writing documentation in-line with code makes it easier to keep your documentation up-to-date as your requirements change. 'Roxygen2' is inspired by the 'Doxygen' system for C++.

Details

See `vignette("roxygen2", package = "roxygen2")` for an overview of the package, `vignette("rd", package = "roxy`
for generating documentation, and `vignette("namespace", package = "roxygen2")` for generating the namespace specification.

If you have existing Rd files, check out the `Rd2roxygen` package for a convenient way of converting Rd files to roxygen comments.

Author(s)

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See Also

Useful links:

- https://github.com/klutometis/roxygen
- Report bugs at https://github.com/klutometis/roxygen/issues

double_escape_md	*Escape % and \\\$ and _ once more, because commonmark removes the escaping. We do this everywhere currently.*

Description

Escape % and \\\$ and _ once more, because commonmark removes the escaping. We do this everywhere currently.

Usage

```
double_escape_md(text)
```

Arguments

text	Input text.

Value

Double-escaped text.

is_s3_generic	*Determine if a function is an S3 generic or S3 method.*

Description

is_s3_generic compares name to .knownS3Generics and .S3PrimitiveGenerics, then looks at the function body to see if it calls [UseMethod()](#).

is_s3_method builds names of all possible generics for that function and then checks if any of them actually is a generic.

Usage

```
is_s3_generic(name, env = parent.frame())

is_s3_method(name, env = parent.frame())
```

Arguments

name	Name of function.
env	Base environment in which to look for function definition.

---

namespace_roclet   *Roclet: make NAMESPACE.*

Description

This roclet automates the production of a NAMESPACE file, see Writing R Extensions. (https://cran.r-project.org/doc/manuals/R-exts.pdf) for details. The NAMESPACE is generated in two passes: the first generates only import directives (because this can be computed without evaluating package code), and the second generates everything (after the packaege has been loaded).

Usage

```
namespace_roclet()
```

See Also

```
vignette("namespace", package = "roxygen2")
```

Other roclets: [rd_roclet](), [vignette_roclet]()

---

object_format   *Default format for data*

Description

This function is called to generate the default "Format" section for each data object. The default implementation will return the class and dimension information.

Usage

```
object_format(x)
```

Arguments

x   A data object

Value

A `character` value with valid Rd syntax, or `NULL`.

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rd_roclet	*Roclet: make Rd files.*

Description

This roclet is the workhorse of roxygen, producing the Rd files that document that functions in your package.

Generally you will not call this function directly but will instead use roxygenise() specifying the rd roclet

Usage

```
rd_roclet()
```

See Also

```
vignette("rd", package = "roxygen2")
```

Other roclets: `namespace_roclet`, `vignette_roclet`

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roclet_find	*Create a roclet from a string.*

Description

This provides a flexible way of specifying a roclet in a string.

Usage

```
roclet_find(x)
```

Arguments

x	Arbitrary R code evaluated in roxygen2 package.

Examples

```
# rd, namespace, and vignette work for backward compatibility
roclet_find("rd")

# But generally you should specify the name of a function that
# returns a roclet
roclet_find("rd_roclet")

# If it lives in another package, you'll need to use ::
roclet_find("roxygen2::rd_roclet")
```

```
# If it takes parameters (which no roclet does currently), you'll need
# to call the function
roclet_find("roxygen2::rd_roclet()")
```

---

roxygenize   *Process a package with the Rd, namespace and collate roclets.*

Description

This is the workhorse function that uses roclets, the built-in document tranformation functions, to build all documentation for a package. See the documentation for the individual roclets, rd_roclet(), namespace_roclet(), and for update_collate(), for more details.

Usage

```
roxygenize(package.dir = ".", roclets = NULL,
  load_code = env_package, clean = FALSE)

roxygenise(package.dir = ".", roclets = NULL,
  load_code = env_package, clean = FALSE)
```

Arguments

package.dir	Location of package top level directory. Default is working directory.
roclets	Character vector of roclet names to use with package. This defaults to NULL, which will use the roclets fields in the list provided in the Roxygen DESCRIPTION field. If none are specified, defaults to c("collate", "namespace", "rd").
load_code	A function used to load all the R code in the package directory. It is called with the path to the package, and it should return an environment containing all the sourced code.
clean	If TRUE, roxygen will delete all files previously created by roxygen before running each roclet.

Details

Note that roxygen2 is a dynamic documentation system: it works by inspecting loaded objects in the package. This means that you must be able to load the package in order to document it.

Value

NULL

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update_collate   *Update Collate field in DESCRIPTION.*

Description

Topologically sort R files and record in Collate field. The topological sort is based on the @include tag, which should specify the filenames (space separated) that should be loaded before the current file. These are typically necessary if you're using S4 or RC classes (because super classes must be defined before subclasses).

Usage

```
update_collate(base_path)
```

Arguments

base_path   Path to package directory.

Details

If there are no @include tags, roxygen2 will leave collate as is. This makes it easier to use roxygen2 with an existing collate directive, but if you remove all your @include tags, you'll need to also manually delete the collate field.

This is not a roclet because roclets need the values of objects in a package, and those values can not be generated unless you've sourced the files, and you can't source the files unless you know the correct order.

Examples

```
#' `example-a.R', `example-b.R' and `example-c.R' reside
#' in the `example' directory, with dependencies
#' a -> {b, c}. This is `example-a.R'.
#' @include example-b.R
#' @include example-c.R
NULL

## Not run:
  update_collate("my_package")

## End(Not run)
```

vignette_roclet	*Re-build outdated vignettes.*

Description

This rebuilds outdated vignettes with tools::buildVignette. By default, it will rebuild all vignettes if the source file is newer than the output pdf or html. (This means it will automatically re-build the vignette if you change the vignette source, but *not* when you change the R code). If you want finer control, add a Makefile to `vignettes/` and roxygen2 will use that instead.

Usage

```
vignette_roclet()
```

Details

To prevent RStudio from re-building the vignettes again when checking your package, add `--no-build-vignettes` to the "Build Source Package" field in your project options.

See Also

Other roclets: `namespace_roclet`, `rd_roclet`

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