

# Package ‘svTools’

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**Title** Wrappers for Tools in Other Packages for IDE Friendliness

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**Imports** utils, codetools, grDevices, svMisc

**Description** Set of tools aimed at wrapping some of the functionalities of the packages tools, utils and codetools into a nicer format so that an IDE can use them.

**License** GPL-2

**URL** <http://www.sciviews.org/SciViews-R>,  
<http://romainfrancois.blog.free.fr/>

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svTools-package	<i>Wrappers for Tools in Other Packages for IDE Friendliness</i>
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### Description

Set of tools aimed at wrapping some of the functionalities of the packages tools, utils and codetools into a nicer format so that an IDE can use them.

### Details

Package: svTools  
 Type: Package  
 Version: 0.9-5  
 Date: 2018-06-28  
 License: GPL 2 or above, at your convenience

### Author(s)

Romain Francois  
 Maintainer: Ph. Grosjean <phgrosjean@sciviews.org>

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bibRNews	<i>A list of papers that where published in R News</i>
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### Description

List all publications in R News (note: it is now replaced by the R Journal).

### Usage

data(bibRNews)

**Format**

A data frame with 205 entries on the following 10 variables

author the author(s) of the paper.  
 title the title of the paper.  
 journal this is always R News in this case.  
 year the year of publication.  
 volume the journal volume.  
 number the journal number in this volume.  
 pages pages for this paper.  
 month the month of publication of this volume.  
 url a link to the downloadable PDF version.  
 issue volume/number - year, month.

**References**

Writing R extensions

**See Also**

[searchBiblio](#)

**Examples**

```
(data(bibRNews))
```

---

completeDescription    *completion for DESCRIPTION files*

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**Description**

Proposes completions for a DESCRIPTION file.

**Usage**

```
completeDescription(file, row, column, text = readLines(file),
  author = getOption("svTools.description.author"))
```

**Arguments**

file	a DESCRIPTION file to complete.
row	line in the file where the cursor is located.
column	column in the file where the cursor is located.
text	text to complete.
author	how to complete Author fields. The default value looks for the "svTools.description.author" option.

**Value**

A list with the following items:

ok	logical indicating if there actually are completions.
data	character matrix. The first column gives the completion, the second a description.
token	token that is being completed.
type	type of results, can be \"package\", \"fields\", \"other\".

**Author(s)**

Romain Francois <francoisromain@free.fr>

**References**

Writing R extensions defines what should be in a DESCRIPTION file

**See Also**

[lintDescription](#)

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completeNamespace	<i>Namespace completion</i>
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**Description**

Provides a completion list in the context of a NAMESPACE file.

**Usage**

```
completeNamespace(line)
```

**Arguments**

line            the line currently edited in the NAMESPACE file.

**Value**

A list with the possible completion items

**Author(s)**

Romain Francois <francoisromain@free.fr>

**See Also**

[lintNamespace](#)

## Examples

```
completeNamespace("import(")
completeNamespace("importFrom(")
completeNamespace("export(") # Not yet!
```

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completeRoxygen	<i>completion for R oxygen entries</i>
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## Description

Proposes completions for R oxygen inline documentation of R functions.

## Usage

```
completeRoxygen(line = "#'")
completeRoxygenParam(file, row, line = "#' @param ")
```

## Arguments

file	a file to complete.
row	location of the cursor (row) in the file.
line	line of code currently edited.

## Value

A list with the following items:

token	token that is being completed.
completions	list of current completions.
tooltip	further explanation about completion items (for completeRoxygen() only).

## Author(s)

Romain Francois <francoisromain@free.fr>

## References

Roxygen. <http://roxygen.org/>

## See Also

[generateRoxygenTemplate](#)

## Examples

```
completeRoxygen("#'")
completeRoxygen("#' @ex")
```

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completion	<i>Code or arguments completion</i>
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### Description

Provide a list of completion candidates for code or arguments like `col`, `lty` or `pch`.

### Usage

```
completeCode(...)  
completeCol(line)  
completeLty(line)  
completePch(line)
```

### Arguments

<code>...</code>	arguments passed to <a href="#">completion</a> .
<code>line</code>	the line of code currently edited.

### Value

For `completeCode()`, a list with these items:

<code>token</code>	the token being completed.
<code>completions</code>	a matrix of potential completions.
<code>fun</code>	in case of function completion, the name of the function.
<code>tooltip</code>	in case of function completion, the function tooltip.

For `completeCol()`, a list with these items:

<code>token</code>	the token being completed.
<code>completions</code>	list of color names.
<code>col.rgb</code>	matrix with RGB values for the corresponding colors.

For the other function, the returned list contains:

<code>token</code>	the token being completed.
<code>completions</code>	list of completion items.

### Author(s)

Romain Francois <francoisromain@free.fr>

### See Also

[completion](#)

**Examples**

```
completeCode("browse")
completeCol("plot(x, y, col = ")
completeLty("plot(x, y, lty = ")
completePch("plot(x, y, pch = ")
```

---

descriptionFields      *List of possible fields in DESCRIPTION files*

---

**Description**

List of possible fields in DESCRIPTION files and their meaning.

**Usage**

```
data(descriptionFields)
```

**Format**

A data frame with 27 entries on the following 3 variables.

field the name of the field as it should appear on the DESCRIPTION file.

optional a factor with levels Mandatory and Optional.

description a description of each field.

**References**

Writing R extensions

**See Also**

[lintDescription](#), [completeDescription](#)

**Examples**

```
(data(descriptionFields))
```

generateRoxygenTemplate

*Roxygen template generator*

---

### Description

Generate a default Roxygen template for this file.

### Usage

```
generateRoxygenTemplate(file, row, column, author = getOption("svTools.roxygen.author"),  
  type = c("verbatim", "superabbrev"))
```

### Arguments

file	code file in which to add a roxygen roclet.
row	line in the file.
column	column in the file.
author	author. The default value uses the option "svTools.roxygen.author".
type	type of output. "verbatim" is plain text. "superabbrev" is specific to jedit

### Value

A character string that contains the roxygen comments to add in the file.

### Author(s)

Romain Francois <francoisromain@free.fr>

### References

Roxygen. <http://roxygen.org/>

### See Also

[completeRoxygen](#)



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lint	<i>Look for error in a R code file</i>
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## Description

Simple wrapper to the `checkUsage()` function of the `codetools` package that calls `checkUsage()` on all objects contained in a source file.

## Usage

```
lint(file, text = NULL, filename = NULL, encoding = getOption("encoding"),
      type = c("data.frame", "flat", "rjson"), sep = "+++")
```

## Arguments

<code>file</code>	file to check.
<code>text</code>	the R source code (as text) to lint; used only if <code>file</code> is not provided.
<code>filename</code>	the filename to flag returned errors.
<code>encoding</code>	encoding to assume for the file.
<code>type</code>	the type of output to produce.
<code>sep</code>	in case of flat output, what is the indicator to use as field separator ?

## Value

A data frame, text output or `rjson` object of the errors/problems in the file or the R code in `'text'` is returned.

## Author(s)

Romain Francois <francoisromain@free.fr> & Philippe Grosjean <phgrosjean@sciviews.org>

## See Also

[checkUsage](#), [lintDescription](#), [lintNamespace](#)

lintDescription      *Description linter*

---

**Description**

Check correctness of the content in a DESCRIPTION file.

**Usage**

```
lintDescription(descfile, txt = readLines(descfile))
```

**Arguments**

descfile      a DESCRIPTION file name.  
txt            the text containing the description; if provided, descfile is ignored.

**Value**

A data frame that contains errors found in the DESCRIPTION file.

**Author(s)**

Romain Francois <francoisromain@free.fr>

**See Also**

[completeDescription](#)

---

lintNamespace      *Namespace linter*

---

**Description**

Check correctness of the code in a NAMESPACE file.

**Usage**

```
lintNamespace(namespace, checkPackages = TRUE)
```

**Arguments**

namespace      a NAMESPACE file name.  
checkPackages   logical; if TRUE, packages that are set to be imported are checked if they are actually installed.

**Value**

A data frame that contains errors found in the NAMESPACE file.

**Author(s)**

Romain Francois <francoisromain@free.fr>

**See Also**

[completeNamespace](#)

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pkgDesc	<i>Get installed or loaded packages, or their description</i>
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**Description**

This is similar to `installed.packages()` but with two additional columns indicating if the package is loaded and default. Description of packages can be retrieved from the local library, or from the Web (default repository).

**Usage**

```
pkgLoaded()
pkgInstalled(pattern = NULL, ...)
pkgDesc(pkg, lib.loc = NULL, fields = NULL, encoding = "")
pkgWebDesc(pkg, repos = getOption("repos"))
```

**Arguments**

pattern	filter on the name or the title of the packages.
...	arguments for <a href="#">installed.packages</a> .
pkg	character. The name of a R package.
lib.loc	the local library where the package is located, or NULL (by default) to search in all known libraries.
fields	which fields do we retrieve. If NULL (by default), all fields in the DESCRIPTION file are returned.
encoding	the encoding to use, or "" for default one.
repos	the repository where to look for the package description.

**Value**

A matrix similar to the result of [installed.packages](#) with two additional columns for `pkgInstalled()`.  
A character string for `pkgLoaded()`, `pkgDesc()` and `pkgWebDesc()`.

**Author(s)**

Romain Francois <francoisromain@free.fr>

**See Also**

[installed.packages](#)

**Examples**

```
pkgLoaded()
pkgInstalled()
pkgDesc("utils")
## Not run:
pkgWebDesc("svTools")

## End(Not run)
```

---

searchEngines

*Various search engines for R documents*

---

**Description**

Documentation about R is widespread and not always easy to find. These functions look for documents in various places.

**Usage**

```
searchBiblio(query, max = 30, url = "http://journal.r-project.org/RJournal.bib",
  add.bibRNews = TRUE, ...)
searchMailing(query, max = 30, groups = "*", prefix = "gmane.comp.lang.r")
searchGraph(query, max = 30)
searchPackage(query, max = 30)
searchWiki(query, max = 30)

## S3 method for class 'search'
print(x, detailed = TRUE, ...)
browse(object, ...)
## S3 method for class 'search'
browse(object, item = 1, ...)
```

**Arguments**

query	one or several topics to search for.
max	maximum number of items to return.
url	the url from where the BibTeX file describing R Journal articles can be downloaded.
add.bibRNews	also add data for R News (local cached version)?

...	further arguments passed to the function or method.
groups	the mailing lists and newsgroups sections to search.
prefix	the gmane tree for the discussion archives.
x	a 'search' object.
detailed	do we print a detailed list of found items?
object	a 'search' object.
item	the index of the found item to browse.

**Value**

All the searchXXX() functions return a 'search' object that inherits from 'data.frame'. It contains the 'type' or search, the 'item' found, the 'page' in the item, a 'snippet' of the relevant text, a 'score' for this hit and the 'url' where the content can be obtained.

The print() method presents the results in a more readable way, and one can browse() one item in the list.

**Author(s)**

Romain Francois <francoisromain@free.fr>

**See Also**

[bibRNews](#), [RSiteSearch](#)

**Examples**

```
## Not run:
searchBiblio("mean")
searchMailing("mean")
searchGraph("mean")
searchPackage("mean")
(res <- searchWiki("mean"))
browse(res, 1) # Display the first item
rm(res)

## End(Not run)
```

---

sidekick

*Builds a tree structure of an R source file*

---

**Description**

The sidekick function builds a tree structure of an R code file by analysing output of the R parser.

**Usage**

```
sidekick(x, ...)  
## S3 method for class 'character'  
sidekick(x, encoding = getOption("encoding"), delete.file = FALSE, ...)  
## Default S3 method:  
sidekick(x, ...)  
## S3 method for class 'function'  
sidekick(x, ...)
```

**Arguments**

x	a file to <a href="#">parse</a> and analyse. If x is a function, it is first dumped into a file.
encoding	encoding to use. Default to the encoding option (see <a href="#">options</a> ).
delete.file	should the file be delete when the function exits?
...	further arguments to pass to the method.

**Value**

A Data frame with columns:

```
id  
parent  
srcref1  
srcref2  
srcref3  
srcref4  
description
```

**Author(s)**

Romain Francois <francoisromain@free.fr>

**See Also**

[parse](#)

**Examples**

```
## Not run:  
sidekick(outer)  
  
## End(Not run)
```

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