

# Package: srr (via r-universe)

November 27, 2024

**Title** 'rOpenSci' Review Roclets

**Version** 0.1.3.026

**Description** Companion package to 'rOpenSci' statistical software review project.

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**URL** <https://docs.ropensci.org/srr/>,  
<https://github.com/ropensci-review-tools/srr>

**BugReports** <https://github.com/ropensci-review-tools/srr/issues>

**Imports** cli, clipr, fs, gert, here, methods, Rcpp, roxygen2

**Suggests** knitr, pkgbuild, rmarkdown, testthat (>= 3.0.0)

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**VignetteBuilder** knitr

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**Config/pak/sysreqs** make libicu-dev libxml2-dev libssl-dev libx11-dev

**Repository** <https://ropensci.r-universe.dev>

**RemoteUrl** <https://github.com/ropensci-review-tools/srr>

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srr_report	<i>Generate report from srr tags.</i>
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### Description

Generate report from srr tags.

### Usage

```
srr_report(path = ".", branch = "", view = TRUE, roxygenise = TRUE)
```

### Arguments

path	Path to package for which report is to be generated
branch	By default a report will be generated from the current branch as set on the local git repository; this parameter can be used to specify any alternative branch.
view	If TRUE (default), a html-formatted version of the report is opened in default system browser. If FALSE, the return object includes the name of a html-rendered version of the report in an attribute named 'file'.
roxygenise	If TRUE (default), documentation will first be updated with the <b>roxygen2</b> package. This requires local installation of the package, which may take some time if the package has not previously been installed. If this parameter is FALSE, the roxygen2 package is not used, documentation is not updated, and reports are generally generated faster.

### Value

(invisibly) Markdown-formatted lines used to generate the final html document.

### Examples

```
## Not run:
path <- srr_stats_pkg_skeleton ()
srr_report (path)

## End(Not run)
```

---

srr\_stats\_categories *Get details of current statistical software categories*

---

### Description

List all currently available categories and associated URLs to full category descriptions.

### Usage

```
srr_stats_categories()
```

### Value

A data.frame with 3 columns of "category" (the categories to be submitted to [srr\\_stats\\_checklist](#)), "title" (the full title), and "url".

### See Also

Other helper: [srr\\_stats\\_checklist\(\)](#), [srr\\_stats\\_checklist\\_check\(\)](#), [srr\\_stats\\_pkg\\_skeleton\(\)](#), [srr\\_stats\\_pre\\_submit\(\)](#)

### Examples

```
srr_stats_categories ()
```

---

srr\_stats\_checklist *Download checklists of statistical software standards*

---

### Description

Obtain rOpenSci standards for statistical software, along with one or more category-specific standards, as a checklist, and store the result in the local clipboard ready to paste.

### Usage

```
srr_stats_checklist(category = NULL, filename = NULL)
```

### Arguments

category	One of the names of files given in the directory contents of <a href="https://github.com/ropensci/statistical-software-review-book/tree/main/standards">https://github.com/ropensci/statistical-software-review-book/tree/main/standards</a> , each of which is ultimately formatted into a sub-section of the standards.
filename	Optional name of local file to save markdown-formatted checklist. A suffix of .md will be automatically appended.

**Value**

A character vector containing a markdown-style checklist of general standards along with standards for any additional categories.

**See Also**

Other helper: [srr\\_stats\\_categories\(\)](#), [srr\\_stats\\_checklist\\_check\(\)](#), [srr\\_stats\\_pkg\\_skeleton\(\)](#), [srr\\_stats\\_pre\\_submit\(\)](#)

**Examples**

```
## Not run:
x <- srr_stats_checklist (category = "regression")
# or write to specified file:
f <- tempfile (fileext = ".md")
x <- srr_stats_checklist (category = "regression", filename = f)

## End(Not run)
```

---

srr\_stats\_checklist\_check

*Check a completed standards checklist*

---

**Description**

Correct any potential formatting issues in a completed standards checklist

**Usage**

```
srr_stats_checklist_check(file)
```

**Arguments**

**file** Name of local file containing a completed checklist. Must be a markdown document in .md format, not .Rmd or anything else.

**See Also**

Other helper: [srr\\_stats\\_categories\(\)](#), [srr\\_stats\\_checklist\(\)](#), [srr\\_stats\\_pkg\\_skeleton\(\)](#), [srr\\_stats\\_pre\\_submit\(\)](#)

**Examples**

```
## Not run:
f <- tempfile (fileext = ".md")
srr_stats_checklist (category = "regression", filename = f)
chk <- srr_stats_checklist_check (f)

## End(Not run)
```

---

`srr_stats_pkg_skeleton`*Make skeleton package to test roclet system*

---

### Description

Make a dummy package skeleton including 'srr' **roxygen2** tags which can be used to try out the functionality of this package. Running the example lines below which activate the 'srr' roclets, and show you what the output of those roclets looks like. Feel free to examine the effect of modifying any of the @srrstats tags within the code as identified by running those lines.

### Usage

```
srr_stats_pkg_skeleton(base_dir = tempdir(), pkg_name = "demo")
```

### Arguments

<code>base_dir</code>	The base directory where the package should be constructed.
<code>pkg_name</code>	The name of the package. The final location of this package will be in <code>file.path(base_dir, pkg_name)</code> .

### Value

The path to the directory holding the newly created package

### See Also

Other helper: [srr\\_stats\\_categories\(\)](#), [srr\\_stats\\_checklist\(\)](#), [srr\\_stats\\_checklist\\_check\(\)](#), [srr\\_stats\\_pre\\_submit\(\)](#)

### Examples

```
d <- srr_stats_pkg_skeleton (pkg_name = "mystatspkg")
# (capture.output of initial compilation messages)
x <- utils::capture.output (roxygen2::roxygenise (d), type = "output")
```

---

`srr_stats_pre_submit` *Perform pre-submission checks*

---

### Description

Check that all standards are present in code, and listed either as '@srrstats' or '@srrstatsNA'

### Usage

```
srr_stats_pre_submit(path = ".", quiet = FALSE)
```

**Arguments**

path            Path to local repository to check  
quiet           If 'FALSE', display information on status of package on screen.

**Value**

(Invisibly) List of any standards missing from code

**See Also**

Other helper: [srr\\_stats\\_categories\(\)](#), [srr\\_stats\\_checklist\(\)](#), [srr\\_stats\\_checklist\\_check\(\)](#), [srr\\_stats\\_pkg\\_skeleton\(\)](#)

**Examples**

```
d <- srr_stats_pkg_skeleton ()  
# The skeleton has 'TODO' standards, and also has only a few from the full  
# list expected for the categories specified there.  
srr_stats_pre_submit (d)
```

---

srr\_stats\_roclet        *srr\_stats\_roclet*

---

**Description**

Get values of all srrstats tags in function documentation

**Usage**

```
srr_stats_roclet()
```

**Details**

Note that this function should never need to be called directly. It only exists to enable "@srrstats" tags to be parsed from **roxygen2** documentation.

**Value**

A **roxygen2** roclet

**See Also**

Other roxygen: [srr\\_stats\\_roxygen\(\)](#)

**Examples**

```
srr_stats_roclet ()
```

---

srr\_stats\_roxygen      *Insert standards into code in **roxygen2** format*

---

### Description

Obtain rOpenSci standards for statistical software, along with one or more category-specific standards, as a checklist, convert to project-specific **roxygen2** format, and save in nominated file.

### Usage

```
srr_stats_roxygen(  
  category = NULL,  
  filename = "srr-stats-standards.R",  
  overwrite = FALSE  
)
```

### Arguments

category	One of the names of files given in the directory contents of <a href="https://github.com/ropensci/statistical-software-review-book/tree/main/standards">https://github.com/ropensci/statistical-software-review-book/tree/main/standards</a> , each of which is ultimately formatted into a sub-section of the standards.
filename	Name of 'R' source file in which to write <b>roxygen2</b> -formatted lists of standards.
overwrite	If FALSE (default) and filename already exists, a dialog will ask whether file should be overwritten.

### Value

Nothing

### See Also

Other roxygen: [srr\\_stats\\_roclet\(\)](#)

### Examples

```
## Not run:  
path <- srr_stats_pkg_skeleton ()  
# contains a few standards; insert all with:  
f <- file.path (path, "R", "srr-stats-standards.R")  
file.exists (f)  
length (readLines (f)) # only 14 lines  
srr_stats_roxygen (  
  category = "regression",  
  file = f,  
  overwrite = TRUE  
)  
length (readLines (f)) # now much longer  
  
## End(Not run)
```

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