

Package ‘BiocBaseUtils’

May 14, 2024

Title General utility functions for developing Bioconductor packages

Version 1.6.0

Description The package provides utility functions related to package development. These include functions that replace slots, and selectors for show methods. It aims to coalesce the various helper functions often re-used throughout the Bioconductor ecosystem.

Imports methods, utils

Depends R (>= 4.2.0)

Suggests knitr, rmarkdown, BiocStyle, tinytest

License Artistic-2.0

Encoding UTF-8

biocViews Software, Infrastructure

BugReports <https://www.github.com/Bioconductor/BiocBaseUtils/issues>

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

VignetteBuilder knitr

Date 2024-04-29

git_url <https://git.bioconductor.org/packages/BiocBaseUtils>

git_branch RELEASE_3_19

git_last_commit 2a04686

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-14

Author Marcel Ramos [aut, cre] (<<https://orcid.org/0000-0002-3242-0582>>),
Martin Morgan [ctb],
Hervé Pagès [ctb]

Maintainer Marcel Ramos <marcel.ramos@roswellpark.org>

Contents

BiocBaseUtils-package	2
askUserYesNo	2
Assertions	3
checkInstalled	5
selectSome	6
setSlots	7
Index	8

BiocBaseUtils-package	<i>BiocBaseUtils: Utility and Internal functions for Bioconductor packages</i>
-----------------------	--

Description

BiocBaseUtils is a package aimed at helping the typical Bioconductor developer formalize often written functions that can be seen scattered throughout the Bioconductor ecosystem. Some of these functions include the ability to replace slots in an object. Other functions work to create a nice show method output by selecting some observations.

Author(s)

Maintainer: Marcel Ramos <marcel.ramos@roswellpark.org> ([ORCID](#))
Other contributors:

- Martin Morgan <martin.morgan@roswellpark.org> [contributor]
- Hervé Pagès <hpages.on.github@gmail.com> [contributor]

See Also

Useful links:

- Report bugs at <https://www.github.com/Bioconductor/BiocBaseUtils/issues>

askUserYesNo	<i>Ask user for a yes/no response</i>
--------------	---------------------------------------

Description

Ask user for a yes/no response

Usage

askUserYesNo(prompt, interactive.only = TRUE)

Arguments

`prompt` `character()` Question form prompt to display to the user without a question mark

`interactive.only` `logical(1)` If TRUE, the function will only prompt the user when the R session is interactive. If FALSE, the function will always prompt the user.

Value

TRUE when user replies with 'yes' to prompt, FALSE when 'no'

Author(s)

Martin M.

Examples

```
askUserYesNo("Do you want to continue")
```

Assertions

Suite of helper functions to test for types

Description

These are a group of helper functions that allow the developer to easily check for common data types in Bioconductor. These include logical, character, and numeric (& integer).

Usage

```
isTRUEorFALSE(x, na.ok = FALSE)

isScalarCharacter(x, na.ok = FALSE, zchar = FALSE)

isScalarInteger(x, na.ok = FALSE)

isScalarNumber(x, na.ok = FALSE, infinite.ok = FALSE)

isScalarLogical(x, na.ok = FALSE)

isCharacter(x, na.ok = FALSE, zchar = FALSE)

isZeroOneCharacter(x, na.ok = FALSE, zchar = FALSE)
```

Arguments

<code>x</code>	The input vector whose type is to be checked
<code>na.ok</code>	logical(1L) Whether it is acceptable to consider NA type inputs (default: FALSE).
<code>zchar</code>	logical(1L) Whether it is acceptable to consider 'zero' characters as defined by <code>nchar</code> , e.g., <code>nchar("")</code> (default: FALSE).
<code>infinite.ok</code>	logical(1L) Whether it is acceptable to consider infinite values as identified by <code>is.finite</code> (default: FALSE).

Details

Some functions such as `isScalarCharacter` allow exceptions to the type checks via the `na.ok` and `zchar` arguments. Others, for example `isScalarNumber` can permit `Inf` with the `infinite.ok` argument.

Value

Either TRUE or FALSE

Functions

- `isTRUEorFALSE()`: Is the input a single logical vector?
- `isScalarCharacter()`: Is the input a single character vector?
- `isScalarInteger()`: Is the input a single integer vector?
- `isScalarNumber()`: Is the input a single numeric vector?
- `isScalarLogical()`: Is the input a single logical vector?
- `isCharacter()`: Is the input a character vector?
- `isZeroOneCharacter()`: Is the input a character vector of zero or one length?

Author(s)

M. Morgan, H. Pagès

Examples

```
isTRUEorFALSE(TRUE)
isTRUEorFALSE(FALSE)
isTRUEorFALSE(NA, na.ok = TRUE)

isScalarCharacter(LETTERS)
isScalarCharacter("L")
isCharacter(LETTERS)
isCharacter(NA_character_, na.ok = TRUE)
isZeroOneCharacter("")
isZeroOneCharacter("", zchar = TRUE)

isScalarInteger(1L)
isScalarInteger(1)
```

```
isScalarNumber(1)
isScalarNumber(1:2)
```

checkInstalled	<i>Check packages are installed otherwise suggest</i>
----------------	---

Description

checkInstalled allows to check if a package is installed. If the package is not available, a convenient copy-and-paste message is provided for package installation with BiocManager. The function is typically used within functions that check for package availability from the Suggests field.

Usage

```
checkInstalled(pkgs)
```

Arguments

pkgs	character() package names required for a function
------	---

Value

TRUE if all packages are installed, otherwise stops with a message and suggests installation of missing packages

Author(s)

M. Morgan, M. Ramos

Examples

```
if (interactive()) {
  checkInstalled(
    c("BiocParallel", "SummarizedExperiment")
  )
}
```

`selectSome`*Select and return only some entries from a vector*

Description

`selectSome` works well in `show` methods. It abbreviates a vector input depending on the `maxToShow` argument.

Usage

```
selectSome(  
  obj,  
  maxToShow = 5,  
  ellipsis = "...",  
  ellipsisPos = c("middle", "end", "start"),  
  quote = FALSE  
)
```

Arguments

<code>obj</code>	<code>character()</code> A vector to be abbreviated for display purposes
<code>maxToShow</code>	<code>numeric(1)</code> The maximum number of values to show in the output (default: 5)
<code>ellipsis</code>	<code>character(1)</code> The symbol used to abbreviate values in the vector (default: "...")
<code>ellipsisPos</code>	<code>character(1)</code> The location for the ellipsis in the output, by default in the "middle" but can be moved to either the "end" or the "start".
<code>quote</code>	<code>logical(1)</code> Whether or not to add a single quote around the <code>obj</code> input. This only works for character type inputs.

Value

An abbreviated output of `obj`

Author(s)

M. Morgan, H. Pagès

Examples

```
letters  
  
selectSome(letters)
```

setSlots	<i>Convenience function to set slot values</i>
----------	--

Description

Given the current object, the function `setSlots` will take name-value pair inputs either as named arguments or a list and replace the values of the specified slots. This is a convenient function for updating slots in an S4 class object.

Usage

```
setSlots(object, ..., check = TRUE)
```

Arguments

<code>object</code>	An S4 object with slots to replace
<code>...</code>	Slot name and value pairs either as named arguments or a named list, e.g., <code>slotName = value</code> .
<code>check</code>	logical(1L) Whether to run <code>validObject</code> after the slot replacement

Value

The object input with updated slot data

Author(s)

H. Pagès

Examples

```
setClass("A", representation = representation(slotA = "character"))  
  
aclass <- new("A", slotA = "A")  
  
setSlots(aclass, slotA = "B")
```

Index

`askUserYesNo`, [2](#)

`Assertions`, [3](#)

`BiocBaseUtils` (`BiocBaseUtils-package`), [2](#)

`BiocBaseUtils-package`, [2](#)

`checkInstalled`, [5](#)

`isCharacter` (`Assertions`), [3](#)

`isScalarCharacter` (`Assertions`), [3](#)

`isScalarInteger` (`Assertions`), [3](#)

`isScalarLogical` (`Assertions`), [3](#)

`isScalarNumber` (`Assertions`), [3](#)

`isTRUEorFALSE` (`Assertions`), [3](#)

`isZeroOneCharacter` (`Assertions`), [3](#)

`replaceSlots` (`setSlots`), [7](#)

`selectSome`, [6](#)

`setSlots`, [7](#)