Package 'BiocBaseUtils'

May 17, 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 2024-05-17

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` *BiocBaseUtils: Utility and Internal functions for Bioconductor packages*

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` *Ask user for a yes/no response*

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

x	The input vector whose type is to be checked
na.ok	logical(1L) Whether it is acceptable to consider NA type inputs (default: FALSE).
zchar	logical(1L) Whether is is acceptable to consider 'zero' characters as defined by nchar, e.g., nchar("") (default: FALSE).
infinite.ok	logical(1L) Whether it is acceptable to consider infinite values as identified by is.finite (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 *Check packages are installed otherwise suggest*

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

obj	character() A vector to be abbreviated for display purposes
maxToShow	numeric(1) The maximum number of values to show in the output (default: 5)
ellipsis	character(1) The symbol used to abbreviate values in the vector (default: "...")
ellipsisPos	character(1) The location for the ellipsis in the output, by default in the "middle" but can be moved to either the "end" or the "start".
quote	logical(1) Whether or not to add a single quote around the obj 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` *Convenience function to set slot values*

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

`object`	An S4 object with slots to replace
`...`	Slot name and value pairs either as named arguments or a named list, e.g., `slotName = value`.
`check`	logical(1L) Whether to run validObject 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