

Package ‘plyxp’

May 19, 2025

Title Data masks for SummarizedExperiment enabling dplyr-like manipulation

Version 1.2.0

Description The package provides `rlang` data masks for the SummarizedExperiment class. The enables the evaluation of unquoted expression in different contexts of the SummarizedExperiment object with optional access to other contexts. The goal for `plyxp` is for evaluation to feel like a data.frame object without ever needing to unwind to a rectangular data.frame.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

VignetteBuilder knitr

Imports dplyr, purrr, rlang, SummarizedExperiment, tidyr, tidyselect, vctrs, tibble, pillar, cli, glue, S7, S4Vectors, utils, methods

Depends R (>= 4.4.0)

Suggests devtools, knitr, rmarkdown, testthat, airway, IRanges, here

LazyData true

URL <https://github.com/jtlandis/plyxp>,
<https://jtlandis.github.io/plyxp>

BugReports <https://www.github.com/jtlandis/plyxp/issues>

biocViews Annotation, GenomeAnnotation, Transcriptomics

Config/testthat/edition 3

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

git_branch RELEASE_3_21

git_last_commit 054beec

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-05-18

Author Justin Landis [aut, cre] (ORCID:
<https://orcid.org/0000-0001-5501-4934>),
Michael Love [aut] (ORCID: <https://orcid.org/0000-0001-8401-0545>)
Maintainer Justin Landis <jtlandis314@gmail.com>

Contents

plyxp-package	2
arrange	3
as.data.frame	4
dot-pronouns	5
filter	6
group_by	7
group_data	8
group_vars	8
mutate	9
new_plyxp	10
plyxp	11
plyxp-context	12
pull	13
reexports	14
se	14
select	17
se_simple	18
summarize	19
vctrs-vec_recycle	20
vctrs-vec_rep	21
vctrs_slice	22
vectors	23
vec_phantom	24
Index	26

plyxp-package	<i>plyxp: Data masks for SummarizedExperiment enabling dplyr-like manipulation</i>
---------------	--

Description

The package provides ‘rlang’ data masks for the SummarizedExperiment class. The enables the evaluation of unquoted expression in different contexts of the SummarizedExperiment object with optional access to other contexts. The goal for ‘plyxp’ is for evaluation to feel like a data.frame object without ever needing to unwind to a rectangular data.frame.

Value

API for using S4 classes with rlang data masks

Author(s)

Maintainer: Justin Landis <jtlandis314@gmail.com> ([ORCID](#))

Authors:

- Michael Love <michaelisaiahlove@gmail.com> ([ORCID](#))

See Also

Useful links:

- <https://github.com/jtlandis/plyxp>
- <https://jtlandis.github.io/plyxp>
- Report bugs at <https://www.github.com/jtlandis/plyxp/issues>

arrange

arrange rows or columns of PlySummarizedExperiment

Description

arrange() orders either the rows or columns of a PlySummarizedExperiment object. Note, to guarantee a valid PlySummarizedExperiment is returned, arranging in the assays evaluation context is disabled.

Unlike other dplyr verbs, arrange() largely ignores grouping. The PlySummarizedExperiment method also provides the same functionality via the .by_group argument.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
arrange(.data, ..., .by_group = FALSE)
```

Arguments

- | | |
|-----------|---|
| .data | An object inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects |
| ... | <data-masking> Variables, or functions of variables. Use desc() to sort a variable in descending order. |
| .by_group | If TRUE, will sort first by grouping variable. Applies to grouped data frames only. |

Value

an object inheriting PlySummarizedExperiment class

Examples

```
# arrange within rows/cols contexts separately
arrange(
  se_simple,
  rows(direction),
  cols(dplyr::desc(condition))
)

# access assay data to compute arrangement
arrange(
  se_simple,
  rows(rowSums(.assays_asis$counts)),
  cols(colSums(.assays_asis$counts))
)

# assay context is disabled
arrange(se_simple, counts) |> try()

# convert to `data.frame` first
as.data.frame(se_simple) |>
  arrange(counts)
```

as.data.frame

create data.frame

Description

create data.frame

Usage

```
## S3 method for class 'PlySummarizedExperiment'
as.data.frame(x, ...)
```

Arguments

x	SummarizedExperiment object
...	unused arguments

Value

a data.frame object

Examples

```
as.data.frame(se_simple)
```

dot-pronouns	<i>contextual plyxp pronouns</i>
--------------	----------------------------------

Description

plyxp utilizes its own version of `rlang::.data` pronouns. These may be used to gain access to other evaluation contexts for a managed set of data-masks.

Similar to `rlang::.data`, `plyxp::.assays` and other exported pronouns are exported to pass R CMD Checks. When using a `plyxp` within your package, import the associated pronoun from `plyxp` but only use the fully unqualified name, `.assays`, `.assays_asis`, etc.

Usage

```
.assays
.assays_asis
.rows
.rows_asis
.cols
.cols_asis
```

Format

```
An object of class NULL of length 0.
An object of class NULL of length 0.
An object of class NULL of length 0.
An object of class NULL of length 0.
An object of class NULL of length 0.
An object of class NULL of length 0.
```

Value

access to specific values behind the `rlang` pronoun

Examples

```
mutate(se_simple,
  # access via pronoun
  rows(sum = rowSums(.assays_asis$counts)),
  cols(sum = vapply(.assays$counts, sum, numeric(1))))
```

filter	<i>filter PlySummarizedExperiment</i>
--------	---------------------------------------

Description

The `filter()` function is used to subset an object, returning the observations that satisfy your conditions. An observation must return `TRUE` for all conditions within a context to be retained. Note, to guarantee a valid `PlySummarizedExperiment` is returned, filtering in the assays evaluation context is disabled.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
filter(.data, ..., .preserve = FALSE)
```

Arguments

<code>.data</code>	An object Inheriting from <code>PlySummarizedExperiment</code> , the wrapper class for <code>SummarizedExperiment</code> objects
<code>...</code>	conditions to filter on. These must be wrapped in <code>cols()</code> and or <code>rows()</code>
<code>.preserve</code>	Relevant when the <code>.data</code> input is grouped. If <code>.preserve = FALSE</code> (the default), the grouping structure is recalculated based on the resulting data, i.e. the number of groups may change.

Value

an object inheriting `PlySummarizedExperiment` class

Examples

```
# example code
filter(
  se_simple,
  rows(length > 30),
  cols(condition == "drug")
)

filter(
  se_simple,
  rows(rowSums(.assays_asis$counts) > 40),
  cols(colSums(.assays_asis$counts) < 50)
)

# assay context is disabled
filter(
  se_simple,
  counts > 12
) |> try()
```

```
# convert to `data.frame` first
as.data.frame(se_simple) |>
  filter(counts > 12)
```

group_by

*apply groups to PlySummarizedExperiment***Description**

create grouping variables about the rowData and colData of a PlySummarizedExperiment object. Unlike the data.frame method the resulting output class is left unchanged. Thus dplyr generics for PlySummarizedExperiment must check grouping information manually.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
group_by(.data, ..., .add = FALSE)

## S3 method for class 'PlySummarizedExperiment'
ungroup(x, ...)
```

Arguments

.data	An object Inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects
	S4 Compatibility: At the moment, grouping on S4 Vectors is not yet supported. This is due to plyxp using [vec_group_loc][vctrs::vec_group_loc] to form grouping information. plyxp will eventually develop a method to handle S4 Vectors.
...	contextual expressions specifying which columns to ungroup. Omitting ... ungroups the entire object.
.add	When FALSE, the default, group_by() will override existing groups.
x	An object Inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects

Value

PlySummarizedExperiment object

Functions

- ungroup(PlySummarizedExperiment): Ungroup a PlySummarizedExperiment object

Examples

```
group_by(se_simple, rows(direction), cols(condition))
```

group_data	<i>get grouping data</i>
------------	--------------------------

Description

retrieve grouping information from a SummarizedExperiment object. This is stored within the metadata() of the object.

Usage

```
## S3 method for class 'PlySummarizedExperiment'  
group_data(.data)
```

Arguments

.data An object Inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects

Value

list of groupings for an SummarizedExperiment

Examples

```
group_by(se_simple, rows(direction), cols(condition)) |> group_data()
```

group_vars	<i>get PlySummarizedExperiment grouping Variables</i>
------------	---

Description

like in `dplyr::group_vars()` will get character strings for groupings with the exection of the return value being a list for each grouped context

Usage

```
## S3 method for class 'PlySummarizedExperiment'  
group_vars(x)
```

Arguments

x PlySummarizedExperiment

Value

NULL or list containing names of grouping columns

Examples

```
out <- group_by(se_simple, rows(direction))
group_vars(out)
```

mutate

*Mutate a PlySummarizedExperiment object***Description**

Mutate a PlySummarizedExperiment object under an data mask. Unlike a few other dplyr implementations, all contextual evaluations of mutate() for SummarizedExperiment are valid.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
mutate(.data, ...)
```

Arguments

.data	An object inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects
...	expressions to evaluate

Value

an object inheriting PlySummarizedExperiment class

Examples

```
mutate(se_simple,
  counts_1 = counts + 1,
  logp_counts = log(counts_1),
  # access assays context with ".assays" pronoun,
  # note that assays are sliced into a list to
  # fit dimensions of cols context
  cols(sum = purrr::map_dbl(.assays$counts, sum)),
  # access assays context "asis" with the same pronoun
  # but with a "_asis" suffix.
  rows(sum = rowSums(.assays_asis$counts))
)
```

`new_plyxp`*SummarizedExperiment Shell Object*

Description

A container object for the `SummarizedExperiment` class.

This S4 class is implemented to bring unique `dplyr` syntax to the `SummarizedExperiment` object without clashing with the `tidySummarizedExperiment` package. As such, this is a simple wrapper that contains one slot, which holds a `SummarizedExperiment` object.

Usage

```
new_plyxp(se)
```

```
PlySummarizedExperiment(se)
```

Arguments

`se` `SummarizedExperiment` object

Value

`PlySummarizedExperiment` object

Slots

`se` contains the underlying `SummarizedExperiment` class.

Examples

```
se <- SummarizedExperiment(  
  assays = list(counts = matrix(1:6, nrow = 3)),  
  colData = S4Vectors::DataFrame(condition = c("A", "B"))  
)  
new_plyxp(se = se)  
# or  
PlySummarizedExperiment(se = se)
```

plyxp

Modify SummarizedExperiment Object

Description

Modify the underlying SummarizedExperiment object with a function.

Usage

```
plyxp(.data, .f, ..., .caller = caller_env())
```

```
plyxp_on(.data, .f, ..., .on, .caller = caller_env())
```

Arguments

<code>.data</code>	a PlySummarizedExperiment object
<code>.f</code>	within <code>plyxp()</code> : a function that returns a SummarizedExperiment object. within <code>plyxp_on()</code> : <code>.f</code> should return a value compatible with <code>.on(se)<-</code>
<code>...</code>	additional arguments passed to <code>.f</code>
<code>.caller</code>	environment in which <code>plyxp</code> should signal an error if one occurs.
<code>.on</code>	a symbol matching an accessor and setter function for the SummarizedExperiment Class.

Value

a PlySummarizedExperiment object

Functions

- `plyxp_on()`: pass a function to the result of an accessor of the SummarizedExperiment Class
This function is a wrapper for the expression:

```
plyxp::plyxp(.data, function(se, ...) {
  .f <- rlang::as_function(.f)
  obj <- .on(se)
  obj <- .f(se, ...)
  .on(se) <- obj
  se
}, ...)
```

where `.on` is the symbol for the accessor function into a SummarizedExperiment Class. Note: the setter variant must exist in the environment that `plyxp_on()` is called. All other arguments are diffused as quosures and will be evaluated in the environment they were quoted.

Examples

```
plyxp(se_simple, function(x) x)
plyxp_on(se_simple,
  .f = lapply, # function to call on `.on` args,
  .on = rowData, # data `.f` will be used on
  paste, "foo") # arguments for `.f`
```

plyxp-context

plyxp contexts

Description

Contextual user-facing helper function for dplyr verbs with SummarizedExperiment objects. These functions are intended to be used as the top level call to any dplyr verbs ... argument, similar to that of across()/if_any()/if_all().

Specifies that the following expressions should be evaluated within the colData context.

Specifies that the following expressions should be evaluated within the rowData context.

Specify a single expression to evaluate in another context

Specify a single expression to evaluate in another context

Specify a single expression to evaluate in another context

Usage

```
cols(...)
```

```
rows(...)
```

```
col_ctx(x, asis = FALSE)
```

```
row_ctx(x, asis = FALSE)
```

```
assay_ctx(x, asis = FALSE)
```

Arguments

`x, ...` expressions to evaluate within its associated context

`asis` `asis = FALSE` (the default) will indicate using active bindings that attempt to coerce the underlying data into a format that is appropriate for the current context. Indicating `TRUE` will instead bind the underlying data as is.

Value

function called for its side-effects

Examples

```
# cols
mutate(se_simple,
  cols(is_drug = condition=="drug"),
  #bind a different context
  effect = col_ctx(counts + (is_drug * rbinom(n(), 20, .3))))
```

pull	<i>extract data from object</i>
------	---------------------------------

Description

similar to `dplyr::pull.data.frame` except allows to extract objects from different contexts.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
pull(.data, var = -1, name = NULL, ...)
```

Arguments

<code>.data</code>	An object Inheriting from <code>PlySummarizedExperiment</code> , the wrapper class for <code>SummarizedExperiment</code> objects
<code>var</code>	A variable as specified by dplyr::pull
<code>name</code>	ignored argument. Due to the range of data types a <code>PlySummarizedExperiment</code> this argument is not supported
<code>...</code>	unused argument

Value

an element from either the assays, rowData, or colData of a `SummarizedExperiment` object

Examples

```
# last element of default context (assays)
pull(se_simple, var = -1)
# first element of rows context
pull(se_simple, var = rows(1))
# element from col context by literal variable name
pull(se_simple, var = cols(condition))

# use `pull()` to return contextual info
mutate(se_simple, rows(counts = .assays$counts)) |>
  # get last stored element
  pull(rows(-1))
```

reexports	<i>Objects exported from other packages</i>
-----------	---

Description

These objects are imported from other packages. Follow the links below to see their documentation.

S4Vectors [metadata](#), [metadata<-](#)

SummarizedExperiment [SummarizedExperiment](#), [assay](#), [assay<-](#), [assays](#), [assays<-](#), [colData](#), [colData<-](#), [rowData](#), [rowData<-](#)

Value

exported functions available from plyxp

See Also

[arrange\(\)](#) [mutate\(\)](#) [filter\(\)](#) [summarize\(\)](#) [select\(\)](#) [pull\(\)](#) [group_by\(\)](#) [group_data\(\)](#) [group_vars\(\)](#) [ungroup\(\)](#)

[PlySummarizedExperiment-methods](#)

Examples

```
arrange(se_simple, rows(direction)) |>
  mutate(logp_counts = log1p(counts)) |>
  filter(cols(condition == "drug"))
```

```
assays(se_simple)
rowData(se_simple)
colData(se_simple)
```

se	<i>PlySummarizedExperiment Methods</i>
----	--

Description

Methods from SummarizedExperiment package re-implemented for PlySummarizedExperiment.

Usage

```
se(x)

## S4 method for signature 'PlySummarizedExperiment'
se(x)

se(x) <- value

## S4 replacement method for signature 'PlySummarizedExperiment'
se(x) <- value

## S4 method for signature 'PlySummarizedExperiment'
assays(x, withDimnames = TRUE, ...)

## S4 replacement method for signature 'PlySummarizedExperiment,list'
assays(x, withDimnames = TRUE, ...) <- value

## S4 replacement method for signature 'PlySummarizedExperiment,SimpleList'
assays(x, withDimnames = TRUE, ...) <- value

## S4 method for signature 'PlySummarizedExperiment,missing'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'PlySummarizedExperiment,numeric'
assay(x, i, withDimnames = TRUE, ...)

## S4 method for signature 'PlySummarizedExperiment,character'
assay(x, i, withDimnames = TRUE, ...)

## S4 replacement method for signature 'PlySummarizedExperiment,missing'
assay(x, i, withDimnames = TRUE, ...) <- value

## S4 replacement method for signature 'PlySummarizedExperiment,numeric'
assay(x, i, withDimnames = TRUE, ...) <- value

## S4 replacement method for signature 'PlySummarizedExperiment,character'
assay(x, i, withDimnames = TRUE, ...) <- value

## S4 method for signature 'PlySummarizedExperiment'
rowData(x, use.names = TRUE, ...)

## S4 replacement method for signature 'PlySummarizedExperiment'
rowData(x, ...) <- value

## S4 method for signature 'PlySummarizedExperiment'
colData(x, ...)

## S4 replacement method for signature 'PlySummarizedExperiment,DataFrame'
```

```
colData(x, ...) <- value

## S4 replacement method for signature 'PlySummarizedExperiment, NULL'
colData(x, ...) <- value
```

Arguments

<code>x</code>	PlySummarizedExperiment object
<code>value</code>	replacement value
<code>withDimnames</code>	logical
<code>...</code>	additional arguments
<code>i</code>	character or numeric index
<code>use.names</code>	logical

Value

Replacement functions return a PlySummarizedExperiment object. Other functions will return the same object as the method from SummarizedExperiment.

Functions

- `se(PlySummarizedExperiment)`: get the se slot of the PlySummarizedExperiment object
- `se(x) <- value`: set the se slot of the PlySummarizedExperiment object
- `se(PlySummarizedExperiment) <- value`: set the se slot of the PlySummarizedExperiment object
- `assays(PlySummarizedExperiment)`: get the assays of the PlySummarizedExperiment object
- `assays(x = PlySummarizedExperiment) <- value`: set the assays of the PlySummarizedExperiment object
- `assays(x = PlySummarizedExperiment) <- value`: set the assays of the PlySummarizedExperiment object
- `assay(x = PlySummarizedExperiment, i = missing)`: get the first assay of the PlySummarizedExperiment object
- `assay(x = PlySummarizedExperiment, i = numeric)`: get assay from a PlySummarizedExperiment object
- `assay(x = PlySummarizedExperiment, i = character)`: get assay from a PlySummarizedExperiment object
- `assay(x = PlySummarizedExperiment, i = missing) <- value`: set assay in a PlySummarizedExperiment object
- `assay(x = PlySummarizedExperiment, i = numeric) <- value`: set assay in a PlySummarizedExperiment object
- `assay(x = PlySummarizedExperiment, i = character) <- value`: set assay in a PlySummarizedExperiment object
- `rowData(PlySummarizedExperiment)`: get rowData in a PlySummarizedExperiment object

- `rowData(PlySummarizedExperiment) <- value`: set `rowData` in a `PlySummarizedExperiment` object
- `colData(PlySummarizedExperiment)`: get `colData` in a `PlySummarizedExperiment` object
- `colData(x = PlySummarizedExperiment) <- value`: set `colData` in a `PlySummarizedExperiment` object

Examples

```
assays(se_simple)
rowData(se_simple)
colData(se_simple)
```

select	<i>select assays, rowData, and colData names</i>
--------	--

Description

Select one or more values from each context. By default omitting an expression for a context is the same as selecting NOTHING from that context.

The `<tidy-select>` implementation within `plyxp` is almost similar to `dplyr` except when used within the `across()` function. When used from `accross()`, the data provided to `eval_select` is a zero length slice of the data. This was an intentional choice to prevent the evaluation of potentially expensive chopping operations for `S4Vectors`. This means that predicate function from `where()` will NOT be able to query the original data.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
select(.data, ...)
```

Arguments

<code>.data</code>	An object Inheriting from <code>PlySummarizedExperiment</code> , the wrapper class for <code>SummarizedExperiment</code> objects
<code>...</code>	<code><tidy-select></code> one or more selection expressions. Supports wrapping expressions within the <code><plyxp-contexts></code> .

Value

an object inheriting `PlySummarizedExperiment` class

Examples

```
# only keep assays, other contexts are dropped
select(se_simple, everything())

# only keep rowData, other contexts are dropped
select(se_simple, rows(everything()))

select(se_simple, rows(where(is.numeric)))

# Note on `where()` clause, all data is available within select
select(se_simple, rows(where(~any(grepl("-", .x)))))

# within an `across()`, only a zero-length slice available, so the
# `where()` predicate cannot access the data
mutate(se_simple,
  rows(
    across(where(~any(grepl("-", .x))),
      ~sprintf("%s foo", .x)))
# here is an acceptable usage of the `where()` predicate
mutate(se_simple,
  rows(
    across(where(is.character),
      ~sprintf("%s foo", .x)))
```

se_simple

Plyxp Simple Example Summarized Experiment

Description

A small data SummarizedExperiment Object of 20 observations, 5 rows and 4 columns.

Usage

```
se_simple
```

Format

```
se_simple:
assays counts sampled data points between 1:20
logcounts log transform of counts
rowData/.features gene fake gene name
length fake gene length
direction fake strand
colData/.samples sample fake sample name
condition control or drug treatment
```

Value

a SummarizedExperiment object

Examples

```
SummarizedExperiment::assays(se_simple)
SummarizedExperiment::rowData(se_simple)
SummarizedExperiment::colData(se_simple)
```

summarize	<i>Summarize PlySummarizedExperiment</i>
-----------	--

Description

Summarize PlySummarizedExperiment

Usage

```
## S3 method for class 'PlySummarizedExperiment'
summarize(.data, ..., .retain = c("auto", "ungrouped", "none"))

## S3 method for class 'PlySummarizedExperiment'
summarise(.data, ..., .retain = c("auto", "ungrouped", "none"))
```

Arguments

<code>.data</code>	An object inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects
<code>...</code>	expressions to summarize the object
<code>.retain</code>	This argument controls how <code>rowData()</code> or <code>colData()</code> is retained after summarizing. When "auto" (the default), <code>.retain</code> behavior depends on the groupings of <code>.data</code> . When exactly one dimension is grouped, "auto" behaves like "ungrouped-dim", and "none" otherwise. When "ungrouped-dim", the ungrouped dimension's data are retained in the resulting SummarizedExperiment object and scalar outputs are recycled to the length of the ungrouped dimension. When "none", all outputs are expected to be scalar and only computed values are retained in <code>rowData()</code> and <code>colData()</code>

Value

an object inheriting PlySummarizedExperiment class

Examples

```
# outputs in assay context may be either
# length 1, or the length of the ungrouped
# dimension while .retain = "auto"/"ungrouped-dim"
se_simple |>
  group_by(rows(direction)) |>
  summarise(
    col_sums = colSums(counts),
    sample = sample(1:20, 1L)
  )

# .retain = "none" will drop ungrouped dimensions and
# outputs of assay context should be length 1.
se_simple |>
  group_by(rows(direction)) |>
  summarise(
    col_sums = list(colSums(counts)),
    .retain = "none"
  )

# using an `across()` function will help
# nest ungrouped dimensions
se_simple |>
  group_by(rows(direction)) |>
  summarise(
    col_sums = list(colSums(counts)),
    cols(across(everything(), list)),
    .retain = "none"
  )
```

vctrs-vec_recycle	<i>Recycle a vector</i>
-------------------	-------------------------

Description

A re-export of `vctrs::vec_recycle` as an S7 generic function to allow S4Vectors.

Usage

```
vec_recycle(x, size, ..., x_arg = "", call = caller_env())
```

Arguments

<code>x</code>	A vector to recycle.
<code>size</code>	Desired output size.
<code>...</code>	Depending on the function used: For <code>vec_recycle_common()</code>, vectors to recycle.

- For `vec_recycle()`, these dots should be empty.
- `x_arg` Argument name for `x`. These are used in error messages to inform the user about which argument has an incompatible size.
- `call` The execution environment of a currently running function, e.g. `caller_env()`. The function will be mentioned in error messages as the source of the error. See the `call` argument of `abort()` for more information.

Value

a S3 or S4 vector

Examples

```
vec_recycle(1L, size = 5L)
vec_recycle(S4Vectors::Rle(1L), size = 5L)
```

vctrs-vec_rep	<i>replicate a vector</i>
---------------	---------------------------

Description

A re-export of `vctrs::vec_rep` and `vctrs::vec_rep_each` as an *S7* generic function to allow `S4Vectors`.

Usage

```
vec_rep(
  x,
  times,
  ...,
  error_call = caller_env(),
  x_arg = "x",
  times_arg = "times"
)

vec_rep_each(
  x,
  times,
  ...,
  error_call = caller_env(),
  x_arg = "x",
  times_arg = "times"
)
```

Arguments

<code>x</code>	A vector.
<code>times</code>	For <code>vec_rep()</code> , a single integer for the number of times to repeat the entire vector. For <code>vec_rep_each()</code> , an integer vector of the number of times to repeat each element of <code>x</code> . <code>times</code> will be recycled to the size of <code>x</code> .
<code>...</code>	These dots are for future extensions and must be empty.
<code>error_call</code>	The execution environment of a currently running function, e.g. <code>caller_env()</code> . The function will be mentioned in error messages as the source of the error. See the <code>call</code> argument of abort() for more information.
<code>x_arg, times_arg</code>	Argument names for errors.

Value

a new S3 or S4 vector replicated by specified times

Examples

```
vec_rep(1:2, times = 5)
vec_rep(S4Vectors::Rle(1:2), times = 5)

vec_rep_each(1:2, times = 5)
vec_rep_each(S4Vectors::Rle(1:2), times = 5)
```

vctrs_slice

Get observations of a vector

Description

This extends `vctrs::vec_slice` to `S4Vectors::Vector` class by masking `vec_slice` with `S7::new_generic`. Atomic vectors and other base S3 classes (`list`, `data.frame`, `factor`, `Dat`, `POSIXct`) will dispatch to the `vctrs::vec_slice` method as normal. Dispatch support on the `S4Vectors::Vector` and `S4Vectors::DataFrame` classes provides a unified framework for working with base R vectors and `S4Vectors`.

S4Vectors::Vector Implementation:

This method will naively call the `[]` method for any S4 class that inherits from the `S4Vectors::Vector` class. This may not be a very efficient way to slice up an S4 class, but will work.

With this implementation, the `x@mc01` data is expected to be retained after a call to `plyxp::vec_slice(x, i)`.

S4Vectors::DataFrame Implementation:

The `DataFrame` implementation works similar to how `vctrs::vec_slice` works on a `data.frame` object. What is being sliced is the rows of `x@listData`. To maintain the size stability of the `DataFrame` object, we change `@nrows` to the appropriate value, and perform a recursive call if `@elementMetadata` is not `NULL`.

Performance:

Depending on the size and complexity of your S4 Vector object, you may find the standard subset operation is extremely slow. For example, consider a SummarizedExperiment whose rowData contains a CompressedGRangesList object assigned to the name "exons" and whose length is 250,000 and underlying @unlistData is length 1,600,000. Performing a by .features grouping operation and attempting to evaluate the exons within the row context would force the CompressedGRangesList object to be chopped element-wise.

Unfortunately, there is a massive performance hit in attempting to construct 250,000 GRanges. Unless you do not mind waiting over an hour for each dplyr verb in which exons gets evaluated, doing so is not recommended.

The plyxp package is planning to export a new generic named plyxp_s4_proxy_vec(). This attempts to reconstruct certain standard S4Vectors::Vectors as standard vectors or tibbles. The equivalent exons object would require much more memory use, but at the advantage of only taking several seconds to construct. When you are done, you can attempt to restore the original S4 Vector with plyxp_restore_s4_proxy().

In development, plyxp_s4_proxy_vec() is faster to work with because there are less checks on the object validity and all @elementMetadata and @metadata are dropped from the objects.

Usage

```
vec_slice(x, i, ...)
```

Arguments

x	A vector
i	An integer, character or logical vector specifying the locations or names of the observations to get/set. Specify TRUE to index all elements (as in x[]), or NULL, FALSE or integer() to index none (as in x[NULL]).
...	These dots are for future extensions and must be empty.

Value

a new S3 or S4 vector subsetting by i

Examples

```
vec_slice(1:10, i = 5)
vec_slice(S4Vectors::Rle(rep(1:3, each = 3)), i = 5)
```

vectors

S7 classes for vctrs and S4 Vectors

Description

A set of S7 classes and Class unions that help establish S7 method dispatch. These classes were made to re-export several vctrs functions such that internals for plyxp were consistent with room for optimization.

Usage

```
class_vctrs

class_s4_vctrs

class_DF
```

Format

An object of class S7_union of length 1.
 An object of class classRepresentation of length 1.
 An object of class classRepresentation of length 1.

Value

S7 class union or base class

See Also

[vec_rep\(\)](#), [vec_recycle\(\)](#), [vec_slice\(\)](#)

vec_phantom

Printing within tibble with S4 objects

Description

plyxp uses [pillar](#) for its printing. If you want to change how your S4 object is printed within plyxp's print method, consider writing a method for this function.

To print S4 objects in a tibble, plyxp hacks a custom integer vector built from [vctrs](#) where the S4 object lives in an attribute named "phantomData". You can create your own S4 phantom vector with [vec_phantom\(\)](#). This function is not used outside of printing for plyxp

The default method for formatting a [vec_phantom\(\)](#) is to call [showAsCell\(\)](#).

Usage

```
vec_phantom(x)

plyxp_pillar_format(x, ...)

show_tidy(x, ...)

use_show_tidy()

use_show_default()
```


Arguments

x The S4 object
 ... other arguments passed from `pillar_shaft`

Value

`plyxp_pillar_format` -> formatted version of your S4 vector `vec_phantom` -> integer vector with arbitrary object in `phantomData` attribute.

tidy printing

By default, `plyxp` will not affect the `show` method for `SummarizedExperiment` objects. The `PlySummarizedExperiment` object will always use the tibble abstraction method. If you want to use tibble abstraction, you may use `use_show_tidy()` to enable or `use_show_default()` #' to disable this feature. These functions are called for their side effects, #' modifying the global option `"show_SummarizedExperiment_as_tibble_abstraction"`.

To show an object as the tibble abstraction regardless of the set option, use the S3 generic `show_tidy(...)`.

Examples

```
if(require("IRanges")) {
  ilist <- IRanges::IntegerList(list(c(1L,2L,3L),c(5L,6L)))
  phantom <- vec_phantom(ilist)
  pillar::pillar_shaft(phantom)

  plyxp_pillar_format.CompressedIntegerList <- function(x) {
    sprintf("Int: [%i]", lengths(x))
  }
  print(pillar::pillar_shaft(phantom))
  rm(plyxp_pillar_format.CompressedIntegerList)
}

# default printing for PlySummarizedExperiment object
se_simple
# default printing for SummarizedExperiment object
se <- se(se_simple)
se
# use `plyxp` tibble abstraction
use_show_tidy()
se
# restore default print
use_show_default()
se
# explicitly using tibble abstraction
show_tidy(se)
```

Index

- * **datasets**
 - dot-pronouns, [5](#)
 - se_simple, [18](#)
 - vectors, [23](#)
- * **internal**
 - plyxp-package, [2](#)
 - reexports, [14](#)
- .assays (dot-pronouns), [5](#)
- .assays_asis (dot-pronouns), [5](#)
- .cols (dot-pronouns), [5](#)
- .cols_asis (dot-pronouns), [5](#)
- .rows (dot-pronouns), [5](#)
- .rows_asis (dot-pronouns), [5](#)
- abort(), [21](#), [22](#)
- arrange, [3](#)
- arrange(), [14](#)
- as.data.frame, [4](#)
- assay, [14](#)
- assay (reexports), [14](#)
- assay, PlySummarizedExperiment, character-method
 - (se), [14](#)
- assay, PlySummarizedExperiment, missing-method
 - (se), [14](#)
- assay, PlySummarizedExperiment, numeric-method
 - (se), [14](#)
- assay<- (reexports), [14](#)
- assay<-, PlySummarizedExperiment, character-method
 - (se), [14](#)
- assay<-, PlySummarizedExperiment, missing-method
 - (se), [14](#)
- assay<-, PlySummarizedExperiment, numeric-method
 - (se), [14](#)
- assay_ctx (plyxp-context), [12](#)
- assays, [14](#)
- assays (reexports), [14](#)
- assays, PlySummarizedExperiment-method
 - (se), [14](#)
- assays<- (reexports), [14](#)
- assays<-, PlySummarizedExperiment, list-method
 - (se), [14](#)
- assays<-, PlySummarizedExperiment, SimpleList-method
 - (se), [14](#)
- class_DF (vectors), [23](#)
- class_s4_vctr (vectors), [23](#)
- class_vctr (vectors), [23](#)
- col_ctx (plyxp-context), [12](#)
- colData, [14](#)
- colData (reexports), [14](#)
- colData, PlySummarizedExperiment-method
 - (se), [14](#)
- colData<- (reexports), [14](#)
- colData<-, PlySummarizedExperiment, DataFrame-method
 - (se), [14](#)
- colData<-, PlySummarizedExperiment, NULL-method
 - (se), [14](#)
- cols (plyxp-context), [12](#)
- contextual expressions, [7](#)
- desc(), [3](#)
- dot-pronouns, [5](#)
- dplyr::group_vars(), [8](#)
- dplyr::pull, [13](#)
- eval_select, [17](#)
- filter, [6](#)
- filter(), [14](#)
- group_by, [7](#)
- group_by(), [14](#)
- group_data, [8](#)
- group_data(), [14](#)
- group_vars, [8](#)
- group_vars(), [14](#)
- metadata, [14](#)
- metadata (reexports), [14](#)
- metadata<- (reexports), [14](#)

- mutate, [9](#)
- mutate(), [14](#)
- new_plyxp, [10](#)
- pillar, [24](#)
- pillar_shaft, [25](#)
- PlySummarizedExperiment (new_plyxp), [10](#)
- PlySummarizedExperiment-class
 - (new_plyxp), [10](#)
- PlySummarizedExperiment-methods, [14](#)
- PlySummarizedExperiment-methods (se), [14](#)
- plyxp, [11](#)
- plyxp-context, [12](#)
- plyxp-package, [2](#)
- plyxp-printing (vec_phantom), [24](#)
- plyxp_on (plyxp), [11](#)
- plyxp_pillar_format (vec_phantom), [24](#)
- pull, [13](#)
- pull(), [14](#)
- recycled, [22](#)
- reexports, [14](#)
- row_ctx (plyxp-context), [12](#)
- rowData, [14](#)
- rowData (reexports), [14](#)
- rowData, PlySummarizedExperiment-method
 - (se), [14](#)
- rowData<- (reexports), [14](#)
- rowData<- , PlySummarizedExperiment-method
 - (se), [14](#)
- rows (plyxp-context), [12](#)
- se, [14](#)
- se, PlySummarizedExperiment-method (se),
 - [14](#)
- se<- (se), [14](#)
- se<- , PlySummarizedExperiment-method
 - (se), [14](#)
- se_simple, [18](#)
- select, [17](#)
- select(), [14](#)
- show_tidy (vec_phantom), [24](#)
- showAsCell(), [24](#)
- summarise (summarize), [19](#)
- summarize, [19](#)
- summarize(), [14](#)
- SummarizedExperiment, [14](#)
- SummarizedExperiment (reexports), [14](#)
- ungroup (group_data), [8](#)
- ungroup(), [14](#)
- ungroup.PlySummarizedExperiment
 - (group_by), [7](#)
- use_show_default (vec_phantom), [24](#)
- use_show_tidy (vec_phantom), [24](#)
- vctrs, [24](#)
- vctrs-vec_recycle, [20](#)
- vctrs-vec_rep, [21](#)
- vctrs::vec_recycle, [20](#)
- vctrs::vec_rep, [21](#)
- vctrs::vec_rep_each, [21](#)
- vctrs_slice, [22](#)
- vec_phantom, [24](#)
- vec_recycle (vctrs-vec_recycle), [20](#)
- vec_recycle(), [24](#)
- vec_rep (vctrs-vec_rep), [21](#)
- vec_rep(), [24](#)
- vec_rep_each (vctrs-vec_rep), [21](#)
- vec_slice (vctrs_slice), [22](#)
- vec_slice(), [24](#)
- vectors, [23](#)
- where(), [17](#)