

# Package ‘plyxp’

November 20, 2024

**Title** Data masks for SummarizedExperiment enabling dplyr-like manipulation

**Version** 1.0.0

**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\_20

**git\_last\_commit** d8f67d5

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2024-11-19

**Author** Justin Landis [aut, cre] (<<https://orcid.org/0000-0001-5501-4934>>),  
Michael Love [aut] (<<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 . . . . .	4
filter . . . . .	5
group_by . . . . .	6
group_data . . . . .	7
group_vars . . . . .	8
mutate . . . . .	8
new_plyxp . . . . .	9
plyxp . . . . .	10
plyxp-context . . . . .	10
pull . . . . .	11
reexports . . . . .	12
se . . . . .	13
select . . . . .	15
se_simple . . . . .	16
summarize . . . . .	17
vttrs-vec_recycle . . . . .	18
vttrs-vec_rep . . . . .	19
vttrs_slice . . . . .	20
vectors . . . . .	21
vec_phantom . . . . .	22
<b>Index</b>	<b>24</b>

---

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	<i>create data.frame</i>
---------------	--------------------------

---

### 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

*filter PlySummarizedExperiment*


---

**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**

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

`...` conditions to filter on. These must be wrapped in `cols()` and or `rows()`

`.preserve` Relevant when the `.data` input is grouped. If `.preserve = FALSE` (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
	<b>S4 Compatibility:</b> 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.
...	<a href="#">contextual expressions</a> 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

*get grouping data*

---

**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 execution 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	<i>Mutate a PlySummarizedExperiment object</i>
--------	------------------------------------------------

---

### 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, ...)
```

### Arguments

.data	a PlySummarizedExperiment object
.f	a function that returns a SummarizedExperiment object
...	additional arguments passed to .f

### Value

a PlySummarizedExperiment object

### Examples

```
plyxp(se_simple, function(x) x)
```

---

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**

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

`var` A variable as specified by `dplyr::pull`

`name` ignored argument. Due to the range of data types a `PlySummarizedExperiment` this argument is not supported

`...` 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

*Objects exported from other packages***Description**

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

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

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

**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)
```

**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

x	PlySummarizedExperiment object
value	replacement value
withDimnames	logical
...	additional arguments
i	character or numeric index
use.names	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          select assays, rowData, and colData names
```

---

## 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 `across()`, 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>&lt;tidy-select&gt;</code> one or more selection expressions. Supports wrapping expressions within the <code>&lt;plyxp-contexts&gt;</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

*Summarize PlySummarizedExperiment*


---

**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 rowData() or colData() is retained after summarizing. When "auto" (the default), .retain behavior depends on the groupings of .data. 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 rowData() and colData()

**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      *Recycle a vector*

---

## 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: <ul style="list-style-type: none"> <li>For <code>vec_recycle_common()</code>, vectors to recycle.</li> <li>For <code>vec_recycle()</code>, these dots should be empty.</li> </ul>
<code>x_arg</code>	Argument name for <code>x</code> . These are used in error messages to inform the user about which argument has an incompatible size.
<code>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 <code>abort()</code> for more information.

## Value

a S3 or S4 vector

## Examples

```
vec_recycle(1L, size = 5L)
vec_recycle(S4Vectors::R1e(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 <a href="#">recycled</a> 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 <code>abort()</code> 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 subsetted 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 <a href="#">pillar_shaft</a>

**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. In order to use a tibble abstraction, 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))
  }
}
```

```
  }
  pillar::pillar_shaft(phantom)
  rm(plyxp_pillar_format.CompressedIntegerList)
}

# default printing
se_simple
# use `plyxp` tibble abstraction
use_show_tidy()
se_simple
# restore default print
use_show_default()
se_simple
# explicitly using tibble abstraction
show_tidy(se_simple)
```

# Index

- \* **datasets**
  - dot-pronouns, 4
  - se\_simple, 16
  - vectors, 21
- \* **internal**
  - plyxp-package, 2
  - reexports, 12
- .assays (dot-pronouns), 4
- .assays\_asis (dot-pronouns), 4
- .cols (dot-pronouns), 4
- .cols\_asis (dot-pronouns), 4
- .rows (dot-pronouns), 4
- .rows\_asis (dot-pronouns), 4
  
- abort(), 18, 19
- arrange, 3
- arrange(), 12
- as.data.frame, 4
- assay, 12
- assay (reexports), 12
- assay, PlySummarizedExperiment, character-method (se), 13
- assay, PlySummarizedExperiment, missing-method (se), 13
- assay, PlySummarizedExperiment, numeric-method (se), 13
- assay<- (reexports), 12
- assay<-, PlySummarizedExperiment, character-method (se), 13
- assay<-, PlySummarizedExperiment, missing-method (se), 13
- assay<-, PlySummarizedExperiment, numeric-method (se), 13
- assay\_ctx (plyxp-context), 10
- assays, 12
- assays (reexports), 12
- assays, PlySummarizedExperiment-method (se), 13
- assays<- (reexports), 12
- assays<-, PlySummarizedExperiment, list-method (se), 13
- assays<-, PlySummarizedExperiment, SimpleList-method (se), 13
  
- class\_DF (vectors), 21
- class\_s4\_vctrs (vectors), 21
- class\_vctrs (vectors), 21
- col\_ctx (plyxp-context), 10
- colData, 12
- colData (reexports), 12
- colData, PlySummarizedExperiment-method (se), 13
- colData<- (reexports), 12
- colData<-, PlySummarizedExperiment, DataFrame-method (se), 13
- colData<-, PlySummarizedExperiment, NULL-method (se), 13
- cols (plyxp-context), 10
- contextual expressions, 7
  
- desc(), 3
- dot-pronouns, 4
- dplyr::group\_vars(), 8
- dplyr::pull, 11
  
- eval\_select, 15
  
- filter, 5
- filter(), 12
  
- group\_by, 6
- group\_by(), 12
- group\_data, 7
- group\_data(), 12
- group\_vars, 8
- group\_vars(), 12
  
- metadata, 12
- metadata (reexports), 12
- metadata<- (reexports), 12
- mutate, 8
- mutate(), 12
  
- new\_plyxp, 9
  
- pillar, 22
- pillar\_shaft, 22
- PlySummarizedExperiment (new\_plyxp), 9



- PlySummarizedExperiment-class
  - (new\_plyxp), 9
- PlySummarizedExperiment-methods, 12
- PlySummarizedExperiment-methods (se), 13
- plyxp, 10
- plyxp-context, 10
- plyxp-package, 2
- plyxp-printing (vec\_phantom), 22
- plyxp\_pillar\_format (vec\_phantom), 22
- pull, 11
- pull(), 12
  
- recycled, 19
- reexports, 12
- row\_ctx (plyxp-context), 10
- rowData, 12
- rowData (reexports), 12
- rowData, PlySummarizedExperiment-method
  - (se), 13
- rowData<- (reexports), 12
- rowData<-, PlySummarizedExperiment-method
  - (se), 13
- rows (plyxp-context), 10
  
- se, 13
- se, PlySummarizedExperiment-method (se),
  - 13
- se<- (se), 13
- se<-, PlySummarizedExperiment-method
  - (se), 13
- se\_simple, 16
- select, 15
- select(), 12
- show\_tidy (vec\_phantom), 22
- showAsCell(), 22
- summarise (summarize), 17
- summarize, 17
- summarize(), 12
- SummarizedExperiment, 12
- SummarizedExperiment (reexports), 12
  
- ungroup (group\_data), 7
- ungroup(), 12
- ungroup.PlySummarizedExperiment
  - (group\_by), 6
- use\_show\_default (vec\_phantom), 22
- use\_show\_tidy (vec\_phantom), 22
  
- vctrs, 22
- vctrs-vec\_recycle, 18
- vctrs-vec\_rep, 19
- vctrs::vec\_recycle, 18
- vctrs::vec\_rep, 19
  
- vctrs::vec\_rep\_each, 19
- vctrs\_slice, 20
- vec\_phantom, 22
- vec\_recycle (vctrs-vec\_recycle), 18
- vec\_recycle(), 21
- vec\_rep (vctrs-vec\_rep), 19
- vec\_rep(), 21
- vec\_rep\_each (vctrs-vec\_rep), 19
- vec\_slice (vctrs\_slice), 20
- vec\_slice(), 21
- vectors, 21
  
- where(), 15