Package 'plyxp'

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Title Data masks for SummarizedExperiment enabling dplyr-like manipulation

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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.

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`plyxp-package` *plyxp: Data masks for SummarizedExperiment enabling dplyr-like manipulation*

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

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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 guarentee 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` *contextual plyxp pronouns*

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 **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` *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_split` *Split a PlySummarizedExperiment based on groups*

Description

Splits a grouped PlySummarizedExperiment based on groups. Note the elements of the return value are ungrouped PlySummarizedExperiment objects.

Usage

```
## S3 method for class 'PlySummarizedExperiment'
group_split(.tbl, ..., .keep = TRUE)
```

Arguments

`.tbl`	a PlySummarizedExperiment object
`...`	ignored if the `.tbl` is grouped, otherwise it is passed to group_by.
`.keep`	logical indicating of grouping variables should be kept

Value

A list of PlySummarizedExperiment objects

Examples

```
gse <- group_by(se_simple, rows(direction), cols(condition))
gse |> group_split()
gse |> group_split(.keep = FALSE)
```

---

group_vars *get PlySummarizedExperiment grouping Variables*

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)
```

---

list_unchop *unchop a list of objects*

Description

A generic version of vctrs::list_unchop meant to support S4 Vectors.

Usage

```
list_unchop(x, ptype = NULL, ..., indices = NULL)
```

Arguments

x	a list
ptype	the expected prototype of the output
...	unused arguments
indices	optional list of integer vectors whose size is equal to that of x. This maps the the final index of each element in the output.

Value

an object of type ptype or the common ptype of elements of x.

---

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

.data	a PlySummarizedExperiment object
.f	within plyxp(): a function that returns a SummarizedExperiment object. within plyxp_on(): .f should return a value compatible with .on(se)<-
...	additional arguments passed to .f
.caller	environment in which plyxp should signal an error if one occurs.
.on	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 *extract data from object*

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() group_split()

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 *PlySummarizedExperiment Methods*

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 'SummarizedExperiment'
se(x)

## S4 replacement method for signature 'SummarizedExperiment'
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

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

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

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

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

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

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

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

## S4 replacement method for signature 'PlySummarizedExperiment,list'
dimnames(x) <- value

## S4 replacement method for signature 'PlySummarizedExperiment,NULL'
dimnames(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
- `se(SummarizedExperiment)`: get the SummarizedExperiment object
- `se(SummarizedExperiment) <- value`: get the SummarizedExperiment object
- `assays(PlySummarizedExperiment)`: get the assays o 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 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 potentionally 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

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

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 avialble, 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)
```

slice *Slice a PlySummarizedExperiment*

Description

`slice()` selects rows and/or columns by position.

Usage

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

Arguments

`.data`	a PlySummarizedExperiment object
`...`	expressions that resolve to integer values to slice, .data by. Note that only the `rows()` and `cols()` contexts are available here.
`.preserve`	Logical value. When FALSE, the default, group combinations are recomputed based on the resulting data. When TRUE, group combinations are retained, despite any groups being empty.

Examples

```
gse <- group_by(se_simple, rows(direction), cols(condition))
sgse <- slice(gse, rows(which(direction == "-")))
group_data(gse)
group_data(sgse)
sgse2 <- slice(gse, rows(which(direction == "-")), .preserve = TRUE)
group_data(sgse2)
```

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

.data	An object Inheriting from PlySummarizedExperiment, the wrapper class for SummarizedExperiment objects
...	expressions to summarize the object
.retain	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_chop *chop a vector*

Description

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

Usage

```
vec_chop(x, ..., indices = NULL)
```

Arguments

x	A vector
...	These dots are for future extensions and must be empty.
indices	For vec_chop(), a list of positive integer vectors to slice x with, or NULL. Can't be used if sizes is already specified. If both indices and sizes are NULL, x is split into its individual elements, equivalent to using an indices of as.list(vec_seq_along(x)). For list_unchop(), a list of positive integer vectors specifying the locations to place elements of x in. Each element of x is recycled to the size of the corresponding index vector. The size of indices must match the size of x. If NULL, x is combined in the order it is provided in, which is equivalent to using vec_c().

Value

a S3 or S4 vector

Examples

```
vec_chop(1L)
vec_chop(S4Vectors::Rle(c(rep(1, 3), rep(4, 5))), indices = list(c(2, 3, 4), c(1, 5:8)))
```

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

x	A vector to recycle.
size	Desired output size.
...	Depending on the function used: • For vec_recycle_common(), 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 *replicate a vector*

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

x	A vector.
times	For vec_rep(), a single integer for the number of times to repeat the entire vector. For vec_rep_each(), an integer vector of the number of times to repeat each element of x. times will be recycled to the size of x.
...	These dots are for future extensions and must be empty.
error_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.
x_arg, times_arg	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@mcol 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()`

Examples

```
# used for defining methods on S7 generics

S7::method(vec_slice, class_s4_vctrs)
```

---

vec_group_id *Create Group Indices*

Description

A alternative to `vctrs::vec_group_id` and `vctrs::vec_group_loc` as an S4 generic function to allow `S4Vectors`.

Usage

```
vec_group_id(x, ...)

vec_group_loc(x, ...)
```

Arguments

x	a vctrs vector or an S4Vector
...	unsued arguments

Value

either a tibble or DataFrame object

Examples

```
data <- S4Vectors::DataFrame(
  letter = sample(letters, 500, TRUE),
  LETTER = sample(letters, 500, TRUE)
)

vec_group_id(data)
vec_group_loc(data)
```

---

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 phatomData 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)
```

`vec_ptype2` *Create a common prototype of two vectors*

Description

given two objects, `vec_ptype2()` finds a common prototype

Usage

```
vec_ptype2(x, y, ...)
```

Arguments

`x`	first object
`y`	second object
`...`	unused arguments

Value

an object of size 0.

vec_ptype_common *find the common ptype*

Description

find the common ptype

Usage

```
vec_ptype_common(..., .ptype = NULL)
```

Arguments

...	<dynamic-dots> a collection of objects
.ptype	the expected prototype

Value

an object of size 0.

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