

Package ‘BiocSet’

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Title Representing Different Biological Sets

Version 1.20.0

Description BiocSet displays different biological sets in a triple tibble format. These three tibbles are `element`, `set`, and `elementset`. The user has the ability to activate one of these three tibbles to perform common functions from the dplyr package. Mapping functionality and accessing web references for elements/sets are also available in BiocSet.

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Author Kayla Morrell [aut, cre],
Martin Morgan [aut],
Kevin Rue-Albrecht [ctb],
Lluís Revilla Sancho [ctb]

Maintainer Kayla Morrell <kayla.morrell16@gmail.com>

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BiocSet

BiocSet class

Description

character()

The BiocSet constructor, the show method, the slot accessors, and creating a BiocSet object from an element set tibble rather than character vector(s).

Usage

```
BiocSet(..., metadata = list(), active = c("elementset", "element", "set"))
```

```
## S4 method for signature 'BiocSet'
show(object)
```

```
es_element(x)
```

```
## S4 method for signature 'BiocSet'
es_element(x)
```

```
es_set(x)
```

```
## S4 method for signature 'BiocSet'
es_set(x)
```

```
es_elementset(x)
```

```
## S4 method for signature 'BiocSet'
es_elementset(x)
```

```
BiocSet_from_elementset(elementset, element, set, metadata)
```

Arguments

| | |
|------------|---|
| ... | Named character() vectors of element sets, or a named list of character() vectors. Each character vector is an element set. The names of the character vectors are the names of the sets. |
| metadata | A list() with arbitrary content, describing the set. |
| active | A character(1) to indicate which tibble is active. The default is "elementset". |
| object | A BiocSet object. |
| x | A BiocSet object. |
| elementset | A tibble with element set information. |
| element | A tibble with element information. |
| set | A tibble with set information. |

Value

An S4 BiocSet object shown as a tripple tibble, where each slot is a tibble.

Slots

| | |
|------------|---|
| element | The element tibble from 'tbl_elementset' |
| set | The set tibble from 'tbl_elementset' |
| elementset | The elementset tibble created from user input |
| active | A character(1), indicates which tibble is active |
| metadata | A list() with arbitrary elements describing the set |

Examples

```
BiocSet(set1 = letters, set2 = LETTERS)
lst <- list(set1 = letters, set2 = LETTERS)
BiocSet(lst)

set.seed(123)
element <-
  tibble(
    element = letters[1:10],
    v1 = sample(10),
    v2 = sample(10)
  )
set <-
  tibble(
    set = LETTERS[1:2],
    v1 = sample(2),
    v2 = sample(2)
  )
elementset <-
  tibble(
    element = letters[1:10],
    set = sample(LETTERS[1:2], 10, TRUE)
  )
BiocSet_from_elementset(elementset, element, set)
```

Description

`es_activate`: which of the three tibbles in the `BiocSet` object should be activated and have the chosen functionality applied to it.

`filter`: choose rows where conditions are true.

`select`: keep only the variables listed.

`mutate`: add new variable and preserve the existing variables.

`summarise`: usually used with `group_by()`, output will have one row for each group.

`arrange`: order rows by an expression involving its variables.

`.tbl_nongroup_vars`: returns only non-grouping variables.

`group_by`: converts an existing tibble into a grouped tibble.

`left_join`: returns all rows from `x`, and all columns from `x` and `y`. If no rows in `x` match with `y` there will be NAs in the new column. If there are multiple matches then all combinations are returned.

`as.list`: coerces argument into a list.

`union`: combines all rows from two `BiocSet` objects and removes duplicate records from the combined `BiocSet` object.

`intersect`: combines all rows from two `BiocSet` objects and returns rows that appear in both `BiocSet` objects.

Usage

```
es_activate(.data, what)

## S3 method for class 'BiocSet'
filter(.data, ...)

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

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

## S3 method for class 'BiocSet'
summarise(.data, ...)

## S3 method for class 'BiocSet'
arrange(.data, ...)

.tbl_nongroup_vars.BiocSet(x)

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

```
## S3 method for class 'BiocSet'
left_join(x, y, by, copy, suffix, ...)

## S3 method for class 'BiocSet'
as.list(x, ...)

## S3 method for class 'BiocSet'
union(x, y, ...)

## S3 method for class 'BiocSet'
intersect(x, y, ...)
```

Arguments

| | |
|---------------------|--|
| <code>.data</code> | The BiocSet object. |
| <code>what</code> | Which of the three tibbles from BiocSet to activate. |
| <code>...</code> | Additional arguments passed to function. |
| <code>x</code> | For <code>.tbl_nongroup_vars</code> (internal), a BiocSet object. For <code>union</code> and <code>intersect</code> the first BiocSet object to perform the operations on. |
| <code>add</code> | logical, whether to add to the existing groups. |
| <code>y</code> | For <code>left_join</code> , a tibble to join. For <code>union</code> and <code>intersect</code> the second BiocSet object used. |
| <code>by</code> | A character vector of variables to join by. |
| <code>copy</code> | logical, allows you to join tables across srcs. |
| <code>suffix</code> | Character vector of length 2, if there are non-joined duplicate variables in 'x' and 'y' these suffixes will be added to the output. |

Value

A BiocSet object.

Examples

```
es <- BiocSet(set1 = letters, set2 = LETTERS)
es_activate(es, element)

es %>% es_activate(element) %>% filter(element == "a")

es %>% select(element)

es %>% es_activate(set) %>% mutate(pval = rnorm(1:2))

es %>% es_activate(set) %>% summarise(n = n())

es %>% es_activate(element) %>% arrange(desc(element))

es %>% mutate(pval = rnorm(1:52)) %>% es_elementset() %>%
  BiocSet:::tbl_nongroup_vars()

es %>% group_by(element, set)

es <- BiocSet(set1 = letters[1:5], set2 = LETTERS[1:5])
```

```
tbl <- tibble(x = 1:10, y = c(letters[1:5], LETTERS[1:5]))
es %>% left_join(tbl, by = c(element = "y"))

library(org.Hs.eg.db)
es <- go_sets(org.Hs.eg.db, "ENSEMBL")
head(as.list(es))

es1 <- BiocSet(set1 = letters[c(1:4)], set2 = LETTERS[c(1:4)])
es2 <- BiocSet(set1 = letters[c(3:8)], set2 = LETTERS[c(3:8)])

dplyr::union(es1, es2)

dplyr::intersect(es1, es2)
```

| | |
|--------|------------------------------|
| coerce | <i>as("BiocSet", "list")</i> |
|--------|------------------------------|

Description

as("BiocSet", "list")

| | |
|-----------------|---|
| elementset_funs | <i>Functions applied to elementsets in a BiocSet object</i> |
|-----------------|---|

Description

All of the major methods applied to a BiocSet object can be explicitly applied to the elementset tibble. These functions bypass the need to use the `es_activate` function by indicating what function should be used on the elementset tibble.

Usage

```
filter_elementset(.data, ...)

select_elementset(.data, ...)

mutate_elementset(.data, ...)

summarise_elementset(.data, ...)

arrange_elementset(.data, ...)

left_join_elementset(.data, ...)

tibble_from_elementset(.data)

data.frame_from_elementset(.data)
```

Arguments

| | |
|--------------------|--|
| <code>.data</code> | A BiocSet object. |
| <code>...</code> | Additional arguments passed to the function. |

Value

A BiocSet object.

For `tibble_from_elementset`, a tibble.

For `data.frame_from_elementset`, a `data.frame`.

Examples

```
es <- BiocSet(set1 = letters, set2 = LETTERS)
filter_elementset(es, element == "a" | element == "A")

es %>% select_elementset(element)

es %>% mutate_elementset(pval = rnorm(1:52))

es %>% summarise_elementset(n = n())

es %>% arrange_elementset(desc(element))

tbl <- tibble(x = 5:6, y = c("set1", "set2"))
es %>% left_join_elementset(tbl, by = c(set = "y"))

tibble_from_elementset(es)

data.frame_from_elementset(es)
```

element_funs

Functions applied to elements in a BiocSet object

Description

All of the major methods applied to a BiocSet object can be explicitly applied to the element tibble. These functions bypass the need to use the `es_activate` function by indicating what function should be used on the element tibble.

Usage

```
filter_element(.data, ...)

select_element(.data, ...)

mutate_element(.data, ...)

summarise_element(.data, ...)

arrange_element(.data, ...)

left_join_element(.data, ...)

tibble_from_element(.data, how = unlist)

data.frame_from_element(.data, how = unlist)
```

Arguments

| | |
|--------------------|--|
| <code>.data</code> | A BiocSet object. |
| <code>...</code> | Additional arguments passed to the function. |
| <code>how</code> | Multiple entries will become a list. |

Value

A BiocSet object.
 For `tibble_from_element`, a tibble.
 For `data.frame_from_element`, a data.frame.

Examples

```
es <- BiocSet(set1 = letters, set2 = LETTERS)
filter_element(es, element == "a")

es %>% select_element(element)

es %>% mutate_element(pval = rnorm(1:52))

es %>% summarise_element(n = n())

es %>% arrange_element(desc(element))

tbl <- tibble(x = 1:5, y = letters[1:5])
es <- BiocSet(set1 = letters[c(1,3,5)], set2 = letters[c(2,4)])
left_join_element(es, tbl, by = c(element = "y"))

tibble_from_element(es)

data.frame_from_element(es)
```

| | |
|-------------------|--------------------------|
| genesetcollection | <i>GeneSetCollection</i> |
|-------------------|--------------------------|

Description

The following functions deal with converting a BiocSet object into a GeneSetCollection object, or vice versa.

Usage

```
GeneSetCollection_from_BiocSet(biocset)

BiocSet_from_GeneSetCollection(gsc)
```

Arguments

| | |
|----------------------|---|
| <code>biocset</code> | The BiocSet object that will become a GeneSetCollection object. |
| <code>gsc</code> | The GeneSetCollection that will become a BiocSet object. |

Value

For 'GeneSetCollection_from_BiocSet()', a GeneSetCollection.

For 'BiocSet_from_GeneSetCollection()', a BiocSet object.

Examples

```
biocset <- BiocSet(set1 = letters, set2 = LETTERS)
gsc <- GeneSetCollection_from_BiocSet(biocset)
gsc

BiocSet_from_GeneSetCollection(gsc)
```

| | |
|--------|----------------------------|
| import | <i>Importing/exporting</i> |
|--------|----------------------------|

Description

Importing/exporting and formatting of element sets as a BiocSet object.

Usage

```
## S4 method for signature 'GMTFile,ANY,ANY'
import(con, format, text, ...)
```

```
## S4 method for signature 'BiocSet,GMTFile,ANY'
export(object, con, format, ...)
```

```
## S4 method for signature 'OBOFile,ANY,ANY'
import(con, format, text, ...)
```

```
## S4 method for signature 'BiocSet,OBOFile,ANY'
export(object, con, format, ...)
```

Arguments

| | |
|--------|--|
| con | For import, the file name or URL the element set is loaded from. For export, the file name or URL the element set is written to. |
| format | For import, the format of the input. For export, the format of the output. |
| text | If con is missing this is a character vector directly providing the element set that should be imported. |
| ... | Parameters to pass to the format-specific method |
| object | For 'export()', the object to be exported. |

Value

For 'import()', a BiocSet object

For 'export()', a GMTFile object representing the location where the BiocSet object was written to

Examples

```
gmtFile <- system.file(package = "BiocSet", "extdata",
  "hallmark.gene.symbol.gmt")
tbl <- import(gmtFile)

tbl2 <- BiocSet(set1 = letters, set2 = LETTERS)
fl <- tempfile(fileext = ".gmt")
gmt <- export(tbl2, fl)

oboFile <- system.file(package = "BiocSet", "extdata", "sample_go.obo")
tst_obo <- import(oboFile)
fl <- system.file("extdata", "sample_go.obo", package = "BiocSet")
tbl <- import(fl)
new_fl <- tempfile(fileext = ".obo")
obo <- export(tbl, new_fl)
```

intersect_single *Intersect on a single BiocSet object*

Description

This function performs an intersection within a single BiocSet object.

Usage

```
intersect_single(x, ...)
```

Arguments

| | |
|-----|--|
| x | A BiocSet object. |
| ... | Additional arguments passed to function. |

Value

A BiocSet object with a single set 'intersect' and intersected elements from x.

Examples

```
es1 <- BiocSet(set1 = letters[c(1:10)], set2 = letters[c(4:20)])
intersect_single(es1)
```

| | |
|-----------------|---|
| mapping_element | <i>Functions for mapping elements in the element tibble to different id types</i> |
|-----------------|---|

Description

Functions for dealing with unique mapping and multiple mapping. `map_add_element` will add the mapping as a new column instead of overwriting the current one used for the mapping.

Usage

```
map_unique(es, org, from, to)

map_multiple(
  es,
  org,
  from,
  to,
  multi = c("list", "filter", "asNA", "CharacterList")
)

map_add_element(es, org, from, add)
```

Arguments

| | |
|--------------------|---|
| <code>es</code> | The BiocSet object to map the elements on. |
| <code>org</code> | The AnnotationDbi object to identify keys/mappings from. |
| <code>from</code> | A character to indicate which identifier to map from. |
| <code>to</code> | A character to indicate which identifier to map to. |
| <code>multi</code> | How should multiple values be returned? Options include: <ul style="list-style-type: none"> • <code>list</code>: This will just return a list object to the end user. • <code>filter</code>: This will remove all elements that contain multiple matches and will therefore return a shorter vector than what came in whenever some of the keys match more than one value. • <code>asNA</code>: This will return an NA value whenever there are multiple matches. • <code>CharacterList</code>: This just returns a SimpleCharacterList object. • <code>FUN</code>: A function can be supplied to the 'multiVals' argument for custom behaviors. |
| <code>add</code> | The id to add to the BiocSet object. |

Value

For `map_unique`, a BiocSet object with unique elements.

For `map_multiple`, a BiocSet object with multiple mappings for certain elements.

For `map_add_element`, a BiocSet object with a new column in the element tibble with the mapping of the new id type.

Examples

```
library(org.Hs.eg.db)
es <- BiocSet(set1 = c("C5", "GANC"), set2 = c("AFM", "CGB1", "ADAM32"))
map_unique(es, org.Hs.eg.db, "SYMBOL", "ENTREZID")

map_multiple(es, org.Hs.eg.db, "SYMBOL", "ENSEMBLTRANS", "asNA")

map <- map_add_element(es, org.Hs.eg.db, "SYMBOL", "ENTREZID")
es %>% mutate_element(entrez = map)
```

mapping_set

*Functions for mapping sets in the set tibble to different id types***Description**

Functions for creating BiocSet objects from GO sets and KEGG sets, and creating a new set mapping from a current BiocSet object. `map_add_set` will add the mapping as a new column instead of overwriting the current one used for the mapping.

Usage

```
go_sets(org, from, go = c("GO", "GOID"), evidence = NULL, ontology = NULL)

kegg_sets(species)

map_set(.data, from, to)

map_add_set(.data, org, from, add)
```

Arguments

| | |
|-----------------------|---|
| <code>org</code> | The AnnotationDbi object to identify keys/mappings from. |
| <code>from</code> | A character to indicate which identifier to map from. |
| <code>go</code> | A character to indicate the column name for the GO ids. Default is "GO". |
| <code>evidence</code> | A character to indicate the evidence codes for GO associations with a gene of interest. Default is all possible evidence codes. |
| <code>ontology</code> | A character to indicate which Gene Ontology to use. Default is BP, CC, and MF. |
| <code>species</code> | Which species the pathways are from. |
| <code>.data</code> | The BiocSet object that contains the set tibble being mapped. |
| <code>to</code> | A character to indicate which identifier to map to. |
| <code>add</code> | The id to add to the BiocSet object. |

Value

For `go_sets`, a BiocSet object with GO ids as the set ids.

For `kegg_sets`, a BiocSet object with Entrez IDs reported as elements (default from KEGGREST) and KEGG pathways as sets.

For `map_set`, a BiocSet object with the mapped set present in the set tibble.

For `map_add_set`, a BiocSet object with a new column in the set tibble with the mapping of the new id type.

Examples

```
library(org.Hs.eg.db)
go <- go_sets(org.Hs.eg.db, "ENSEMBL")

kegg_sets("hsa")

es <- BiocSet(set1 = letters, set2 = LETTERS)
es %>% map_set("set1", "foo")

library(GO.db)
map <- map_add_set(go, GO.db, "GOID", "DEFINITION")
go %>% mutate_set(definition = map)
```

OBOSet

OBOSet class

Description

A class representing the 'OBO' file format as a BiocSet.

Usage

```
OBOSet(elementset, element, set, metadata)
```

Arguments

| | |
|------------|--|
| elementset | A tibble with element set information. |
| element | A tibble with element information. |
| set | A tibble with set information. |
| metadata | A tibble with key-value pairs describing OBO file format header data |

Value

An S4 OBOSet object. OBO sets conform to the 'obo' file format, with OBO 'Term' entries corresponding to elements. Parent / child relationships (e.g., 'is_a') are summarized as 'parents', 'ancestors', and 'children' character list columns of 'set'.

Examples

```
OBOSet()
oboFile <- system.file(package = "BiocSet", "extdata", "sample_go.obo")
import(oboFile)
```

`obo_relations`*Functions to display relationships of an OBOSet object*

Description

These functions will display the relationships (children, parents, or ancestors) for either the elements or the sets of an OBOSet object.

Usage

```
oboset_element_children(oboset)
oboset_element_parents(oboset)
oboset_element_ancestors(oboset)
oboset_set_children(oboset)
oboset_set_parents(oboset)
oboset_set_ancestors(oboset)
```

Arguments

`oboset` The OBOSet of interest.

Value

A 2 column tibble.

Examples

```
oboFile <- system.file("extdata", "sample_go.obo", package = "BiocSet")
obo <- import(oboFile)
oboset_element_children(obo)

oboset_element_parents(obo)

oboset_element_ancestors(obo)

oboset_set_children(obo)

oboset_set_parents(obo)

oboset_set_ancestors(obo)
```

Description

All of the major methods applied to a BiocSet object can be explicitly applied to the set tibble. These functions bypass the need to use the `es_activate` function by indicating what function should be used on the element tibble.

Usage

```
filter_set(.data, ...)  
select_set(.data, ...)  
mutate_set(.data, ...)  
summarise_set(.data, ...)  
arrange_set(.data, ...)  
left_join_set(.data, ...)  
tibble_from_set(.data, how = unlist)  
data.frame_from_set(.data, how = unlist)
```

Arguments

| | |
|--------------------|---|
| <code>.data</code> | A BiocSet object. |
| <code>...</code> | Additional argument passed to the function. |
| <code>how</code> | Multiple entries will become a list. |

Value

A BiocSet object.
For `tibble_from_set`, a tibble.
For `data.frame_from_set`, a data.frame.

Examples

```
es <- BiocSet(set1 = letters, set2 = LETTERS)  
filter_set(es, set == "set1")  
  
es %>% select_set(set)  
  
es %>% mutate_set(pval = rnorm(1:2))  
  
es %>% summarise_set(n = n())  
  
es %>% arrange_set(desc(set))
```

```
tbl <- tibble(x = 10:11, y = c("set1", "set2"))
es <- BiocSet(set1 = letters[c(1,3,5)], set2 = letters[c(2,4)])
left_join_set(es, tbl, by = c(set = "y"))

tibble_from_set(es)

data.frame_from_set(es)
```

| | |
|-------------|---|
| tbl_element | <i>Element representation as an S3 class tibble</i> |
|-------------|---|

Description

Element representation as an S3 class tibble

Usage

```
.tbl_element(tbl_elementset)
```

Arguments

tbl_elementset An S3 elementset tibble.

Value

An S3 element object in a tibble representation.

Examples

```
tbl <- BiocSet:::tbl_elementset(set1 = letters, set2 = LETTERS)
BiocSet:::tbl_element(tbl)
```

| | |
|----------------|---|
| tbl_elementset | <i>Element set representation as an S3 class tibble</i> |
|----------------|---|

Description

Element set representation as an S3 class tibble

Usage

```
.tbl_elementset(...)

.is_tbl_elementset(x)
```

Arguments

... For `tbl_elementset`, named character vectors of gene sets. Each character vector is a element set. The name of the character vector is the name of the element set.

x A tibble that may or may not be an elementset

Value

For `tbl_elementset`, an S3 elementset object in a tibble representation.

For `.is_tbl_elementset` (internal), a logical indicating if the tibble is an elementset.

Examples

```
es <- BiocSet:::tbl_elementset(set1 = letters, set2 = LETTERS)
BiocSet:::is_tbl_elementset(es)
```

| | |
|--------|---|
| tblset | <i>Set representation as an S3 class tibble</i> |
|--------|---|

Description

Set representation as an S3 class tibble

Usage

```
.tbl_set(tbl_elementset)
```

Arguments

`tbl_elementset` An S3 elementset tibble.

Value

An S3 set object in a tibble representation.

Examples

```
tbl <- BiocSet:::tbl_elementset(set1 = letters, set2 = LETTERS)
BiocSet:::tbl_set(tbl)
```

| | |
|--------------|---|
| union_single | <i>Union on a single BiocSet object</i> |
|--------------|---|

Description

This function performs a union within a single BiocSet object.

Usage

```
union_single(x, ...)
```

Arguments

`x` A BiocSet object.
`...` Additional arguments passed to function.

Value

For `union_single`, a `BiocSet` object with a single set union and unioned elements from `x`.

Examples

```
es3 <- BiocSet(set1 = letters[c(1:10)], set2 = letters[c(4:20)])
union_single(es3)
```

`url_ref`*Functions to access reference urls for different identifiers*

Description

Functions to access reference urls for different identifiers

Usage

```
url_ref_element(es)
```

```
url_ref_set(es)
```

```
url_ref(es)
```

Arguments

`es` A `BiocSet` object that the reference urls should be added to.

Value

For `url_ref_element`, a `BiocSet` object with the `url` column added to the element tibble.

For `url_ref_set`, a `BiocSet` object with the `url` column added to the set tibble.

For `url_ref`, a `BiocSet` object with the `url` column added to both the element and set tibbles.

Examples

```
es <- BiocSet("GO:0000002" = c("TP53", "TNF"), "GO:0000003" = c("IL6"))
url_ref_element(es)

url_ref_set(es)

url_ref(es)
```

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