Package ‘BiocSet’

April 3, 2024

Title  Representing Different Biological Sets
Version  1.16.1
Description  BiocSet displays different biological sets in a triple tibble format. These three tibbles are `element`, `set`, and `elements`. 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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BiocSet

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)
## S4 method for signature 'BiocSet'

```r
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

```r
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 <-
```r
library(tibble)

# Create a tibble with two sets
set1 <- LETTERS[1:2]
v1 <- sample(2)
v2 <- sample(2)
tibble(set = set1, v1 = v1, v2 = v2)

elementset <-
tibble(element = letters[1:10], set = sample(LETTERS[1:2], 10, TRUE))

BiocSet_from_elementset(elementset, element, set)
```

**BiocSet-methods**

**BiocSet methods**

### 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 tbl into a grouped tbl.
- **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)**

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

  ```r
  # 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

.data The BiocSet object.

what Which of the three tibbles from BiocSet to activate.

... Additional arguments passed to function.

x For .tbl_nongroup_vars (internal), a BiocSet object. For union and intersect the first BiocSet object to perform the operations on.

add logical, whether to add to the existing groups.

y For left_join, a tibble to join. For union and intersect the second BiocSet object used.

by A character vector of variables to join by.

copy logical, allows you to join tables across srcs.

suffix 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

```r
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)
```

```r
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"))
```

```r
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**

as("BiocSet", "list")

---

**Description**

as("BiocSet", "list")

---

**elementset_funs**

*Functions applied to elementsets in a BiocSet object*

---

**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.
elementset_funs

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

.data A BiocSet object.
... 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)
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

```r
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

- `.data` A BiocSet object.
- `...` Additional arguments passed to the function.
- `how` 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

```r
es <- BiocSet(set1 = letters, set2 = LETTERS)  
filter_element(es, element == "a")  
es %>% select_element(element)
```
```r
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 | GeneSetCollection

**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**

- `biocset` The BiocSet object that will become a GeneSetCollection object.
- `gsc` The GeneSetCollection that will become a BiocSet object.

**Value**

For `GeneSetCollection_from_BiocSet()`, a GeneSetCollection.
For `BiocSet_from_GeneSetCollection()`, a BiocSet object.

**Examples**

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

BiocSet_from_GeneSetCollection(gsc)
```
import

Importing/exporting

Description

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

Usage

```r
## 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

```r
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)
```
**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

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

**mapping_element**

Functions for mapping elements in the element tibble to different id types

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

es The BiocSet object to map the elements on.
org The AnnotationDbi object to identify keys/mappings from.
from A character to indicate which identifier to map from.
to A character to indicate which identifier to map to.
multi How should multiple values be returned? Options include:
  • list: This will just return a list object to the end user.
  • filter: 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.
  • asNA: This will return an NA value whenever there are multiple matches.
  • CharacterList: This just returns a SimpleCharacterList object.
  • FUN: A function can be supplied to the 'multiVals' argument for custom behaviors.

add 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

```r
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

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

```r
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**

```r
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**

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

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

Usage

obo_set_element_children(oboset)
obo_set_element_parents(oboset)
obo_set_element_ancestors(oboset)
obo_set_set_children(oboset)
obo_set_set_parents(oboset)
obo_set_set_ancestors(oboset)

Arguments

oboset The OBOSet of interest.

Value

A 2 column tibble.

Examples

oboFile <- system.file("extdata", "sample_go.obo", package = "BiocSet")
oboset <- import(oboFile)
oboset_element_children(oboset)
oboset_element_parents(oboset)
oboset_element_ancestors(oboset)
oboset_set_children(oboset)
oboset_set_parents(oboset)
oboset_set_ancestors(oboset)
set_funs

Functions applied to sets in a BiocSet object

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

.data A BiocSet object.
... Additional argument passed to the function.
how 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)

---

tblelement  

**Element representation as an S3 class tibble**

**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)
```
### tblset

**Description**

Set representation as an S3 class tibble

**Usage**

`.tbl_set(tbl_elementset)`

**Arguments**

- `tbl_elementset` An S3 elementset tibble.
**union_single**

**Value**

An S3 set object in a tibble representation.

**Examples**

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

---

**Description**

This function performs a union within a single BiocSet object.

**Usage**

```r
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**

```r
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**

```r
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

```r
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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