

Package: BiocSet (via r-universe)

May 30, 2026

Title Representing Different Biological Sets

Version 1.26.0

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.

Depends R (>= 3.6), dplyr

Imports methods, tibble, utils, rlang, plyr, S4Vectors, BiocIO, AnnotationDbi, KEGGREST, ontologyIndex, tidyr

Suggests GSEABase, airway, org.Hs.eg.db, DESeq2, limma, BiocFileCache, GO.db, testthat, knitr, rmarkdown, BiocStyle

biocViews GeneExpression, GO, KEGG, Software

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Encoding UTF-8

RoxygenNote 7.2.3

VignetteBuilder knitr

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository <https://bioc-release.r-universe.dev>

Date/Publication 2026-04-28 12:51:26 UTC

RemoteUrl <https://github.com/bioc/BiocSet>

RemoteRef RELEASE_3_23

RemoteSha f83c337e7da7be859f9d146daa227ddff5f7efa

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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)
```

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

```
as("BiocSet", "list")
```

element_funs	<i>Functions applied to elements in a BiocSet object</i>
--------------	--

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)
```

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.

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)
```

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)
```


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)
```

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)
```

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)
```

`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

<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)
```

union_single

Union on a single BiocSet object

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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