Package 'AnnotationFilter'

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Title Facilities for Filtering Bioconductor Annotation Resources

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BugReports https://github.com/Bioconductor/AnnotationFilter/issues

Description This package provides class and other infrastructure to implement filters for manipulating Bioconductor annotation resources. The filters will be used by ensembldb, Organism.dplyr, and other packages.

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`AnnotationFilter` *Filters for annotation objects*

Description

The filters extending the base `AnnotationFilter` class represent a simple filtering concept for annotation resources. Each filter object is thought to filter on a single (database) table column using the provided values and the defined condition.

Filter instances created using the constructor functions (e.g. `GeneIdFilter`).

`supportedFilters()` lists all defined filters. It returns a two column `data.frame` with the filter class name and its default field. Packages using `AnnotationFilter` should implement the `supportedFilters` for their annotation resource object (e.g. for `object = "EnsDb"` in the `ensembldb` package) to list all supported filters for the specific resource.

`condition()` get the `condition` value for the filter `object`.

`value()` get the `value` for the filter `object`.

`field()` get the `field` for the filter `object`.

`not()` get the `not` for the filter `object`.

`feature()` get the `feature` for the `GRangesFilter` `object`.

Converts an `AnnotationFilter` object to a `character(1)` giving an equation that can be used as input to a `dplyr` filter.

`AnnotationFilter` *translates* a filter expression such as `~ gene_id == "BCL2"` into a filter object extending the `AnnotationFilter` class (in the example a `GeneIdFilter` object) or an `AnnotationFilterList` if the expression contains multiple conditions (see examples below). Filter expressions have to be written in the form `~ <field> <condition> <value>`, with `<field>` being the default field of the filter class (use the `supportedFilter` function to list all fields and filter classes), `<condition>` the logical expression and `<value>` the value for the filter.

Usage

```
CdsStartFilter(value, condition = "==", not = FALSE)
CdsEndFilter(value, condition = "==", not = FALSE)
ExonIdFilter(value, condition = "==", not = FALSE)
ExonNameFilter(value, condition = "==", not = FALSE)
ExonRankFilter(value, condition = "==", not = FALSE)
ExonStartFilter(value, condition = "==", not = FALSE)
ExonEndFilter(value, condition = "==", not = FALSE)
GeneIdFilter(value, condition = "==", not = FALSE)
```

```
GeneNameFilter(value, condition = "==", not = FALSE)
GeneBiotypeFilter(value, condition = "==", not = FALSE)
GeneStartFilter(value, condition = "==", not = FALSE)
GeneEndFilter(value, condition = "==", not = FALSE)
EntrezFilter(value, condition = "==", not = FALSE)
SymbolFilter(value, condition = "==", not = FALSE)
TxIdFilter(value, condition = "==", not = FALSE)
TxNameFilter(value, condition = "==", not = FALSE)
TxBiotypeFilter(value, condition = "==", not = FALSE)
TxStartFilter(value, condition = "==", not = FALSE)
TxEndFilter(value, condition = "==", not = FALSE)
ProteinIdFilter(value, condition = "==", not = FALSE)
UniprotFilter(value, condition = "==", not = FALSE)
SeqNameFilter(value, condition = "==", not = FALSE)
SeqStrandFilter(value, condition = "==", not = FALSE)

## S4 method for signature 'AnnotationFilter'
condition(object)

## S4 method for signature 'AnnotationFilter'
value(object)

## S4 method for signature 'AnnotationFilter'
field(object)

## S4 method for signature 'AnnotationFilter'
not(object)

GRangesFilter(value, feature = "gene", type = c("any", "start", "end",
  "within", "equal"))

feature(object)

## S4 method for signature 'AnnotationFilter,missing'
convertFilter(object)

## S4 method for signature 'missing'
supportedFilters(object)

AnnotationFilter(expr)
```

Arguments

object	An AnnotationFilter object.
value	character(), integer(), or GRanges() value for the filter
feature	character(1) defining on what feature the GRangesFilter should be applied. Choices could be "gene", "tx" or "exon".

type	character(1) indicating how overlaps are to be filtered. See findOverlaps in the IRanges package for a description of this argument.
expr	A filter expression, written as a formula, to be converted to an AnnotationFilter or AnnotationFilterList class. See below for examples.
condition	character(1) defining the condition to be used in the filter. For IntegerFilter or DoubleFilter, one of "==", "!=", ">", "<", ">=" or "<=". For CharacterFilter, one of "==", "!=", "startsWith", "endsWith" or "contains". Default condition is "==".
not	logical(1) whether the AnnotationFilter is negated. TRUE indicates is negated (!). FALSE indicates not negated. Default not is FALSE.

Details

By default filters are only available for tables containing the field on which the filter acts (i.e. that contain a column with the name matching the value of the field slot of the object). See the vignette for a description to use filters for databases in which the database table column name differs from the default field of the filter.

Filter expressions for the AnnotationFilter class have to be written as formulas, i.e. starting with a ~.

Value

The constructor function return an object extending AnnotationFilter. For the return value of the other methods see the methods' descriptions.

character(1) that can be used as input to a dplyr filter.

AnnotationFilter returns an AnnotationFilter or an AnnotationFilterList.

Note

Translation of nested filter expressions using the AnnotationFilter function is not yet supported.

See Also

AnnotationFilterList for combining AnnotationFilter objects.

Examples

```
## filter by GRanges
GRangesFilter(GenomicRanges::GRanges("chr10:87869000-87876000"))
## Create a SymbolFilter to filter on a gene's symbol.
sf <- SymbolFilter("BCL2")
sf

## Create a GeneStartFilter to filter based on the genes' chromosomal start
## coordinates
gsf <- GeneStartFilter(10000, condition = ">")
gsf

filter <- SymbolFilter("ADA", "==")
```

```
result <- convertFilter(filter)
result
supportedFilters()

## Convert a filter expression based on a gene ID to a GeneIdFilter
gnf <- AnnotationFilter(~ gene_id == "BCL2")
gnf

## Same conversion but for two gene IDs.
gnf <- AnnotationFilter(~ gene_id %in% c("BCL2", "BCL2L11"))
gnf

## Converting an expression that combines multiple filters. As a result we
## get an AnnotationFilterList containing the corresponding filters.
## Be aware that nesting of expressions/filters does not work.
flt <- AnnotationFilter(~ gene_id %in% c("BCL2", "BCL2L11") &
                        tx_biotype == "nonsense_mediated_decay" |
                        seq_name == "Y")
flt
```

AnnotationFilterList *Combining annotation filters*

Description

The AnnotationFilterList allows to combine filter objects extending the AnnotationFilter class to construct more complex queries. Consecutive filter objects in the AnnotationFilterList can be combined by a logical *and* (&) or *or* (|). The AnnotationFilterList extends list, individual elements can thus be accessed with [[.

value() get a list with the AnnotationFilter objects. Use [[to access individual filters.

logicOp() gets the logical operators separating successive AnnotationFilter.

not() gets the logical operators separating successive AnnotationFilter.

Converts an AnnotationFilterList object to a character(1) giving an equation that can be used as input to a dplyr filter.

Usage

```
AnnotationFilterList(..., logicOp = character(), logOp = character(),
  not = FALSE, .groupingFlag = FALSE)

## S4 method for signature 'AnnotationFilterList'
value(object)

## S4 method for signature 'AnnotationFilterList'
logicOp(object)
```

```
## S4 method for signature 'AnnotationFilterList'
not(object)

## S4 method for signature 'AnnotationFilterList'
distributeNegation(object,
  .prior_negation = FALSE)

## S4 method for signature 'AnnotationFilterList,missing'
convertFilter(object)

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

Arguments

`...`	individual `AnnotationFilter` objects or a mixture of `AnnotationFilter` and `AnnotationFilterList` objects.
`logicOp`	`character` of length equal to the number of submitted `AnnotationFilter` objects - 1. Each value representing the logical operation to combine consecutive filters, i.e. the first element being the logical operation to combine the first and second `AnnotationFilter`, the second element being the logical operation to combine the second and third `AnnotationFilter` and so on. Allowed values are `"&"` and `"|"`. The function assumes a logical *and* between all elements by default.
`logOp`	Deprecated; use `logicOp=`.
`not`	`logical` of length one. Indicates whether the grouping of `AnnotationFilters` are to be negated.
`.groupingFlag`	Flag desginated for internal use only.
`object`	An object of class `AnnotationFilterList`.
`.prior_negation`	`logical(1)` unused argument.

Value

`AnnotationFilterList` returns an `AnnotationFilterList`.

`value()` returns a `list` with `AnnotationFilter` objects.

`logicOp()` returns a `character()` vector of "&" or "|" symbols.

`not()` returns a `character()` vector of "&" or "|" symbols.

`AnnotationFilterList` object with DeMorgan's law applied to it such that it is equal to the original `AnnotationFilterList` object but all `!`'s are distributed out of the `AnnotationFilterList` object and to the nested `AnnotationFilter` objects.

`character(1)` that can be used as input to a `dplyr` filter.

Note

The `AnnotationFilterList` does not support containing empty elements, hence all elements of `length == 0` are removed in the constructor function.

See Also

supportedFilters for available AnnotationFilter objects

Examples

```
## Create some AnnotationFilters
gf <- GeneNameFilter(c("BCL2", "BCL2L11"))
tbtf <- TxBiotypeFilter("protein_coding", condition = "!=")

## Combine both to an AnnotationFilterList. By default elements are combined
## using a logical "and" operator. The filter list represents thus a query
## like: get all features where the gene name is either ("BCL2" or "BCL2L11")
## and the transcript biotype is not "protein_coding".
afl <- AnnotationFilterList(gf, tbtf)
afl

## Access individual filters.
afl[[1]]

## Create a filter in the form of: get all features where the gene name is
## either ("BCL2" or "BCL2L11") and the transcript biotype is not
## "protein_coding" or the seq_name is "Y". Hence, this will get all feature
## also found by the previous AnnotationFilterList and returns also all
## features on chromosome Y.
afl <- AnnotationFilterList(gf, tbtf, SeqNameFilter("Y"),
                            logicOp = c("&", "|"))
afl

afl <- AnnotationFilter(~!(symbol == 'ADA' | symbol %startsWith% 'SNORD'))
afl <- distributeNegation(afl)
afl
afl <- AnnotationFilter(~symbol=="ADA" & tx_start > "400000")
result <- convertFilter(afl)
result
```

GenenameFilter *DEPRECATED Gene name filter*

Description

The GenenameFilter class and functions are deprecated. Please use the GeneNameFilter() instead.

Usage

```
GenenameFilter(value, condition = "==", not = FALSE)
```

Arguments

value	character() value for the filter
condition	character(1) defining the condition to be used in the filter. One of "==", "!=", "startsWith", "endsWith" or "contains". Default condition is "==".
not	logical(1) whether the AnnotationFilter is negated. TRUE indicates is negated (!). FALSE indicates not negated. Default not is FALSE.

Value

The constructor function return a GenenameFilter.

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