

# Package ‘BREW3R.r’

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**Type** Package

**Title** R package associated to BREW3R

**Version** 1.3.0

**Description** This R package provide functions that are used in the BREW3R workflow. This mainly contains a function that extend a gtf as GRanges using information from another gtf (also as GRanges). The process allows to extend gene annotation without increasing the overlap between gene ids.

**License** GPL-3

**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 7.3.1

**Imports** GenomicRanges, methods, rlang, S4Vectors, utils

**Suggests** testthat (>= 3.0.0), IRanges, knitr, rmarkdown, BiocStyle, rtracklayer

**biocViews** GenomeAnnotation

**Config/testthat/edition** 3

**URL** <https://github.com/lldelisle/BREW3R.r>

**BugReports** <https://github.com/lldelisle/BREW3R.r/issues/>

**VignetteBuilder** knitr

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**Author** Lucille Lopez-Delisle [aut, cre] (ORCID:  
<<https://orcid.org/0000-0002-1964-4960>>)

**Maintainer** Lucille Lopez-Delisle <[lucille.delisle@epfl.ch](mailto:lucille.delisle@epfl.ch)>

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add_new_exons	<i>Add new exons</i>
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### Description

A function that from 2 GRanges add exons from the second one to the first one if the 3p of the last exon of the transcript in the first GRanges matches the 3p of an exon in the second one

### Usage

```
add_new_exons(input_gr_to_extend, input_gr_with_new_exons)
```

### Arguments

input\_gr\_to\_extend  
 A GRanges to be complemented

input\_gr\_with\_new\_exons  
 A GRanges with exons to be added to the first one (exons with strand '\*' are excluded)

### Details

Potential new exons will be filtered for collision with exons present in the first GRanges even if they belong to the same gene\_id. For the moment all potential exons extensions are added to the same existing transcript\_id so introns maybe artificial introns.

### Value

A GRanges identical to 'input\_gr\_to\_extend' with new exons whose 'exon\_id' contains BREW3R. 'exon\_number' may have changed.

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adjust\_for\_collision    *Adjust for collision*

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**Description**

A function that from a GRanges with 'old\_width' Change the starts and ends to prevent collisions larger than with old coordinates

**Usage**

```
adjust_for_collision(input_gr)
```

**Arguments**

input\_gr            A GRanges with 1 meta: 'old\_width'

**Value**

A list with: - 'pot\_issues': A dataframe with exons which overlaps between 'input\_gr' and itself while gene\_ids are different - 'new\_gr': A GRanges identical to 'input\_gr' except that start/end have been adjusted to prevent collisions.

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debug\_msg            *Display debug messages if verbose allows it*

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**Description**

A function that extend rlang::inform to display a message if the verbose is at "debug" and show content of the variable

**Usage**

```
debug_msg(message = NULL, ...)
```

**Arguments**

message            String to display  
...                Other parameters for rlang::inform

**Value**

Nothing

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extend_granges	<i>Extend GRanges</i>
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### Description

A function that from a GRanges from gtf will extend the 3' of transcripts using another GRanges from gtf as a template

### Usage

```
extend_granges(
  input_gr_to_extend,
  input_gr_to_overlap,
  extend_existing_exons = TRUE,
  add_new_exons = TRUE,
  overlap_resolution_fn = NULL
)
```

### Arguments

`input_gr_to_extend`  
A GRanges to extend (only exons are kept and strand \* are excluded)

`input_gr_to_overlap`  
A GRanges with intervals to overlap

`extend_existing_exons`  
A boolean that indicates if existing exons should be extended

`add_new_exons`  
A boolean that indicates if new exons with compatible splicing event should be added

`overlap_resolution_fn`  
A file path where the dataframe giving details on the collision resolution is written

### Details

During the extension process a special care is taking to prevent extension which would lead to overlap between different gene\_ids.

### Value

A GRanges based on 'input\_gr\_to\_extend' where exons are extended and new exons can be added. Exons extended will have a '.ext' suffix to the original exon\_id. Exons added will have a exon\_id starting with 'BREW3R'.

**Examples**

```

# Very simple case
# input_gr:      ----->          ----->
# to_overlap:    ----->

# output:        ----->          ----->

input_gr <- GenomicRanges::GRanges(
  seqnames = "chr1",
  ranges = IRanges::IRanges(
    start = c(5, 20),
    end = c(10, 30)
  ),
  strand = "+",
  gene_id = c("gene1", "gene2"),
  transcript_id = c("transcript1", "transcript2"),
  type = "exon",
  exon_id = c("exon1", "exon2")
)

input_gr_to_overlap <- GenomicRanges::GRanges(
  seqnames = "chr1",
  ranges = IRanges::IRanges(
    start = 3,
    end = 15
  ),
  strand = "+",
  gene_id = "geneA",
  transcript_id = "transcriptA",
  type = "exon",
  exon_id = "exonA"
)

extend_granges(input_gr, input_gr_to_overlap)

```

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extend\_using\_overlap *Overlap exons and extend three prime end*

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**Description**

A function that from 2 GRanges returns a subset of the first GRanges which have been extended using the second GRanges

**Usage**

```
extend_using_overlap(input_gr_to_extend, input_gr_to_overlap)
```

**Arguments**

input\_gr\_to\_extend  
 A GRanges with exons to extend (strand \* are excluded)

input\_gr\_to\_overlap  
 A GRanges with intervals to overlap

**Value**

A GRanges which is a subset of 'input\_gr\_to\_extend' where 3' end have been modified to match the 3' end of 'input\_gr\_to\_overlap' if they overlap (initial width have been stored into old\_width)

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extract\_last\_exons      *Extract last exons*

---

**Description**

A function that from a GRanges from gtf select only entries for the last exons. If multiple exons overlap the last base of the grouping\_variable, they will all be reported.

**Usage**

```
extract_last_exons(
  input_gr,
  grouping_variable = "transcript_id",
  invert = FALSE
)
```

**Arguments**

input\_gr            A GRanges from a gtf

grouping\_variable  
 A string with the name of the metadata which should be used to group

invert            A boolean that indicates if you want all except the last exons

**Value**

A GRanges which contains a subset of 'input\_gr'

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filter_new_exons	<i>Filter new exons for collision</i>
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**Description**

A function that from 2 GRanges filter exons from the first one so they do not go three prime to the first collision with the second one.

**Usage**

```
filter_new_exons(all_exons_interesting, input_gr_to_extend)
```

**Arguments**

all\_exons\_interesting  
A GRanges with exons to trim and filter

input\_gr\_to\_extend  
A GRanges to overlap

**Value**

A GRanges subset of 'all\_exons\_interesting'

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five_prime_pos	<i>Get five prime position</i>
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**Description**

A function that from a GRanges gives the 5' position

**Usage**

```
five_prime_pos(input_gr)
```

**Arguments**

input\_gr A GRanges or GRangesList

**Value**

A vector of integers

overlap\_different\_genes

*Get overlaps from different genes*

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### Description

A function that from 2 GRanges generates a dataframe With queryHits, subjectHits when the gene\_id is different

### Usage

```
overlap_different_genes(gr1, gr2)
```

### Arguments

gr1	A GRanges with 'gene_id'
gr2	A GRanges with 'gene_id'

### Value

a data.frame with overlaps between gr1 and gr2 when gene\_id from gr1 is different from gene\_id from gr2. The data.frame has 4 columns: 'queryHits', 'subjectHits', 'query\_gene\_id' and 'subject\_gene\_id'

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progression\_msg

*Display progression messages if verbose allows it*

---

### Description

A function that extend rlang::inform to display a message if the verbose is at "debug" or "progression"

### Usage

```
progression_msg(...)
```

### Arguments

...	Parameters for rlang::inform
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### Value

Nothing



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<code>three_prime_pos</code>	<i>Get three prime position</i>
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**Description**

A function that from a GRanges gives the 3' position

**Usage**

```
three_prime_pos(input_gr)
```

**Arguments**

`input_gr`      A GRanges or GRangelist

**Value**

A vector of integers

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