Package 'ADARR'

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Type Package

Title ADAR R Package

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Description Functions to interpret and annotate data from Sprint and RNA editing identificaiton tools

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

R topics documented:

AD_DP *Obtain editing levels for results Reformats results from Sprint file*

Description

Obtain editing levels for results Reformats results from Sprint file

Usage

```
AD_DP(RES.table)
```

Arguments

RES.table	data frame of RES table from Sprint obtained from read.delim() function

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`annotate_regions` *A function to intersect user region data with annotation data Taken from annotatr package Annotate genomic regions to selected genomic annotations while preserving the data associated with the genomic regions.*

Description

A function to intersect user region data with annotation data Taken from annotatr package Annotate genomic regions to selected genomic annotations while preserving the data associated with the genomic regions.

Usage

```
annotate_regions(
  regions,
  annotations = hg38_annotations,
  minoverlap = 1L,
  ignore.strand = TRUE,
  quiet = FALSE
)
```

Arguments

regions	The GRanges object to annotate
annotations	The annotations to overlap with
minoverlap	A scalar, positive integer, indicating the minimum required overlap of regions with annotations.
ignore.strand	Logical indicating whether strandedness should be respected in findOverlaps(). Default FALSE.
quiet	Print progress messages (FALSE) or not (TRUE).
	' @export

filter_annotated_results

A function for filtering annotated Sprint results by editing ratio and/or number of supporting reads

Description

A function for filtering annotated Sprint results by editing ratio and/or number of supporting reads

Usage

```
filter_annotated_results(input.sprint, editing_ratio = 0, supporting_reads = 1)
```

Arguments

input.sprint	The Sprint data frame to input
editing_ratio	The minimum editing ratio to have
supporting_reads	The minimum number of supporting reads needed

filter_by_transitions

A function for filtering annotated Sprint results by type of transitions

Description

A function for filtering annotated Sprint results by type of transitions

Usage

```
filter_by_transitions(input.sprint, transitions_list = c("AG", "TC"))
```

Arguments

input.sprint	The Sprint data frame to input
transitions_list	The list of transitions you want

`getGeneMatrix` *A function for obtaining a gene matrix from a list of tables of identified genes*

Description

A function for obtaining a gene matrix from a list of tables of identified genes

Usage

```
getGeneMatrix(list_table_identified_genes)
```

Arguments

`list_table_identified_genes`
: A list of tables from table_identified_genes() with names of tables being sample names

`hello` *Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

`partition_files` *A function for annotating the Sprint results with genomic regions and repeats (allows for partition)*

Description

A function for annotating the Sprint results with genomic regions and repeats (allows for partition)

Usage

```
partition_files(
  input.file.path,
  partition.path = "partitions",
  partition = 10000
)
```

Arguments

input.file.path	The input file path
partition.path	Directory to export partitions to
partition	the number of RES to partition by

RES.name *Obtain site names for RES results*

Description

Assigns each RES from a Sprint output table a site name denoting position and type of change

Usage

```
RES.name(RES.table)
```

Arguments

RES.table	data frame of RES table from Sprint obtained from read.delim() function

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run_ADARR *A function for annotating the Sprint results with genomic regions and repeats*

Description

A function for annotating the Sprint results with genomic regions and repeats

Usage

```
run_ADARR(input.file.path, annotation.granges.path, complete.annotated.path)
```

Arguments

input.file.path	The input file path
annotation.granges.path	The path to output initial annotations
complete.annotated.path	The path to output the complete annotations

`run_ADARR_from_df` *A function for annotating the Sprint results with genomic regions and repeats This requires inputting a data frame rather than a file path*

Description

A function for annotating the Sprint results with genomic regions and repeats This requires inputting a data frame rather than a file path

Usage

```
run_ADARR_from_df(
  input.sprint,
  annotation.granges.path,
  complete.annotated.path
)
```

Arguments

`input.sprint` The input file path

`annotation.granges.path`
: The path to output initial annotations

`complete.annotated.path`
: The path to output the complete annotations

`run_ADARR_partition`
A function for annotating the Sprint results with genomic regions and repeats (allows for partition)

Description

A function for annotating the Sprint results with genomic regions and repeats (allows for partition)

Usage

```
run_ADARR_partition(
  input.file.path,
  annotation.granges.path,
  complete.annotated.path,
  partition = 10000
)
```

Arguments

`input.file.path`	The input file path
`annotation.granges.path`	The path to output initial annotations
`complete.annotated.path`	The path to output the complete annotations
`partition`	the number of RES to partition by

`table_identified_genes` *A function for obtaining table of identified genes*

Description

A function for obtaining table of identified genes

Usage

```
table_identified_genes(input.sprint)
```

Arguments

`input.sprint`	The Sprint data frame to input

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