

Package ‘alignr’

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Type Package

Title alignr 0.1.0: An R package to call a single full length TCR from a 10X genomics single cell RNA sequencing contain annotations JSON file.

Version 0.1.0

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Description alignr is a package that can be used to make full length TCR transgenes from single cell RNA sequencing experiments.

License BSD2

Encoding UTF-8

LazyData true

Imports curl, readr, Rcpp, rjson

RoxygenNote 7.3.2

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GetTCRs	<i>Code to pull the full length TCR sequence from 10X genomics all_contig_annotations.json file</i>
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Description

This function will import a set of single cell barcodes, extract the full length TCR transcript details and output the details ranked by the cell with the greatest functional score.

Usage

```
GetTCRs(
  barcodes,
  contig.annotations,
  json.path = ".",
  save.dir = ".",
  score = "",
  ranked.sheet = FALSE,
  verbose = TRUE
)
```

Arguments

barcodes	Barcodes used to identify cells in full contig annotations JSON file.
contig.annotations	contig_annotations.csv file.
json.path	Directory where JSON file is saved.
save.dir	Directory where full length TCR transcripts will be saved.
score	Orders the cells by classification score.
ranked.sheet	False. If true implements and saves the cells by their characteristic rank.
verbose	Print progress bars and output

Value

Void

MakeReceptor	<i>This function will import a set of single cell barcodes, extract the full length TCR transcript details and output the details ranked by the cell with the greatest functional score.</i>
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Description

This function will import a set of single cell barcodes, extract the full length TCR transcript details and output the details ranked by the cell with the greatest functional score.

Usage

```
MakeReceptor(n.cells, path = ".", save.dir = ".")
```

Arguments

n.cells	Number of cells processed.
path	Path to output files from alignr::GetTCRs
save.dir	Directory where full length receptor sequences will be saved.
verbose	Print progress bars and output

Value

Void

RankTCRs

This function will import a set of single cell barcodes, extract the full length TCR transcript details and output the details ranked by the cell with the greatest functional score.

Description

This function will import a set of single cell barcodes, extract the full length TCR transcript details and output the details ranked by the cell with the greatest functional score.

Usage

```
RankTCRs(  
  cell.data,  
  gene = "IFNG",  
  meta.data = FALSE,  
  data.name = "Mdist",  
  save.dir = ".",  
  verbose = TRUE  
)
```

Arguments

<code>cell.data</code>	single cell RNA sequencing data processed by aocseq.
<code>gene</code>	gene list for UMI ranked cell types.
<code>meta.data</code>	select a metadata column to rank cell types.
<code>data.name</code>	name of metadata used for ranking.
<code>verbose</code>	Print progress bars and output.

Value

Void

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