

Package ‘rTCRBCRr’

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Type Package

Title Repertoire Analysis of the Detected Clonotype

Version 0.1.1

Description The 'TRUST4' or 'MiXCR' is used to identify the clonotypes.

The goal of 'rTCRBCRr' is to process the results from these clonotyping tools,
and analyze the clonotype repertoire metrics based on chain names and IGH isotypes.

The manuscript is still under preparation for publication for now.

The references describing the methods in this package will be added later.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Imports magrittr, readr, tidyr, tidysselect

Depends R (>= 2.10)

Suggests rmarkdown, knitr

VignetteBuilder knitr

NeedsCompilation no

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all_sample_all_chain_all_metrics_wide_format_dataframe
a dataframe of wide format

Description

The data frame must be generated from combine_all_sample_repertoire_metrics function

Usage

```
all_sample_all_chain_all_metrics_wide_format_dataframe
```

Format

A data frame with m rows and n variables:

Source

<https://www.rdocumentation.org/packages/base/versions/3.6.2/topics/list>

`all_sample_all_chain_all_metrics_wide_format_dataframe_list`
a dataframe list to combine rowwise.

Description

The element data frame must be generated from `compute_repertoire_metrics_by_chain_name` function

Usage

`all_sample_all_chain_all_metrics_wide_format_dataframe_list`

Format

A list of data frames with m rows and n variables:

Source

<https://www.rdocumentation.org/packages/base/versions/3.6.2/topics/list>

`all_sample_all_chain_individual_metrics_dataframe_list`
a list of dataframes

Description

The list of data frames generated from `get_item_name_x_sample_name_for_each_metric`

Usage

`all_sample_all_chain_individual_metrics_dataframe_list`

Format

A list of data frame with m rows and n variables:

Source

<https://www.rdocumentation.org/packages/base/versions/3.6.2/topics/list>

`all_sample_IGH_chain_all_metrics_wide_format_dataframe`
a dataframe of wide format

Description

The data frame must be generated from `combine_all_sample_repertoire_metrics` function

Usage

```
all_sample_IGH_chain_all_metrics_wide_format_dataframe
```

Format

A data frame with m rows and n variables:

Source

<https://www.rdocumentation.org/packages/base/versions/3.6.2/topics/list>

`all_sample_IGH_chain_all_metrics_wide_format_dataframe_list`
a dataframe list to combine rowwise.

Description

The element data frame must be generated from `calculate_IGH_isotype_proportion` function

Usage

```
all_sample_IGH_chain_all_metrics_wide_format_dataframe_list
```

Format

A list of data frames with m rows and n variables:

Source

<https://www.rdocumentation.org/packages/base/versions/3.6.2/topics/list>

`all_sample_IGH_chain_individual_metrics_dataframe_list`
a list of dataframes

Description

The list of data frames generated from `get_item_name_x_sample_name_for_each_metric`

Usage

`all_sample_IGH_chain_individual_metrics_dataframe_list`

Format

A list of data frame with m rows and n variables:

Source

<https://www.rdocumentation.org/packages/base/versions/3.6.2/topics/list>

`annotate_chain_name_and_isotype_name`
Annotate chain name and isotype name

Description

Annotate chain name and isotype name

Usage

`annotate_chain_name_and_isotype_name(input_dataframe)`

Arguments

`input_dataframe`
A dataframe of clonotype of immunarch format

Value

A dataframe of clonotype of immunarch format

Examples

`annotate_chain_name_and_isotype_name(nonproductive_CDR3aa_removed_dataframe)`

```
calculate_IGH_isotype_proportion  
    calculate_IGH_isotype_proportion
```

Description

calculate_IGH_isotype_proportion

Usage

```
calculate_IGH_isotype_proportion(input_dataframe)
```

Arguments

```
input_dataframe  
    a clonotype dataframe with chain name and isotype name information
```

Value

a dataframe of count and proportion of isotypes of IGH chain.

Examples

```
calculate_IGH_isotype_proportion(convergent_clonotype_merged_dataframe)
```

```
calculate_repertoire_metrics  
    calculate_repertoire_metrics
```

Description

calculate_repertoire_metrics

Usage

```
calculate_repertoire_metrics(named_species_vector)
```

Arguments

```
named_species_vector  
    a named vector
```

Value

a named vector

Examples

```
a_named_vector <- c("apple" = 1, "banana" = 3, "cranberry" = 7, "date" = 10)
calculate_repertoire_metrics(a_named_vector)
```

```
calibrate_proportion_by_clones
  calibrate_proportion_by_clones
```

Description

calibrate_proportion_by_clones

Usage

```
calibrate_proportion_by_clones(a_dataframe)
```

Arguments

a_dataframe a dataframe

Value

a dataframe

```
chain_separated_dataframe
  a dataframe separated by chain name
```

Description

an example dataframe separated by chain name

Usage

```
chain_separated_dataframe
```

Format

A data frame with m rows and n variables:

Source

https://en.wikipedia.org/wiki/T-cell_receptor

`combine_all_sample_repertoire_metrics`
combine_all_sample_repertoire_metrics

Description

`combine_all_sample_repertoire_metrics`

Usage

`combine_all_sample_repertoire_metrics(input_dataframe_list)`

Arguments

`input_dataframe_list`
a list of dataframes with repertoire metrics by chain name

Value

a wide table with all samples' all chains' all repertoire metrics

Examples

```
combine_all_sample_repertoire_metrics(all_sample_all_chain_all_metrics_wide_format_dataframe_list)
combine_all_sample_repertoire_metrics(all_sample_IGH_chain_all_metrics_wide_format_dataframe_list)
```

`compute_repertoire_metrics_by_chain_name`
compute_repertoire_metrics_by_chain_name

Description

`compute_repertoire_metrics_by_chain_name`

Usage

`compute_repertoire_metrics_by_chain_name(input_dataframe)`

Arguments

`input_dataframe`
a clonotype dataframe with chain name information

Value

repertoire metrics by chain name.

Examples

```
compute_repertoire_metrics_by_chain_name(convergent_clonotype_merged_dataframe)
```

convergent_clonotype_merged_dataframe
a dataframe where convergent clonotypes are merged

Description

an example dataframe where convergent clonotypes are merged

Usage

```
convergent_clonotype_merged_dataframe
```

Format

A data frame with m rows and n variables:

Source

<https://www.frontiersin.org/articles/10.3389/fimmu.2019.02985/full>

format_clonotype_to_immunarch_style
Convert clonotype dataframe to immunarch format

Description

Convert clonotype dataframe to immunarch format

Usage

```
format_clonotype_to_immunarch_style(input_dataframe, clonotyping_tool)
```

Arguments

input_dataframe
a clonotype dataframe from an upstream clonotyping tool

clonotyping_tool
choose from c("mixcr", "trust")

Value

a clonotype dataframe of immunarch format

Examples

```
format_clonotype_to_immunarch_style(raw_input_clonotype_dataframe, "trust")
```

```
get_item_name_x_sample_name_for_each_metric  
get_item_name_x_sample_name_for_each_metric
```

Description

get_item_name_x_sample_name_for_each_metric

Usage

```
get_item_name_x_sample_name_for_each_metric(input_dataframe)
```

Arguments

input_dataframe
a dataframe with repertoire metrics calculated for each item name

Value

a list of dataframes that is one single repertoire metric for all items in all samples

Examples

```
get_item_name_x_sample_name_for_each_metric(all_sample_all_chain_all_metrics_wide_format_dataframe)
```

```
immunarch_style_dataframe  
An converted dataframe to immunarch format
```

Description

An example dataframe converted to immunarch format

Usage

```
immunarch_style_dataframe
```

Format

A data frame with m rows and n variables:

Source

<https://github.com/immunomind/immunarch/>

merge_convergent_clonotype
Merge convergent clonotype

Description

Merge convergent clonotype

Usage

```
merge_convergent_clonotype(input_dataframe)
```

Arguments

input_dataframe
A dataframe of clonotype of immunarch format

Value

A dataframe of clonotype of immunarch format merge_convergent_clonotype_function(an_immunarch_format_clonotype_d

Examples

```
merge_convergent_clonotype(chain_separated_dataframe)
```

nonproductive_CDR3aa_removed_dataframe
a dataframe with nonproductive CDR3aa removed

Description

an example dataframe with nonproductive CDR3aa removed

Usage

```
nonproductive_CDR3aa_removed_dataframe
```

Format

A data frame with m rows and n variables:

Source

<https://mixcr.readthedocs.io/en/master/analyze.html>

`parse_mixcr`*Parse mixcr format*

Description

Parse mixcr format

Usage

```
parse_mixcr(input_clone_dataframe)
```

Arguments

`input_clone_dataframe`
Generated from mixcr program

Value

A dataframe of immunarch format

`parse_trust4`*Parse trust4 format*

Description

Parse trust4 format

Usage

```
parse_trust4(input_clone_dataframe)
```

Arguments

`input_clone_dataframe`
Generated from trust4 program

Value

A dataframe of immunarch format

raw_input_clonotype_dataframe
Raw clonotype output from trust4

Description

An example dataframe for raw clonotype identified by trust4

Usage

raw_input_clonotype_dataframe

Format

A data frame with m rows and n variables:

Source

<https://github.com/liulab-dfci/TRUST4>

remove_nonproductive_CDR3aa
Clean the clonotype dataframe

Description

Clean the clonotype dataframe

Usage

remove_nonproductive_CDR3aa(input_dataframe)

Arguments

input_dataframe
A dataframe of clonotype of immunarch format

Value

A dataframe of clonotype of immunarch format

Examples

remove_nonproductive_CDR3aa(immunarch_style_dataframe)

summarize_convergence_function
summarize_convergence_function

Description

summarize_convergence_function

Usage

summarize_convergence_function(a_dataframe)

Arguments

a_dataframe a dataframe

Value

a dataframe

summarize_repertoire_metrics
summarize_repertoire_metrics

Description

summarize_repertoire_metrics

Usage

summarize_repertoire_metrics(one_sample_dataframe)

Arguments

one_sample_dataframe
 a dataframe of clonotype in immunarch format

Value

a named vector

the global variables *Make variable names global to avoid CHECK notes*

Description

Global variables

the_divergent_clonotype_dataframe_list
a list of dataframe where convergent clonotypes are merged

Description

an list of example dataframes where convergent clonotypes are merged

Usage

the_divergent_clonotype_dataframe_list

Format

A list of data frame with m rows and n variables:

Source

<https://www.frontiersin.org/articles/10.3389/fimmu.2019.02985/full>

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