Package: rTCRBCRr (via r-universe)

September 2, 2024

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.

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Imports magrittr, readr, tidyr, tidyselect

Depends R (>= 2.10)

Suggests rmarkdown, knitr

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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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_da

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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