

Package ‘scImmuneGraph’

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Type Package

Title Visualize the Basic Characteristics of Single-Cell Immune Repertoire

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Description Statistics and visualization of the distribution, diversity and composition of clonotypes, the abundance and length distribution of CDR3, the respective abundance distribution of V and J genes, and the abundance of V-J gene pairs are the basic requirements for single-cell immune group analysis. 'scImmuneGraph' is designed to process data from 10x Genomics Chromium Immune Profiling for T cell receptor (TCR) and immunoglobulin (Ig) enrichment workflows.

URL <https://github.com/zff-excellent/scImmuneGraph>

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Depends R (>= 4.0)

Imports RColorBrewer, scales, ggplot2, cowplot, tibble, stringr, tidyverse, readr, tidyr, dplyr, purrr, gtools, plyr, forcats, easypackages, BiocStyle

Suggests rmarkdown, knitr, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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BasicPlot	<i>Draw a variety of diagrams</i>
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Description

Draw a variety of diagrams

Usage

```
BasicPlot(plot_fun, contigList, sampleName)
```

Arguments

plot_fun	Drawing function.
contigList	List which produced by TCR.ContigList() or BCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```

project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")

contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)
BasicPlot(TCR.ClonalStateDistribution, contig_list, sample_name)

```

bcontig_list	<i>Single chain immune repertoire dataset</i>
--------------	---

Description

A dataset with single chain BCR data for testing and exemplary purposes.

Usage

```
bcontig_list
```

Format

A list of two elements. First element ("data") is a list with data frames with clonotype tables. Second element ("meta") is a metadata table.

data List of immune repertoire data frames.

meta Metadata ...

BCR.CDR3ntLengthDistribution	<i>CDR3 nucleic acid length distribution in the sample</i>
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Description

CDR3 nucleic acid length distribution in the sample

Usage

```
BCR.CDR3ntLengthDistribution(contigList, sampleName)
```

Arguments

contigList	The product of BCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(BCR.CDR3ntLengthDistribution, contig_list, sample_name)
```

BCR.ClonalStateDistribution

Distribution of clonal status of single-cell BCR clonotypes

Description

Distribution of clonal status of single-cell BCR clonotypes

Usage

```
BCR.ClonalStateDistribution(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList() or BCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")

contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

TCR.ClonalStateDistribution(contig_list, sample_name)

BasicPlot(TCR.ClonalStateDistribution, contig_list, sample_name)
```

`BCR.ClonotypeComposition`*The composition of single-cell BCR clonotypes in the sample*

Description

The composition of single-cell BCR clonotypes in the sample

Usage

```
BCR.ClonotypeComposition(contigList, sampleName)
```

Arguments

<code>contigList</code>	The product of <code>BCR.ContigList()</code> .
<code>sampleName</code>	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"  
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)  
group_name <- c("A", "A", "B", "B")  
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)  
  
BasicPlot(BCR.ClonotypeComposition, contig_list, sample_name)
```

`BCR.ContigList`*Converting 10X genomics produced B cell contigs file(s) as a list outputed*

Description

Converting 10X genomics produced B cell contigs file(s) as a list outputed

Usage

```
BCR.ContigList(datasetDir, sampleName, groupName)
```

Arguments

datasetDir The single-cell samples' directory containing file filtered_contig_annotations.csv.
 sampleName The sample name of single cell sample.
 groupName The group name of single cell sample.

Value

List of clonotypes for individual cell barcodes.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")

TCR.ContigList(project_data_dir, sample_name, group_name)
```

BCR.JgeneAbundance *J gene abundance distribution in the sample*

Description

J gene abundance distribution in the sample

Usage

```
BCR.JgeneAbundance(contigList, sampleName)
```

Arguments

contigList The product of BCR.ContigList().
 sampleName The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(BCR.JgeneAbundance, contig_list, sample_name)
```

```
BCR.top100CDR3Abundance
      #' Get the 100 most abundant CDR3
```

Description

#' Get the 100 most abundant CDR3

Usage

```
BCR.top100CDR3Abundance(contigList, sampleName)
```

Arguments

contigList The product of TCR.ContigList().
sampleName The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(BCR.top100CDR3Abundance, contig_list, sample_name)
```

```
BCR.top100ClonotypeAbundance
      Get the 100 most abundant clonotypes
```

Description

Get the 100 most abundant clonotypes

Usage

```
BCR.top100ClonotypeAbundance(contigList, sampleName)
```

Arguments

contigList The product of BCR.ContigList().
sampleName The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(BCR.top100ClonotypeAbundance, contig_list, sample_name)
```

BCR.VgeneAbundance	<i>V gene abundance distribution in the sample</i>
--------------------	--

Description

V gene abundance distribution in the sample

Usage

```
BCR.VgeneAbundance(contigList, sampleName)
```

Arguments

contiglist	The product of BCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(BCR.VgeneAbundance, contig_list, sample_name)
```

BCR.VJgenePair	<i>VJ gene pair abundance distribution in the sample</i>
----------------	--

Description

VJ gene pair abundance distribution in the sample

Usage

```
BCR.VJgenePair(contigList, sampleName)
```

Arguments

contigList	The product of BCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/bcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- BCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(BCR.VJgenePair, contig_list, sample_name)
```

tcontig_list	<i>Single chain immune repertoire dataset</i>
--------------	---

Description

A dataset with single chain TCR data for testing and exemplary purposes.

Usage

```
tcontig_list
```

Format

A list of two elements. First element ("data") is a list with data frames with clonotype tables. Second element ("meta") is a metadata table.

data List of immune repertoire data frames.

meta Metadata ...

TCR.CDR3ntLengthDistribution

CDR3 nucleic acid length distribution in the sample

Description

CDR3 nucleic acid length distribution in the sample

Usage

```
TCR.CDR3ntLengthDistribution(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"  
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)  
group_name <- c("A", "A", "B", "B")  
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)  
  
BasicPlot(TCR.CDR3ntLengthDistribution, contig_list, sample_name)
```

TCR.ClonalStateDistribution

Distribution of clonal status of single-cell TCR clonotypes

Description

Distribution of clonal status of single-cell TCR clonotypes

Usage

```
TCR.ClonalStateDistribution(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList() or BCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")

contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)

TCR.ClonalStateDistribution(contig_list, sample_name)

BasicPlot(TCR.ClonalStateDistribution, contig_list, sample_name)
```

TCR.ClonotypeComposition

The composition of single-cell TCR clonotypes in the sample

Description

The composition of single-cell TCR clonotypes in the sample

Usage

```
TCR.ClonotypeComposition(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(TCR.ClonotypeComposition, contig_list, sample_name)
```

TCR.ContigList	<i>Converting 10X genomics produced T cell contigs file(s) as a list outputed</i>
----------------	---

Description

Converting 10X genomics produced T cell contigs file(s) as a list outputed

Usage

```
TCR.ContigList(datasetDir, sampleName, groupName)
```

Arguments

datasetDir	The single-cell samples' directory containing file filtered_contig_annotations.csv.
sampleName	The sample name of single cell sample.
groupName	The group name of single cell sample.

Value

List of clonotypes for individual cell barcodes.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")

TCR.ContigList(project_data_dir, sample_name, group_name)
```

TCR.JgeneAbundance	<i>J gene abundance distribution in the sample</i>
--------------------	--

Description

J gene abundance distribution in the sample

Usage

```
TCR.JgeneAbundance(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(TCR.JgeneAbundance, contig_list, sample_name)
```

```
TCR.top100CDR3Abundance
      #' Get the 100 most abundant CDR3
```

Description

#' Get the 100 most abundant CDR3

Usage

```
TCR.top100CDR3Abundance(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(TCR.top100CDR3Abundance, contig_list, sample_name)
```

TCR.top100ClonotypeAbundance

Get the 100 most abundant clonotypes

Description

Get the 100 most abundant clonotypes

Usage

```
TCR.top100ClonotypeAbundance(contigList, sampleName)
```

Arguments

`contigList` The product of `TCR.ContigList()` or `BCR.ContigList()`.
`sampleName` The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"  
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)  
group_name <- c("A", "A", "B", "B")  
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)  
  
BasicPlot(TCR.top100ClonotypeAbundance, contig_list, sample_name)
```

TCR.VgeneAbundance *V gene abundance distribution in the sample*

Description

V gene abundance distribution in the sample

Usage

```
TCR.VgeneAbundance(contigList, sampleName)
```

Arguments

`contigList` The product of `TCR.ContigList()`.
`sampleName` The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(TCR.VgeneAbundance, contig_list, sample_name)
```

TCR.VJgenePair	<i>VJ gene pair abundance distribution in the sample</i>
----------------	--

Description

VJ gene pair abundance distribution in the sample

Usage

```
TCR.VJgenePair(contigList, sampleName)
```

Arguments

contigList	The product of TCR.ContigList().
sampleName	The sample name of single cell sample.

Value

Multiple pictures in the form of a list.

Examples

```
project_data_dir <- "F:/R_Language/data/tcr"
sample_name <- list.dirs(project_data_dir, full.names = FALSE, recursive = FALSE)
group_name <- c("A", "A", "B", "B")
contig_list <- TCR.ContigList(project_data_dir, sample_name, group_name)

BasicPlot(TCR.VJgenePair, contig_list, sample_name)
```

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