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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R topics documented:

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BasicPlot

Draw a variety of diagrams

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.
bcontig_list

Examples

```r
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  Single chain immune repertoire dataset

Description

A dataset with single chain BCR data for testing and examplatory 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

*CDR3 nucleic acid length distribution in the sample*

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.
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

```r
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)

BCR.ClonalStateDistribution(contig_list, sample_name)
```

```r
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**

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

**Value**

Multiple pictures in the form of a list.

**Examples**

```r
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)
```
BCR.JgeneAbundance

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

```r
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")

BCR.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

```r
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.
**BCR.VgeneAbundance**

**Value**

Multiple pictures in the form of a list.

**Examples**

```r
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**  
*V gene abundance distribution in the sample*

**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**

```r
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

VJ gene pair abundance distribution in the sample

**Description**

VJ gene pair abundance distribution in the sample

**Usage**

```r
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**

```r
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

Single chain immune repertoire dataset

**Description**

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

**Usage**

```r
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

```r
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.
**TCR.ClonotypeComposition**

*The composition of single-cell TCR clonotypes in the sample*

**Description**

The composition of single-cell TCR clonotypes in the sample

**Usage**

```r
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**

```r
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.ClonotypeComposition, contig_list, sample_name)
```
TCR.ContigList

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

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

J gene abundance distribution in the sample

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.
TCR.top100CDR3Abundance

Value

Multiple pictures in the form of a list.

Examples

```r
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

```r
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**

```r
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**

```r
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**

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

**Arguments**

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

**Value**

Multiple pictures in the form of a list.

**Examples**

```r
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**

**VJ gene pair abundance distribution in the sample**

**Description**

VJ gene pair abundance distribution in the sample

**Usage**

```r
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**

```r
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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