Package ‘seAMLess’

September 5, 2022

Type Package

Title A Single Cell Transcriptomics Based Deconvolution Pipeline for
Leukemia

Description Given a bulk transcriptomic (RNA-seq) sample of an Myeloid Leukemia patient calculates immune composition and drug resistance for different small-molecule inhibitors.

Version 0.1.0

biocViews

Depends R (>= 3.5.0)

Imports Biobase, ggplot2, ggtern, randomForest

Suggests xbioc, MuSiC, seAMLessData

Additional_repositories `https://eonurk.github.io/drat/`

URL `https://github.com/eonurk/seAMLess`

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

NeedsCompilation no

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Repository CRAN

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R topics documented:

`exampleTCGA` *TCGA-LAML bulk RNA-seq data downloaded from GDC*

Description

TCGA-LAML bulk RNA-seq data downloaded from GDC

Usage

```
data(exampleTCGA)
```

Format

An object of class `data.frame` with 60483 rows and 21 columns.

`exampleTCGAmeta` *TCGA-LAML example data meta file downloaded from GDC*

Description

TCGA-LAML example data meta file downloaded from GDC

Usage

```
data(exampleTCGAmeta)
```

Format

An object of class `data.frame` with 20 rows and 34 columns.

`grch38` *Grch38*

Description

Grch38

Usage

```
data(grch38)
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 67495 rows and 3 columns.

`minRes` *A minimal seAMLess result list object*

Description

A minimal seAMLess result list object

Usage

```
data(minRes)
```

Format

An object of class `list` of length 2.

`seAMLess` *Given the count matrices of bulk-RNA samples, this function deconvolutes each sample into its cell types using a healthy BM reference, and calculates the sample's in vitro resistance to Venetoclax.*

Description

Given the count matrices of bulk-RNA samples, this function deconvolutes each sample into its cell types using a healthy BM reference, and calculates the sample's in vitro resistance to Venetoclax.

Usage

```
seAMLess(mat, verbose = TRUE)
```

Arguments

`mat`	count matrix (genes by 1+samples).
`verbose`	prints detailed messages

Value

List of deconvoluted cell type percentages and predicted drug resistances

`ternaryPlot` *Given the immune compositions (ICs) of bulk-RNA samples, this function creates a ternary plot similar to ALOT tube from EuroFlow analysis and Figure 1E of our paper.*

Description

Given the immune compositions (ICs) of bulk-RNA samples, this function creates a ternary plot similar to ALOT tube from EuroFlow analysis and Figure 1E of our paper.

Usage

```
ternaryPlot(res)
```

Arguments

`res`	seAMLess object.

Value

ggplot2 object

Examples

```
library(seAMLess)

data(minRes)
ternaryPlot(minRes)
```

venoModel *Trained RF model on Venetoclax Resistance*

Description

Trained RF model on Venetoclax Resistance

Usage

```
data(venoModel)
```

Format

An object of class `randomForest` of length 17.

verboseFn *verboseFn*

Description

returns a printing function to be used with in the script

Usage

```
verboseFn(verbose)
```

Arguments

verbose	boolean, determines whether the output going be printed or not

Value

print function

Examples

```
# Prints output
verbosePrint <- verboseFn(TRUE)
verbosePrint("Hello World!")
# > "Hello World!"

# Does not print
verbosePrint <- verboseFn(FALSE)
verbosePrint("Hello World!")
```

wrangleMat *removes ERCC peaks and duplicated genes*

Description

removes ERCC peaks and duplicated genes

Usage

```
wrangleMat(mat)
```

Arguments

`mat`	pre-filters and orders bulk rna-seq data

Value

filtered and ordered count-matrix

Examples

```
library(seAMLess)

data("exampleTCGA")

exampleTCGA <- wrangleMat(exampleTCGA)
```

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