

Package ‘seAMLess’

July 23, 2025

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. Published in <<https://www.nature.com/articles/s41698-024-00596-9>>.

Version 0.1.1

Depends R (>= 3.5.0)

Imports Biobase, ggplot2, optparse, data.table,

Suggests MuSiC, ggtern, seAMLessData, randomForest

Additional_repositories <https://eonurk.github.io/drat/>

URL <https://github.com/eonurk/seAMLess>

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-11-11 12:50:02 UTC

Contents

cli	2
exampleTCGA	2
exampleTCGAmeta	3
grch38	3

minRes	3
seAMLess	4
ternaryPlot	4
venoModel	5
verboseFn	5
wrangleMat	6
Index	7

cli	<i>Command Line Interface for seAMLess</i>
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Description

Provides a command line interface to run seAMLess deconvolution analysis on bulk RNA-seq data.

Usage

cli()

Value

List of validated command line options

exampleTCGA	<i>TCGA-LAML bulk RNA-seq data downloaded from GDC</i>
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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	<i>TCGA-LAML example data meta file downloaded from GDC</i>
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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	<i>Grch38</i>
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Description

Grch38

Usage

```
data(grch38)
```

Format

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

minRes	<i>A minimal seAMLess result list object</i>
--------	--

Description

A minimal seAMLess result list object

Usage

```
data(minRes)
```

Format

An object of class `list` of length 2.

seAMLess	<i>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.</i>
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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,
  scRef = seAMLessData::scRef,
  scRef.sample = "Sample",
  scRef.label = "label.new",
  verbose = TRUE
)
```

Arguments

mat	count matrix (genes by 1+samples).
scRef	reference matrix for single cell data
scRef.sample	column name for the samples in single cell reference
scRef.label	column name for the cell names in single cell reference
verbose	prints detailed messages

Value

List of deconvoluted cell type percentages and predicted drug resistances

ternaryPlot	<i>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.</i>
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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	<i>Trained RF model on Venetoclax Resistance</i>
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Description

Trained RF model on Venetoclax Resistance

Usage

```
data(venoModel)
```

Format

An object of class randomForest of length 17.

verboseFn	<i>verboseFn</i>
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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	<i>removes ERCC peaks and duplicated genes</i>
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Description

removes ERCC peaks and duplicated genes

Usage

```
wrangleMat(mat)
```

Arguments

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

filtered and ordered count-matrix

Examples

```
library(seAMless)

data("exampleTCGA")

exampleTCGA <- wrangleMat(exampleTCGA)
```

Index

* **datasets**

- exampleTCGA, [2](#)
- exampleTCGAMeta, [3](#)
- grch38, [3](#)
- minRes, [3](#)
- venoModel, [5](#)

cli, [2](#)

exampleTCGA, [2](#)
exampleTCGAMeta, [3](#)

grch38, [3](#)

minRes, [3](#)

seAMLess, [4](#)

ternaryPlot, [4](#)

venoModel, [5](#)
verboseFn, [5](#)

wrangleMat, [6](#)