

# Package ‘seAMLess’

November 11, 2024

**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

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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

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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.

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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.

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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.

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minRes	<i>A minimal seAMLess result list object</i>
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**Description**

A minimal seAMLess result list object

**Usage**

```
data(minRes)
```

**Format**

An object of class `list` of length 2.

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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

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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                    *Trained RF model on Venetoclax Resistance*

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**Description**

Trained RF model on Venetoclax Resistance

**Usage**

```
data(venoModel)
```

**Format**

An object of class randomForest of length 17.

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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!")
```

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wrangleMat

*removes ERCC peaks and duplicated genes*

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**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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