

Package ‘Twenty’

May 6, 2022

Version 5.0

Date 04-May-2022

Title Twenty, A data manipulation package created by the members of group number 20

Description Functions used during data cleaning, augmentation, modelling and data visualisation.

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RoxygenNote 7.1.2

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Encoding UTF-8

Depends magrittr

Imports broom,

dplyr,
ggplot2,
ggrepel,
stringr,
tidyr,
tidyselect

Suggests knitr,
rmarkdown

VignetteBuilder knitr

URL <https://rforbiodatascience22.github.io/Twenty/>

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convert_to_long	<i>Table of Genes in a long format</i>
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Description

Transformation of a gene expression matrix into a 3 column table.

Usage

```
convert_to_long(the_dataset)
```

Arguments

the_dataset This is a dataset often in a wide format.

Value

gene_data

Author(s)

Oriade Latifah Simpson

Examples

```
data("data_two")
my_data_two
my_long_data <- convert_to_long(my_data_two)
my_long_data
```

make_nested	<i>Nested dataset to use downstream</i>
-------------	---

Description

Creates nested table of grouped genes that may be useful for further modelling.

Usage

```
make_nested(long_dataset, Gene, value, expression_level)
```

Arguments

long_dataset This is the dataset provided
 Gene This is the list of genes.
 value The is the value variable.
 expression_level This is the expression level variable.

Value

nested_outcome

Author(s)

Miss Oriade Latifah Simpson, <s172084@dtu.dk>

Examples

```
data("data_two")
```

make_rotation_table	Create a rotation table from a modelled PCA object.
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Description

Create a rotation table from a modelled PCA object.

Usage

```
make_rotation_table(pca_fit)
```

Arguments

pca_fit	This is a model object.
---------	-------------------------

Value

rt

Author(s)

Miss Oriade Latifah Simpson, <s172084@dtu.dk>

Examples

```
data("wide_wide_west")
west_data_wide
fitted_pca_object <- perform_pca(west_data_wide)
fitted_pca_object
rot_tab <- make_rotation_table(fitted_pca_object)
rot_tab
```

my_data_one	<i>Example dataset 01_my_data</i>
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Description

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(my_data_one)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(my_data_one)
```

my_data_three	<i>Example dataset 03_my_data_clean_aug The augmented dataset</i>
---------------	---

Description

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(my_data_three)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(my_data_three)
```

my_data_two*Example dataset 02_my_data_clean The cleaned dataset*

Description

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(my_data_two)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(my_data_two)
```

perform_pca*Example dataset Model data using Principal Components analysis*

Description

Perform data modelling using principal components analysis

Usage

```
perform_pca(provided_dataset)
```

Arguments

provided_dataset

This is the dataset that is provided to the function

Value

modelled_data

Author(s)

Miss Oriade Latifah Simpson, <s172084@dtu.dk>

Examples

```
data("wide_wide_west")
west_data_wide
pca_fit <- perform_pca(west_data_wide)
pca_fit
```

results_grand_pca	<i>Example dataset results_grand_pca A PCA table</i>
-------------------	--

Description

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(results_grand_pca)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(results_grand_pca)
```

results_kmean_aug	<i>Example dataset The Augmented KMeans Results</i>
-------------------	---

Description

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(results_kmean_aug)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(results_kmean_aug)
```

`results_pca_eig`

*Example dataset PCA Eigenvalues***Description**

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(results_pca_eig)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(results_pca_eig)
```

`west`

*Example dataset The original raw data***Description**

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(west)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(west)
```

west_data_wide

Example dataset west_data_wide A wide dataset

Description

Data from Predicting the clinical status of human breast cancer by using gene expression profiles

Usage

```
data(west_data_wide)
```

Format

A dataframe

Source

<https://github.com/ramhiser/datamicroarray/blob/master/data/west.RData>

References

Predicting the clinical status of human breast cancer by using gene expression profiles DOI: 10.1073/pnas.201162998

Examples

```
data(west_data_wide)
```


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