CompSign: Analysis of Mutational Signatures

November 19, 2018

Breast560   *Normalised exposures of 560 Breast Cancer genomes from the paper Landscape of somatic mutations in 560 breast cancer whole-genome sequences*

Description

It contains 12 signatures

Usage

Breast560

Format

A merged_compositional object with a 560x12 exposure matrix and a data frame with clinical data, of dimension 560x47.

price price, in US dollars

carat weight of the diamond, in carats

donor_gender

donor_age_at_diagnosis

donor_age_at_last_follow.up

specimen_type

donor_vital_status

disease_status_last_follow.up

donor_relapse_interval__in_DAYS

donor_survival_time_in_DAYS

donor_interval_of_last_follow.up_in_DAYS

tumour_grade

T_stage

N_stage

M_stage

known_germline_mutations

sample_removed_pre_or_post.treatment

source_of_normal

X._tumour_cellularity

smoking.history

other.exposure

parity

age_at_birth_of_first_child_.years.

oral_contraception_exposure

oral_contraception_years

menopausal_status_at_diagnosis

HRT_history_years

number_of_positive_lymph_nodes

DCIS_Grade

Histopathological_subtype

tubule_score

pleomorphism_score

mitotic_score

total_mitoses

grade

Lymphovascular_invasion

Lymphocyte_infiltration

tumour_border

Central_scar.fibrosis

Necrosis

X._Invasive_tumour

X._CIS

X._Stroma

X._Lymphocytes

X._Adipose_tissue

X._Normal_epithelium

final.ER

final.PR

final.HER2

CONTINUE yadayada ...

Source

https://www.nature.com/articles/nature17676

addPseudoCounts	*Add pseudocounts; renormalise*

Description

Add pseudocounts; renormalise

Usage

```
addPseudoCounts(count_matrix, pseudocount = 1e-05)
```

comp_lda	*It computes the LDA for categorical responses (??? need to change? they are actually the predictors)*

Description

It computes the LDA for categorical responses (??? need to change? they are actually the predictors)

Usage

```
comp_lda(x, indices_response)
```

comp_lm	*(ongoing) Linear regression with compositional data as the response It computes a linear regression with some numerical value as the predictor and the compositions as response*

Description

(ongoing) Linear regression with compositional data as the response It computes a linear regression with some numerical value as the predictor and the compositions as response

Usage

```
comp_lm(x, indices_predictor)
```

---

comp_logistic   *Perform logistic regression*

Description

Perform logistic regression

Usage

```
comp_logistic(merged_obj, colname)
```

Arguments

merged_obj	a merged_compositional object
colname	either the name or the index of the column in metadata(merged_compositional) with which to perform logistic regression

Value

The summary of a logistic regression

---

compare_populations   *Compare two groups*

Description

Compare two groups

Usage

```
compare_populations(predictors, response, ...)
```

---

count_matrix<-   *Assign count matrix from object of class sign*

Description

Assign count matrix from object of class sign

Usage

```
count_matrix(object) <- value
```

count_matrix	*Retrieve count matrix from object of class sign.*

Description

Retrieve count matrix from object of class sign.

Usage

```
count_matrix(X)
```

Arguments

X	object of class sign

createDendrogram	*Create a dendrogram, using Aithchison distance, of the samples in a merged object. The labels are coloured according to the one of the columns of its metadata dataframe (to be specified in name_clinical). There is also an option (bool_comparison) to add a second dendrogram using Euclidean distance, for comparison. Arguments for plot() are inherited (not tested). WARNING! colours for the second dendrogram need fixing*

Description

Create a dendrogram, using Aithchison distance, of the samples in a merged object. The labels are coloured according to the one of the columns of its metadata dataframe (to be specified in name_clinical). There is also an option (bool_comparison) to add a second dendrogram using Euclidean distance, for comparison. Arguments for plot() are inherited (not tested). WARNING! colours for the second dendrogram need fixing

Usage

```
createDendrogram(merged_object, name_clinical, bool_comparison, ...)
```

hello	*Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

---

id<-   *Add name to object of class sign or merged_compositional*

Description

Add name to object of class sign or merged_compositional

Usage

```
id(object) <- value
```

---

merged_compositional-class

> *Class whiuch inludes features of both metadata and mutational signatures. types_metadata is a vector indicating which type of data each column in df (metadata) is.*

Description

Class whiuch inludes features of both metadata and mutational signatures. types_metadata is a vector indicating which type of data each column in df (metadata) is.

---

merged_compositional_to_sign

> *Convert a 'sign' object to a 'merged_compositional_to_sign' (note loss of information)*

Description

Convert a 'sign' object to a 'merged_compositional_to_sign' (note loss of information)

Usage

```
merged_compositional_to_sign(x)
```

---

metadata<-   *Assign metadata to object of class sign*

Description

Assign metadata to object of class sign

Usage

```
metadata(object) <- value
```

metadata	*Retrieve count matrix from object of class sign.*

Description

Retrieve count matrix from object of class sign.

Usage

```
metadata(X)
```

Arguments

X   object of class sign

to_sign	*Converts a matrix to a sign object*

Description

Converts a matrix to a sign object

Usage

```
to_sign(x)
```

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