# CompSign: Analysis of Mutational Signatures

October 24, 2018

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Breast560

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

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**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

| 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 | *It computes a linear regression with some numerical value as the predictor and the compositions as response* |
|---|---|

### Description

It computes a linear regression with some numerical value as the predictor and the compositions as response

### Usage

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

| 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. X is of class sign* |
|---|---|

## Description

Retrieve count matrix from object of class sign. X is of class sign

## Usage

```
count_matrix(X)
```

| 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()
```

## 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. X is of class sign*

### Description

Retrieve count matrix from object of class sign. X is of class sign

### Usage

```
metadata(X)
```

## 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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