

# Package ‘YAPSA’

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**Description** This package provides functions and routines useful in the analysis of somatic signatures (cf. L. Alexandrov et al., Nature 2013). In particular, functions to perform a signature analysis with known signatures (LCD = linear combination decomposition) and a signature analysis on stratified mutational catalogue (SMC = stratify mutational catalogue) are provided.

**License** GPL-3

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<code>add_annotation</code>	<i>Add information to an annotation data structure</i>
-----------------------------	--

---

## Description

Function to iteratively add information to an annotation data structure as needed for [HeatmapAnnotation](#) and especially for [annotation\\_exposures\\_barplot](#)

## Usage

```
add_annotation(in_annotation_col, in_annotation_df, in_attribution_vector,
              in_colour_vector, in_name)
```

## Arguments

- `in_annotation_col`  
List, every element of which refers to one layer of annotation. List elements are structures corresponding to named colour vectors
- `in_annotation_df`  
Data frame, every column of which corresponds to a layer of annotation. It has as many rows as there are samples, every entry in a row corresponding to the attribute the samples has for the corresponding layer of annotation. The factor levels of a column of `in_annotation_df` correspond to the names of the corresponding element in `in_annotation_col`
- `in_attribution_vector`  
A vector which is going to be cbinded to `in_annotation_df`, carrying the annotation information of the new layer to be added
- `in_colour_vector`  
Named vector of colours to be attributed to the new annotation
- `in_name`  
Name of the new layer of annotation

**Value**

A list with entries

- `annotation_col`: A list as in `in_annotation_col` but with one additional layer of annotation
- `annotation_df`: A data frame as in `in_annotation_df` but with one additional layer of annotation

**Examples**

NULL

---

`add_as_fist_to_list`     *Add an element as first entry to a list*

---

**Description**

Works for all types of lists and inputs

**Usage**

```
add_as_fist_to_list(in_list, in_element)
```

**Arguments**

<code>in_list</code>	List to which an element is to be added
<code>in_element</code>	Element to be added

**Value**

List with input element as first entry.

**Examples**

NULL

---

`aggregate_exposures_by_category`  
*Aggregate exposures by category*

---

**Description**

If a valid category (i.e. it matches to a category specified in `in_sig_ind_df`) is supplied, then the exposures are aggregated over this category.

**Usage**

```
aggregate_exposures_by_category(in_exposures_df, in_sig_ind_df, in_category)
```

### Arguments

in_exposures_df	Input data frame of exposures.
in_sig_ind_df	Input data frame of meta information on the signatures. Has to match the signatures in in_exposures_df
in_category	Category to be aggregated over

### Value

A list with entries:

- exposures: The exposures H, a numeric data frame with  $l$  rows and  $m$  columns,  $l$  being the number of aggregated signatures and  $m$  being the number of samples
- norm\_exposures: The normalized exposures H, a numeric data frame with  $l$  rows and  $m$  columns,  $l$  being the number of aggregated signatures and  $m$  being the number of samples
- out\_sig\_ind\_df: Data frame of the type signature\_indices\_df, i.e. indicating name, function and meta-information of the aggregated signatures..

### See Also

[LCD\\_complex\\_cutoff](#)

### Examples

NULL

annotate\_intermut\_dist\_cohort

*Annotate the intermutation distance of variants cohort-wide*

### Description

The function annotates the intermutational distance to a cohort wide data frame by applying [annotate\\_intermut\\_dist\\_PID](#) to every PID-specific subfraction of the cohort wide data. Note that [annotate\\_intermut\\_dist\\_PID](#) calls [rainfallTransform](#). If the PID information is missing, [annotate\\_intermut\\_dist\\_PID](#) is called directly for the whole input.

### Usage

```
annotate_intermut_dist_cohort(in_dat, in_CHROM.field = "CHROM",
  in_POS.field = "POS", in_PID.field = NULL, in_mode = "min",
  in_verbose = FALSE)
```

**Arguments**

<code>in_dat</code>	VRanges object, VRangesList, data frame or list of data frames which carries (at least) one column for the chromosome and one column for the position. Optionally, a column to specify the PID can be provided.
<code>in_CHROM.field</code>	String indicating which column of <code>in_df</code> carries the chromosome information
<code>in_POS.field</code>	String indicating which column of <code>in_df</code> carries the position information
<code>in_PID.field</code>	String indicating which column of <code>in_df</code> carries the PID information
<code>in_mode</code>	String passed through <code>annotate_intermut_dist_PID</code> to <code>rainfallTransform</code> indicating which method to choose for the computation of the intermutational distance.
<code>in_verbose</code>	Whether verbose or not.

**Value**

VRanges object, VRangesList, data frame or list of data frames identical to `in_df` (reordered by `in_PID.field`), but with the intermutation distance annotated as an additional column on the right named `dist`.

**See Also**

[annotate\\_intermut\\_dist\\_PID](#)

[rainfallTransform](#)

**Examples**

```
test_df <- data.frame(CHROM=c(1,1,1,2,2,2,3,3,3,4,4,4,5,5),
                     POS=c(1,2,4,4,6,9,1,4,8,10,20,40,100,200),
                     REF=c("C","C","C","T","T","T","A",
                            "A","A","G","G","G","N","A"),
                     ALT=c("A","G","T","A","C","G","C",
                            "G","T","A","C","T","A","N"),
                     PID=c(1,1,1,2,2,2,1,1,2,2,2,1,1,2))
test_df <- test_df[order(test_df$PID, test_df$CHROM, test_df$POS),]
min_dist_df <-
  annotate_intermut_dist_cohort(test_df, in_CHROM.field="CHROM",
                              in_POS.field="POS", in_PID.field="PID",
                              in_mode="min")
max_dist_df <-
  annotate_intermut_dist_cohort(test_df, in_CHROM.field="CHROM",
                              in_POS.field="POS", in_PID.field="PID",
                              in_mode="max")

min_dist_df
max_dist_df
```

annotate\_intermut\_dist\_PID

*Annotate the intermutation distance of variants per PID*

## Description

The function annotates the intermutational distance to a PID wide data frame by applying [rainfallTransform](#) to every chromosome-specific subfraction of the PID wide data.

## Usage

```
annotate_intermut_dist_PID(in_dat, in_CHROM.field = "CHROM",
  in_POS.field = "POS", in_mode = "min", in_verbose = FALSE)
```

## Arguments

in_dat	VRanges object or data frame which carries (at least) one column for the chromosome and one column for the position.
in_CHROM.field	String indicating which column of in_dat carries the chromosome information if dealing with data frames.
in_POS.field	String indicating which column of in_dat carries the position information if dealing with data frames.
in_mode	String passed to <a href="#">rainfallTransform</a> indicating which method to choose for the computation of the intermutational distance.
in_verbose	Whether verbose or not.

## Value

VRanges object or data frame identical to in\_dat, but with the intermutation distance annotated as an additional column on the right named dist.

## See Also

[annotate\\_intermut\\_dist\\_cohort](#)  
[rainfallTransform](#)

## Examples

```
test_df <- data.frame(
  CHROM=c(1,1,1,2,2,2,3,3,3,4,4,4,5,5),
  POS=c(1,2,4,4,6,9,1,4,8,10,20,40,100,200),
  REF=c("C","C","C","T","T","T","A","A","A","G","G","G","N","A"),
  ALT=c("A","G","T","A","C","G","C","G","T","A","C","T","A","N"))
min_dist_df <- annotate_intermut_dist_PID(test_df,in_CHROM.field="CHROM",
  in_POS.field="POS",
  in_mode="min")
max_dist_df <- annotate_intermut_dist_PID(test_df,in_CHROM.field="CHROM",
  in_POS.field="POS",
  in_mode="max")

min_dist_df
max_dist_df
```

---

 annotation\_exposures\_barplot

*Plot the exposures of a cohort with different layers of annotation*


---

## Description

The exposures  $H$ , determined by NMF or by LCD, are displayed as a stacked barplot by calling [Heatmap](#). The x-axis displays the PIDs (patient identifier or sample), the y-axis the counts attributed to the different signatures with their respective colours per PID. It is analogous to [plot\\_exposures](#). As many layers of information as desired can be added via an annotation data frame. The annotation data is handled in a way similar to [annotation\\_heatmap\\_exposures](#). This function calls:

- [rowAnnotation](#),
- [HeatmapAnnotation](#) and
- [Heatmap](#)

## Usage

```
annotation_exposures_barplot(in_exposures_df, in_signatures_ind_df,
  in_subgroups_df, in_annotation_df, in_annotation_col, ylab = NULL,
  title = "", in_labels = FALSE, in_barplot_borders = TRUE,
  in_column_anno_borders = FALSE, in_annotation_legend_side = "right")
```

## Arguments

in_exposures_df	Numerical data frame encoding the exposures $H$ , i.e. which signature contributes how much to which PID (patient identifier or sample).
in_signatures_ind_df	A data frame containing meta information about the signatures
in_subgroups_df	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup
in_annotation_df	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup for all layers of annotation
in_annotation_col	A list indicating colour attributions for all layers of annotation
ylab	String indicating the column name in in_subgroups_df to take the subgroup information from.
title	Title for the plot to be created.
in_labels	Whether or not to show the names of the samples.
in_barplot_borders	Whether or not to show border lines in barplot
in_column_anno_borders	Whether or not to draw separating lines between the fields in the annotation
in_annotation_legend_side	Where to put the legends of the annotation df, default is right.



## Details

It might be necessary to install the newest version of the development branch of the packages **cir-clize** and **ComplexHeatmap** by Zuguang Gu: `devtools::install_github("jokergoo/circlize")` and `devtools::install_github("jokergoo/ComplexHeatmap")`

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## Value

The function doesn't return any value.

## See Also

[HeatmapAnnotation](#)

[Heatmap](#)

[decorate\\_heatmap\\_body](#)

[annotation\\_heatmap\\_exposures](#)

[plot\\_exposures](#)

## Examples

```
NULL
```

---

annotation\_heatmap\_exposures

*Heatmap to cluster the PIDs on their signature exposures (Complex-Heatmap)*

---

## Description

The PIDs are clustered according to their signature exposures. The procedure is analogous to [complex\\_heatmap\\_exposures](#), but enabling more than one annotation row for the PIDs. This function calls:

- [rowAnnotation](#),
- [HeatmapAnnotation](#) and
- [Heatmap](#)

## Usage

```
annotation_heatmap_exposures(in_exposures_df, in_annotation_df,  
  in_annotation_col, in_signatures_ind_df, in_data_type = "norm exposures",  
  in_method = "manhattan", in_palette = colorRamp2(c(0, 0.2, 0.4, 0.6),  
  c("white", "yellow", "orange", "red")), in_cutoff = 0, in_filename = NULL,  
  in_column_anno_borders = FALSE, in_row_anno_borders = FALSE,  
  in_show_PIDs = TRUE, in_annotation_legend_side = "right")
```

**Arguments**

<code>in_exposures_df</code>	Numerical data frame encoding the exposures H, i.e. which signature contributes how much to which PID (patient identifier or sample).
<code>in_annotation_df</code>	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup for all layers of annotation
<code>in_annotation_col</code>	A list indicating colour attributions for all layers of annotation
<code>in_signatures_ind_df</code>	A data frame containing meta information about the signatures, especially the asserted colour
<code>in_data_type</code>	Title in the figure
<code>in_method</code>	Method of the clustering to be supplied to <code>dist</code> . Can be either of: euclidean, maximum, manhattan, canberra, binary or minkowski
<code>in_palette</code>	Palette with colours or colour codes for the heatmap. Default is <code>colorRamp2(c(0, 0.2, 0.4, 0.6),</code>
<code>in_cutoff</code>	A numeric value less than 1. Signatures from within W with an overall exposure less than <code>in_cutoff</code> will be discarded for the clustering.
<code>in_filename</code>	A path to save the heatmap. If none is specified, the figure will be plotted to the running environment.
<code>in_column_anno_borders</code>	Whether or not to draw separating lines between the fields in the annotation
<code>in_row_anno_borders</code>	Whether or not to draw separating lines between the fields in the annotation
<code>in_show_PIDs</code>	Whether or not to show the PIDs on the x-axis
<code>in_annotation_legend_side</code>	Where to put the legends of the annotation df, default is right.

**Details**

One additional parameter, `in_show_legend_bool_vector`, indicating which legends to display, is planned but deactivated in this version of the package. In order to use this features, it will be necessary to install the newest version of the packages **circlize** and **ComplexHeatmap** by Zuguang Gu: `devtools::install_github("jokergoo/circlize")` and `devtools::install_github("jokergoo/ComplexHeatmap")`

**Value**

The function doesn't return any value.

**See Also**

[Heatmap](#)  
[complex\\_heatmap\\_exposures](#)

**Examples**

NULL

---

 attribute\_nucleotide\_exchanges

*Attribute the nucleotide exchange for an SNV*


---

### Description

SNVs are grouped into 6 different categories (12/2 as reverse complements are summed over). This function defines the attribution.

### Usage

```
attribute_nucleotide_exchanges(in_dat, in_REF.field = "REF",
  in_ALT.field = "ALT", in_verbose = FALSE)
```

### Arguments

in_dat	VRanges object or data frame which carries one column for the reference base and one column for the variant base
in_REF.field	String indicating which column of in_dat carries the reference base if dealing with data frames
in_ALT.field	String indicating which column of in_dat carries the variant base if dealing with data frames
in_verbose	Whether verbose or not.

### Value

A character vector with as many rows as there are in in\_dat which can be annotated (i.e. appended) to the input data frame.

### Examples

```
test_df <- data.frame(
  CHROM=c(1,1,1,2,2,2,3,3,3,4,4,4,5,5),
  POS=c(1,2,3,4,5,6,1,2,3,4,5,6,7,8),
  REF=c("C","C","C","T","T","T","A","A","A","G","G","G","N","A"),
  ALT=c("A","G","T","A","C","G","C","G","T","A","C","T","A","N"))
test_df$change <- attribute_nucleotide_exchanges(
  test_df,in_REF.field = "REF",in_ALT.field = "ALT")
test_df
```

---

 build\_gene\_list\_for\_pathway

*Build a gene list for a given pathway name*


---

### Description

Build a gene list for a given pathway name

**Usage**

```
build_gene_list_for_pathway(in_string, in_organism)
```

**Arguments**

```
in_string      Name or description of the pathway
in_organism    Name of the taxon to be searched in
```

**Value**

A character vector of gene names

**See Also**

[keggLink](#)  
[keggFind](#)  
[extract\\_names\\_from\\_gene\\_list](#)

**Examples**

```
NULL
## Not run:
species <- "hsa"
gene_lists_meta_df <- data.frame(
  name=c("BER", "NHEJ", "MMR"),
  explanation=c("base excision repair",
                "non homologous end joining",
                "mismatch repair"))
number_of_pathways <- dim(gene_lists_meta_df)[1]
gene_lists_list <- list()
for (i in seq_len(number_of_pathways)) {
  temp_list <-
    build_gene_list_for_pathway(gene_lists_meta_df$explanation[i],
                               species)
  gene_lists_list <- c(gene_lists_list, list(temp_list))
}
gene_lists_list

## End(Not run)
```

---

compare_exposures	<i>Compares alternative exposures</i>
-------------------	---------------------------------------

---

**Description**

Compares exposures computed by two alternative approaches for the same cohort

**Usage**

```
compare_exposures(in_exposures1_df, in_exposures2_df, deselect_flag = TRUE)
```

**Arguments**

- `in_exposures1_df` Numeric data frame with exposures, ideally the smaller exposure data is supplied first.
- `in_exposures2_df` Numeric data frame with exposures, ideally the bigger exposure data is supplied second.
- `deselect_flag` Whether signatures absent in both exposure data frames should be removed.

**Value**

A list with entries `merge_df`, `all_cor.coeff`, `all_p.value`, `cor.coeff_vector`, `p.value_vector`, `all_cor.test`, and `cor.test_list`.

- `merge_df`: Merged molten input exposure data frames
- `all_cor.coeff`: Pearson correlation coefficient for all data points, i.e. taken all signatures together
- `all_p.value`: P-value of the Pearson test for all data points, i.e. taken all signatures together
- `cor.coeff_vector`: A vector of Pearson correlation coefficients evaluated for every signature independently
- `p.value_vector`: A vector of p-values of the Pearson tests evaluated for every signature independently
- `all_cor.test`: A data structure as returned by `cor.test` for all data points, i.e. taken all signatures together
- `cor.test_list`: A list of data structures as returned by `cor.test`, but evaluated for every signature independently

**Examples**

NULL

---

<code>compare_sets</code>	<i>Compare two sets of signatures by cosine distance</i>
---------------------------	--

---

**Description**

Compare two sets of signatures, stored in numerical data frames W1 and W2, by computing the column-wise cosine distance

**Usage**

```
compare_sets(in_df_small, in_df_big)
```

**Arguments**

- `in_df_small`, `in_df_big` Numerical data frames W1 and W2, ideally the bigger one first, both with `n` rows and `l1` and `l2` columns, `n` being the number of features and `l1` and `l2` being the respective numbers of signatures of W1 and W2

**Value**

A list with entries `distance`, `hierarchy_small` and `hierarchy_big`.

- `distance`: A numerical data frame with the cosine distances between the columns of W1, indexing the rows, and W2, indexing the columns
- `hierarchy_small`: A data frame carrying the information of ranked similarity between the signatures in W2 with the signatures in W1
- `hierarchy_big`: A data frame carrying the information of ranked similarity between the signatures in W1 with the signatures in W2

**See Also**

[cosineDist](#)

**Examples**

```
sig_1_df <- data.frame(matrix(c(1,0,0,0,0,1,0,0,0,0,1,0),ncol=3))
names(sig_1_df) <- paste0("B",seq_len(dim(sig_1_df)[2]))
sig_2_df <- data.frame(matrix(c(1,1,0,0,0,0,1,1),ncol=2))
compare_sets(sig_1_df,sig_2_df)
```

---

compare\_SMCs

*Compare all strata from different stratifications*

---

**Description**

Compare all strata from different orthogonal stratification axes, i.e. orthogonal SMCs by cosine similarity of signature exposures. First calls

- `make_strata_df`, then
- `plot_strata` and finally
- `make_comparison_matrix`

**Usage**

```
compare_SMCs(in_stratification_lists_list, in_signatures_ind_df, output_path,
             in_nrect = 5, in_attribute = "")
```

**Arguments**

<code>in_stratification_lists_list</code>	List of lists with entries from different (orthogonal) stratification axes or SMCs
<code>in_signatures_ind_df</code>	A data frame containing meta information about the signatures
<code>output_path</code>	Path to directory where the results, especially the figure produced by <code>corrplot</code> is going to be stored.
<code>in_nrect</code>	Number of clusters in the clustering procedure provided by <code>corrplot</code>
<code>in_attribute</code>	Additional string for the file name where the figure produced by <code>corrplot</code> is going to be stored.

**Value**

The comparison matrix of cosine similarities.

**See Also**

[plot\\_strata](#)

[make\\_comparison\\_matrix](#)

**Examples**

NULL

---

compare\_to\_catalogues *Compare one mutational catalogue to reference mutational catalogues*

---

**Description**

Compare one mutational catalogue (e.g. of one index patient) to a list of reference mutational catalogues (e.g. from the initial Alexandrov publication) by cosine similarities

**Usage**

```
compare_to_catalogues(in_index_df, in_comparison_list)
```

**Arguments**

`in_index_df` Data frame containing the mutational catalogue of interest

`in_comparison_list`

List of data frames (ideally named) containing the reference mutational catalogues

**Value**

A similarity dataframe

**Examples**

NULL

---

complex\_heatmap\_exposures

*Heatmap to cluster the PIDs on their signature exposures (Complex-Heatmap)*

---

## Description

The PIDs are clustered according to their signature exposures. uses package **ComplexHeatmap** by Zuguang Gu. This function calls:

- [rowAnnotation](#),
- [HeatmapAnnotation](#) and
- [Heatmap](#)

## Usage

```
complex_heatmap_exposures(in_exposures_df, in_subgroups_df,
  in_signatures_ind_df, in_data_type = "norm exposures",
  in_method = "manhattan", in_subgroup_column = "subgroup",
  in_subgroup_colour_column = NULL, in_palette = colorRamp2(c(0, 0.2, 0.4,
  0.6), c("white", "yellow", "orange", "red")), in_cutoff = 0,
  in_filename = NULL, in_column_anno_borders = FALSE,
  in_row_anno_borders = FALSE)
```

## Arguments

<code>in_exposures_df</code>	Numerical data frame encoding the exposures H, i.e. which signature contributes how much to which PID (patient identifier or sample).
<code>in_subgroups_df</code>	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup
<code>in_signatures_ind_df</code>	A data frame containing meta information about the signatures, especially the asserted colour
<code>in_data_type</code>	Title in the figure
<code>in_method</code>	Method of the clustering to be supplied to <a href="#">dist</a> . Can be either of: euclidean, maximum, manhattan, canberra, binary or minkowski
<code>in_subgroup_column</code>	Indicates the name of the column in which the subgroup information is encoded in <code>in_subgroups_df</code>
<code>in_subgroup_colour_column</code>	Indicates the name of the column in which the colour information for subgroups is encoded in <code>in_subgroups_df</code> . If NULL, a rainbow palette is used instead.
<code>in_palette</code>	Palette with colours for the heatmap. Default is <code>colorRamp2(c(0, 0.2, 0.4, 0.6), c('white', 'y</code>
<code>in_cutoff</code>	A numeric value less than 1. Signatures from within W with an overall exposure less than <code>in_cutoff</code> will be discarded for the clustering.
<code>in_filename</code>	A path to save the heatmap. If none is specified, the figure will be plotted to the running environment.



in\_column\_anno\_borders

Whether or not to draw separating lines between the fields in the annotation

in\_row\_anno\_borders

Whether or not to draw separating lines between the fields in the annotation

### Details

It might be necessary to install the newest version of the development branch of the packages **circlize** and **ComplexHeatmap** by Zuguang Gu: `devtools::install_github("jokergoo/circlize")` and `devtools::install_github("jokergoo/ComplexHeatmap")`

### Value

The function doesn't return any value.

### See Also

[Heatmap](#)

### Examples

```
data(lymphoma_cohort_LCD_results)
complex_heatmap_exposures(
  rel_lymphoma_Nature2013_COSMIC_cutoff_exposures_df,
  COSMIC_subgroups_df,
  chosen_signatures_indices_df,
  in_data_type="norm exposures",
  in_subgroup_colour_column="col",
  in_method="manhattan",
  in_subgroup_column="subgroup")
```

---

compute\_comparison\_stat\_df

*Extract statistical measures for entity comparison*

---

### Description

Compare one mutational catalogue (e.g. of one index patient) to a list of reference mutational catalogues (e.g. from the initial Alexandrov publication) by cosine similarities

### Usage

```
compute_comparison_stat_df(in_sim_df)
```

### Arguments

in\_sim\_df      A similarity data frame as extracted by [compare\\_to\\_catalogues](#)

### Value

A dataframe containing statistical measures, prepared for bar plot

**Examples**

NULL

---

cosineDist	<i>Compute the cosine distance of two vectors</i>
------------	---

---

**Description**

Compute the cosine distance of two vectors

**Usage**

```
cosineDist(a, b)
```

**Arguments**

a, b                      Numerical vectors of same length

**Value**

The scalar product of the two input vectors divided by the product of the norms of the two input vectors

**Examples**

```
## 1. Orthogonal vectors:
cosineDist(c(1,0),c(0,1))
## 2. Non-orthogonal vectors:
cosineDist(c(1,0),c(1,1))
## Compare trigonometry:
1-cos(pi/4)
```

---

create_mutation_catalogue_from_df	<i>Create a Mutational Catalogue from a data frame</i>
-----------------------------------	--

---

**Description**

This function creates a mutational catalogue from a data frame. It is a wrapper function for [create\\_mutation\\_catalogue\\_from\\_VR](#): it first creates a VRanges object from the data frame by [makeVRangesFromDataFrame](#) and then passes this object on to the above mentioned custom function.

**Usage**

```
create_mutation_catalogue_from_df(this_df, this_refGenome_Seqinfo = NULL,
  this_seqnames.field = "X.CHROM", this_start.field = "POS",
  this_end.field = "POS", this_PID.field = "PID",
  this_subgroup.field = "subgroup", this_refGenome, this_wordLength,
  this_verbose = 1, this_rownames = c(), this_adapt_rownames = 1)
```

**Arguments**

<code>this_df</code>	A data frame constructed from a vcf-like file of a whole cohort. The first columns are those of a standard vcf file, followed by an arbitrary number of custom or used defined columns. One of these can carry a PID (patient or sample identifier) and one can carry subgroup information.
<code>this_refGenome_Seqinfo</code>	A <code>seqInfo</code> object, referring to the reference genome used. Argument passed on to <a href="#">makeGRangesFromDataFrame</a> and thus indirectly to <a href="#">makeGRangesFromDataFrame</a> .
<code>this_seqnames.field</code>	Indicates the name of the column in which the chromosome is encoded
<code>this_start.field</code>	Indicates the name of the column in which the start coordinate is encoded
<code>this_end.field</code>	Indicates the name of the column in which the end coordinate is encoded
<code>this_PID.field</code>	Indicates the name of the column in which the PID (patient or sample identifier) is encoded
<code>this_subgroup.field</code>	Indicates the name of the column in which the subgroup information is encoded
<code>this_refGenome</code>	The reference genome handed over to <a href="#">create_mutation_catalogue_from_VR</a> and indirectly to <a href="#">mutationContext</a> and used to extract the motif context of the variants in <code>in_vr</code> .
<code>this_wordLength</code>	The size of the motifs to be extracted by <a href="#">mutationContext</a>
<code>this_verbose</code>	Verbose if <code>this_verbose=1</code>
<code>this_rownames</code>	Optional parameter to specify rownames of the mutational catalogue V i.e. the names of the features.
<code>this_adapt_rownames</code>	Rownames of the output matrix will be adapted if <code>this_adapt_rownames=1</code>

**Value**

A list with entries `matrix` and `frame` obtained from [create\\_mutation\\_catalogue\\_from\\_VR](#):

- `matrix`: The mutational catalogue V
- `frame`: Additional and meta information on rownames (features), colnames (PIDs) and subgroup attribution.

**See Also**

[makeVRangesFromDataFrame](#)

[create\\_mutation\\_catalogue\\_from\\_VR](#)

**Examples**

```
library(BSgenome.Hsapiens.UCSC.hg19)
data(lymphoma_test)
word_length <- 3
temp_list <- create_mutation_catalogue_from_df(
  lymphoma_test_df, this_seqnames.field = "CHROM",
  this_start.field = "POS", this_end.field = "POS",
  this_PID.field = "PID", this_subgroup.field = "SUBGROUP",
  this_refGenome = BSgenome.Hsapiens.UCSC.hg19,
```

```

this_wordLength = word_length)
dim(temp_list$matrix)
head(temp_list$matrix)

```

---

```
create_mutation_catalogue_from_VR
```

*Create a Mutational Catalogue from a VRanges Object*

---

## Description

This function creates a mutational catalogue from a VRanges Object by first calling [mutationContext](#) to establish the motif context of the variants in the input VRanges and then calling [motifMatrix](#) to build the mutational catalogue V.

## Usage

```

create_mutation_catalogue_from_VR(in_vr, in_refGenome, in_wordLength,
  in_PID.field = "PID", in_verbose = 0, in_rownames = c(),
  adapt_rownames = 1)

```

## Arguments

<code>in_vr</code>	A VRanges object constructed from a vcf-like file of a whole cohort. The first columns are those of a standard vcf file, followed by an arbitrary number of custom or used defined columns. One of these can carry a PID (patient or sample identifier) and one can carry subgroup information.
<code>in_refGenome</code>	The reference genome handed over to <a href="#">mutationContext</a> and used to extract the motif context of the variants in <code>in_vr</code> .
<code>in_wordLength</code>	The size of the motifs to be extracted by <a href="#">mutationContext</a>
<code>in_PID.field</code>	Indicates the name of the column in which the PID (patient or sample identifier) is encoded
<code>in_verbose</code>	Verbose if <code>in_verbose=1</code>
<code>in_rownames</code>	Optional parameter to specify rownames of the mutational catalogue V i.e. the names of the features.
<code>adapt_rownames</code>	Rownames of the output matrix will be adapted if <code>adapt_rownames=1</code>

## Value

A list with entries `matrix`, `frame`,

- `matrix`: The mutational catalogue V
- `frame`: Additional and meta information on rownames (features), colnames (PIDs) and subgroup attribution.

## See Also

[mutationContext](#)

[motifMatrix](#)

**Examples**

```

library(BSgenome.Hsapiens.UCSC.hg19)
data(lymphoma_test)
data(sigs)
word_length <- 3
temp_vr <- makeVRangesFromDataFrame(
  lymphoma_test_df, in_seqnames.field="CHROM",
  in_subgroup.field="SUBGROUP", verbose_flag=1)
temp_list <- create_mutation_catalogue_from_VR(
  temp_vr, in_refGenome=BSgenome.Hsapiens.UCSC.hg19,
  in_wordLength=word_length, in_PID.field="PID",
  in_verbose=1)
dim(temp_list$matrix)
head(temp_list$matrix)
test_list <- split(lymphoma_test_df, f=lymphoma_test_df$PID)
other_list <- list()
for(i in seq_len(length(test_list))){
  other_list[[i]] <- test_list[[i]][c(1:80),]
}
other_df <- do.call(rbind, other_list)
other_vr <- makeVRangesFromDataFrame(
  other_df, in_seqnames.field="CHROM",
  in_subgroup.field="SUBGROUP", verbose_flag=1)
other_list <- create_mutation_catalogue_from_VR(
  other_vr, in_refGenome=BSgenome.Hsapiens.UCSC.hg19,
  in_wordLength=word_length, in_PID.field="PID",
  in_verbose=1, in_rownames=rownames(AlexCosmicValid_sig_df))
dim(other_list$matrix)
head(other_list$matrix)

```

cutoffs

*Cutoffs for a supervised analysis of mutational signatures.***Description**

Series of data frames with signature-specific cutoffs. All values represent optimal cutoffs. The optimal cutoffs were determined for different choices of parameters in the cost function of the optimization. The row index is equivalent to the ratio between costs for false negative attribution and false positive attribution. The columns correspond to the different signatures. To be used with [LCD\\_complex\\_cutoff](#).

cutoffCosmicValid\_rel\_df: Optimal cutoffs for [AlexCosmicValid\\_sig\\_df](#), i.e. COSMIC signatures, only validated, trained on relative exposures.

cutoffCosmicArtif\_rel\_df: Optimal cutoffs for [AlexCosmicArtif\\_sig\\_df](#), i.e. COSMIC signatures, including artifact signatures, trained on relative exposures.

cutoffCosmicValid\_abs\_df: Optimal cutoffs for [AlexCosmicValid\\_sig\\_df](#), i.e. COSMIC signatures, only validated, trained on absolute exposures.

cutoffCosmicArtif\_abs\_df: Optimal cutoffs for [AlexCosmicArtif\\_sig\\_df](#), i.e. COSMIC signatures, including artifact signatures, trained on absolute exposures.

cutoffInitialValid\_rel\_df: Optimal cutoffs for [AlexInitialValid\\_sig\\_df](#), i.e. initially published signatures, only validated signatures, trained on relative exposures.

cutoffInitialArtif\_rel\_df: Optimal cutoffs for `AlexInitialArtif_sig_df`, i.e. initially published signatures, including artifact signatures, trained on relative exposures.

cutoffInitialValid\_abs\_df: Optimal cutoffs for `AlexInitialValid_sig_df`, i.e. initially published signatures, only validated signatures, trained on absolute exposures.

cutoffInitialArtif\_abs\_df: Optimal cutoffs for `AlexInitialArtif_sig_df`, i.e. initially published signatures, including artifact signatures, trained on absolute exposures.

### Usage

```
data(cutoffs)
```

### Author(s)

Daniel Huebschmann <huebschmann.daniel@gmail.com>

---

cut\_breaks\_as\_intervals

*Wrapper for cut*

---

### Description

In this wrapper function for the known `cut` function, the breaks vector need not be supplied directly, instead, for every break, an interval is supplied and the function optimizes the choice of the breakpoint by choosing a local minimum of the distribution.

### Usage

```
cut_breaks_as_intervals(in_vector, in_outlier_cutoffs = c(0, 3000),
  in_cutoff_ranges_list = list(c(60, 69), c(25, 32)), in_labels = c("late",
  "intermediate", "early"), in_name = "", output_path = NULL)
```

### Arguments

<code>in_vector</code>	Vector of numerical continuously distributed input
<code>in_outlier_cutoffs</code>	Interval specifying the upper and lower bounds of the range to be considered
<code>in_cutoff_ranges_list</code>	List of intervals in which the cutoffs for <code>cut</code> have to be optimized.
<code>in_labels</code>	Labels assigned to the strata or factors returned
<code>in_name</code>	String specifying the name of the quantity analyzed (and plotted on the x-axis of the figure to be created).
<code>output_path</code>	Path where the figure produced by the density function should be stored if non-NULL.

### Value

A list with entries `category_vector`, `density_plot` and `cutoffs`

- `category_vector`: Factor vector of the categories or strata, of the same length as `in_vector`
- `density_plot`: Density plot produced by the density function and indication of the chosen cutoffs.
- `cutoffs`: Vector of the computed optimal cutoffs

**See Also**

[cut](#)  
[density](#)

**Examples**

```
data(lymphoma_test)
lymphoma_test_df$random_norm <- rnorm(dim(lymphoma_test_df)[1])
temp_list <- cut_breaks_as_intervals(
  lymphoma_test_df$random_norm,
  in_outlier_cutoffs=c(-4,4),
  in_cutoff_ranges_list=list(c(-2.5,-1.5),c(0.5,1.5)),
  in_labels=c("small","intermediate","big"))
temp_list$density_plot
```

---

exampleYAPSA

*Test and example data*

---

**Description**

Data structures used in examples, tests and the vignette of the YAPSA package.

`lymphoma_PID_df`: A data frame carrying subgroup information for a subcohort of samples used in the vignette. Data in the vignette is downloaded from [ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic\\_mutation\\_data/LymphomaB-cell/LymphomaB-cell\\_clean\\_somatic\\_mutations\\_for\\_signature\\_analysis.txt](ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic_mutation_data/LymphomaB-cell/LymphomaB-cell_clean_somatic_mutations_for_signature_analysis.txt). In the file available under that link somatic point mutation calls from several samples are listed in a vcf-like format. One column encodes the sample the variant was found in. In the vignette we want to restrict the analysis to only a fraction of these involved samples. The data frame `lymphoma_PID_df` carries the sample identifiers (PID) as row-names and the attributed subgroup in a column called subgroup.

`lymphoma_test_df`: A data frame carrying point mutation calls. It represents a subset of the data stored in [ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic\\_mutation\\_data/LymphomaB-cell/LymphomaB-cell\\_clean\\_somatic\\_mutations\\_for\\_signature\\_analysis.txt](ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic_mutation_data/LymphomaB-cell/LymphomaB-cell_clean_somatic_mutations_for_signature_analysis.txt). In the file available under that link somatic point mutation calls from several samples are listed in a vcf-like format. One column encodes the sample the variant was found in. The data frame `lymphoma_test_df` has only the variants occurring in the sample identifiers (PIDs) 4112512, 4194218 and 4121361.

`lymphoma_Nature2013_raw_df`: A data frame carrying point mutation calls. It represents a subset of the data stored in [ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic\\_mutation\\_data/LymphomaB-cell/LymphomaB-cell\\_clean\\_somatic\\_mutations\\_for\\_signature\\_analysis.txt](ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic_mutation_data/LymphomaB-cell/LymphomaB-cell_clean_somatic_mutations_for_signature_analysis.txt). In the file available under that link somatic point mutation calls from several samples are listed in a vcf-like format. One column encodes the sample the variant was found in.

`lymphoma_Nature2013_COSMIC_cutoff_exposures_df`: Data frame with exposures for testing the plot functions. Data taken from [ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic\\_mutation\\_data/LymphomaB-cell/LymphomaB-cell\\_clean\\_somatic\\_mutations\\_for\\_signature\\_analysis.txt](ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/somatic_mutation_data/LymphomaB-cell/LymphomaB-cell_clean_somatic_mutations_for_signature_analysis.txt).

`rel_lymphoma_Nature2013_COSMIC_cutoff_exposures_df`: Data frame with normalized or relative exposures for testing the plot functions. Data taken from <ftp://ftp.sanger.ac.uk/pub/>

[cancer/AlexandrovEtAl/somatic\\_mutation\\_data/LymphomaB-cell/LymphomaB-cell\\_clean\\_somatic\\_mutations\\_for\\_signature\\_analysis.txt](#).

COSMIC\_subgroups\_df: Subgroup information for the data stored in [lymphoma\\_Nature2013\\_COSMIC\\_cutoff\\_exposures\\_df](#) and [rel\\_lymphoma\\_Nature2013\\_COSMIC\\_cutoff\\_exposures\\_df](#).

chosen\_AlexInitialArtif\_sigInd\_df: Signature information for the data stored in [lymphoma\\_Nature2013\\_COSMIC\\_cutoff\\_exposures\\_df](#) and [rel\\_lymphoma\\_Nature2013\\_COSMIC\\_cutoff\\_exposures\\_df](#).

chosen\_signatures\_indices\_df: Signature information for the data stored in [lymphoma\\_Nature2013\\_COSMIC\\_cutoff\\_exposures\\_df](#) and [rel\\_lymphoma\\_Nature2013\\_COSMIC\\_cutoff\\_exposures\\_df](#).

## Usage

```
data(lymphoma_PID)

data(lymphoma_test)

data(lymphoma_Nature2013_raw)

data(lymphoma_cohort_LCD_results)

data(lymphoma_cohort_LCD_results)

data(lymphoma_cohort_LCD_results)

data(lymphoma_cohort_LCD_results)

data(lymphoma_cohort_LCD_results)
```

## Author(s)

Daniel Huebschmann <[huebschmann.daniel@gmail.com](mailto:huebschmann.daniel@gmail.com)>

## References

<http://www.ncbi.nlm.nih.gov/pubmed/23945592>

## Examples

```
data(lymphoma_test)
head(lymphoma_test_df)
dim(lymphoma_test_df)
table(lymphoma_test_df$PID)

data(lymphoma_Nature2013_raw)
head(lymphoma_Nature2013_raw_df)
dim(lymphoma_Nature2013_raw_df)
```



---

 exchange\_colour\_vector

*Colours codes for displaying SNVs*


---

**Description**

Vector attributing colours to nucleotide exchanges used when displaying SNV information, e.g. in a rainfall plot.

**Usage**

```
data(exchange_colour_vector)
```

**Value**

A named character vector

**Author(s)**

Daniel Huebschmann <huebschmann.daniel@gmail.com>

---

exposures\_barplot

*Wrapper for enhanced\_barplot*


---

**Description**

Wrapper for enhanced\_barplot

**Usage**

```
exposures_barplot(in_exposures_df, in_signatures_ind_df = NULL,
  in_subgroups_df = NULL, in_sum_ind = NULL,
  in_subgroups.field = "subgroup", in_title = "", in_labels = TRUE,
  in_show_subgroups = TRUE, ylab = NULL, in_barplot_borders = TRUE,
  in_column_anno_borders = FALSE)
```

**Arguments**

in\_exposures\_df

Numerical data frame encoding the exposures H, i.e. which signature contributes how much to which PID (patient identifier or sample).

in\_signatures\_ind\_df

A data frame containing meta information about the signatures. If NULL, the colour information for the signatures is taken from a rainbow palette.

in\_subgroups\_df

A data frame indicating which PID (patient or sample identifier) belongs to which subgroup. If NULL, it is assumed that all PIDs belong to one common subgroup. The colour coding for the default subgroup is red.

in\_sum\_ind

Index vector influencing the order in which the PIDs are going to be displayed

<code>in_subgroups.field</code>	String indicating the column name in <code>in_subgroups_df</code> to take the subgroup information from.
<code>in_title</code>	Title for the plot to be created.
<code>in_labels</code>	Flag, if TRUE the PIDs are displayed on the x-axis
<code>in_show_subgroups</code>	Flag, if TRUE then PIDs are grouped by subgroups
<code>ylab</code>	Label of the y-axis on the plot to be generate
<code>in_barplot_borders</code>	Whether or not to show border lines in barplot
<code>in_column_anno_borders</code>	Whether or not to draw separating lines between the fields in the annotation

**Value**

The generated barplot - a ggplot2 plot

**Examples**

```
data(lymphoma_cohort_LCD_results)
exposures_barplot(lymphoma_Nature2013_COSMIC_cutoff_exposures_df,
                  chosen_signatures_indices_df,
                  COSMIC_subgroups_df)
```

---

`extract_names_from_gene_list`

*Return gene names from gene lists*

---

**Description**

Return gene names from gene lists

**Usage**

```
extract_names_from_gene_list(in_KEGG_gene_list, 1)
```

**Arguments**

<code>in_KEGG_gene_list</code>	Gene list to extract names from
<code>1</code>	Index of the gene to be extracted

**Value**

The gene name.

**See Also**

[keggGet](#)

[build\\_gene\\_list\\_for\\_pathway](#)

**Examples**

NULL

---

find\_affected\_PIDs      *Find samples affected*

---

**Description**

Find samples affected by SNVs in a certain pathway

**Usage**

```
find_affected_PIDs(in_gene_list, in_gene_vector, in_PID_vector)
```

**Arguments**

in\_gene\_list      List of genes in the pathway of interest.  
in\_gene\_vector    Character vector for genes annotated to SNVs as in vcf\_like\_df.  
in\_PID\_vector     Character vector for sample names annotated to SNVs as in vcf\_like\_df.

**Value**

A character vector of the names of the affected samples

**Examples**

NULL

---

get\_extreme\_PIDs      *Return those PIDs which have an extreme pattern for signature exposure*

---

**Description**

For all signatures found in a project, this function returns the sample identifiers (PIDs) with extremely high or extremely low exposures of the respective signatures.

**Usage**

```
get_extreme_PIDs(in_exposures_df, in_quantile = 0.03)
```

**Arguments**

in\_exposures\_df      Data frame with the signature exposures  
in\_quantile          Quantile for the amount of extreme PIDs to be selected.

**Value**

A data frame with 4 rows per signature (high PIDs, high exposures, low PIDs, low exposures); the number of columns depends on the quantile chosen.

**Examples**

```
data(lymphoma_cohort_LCD_results)
get_extreme_PIDs(lymphoma_Nature2013_COSMIC_cutoff_exposures_df, 0.05)
```

---

hclust\_exposures

*Cluster the PIDs according to their signature exposures*

---

**Description**

The PIDs are clustered according to their signature exposures by calling first creating a distance matrix:

- `dist`, then
- `hclust` and then
- `labels_colors` to colour the labels (the text) of the leaves in the dendrogram.

Typically one colour per subgroup.

**Usage**

```
hclust_exposures(in_exposures_df, in_subgroups_df, in_method = "manhattan",
  in_subgroup_column = "subgroup", in_palette = NULL, in_cutoff = 0,
  in_filename = NULL, in_shift_factor = 0.3, in_cex = 0.2,
  in_title = "", in_plot_flag = FALSE)
```

**Arguments**

- |                                 |  |
|---------------------------------|--|
| <code>in_exposures_df</code>    | Numerical data frame encoding the exposures H, i.e. which signature contributes how much to which PID (patient identifier or sample).  |
| <code>in_subgroups_df</code>    | A data frame indicating which PID (patient or sample identifier) belongs to which subgroup   |
| <code>in_method</code>          | Method of the clustering to be supplied to <code>dist</code> . Can be either of: euclidean, maximum, manhattan, canberra, binary or minkowski  |
| <code>in_subgroup_column</code> | Indicates the name of the column in which the subgroup information is encoded in <code>in_subgroups_df</code>  |
| <code>in_palette</code>         | Palette with colours or colour codes for the labels (the text) of the leaves in the dendrogram. Typically one colour per subgroup. If none is specified, a rainbow palette of the length of the number of subgroups will be used as default. |
| <code>in_cutoff</code>          | A numeric value less than 1. Signatures from within W with an overall exposure less than <code>in_cutoff</code> will be discarded for the clustering.  |

<code>in_filename</code>	A path to save the dendrogram. If none is specified, the figure will be plotted to the running environment.
<code>in_shift_factor</code>	Graphical parameter to adjust figure to be created
<code>in_cex</code>	Graphical parameter to adjust figure to be created
<code>in_title</code>	Title in the figure to be created under <code>in_filename</code>
<code>in_plot_flag</code>	Whether or not to display the dendrogram

### Value

A list with entries `hclust` and `dendrogram`.

- `hclust`: The object created by [hclust](#)
- `dendrogram`: The above object wrapped in [as.dendrogram](#)

### See Also

[hclust](#)

[dist](#)

[labels\\_colors](#)

### Examples

```
data(lymphoma_cohort_LCD_results)
hclust_exposures(rel_lymphoma_Nature2013_COSMIC_cutoff_exposures_df,
                 COSMIC_subgroups_df,
                 in_method="manhattan",
                 in_subgroup_column="subgroup")
```

### Description

LCD performs a mutational signatures decomposition of a given mutational catalogue  $V$  with known signatures  $W$  by solving the minimization problem  $\min(\|W * H - V\|)$  with additional constraints of non-negativity on  $H$  where  $W$  and  $V$  are known

### Usage

```
LCD(in_mutation_catalogue_df, in_signatures_df, in_per_sample_cutoff = 0)
```

**Arguments**

- `in_mutation_catalogue_df`  
A numeric data frame  $V$  with  $n$  rows and  $m$  columns,  $n$  being the number of features and  $m$  being the number of samples
- `in_signatures_df`  
A numeric data frame  $W$  with  $n$  rows and  $l$  columns,  $n$  being the number of features and  $l$  being the number of signatures
- `in_per_sample_cutoff`  
A numeric value less than 1. Signatures from within  $W$  with an exposure per sample less than `in_cutoff` will be discarded.

**Value**

The exposures  $H$ , a numeric data frame with  $l$  rows and  $m$  columns,  $l$  being the number of signatures and  $m$  being the number of samples

**See Also**

[lsei](#)

**Examples**

```
## define raw data
W_prim <- matrix(c(1,2,3,4,5,6),ncol=2)
W_prim_df <- as.data.frame(W_prim)
W_df <- YAPSA::normalize_df_per_dim(W_prim_df,2) # corresponds to the sigs
W <- as.matrix(W_df)
## 1. Simple case: non-negativity already in raw data
H <- matrix(c(2,5,3,6,1,9,1,2),ncol=4)
H_df <- as.data.frame(H) # corresponds to the exposures
V <- W %*% H # matrix multiplication
V_df <- as.data.frame(V) # corresponds to the mutational catalogue
exposures_df <- YAPSA::LCD(V_df,W_df)
## 2. more complicated: raw data already contains negative elements
## define indices where sign is going to be swapped
sign_ind <- c(5,7)
## now compute the indices of the other fields in the columns affected
## by the sign change
row_ind <- sign_ind %*% dim(H)[1]
temp_ind <- 2*row_ind -1
other_ind <- sign_ind + temp_ind
## alter the matrix H to yield a new mutational catalogue
H_compl <- H
H_compl[sign_ind] <- (-1)*H[sign_ind]
H_compl_df <- as.data.frame(H_compl) # corresponds to the exposures
V_compl <- W %*% H_compl # matrix multiplication
V_compl_df <- as.data.frame(V_compl) # corresponds to the mutational catalog
exposures_df <- YAPSA::LCD(V_compl_df,W_df)
exposures <- as.matrix(exposures_df)
```

---

LCD\_complex\_cutoff      *LCD with a signature-specific cutoff on exposures*

---

### Description

LCD\_cutoff performs a mutational signatures decomposition by Linear Combination Decomposition (LCD) of a given mutational catalogue  $V$  with known signatures  $W$  by solving the minimization problem  $\min(\|W * H - V\|)$  with additional constraints of non-negativity on  $H$  where  $W$  and  $V$  are known, but excludes signatures with an overall contribution less than a given signature-specific cutoff (and thereby accounting for a background model) over the whole cohort.

LCD\_complex\_cutoff\_perPID is a wrapper for `LCD_complex_cutoff` and runs individually for every PID.

### Usage

```
LCD_complex_cutoff(in_mutation_catalogue_df, in_signatures_df,
  in_cutoff_vector = NULL, in_filename = NULL, in_method = "abs",
  in_per_sample_cutoff = 0, in_rescale = TRUE, in_sig_ind_df = NULL,
  in_cat_list = NULL)
```

```
LCD_complex_cutoff_perPID(in_mutation_catalogue_df, in_signatures_df,
  in_cutoff_vector = NULL, in_filename = NULL, in_method = "abs",
  in_rescale = TRUE, in_sig_ind_df = NULL, in_cat_list = NULL)
```

### Arguments

<code>in_mutation_catalogue_df</code>	A numeric data frame $V$ with $n$ rows and $m$ columns, $n$ being the number of features and $m$ being the number of samples
<code>in_signatures_df</code>	A numeric data frame $W$ with $n$ rows and $l$ columns, $n$ being the number of features and $l$ being the number of signatures
<code>in_cutoff_vector</code>	A numeric vector of values less than 1. Signatures from within $W$ with an overall exposure less than the respective value in <code>in_cutoff_vector</code> will be discarded.
<code>in_filename</code>	A path to generate a histogram of the signature exposures if non-NULL
<code>in_method</code>	Indicate to which data the cutoff shall be applied: absolute exposures, relative exposures
<code>in_per_sample_cutoff</code>	A numeric value less than 1. Signatures from within $W$ with an exposure per sample less than <code>in_per_sample_cutoff</code> will be discarded.
<code>in_rescale</code>	Boolean, if TRUE (default) the exposures are rescaled such that colSums over exposures match colSums over mutational catalogue
<code>in_sig_ind_df</code>	Data frame of type <code>signature_indices_df</code> , i.e. indicating name, function and meta-information of the signatures. Default is NULL.
<code>in_cat_list</code>	List of categories for aggregation. Have to be among the column names of <code>in_sig_ind_df</code> . Default is NULL.

**Value**

A list with entries:

- `exposures`: The exposures  $H$ , a numeric data frame with  $l$  rows and  $m$  columns,  $l$  being the number of signatures and  $m$  being the number of samples
- `norm_exposures`: The normalized exposures  $H$ , a numeric data frame with  $l$  rows and  $m$  columns,  $l$  being the number of signatures and  $m$  being the number of samples
- `signatures`: The reduced signatures that have exposures bigger than `in_cutoff`
- `choice`: Index vector of the reduced signatures in the input signatures
- `order`: Order vector of the signatures by exposure
- `residual_catalogue`: Numerical data frame (matrix) of the difference between fit (product of signatures and exposures) and input mutational catalogue
- `rss`: Residual sum of squares (i.e. sum of squares of the residual catalogue)
- `cosDist_fit_orig_per_matrix`: Cosine distance between the fit (product of signatures and exposures) and input mutational catalogue computed after putting the matrix into vector format (i.e. one scalar product for the whole matrix)
- `cosDist_fit_orig_per_col`: Cosine distance between the fit (product of signatures and exposures) and input mutational catalogue computed per column (i.e. per sample, i.e. as many scalar products as there are samples in the cohort)
- `sum_ind`: Decreasing order of mutational loads based on the input mutational catalogue
- `out_sig_ind`: Data frame of the type `signature_indices_df`, i.e. indicating name, function and meta-information of the signatures. Default is `NULL`, non-`NULL` only if `in_sig_ind_df` is non-`NULL`.
- `aggregate_exposures_list`: List of exposure data frames aggregated over different categories. Default is `NULL`, non-`NULL` only if `in_sig_ind_df` and `in_cat_list` are non-`NULL` and if the categories specified in `in_cat_list` are among the column names of `in_sig_ind_df`.

**See Also**

[LCD](#)

[aggregate\\_exposures\\_by\\_category](#)

[lsei](#)

**Examples**

`NULL`

---

`makeVRangesFromDataFrame`

*Construct a VRanges Object from a data frame*

---

**Description**

In this package, big data frames are generated from cohort wide vcf-like files. This function constructs a `VRanges` object from such a data frame by using [makeGRangesFromDataFrame](#) from the package [GenomicRanges](#)



## Usage

```
makeVRangesFromDataFrame(in_df, in_keep.extra.columns = TRUE,  
  in_seqinfo = NULL, in_seqnames.field = "X.CHROM",  
  in_start.field = "POS", in_end.field = "POS", in_PID.field = "PID",  
  in_subgroup.field = "subgroup", in_strand.field = "strand",  
  verbose_flag = 1)
```

## Arguments

`in_df` A big dataframe constructed from a vcf-like file of a whole cohort. The first columns are those of a standard vcf file, followed by an arbitrary number of custom or user defined columns. One of these can carry a PID (patient or sample identifier) and one can carry subgroup information.

`in_keep.extra.columns` `in_seqinfo` Argument passed on to [makeGRangesFromDataFrame](#)

`in_seqinfo` A seqInfo object, referring to the reference genome used. Argument passed on to [makeGRangesFromDataFrame](#)

`in_seqnames.field` Indicates the name of the column in which the chromosome is encoded

`in_start.field` Indicates the name of the column in which the start coordinate is encoded

`in_end.field` Indicates the name of the column in which the end coordinate is encoded

`in_PID.field` Indicates the name of the column in which the PID (patient or sample identifier) is encoded

`in_subgroup.field` Indicates the name of the column in which the subgroup information is encoded

`in_strand.field` Indicates the name of the column in which the strandedness is encoded

`verbose_flag` Verbose if 1

## Value

The constructed VRanges object

## See Also

[makeGRangesFromDataFrame](#)

## Examples

```
data(lymphoma_test)  
temp_vr <- makeVRangesFromDataFrame(lymphoma_test_df,  
  in_seqnames.field="CHROM",  
  in_subgroup.field="SUBGROUP",  
  verbose_flag=1)
```

---

`make_catalogue_strata_df`*Group strata from different stratification axes*

---

### Description

For a comparison of the strata from different orthogonal stratification axes, i.e. orthogonal SMCs, the strata have to be grouped and reformatted. This function does this task for the comparison by cosine similarity of mutational catalogues. Output of this function is the basis for applying [make\\_comparison\\_matrix](#). It is called by the wrapper function [run\\_comparison\\_catalogues](#).

### Usage

```
make_catalogue_strata_df(in_stratification_lists_list,  
                        in_additional_stratum = NULL)
```

### Arguments

`in_stratification_lists_list`

List of lists with entries from different (orthogonal) stratification axes or SMCs

`in_additional_stratum`

Include an additionally supplied stratum in comparison in non-NULL.

### Value

A list with entries `strata_df`, `number_of_SMCs`, `number_of_strata`.

- `strata_df`: Pasted numerical data frame of all strata (these are going to be compared e.g. by [make\\_comparison\\_matrix](#)).
- `number_of_SMCs`: Number of orthogonal stratifications in `in_stratification_lists_list` and additional ones.
- `number_of_strata`: Cumulative number of strata (sum over the numbers of strata of the different stratifications in `in_stratification_lists_list`) and additional ones.

### See Also

[plot\\_strata](#)

[make\\_comparison\\_matrix](#)

[run\\_comparison\\_catalogues](#)

### Examples

NULL

---

`make_comparison_matrix`*Compute a similarity matrix for different strata*

---

## Description

Compute and plot a similarity matrix for different strata from different stratification axes together. First, `compare_sets` is called on `in_strata_df` with itself, yielding a distance matrix (a numerical data frame) `dist_df` of the strata. The corresponding similarity matrix `1-dist_df` is then passed to `corrplot`.

## Usage

```
make_comparison_matrix(in_strata_df, output_path = NULL, in_nrect = 5,  
  in_attribute = "", in_palette = NULL)
```

## Arguments

<code>in_strata_df</code>	Numerical data frame of all strata to be compared.
<code>output_path</code>	Path to directory where the results, especially the figure produced by <code>corrplot</code> is going to be stored.
<code>in_nrect</code>	Number of clusters in the clustering procedure provided by <code>corrplot</code>
<code>in_attribute</code>	Additional string for the file name where the figure produced by <code>corrplot</code> is going to be stored.
<code>in_palette</code>	Colour palette for the matrix

## Value

The comparison matrix of cosine similarities.

## See Also

[compare\\_SMCs](#)

## Examples

```
data(sigs)  
make_comparison_matrix(  
  AlexCosmicValid_sig_df, in_nrect=9,  
  in_palette=colorRampPalette(c("blue", "green", "red"))(n=100))
```

---

make_strata_df	<i>Group strata from different stratification axes</i>
----------------	--

---

### Description

For a comparison of the strata from different orthogonal stratification axes, i.e. orthogonal SMCs, the strata have to be grouped and reformatted. This function does this task for the comparison by cosine similarity of signature exposures. Output of this function is the basis for applying [plot\\_strata](#) and [make\\_comparison\\_matrix](#). It is called by the wrapper functions [compare\\_SMCs](#), [run\\_plot\\_strata\\_general](#) or [run\\_comparison\\_general](#).

### Usage

```
make_strata_df(in_stratification_lists_list, in_remove_signature_ind = NULL,
              in_additional_stratum = NULL)
```

### Arguments

`in_stratification_lists_list`  
List of lists with entries from different (orthogonal) stratification axes or SMCs

`in_remove_signature_ind`  
Omit one of the signatures in `in_signatures_ind_df` for the comparison if non-NULL. The parameter specifies the index of the signature to be removed.

`in_additional_stratum`  
Include an additionally supplied stratum in comparison in non-NULL.

### Value

A list with entries `strata_df`, `number_of_SMCs`, `number_of_strata`.

- `strata_df`: Pasted numerical data frame of all strata (these are going to be compared e.g. by [make\\_comparison\\_matrix](#)).
- `number_of_SMCs`: Number of orthogonal stratifications in `in_stratification_lists_list` and additional ones.
- `number_of_strata`: Cumulative number of strata (sum over the numbers of strata of the different stratifications in `in_stratification_lists_list`) and additional ones.

### See Also

[plot\\_strata](#)  
[make\\_comparison\\_matrix](#)  
[compare\\_SMCs](#)  
[run\\_plot\\_strata\\_general](#)  
[run\\_comparison\\_general](#)

### Examples

```
NULL
```

---

make\_subgroups\_df      *Make a custom data structure for subgroups*

---

## Description

Creates a data frame carrying the subgroup information and the order in which the PIDs have to be displayed. Calls [aggregate](#) on `in_vcf_like_df`.

## Usage

```
make_subgroups_df(in_vcf_like_df, in_exposures_df = NULL, in_palette = NULL,
  in_subgroup.field = "SUBGROUP", in_PID.field = "PID",
  in_verbose = FALSE)
```

## Arguments

<code>in_vcf_like_df</code>	vcf-like data frame with point mutation calls
<code>in_exposures_df</code>	Data frame with the signature exposures
<code>in_palette</code>	Palette for colour attribution to the subgroups if non-NULL
<code>in_subgroup.field</code>	String indicating which column of <code>in_vcf_like_df</code> carries the subgroup information
<code>in_PID.field</code>	String indicating which column of <code>in_vcf_like_df</code> and of <code>in_exposures_df</code> carries the PID information
<code>in_verbose</code>	Whether verbose or not.

## Value

`subgroups_df`: A data frame carrying the subgroup and rank information.

## See Also

[aggregate](#)

## Examples

```
data(lymphoma_test)
data(lymphoma_cohort_LCD_results)
choice_ind <- (names(lymphoma_Nature2013_COSMIC_cutoff_exposures_df)
  %in% unique(lymphoma_test_df$PID))
lymphoma_test_exposures_df <-
  lymphoma_Nature2013_COSMIC_cutoff_exposures_df[,choice_ind]
make_subgroups_df(lymphoma_test_df, lymphoma_test_exposures_df)
```

---

melt_exposures	<i>Generically melts exposure data frames</i>
----------------	---

---

**Description**

Melt an exposure data frame with signatures as ID variables.

**Usage**

```
melt_exposures(in_df)
```

**Arguments**

`in_df` Numeric data frame with exposures.

**Value**

A data frame with the molten exposures.

**Examples**

```
NULL
```

---

merge_exposures	<i>Merge exposure data frames</i>
-----------------	-----------------------------------

---

**Description**

Merges with the special feature of preserving the signatures and signature order.

**Usage**

```
merge_exposures(in_exposures_list, in_signatures_df)
```

**Arguments**

`in_exposures_list` List of data frames (carrying information on exposures).

`in_signatures_df` Data frame W in which the columns represent the signatures.

**Value**

A data frame with the merged exposures.

**Examples**

```
NULL
```

---

`normalizeMotifs_otherRownames`*Normalize Somatic Motifs with different rownames*

---

### Description

This is a wrapper function to `normalizeMotifs`. The rownames are first transformed to fit the convention of the `SomaticSignatures` package and then passed on to the above mentioned function.

### Usage

```
normalizeMotifs_otherRownames(in_matrix, in_norms, adjust_counts = TRUE)
```

### Arguments

`in_matrix`, `in_norms`

Arguments to `normalizeMotifs`

`adjust_counts` Whether to rescale the counts after adaption or not. Default is true.

### Value

The matrix returned by `normalizeMotifs`, but with rownames transformed back to the convention of the input

### Examples

```
NULL
```

---

`normalize_df_per_dim` *Useful functions on data frames*

---

### Description

`normalize_df_per_dim`: Normalization is carried out by dividing by `rowSums` or `colSums`; for rows with `rowSums=0` or columns with `colSums=0`, the normalization is left out.

`average_over_present`: If averaging over columns, zero rows (i.e. those with `rowSums=0`) are left out, if averaging over rows, zero columns (i.e. those with `colSums=0`) are left out.

`sd_over_present`: If computing the standard deviation over columns, zero rows (i.e. those with `rowSums=0`) are left out, if computing the standard deviation over rows, zero columns (i.e. those with `colSums=0`) are left out.

`stderrmean_over_present`: If computing the standard error of the mean over columns, zero rows (i.e. those with `rowSums=0`) are left out, if computing the standard error of the mean over rows, zero columns (i.e. those with `colSums=0`) are left out. Uses the function `stderrmean`

**Usage**

```
normalize_df_per_dim(in_df, in_dimension)

average_over_present(in_df, in_dimension)

sd_over_present(in_df, in_dimension)

stderrmean_over_present(in_df, in_dimension)
```

**Arguments**

```
in_df          Data frame to be normalized
in_dimension   Dimension along which the operation will be carried out
```

**Value**

The normalized numerical data frame (normalize\_df\_per\_dim)  
 A vector of the means (average\_over\_present)  
 A vector of the standard deviations (sd\_over\_present)  
 A vector of the standard errors of the mean (stderrmean\_over\_present)

**See Also**

[stderrmean](#)

**Examples**

```
test_df <- data.frame(matrix(c(1,2,3,0,5,2,3,4,0,6,0,0,0,0,0,4,5,6,0,7),
                             ncol=4))
## 1. Normalize over rows:
normalize_df_per_dim(test_df,1)
## 2. Normalize over columns:
normalize_df_per_dim(test_df,2)

test_df <- data.frame(matrix(c(1,2,3,0,5,2,3,4,0,6,0,0,0,0,0,4,5,6,0,7),
                             ncol=4))
## 1. Average over non-zero rows:
average_over_present(test_df,1)
## 2. Average over non-zero columns:
average_over_present(test_df,2)

test_df <- data.frame(matrix(c(1,2,3,0,5,2,3,4,0,6,0,0,0,0,0,4,5,6,0,7),
                             ncol=4))
## 1. Compute standard deviation over non-zero rows:
sd_over_present(test_df,1)
## 2. Compute standard deviation over non-zero columns:
sd_over_present(test_df,2)

test_df <- data.frame(matrix(c(1,2,3,0,5,2,3,4,0,6,0,0,0,0,0,4,5,6,0,7),
                             ncol=4))
## 1. Compute standard deviation over non-zero rows:
stderrmean_over_present(test_df,1)
## 2. Compute standard deviation over non-zero columns:
stderrmean_over_present(test_df,2)
```



---

plotExchangeSpectra *Plot the spectra of nucleotide exchanges*

---

### Description

Plots the spectra of nucleotide exchanges in their triplet contexts. If several columns are present in the input data frame, the spectra are plotted for every column separately.

### Usage

```
plotExchangeSpectra(in_catalogue_df, in_colour_vector = NULL,  
  in_show_triplets = FALSE, in_show_axis_title = FALSE)
```

### Arguments

`in_catalogue_df`  
Numerical data frame encoding the exchange spectra to be displayed, either a mutational catalogue *V* or a signatures matrix *W*.

`in_colour_vector`  
Specifies the colours of the 6 nucleotide exchanges if non-null.

`in_show_triplets`  
Whether or not to show the triplets on the x-axis

`in_show_axis_title`  
Whether or not to show the name of the y-axis

### Value

The generated barplot - a ggplot2 plot

### See Also

[geom\\_bar](#)  
[facet\\_grid](#)

### Examples

```
NULL
```

---

plot\_exposures                      *Plot the exposures of a cohort*

---

## Description

plot\_exposures: The exposures H, determined by NMF or by LCD, are displayed as a stacked barplot by calling

- `geom_bar` and optionally
- `geom_text`.

The x-axis displays the PIDs (patient identifier or sample), the y-axis the counts attributed to the different signatures with their respective colours per PID. Is called by `plot_relative_exposures`.

plot\_relative\_exposures: Plot the relative or normalized exposures of a cohort. This function first normalizes its input and then sends the normalized data to `plot_exposures`.

## Usage

```
plot_exposures(in_exposures_df, in_signatures_ind_df, in_subgroups_df = NULL,
              in_sum_ind = NULL, in_subgroups.field = "subgroup", in_title = "",
              in_labels = TRUE, in_show_subgroups = TRUE, legend_height = 10)
```

```
plot_relative_exposures(in_exposures_df, in_signatures_ind_df, in_subgroups_df,
                      in_sum_ind = NULL, in_subgroups.field = "subgroup", in_title = "",
                      in_labels = TRUE, in_show_subgroups = TRUE)
```

## Arguments

<code>in_exposures_df</code>	Numerical data frame encoding the exposures H, i.e. which signature contributes how much to which PID (patient identifier or sample).
<code>in_signatures_ind_df</code>	A data frame containing meta information about the signatures
<code>in_subgroups_df</code>	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup
<code>in_sum_ind</code>	Index vector influencing the order in which the PIDs are going to be displayed
<code>in_subgroups.field</code>	String indicating the column name in <code>in_subgroups_df</code> to take the subgroup information from.
<code>in_title</code>	Title for the plot to be created.
<code>in_labels</code>	Flag, if TRUE the PIDs are displayed on the x-axis
<code>in_show_subgroups</code>	Flag, if TRUE then PIDs are grouped by subgroups
<code>legend_height</code>	How many signatures should be displayed in one column together at most.

## Value

The generated barplot - a ggplot2 plot

**See Also**

[LCD](#)  
[geom\\_bar](#)  
[geom\\_text](#)

**Examples**

```
data(lymphoma_cohort_LCD_results)
plot_exposures(lymphoma_Nature2013_COSMIC_cutoff_exposures_df,
               chosen_signatures_indices_df,
               COSMIC_subgroups_df)

data(lymphoma_cohort_LCD_results)
plot_relative_exposures(lymphoma_Nature2013_COSMIC_cutoff_exposures_df,
                       chosen_signatures_indices_df,
                       COSMIC_subgroups_df)
```

---

plot\_SMC

---

*Plot results of the Stratification of a Mutational Catalogue*


---

**Description**

Plot a big composite figure with 3 columns: in the left column the per-PID absolute exposures will be shown, in the middle column the per\_PID relative or normalized exposures will be shown, in the right column the cohort-wide exposures are shown (averaged over PIDs).

**Usage**

```
plot_SMC(number_of_strata, output_path, decomposition_method, number_of_sigs,
         name_list, exposures_strata_list, this_signatures_ind_df, this_subgroups_df,
         in_strata_order_ind, exposures_both_rel_df_list, cohort_method_flag,
         fig_width = 1200, fig_height = 900, fig_type = "png",
         in_label_orientation = "turn", this_sum_ind = NULL)
```

**Arguments**

`number_of_strata` Number of strata as deduced from `link{SMC}`

`output_path` Path to file where the results are going to be stored. If `NULL`, the results will be plotted to the running environment.

`decomposition_method` String for the filename of the generated barplot.

`number_of_sigs` Number of signatures

`name_list` Names of the constructed strata.

`exposures_strata_list` The list of `s` strata specific exposures  $H_i$ , all are numerical data frames with `l` rows and `m` columns, `l` being the number of signatures and `m` being the number of samples

this_signatures_ind_df	A data frame containing meta information about the signatures
this_subgroups_df	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup
in_strata_order_ind	Index vector defining reordering of the strata
exposures_both_rel_df_list	A list of s strata specific cohortwide (i.e. averaged over cohort) normalized exposures
cohort_method_flag	Either or several of c("all_PIDs", "cohort", "norm_PIDs"), representing alternative ways to average over the cohort.
fig_width	Width of the figure to be plotted
fig_height	Height of the figure to be plotted
fig_type	png or pdf
in_label_orientation	Whether or not to turn the labels on the x-axis.
this_sum_ind	Optional set of indices for reordering the PIDs

**Value**

The function doesn't return any value.

**Examples**

NULL

---

plot_strata	<i>Plot all strata from different stratification axes together</i>
-------------	--

---

**Description**

Plot the cohort wide signature exposures of all strata from different stratification axes together. Naturally called by [compare\\_SMCs](#).

**Usage**

```
plot_strata(in_strata_list, in_signatures_ind_df, output_path = NULL,
           in_attribute = "")
```

**Arguments**

in_strata_list	Data structure created by <code>make_strata_df</code> or <code>make_catalogue_strata_df</code> in which the strata from different orthogonal stratification axes are reorganized in a consistent structure.
in_signatures_ind_df	A data frame containing meta information about the signatures
output_path	Path to directory where the results, especially the figure produced, are going to be stored.
in_attribute	Additional string for the file name where the figure output is going to be stored.

**Value**

The function doesn't return any value.

**See Also**

[compare\\_SMCs](#)

**Examples**

```
NULL
```

---

repeat\_df

*Create a data frame with default values*

---

**Description**

Create a data frame with default values

**Usage**

```
repeat_df(in_value, in_rows, in_cols)
```

**Arguments**

`in_value` Default entry to be repeated in the data frame  
`in_rows, in_cols` Dimensions of the data frame to be created

**Value**

The created data frame

**Examples**

```
## 1. Initialize with numeric value:  
repeat_df(1,2,3)  
## 2. Initialize with NA value:  
repeat_df(NA,3,2)  
## 3. Initialize with character:  
repeat_df("a",4,3)
```

---

run\_annotate\_vcf\_pl     *Wrapper function to annotate addition information*

---

### Description

Wrapper function to the perl script `annotate_vcf.pl` which annotates data of a track stored in `file_B` (may be different formats) to called variants stored in a vcf-like `file_A`.

### Usage

```
run_annotate_vcf_pl(in_data_file, in_anno_track_file, in_new_column_name,  
out_file, in_data_file_type = "custom", in_anno_track_file_type = "bed",  
in_data_CHROM.field = "CHROM", in_data_POS.field = "POS",  
in_data_END.field = "POS")
```

### Arguments

`in_data_file`     Path to the input vcf-like file to be annotated

`in_anno_track_file`  
                  Path to the input file containing the annotation track

`in_new_column_name`  
                  String indicating the name of the column to be created for annotation.

`out_file`        Path where the created files can be stored.

`in_data_file_type`  
                  custom for vcf-like

`in_anno_track_file_type`  
                  Type of the file `in_anno_track_file` containing the annotation track.

`in_data_CHROM.field`  
                  String indicating which column of `in_data_file` contains the chromosome information.

`in_data_POS.field`  
                  String indicating which column of `in_data_file` contains the position information.

`in_data_END.field`  
                  String indicating which column of `in_data_file` contains the end information if regions are considered.

### Value

Return zero if no problems occur.

### Examples

NULL

---

`run_comparison_catalogues`*Compare all strata from different stratifications*

---

## Description

Compare all strata from different orthogonal stratification axes, i.e. orthogonal SMCs by cosine similarity of mutational catalogues. Function similar to [run\\_comparison\\_general](#). First calls

- [make\\_catalogue\\_strata\\_df](#), then
- [make\\_comparison\\_matrix](#)

## Usage

```
run_comparison_catalogues(in_stratification_lists_list, output_path = NULL,  
                          in_nrect = 5, in_attribute = "")
```

## Arguments

<code>in_stratification_lists_list</code>	List of lists with entries from different (orthogonal) stratification axes or SMCs
<code>output_path</code>	Path to directory where the results, especially the figure produced by <a href="#">corrplot</a> is going to be stored.
<code>in_nrect</code>	Number of clusters in the clustering procedure provided by <a href="#">corrplot</a>
<code>in_attribute</code>	Additional string for the file name where the figure produced by

## Value

The comparison matrix of cosine similarities.

## See Also

[make\\_comparison\\_matrix](#)

[run\\_comparison\\_general](#)

## Examples

```
NULL
```

---

`run_comparison_general`*Compare all strata from different stratifications*

---

### Description

Compare all strata from different orthogonal stratification axes, i.e. orthogonal SMCs by cosine similarity of signature exposures. Function similar to [compare\\_SMCs](#), but without calling [plot\\_strata](#). First calls

- [make\\_strata\\_df](#), then
- [make\\_comparison\\_matrix](#)

### Usage

```
run_comparison_general(in_stratification_lists_list, output_path = NULL,  
                      in_nrect = 5, in_attribute = "", in_remove_signature_ind = NULL,  
                      in_additional_stratum = NULL)
```

### Arguments

<code>in_stratification_lists_list</code>	List of lists with entries from different (orthogonal) stratification axes or SMCs
<code>output_path</code>	Path to directory where the results, especially the figure produced by <a href="#">corrplot</a> is going to be stored.
<code>in_nrect</code>	Number of clusters in the clustering procedure provided by <a href="#">corrplot</a>
<code>in_attribute</code>	Additional string for the file name where the figure produced by <a href="#">corrplot</a> is going to be stored.
<code>in_remove_signature_ind</code>	Omit one of the signatures in <code>in_signatures_ind_df</code> for the comparison if non-NULL. The parameter specifies the index of the signature to be removed.
<code>in_additional_stratum</code>	Include an additionally supplied stratum in comparison in non-NULL.

### Value

The comparison matrix of cosine similarities.

### See Also

[make\\_comparison\\_matrix](#)  
[compare\\_SMCs](#)  
[run\\_comparison\\_catalogues](#)

### Examples

```
NULL
```



---

`run_kmer_frequency_correction`*Provide comprehensive correction factors for kmer content*

---

## Description

This function is analogous to [normalizeMotifs](#). If an analysis of mutational signatures is performed on e.g. Whole Exome Sequencing (WES) data, the signatures and exposures have to be adapted to the potentially different kmer (trinucleotide) content of the target capture. The present function takes as arguments paths to the used reference genome and target capture file. It extracts the sequence of the target capture by calling `bedtools getfasta` on the system command prompt. `run_kmer_frequency_normalization` then calls a custom made perl script `kmer_frequencies.pl` also included in this package to count the occurrences of the triplets in both the whole reference genome and the created target capture sequence. These counts are used for normalization as in [normalizeMotifs](#). Note that [kmerFrequency](#) provides a solution to approximate kmer frequencies by random sampling. As opposed to that approach, the function described here deterministically counts all occurrences of the kmers in the respective genome.

## Usage

```
run_kmer_frequency_correction(in_ref_genome_fasta, in_target_capture_bed,  
                             in_word_length, project_folder, target_capture_fasta = "targetCapture.fa",  
                             in_verbose = 1)
```

## Arguments

<code>in_ref_genome_fasta</code>	Path to the reference genome fasta file used.
<code>in_target_capture_bed</code>	Path to a bed file containing the information on the used target capture. May also be a compressed bed.
<code>in_word_length</code>	Integer number defining the length of the features or motifs, e.g. 3 for triplets or 5 for pentamers
<code>project_folder</code>	Path where the created files, especially the fasta file with the sequence of the target capture and the count matrices, can be stored.
<code>target_capture_fasta</code>	Name of the fasta file of the target capture to be created if not yet existent.
<code>in_verbose</code>	Verbose if <code>in_verbose=1</code>

## Value

A list with 2 entries:

- `rel_cor`: The correction factors after normalization as in [run\\_kmer\\_frequency\\_normalization](#)
- `abs_cor`: The correction factors without normalization.

## See Also

[normalizeMotifs](#)

## Examples

NULL

---

run\_kmer\_frequency\_normalization

*Provide normalized correction factors for kmer content*

---

## Description

This function is analogous to [normalizeMotifs](#). If an analysis of mutational signatures is performed on e.g. Whole Exome Sequencing (WES) data, the signatures and exposures have to be adapted to the potentially different kmer (trinucleotide) content of the target capture. The present function takes as arguments paths to the used reference genome and target capture file. It then extracts the sequence of the target capture by calling `bedtools getfasta` on the system command prompt. `run_kmer_frequency_normalization` then calls a custom made perl script `kmer_frequencies.pl` also included in this package to count the occurrences of the triplets in both the whole reference genome and the created target capture sequence. These counts are used for normalization as in [normalizeMotifs](#). Note that [kmerFrequency](#) provides a solution to approximate kmer frequencies by random sampling. As opposed to that approach, the function described here deterministically counts all occurrences of the kmers in the respective genome.

## Usage

```
run_kmer_frequency_normalization(in_ref_genome_fasta, in_target_capture_bed,  
                                in_word_length, project_folder, in_verbose = 1)
```

## Arguments

<code>in_ref_genome_fasta</code>	Path to the reference genome fasta file used.
<code>in_target_capture_bed</code>	Path to a bed file containing the information on the used target capture. May also be a compressed bed.
<code>in_word_length</code>	Integer number defining the length of the features or motifs, e.g. 3 for triplets or 5 for pentamers
<code>project_folder</code>	Path where the created files, especially the fasta file with the sequence of the target capture and the count matrices, can be stored.
<code>in_verbose</code>	Verbose if <code>in_verbose=1</code>

## Value

A numeric vector with correction factors

## See Also

[normalizeMotifs](#)

## Examples

NULL

---

`run_plot_strata_general`*Wrapper function for plot\_strata*

---

**Description**

First calls

- `make_strata_df`, then
- `plot_strata`

**Usage**

```
run_plot_strata_general(in_stratification_lists_list, in_signatures_ind_df,  
                        output_path = NULL, in_attribute = "", in_remove_signature_ind = NULL,  
                        in_additional_stratum = NULL)
```

**Arguments**

<code>in_stratification_lists_list</code>	List of lists with entries from different (orthogonal) stratification axes or SMCs
<code>in_signatures_ind_df</code>	A data frame containing meta information about the signatures
<code>output_path</code>	Path to directory where the results, especially the figure produced by <code>plot_strata</code> is going to be stored.
<code>in_attribute</code>	Additional string for the file name where the figure produced by <code>plot_strata</code> is going to be stored.
<code>in_remove_signature_ind</code>	Omit one of the signatures in <code>in_signatures_ind_df</code> for the comparison if non-NULL. The parameter specifies the index of the signature to be removed.
<code>in_additional_stratum</code>	Include an additionally supplied stratum in comparison in non-NULL.

**Value**

The function doesn't return any value.

**See Also**

`plot_strata`

**Examples**

```
NULL
```

run\_SMC

*Wrapper function for the Stratification of a Mutational Catalogue***Description**

run\_SMC takes as input a big dataframe constructed from a vcf-like file of a whole cohort. This wrapper function calls custom functions to construct a mutational catalogue and stratify it according to categories indicated by a special column in the input dataframe:

- [create\\_mutation\\_catalogue\\_from\\_df](#)
- [adjust\\_number\\_of\\_columns\\_in\\_list\\_of\\_catalogues](#)

This stratification yields a collection of stratified mutational catalogues, these are reformatted and sent to the custom function SMC and thus indirectly to LCD\_SMC to perform a signature analysis of the stratified mutational catalogues. The result is then handed over to [plot\\_SMC](#) for visualization.

**Usage**

```
run_SMC(my_table, this_signatures_df, this_signatures_ind_df, this_subgroups_df,
        column_name, refGenome, cohort_method_flag = "all_PIDs",
        in_strata_order_ind = seq_len(length(unique(my_table[, column_name]))),
        wordLength = 3, verbose_flag = 1, target_dir = NULL,
        strata_dir = NULL, output_path = NULL, in_all_exposures_df = NULL,
        in_rownames = c(), in_norms = NULL, in_label_orientation = "turn",
        this_sum_ind = NULL)
```

**Arguments**

my_table	A big dataframe constructed from a vcf-like file of a whole cohort. The first columns are those of a standard vcf file, followed by an arbitrary number of custom or user defined columns. One of these must carry a PID (patient or sample identifier) and one must be the category used for stratification.
this_signatures_df	A numeric data frame W in with n rows and l columns, n being the number of features and l being the number of signatures
this_signatures_ind_df	A data frame containing meta information about the signatures
this_subgroups_df	A data frame indicating which PID (patient or sample identifier) belongs to which subgroup
column_name	Name of the column in my_table which is going to be used for stratification
refGenome	FaFile of the reference genome to extract the motif context of the variants in my_table
cohort_method_flag	Either or several of c("all_PIDs", "cohort", "norm_PIDs"), representing alternative ways to average over the cohort.
in_strata_order_ind	Index vector defining reordering of the strata
wordLength	Integer number defining the length of the features or motifs, e.g. 3 for triplets or 5 for pentamers

verbose_flag	Verbose if verbose_flag=1
target_dir	Path to directory where the results of the stratification procedure are going to be stored if non-NULL.
strata_dir	Path to directory where the mutational catalogues of the different strata are going to be stored if non-NULL
output_path	Path to directory where the results, especially the figures produced by <code>plot_SMC</code> are going to be stored.
in_all_exposures_df	Optional argument, if specified, H, i.e. the overall exposures without stratification, is set to equal <code>in_all_exposures_df</code> . This is equivalent to forcing the LCD_SMC procedure to use e.g. the exposures of a previously performed NMF decomposition.
in_rownames	Optional parameter to specify rownames of the mutational catalogue V i.e. the names of the features.
in_norms	If specified, vector of the correction factors for every motif due to differing trinucleotide content. If null, no correction is applied.
in_label_orientation	Whether or not to turn the labels on the x-axis.
this_sum_ind	Optional set of indices for reordering the PIDs

### Value

A list with entries `exposures_list`, `catalogues_list`, `cohort` and `name_list`.

- `exposures_list`: The list of `s` strata specific exposures  $H_i$ , all are numerical data frames with `l` rows and `m` columns, `l` being the number of signatures and `m` being the number of samples
- `catalogues_list`: A list of `s` strata specific cohortwide (i.e. averaged over cohort) normalized exposures
- `cohort`: `subgroups_df` adjusted for plotting
- `name_list`: Names of the constructed strata.

### See Also

[create\\_mutation\\_catalogue\\_from\\_df](#)  
[normalizeMotifs\\_otherRownames](#)  
[plot\\_SMC](#)

### Examples

```
library(BSgenome.Hsapiens.UCSC.hg19)
data(sigs)
data(lymphoma_test)
data(lymphoma_cohort_LCD_results)
strata_list <-
  cut_breaks_as_intervals(lymphoma_test_df$random_norm,
                        in_outlier_cutoffs=c(-4,4),
                        in_cutoff_ranges_list=list(c(-2.5,-1.5),
                                                  c(0.5,1.5)),
                        in_labels=c("small", "intermediate", "big"))
lymphoma_test_df$random_cat <- strata_list$category_vector
choice_ind <- (names(lymphoma_Nature2013_COSMIC_cutoff_exposures_df))
```

```
      %in% unique(lymphoma_test_df$PID))
lymphoma_test_exposures_df <-
  lymphoma_Nature2013_COSMIC_cutoff_exposures_df[,choice_ind]
temp_subgroups_df <- make_subgroups_df(lymphoma_test_df,
                                       lymphoma_test_exposures_df)
mut_density_list <- run_SMC(lymphoma_test_df,
                           AlexCosmicValid_sig_df,
                           AlexCosmicValid_sigInd_df,
                           temp_subgroups_df,
                           column_name="random_cat",
                           refGenome=BSgenome.Hsapiens.UCSC.hg19,
                           cohort_method_flag="norm_PIDs",
                           in_rownames = rownames(AlexCosmicValid_sig_df))
```

---

shapiro\_if\_possible    *Wrapper for Shapiro test but allow for all identical values*

---

### Description

Wrapper for Shapiro test but allow for all identical values

### Usage

```
shapiro_if_possible(in_vector)
```

### Arguments

`in_vector`       Numerical vector the Shapiro-Wilk test is computed on

### Value

p-value of the Shapiro-Wilk test, zero if all entries in the input vector `in_vector` are identical.

### See Also

[shapiro.test](#)

### Examples

```
shapiro_if_possible(runif(100,min=2,max=4))
shapiro_if_possible(rnorm(100,mean=5,sd=3))
shapiro_if_possible(rep(4.3,100))
shapiro_if_possible(c("Hello", "World"))
```

sigs

*Data for mutational signatures***Description**

The numerical data of the mutational signatures published initially by Alexandrov et al. (Nature 2013) is stored in data frames with endings `_sig_df`, the associated meta-information is stored in data frames with endings `_sigInd_df`. There are several instances of `_sig_df` and `_sigInd_df`, corresponding to results and data obtained at different times and with different raw data. There always is a one-to-one correspondence between a `_sig_df` and a `_sigInd_df`. The data frames of type `_sig_df` have as many rows as there are features, i.e. 96 if analyzing mutational signatures of SNVs in a triplet context, and as many columns as there are signatures. Data frames of type `_sigInd_df` have as many rows as there are signatures in the corresponding `_sig_df` and several columns:

- `sig`: signature name
- `index`: corresponding to the row index of the signature
- `colour`: colour for visualization in stacked barplots
- `process`: asserted biological process
- `cat.coarse`: categorization of the signatures according to the asserted biological processes at low level of detail
- `cat.medium`: categorization of the signatures according to the asserted biological processes at intermediate level of detail
- `cat.high`: categorization of the signatures according to the asserted biological processes at high level of detail
- `cat.putative`: categorization of the signatures according to the asserted biological processes based on clustering and inference

`AlexInitialArtif_sig_df`: Data frame of the signatures published initially by Alexandrov et al. (Nature 2013). There are 27 signatures which constitute the columns, 22 of which were validated by an orthogonal sequencing technology. These 22 are in the first 22 columns of the data frame. The column names are *A* pasted to the number of the signature, e.g. *A5*. The nonvalidated signatures have an additional letter in their naming convention: either *AR1 - AR3* or *AU1 - AU2*. The rownames are the features, i.e. an encoding of the nucleotide exchanges in their trinucleotide context, e.g. *C>A ACA*. In total there are 96 different features and therefore 96 rows when dealing with a trinucleotide context.

`AlexInitialArtif_sigInd_df`: Meta-information for `AlexInitialArtif_sig_df`

`AlexInitialValid_sig_df`: Data frame of only the validated signatures published initially by Alexandrov et al. (Nature 2013), corresponding to the first 22 columns of `AlexInitialArtif_sig_df`

`AlexInitialValid_sigInd_df`: Meta-information for `AlexInitialValid_sig_df`

`AlexCosmicValid_sig_df`: Data frame of the updated signatures list maintained by Ludmil Alexandrov at <http://cancer.sanger.ac.uk/cosmic/signatures>. The column names are *AC* pasted to the number of the signature, e.g. *AC5*. The naming convention for the rows is as described for `AlexInitialArtif_sig_df`.

`AlexCosmicValid_sigInd_df`: Meta-information for `AlexCosmicValid_sig_df`

`AlexCosmicArtif_sig_df`: Data frame of the updated signatures list maintained by Ludmil Alexandrov at <http://cancer.sanger.ac.uk/cosmic/signatures> and complemented by the artifact

signatures from the initial publication, i.e. the last 5 columns of `AlexInitialArtif_sig_df`. The column names are `AC` pasted to the number of the signature, e.g. `AC5`. The naming convention for the rows is as described for `AlexInitialArtif_sig_df`.

`AlexCosmicArtif_sigInd_df`: Meta-information for `AlexCosmicArtif_sig_df`

### Usage

```
data(sigs)
```

### Author(s)

Daniel Huebschmann <huebschmann.daniel@googlemail.com>

### Source

AlexInitial: <ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/signatures.txt>

AlexCosmic: [http://cancer.sanger.ac.uk/cancergenome/assets/signatures\\_probabilities.txt](http://cancer.sanger.ac.uk/cancergenome/assets/signatures_probabilities.txt)

### References

Alexandrov et al. (Nature 2013)

---

split\_exposures\_by\_subgroups

*Split an exposures data frame by subgroups*

---

### Description

If a cohort consists of different subgroups, this function enables to split the data frame storing the signature exposures into a list of data frames with signature exposures, one per subgroup. This functionality is needed for `stat_test_subgroups` and `stat_plot_subgroups`

### Usage

```
split_exposures_by_subgroups(in_exposures_df, in_subgroups_df,
  in_subgroups.field = "subgroup", in_PID.field = "PID")
```

### Arguments

<code>in_exposures_df</code>	Numerical data frame of the exposures (i.e. contributions of the different signatures to the number of point mutations per PID)
<code>in_subgroups_df</code>	Data frame indicating which PID belongs to which subgroup
<code>in_subgroups.field</code>	Name indicating which column in <code>in_subgroups_df</code> contains the subgroup information
<code>in_PID.field</code>	Name indicating which column in <code>in_subgroups_df</code> contains the PID information



**Value**

List of data frames with the subgroup specific signature exposures.

**See Also**

[stat\\_test\\_subgroups](#)

[stat\\_plot\\_subgroups](#)

**Examples**

NULL

---

stat\_plot\_subgroups     *Plot averaged signature exposures per subgroup*

---

**Description**

Plot one averaged signature exposure pattern per subgroup. Uses [split\\_exposures\\_by\\_subgroups](#).

**Usage**

```
stat_plot_subgroups(in_exposures_df, in_subgroups_df, in_signatures_ind_df,
                    in_subgroups.field = "subgroup", in_PID.field = "PID",
                    in_colour_vector = NULL)
```

**Arguments**

in_exposures_df	Numerical data frame of the exposures (i.e. contributions of the different signatures to the number of point mutations per PID)
in_subgroups_df	Data frame indicating which PID belongs to which subgroup
in_signatures_ind_df	Data frame carrying additional information on the signatures
in_subgroups.field	Name indicating which column in in_subgroups_df contains the subgroup information
in_PID.field	Name indicating which column in in_subgroups_df contains the PID information
in_colour_vector	If non-null, specifies the colours attributed to the subgroups

**Value**

The function doesn't return any value, it plots instead.

**See Also**

[split\\_exposures\\_by\\_subgroups](#)

**Examples**

NULL

---

<code>stat_test_SMC</code>	<i>Apply statistical tests to a stratification (SMC)</i>
----------------------------	--

---

**Description**

`stat_test_SMC` tests for enrichment or depletion in the different strata of a stratification of the mutational catalogue for every signature independently by applying Kruskal Wallis tests. For those signatures where the Kruskal Wallis test gives a significant p-value, pairwise posthoc tests are carried out by calling `posthoc.kruskal.nemenyi.test`. Additionally all data is tested for normality by Shapiro Wilk tests, so that the user may apply ANOVA and pairwise posthoc t-test where allowed.

**Usage**

```
stat_test_SMC(in_strat_list, in_flag = "norm")
```

**Arguments**

`in_strat_list` A list with entries `exposures_list`, `catalogues_list`, `cohort` and `name_list` as in the output of `run_SMC`.

- `exposures_list`: The list of `s` strata specific exposures  $H_i$ , all are numerical data frames with `l` rows and `m` columns, `l` being the number of signatures and `m` being the number of samples
- `catalogues_list`: A list of `s` strata specific cohortwide (i.e. averaged over cohort) normalized exposures
- `cohort`: `subgroups_df` adjusted for plotting
- `name_list`: Names of the constructed strata.

`in_flag` If "norm", all tests are performed on normalized exposures, otherwise the absolute exposures are taken.

**Value**

A list with entries `kruskal_df`, `shapiro_df`, `kruskal_posthoc_list`,

- `kruskal_df`: A data frame containing results (statistic and p values) of the Kruskal Wallis tests (tests for enrichment or depletion in the different strata for every signature independently).
- `shapiro_df`: A data frame containing results (p values) of the Shapiro Wilk tests (tests for normal distribution in the different strata for every signature independently).
- `kruskal_posthoc_list`: A list of results of pairwise posthoc tests carried out for those signatures where the Kruskal Wallis test yielded a significant p-value (carried out by `posthoc.kruskal.nemenyi.test`).

**See Also**

[run\\_SMC](#)  
[posthoc.kruskal.nemenyi.test](#)  
[kruskal.test](#)  
[shapiro\\_if\\_possible](#)  
[shapiro.test](#)

**Examples**

NULL

---

stat\_test\_subgroups     *Test for differences in average signature exposures between subgroups*

---

**Description**

Apply Kruskal-Wallis tests to detect differences in the signature exposures between different subgroups. Uses [split\\_exposures\\_by\\_subgroups](#). Algorithm analogous to [stat\\_test\\_SMC](#).

**Usage**

```
stat_test_subgroups(in_exposures_df, in_subgroups_df,
  in_subgroups.field = "subgroup", in_PID.field = "PID")
```

**Arguments**

**in\_exposures\_df**     Numerical data frame of the exposures (i.e. contributions of the different signatures to the number of point mutations per PID)  
**in\_subgroups\_df**     Data frame indicating which PID belongs to which subgroup  
**in\_subgroups.field**     Name indicating which column in `in_subgroups_df` contains the subgroup information  
**in\_PID.field**     Name indicating which column in `in_subgroups_df` contains the PID information

**Value**

A list with entries `kruskal_df`, `kruskal_posthoc_list`,

- `kruskal_df`: A data frame containing results (statistic and p values) of the Kruskal Wallis tests (tests for enrichment or depletion in the different strata for every signature independently).
- `kruskal_posthoc_list`: A list of results of pairwise posthoc tests carried out for those signatures where the Kruskal Wallis test yielded a significant p-value (carried out by [posthoc.kruskal.nemenyi.test](#)).

**See Also**[split\\_exposures\\_by\\_subgroups](#)[stat\\_test\\_SMC](#)[posthoc.kruskal.nemenyi.test](#)[kruskal.test](#)**Examples**

NULL

---

`stderrmean`*Compute the standard error of the mean*

---

**Description**

This function returns the standard deviation of an input numerical vector divided by the square root of the length of the input vector

**Usage**`stderrmean(x)`**Arguments**

`x`                    A numerical vector

**Value**

Standard deviation of an input numerical vector divided by the square root of the length of the input vector

**Examples**

```
A <- c(1,2,3)
sd(A)
stderrmean(A)
```

---

sum\_over\_list\_of\_df     *Elementwise sum over a list of (numerical) data frames*

---

**Description**

Elementwise sum over a list of (numerical) data frames

**Usage**

```
sum_over_list_of_df(in_df_list)
```

**Arguments**

in\_df\_list     List of (numerical) data frames

**Value**

A numerical data frame with the same dimensions as the entries of in\_df\_list with elementwise sums

**Examples**

```
A <- data.frame(matrix(c(1,1,1,2,2,2),ncol=2))
B <- data.frame(matrix(c(3,3,3,4,4,4),ncol=2))
df_list <- list(A=A,B=B)
sum_over_list_of_df(df_list)
```

---

targetCapture\_cor\_factors

*Correction factors for different target capture kits*

---

**Description**

List of lists with correction factors for different target capture kits. The elements of the overall list are lists, every one carrying information for one target capture kit (and named after it). The elements of these sublists are 64 dimensional vectors with correction factors for all triplets. They were computed using counts of occurrence of the respective triplets in the target capture and in the reference genome and making ratios (either for the counts themselves as in `abs_cor` or for the relative occurrences in `rel_cor`). The information in this data structure may be used as input to [normalizeMotifs\\_otherRownames](#).

**Usage**

```
data(targetCapture_cor_factors)
```

**Value**

A list of lists of data frames

**Author(s)**

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test\_exposureAffected *Test significance of association*

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**Description**

Test significance of association between a vector of exposures and a selection of samples, e.g. those affected by mutations in a pathway as returned by [find\\_affected\\_PIDs](#)

**Usage**

```
test_exposureAffected(in_exposure_vector, in_affected_PIDs,  
  in_mutation_label = NULL, in_exposure_label = NULL)
```

**Arguments**

`in_exposure_vector`  
Named vector of a phenotype (e.g. exposures to a specific signature)

`in_affected_PIDs`  
Character vector of samples affected by some criterion, e.g. mutations in a pathway as returned by [find\\_affected\\_PIDs](#)

`in_mutation_label`  
If non-NULL, prefix to the mutation status (x-axis label) in the produced boxplot

`in_exposure_label`  
If non-NULL, prefix to the exposures (y-axis label) in the produced boxplot

**Value**

A list with entries:

- `current_kruskal`: Kruskal test object from testing phenotype against affection
- `current_boxplot`: Boxplot of phenotype against affection

**Examples**

```
NULL
```

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`test_gene_list_in_exposures`*Test if mutated PIDs are enriched in signatures*

---

**Description**

For all signatures found in a project, this function tests whether PIDs having mutations in a specified list of genes of interest have significantly higher exposures.

**Usage**

```
test_gene_list_in_exposures(in_gene_list, in_exposure_df, in_mut_table,  
  in_gene.field = "GENE_short", in_p_cutoff = 0.05)
```

**Arguments**

`in_gene_list` List with genes of interest  
`in_exposure_df` Data frame with the signature exposures  
`in_mut_table` Data frame or table of mutations (derived from vcf-format)  
`in_gene.field` Name of the column in which the gene names are to be looked up  
`in_p_cutoff` Significance threshold

**Value**

A list with entries `pvals`, `exposure_df`, `number_of_mutated`,

- `pvals`: p-values of the t-tests performed on mutated vs. unmutated PIDs
- `exposure_df`: Transposed input exposures data frame with additional annotations for mutation status
- `number_of_mutated`: Number of PIDs carrying a mutation

**Examples**

```
NULL
```

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`transform_rownames_R_to_MATLAB`*Change rownames from one naming convention to another*

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**Description**

Rownames or names of the features used differ between the different contexts a signature analysis is carried out in. The function `transform_rownames_R_to_MATLAB` changes from the convention used in the YAPSA package to the one used by Alexandrov et al. in the MATLAB framework.

The function `transform_rownames_MATLAB_to_R` changes from the convention used in Alexandrov et al. in the MATLAB framework to the one used by the YAPSA package.

The function `transform_rownames_MATLAB_to_R` changes from the convention used in stored mutational catalogues by Alexandrov et al. to the one used by the YAPSA package.

The function `transform_rownames_YAPSA_to_deconstructSigs` changes from the convention used in the YAPSA package to the one used by the `deconstructSigs` package.

The function `transform_rownames_YAPSA_to_deconstructSigs` changes from the convention used in the `deconstructSigs` package to the one used by the YAPSA package.

**Usage**

```
transform_rownames_R_to_MATLAB(in_rownames, wordLength = 3)
```

```
transform_rownames_MATLAB_to_R(in_rownames, wordLength = 3)
```

```
transform_rownames_nature_to_R(in_rownames, wordLength = 3)
```

```
transform_rownames_YAPSA_to_deconstructSigs(in_rownames, wordLength = 3)
```

```
transform_rownames_deconstructSigs_to_YAPSA(in_rownames, wordLength = 3)
```

**Arguments**

<code>in_rownames</code>	Character vector of input rownames
<code>wordLength</code>	Size of the considered motif context

**Value**

A character vector of the translated rownames.

**Examples**

```
NULL
```

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<code>translate_to_hg19</code>	<i>Translate chromosome names to the hg19 naming convention</i>
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**Description**

`translate_to_hg19`: In hg19 naming convention, chromosome names start with the prefix *chr* and the gonosomes are called *X* and *Y*. If data analysis is performed e.g. with [BSgenome.Hsapiens.UCSC.hg19](#), this naming convention is needed. The inverse transform is done with [translate\\_to\\_1kG](#).

`translate_to_1kG`: In 1kG, i.e. 1000 genomes naming convention, chromosome names have no prefix *chr* and the gonosomes are called *23* for *X* and *24* for *Y*. If data analysis is performed e.g. with `hs37d5.fa`, this naming convention is needed. The inverse transform is done with [translate\\_to\\_hg19](#).



**Usage**

```
translate_to_hg19(in_dat, in_CHROM.field = "CHROM", in_verbose = FALSE)

translate_to_1kG(in_dat, in_CHROM.field = "chr", in_verbose = FALSE)
```

**Arguments**

`in_dat` GRanges object, VRanges object or data frame which carries one column with chromosome information to be reformatted.

`in_CHROM.field` String indicating which column of `in_dat` carries the chromosome information

`in_verbose` Whether verbose or not.

**Value**

GRanges object, VRanges object or data frame identical to `in_dat`, but with the names in the chromosome column replaced (if dealing with data frames) or alternatively the seqlevels replaced (if dealing with GRanges or VRanges objects).

**Examples**

```
test_df <- data.frame(CHROM=c(1,2,23,24),POS=c(100,120000000,300000,25000),
                     dummy=c("a","b","c","d"))
hg19_df <- translate_to_hg19(test_df, in_CHROM.field = "CHROM")
hg19_df

test_df <- data.frame(CHROM=c(1,2,23,24),POS=c(100,120000000,300000,25000),
                     dummy=c("a","b","c","d"))
hg19_df <- translate_to_hg19(test_df, in_CHROM.field = "CHROM")
onekG_df <- translate_to_1kG(hg19_df, in_CHROM.field = "CHROM")
onekG_df
```

---

`trellis_rainfall_plot` *Create a rainfall plot in a trellis structure*

---

**Description**

A trellis is a plot structure which allows space optimized multi-panel multi track plots. This function uses the package **gtrellis** developed by Zuguang Gu, also available at <http://www.bioconductor.org/packages/release/bioc/html/gtrellis.html>. The graphics in the tracks within a gtrellis plot are mostly drawn with functions from the package **grid**. Note that for technical reasons, the column indicating the chromosome MUST have the name *chr* and be the first column in the data frame supplied to the gtrellis functions. Therefore reformatting is performed in this function before calling gtrellis functions.

**Usage**

```
trellis_rainfall_plot(in_rainfall_dat, in_point_size = unit(1, "mm"),
                     in_rect_list = NULL, in_title = "", in_CHROM.field = "CHROM",
                     in_POS.field = "POS", in_dist.field = "dist", in_col.field = "col")
```

## Arguments

<code>in_rainfall_dat</code>	Data frame which has to contain at least columns for chromosome, position, intermutational distance and colour information
<code>in_point_size</code>	size of the points in the rainfall plot to be created has to be provided with appropriate units, e.g. <code>in_point_size=unit(0.5,"mm")</code>
<code>in_rect_list</code>	Optional argument, if present, will lead to highlighting of specified regions by coloured but transparent rectangles
<code>in_title</code>	Title in the figure to be created.
<code>in_CHROM.field</code>	String indicating which column of <code>in_rainfall_dat</code> carries the chromosome information
<code>in_POS.field</code>	String indicating which column of <code>in_rainfall_dat</code> carries the position information
<code>in_dist.field</code>	String indicating which column of <code>in_rainfall_dat</code> carries the intermutational distance information
<code>in_col.field</code>	String indicating which column of <code>in_rainfall_dat</code> carries the colour information encoding the nucleotide exchange

## Value

The function doesn't return any value.

## See Also

[gtrellis\\_layout](#)  
[add\\_track](#)  
[grid.points](#)

## Examples

```
data(lymphoma_test)
choice_PID <- "4121361"
PID_df <- subset(lymphoma_test_df, PID==choice_PID)
trellis_rainfall_plot(PID_df, in_point_size=unit(0.5, "mm"))
```

## Description

Yet Another Package for mutational Signature analysis

## Details

This package provides functions and routines useful in the analysis of mutational signatures (cf. L. Alexandrov et al., Nature 2013). In particular, functions to perform a signature analysis with known signatures (`LCD` = linear combination decomposition) and a signature analysis on stratified mutational catalogue (`run_SMC` = stratify mutational catalogue) are provided.

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