

Package: CHOIRBM (via r-universe)

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Title Plots the CHOIR Body Map

Version 0.0.3

Description Collection of utility functions for visualizing body map data collected with the Collaborative Health Outcomes Information Registry.

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URL <https://github.com/emcramer/CHOIRBM>

BugReports <https://github.com/emcramer/CHOIRBM/issues>

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agg_choirbm_list	<i>Converts a list of CBMs to a single data frame</i>
------------------	---

Description

Takes a list of data frames where each data frame is the CBM of a patient and the values column is a binary endorsement of the CBM segment. Then it collapses the information to a single data frame for plotting by adding the 'value' columns of each data frame.

Usage

```
agg_choirbm_list(cbm_list)
```

Arguments

cbm_list a list of CBMs to collapse

Value

map_df a single CBM data frame with the value column summed.

Examples

```
## Not run:
data(validation)
cbm_list <- lapply(validation[["bodymap_regions_csv"]], string_to_map)
agg_df <- agg_choirbm_list(cbm_list)

## End(Not run)
```

comp_choirbm_chi	<i>Compare CBM segment endorsement across categorical variable using Chi-Square</i>
------------------	---

Description

Compare CBM segment endorsement across categorical variable using Chi-Square

Usage

```
comp_choirbm_chi(cbm_list, ...)
```

Arguments

cbm_list	a named list of CBMs
...	additional parameters passed to p.adjust()

Value

a data frame with the p-values, chi statistic, and degrees of freedom

Examples

```
## Not run:
data(validation)
# split male and female data
male_data <- validation[validation[['gender']] == "Male", ]
male_bodymap_list <- lapply(
  male_data[["bodymap_regions_csv"]]
  , string_to_map)
male_bodymap_df <- agg_choirbm_list(male_bodymap_list)
female_data <- validation[validation[['gender']] == "Female", ]
female_bodymap_list <- lapply(
  female_data[["bodymap_regions_csv"]]
  , string_to_map)
female_bodymap_df <- agg_choirbm_list(female_bodymap_list)
# compare with chi square test
chi_res <- comp_choirbm_chi(
  list("male" = male_bodymap_df
    , "female" = female_bodymap_df)
  , method = 'bonferroni'
)

## End(Not run)
```

comp_chairbm_glm	<i>Examine the effect of a continuous variable on CBM location endorsement</i>
------------------	--

Description

Examine the effect of a continuous variable on CBM location endorsement

Usage

```
comp_chairbm_glm(in_df, comp_var, method = "bonferroni", ...)
```

Arguments

in_df	a data.frame with at least one column for the CBM as a delimited string, and another column as the continuous variable for modeling.
comp_var	the name of the variable to model as a string
method	the method for p-value corrections
...	additional parameters passed to glm.

Value

a data.frame with the following columns: id, term, estimate, std.error, statistic, p.value. Each row is the result of one glm using the continuous variable to predict CBM location endorsement.

Examples

```
## Not run:
data(validation)
set.seed(123)
sampled_data <- validation[sample(1:nrow(validation), 100, replace = FALSE),]
model_output <- comp_chairbm_glm(sampled_data, "age")

## End(Not run)
```

comp_chairbm_ztest	<i>Compare CBM segment endorsement across categorical variable using z-test(s)</i>
--------------------	--

Description

Compare CBM segment endorsement across categorical variable using z-test(s)

Usage

```
comp_choirbm_ztest(cbm_list, tail = "two", p.method = "bonferroni")
```

Arguments

cbm_list a named list of CBMs

tail whether to do a single or two tailed z test

p.method the method for p-value corrections

Value

a data frame with the p-values and z statistic

Examples

```
library(CHOIRBM)
# isolate and process male data
male_data <- validation[validation[["gender"]] == "Male", ]
# isolate and process female data
female_data <- validation[validation[["gender"]] == "Female", ]
comp_choirbm_ztest(list( "male" = male_data, "female" = female_data), tail = "two")
```

comp_cooccurrence	<i>Calculate the co-occurrence between locations on the CBM</i>
-------------------	---

Description

Calculates the raw number of times two locations on the CBM are endorsed together in a data set.

Usage

```
comp_cooccurrence(df)
```

Arguments

df a data.frame with the CBMs as delimited strings in a single column.

Value

a data.frame with every combination of CBM locations and the number of times those locations occur together (the "co-occurrence").

Examples

```
## Not run:
set.seed(123)
sampled_data <- validation[sample(1:nrow(validation), 100, replace = FALSE),]
colnames(sampled_data)[5] <- "bodymap"
con_mat <- comp_cooccurrence(sampled_data)

## End(Not run)
```

convert_bodymap	<i>convert_bodymap Helper function to convert a single bodymap</i>
-----------------	--

Description

convert_bodymap Helper function to convert a single bodymap

Usage

```
convert_bodymap(segments)
```

Arguments

segments	a character vector containing segment numbers as individual strings in the vector that need to be adjusted/standardized
----------	---

Value

a character vector containing standardized segment numbers as individual strings in the vector

Examples

```
exampledata <- data.frame(
  GENDER = as.character(c("Male", "Female", "Female")),
  BODYMAP_CSV = as.character(c("112,125","112,113","128,117"))
)
convert_bodymap(exampledata[2,2])
```

convert_bodymaps	<i>convert_bodymaps Function to convert multiple bodymaps</i>
------------------	---

Description

convert_bodymaps Function to convert multiple bodymaps

Usage

```
convert_bodymaps(f_maps)
```

Arguments

f_maps a character vector where each string is a CHOIR bodymap in csv form

Value

a character vector of bodymaps using the male CHOIR bodymap numberings as a standard. Each bodymap is in csv form

Examples

```

exempladata <- data.frame(
  GENDER = as.character(c("Male", "Female", "Female")),
  BODYMAP_CSV = as.character(c("112,125","112,113","128,117"))
)
convert_bodymaps(
  as.character(
    exempladata$BODYMAP_CSV[exempladata$GENDER == 'Female']
  )
)

```

gen_example_data	<i>Generate Simple Example Data</i>
------------------	-------------------------------------

Description

Creates a data frame with CHOIR Body Map segment IDs and a randomly associated value. Also adds grouping information for facetting while plotting.

Usage

```
gen_example_data(seed = 123)
```

Arguments

seed integer to seed the random number generator

Value

values data.frame

Examples

```
cbm_df <- gen_example_data()
head(cbm_df)
```

num_areas	<i>Count the number of areas indicated in a CBM</i>
-----------	---

Description

Counts the number of areas a person endorses/indicates on their CHOIR Body Map.

Usage

```
num_areas(cbm_str, delim = ",")
```

Arguments

cbm_str a delimited string of 3-digit codes indicating CBM areas.
delim the delimiter character, defaults to a comma.

Value

nareas

Examples

```
cbm_str <- c("101,102,103,104")
num_areas(cbm_str, ",")
```

plot_cooccurrence	<i>Plot a concurrence matrix</i>
-------------------	----------------------------------

Description

Generates a concurrence matrix as a heatmap to show which CBM locations are commonly endorsed together.

Usage

```
plot_cooccurrence(con_mat, ...)
```

Arguments

con_mat	a long form data frame or matrix produced by the plot_concurrence function, with every combination of locations and the number of times each combination occurs.
...	additional parameters for plotting

Value

a ggplot heatmap of the concurrence.

Examples

```
## Not run:
set.seed(123)
sampled_data <- validation[sample(1:nrow(validation), 100, replace = FALSE),]
con_mat <- comp_cooccurrence(sampled_data)
plot_cooccurrence(con_mat)

## End(Not run)
```

plot_female_choirbm	<i>Plot the male CHOIR Body Map</i>
---------------------	-------------------------------------

Description

Creates a new plot of the front and back of the female CHOIR body map.

Usage

```
plot_female_choirbm(df, value)
```

Arguments

df	data.frame
value	string

Value

ggrob

Examples

```
cbm_df <- gen_example_data()
plot_female_choirbm(cbm_df, "value")
```

plot_male_choirbm	<i>Plot the male CHOIR Body Map</i>
-------------------	-------------------------------------

Description

Creates a new plot of the male CHOIR body map.

Usage

```
plot_male_choirbm(df, value)
```

Arguments

df	data.frame
value	string

Value

ggrob

Examples

```
cbm_df <- gen_example_data()
plot_male_choirbm(cbm_df, "value")
```

plot_nareas_histogram	<i>Plots a histogram of the number of CBM areas indicated</i>
-----------------------	---

Description

This is a wrapper for ggplot2's histogram function that incorporates calculating the number of CBM areas each individual indicates.

Usage

```
plot_nareas_histogram(cbms, ...)
```

Arguments

cbms	a list of delimited CBM strings
...	additional arguments passed to geom_histogram

Value

a histogram of the number of CBM areas endorsed by individuals in the dataset.

Examples

```
## Not run:
data(validation)
below20 <- validation[
  sapply(validation$bodymap_regions_csv, num_areas) < 20
, ]
plot_nareas_histogram(
  below20$bodymap_regions_csv
  , binwidth = 1
  , fill = "grey"
  , color = "white")

## End(Not run)
```

prep_bodymaps	<i>prep_bodymaps converts a single charcter vector of bodymaps into a list of character vectors, each a bodymap</i>
---------------	---

Description

prep_bodymaps converts a single charcter vector of bodymaps into a list of character vectors, each a bodymap

Usage

```
prep_bodymaps(maps)
```

Arguments

maps	a character vector containing the endorsed bodymap segments of patients in csv form
------	---

Value

a list of character vectors, where each vector contains the patient's endorsed segments

Examples

```
exampledata <- data.frame(
  GENDER = as.character(c("Male", "Female", "Female")),
  BODYMAP_CSV = as.character(c("112,125","112,113","128,117"))
)
prep_bodymaps(as.character(exampledata$BODYMAP_CSV))
```

string_to_map	<i>Converts a comma-separated string to a CHOIR BM</i>
---------------	--

Description

Takes a string of IDs that are separated by a comma and converts the information into a data frame with a binary indication of whether or not an ID appeared. Useful for plotting an individual’s CHOIR BM or for isolating particular sections to highlight.

Usage

```
string_to_map(map_str = "", delim = ",")
```

Arguments

map_str	The delimited CBM string.
delim	The delimiter for the CBM string.

Value

ret_df data.frame with all of the CHOIR BM segment IDs with a 1 if the segment was present and 0 otherwise.

Examples

```
# from a choir database
cbm_str <- "101,102,103,104,201,202"
cbm_df <- string_to_map(cbm_str)
# plot in a male or female bodymap...
plot_male_choirbm(cbm_df, "value")

# from a REDCap project
cbm_str <- "b07,b18,b19,b23,b24,b28,b33,f01,f03,f08,f17,f27,f29"
cbm_df <- string_to_map(cbm_str)
# plot in a male or female bodymap...
plot_male_choirbm(cbm_df, "value")
```

validation	<i>CHOIR Body Map data for approximately 7,000 patients</i>
------------	---

Description

A non-identifiable, simulated data set generated by randomly permuting data from the CHOIR Body Map validation study.

Usage

```
data(validation)
```

Format

An object of class "data.frame"

id A randomly generated numeric code for each patient.

gender The patient's gender.

race The patient's race.

age The patient's age.

bodymap_regions_csv The patient's CHOIR Body Map in a comma separated string.

score A simulated pain score for demonstration purposes.

References

This data set was derived from the data collected during the study validating the CHOIR Body Map as an instrument for recording a patient's anatomical pain location. [doi:10.1097/pr9.0000000000000880](https://doi.org/10.1097/pr9.0000000000000880)

Examples

```
data(validation)
head(validation)
```

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