

# Package ‘CHOIRBM’

February 15, 2021

**Title** Plots the CHOIR Body Map

**Version** 0.0.2

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

**License** MIT + file LICENSE

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

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

**Depends** R (>= 3.5.0)

**Imports** ggplot2, rlang, stringr

**Suggests** knitr, rmarkdown, testthat (>= 2.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 2

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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**Repository** CRAN

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gen_example_data	<i>Generate Simple Example Data</i>
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**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
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**Value**

values data.frame

**Examples**

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

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plot_female_choirbm	<i>Plot the male CHOIR Body Map</i>
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**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")
```

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plot_male_choirbm	<i>Plot the male CHOIR Body Map</i>
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**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")
```

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

```
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")
```

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validation

*CHOIR Body Map data for approximately 7,000 patients*


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**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)

*validation*

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### **Examples**

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

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