Package ‘healthyR’

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Title Hospital Data Analysis Workflow Tools
Version 0.2.0
Description Hospital data analysis workflow tools, modeling, and automations. This library provides many useful tools to review common administrative hospital data. Some of these include average length of stay, readmission rates, average net pay amounts by service lines just to name a few. The aim is to provide a simple and consistent verb framework that takes the guesswork out of everything.
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**Description**

Get the counts of a column by a particular grouping if supplied, otherwise just get counts of a column.
Usage

category_counts_tbl(.data, .count_col, .arrange_value = TRUE, ...)

Arguments

.data The data.frame/tibble supplied.
.count_col The column that has the values you want to count.
.arrange_value Defaults to true, this will arrange the resulting tibble in descending order by .count_col
...

Place the values you want to pass in for grouping here.

Details

• Requires a data.frame/tibble.
• Requires a value column, a column that is going to counted.

Author(s)

Steven P. Sanderson II, MPH

Examples

library(healthyR.data)
library(dplyr)

healthyR_data %>%
category_counts_tbl(  
 .count_col = payer_grouping  
 , .arrange = TRUE  
 , ip_op_flag  
 )

healthyR_data %>%
category_counts_tbl(  
 .count_col = ip_op_flag  
 , .arrange_value = TRUE  
 , service_line  
 )

Description

8 Hex RGB color definitions suitable for charts for colorblind people.
Usage

color_blind()

Details

This function is used in others in order to help render plots for those that are color blind.

Value

A vector of 8 Hex RGB definitions.

Author(s)

Steven P. Sanderson II, MPH

Examples

color_blind()

---

diverging_bar_plt  Diverging Bar Chart

Description

Diverging Bars is a bar chart that can handle both negative and positive values. This can be implemented by a smart tweak with \texttt{geom_bar()}. But the usage of \texttt{geom_bar()} can be quite confusing. That's because, it can be used to make a bar chart as well as a histogram. Let me explain.

By default, \texttt{geom_bar()} has the stat set to count. That means, when you provide just a continuous \(X\) variable (and no \(Y\) variable), it tries to make a histogram out of the data.

In order to make a bar chart create bars instead of histogram, you need to do two things. Set \texttt{stat = identity} and provide both \(x\) and \(y\) inside \texttt{aes()} where, \(x\) is either character or factor and \(y\) is numeric. In order to make sure you get diverging bars instead of just bars, make sure, your categorical variable has 2 categories that changes values at a certain threshold of the continuous variable. In below example, the mpg from mtcars data set is normalized by computing the \(z\) score. Those vehicles with mpg above zero are marked green and those below are marked red.

Usage

diverging_bar_plt(
   .data,
   .x_axis,
   .y_axis,
   .fill_col,
   .plot_title = NULL,
   .plot_subtitle = NULL,
   .plot_caption = NULL,
)
**diverging_bar_plt**

```r

.data = mtcars,
.x_axis = car_name,
.y_axis = mpg_z,
.fill_col = mpg_type

```

### Arguments

- `.data` The data to pass to the function, must be a tibble/data.frame.
- `.x_axis` The data that is passed to the x-axis.
- `.y_axis` The data that is passed to the y-axis. This will also equal the parameter `label`.
- `.fill_col` The column that will be used to fill the color of the bars.
- `.plot_title` Default is NULL
- `.plot_subtitle` Default is NULL
- `.plot_caption` Default is NULL
- `.interactive` Default is FALSE. TRUE returns a plotly plot

### Details

This function takes only a few arguments and returns a ggplot2 object.

### Value

A plotly plot or a ggplot2 static plot

### Author(s)

Steven P. Sanderson II, MPH

### Examples

```r
suppressPackageStartupMessages(library(ggplot2))
data("mtcars")
mtcars$car_name <- rownames(mtcars)
mtcars$mpg_z <- round((mtcars$mpg - mean(mtcars$mpg))/sd(mtcars$mpg), 2)
mtcars$mpg_type <- ifelse(mtcars$mpg_z < 0, "below", "above")
mtcars <- mtcars[order(mtcars$mpg_z), ] # sort
mtcars$car_name <- factor(mtcars$car_name, levels = mtcars$car_name)

diverging_bar_plt(
  .data = mtcars,
  .x_axis = car_name,
  .y_axis = mpg_z,
  .fill_col = mpg_type,
  .interactive = FALSE
)
```
diverging_lollipop_plt

Diverging Lollipop Chart

Description
This is a diverging lollipop function. Lollipop chart conveys the same information as bar chart and diverging bar. Except that it looks more modern. Instead of geom_bar, I use geom_point and geom_segment to get the lollipops right. Let’s draw a lollipop using the same data I prepared in the previous example of diverging bars.

Usage
diverging_lollipop_plt(
  .data,
  .x_axis,
  .y_axis,
  .plot_title = NULL,
  .plot_subtitle = NULL,
  .plot_caption = NULL,
  .interactive = FALSE
)

Arguments
.data The data to pass to the function, must be a tibble/data.frame.
.x_axis The data that is passed to the x-axis. This will also be the x and xend parameters of the geom_segment
.y_axis The data that is passed to the y-axis. This will also equal the parameters of yend and label
.plot_title Default is NULL
.plot_subtitle Default is NULL
.plot_caption Default is NULL
.interactive Default is FALSE. TRUE returns a plotly plot

Details
This function takes only a few arguments and returns a ggplot2 object.

Value
A plotly plot or a ggplot2 static plot

Author(s)
Steven P. Sanderson II, MPH
Examples

```r
suppressPackageStartupMessages(library(ggplot2))

data("mtcars")
mtcars$car_name <- rownames(mtcars)
mtcars$mpg_z <- round((mtcars$mpg - mean(mtcars$mpg))/sd(mtcars$mpg), 2)
mtcars$mpg_type <- ifelse(mtcars$mpg_z < 0, "below", "above")
mtcars <- mtcars[order(mtcars$mpg_z), ] # sort
mtcars$car_name <- factor(mtcars$car_name, levels = mtcars$car_name)

diverging_lollipop_plt(.data = mtcars, .x_axis = car_name
, .y_axis = mpg_z)
```

**dx_cc_mapping**

*Diagnosis to Condition Code Mapping file*

**Description**

A dataset containing the Diagnosis Code to AHRQ Condition Code Mapping that is used in helping to define service lines for inpatient discharges.

**Usage**

```r
data(dx_cc_mapping)
```

**Format**

A data frame with 86852 rows and 5 variables

**Details**

- **CC_Code.** DX_1, DX_2, ..., DX_n
- **CC_Desc.** DX_1 = Conduction disorders, DX_n = description
- **ICD Ver_Flag.** ICD Version 10 or 9
- **ICDCode.** ICD-9 or ICD-10 Code
- **Diagnosis.** Long QT Syndrome
gartner_magic_chart_plt

Gartner Magic Chart - Plotting of two continuous variables

Description

Plot a Gartner Magic Chart of two continuous variables

Usage

```r
gartner_magic_chart_plt(
  .data,
  .x_col,
  .y_col,
  .point_size_col = NULL,
  .y_lab,
  .x_lab,
  .plt_title,
  .tl_lbl,
  .tr_lbl,
  .br_lbl,
  .bl_lbl
)
```

Arguments

- `.data` The data set you want to plot
- `.x_col` The x-axis for the plot
- `.y_col` The y-axis for the plot
- `.point_size_col` The default is NULL, if you want to size the dots by a column in the data.frame/tibble then enter the column name here.
- `.y_lab` The y-axis label
- `.x_lab` The x-axis label
- `.plt_title` The title of the plot
- `.tl_lbl` The top left label
- `.tr_lbl` The top right label
- `.br_lbl` The bottom right label
- `.bl_lbl` The bottom left label

Details

- Supply a data frame with at least two continuous variables to plot against each other
Value
A ggplot plot

Author(s)
Steven P. Sanderson II, MPH

Examples
library(dplyr)

data_tbl <- tibble(
  x = rnorm(100, 0, 1),
  y = rnorm(100, 0, 1),
  z = abs(x) + abs(y)
)
gartner_magic_chart_plt(
  .data = data_tbl,
  .x_col = x,
  .y_col = y,
  .point_size = z,
  .x_lab = "los",
  .y_lab = "ra",
  .plt_title = "tst",
  .tr_lbl = "High RA-LOS",
  .tl_lbl = "High RA",
  .bl_lbl = "Leader",
  .br_lbl = "High LOS"
)
gartner_magic_chart_plt(
  .data = data_tbl,
  .x_col = x,
  .y_col = y,
  .point_size = NULL,
  .x_lab = "los",
  .y_lab = "ra",
  .plt_title = "tst",
  .tr_lbl = "High RA-LOS",
  .tl_lbl = "High RA",
  .bl_lbl = "Leader",
  .br_lbl = "High LOS"
)
hr_scale_fill_colorblind

Description
8 Hex RGB color definitions suitable for charts for colorblind people.

Usage
hr_scale_color_colorblind(..., theme = "hr")

Arguments
... Data passed in from a ggplot object
theme Right now this is hr only. Anything else will render an error.

Details
This function is used in others in order to help render plots for those that are color blind.

Value
A ggplot layer

Author(s)
Steven P. Sanderson II, MPH
kmeans_mapped.tbl

Author(s)

Steven P. Sanderson II, MPH

---

**kmeans_mapped.tbl  K-Means Mapper**

Description

Create a tibble that maps the `kmeans_obj()` using `purrr::map()` to create a nested data.frame/tibble that holds n centers. This tibble will be used to help create a scree plot.

Usage

```r
kmeans_mapped_tbl(.data, .centers = 15)
```

Arguments

- `.data` You must have a tibble in the working environment from the `kmeans_user_item_tbl()`
- `.centers` How many different centers do you want to try

Details

Takes in a single parameter of .centers. This is used to create the tibble and map the `kmeans_obj()` function down the list creating a nested tibble.

Value

A nested tibble

Author(s)

Steven P. Sanderson II, MPH

See Also

https://en.wikipedia.org/wiki/Scree_plot

Examples

```r
call <- healthyR.data%>%
  filter(ip_op_flag == "I") %>%
  filter(payer_grouping != "Medicare B") %>%
  filter(payer_grouping != "?"
  ) %>%
select(service_line, payer_grouping) %>%
mutate(record = 1) %>%
```
as_tibble()

ui_tbl <- kmeans_user_item_tbl(
  .data = data_tbl,
  .row_input = service_line,
  .col_input = payer_grouping,
  .record_input = record
)

kmeans_mapped_tbl(ui_tbl)

---

### kmeans_obj

**K-Means Functions**

**Description**

Takes the output of the `kmeans_user_item_tbl()` function and applies the k-means algorithm to it using `stats::kmeans()`

**Usage**

```r
kmeans_obj(.data, .centers = 5)
```

**Arguments**

- `.data`: The data that gets passed from `kmeans_user_item_tbl()`
- `.centers`: How many initial centers to start with

**Details**

Uses the `stats::kmeans()` function and creates a wrapper around it.

**Value**

A stats k-means object

**Author(s)**

Steven P. Sanderson II, MPH

**Examples**

```r
library(healthyR.data)
library(dplyr)

data_tbl <- healthyR_data%>%filter(ip_op_flag == "I")%>%filter(payer_grouping != "Medicare B")
```
filter(payer_grouping != ")") %>%
select(service_line, payer_grouping) %>%
mutate(record = 1) %>%
as_tibble()

kmeans_user_item_tbl(
  .data = data_tbl,
  .row_input = service_line,
  .col_input = payer_grouping,
  .record_input = record
) %>%
kmeans_obj()

---

**kmeans_scree_data_tbl  K-Means Scree Plot Data Table**

**Description**

Take data from the `kmeans_mapped_tbl()` and unnest it into a tibble for inspection and for use in the `kmeans_scree_plt()` function.

**Usage**

`kmeans_scree_data_tbl(.data)`

**Arguments**

`.data` You must have a tibble in the working environment from the `kmeans_mapped_tbl()`

**Details**

Takes in a single parameter of `.data` from `kmeans_mapped_tbl()` and transforms it into a tibble that is used for `kmeans_scree_plt()`. It will show the values (tot.withinss) at each center.

**Value**

A nested tibble

**Author(s)**

Steven P. Sanderson II, MPH
Examples

```r
library(healthyR.data)
library(dplyr)

data_tbl <- healthyR_data%>%
    filter(ip_op_flag == "I") %>%
    filter(payer_grouping != "Medicare B") %>%
    filter(payer_grouping != "?") %>%
    select(service_line, payer_grouping) %>%
    mutate(record = 1) %>%
    as_tibble()

ui_tbl <- kmeans_user_item_tbl(
  .data = data_tbl
  , .row_input = service_line
  , .col_input = payer_grouping
  , .record_input = record
)

kmm_tbl <- kmeans_mapped_tbl(ui_tbl)

kmeans_scree_data_tbl(kmm_tbl)
```

---

**kmeans_scree_plt**  
*K-Means Scree Plot*

**Description**

Create a scree-plot from the `kmeans_mapped_tbl()` function.

**Usage**

```r
kmeans_scree_plt(.data)
```

**Arguments**

- `.data`  
The data from the `kmeans_mapped_tbl()` function

**Details**

Outputs a scree-plot

**Value**

A ggplot2 plot

**Author(s)**

Steven P. Sanderson II, MPH
kmeans_tidy_tbl

See Also

https://en.wikipedia.org/wiki/Scree_plot

Examples

library(healthyR.data)
library(dplyr)

data_tbl <- healthyR_data%>%
  filter(ip_op_flag == "I")%>%
  filter(payer_grouping != "Medicare B")%>%
  filter(payer_grouping != "?")%>%
  select(service_line, payer_grouping)%>%
  mutate(record = 1)%>%
  as_tibble()

ui_tbl <- kmeans_user_item_tbl(
  .data = data_tbl,
  .row_input = service_line,
  .col_input = payer_grouping,
  .record_input = record
)

kmm_tbl <- kmeans_mapped_tbl(ui_tbl)

kmeans_scree_plt(.data = kmm_tbl)

---

kmeans_tidy_tbl  K-Means tidy Functions

Description

K-Means tidy functions

Usage

kmeans_tidy_tbl(.kmeans_obj, .data, .tidy_type = "tidy")

Arguments

.kmeans_obj A stats::kmeans() object
.data The user item tibble created from kmeans_user_item_tbl()
.tidy_type "tidy","glance", or "augment"

Details

Takes in a k-means object and its associated user item tibble and then returns one of the items asked for. Either: broom::tidy(), broom::glance() or broom::augment(). The function defaults to broom::tidy().
Value

A tibble

Author(s)

Steven P. Sanderson II, MPH

Examples

library(healthyR.data)
library(dplyr)
library(broom)

data_tbl <- healthyR_data%>%
  filter(ip_op_flag == "I") %>%
  filter(payer_grouping != "Medicare B") %>%
  filter(payer_grouping != "?") %>%
  select(service_line, payer_grouping) %>%
  mutate(record = 1) %>%
  as_tibble()

uit_tbl <- kmeans_user_item_tbl(
  .data = data_tbl
  , .row_input = service_line
  , .col_input = payer_grouping
  , .record_input = record
)

km_obj <- kmeans_obj(uit_tbl)

kmeans_tidy_tbl(
  .kmeans_obj = km_obj
  , .data = uit_tbl
  , .tidy_type = "augment"
)

kmeans_tidy_tbl(
  .kmeans_obj = km_obj
  , .data = uit_tbl
  , .tidy_type = "glance"
)

kmeans_tidy_tbl(
  .kmeans_obj = km_obj
  , .data = uit_tbl
  , .tidy_type = "tidy"
) %>%
glimpse()
**kmeans_user_item_tbl**  
**K-Means Functions**

**Description**
Takes in a data.frame/tibble and transforms it into an aggregated/normalized user-item tibble of proportions. The user will need to input the parameters for the rows/user and the columns/items.

**Usage**

```r
kmeans_user_item_tbl(.data, .row_input, .col_input, .record_input)
```

**Arguments**

- `.data`: The data that you want to transform
- `.row_input`: The column that is going to be the row (user)
- `.col_input`: The column that is going to be the column (item)
- `.record_input`: The column that is going to be summed up for the aggregation and normalization process.

**Details**
This function should be used before using a k-mean model. This is commonly referred to as a user item matrix because "users" tend to be on the rows and "items" (e.g. orders) on the columns. You must supply a column that can be summed for the aggregation and normalization process to occur.

**Value**
A aggregated/normalized user item tibble

**Author(s)**
Steven P. Sanderson II, MPH

**Examples**

```r
library(healthyR.data)  # assuming healthyR.data is a package
library(dplyr)

data_tbl <- healthyR.data%>%
  filter(ip_op_flag == "I") %>%
  filter(payer_grouping != "Medicare B") %>%
  filter(payer_grouping != "?") %>%
  select(service_line, payer_grouping) %>%
  mutate(record = 1) %>%
  as_tibble()

kmeans_user_item_tbl(
```
los_ra_index_plt  

Plot LOS and Readmit Index with Variance

Description
Plot the index of the length of stay and readmit rate against each other along with the variance

Usage
los_ra_index_plt(.data)

Arguments
.data  The data supplied from los_ra_index_summary_tbl()

Details
- Expects a tibble
- Expects a Length of Stay and Readmit column, must be numeric
- Uses cowplot to stack plots

Value
A patchwork ggplot2 plot

Author(s)
Steven P. Sanderson II, MPH

Examples

suppressPackageStartupMessages(library(dplyr))
data_tbl <- tibble("alos" = runif(186, 1, 20),
                   "elos" = runif(186, 1, 17),
                   "readmit_rate" = runif(186, 0, .25),
                   "readmit_rate_bench" = runif(186, 0, .2))

los_ra_index_summary_tbl(
los_ra_index_summary_tbl

Description

Create the length of stay and readmit index summary tibble

Usage

los_ra_index_summary_tbl(
  .data,
  .max_los = 15,
  .alos_col,
  .elos_col,
  .readmit_rate,
  .readmit_bench
)

Arguments

.data The data you are going to analyze.
.max_los You can give a maximum LOS value. Lets say you typically do not see los over 15 days, you would then set .max_los to 15 and all values greater than .max_los will be grouped to .max_los
.alos_col The Average Length of Stay column
.elos_col The Expected Length of Stay column
.readmit_rate The Actual Readmit Rate column
.readmit_bench The Expected Readmit Rate column
Details

- Expects a tibble
- Expects the following columns and there should only be these 4
  - Length Of Stay Actual - Should be an integer
  - Length Of Stacy Benchmark - Should be an integer
  - Readmit Rate Actual - Should be 0/1 for each record, 1 = readmitted, 0 did not.
  - Readmit Rate Benchmark - Should be a percentage from the benchmark file.
- This will add a column called visits that will be the count of records per length of stay from 1 to .max_los
- The .max_los param can be left blank and the function will default to 15. If this is not a good default and you don't know what it should be then set it to 75 percentile from the \texttt{stats::quantile()} function using the defaults, like so .max_los = \texttt{stats::quantile(data_tbl$alos)[[4]]}
- Uses all data to compute variance, if you want it for a particular time frame you will have to filter the data that goes into the \texttt{.data} argument. It is suggested to use \texttt{timetk::filter_by_time()}
- The index is computed as the excess of the length of stay or readmit rates over their respective expectations.

Value

A tibble

Author(s)

Steven P. Sanderson II, MPH

Examples

```r
suppressPackageStartupMessages(library(dplyr))

data_tbl <- tibble(
  "alos" = runif(186, 1, 20),
  "elos" = runif(186, 1, 17),
  "readmit_rate" = runif(186, 0, .25),
  "readmit_bench" = runif(186, 0, .2)
)

los_ra_index_summary_tbl(
  .data = data_tbl,
  .max_los = 15,
  .alos_col = alos,
  .elos_col = elos,
  .readmit_rate = readmit_rate,
  .readmit_bench = readmit_bench
)

los_ra_index_summary_tbl(
  .data = data_tbl
)
named_item_list

, .max_los = 10
, .alos_col = alos
, .elos_col = elos
, .readmit_rate = readmit_rate
, .readmit_bench = readmit_bench

Tibble to named list

Description

Takes in a data.frame/tibble and creates a named list from a supplied grouping variable. Can be used in conjunction with `save_to_excel()` to create a new sheet for each group of data.

Usage

`named_item_list(.data, .group_col)`

Arguments

- `.data` The data.frame/tibble.
- `.group_col` The column that contains the groupings.

Details

- Requires a data.frame/tibble and a grouping column.

Author(s)

Steven P. Sanderson II, MPH

Examples

```r
library(healthyR.data)

df <- healthyR_data
df_list <- named_item_list(.data = df, .group_col = service_line)
df_list
```
Get the optimal binwidth for a histogram

Description

Gives the optimal binwidth for a histogram given a data set, its value and the desired amount of bins.

Usage

`opt_bin(.data, .value_col, .iters = 30)`

Arguments

- `.data` The data set in question
- `.value_col` The column that holds the values
- `.iters` How many times the cost function loop should run

Details

Modified from Hideaki Shimazaki Department of Physics, Kyoto University shimazaki at ton.scphys.kyoto-u.ac.jp Feel free to modify/distribute this program.

- Supply a data.frame/tibble with a value column. From this an optimal binwidth will be computed for the amount of bins desired.

Value

A tibble of histogram breakpoints

Examples

```r
suppressPackageStartupMessages(library(purrr))
suppressPackageStartupMessages(library(dplyr))

df_tbl <- rnorm(n = 1000, mean = 0, sd = 1)
df_tbl <- df_tbl %>%
  as_tibble() %>%
  set_names("value")

df_tbl %>%
opt_bin(
  .value_col = value,
  .iters = 100
)
```
px_cc_mapping

Procedure to Condition Code Mapping file

Description
A dataset containing the Procedure Code to AHRQ Condition Code Mapping that is used in helping to define service lines for inpatient discharges.

Usage
data(px_cc_mapping)

Format
A data frame with 79721 rows and 5 variables

Details
• CC_Code. PX_1, PX_2, ..., PX_n
• CC_Desc. PX_1 = Genitourinary incontinence procedures
• ICD_Ver_Flag. 10 or 9
• ICDCode. ICD-9 or ICD-10 Code
• Procedure. Inject Implant Urethra

save_to_excel
Save a file to Excel

Description
Save a tibble/data.frame to an excel .xlsx file. The file will automatically with a save_dtime in the format of 20201109_132416 for November 11th, 2020 at 1:24:16PM.

Usage
save_to_excel(.data, .file_name)

Arguments
.data The tibble/data.frame that you want to save as an .xlsx file.
.file_name the name you want to give to the file.

Details
• Requires a tibble/data.frame to be passed to it.
Value

A saved excel file

Author(s)

Steven P. Sanderson II, MPH

---

**service_line_augment**  
*Service Line Grouper Augment Function*

**Description**

Takes a few arguments from a data.frame/tibble and returns a service line augmented to a data.frame/tibble for a set of patients.

**Usage**

```r
service_line_augment(.data, .dx_col, .px_col, .drg_col)
```

**Arguments**

- `.data` The data being passed that will be augmented by the function.
- `.dx_col` The column containing the Principal Diagnosis for the discharge.
- `.px_col` The column containing the Principal Coded Procedure for the discharge. It is possible that this could be blank.
- `.drg_col` The DRG Number coded to the inpatient discharge.

**Details**

This is an augment function in that appends a vector to an data.frame/tibble that is passed to the `.data` parameter. A data.frame/tibble is required, along with a principal diagnosis column, a principal procedure column, and a column for the DRG number. These are needed so that the function can join the dx_cc_mapping and px_cc_mapping columns to provide the service line. This function only works on visits that are coded using ICD Version 10 only.

Let's take an example discharge, the DRG is 896 and the Principal Diagnosis code maps to DX_660, then this visit would get grouped to alcohol_abuse

**DRG 896: ALCOHOL, DRUG ABUSE OR DEPENDENCE WITHOUT REHABILITATION THERAPY WITH MAJOR COMPLICATION OR COMORBIDITY (MCC)**

DX_660 Maps to the following ICD-10 Codes ie F1010 Alcohol abuse, uncomplicated:

```r
library(healthyR)
dx_cc_mapping %>%
  filter(CC_Code == "DX_660", ICD_Ver_Flag == "10")
```
Value

An augmented data.frame/tibble with the service line appended as a new column.

Author(s)

Steven P. Sanderson II, MPH

Examples

df <- data.frame(
  dx_col = "F10.10",
  px_col = NA,
  drg_col = "896"
)

service_line_augment(
  .data = df,
  .dx_col = dx_col,
  .px_col = px_col,
  .drg_col = drg_col
)

<table>
<thead>
<tr>
<th>service_line_vec</th>
<th>Service Line Grouper Vectorized Function</th>
</tr>
</thead>
</table>

Description

Takes a few arguments from a data.frame/tibble and returns a service line vector for a set of patients.

Usage

service_line_vec(.data, .dx_col, .px_col, .drg_col)

Arguments

| .data | The data being passed that will be augmented by the function. |
| .dx_col | The column containing the Principal Diagnosis for the discharge. |
| .px_col | The column containing the Principal Coded Procedure for the discharge. It is possible that this could be blank. |
| .drg_col | The DRG Number coded to the inpatient discharge. |
**Details**

This is a vectorized function in that it returns a vector. It can be applied inside of a `mutate` statement when using `dplyr` if desired. A `data.frame/tibble` is required, along with a principal diagnosis column, a principal procedure column, and a column for the DRG number. These are needed so that the function can join the `dx_cc_mapping` and `px_cc_mapping` columns to provide the service line. This function only works on visits that are coded using ICD Version 10 only.

Let's take an example discharge, the DRG is 896 and the Principal Diagnosis code maps to `DX_660`, then this visit would get grouped to `alcohol_abuse`:

**DRG 896: ALCOHOL, DRUG ABUSE OR DEPENDENCE WITHOUT REHABILITATION THERAPY WITH MAJOR COMPLICATION OR COMORBIDITY (MCC)**

`DX_660` Maps to the following ICD-10 Codes ie F1010 Alcohol abuse, uncomplicated:

```r
library(healthyR)
dx_cc_mapping %>%
  filter(CC_Code == "DX_660", ICD_Ver_Flag == "10")
```

**Value**

A vector of service line assignments.

**Author(s)**

Steven P. Sanderson II, MPH

**Examples**

```r
df <- data.frame(
  dx_col = "F10.10",
  px_col = NA,
  drg_col = "896"
)

service_line_vec(
  .data = df,
  .dx_col = dx_col,
  .px_col = px_col,
  .drg_col = drg_col
)
```

---

**Use SQL LEFT type function**

**Description**

Perform an SQL `LEFT()` type function on a piece of text
sql_left

Usage

sql_left(.text, .num_char)

Arguments

.text	A piece of text/string to be manipulated
.num_char	How many characters do you want to grab

Details

• You must supply data that you want to manipulate.

Examples

sql_left("text", 3)

sql_mid

Use SQL MID type function

Description

Perform an SQL SUBSTRING type function

Usage

sql_mid(.text, .start_num, .num_char)

Arguments

.text	A piece of text/string to be manipulated
.start_num	What place to start at
.num_char	How many characters do you want to grab

Details

• You must supply data that you want to manipulate.

Examples

sql_mid("this is some text", 6, 2)
**sql_right**  
*Use SQL RIGHT type functions*

**Description**
Perform an SQL RIGHT type function

**Usage**
```
sql_right(.text, .num_char)
```

**Arguments**
- `.text`: A piece of text/string to be manipulated
- `.num_char`: How many characters do you want to grab

**Details**
- You must supply data that you want to manipulate.

**Examples**
```
sql_right("this is some more text", 3)
```

---

**top_n_tbl**  
*Top N tibble*

**Description**
Get a tibble returned with n records sorted either by descending order (default) or ascending order.

**Usage**
```
top_n_tbl(.data, .n_records, .arrange_value = TRUE, ...)
```

**Arguments**
- `.data`: The data you want to pass to the function
- `.n_records`: How many records you want returned
- `.arrange_value`: A boolean with TRUE as the default. TRUE sorts data in descending order
- `...`: The columns you want to pass to the function.
Details

- Requires a data.frame/tibble
- Requires at least one column to be chosen inside of the ...
- Will return the tibble in sorted order that is chosen with descending as the default

Author(s)

Steven P. Sanderson II, MPH

Examples

```r
library(healthyR.data)

df <- healthyR.data

df_tbl <- top_n_tbl(
  .data = df
, .n_records = 3
, .arrange_value = TRUE
, service_line
, payer_grouping
)

print(df_tbl)
```

---

**ts_alos_plt**  
*Plot ALOS - Average Length of Stay*

Description

Plot ALOS - Average Length of Stay

Usage

```r
ts_alos_plt(.data, .date_col, .value_col, .by_grouping, .interactive)
```

Arguments

- `.data` The time series data you need to pass
- `.date_col` The date column
- `.value_col` The value column
- `.by_grouping` How you want the data summarized - "sec", "min", "hour", "day", "week", "month", "quarter" or "year"
- `.interactive` TRUE or FALSE. TRUE returns a plotly plot and FALSE returns a static ggplot2 plot
Details

- Expects a tibble with a date time column and a value column
- Uses timetk for underlying summarization and plot
- If .by_grouping is missing it will default to "day"
- A static ggplot2 object is return if the .interactive function is FALSE otherwise a plotly plot is returned.

Value

A timetk time series plot

Author(s)

Steven P. Sanderson II, MPH

Examples

library(healthyR)
library(healthyR.data)
library(timetk)
library(dplyr)
library(purrr)

# Make A Series of Dates ----
data_tbl <- healthyR_data

df_tbl <- data_tbl %>%
  filter(ip_op_flag == "I") %>%
  select(visit_end_date_time, length_of_stay) %>%
  summarise_by_time(
    .date_var = visit_end_date_time,
    , .by = "day",
    , visits = mean(length_of_stay, na.rm = TRUE)
  ) %>%
  filter_by_time(
    .date_var = visit_end_date_time,
    , .start_date = "2012",
    , .end_date = "2019"
  ) %>%
  set_names("Date","Values")

ts_alos_plt(
  .data = df_tbl,
  , .date_col = Date
  , .value_col = Values
  , .by = "month"
  , .interactive = FALSE
)
Description

Sometimes it is important to know what the census was on any given day, or what the average length of stay is on given day, including for those patients that are not yet discharged. This can be easily achieved. This will return one record for every account so the data will still need to be summarized. If there are multiple entries per day then those records will show up and you will therefore have multiple entries in the column date in the resulting tibble. If you want to aggregate from there you should be able to do so easily.

If you have a record where the .start_date_col is filled in but the corresponding end_date is null then the end date will be set equal to Sys.Date()

If a record has a start_date that is NA then it will be discarded.

This function can take a little bit of time to run while the join comparison runs.

Usage

ts_census_los_daily_tbl(
  .data,
  .keep_nulls_only = FALSE,
  .start_date_col,
  .end_date_col,
  .by_time = "day"
)

Arguments

.data The data you want to pass to the function
.keep_nulls_only A boolean that will keep only those records that have a NULL end date, meaning the patient is still admitted. The default is FALSE which brings back all records.
.start_date_col The column containing the start date for the record
.end_date_col The column containing the end date for the record.
.by_time How you want the data presented, defaults to day and should remain that way unless you need more granular data.

Details

• Requires a dataset that has at least a start date column and an end date column
• Takes a single boolean parameter
ts_median_excess_plt

Value

A tibble object

Author(s)

Steven P. Sanderson II, MPH

Examples

```r
library(healthyR)
library(healthyR.data)
library(dplyr)

df <- healthyR_data

df_tbl <- df %>%
  filter(ip_op_flag == "I") %>%
  select(visit_start_date_time, visit_end_date_time) %>%
  timetk::filter_by_time(.date_var = visit_start_date_time, .start_date = "2020")

ts_census_los_daily_tbl(
  .data = df_tbl,
  .keep_nulls_only = FALSE,
  .start_date_col = visit_start_date_time,
  .end_date_col = visit_end_date_time
)
```

---

### ts_median_excess_plt

Create a plot showing the excess of the median value

**Description**

Plot out the excess +/- of the median value grouped by certain time parameters.

**Usage**

```r
ts_median_excess_plt(
  .data, .date_col, .value_col, .x_axis, .ggplot_group_var, .years_back
)
```
Arguments

- `.data` The data that is being analyzed, data must be a tibble/data.frame.
- `.date_col` The column of the tibble that holds the date.
- `.value_col` The column that holds the value of interest.
- `.x_axis` What is the be the x-axis, day, week, etc.
- `.ggplot_group_var` The variable to group the ggplot on.
- `.years_back` How many years back do you want to go in order to compute the median value.

Details

- Supply data that you want to view and you will see the excess +/- of the median values over a specified time series tibble.

Value

A ggplot2 plot

Examples

```r
suppressPackageStartupMessages(library(timetk))

ts_signature_tbl(
  .data = m4_daily,
  .date_col = date
)

%%

ts_median_excess_plt(
  .date_col = date,
  .value_col = value,
  .x_axis = month,
  .ggplot_group_var = year,
  .years_back = 1
)
```

Description

This is a wrapper function to the `timetk::plot_time_series()` function with a limited functionality parameter set. To see the full reference please visit the timetk package site.
Usage

ts_plt(
  .data,
  .date_col,
  .value_col,
  .color_col = NULL,
  .facet_col = NULL,
  .facet_ncol = NULL,
  .interactive = FALSE
)

Arguments

.data The data to pass to the function, must be a tibble/data.frame.
.date_col The column holding the date.
.value_col The column holding the value.
.color_col The column holding the variable for color.
.facet_col The column holding the variable for faceting.
.facet_ncol How many columns do you want.
.interactive Return a plotly plot if set to TRUE and a static ggplot2 plot if set to FALSE. The default is FALSE.

Details

This function takes only a few of the arguments in the function and presets others while choosing the defaults on others. The smoother functionality is turned off.

Value

A plotly plot or a ggplot2 static plot

Author(s)

Steven P. Sanderson II, MPH

See Also


Examples

suppressPackageStartupMessages(library(dplyr))
library(timetk)
library(healthyR.data)

healthyR.data::healthyR_data %>%
  filter(ip_op_flag == "I") %>%
  select(visit_end_date_time, service_line) %>%
```
filter_by_time(
 .date_var = visit_end_date_time
 , .start_date = "2020"
 ) %>%
group_by(service_line) %>%
summarize_by_time(
 .date_var = visit_end_date_time
 , .by = "month"
 , visits = n()
 ) %>%
ungroup() %>%
ts_plt(
 .date_col = visit_end_date_time
 , .value_col = visits
 , .color_col = service_line
)
```

---

### ts_readmit_rate_plt

**Plot Readmit Rate**

#### Description

Plot Readmit Rate

#### Usage

```
ts_readmit_rate_plt(.data, .date_col, .value_col, .by_grouping, .interactive)
```

#### Arguments

- `.data` - The data you need to pass.
- `.date_col` - The date column.
- `.value_col` - The value column.
- `.by_grouping` - How you want the data summarized - "sec", "min", "hour", "day", "week", "month", "quarter" or "year".
- `.interactive` - TRUE or FALSE. TRUE returns a plotly plot and FALSE returns a static ggplot2 plot.

#### Details

- Expects a tibble with a date time column and a value column
- Uses timetk for underlying sumarization and plot
- If `.by_grouping` is missing it will default to "day"

#### Value

A timetk time series plot that is interactive
Author(s)
Steven P. Sanderson II, MPH

Examples

```r
set.seed(123)

suppressPackageStartupMessages(library(timetk))
suppressPackageStartupMessages(library(purrr))
suppressPackageStartupMessages(library(dplyr))

ts_tbl <- tk_make_timeseries(
  start = "2019-01-01",
  by = "day",
  length_out = "1 year 6 months"
)

values <- arima.sim(
  model = list(
    order = c(0, 1, 0)
    , n = 547
    , mean = 1
    , sd = 5
  )
)

df_tbl <- tibble(
  x = ts_tbl
  , y = values
) %>%
  set_names("Date","Values")

ts_readmit_rate_plt(
  .data = df_tbl
  , .date_col = Date
  , .value_col = Values
  , .by = "month"
  , .interactive = FALSE
)
```

---

### ts_signature_tbl

**Make a Time Enhanced Tibble**

**Description**

Returns a tibble that adds the time series signature from the `timetk::tk_augment_timeseries_signature()` function. All added from a chosen date column defined by the `.date_col` parameter.

**Usage**

```r
ts_signature_tbl(.data, .date_col, .pad_time = TRUE, ...)
```
umap_list

Arguments

.data The data that is being analyzed.
.date_col The column that holds the date.
.pad_time Boolean TRUE/FALSE. If TRUE then the `timetk::pad_by_time()` function is called and used on the data.frame before the modification. The default is TRUE.
...

Details

- Supply data with a date column and this will add the year, month, week, week day and hour to the tibble. The original date column is kept.
- Returns a time-series signature tibble.
- You must know the data going into the function and if certain columns should be dropped or kept when using further functions

Value

A tibble

Examples

library(timetk)

ts_signature_tbl(
  .data = m4_daily,
  .date_col = date,
  .pad_time = TRUE,
  id = id
)

umap_list

Description

Create a umap object from the uwot::umap() function.

Usage

umap_list(.data, .kmeans_map_tbl, .k_cluster = 5)

Arguments

.data The data from the kmeans_user_item_tbl() function.
.kmeans_map_tbl The data from the kmeans_mapped_tbl().
.k_cluster Pick the desired amount of clusters from your analysis of the scree plot.
Details

This takes in the user item table/matrix that is produced by `kmeans_user_item_tbl()` function. This function uses the defaults of `uwot::umap()`.

Value

A list of tibbles and the umap object

Author(s)

Steven P. Sanderson II, MPH

See Also

• https://cran.r-project.org/package=uwot (CRAN)
• https://github.com/jlmelville/uwot (GitHub)
• https://github.com/jlmelville/uwot (arXiv paper)

Examples

```r
library(healthyR.data)
library(healthyR)
library(dplyr)
library(broom)

data_tbl <- healthyR_data %>%
  filter(ip_op_flag == "I") %>%
  filter(payer_grouping != "Medicare B") %>%
  filter(payer_grouping != "?") %>%
  select(service_line, payer_grouping) %>%
  mutate(record = 1) %>%
  as_tibble()

uit_tbl <- kmeans_user_item_tbl(
  .data = data_tbl
  , .row_input = service_line
  , .col_input = payer_grouping
  , .record_input = record
)

kmm_tbl <- kmeans_mapped_tbl(uit_tbl)

umap_list(.data = uit_tbl, kmm_tbl, 3)
```
**Description**
Create a UMAP Projection plot.

**Usage**
```r
umap_plt(.data, .point_size = 2, .label = TRUE)
```

**Arguments**

- `.data` The data from the `umap_list()` function.
- `.point_size` The desired size for the points of the plot.
- `.label` Should `ggrepel::geom_label_repel()` be used to display cluster user labels.

**Details**
This takes in `umap_kmeans_cluster_results_tbl` from the `umap_list()` function output.

**Value**
A ggplot2 UMAP Projection with clusters represented by colors.

**Author(s)**
Steven P. Sanderson II, MPH

**See Also**
- [https://cran.r-project.org/package=uwot](https://cran.r-project.org/package=uwot) (CRAN)
- [https://github.com/jlmelville/uwot](https://github.com/jlmelville/uwot) (GitHub)
- [https://github.com/jlmelville/uwot](https://github.com/jlmelville/uwot) (arXiv paper)

**Examples**
```r
library(healthyR.data)
library(healthyR)
library(dplyr)
library(broom)
library(ggplot2)

data_tbl <- healthyR_data %>%
  filter(ip_op_flag == "I") %>%
  filter(payer_grouping != "Medicare B") %>%
  filter(payer_grouping != "?") %>%
  select(service_line, payer_grouping)
```
```r
mutate(record = 1) %>%
as_tibble()

uit_tbl <- kmeans_user_item_tbl(
  .data = data_tbl,
  .row_input = service_line,
  .col_input = payer_grouping,
  .record_input = record
)

kmm_tbl <- kmeans_mapped_tbl(uit_tbl)

ump_lst <- umap_list(.data = uit_tbl, kmm_tbl, 3)

umap_plt(.data = ump_lst, .point_size = 3)
```
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