Package ‘cmpsR’

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Title R Implementation of Congruent Matching Profile Segments Method
Version 0.1.2
Description This is an open-source implementation of the Congruent Matching Profile Segments (CMPS) method (Chen et al. 2019)<doi:10.1016/j.forsciint.2019.109964>. In general, it can be used for objective comparison of striated tool marks, and in our examples, we specifically use it for bullet signatures comparisons. The CMPS score is expected to be large if two signatures are similar. So it can also be considered as a feature that measures the similarity of two bullet signatures.
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Author Wangqian Ju [aut, cre] (<https://orcid.org/0000-0002-9977-377X>), Heike Hofmann [ctb] (<https://orcid.org/0000-0001-6216-5183>)
Maintainer Wangqian Ju <wju@iastate.edu>
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bullets

**Description**

A dataset containing pre-processed information of two bullets. They are used as examples in Chapter 3.5 of Open Forensic Science in R.

**Usage**

```r
bullets
```

**Format**

A data frame/tbl/tbl_df with 12 rows and 3 variables:

- **source**: source of the bullet data
- **sigs**: bullet signatures, detailed information about how to get the signatures can be found at https://sctyner.github.io/OpenForSciR/bullets.html
- **bulletland**: label of the signatures

**Source**

**cmps_na_trim**

Remove the leading and trailing missing values in a numeric vector

**Description**

Remove the leading and trailing missing values in a numeric vector

**Usage**

```r
cmps_na_trim(x)
```

**Arguments**

- `x` numeric vector

**Value**

a numeric vector; only the leading and trailing missing values are removed

**Examples**

```r
x <- c(NA, 1, 2, 3, 4, NA)
cmps_na_trim(x)
```

---

**cmps_segment_plot**

Plot the selected basis segment and its cross-correlation curve at all scales based on the results of CMPS algorithm

**Description**

This function plots the selected basis segment with the comparison signature. One can visualize the scaled segment and its corresponding cross-correlation curve. The number of marked correlation peaks at each segment scale is determined by npeaks_set of extract_feature_cmps. The red vertical dashed line indicates the congruent registration position for all segments; the green vertical dashed line indicates the position of the consistent correlation peak (if any); the blue vertical dashed line indicates the tolerance zone (determined by Tx)

**Usage**

```r
cmps_segment_plot(cmps_result, seg_idx = 1)
```
**cmps_signature_plot**

- **Arguments**
  - `cmps_result`: A list generated by `extract_feature_cmps`. `cmps_result` is required to have the following names: parameters, congruent_pos, segments, nseg, i.e. one should at least have include = c("parameters", "congruent_pos", "segments", "nseg") when computing `cmps_result`. However, include = "full_result" is still recommended.
  - `seg_idx`: An integer. The index of a basis segment that we want to plot for.

- **Value**
  - A list of n elements, where n is the length of npeaks_set, i.e. the number of scales for each basis segment. And each one of these n elements is also a list, a list of two plots:
    - `segment_plot`: The basis segment of current scale is plotted at different positions where the segment obtains correlation peak. The comparison signature is also plotted.
    - `scale_ccf_plot`: This is the plot of the cross-correlation curve between the comparison signature and the segment of the current scale.

- **Examples**
  ```r
  library(cmpsR)
  library(ggpubr)
  data("bullets")
  land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][[1]]
  land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][[1]]
  
  # compute cmps
  # algorithm with multi-peak insepction at three different segment scales
  cmps_with_multi_scale <- extract_feature_cmps(land2_3$sig, land1_2$sig, include = "full_result")
  
  # generate plots using cmps_signature_plot
  seg_plot <- cmps_segment_plot(cmps_with_multi_scale, seg_idx = 3)
  pp <- ggarrange(plotlist = unlist(seg_plot, recursive = FALSE), nrow = 3, ncol = 2)
  ```

**Description**

This function aligns two signatures and shows which basis segments find the congruent registration position.
**Usage**

```r
cmps_signature_plot(cmps_result, add_background = TRUE)
```

**Arguments**

- **cmps_result**: a list generated by `extract_feature_cmps`. `cmps_result` is required to have the following names: `parameters`, `congruent_seg`, `congruent_pos`, `segments`, `cpp_list`. So `include = "full_result"` is recommended when computing `cmps_result`.
- **add_background**: boolean; whether or not to add zebra-striped background under each basis segment; default is `TRUE`.

**Value**

- a list

  - **segment_shift_plot**: a plot object generated by `ggplot2`. In this plot only basis segments that are congruent matching profile segments (CMPS) are plotted along with the comparison profile; each basis segment is shifted to the position where it obtains either a consistent correlation peak or a cross-correlation peak closest to the congruent registration position.
  - **signature_shift_plot**: a plot object generated by `ggplot2`. In this plot both the reference signature and the comparison signature are plotted, and CMPS are highlighted. The alignment of the two signatures is achieved by shifting the reference signature to the congruent registration position.
  - **seg_shift**: a data.frame. This data frame shows which basis segments are plotted (are CMPS) and the units by which each segment shifted when plotting `segment_shift_plot`.
  - **sig_shift**: a numeric value. The number of units by which the reference signature shifted when plotting `signature_shift_plot`.

**Examples**

```r
library(cmpsR)

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][[1]]
land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][[1]]

# compute cmps

# algorithm with multi-peak insepection at three different segment scales
cmps_with_multi_scale <- extract_feature_cmps(land2_3$sig, land1_2$sig, include = "full_result")

# generate plots using cmps_signature_plot
sig_plot <- cmps_signature_plot(cmps_with_multi_scale)
```
**compute_cross_corr**  
Wrapper function for compute_cross_corr

**Description**
Wrapper function for compute_cross_corr

**Usage**
```
compute_cross_corr(x, y, min.overlap)
```

**Arguments**
- `x` numeric vector, the longer sequence
- `y` numeric vector, the shorter sequence
- `min.overlap` numeric scalar, set the length of the minimum overlapping part

**compute_diff_phase**  
Compute a Statistic for the Foreground Phase and the Background Phases

**Description**
Compute a statistic (for example, a mean) based on all matching comparisons (foreground phase) and the same statistic based on all non-matching comparisons (background phases)

**Usage**
```
compute_diff_phase(scores_list, FUNC = mean, na.rm = TRUE, both = FALSE)
```

**Arguments**
- `scores_list` a list of all phases
- `FUNC` a function to be applied to both the foreground phase and the background phases
- `na.rm` a logical value indicating whether NA values should be stripped before the computation proceeds
- `both` logical value. If TRUE, return the values of the FUNC for both the foreground phase and the background phases; if FALSE, return their difference

**Value**
If both = TRUE, return the values of the statistic (calculated by FUNC) for both the foreground phase and the background phases; if both = FALSE, return the difference
Examples

library(tidyverse)

data("bullets")

lands <- unique(bullets$bulletland)

comparisons <- data.frame(expand.grid(land1 = lands[1:6], land2 = lands[7:12]),
                           stringsAsFactors = FALSE)

comparisons <- comparisons %>%
  left_join(bullets %>% select(bulletland, sig1=sigs),
            by = c("land1" = "bulletland")) %>%
  left_join(bullets %>% select(bulletland, sig2=sigs),
            by = c("land2" = "bulletland"))

comparisons <- comparisons %>%
  mutate(cmps = purrr::map2(sig1, sig2, .f = function(x, y) {
    extract_feature_cmps(x$sig, y$sig, include = "full_result")
  }))

comparisons <- comparisons %>%
  mutate(
    cmps_score = sapply(comparisons$cmps, function(x) x$CMPS_score),
    cmps_nseg = sapply(comparisons$cmps, function(x) x$nseg)
  )

cp1 <- comparisons %>% select(land1, land2, cmps_score, cmps_nseg)
cp1 <- cp1 %>%
  mutate(
    land1idx = land1 %>% str_sub(-1, -1) %>% as.numeric(),
    land2idx = land2 %>% str_sub(-1, -1) %>% as.numeric()
  )

phases <- with(cp1, {
  get_all_phases(land1idx, land2idx, cmps_score, addNA = TRUE)
})

compute_diff_phase(phases)
Usage

compute_score_metrics(
  land1,
  land2,
  score,
  addNA = TRUE,
  na.rm = TRUE,
  include = NULL,
  out_names = NULL
)

Arguments

land1 (numeric) vector with land ids of bullet 1
land2 (numeric) vector with land ids of bullet 2
score numeric vector of scores to be summarized into a single number
addNA logical value. In case of missing lands, are scores set to 0 (addNA = FALSE) or set to NA (addNA = TRUE)
na.rm a logical value indicating whether NA values should be stripped before the computation proceeds
include a character vector specifying which metrics to be included in the result; if include = NULL, including all metrics
out_names a character vector specifying the variable names of each metric; if out_names = NULL, using the default names

Details

By default, this helper function computes four metrics.
diff: the difference between the mean score of the foreground phase and the mean score of the background phases
diff.med: the difference between the median score of the foreground phase and the median score of the background phases
max: the max score
maxbar: the mean score of the foreground phase

Value

a data frame containing values of the metrics

Examples

library(tidyverse)

data("bullets")

lands <- unique(bullets$bulletland)

comparisons <- data.frame(expand.grid(land1 = lands[1:6], land2 = lands[7:12]),
                          stringsAsFactors = FALSE)
compute_ss_ratio

```r
comparisons <- comparisons %>%
  left_join(bullets %>% select(bulletland, sig1=sigs),
            by = c("land1" = "bulletland")) %>%
  left_join(bullets %>% select(bulletland, sig2=sigs),
            by = c("land2" = "bulletland"))

comparisons <- comparisons %>%
  mutate(cmps = purrr::map2(sig1, sig2, .f = function(x, y) {
    extract_feature_cmps(x$sig, y$sig, include = "full_result")
  })),

comparisons <- comparisons %>%
  mutate(cmps_score = sapply(comparisons$cmps, function(x) x$CMPS_score),
         cmps_nseg = sapply(comparisons$cmps, function(x) x$nseg))

cp1 <- comparisons %>% select(land1, land2, cmps_score, cmps_nseg)
cp1 <- cp1 %>%
  mutate(land1idx = land1 %>% str_sub(-1, -1) %>% as.numeric(),
          land2idx = land2 %>% str_sub(-1, -1) %>% as.numeric())

with(cp1, {
  compute_score_metrics(land1idx, land2idx, cmps_score)
})
```

---

**compute_ss_ratio** # 'Compute the Sum of Squares Ratio

**Description**

#' Compute the Sum of Squares Ratio

**Usage**

`compute_ss_ratio(score, label, MS = FALSE)`

**Arguments**

- `score` a numeric vector, scores
- `label` a character vector, the label of each score
- `MS` boolean, whether to compute the mean squares instead of the sum of squares. Default is FALSE

**Value**

the sum of squares ratio
extract_feature_cmps

**Examples**

```r
c(score <- c(rnorm(100), rnorm(100, mean = 5)))
l(label <- c(rep("a", 100), rep("b", 100)))
c(compute_ss_ratio(score, label))
```

**Description**

Compute the Congruent Matching Profile Segments (CMPS) score based on two bullet profiles/signatures. The reference profile will be divided into consecutive, non-overlapping, basis segments of the same length. Then the number of segments that are congruent matching will be found as the CMPS score. By default, `extract_feature_cmps` implements the algorithm with multi-peak inspection at three different segment scale levels. By setting `npeaks_set` as a single-length vector, users can switch to the algorithm with multi-peak inspection at the basis scale level only.

**Usage**

```r
eextract_feature_cmps(
  x,
  y,
  seg_length = 50,
  Tx = 25,
  npeaks_set = c(5, 3, 1),
  include = NULL,
  outlength = NULL
)
```

**Arguments**

- **x**
  - a numeric vector, vector of the reference bullet signature/profile that will be divided into basis segments
- **y**
  - a numeric vector, vector of the comparison bullet signature/profile
- **seg_length**
  - a positive integer, the length of a basis segment
- **Tx**
  - a positive integer, the tolerance zone is +/- Tx
- **npeaks_set**
  - a numeric vector, specify the number of peaks to be found at each segment scale level
    - If `length(npeaks_set) == 1`, the algorithm uses multi-peak inspection only at the basis scale level;
    - If `length(npeaks_set) > 1`, the algorithm uses multi-peak inspection at different segment scale levels.
    - By default, `npeaks_set = c(5, 3, 1)`. Including more segment scale levels will reduce the number of false positive results
extract_feature_cmps

include

NULL or a vector of character strings indicating what additional information should be included in the output of `extract_feature_cmps`. All possible options are: "nseg", "congruent_pos", "congruent_seg", "congruent_seg_idx", "pos_df", "ccp_list", "segments", and "parameters". If one wants to include them all, one can use `include = "full_result"`. By default, `include = NULL` and only the CMPS score is returned.

outlength

NULL or a numeric vector, specify the segment length of each level of the basis segment when the multi-segment lengths strategy is being used. If `outlength = NULL`, then the length of a basis segment will be doubled at each segment level.

Value

a numeric value or a list

- if `include = NULL`, returns the CMPS score (a numeric value) only
- if `include = ` one or a vector of strings listed above:
  - `nseg`: number of basis segments
  - `congruent_seg`: a vector of boolean values. TRUE means this basis segment is a congruent matching profile segment (CMPS)
  - `congruent_seg_idx`: the indices of all CMPS
  - `pos_df`: a dataframe that includes positions of correlation peaks and the CMPS score of these positions
  - `ccp_list`: a list of consistent correlation peaks of each basis segment.
  - `segments`: a list of all basis segments
  - `parameters`: a list that stores all parameters used in the function call

References


Examples

```r
library(tidyverse)
library(cmpsR)

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][[1]]
land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][[1]]

# compute cmps

cmps_with_multi_scale <- extract_feature_cmps(land2_3$sig, land1_2$sig, include = "full_result")
cmps_without_multi_scale <- extract_feature_cmps(land2_3$sig, land1_2$sig, npeaks_set = 5, include = "full_result")
```
# Another example
library(tidyverse)
data("bullets")
lands <- unique(bullets$bulletland)
comparisons <- data.frame(expand.grid(land1 = lands[1:6], land2 = lands[7:12]),
                          stringsAsFactors = FALSE)
comparisons <- comparisons %>%
  left_join(bullets %>% select(bulletland, sig1=sigs),
            by = c("land1" = "bulletland")) %>%
  left_join(bullets %>% select(bulletland, sig2=sigs),
            by = c("land2" = "bulletland"))
comparisons <- comparisons %>%
  mutate(cmps = purrr::map2(sig1, sig2, .f = function(x, y) {
    extract_feature_cmps(x$sig, y$sig, include = "full_result")
  } ))
comparisons <- comparisons %>%
  mutate(
    cmps_score = sapply(comparisons$cmps, function(x) x$CMPS_score),
    cmps_nseg = sapply(comparisons$cmps, function(x) x$nseg)
  )
cp1 <- comparisons %>% select(land1, land2, cmps_score, cmps_nseg)

get_all_phases

Obtain a list of all phases of a bullet-by-bullet comparison

description
Obtain a list of all phases of a bullet-by-bullet comparison

usage
get_all_phases(land1, land2, score, addNA = FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>land1</td>
<td>(numeric) vector with land ids of bullet 1</td>
</tr>
<tr>
<td>land2</td>
<td>(numeric) vector with land ids of bullet 2</td>
</tr>
<tr>
<td>score</td>
<td>numeric vector of scores to be summarized into a single number</td>
</tr>
<tr>
<td>addNA</td>
<td>logical value. In case of missing lands, are scores set to 0 (addNA = FALSE) or set to NA (addNA = TRUE)</td>
</tr>
</tbody>
</table>
Value

a list of all phases

Examples

```r
call_value <- library(tidyverse)
data("bullets")
lands <- unique(bullets$bulletland)
comparisons <- data.frame(expand.grid(land1 = lands[1:6], land2 = lands[7:12]),
    stringsAsFactors = FALSE)
comparisons <- comparisons %>%
    left_join(bullets %>% select(bulletland, sig1=sigs),
        by = c("land1" = "bulletland")) %>%
    left_join(bullets %>% select(bulletland, sig2=sigs),
        by = c("land2" = "bulletland"))
comparisons <- comparisons %>% mutate(
    cmps = purrr::map2(sig1, sig2, .f = function(x, y) {
        extract_feature_cmps(x$sig, y$sig, include = "full_result")
    })
)
comparisons <- comparisons %>%
    mutate(
        cmps_score = sapply(comparisons$cmps, function(x) x$CMPS_score),
        cmps_nseg = sapply(comparisons$cmps, function(x) x$nseg)
    )

cp1 <- comparisons %>% select(land1, land2, cmps_score, cmps_nseg)
cp1 <- cp1 %>% mutate(
    land1idx = land1 %>% str_sub(-1, -1) %>% as.numeric(),
    land2idx = land2 %>% str_sub(-1, -1) %>% as.numeric()
)

with(cp1, {
    get_all_phases(land1idx, land2idx, cmps_score, addNA = TRUE)
})
```

---

**get_ccf4**  
*Function to calculate the cross-correlation between two sequences*

**Description**

This function is used for CMPS algorithm.
Usage

get_ccf4(x, y, min.overlap = round(0.1 * max(length(x), length(y))))

Arguments

x numeric sequence of values
y numeric sequence of values
min.overlap integer, minimal number of values in the overlap between sequences x and y to calculate a correlation value. Set to 10 percent of the maximum length of either sequence (HH: this might be problematic for CMPS)

Value

list consisting of the lag where the maximum correlation is achieved, and the maximum correlation value.

Examples

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][[1]]
land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][[1]]
x <- land2_3$sig
y <- land1_2$sig

segments <- get_segs(x, len = 50)

ccr <- get_ccf4(y, segments$segs[[7]],
                min.overlap = length(segments$segs[[7]])

get_ccp

Identify at most one consistent correlation peak (ccp)

Description

If multi segment lengths strategy is being used, at most one consistent correlation peak (ccp) will be found for the corresponding basis segment. If the ccp cannot be identified, return NULL

Usage

get_ccp(ccr_list, Tx = 25)

Arguments

crr_list list, obtained by get_ccr_peaks
Tx integer, the tolerance zone is +/- Tx
get_crr_peaks

Value

integer, the position of the ccp if it is identified; NULL otherwise.

Examples

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][]
land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][]

x <- land2_3$sig
y <- land1_2$sig

segments <- get_segs(x, len = 50)

# identify the consistent correlation peak when ccf curves are computed
# based on y and segment 7 in 3 different scales;
# the number of peaks identified in each scale are 5, 3, and 1, respectively.
seg_scale_max <- 3
npeaks_set <- c(5, 3, 1)
outlength <- c(50, 100, 200)

ccr_list <- lapply(1:seg_scale_max, function(seg_scale) {
  get_crr_peaks(y, segments, seg_outlength = outlength[seg_scale], nseg = 7,
  npeaks = npeaks_set[seg_scale])
})

getc(crr_list, Tx = 25)

---

get_crr_peaks

Identify peaks of a cross correlation curve

Description

Given a comparison profile and a segment, get_crr_peaks computes the cross correlation curve
and finds peaks of the curve.

Usage

getc(r_peaks(comp, segments, seg_outlength, nseg = 1, npeaks = 5)

Arguments

comp
  a numeric vector, vector of the bullet comparison profile
segments
  list with basis segments and their corresponding indices in the original profile,
  obtained by get_segs()
seg_outlength
  length of the enlarged segment
nseg
  integer. nseg = 3: the third segment in segments
npeaks
  integer. the number of peaks to be identified.
get_CMPS

Value

a list consisting of:

- ccr: the cross correlation curve
- adj_pos: indices of the curve
- peaks_pos: position of the identified peaks
- peaks_heights: the cross correlation value (height of the curve) of the peaks

Examples

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][[1]]
land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][[1]]
x <- land2_3$sig
y <- land1_2$sig

segments <- get_segs(x, len = 50)

# compute ccf based on y and segment 7 with scale 1, then identify 5 highest peaks
ccrpeaks <- get_ccr_peaks(y, segments = segments, seg_outlength = 50,
                        nseg = 7, npeaks = 5)

get_CMPS

Compute the CMPS score

Description

Compute the CMPS score from a list of positions of (consistent) correlation peaks.

Usage

get_CMPS(input_ccp, Tx = 25)

Arguments

input_ccp a list of positions for (consistent) correlation peaks
Tx integer, the tolerance zone is +/- Tx

Value

a list of six components:

- CMPS_score: computed CMPS score
- nseg: the number of basis segments
- congruent_pos: the congruent position that results in the CMPS score
- congruent_seg: a boolean vector of the congruent matching profile segments
- congruent_seg_idx: the index of the congruent matching profile segments
- pos_df: a dataframe that includes all positions and their corresponding CMPS score
get_segs

Divide a bullet signature/profile into basis segments of desired length

Description

get_segs divides a bullet signature/profile (a numeric vector) into consecutive, non-overlapping, basis segments of the same desired length. If the profile starts or ends with a sequence of NA (missing values), the NAs will be trimmed. If the very last segment does not have the desired length, it will be dropped.

Usage

get_segs(x, len = 50)

Arguments

x
a numeric vector, vector of the bullet signature/profile

len
integer: the desired length of a basis segment

Value

list with basis segments and their corresponding indices in the profile

Examples

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][[1]]
land1_2 <- bullets$sigs[bullets$bulletland == "1-2"][[1]]
x <- land2_3$sig
y <- land1_2$sig
segments <- get_segs(x, len = 50)
nseg <- length(segments$segs)
seg_scale_max <- 3
npeaks_set <- c(5, 3, 1)
outlength <- c(50, 100, 200)

ccp_list <- lapply(1:nseg, function(nseg) {
  ccr_list <- lapply(1:seg_scale_max, function(seg_scale) {
    get_ccr_peaks(y, segments, seg_outlength = outlength[seg_scale],
                 nseg = nseg, npeaks = npeaks_set[seg_scale])
  })
  get_ccp(ccr_list, Tx = 25)
})
cmps <- get_CMPS(ccp_list, Tx = 25)
Examples

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][-1]

x <- land2_3$seg

segments <- get_segs(x, len = 50)

getSegscale <- get_segscale(segments, nseg = 5, out_length = 50)

get_segscale  
Change the scale of a segment

Description

In order to identify the congruent registration position of a basis segment, the length of the basis segment will be doubled to compute the correlation curve. get_segscale computes the increased segment, which has the same center as the basis segment.

Usage

get_segscale(segments, nseg, out_length)

Arguments

segments  list with basis segments and their corresponding indices in the original profile, obtained by get_segs()

nseg  integer. nseg = 3: increase the length of the third basis segment.

out_length  integer. The length of the enlarged segment

Value

list consisting of

• aug_seg: the increased segment

• aug_idx: the corresponding indices in the profile

Examples

data("bullets")
land2_3 <- bullets$sigs[bullets$bulletland == "2-3"][-1]

x <- land2_3$seg

segments <- get_segs(x, len = 50)

seg5_scale3 <- get_segscale(segments, nseg = 5, out_length = 50)
local_max_cmps  

**Description**
find local maximums

**Usage**
local_max_cmps(x, find_max = 0)

**Arguments**
- **x**  numeric vector, the input sequence
- **find_max**  a numeric scalor, the function finds maximums if `find_max = 0` finds minimums if otherwise.

---

metric_plot_helper  

**Description**
Helper Function for Plotting the Distribution of a Metric

**Usage**
metric_plot_helper(
    cmps_metric,    
    metric,    
    scaled = FALSE,    
    SSratio = TRUE,    
    plot_density = TRUE,    
    ...    
)

**Arguments**
- **cmps_metric**  a data frame containing values of the metric and the labels
- **metric**  string. Which metric to be plotted
- **scaled**  logical value. If `scaled = TRUE`, the values should be within the interval of `[0, 1]`
- **SSratio**  logical value. Whether to show the sum of squares ratio value
- **plot_density**  logical value. If `plot_density = TRUE`, the function plots group density on the y-axis; if `plot_density = FALSE`, it plots the count of a certain bin.
- **...**  other arguments for plotting: breaks, binwidth, and subtitle
Value

a ggplot object

Description

Wrapper function for `na_trim`

Usage

`na_trim_cmns(x)`

Arguments

`x` numeric vector
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