Package 'ultrapolaRplot'

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Type Package

Title Plotting Ultrasound Tongue Traces

Version 0.2.1

Depends R (>= 4.1.0)

Imports RColorBrewer, tibble, rjson, ggplot2, Cairo, purrr, plyr, tidyr, readr, stringr, ggsignif, ggpubr, car, rstatix, vegan

Description Plots traced ultrasound tongue imaging data according to a polar coordinate system. There is currently support for plotting means and standard deviations of each category's trace; Smoothing Splines Analysis of Variance (SSANOVA) could be implemented as well. The origin of the
polar coordinates may be defined manually or automatically determined based on different algorithms.
Points for each category can be split into two groups (anterior and posterior) at the point of maximum curvature of each trace. User can specify rays to intersect various parts of the tongue; intersections along these rays serve as input for a pairwise t-test to measure significant contrasts between segments.
Currently 'ultrapolaRplot' supports ultrasound tongue imaging trace data from 'UltraTrace' (<https://github.com/SwatPhonLab/UltraTrace>). 'UltraTrace' is capable of importing data from Articulate Instruments AAA.
'read_textgrid.R' is required for opening TextGrids to determine category and alignment information of ultrasound traces.

License GPL-3

Encoding UTF-8

NeedsCompilation no

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Repository CRAN

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Contents

`loadAllTracesMidPoint` *Processes metadata and TextGrids*

Description

Processes layers, tiers, and categories within TextGrids. Extracts x and y coordinate data from metadata.

Usage

```
loadAllTracesMidPoint(directory_name)
```

Arguments

`directory_name`	a (readable binary-mode) connection or a character string giving the name of the folder containing metadata and textgrid files to load (when tilde expansion is done).

Value

Returns dataframe of filename, annotation number in file, segment, x-coordinate, y-coordinate, list of tiers, layer, segment text.

`plotTraces` *Plots ultrasound polar coordinate data*

Description

Filters rawTraces by categories, tiers, and layers. Plots extracted segments with means and standard deviation bands calculated through use of polar coordinates. Compares significant constasts between segments along various parts of the tongue.

Usage

```
plotTraces(rawTraces, polarTraces = "", tiernameAll = c(NA),
                  categoriesAll = list(c(NA)), layersAll = c(NA),
                  seg_filter = list(c(NA)), mergeCategories = c(FALSE),
                  origin.algorithm = "BottomMiddle", origin.x = NA,
                  scaling.factor = 800/600,  interval = 1, mean.lines =
                  TRUE, points.display = FALSE, palette = c(),
                  bands.lines = FALSE, bands.fill = TRUE,
                  legend.position = "topleft", means.styles = c(),
                  standard.deviation.styles = "l", plot.ticks = FALSE,
                  plot.labels = FALSE, legend.size = 3, transparency =
                  0.37, pdf.filename = c(), bands.linewidth = 0.3,
                  png.filename = c(), legend.linewidth = 5,
                  means.linewidth = 3, tick.size = 2, maskCategories =
                  c(), rays = list(), bestFitRays = FALSE,
                  bestFitRays.show_elbows = FALSE,
                  bestFitRays.start_point_density = 1,
                  bestFitRays.intersection_rays.negative = c(),
                  bestFitRays.intersection_rays.positive = c(),
                  angle_neg_rotate = c(), angle_pos_rotate = c(),
                  ray_color = "darkgrey", elbow_color = "black", bubble = FALSE,
                  x_coor = 0, y_coor = 0, difference_plot = FALSE,
                  angle_between_best_fit = FALSE, debug_intersections = FALSE)
```

Arguments

rawTraces	data frame returned from loadAllTracesMidPoint()
polarTraces	returned from makeTracesPolar(), optional, outdated
tiernameAll	respective tiers (if applicable) within layers. If none specified, all tiers are checked.
categoriesAll	respective categories of segments to extract within tiers.
layersAll	list of layers within metadata to extract x and y coodinate data from. Defaults to 'tongue' layer.
mergeCategories	boolean or boolean array, as to whether to merge respective categories.
seg_filter	respective segment_text for additional filtering
origin.algorithm	takes list of all extracted x-coordinates and sets
origin.x	override x coordinate of origin
scaling.factor	default 800/600
x_coor	x_coor of transducer (default = 0)
y_coor	y_coor of transducer (default = 0)
angle_between_best_fit	boolean, whether or not to display violin plot of angles between the bestfit lines per category

`bands.fill` boolean, whether or not to show standard deviation bands

`bands.lines` boolean, whether or not to show lines on edges of standard deviation bands

`bands.linewidth`
line thickness of standard deviation bands

`bestFitRays` boolean, whether or not to display lines of best fit for tongue body and tongue root

`bestFitRays.start_point_density`
Number of intersecting traces per category needed to extend bestFitRays until (default = 1), 0 would be until farthest points, 2 would be until each segment has standard deviation

`bestFitRays.intersection_rays.negative`
List of percentages along bestfit ray on left side to intersect data

`bestFitRays.intersection_rays.positive`
List of percentages along bestfit ray on right side to intersect data

`angle_neg_rotate`
Corresponding angles to bestFitRays.intersection_rays.negative (default = 0) to rotate rays while still keeping the intersections with the bestfit line the same

`angle_pos_rotate`
Corresponding angles to bestFitRays.intersection_rays.positive (default = 0) to rotate rays while still keeping the intersections with the bestfit line the same

`rays` list of arrays to specify (x,y), and angle of intersecting ray

`bestFitRays.show_elbows`
boolean, whether or not to show PMC along means

`bubble` boolean, whether or not to display PMC cluster graph

`difference_plot`
boolean, whether or not to display difference_plot for the first two segments

`debug_intersections`
boolean, whether or not to print data frame of segments and their intersections with the perpedicular ray(s)

`elbow_color` color of PMC along means (default = "black")

`interval` sampling interval, in degrees, for finding intersections with existing traces (default = ‘1‘)

`mean.lines` boolean, whether or not to display mean lines

`means.styles` array to override default solid line (sequentially in order of categories)

`means.linewidth`
size of mean lines

`standard.deviation.styles`
line type for standard deviation upper and low bands, (default = "l")

`transparency` transparency of standard deviation bands (default = 0.37)

`palette` array to override default colour palette

`pdf.filename` pdf file name, saves in current directory

`png.filename` png file name, saves in current directory

`plot.labels` boolean, whether or not to show labels

plot.ticks	boolean, whether or not to show tick marks
tick.size	size of label scaling on axises
points.display	boolean, whether or not to show original annotated points
ray_color	color of bestFitRays.intersection_rays.negative and bestFitRays.intersection_rays.positive (default = "darkgrey")
labels	array to override labels
legend.position	default "center", with an option of "topleft", "bottomright"
legend.size	size of legend (default = 0.6)
legend.linewidth	size of displayed legend lines
maskCategories	array to override current segment labels

Value

Returns a dataframe of filename, annotation number in file, segment, x-coordinate, y-coordinate, segment text; Displays and pairwise comparisons. User can export output to pdf or png.

`ultrapolaRplot` *ultrapolaRplot*

Description

The ultrapolaRplot library for R is designed for plotting traced ultrasound tongue imaging data according to a polar coordinate system. There is currently support for plotting means and standard deviations of each category's trace; SSANOVA could be implemented as well. The origin of the polar coordinates may be defined manually or automatically determined based on different algorithms. Points for each category can be split into two groups (anterior and posterior) at the point of maximum curvature of each trace. User can specify rays to intersect various parts of the tongue; intersections along these rays serve as input for a pairwise t-test to measure significant contrasts between segments. Currently ultrapolaRplot supports ultrasound tongue imaging trace data from UltraTrace (<https://github.com/SwatPhonLab/UltraTrace>). UltraTrace is capable of importing data from Articulate Instruments AAA.

Examples

```
## Not run:
library(ultrapolaRplot)
filepath <- system.file("extdata", package = "ultrapolaRplot")
rawTraces <- loadAllTracesMidPoint(filepath)
filteredTraces <- plotTraces(rawTraces,
categoriesAll = c("o", "i"), bestFitRays = TRUE,
bestFitRays.intersection_rays.positive = c(0.5))

## End(Not run)
```

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