## PlotPolarGAMM\_demo

#### **Benson**

#### 3/18/2024

PlotPolarGAMM is a function that allows you to visualize and plot Plotly figures of GAMM-fitted ultrasound tongue contours with provided GAMM models.

```
plotPolarGAMM(
model,
targetName,
targetL,
rmax,
view='X',
showLegend=T,
showDiff=T,
fontSize=25,
returnData=F
)
```

#### **Arguments**

#### model

A GAMM model, resulting from the functions gam or bam.

#### target

The name of the categories of different types of sounds (e.g. *vowel* for tokens of /i/, /a/, and /u/, or *place* for alveolar and velar sounds.)

#### targetL

The categories of the target (e.g. use c('i', 'a', 'u') for the *vowel* example previously, or c('velar', 'alvolar') for the *place* example.)

#### rmax

The maximum radius of the plot.

#### view

The predictor, usually 'X'.

#### showLegend

Whether to show the legend.

#### showDiff

Whether to plot the different areas, indicated by gray color blocks.

#### **fontSize**

The font size.

#### returnData

Whether to return the fitted data as a dataframe. If False, it will return a Plotly plot.

# Import plot\_polar\_GAMM and the other two modules used to perform polar GAMM.

```
source('plot_polar_GAMM.R')
library(itsadug)

## Loading required package: mgcv

## Loading required package: nlme

## This is mgcv 1.8-38. For overview type 'help("mgcv-package")'.

## Loading required package: plotfunctions

## Loaded package itsadug 2.4 (see 'help("itsadug")' ).

library(rticulate)
```

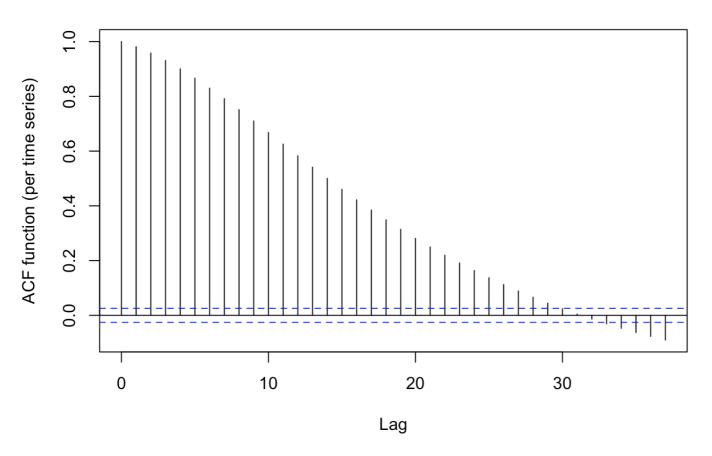
# Import the ultrasound contour data. In contours\_demo.csv, there are the tongue contour tracings of /i/, /u/, and /y/ at the mid time point.

```
df <- read.csv('contours_demo.csv')
df$vowel <- factor(df$vowel)
df$token <- factor(df$token)
df$X <- df$x
df$Y <- df$y
df <- start_event(df, event=c('token', 'vowel'), column="time_point")</pre>
```

### Construct teh GAMM model.

```
model <- polar_gam(
    Y~ vowel +
        s(X, by=vowel) +
        s(token, bs='re'),
    data=df,
    origin=c(562, 573)
)
model.Acf <- acf_resid(model)</pre>
```

#### ACF resid\_gam(model)



```
model <- polar_gam(
    Y ~ vowel +
        s(X, by=vowel) +
        s(token, bs='re'),
    data=df,
    origin=c(562, 573),
    rho=model.Acf[2],
    AR.start=df$start.event
)</pre>
```

## Put the model into the function, and you will get the plot.

```
plotPolarGAM(model=model,
             targetName='vowel',
             targetL=c('i', 'u', 'y'),
             rmax=max(df$Y)*1.05,
             view='X',
             showDiff=F,
             returnData=F)
## Loading required package: gss
## Loading required package: ggplot2
##
## Attaching package: 'ggplot2'
## The following object is masked from 'package:plotfunctions':
##
##
       alpha
## Loading required package: plotly
##
## Attaching package: 'plotly'
## The following object is masked from 'package:ggplot2':
##
##
       last_plot
## The following object is masked from 'package:plotfunctions':
##
##
       add_bars
## The following object is masked from 'package:stats':
##
##
       filter
## The following object is masked from 'package:graphics':
##
##
       layout
## Loading required package: sets
```

```
## Registered S3 method overwritten by 'sets':
## method from
## print.element ggplot2

##
## Attaching package: 'sets'
```

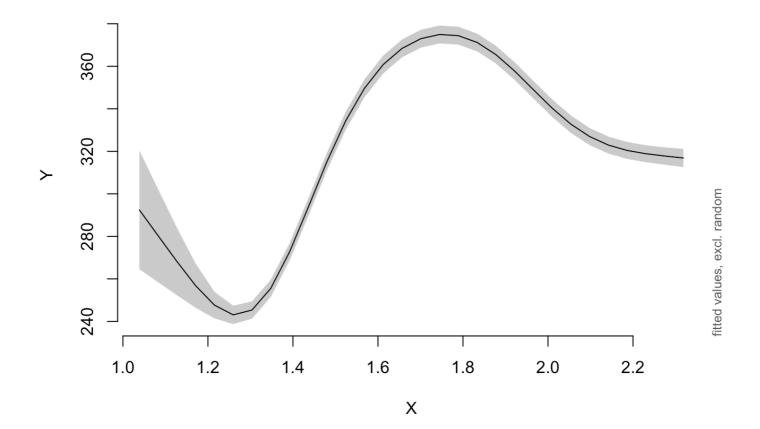
```
## Accaching package. secs

## The following object is masked from 'package:plotly':
##
## %>%
```

## Loading required package: RColorBrewer

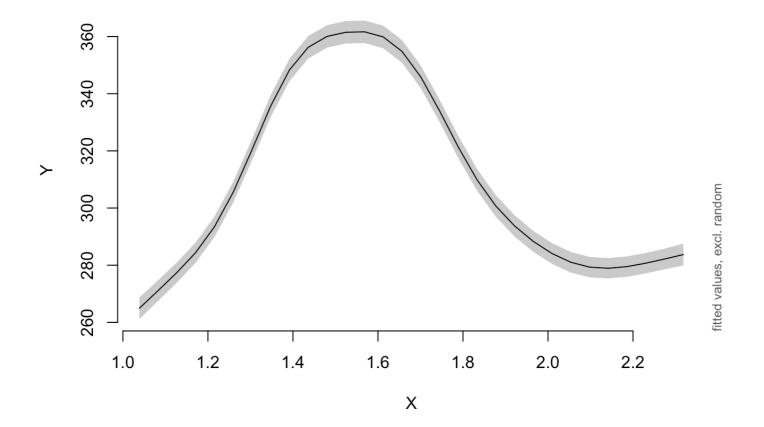
```
## Summary:
## * vowel : factor; set to the value(s): i.
## * X : numeric predictor; with 30 values ranging from 1.038784 to 2.318545.
## * token : factor; set to the value(s): 0. (Might be canceled as random effect, check below.)
## * NOTE : The following random effects columns are canceled: s(token)
##
```

```
## Warning in plotL[i] <- plot_smooth(model, view = view, cond =
## changeName(list(c(targetL[i])), : number of items to replace is not a multiple
## of replacement length</pre>
```



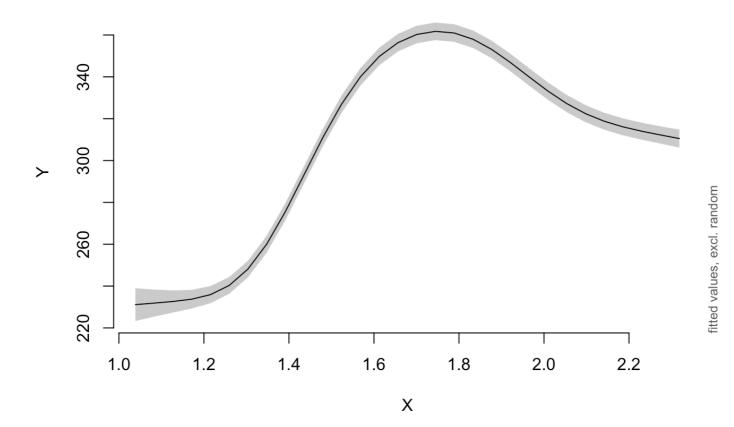
```
## Summary:
## * vowel : factor; set to the value(s): u.
## * X : numeric predictor; with 30 values ranging from 1.038784 to 2.318545.
## * token : factor; set to the value(s): 0. (Might be canceled as random effect, check below.)
## * NOTE : The following random effects columns are canceled: s(token)
##
```

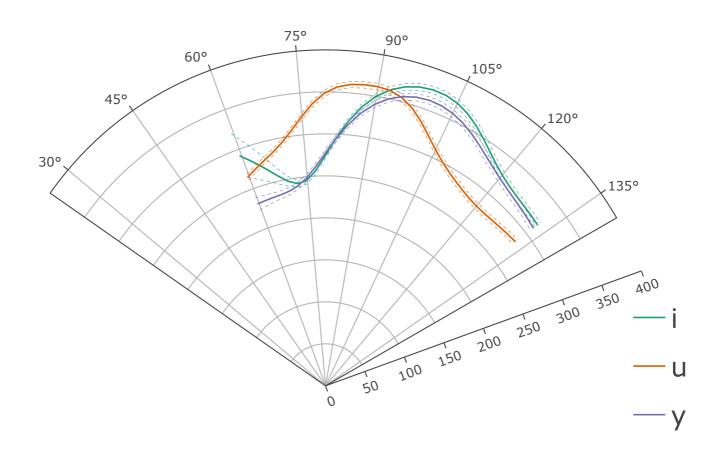
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## changeName(list(c(targetL[i])), : number of items to replace is not a multiple
## of replacement length</pre>
```



```
## Summary:
## * vowel : factor; set to the value(s): y.
## * X : numeric predictor; with 30 values ranging from 1.038784 to 2.318545.
## * token : factor; set to the value(s): 0. (Might be canceled as random effect, check below.)
## * NOTE : The following random effects columns are canceled: s(token)
##
```

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## changeName(list(c(targetL[i])), : number of items to replace is not a multiple
## of replacement length</pre>
```

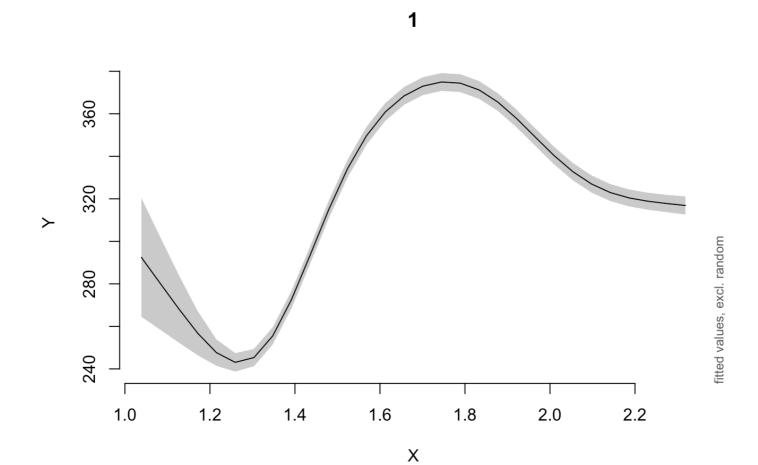




# You can also set returnData to True, and get the estimated contours.

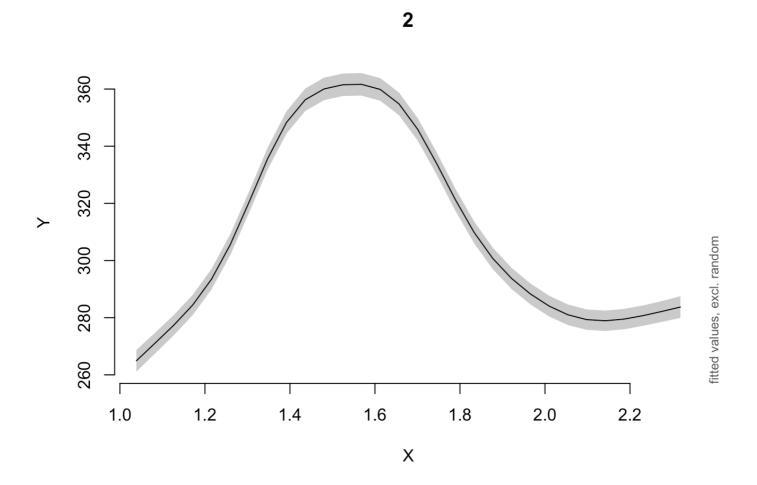
```
## Summary:
## * vowel : factor; set to the value(s): i.
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## * token : factor; set to the value(s): 0. (Might be canceled as random effect, check below.)
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##
```

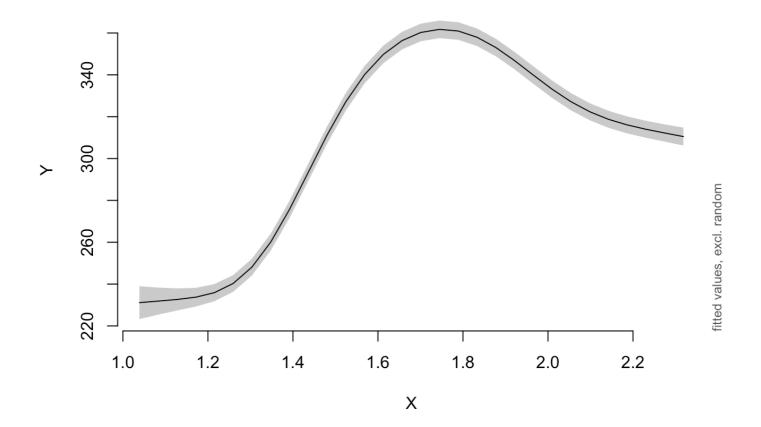
```
## Warning in plotL[i] <- plot_smooth(model, view = view, cond =
## changeName(list(c(targetL[i])), : number of items to replace is not a multiple
## of replacement length</pre>
```



```
## Summary:
## * vowel : factor; set to the value(s): y.
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## * token : factor; set to the value(s): 0. (Might be canceled as random effect, check below.)
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```
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## changeName(list(c(targetL[i])), : number of items to replace is not a multiple
## of replacement length</pre>
```





write.csv(df, 'results.csv')