Cognitive influences in language evolution: Dutch data

Introduction

This is the model code for Monaghan & Roberts, "Cognitive influences in language evolution: Psycholinguistic predictors of loan word borrowing". It takes data from the WOLD database of borrowing for Dutch and tries to predict whether a word has been borrowed or not according to various psycholinguitic measures.

Load libraries

```
library(mgcv)
library(sjPlot)
library(lattice)
library(ggplot2)
library(gplots)
library(dplyr)
library(party)
library(lmtest)
library(gridExtra)
library(itsadug)
library(car)
library(caret)
library(scales)
library(binom)


logit2per = function(X){
  return(exp(X)/(1+exp(X)))
}

rescaleGam = function(px, n, xvar, xlab="",breaks=NULL,xlim=NULL){
  y = logit2per(px[[n]]$fit)
  x = px[[n]]$x *attr(xvar,"scaled:scale") + attr(xvar,"scaled:center")
  se.upper = logit2per(px[[n]]$fit+px[[n]]$se)
  se.lower = logit2per(px[[n]]$fit-px[[n]]$se)
  dx = data.frame(x=x,y=y,ci.upper=se.upper,ci.lower=se.lower)
  plen = ggplot(dx, aes(x=x,y=y))+
    geom_ribbon(aes(ymin=ci.lower,ymax=ci.upper), alpha=0.3)+
    geom_line(size=0.5,linetype=3) +
    xlab(xlab)+
    ylab("Probability of borrowing")
  if(!is.null(breaks)){
    plen = plen + scale_x_continuous(breaks = breaks)
  }
  if(!is.null(xlim)){
   plen = plen + coord_cartesian(ylim = c(0,1),xlim=xlim)
  } else{
    plen = plen + coord_cartesian(ylim = c(0,1))
  }
```

```
  return(plen)
}

source("GAM_derivaties.R")
```

Load data

The Dutch data is processed very similarly to the English data. The full process can be found in the `processing` folder, but here we just load the final prepared data frame:

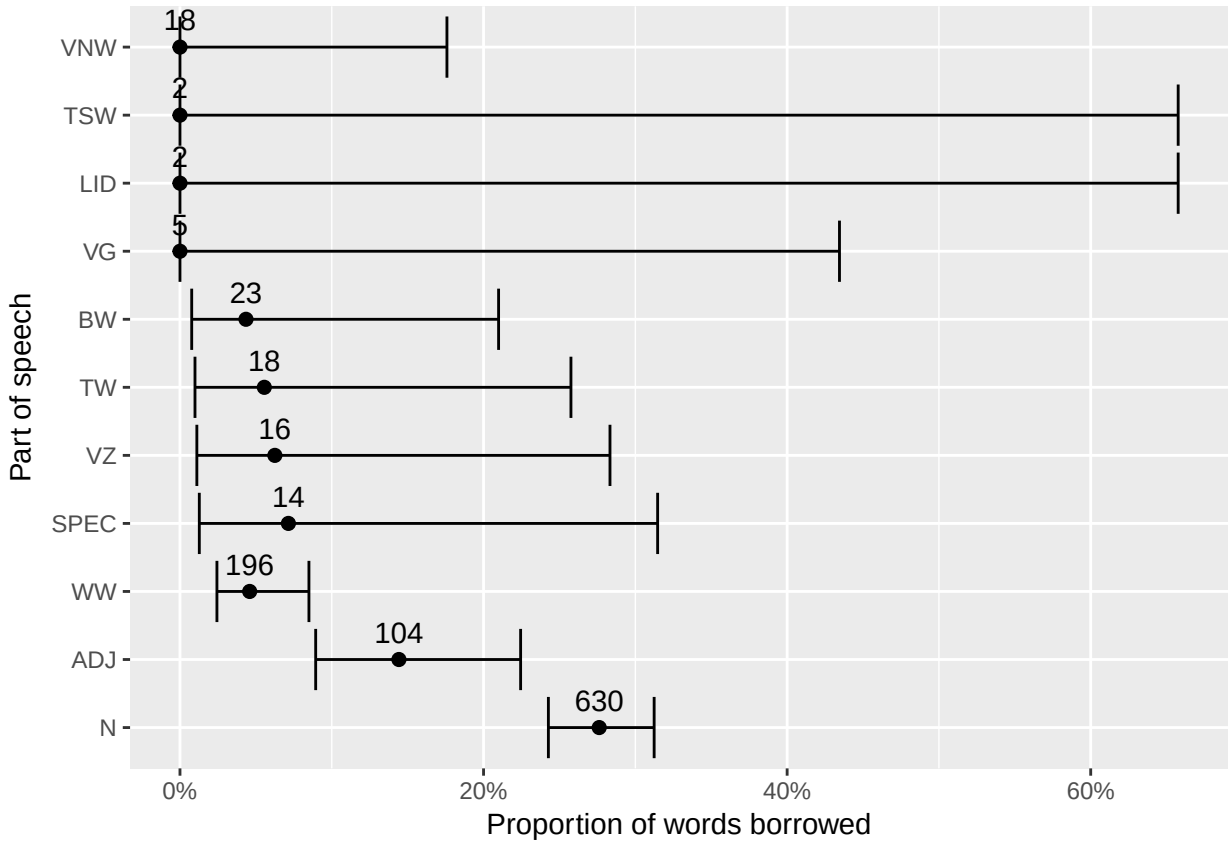
```
load("../data/loanwords_Dutch.Rdat")
```

Part of speech

We calculate the means, but the number of observations is very different for each category. We estimate confidence intervals around the mean with Wilson's binomial confidence interval method.

```
catx = data.frame(
  PoS = tapply(dutch$cat, dutch$cat, function(X){as.character(X[1])}),
  mean = tapply(dutch$bor15, dutch$cat, mean),
  n = tapply(dutch$bor15, dutch$cat, length),
  confint = binom.confint(
    tapply(dutch$bor15, dutch$cat, sum),
    tapply(dutch$bor15, dutch$cat, length),
    methods="wilson"
  )
)
catx = catx[order(catx$confint.lower, decreasing = T),]
catx$PoS = factor(catx$PoS, levels = catx[order(catx$confint.lower, decreasing = T),]$PoS)

posg = ggplot(catx, aes(x=mean, y=PoS)) +
  geom_point(size=2) +
  ylab("Part of speech") +
  xlab("Proportion of words borrowed")+
  scale_x_continuous(labels=percent_format()) +
  geom_text(aes(label=n), nudge_y=0.4) +
  geom_errorbarh(aes(xmin=confint.lower, xmax=confint.upper))
posg
```




```
pdf("../results/graphs/POS_Borrowing_Dutch.pdf",
    width = 6,
    height = 4)
posg
dev.off()
```

```
## pdf
##   2
```

```
catx$mean= catx$mean*100
catx$confint.lower= catx$confint.lower*100
catx$confint.upper= catx$confint.upper*100
write.csv(catx[,c("PoS","mean",
                  'n','confint.lower','confint.upper')],
    "../results/Dutch_POS_BorrowingProportions.csv",
    row.names = F)
```

GAM model

Dutch data has 1028 datapoints.

The range of the length variable limits the number of knots that the gam model can fit. We use k=4, suggested by the rule of thumb in Winter & Wieling (2016) being less than half of the number of unique values.

```
m0.dutch = bam(bor15.cat ~
      s(phonlengthscale, k=4) +
      s(AoAscale) +
```

```
      s(subtlexzipfscale) +
      s(concscale) +
      s(cat,bs='re')+
      s(cat,phonlengthscale,bs='re')+
      s(cat,AoAscale,bs='re')+
      s(cat,subtlexzipfscale,bs='re')+
      s(cat,concscale,bs='re'),
    data = dutch,
    family='binomial')
```

```
summary(m0.dutch)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## bor15.cat ~ s(phonlengthscale, k = 4) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re")
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.3492     0.3773  -6.226 4.78e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                               edf Ref.df Chi.sq  p-value
## s(phonlengthscale)      2.644e+00  2.904 16.919 0.000425 ***
## s(AoAscale)             1.386e+00  1.683 11.311 0.006505 **
## s(subtlexzipfscale)     3.667e+00  4.606 12.048 0.021505 *
## s(concscale)            1.653e+00  2.046  3.036 0.232210
## s(cat)                  3.715e+00 10.000 38.590 2.86e-08 ***
## s(cat,phonlengthscale)  6.887e-05 10.000  0.000 0.364693
## s(cat,AoAscale)         7.494e-06 10.000  0.000 0.966115
## s(cat,subtlexzipfscale) 1.346e-05 10.000  0.000 0.668251
## s(cat,concscale)        1.233e+00 10.000  3.255 0.094333 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.115   Deviance explained = 13.7%
## fREML = 1431.8  Scale est. = 1         n = 1028
```

Interactions

Test whether an interaction between AoA and frequency is warranted:

```
m1.dutch = bam(bor15.cat ~
      s(phonlengthscale, k=3) +
      s(AoAscale) +
      s(subtlexzipfscale) +
      s(concscale) +
      s(cat,bs='re')+
      s(cat,phonlengthscale,bs='re')+
      s(cat,AoAscale,bs='re')+
      s(cat,subtlexzipfscale,bs='re')+
      s(cat,concscale,bs='re') +
      te(AoAscale,subtlexzipfscale),
    data = dutch,
    family='binomial')

lrtest(m0.dutch,m1.dutch)
```

```
## Likelihood ratio test
##
## Model 1: bor15.cat ~ s(phonlengthscale, k = 4) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re")
## Model 2: bor15.cat ~ s(phonlengthscale, k = 3) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re") + te(AoAscale,
##     subtlexzipfscale)
##      #Df  LogLik     Df  Chisq Pr(>Chisq)
## 1 19.272 -439.79
## 2 20.348 -439.66 1.0755 0.2535     0.6146
```

No significant improvement.

Test whether an interaction between AoA and length is warranted:

```
m2.dutch = bam(bor15.cat ~
      s(phonlengthscale, k=3) +
      s(AoAscale) +
      s(subtlexzipfscale) +
      s(concscale) +
      s(cat,bs='re')+
      s(cat,phonlengthscale,bs='re')+
      s(cat,AoAscale,bs='re')+
      s(cat,subtlexzipfscale,bs='re')+
      s(cat,concscale,bs='re') +
      te(AoAscale,phonlengthscale),
    data = dutch,
    family='binomial')

lrtest(m0.dutch,m2.dutch)
```

```
## Likelihood ratio test
```

```
##
## Model 1: bor15.cat ~ s(phonlengthscale, k = 4) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re")
## Model 2: bor15.cat ~ s(phonlengthscale, k = 3) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re") + te(AoAscale,
##     phonlengthscale)
##      #Df  LogLik     Df  Chisq Pr(>Chisq)
## 1 19.272 -439.79
## 2 21.220 -439.07 1.9473 1.4249     0.4904
```

There is no improvement in log likelihood.

Test whether an interaction between Frequency and length is warranted:

```
m3.dutch = bam(bor15.cat ~
      s(phonlengthscale, k=3) +
      s(AoAscale) +
      s(subtlexzipfscale) +
      s(concscale) +
      s(cat,bs='re')+
      s(cat,phonlengthscale,bs='re')+
      s(cat,AoAscale,bs='re')+
      s(cat,subtlexzipfscale,bs='re')+
      s(cat,concscale,bs='re') +
      te(subtlexzipfscale,phonlengthscale),
    data = dutch,
    family='binomial')

lrtest(m0.dutch,m3.dutch)
```

```
## Likelihood ratio test
##
## Model 1: bor15.cat ~ s(phonlengthscale, k = 4) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re")
## Model 2: bor15.cat ~ s(phonlengthscale, k = 3) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re") + te(subtlexzipfscale,
##     phonlengthscale)
##      #Df  LogLik     Df  Chisq Pr(>Chisq)
## 1 19.272 -439.79
## 2 22.040 -437.60 2.7677 4.3719      0.224
```

No significant improvement.

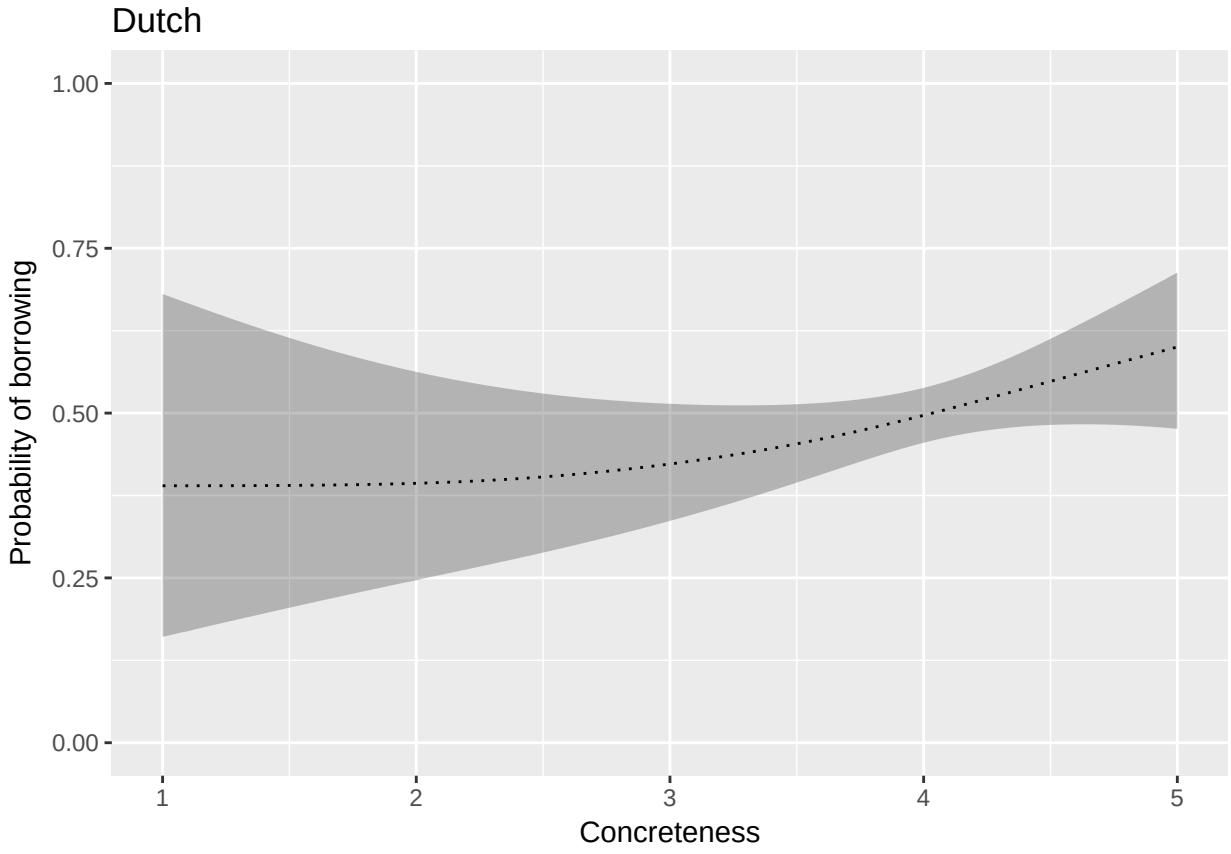
So no interactions are necessary.

Model estiamtes

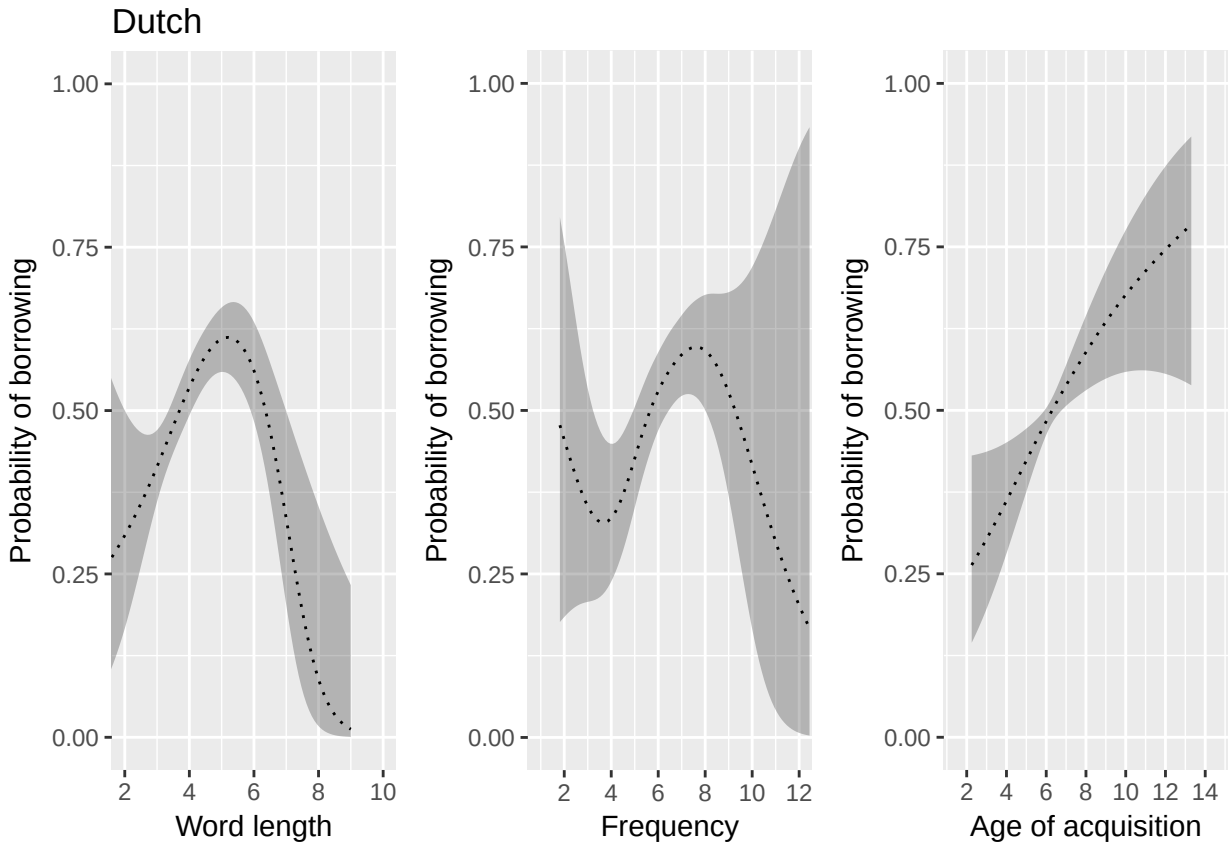
Plot the model estimates, changing the dependent scale to probability and the independent variables to their original scales (code is hidden, but available in the Rmd file).

```
plen = rescaleGam(px, 1, dutch$phonlengthscale,"Word length",
                  xlim = c(2,10), breaks = c(2,4,6,8,10)) + ggtitle("Dutch")
paoa = rescaleGam(px, 2, dutch$AoAscale,"Age of acquisition",
                  xlim=c(1.5,14.5),breaks=c(2,4,6,8,10,12,14)) + ggtitle("")
pfreq = rescaleGam(px, 3, dutch$AoAscale,"Frequency",
                   xlim = c(1,12), breaks=c(2,4,6,8,10,12)) + ggtitle("")
pconc = rescaleGam(px, 4, dutch$concscale,"Concreteness") + ggtitle("Dutch")

pconc
```



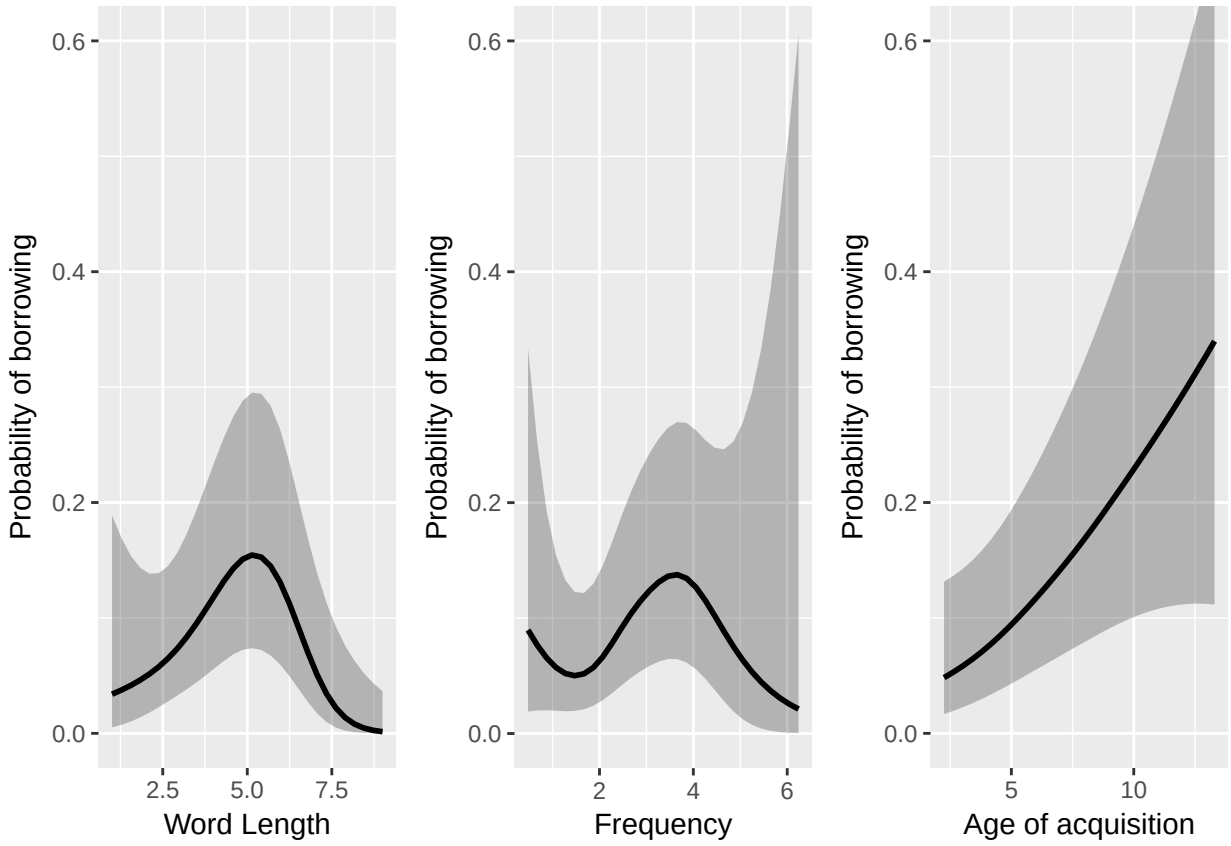

```
grid.arrange(plen,pfreq,paoa, nrow=1)
```




```
pdf(file='../results/graphs/Dutch_ModelResults.pdf',
    height =3,width = 8)
grid.arrange(plen,pfreq,paoa, nrow=1)
dev.off()
```

```
## pdf
##   2
```

Plot the model estimates, removing the influence of the random effects using the library `itsadug` (code is hidden, but available in the Rmd file).




```
## pdf
##   2
```

Random effects for Part of speech

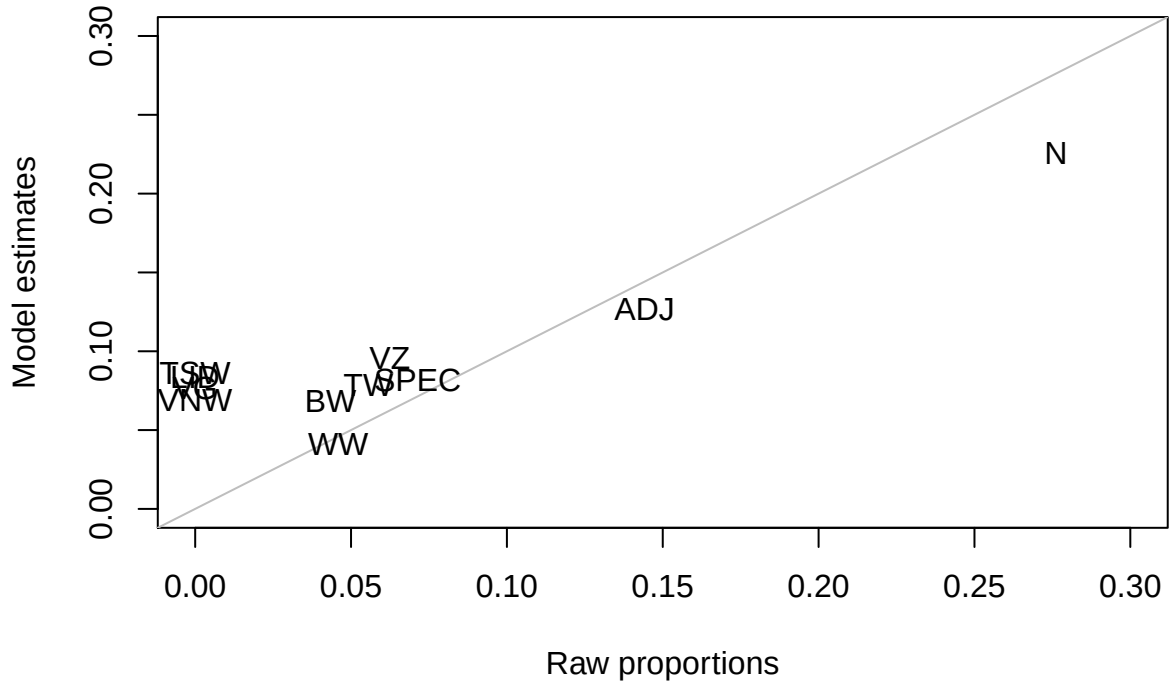
```
mc = m0.dutch$coefficients
mc[grepl("s\\(cat\\)",names(mc))]
```

```
##     s(cat).1     s(cat).2     s(cat).3     s(cat).4     s(cat).5
##  1.118766823  0.418169254 -0.258757264 -0.038467724 -0.069267143
##     s(cat).6     s(cat).7     s(cat).8     s(cat).9    s(cat).10
## -0.007058009 -0.107870765 -0.132337453 -0.242556253  0.104322001
##    s(cat).11
## -0.784943467
```

```
raw = tapply(dutch$bor15,dutch$cat,mean)
model.est = logit2per(m0.dutch$coefficients[1] +
              mc[grepl("s\\(cat\\)",names(mc))])

plot(raw, model.est,
  xlab="Raw proportions",
  ylab="Model estimates",
  col="white",
     ylim=c(0,0.3),
     xlim=c(0,0.3))
abline(0,1,col='gray')
```

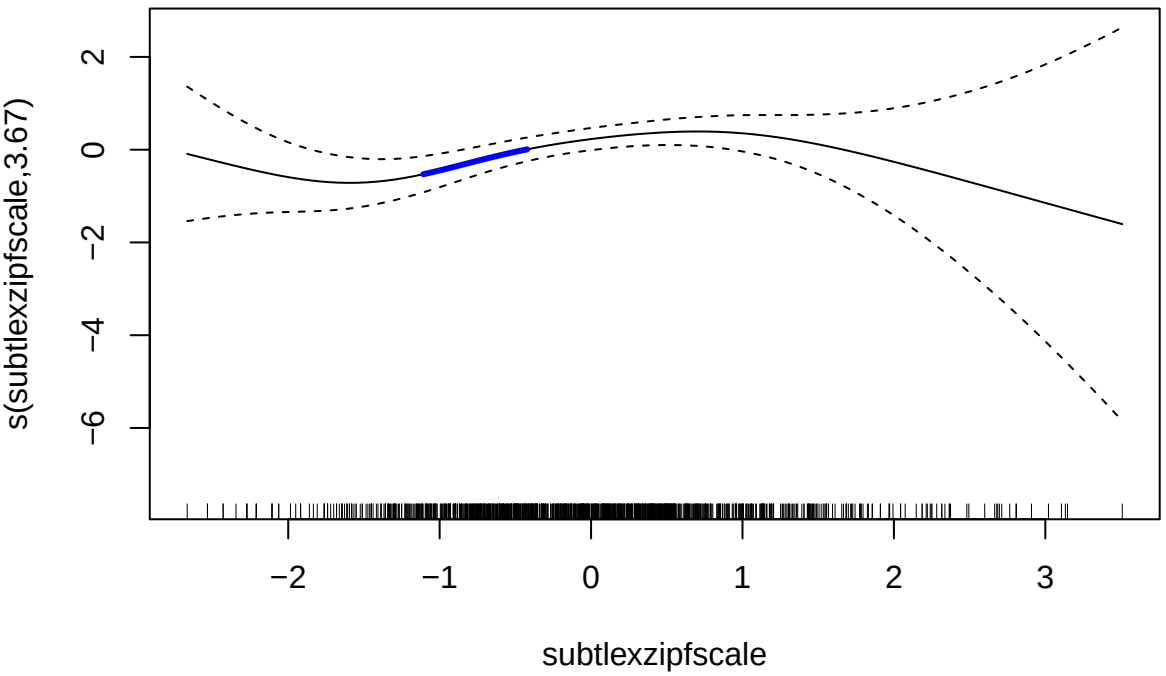
```
text(raw, model.est, names(raw))
```



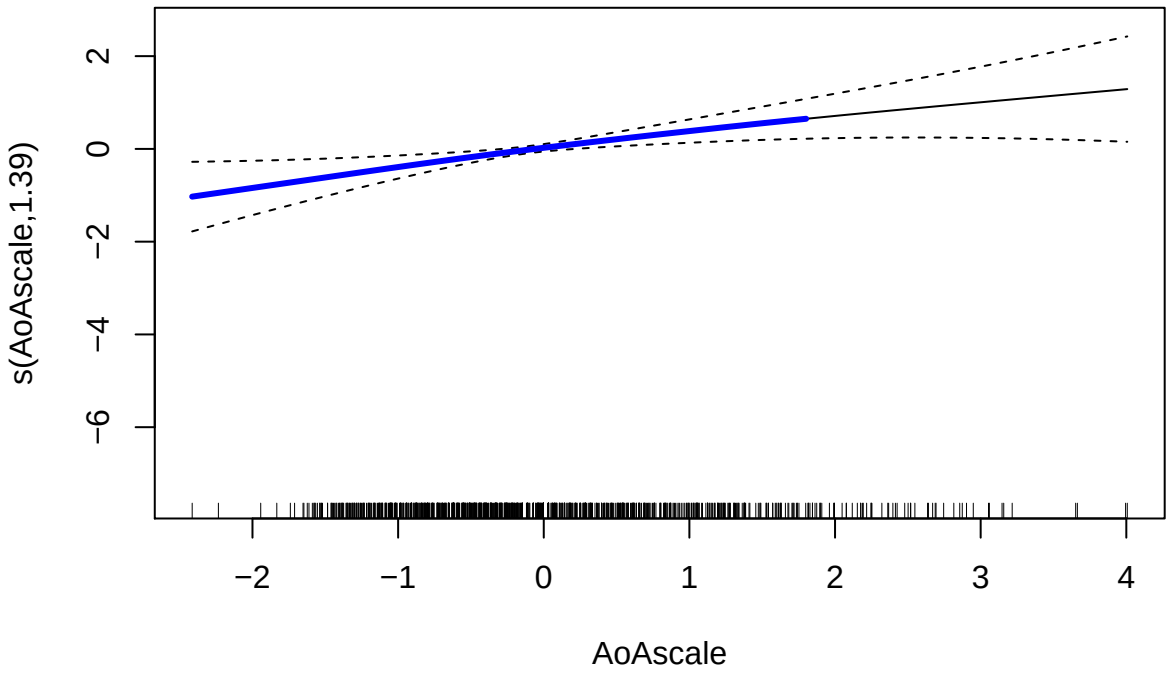
Derivatives test

The plots below highlight which sections of the GAM splines are significantly increasing or decreasing.

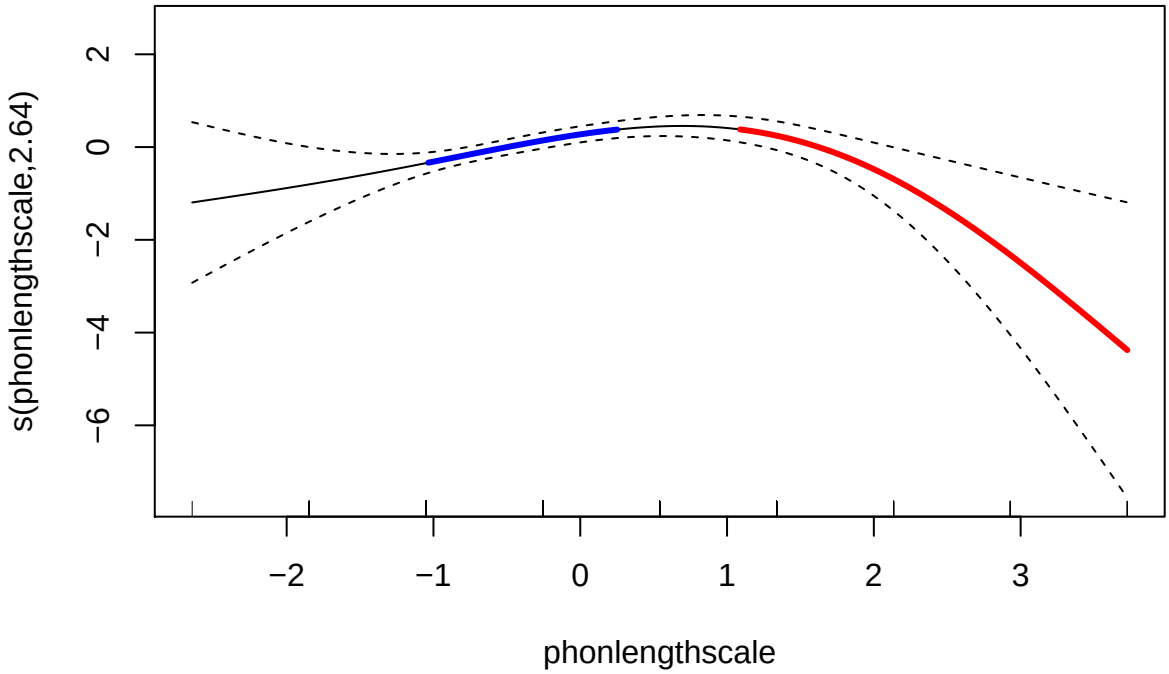
```
pSigFreq = plotGAMSignificantSlopes(m0.dutch,"subtlexzipfscale","Frequency")
```



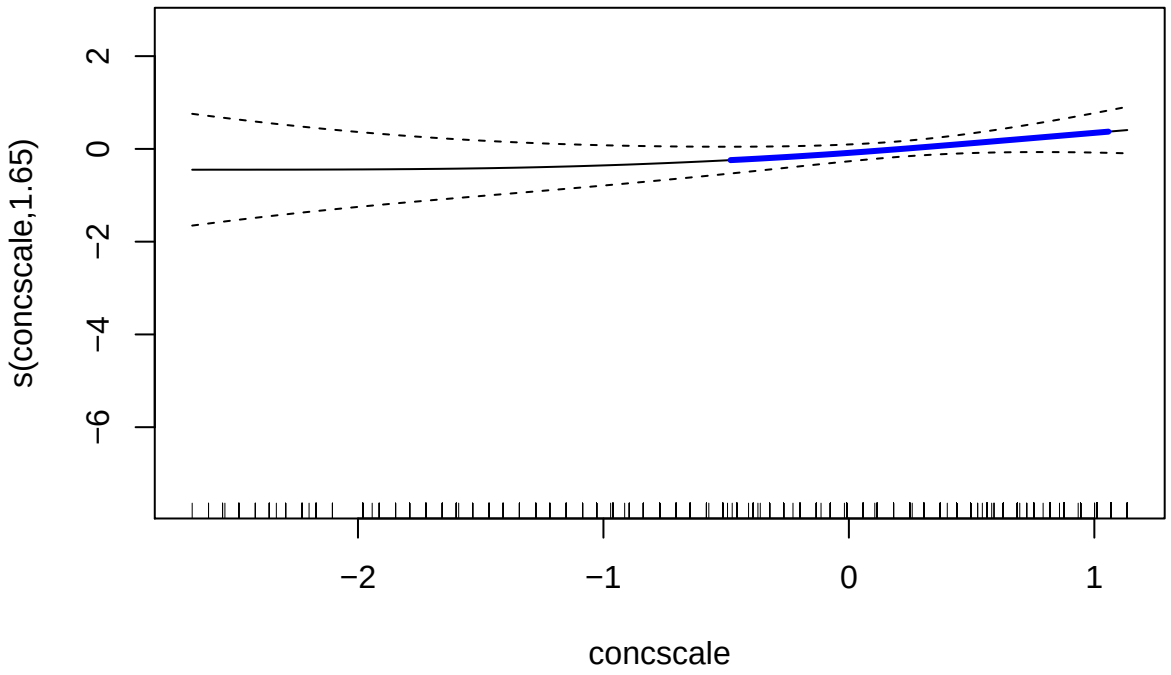

```
pSigAoA = plotGAMSignificantSlopes(m0.dutch,"AoAscale","AoA")
```

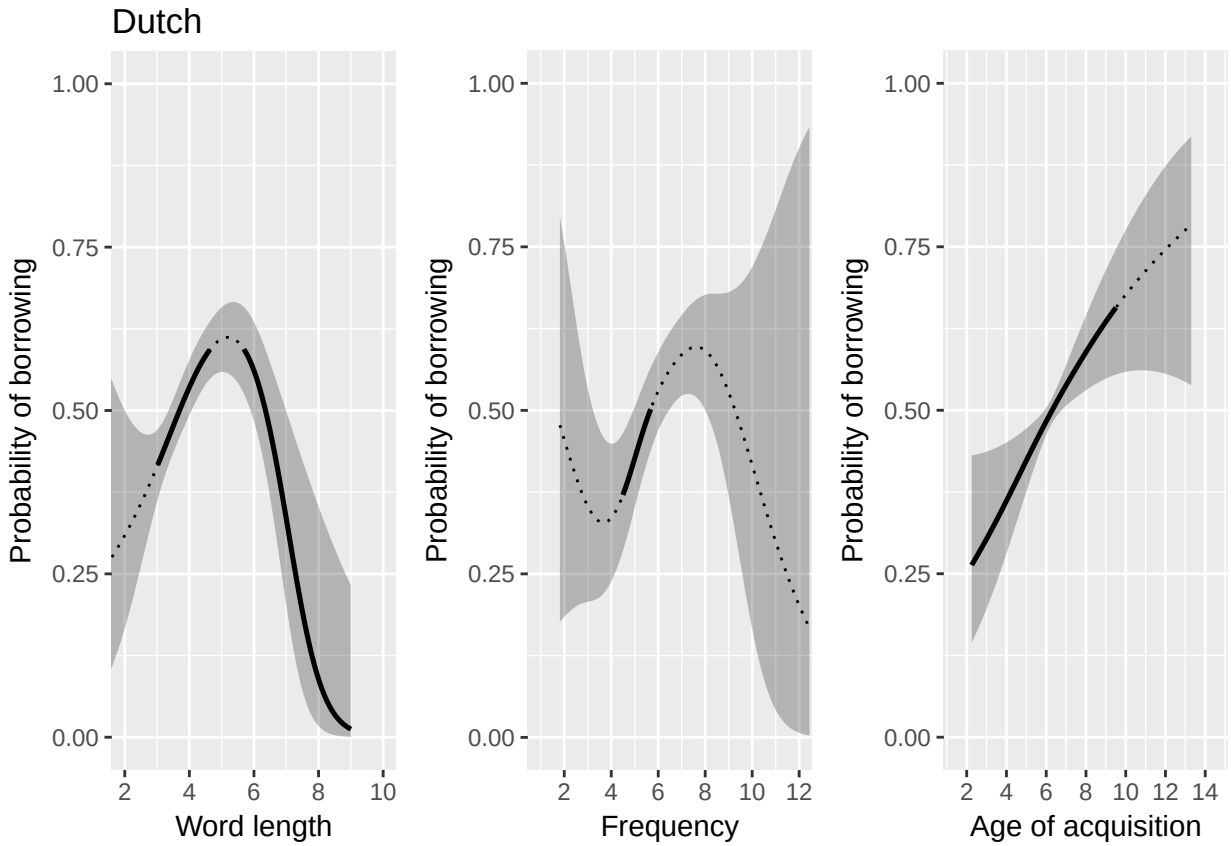



```
pSigLen = plotGAMSignificantSlopes(m0.dutch,"phonlengthscale","length")
```




```
pSigConc = plotGAMSignificantSlopes(m0.dutch,"concscale","Concreteness")
```


s(concscale,1.65)
2
0
−2
−4
−6
−2
−1
0
1
concscale


Dutch
Probability of borrowing
1.00
0.75
0.50
0.25
0.00
2
4
6
8
10
Word length
Probability of borrowing
1.00
0.75
0.50
0.25
0.00
2
4
6
8
10
12
Frequency
Probability of borrowing
1.00
0.75
0.50
0.25
0.00
2
4
6
8
10
12
14
Age of acquisition

```
## pdf
##   2
```

Number of morphemes

The big difference between English and Dutch is the effect of word length. This could reflect the role of agglutination in Dutch, where longer words may be composed of multiple morphemes. We can allow the effect of length to vary by whether the word is monomorphemic or not.

```
dutch$morphology = "other"
dutch$morphology[grepl("monomorphemic",dutch$celex.morphology)] = "monomorphemic"
#dutch$morphology[grepl("complex",dutch$celex.morphology)] = "complex"
dutch$morphology = factor(dutch$morphology)
```

```
mMorph.dutch = bam(bor15.cat ~
      s(phonlengthscale, by=morphology, k=4) +
      s(AoAscale) +
      s(subtlexzipfscale) +
      s(concscale) +
      s(cat,bs='re')+
      s(cat,phonlengthscale,bs='re')+
      s(cat,AoAscale,bs='re')+
      s(cat,subtlexzipfscale,bs='re')+
      s(cat,concscale,bs='re'),
    data = dutch,
    family='binomial')
lrtest(m0.dutch,mMorph.dutch)
```

```
## Likelihood ratio test
##
## Model 1: bor15.cat ~ s(phonlengthscale, k = 4) + s(AoAscale) + s(subtlexzipfscale) +
##     s(concscale) + s(cat, bs = "re") + s(cat, phonlengthscale,
##     bs = "re") + s(cat, AoAscale, bs = "re") + s(cat, subtlexzipfscale,
##     bs = "re") + s(cat, concscale, bs = "re")
## Model 2: bor15.cat ~ s(phonlengthscale, by = morphology, k = 4) + s(AoAscale) +
##     s(subtlexzipfscale) + s(concscale) + s(cat, bs = "re") +
##     s(cat, phonlengthscale, bs = "re") + s(cat, AoAscale, bs = "re") +
##     s(cat, subtlexzipfscale, bs = "re") + s(cat, concscale, bs = "re")
##      #Df  LogLik     Df  Chisq Pr(>Chisq)
## 1 19.272 -439.79
## 2 20.382 -435.02 1.1094 9.5326   0.002019 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

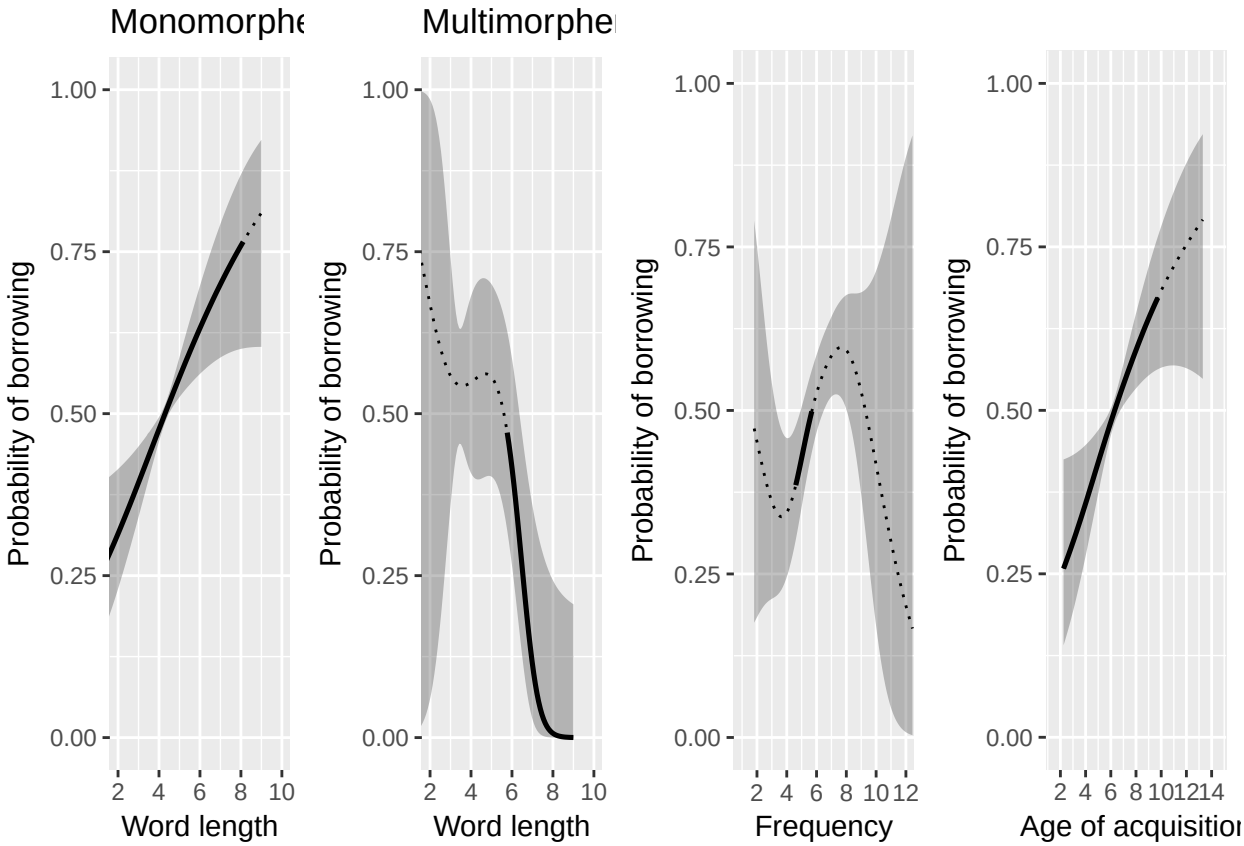
Adding an interaction with morphology signficantly imporves the fit of the model. The model stats are very similar to the model above:

```
summary(mMorph.dutch)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## bor15.cat ~ s(phonlengthscale, by = morphology, k = 4) + s(AoAscale) +
##     s(subtlexzipfscale) + s(concscale) + s(cat, bs = "re") +
##     s(cat, phonlengthscale, bs = "re") + s(cat, AoAscale, bs = "re") +
##     s(cat, subtlexzipfscale, bs = "re") + s(cat, concscale, bs = "re")
##
```

```
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.2209     0.3819  -5.815 6.06e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                                                edf Ref.df Chi.sq
## s(phonlengthscale):morphologymonomorphemic 1.087e+00  1.167 14.815
## s(phonlengthscale):morphologyother         2.202e+00  2.516  9.202
## s(AoAscale)                                1.384e+00  1.679 11.954
## s(subtlexzipfscale)                        3.579e+00  4.504 11.253
## s(concscale)                               1.664e+00  2.063  2.368
## s(cat)                                     3.689e+00 10.000 39.371
## s(cat,phonlengthscale)                     1.246e-05 10.000  0.000
## s(cat,AoAscale)                            3.387e-06 10.000  0.000
## s(cat,subtlexzipfscale)                    7.712e-06 10.000  0.000
## s(cat,concscale)                           1.568e+00 10.000  5.177
##                                             p-value
## s(phonlengthscale):morphologymonomorphemic 0.000313 ***
## s(phonlengthscale):morphologyother         0.058796 .
## s(AoAscale)                                0.004962 **
## s(subtlexzipfscale)                        0.028609 *
## s(concscale)                               0.330308
## s(cat)                                      6.2e-08 ***
## s(cat,phonlengthscale)                     0.475597
## s(cat,AoAscale)                            1.000000
## s(cat,subtlexzipfscale)                    0.625217
## s(cat,concscale)                           0.054537 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.12   Deviance explained = 14.6%
## fREML = 1420.9  Scale est. = 1         n = 1028
```

Plot the results from the new model. Monomorphemic words have an almost linear positive relationship between word length and probability of borrowing, just like English.


Monomorphe
Multimorphe
Probability of borrowing
1.00
0.75
0.50
0.25
0.00
2 4 6 8 10
Word length
2 4 6 8 10
Word length
2 4 6 8 10 12
Frequency
2 4 6 8 10 12 14
Age of acquisitio

```
## pdf
##   2
```

```
## pdf
##   2
```