Supporting Materials for ‘The Integration of Norse-Derived Terms in English’

Contents

1 Introduction

The analysis covers the following sources:

- FCPC Peterborough, 1154 (12th C)
- Ormulum South Lincolnshire, ca. 1180 (12th C)
- Havelok, composed in Lincolnshire, but manuscript from West Norfolk 13th century (13th C)
- Genesis and Exodus, composed in East Midlands, manuscript from West Norfolk 13th/14th century (14th C)
- Cursor mundi, c. 1300 (14th C)
- Gawain-poet Cheshire / Staffordshire, ca. 1380 (14th C)
- St Erkenwald, written late fourteenth or the early fifteenth century, manuscript from 1477 (15th C)
- Mannyng South Lincolnshire, ca. 1450 (15th C)
- Wars of Alexander northern England, ca. 1450 (15th C)
- Texts from Lincolnshire, Norfolk and Nottinghamshire from the Corpus of Middle English (1399-1525), (15th C)
- Texts by Richard Rolle (before 1465), (15thC)

The data analysed here is the product of several processing steps. The file `data/SharedIntegrationOfCognatesData.xls` has the original transcribed data. This is cleaned and processed by the script `analysis/analyseTextDistances.py`, which draws some code from `analysis/CLTSFeatureBasedAlignment.py` which is mainly contributed by Johann Mattis List (see https://calc.hypotheses.org/1962 and https://gist.github.com/LinguList/7fac44813572f65259c872ef89fa64ad). The script calculates the distances between pairs of Norse and English forms according to three measures:

- Simple distance from Keller (2023).
- A feature-based distance.
- A historical distance that uses the likelihood of one segment historically replacing another.

Each row in the data represents a comparison between a Norse form and an English form within a given cognate set, including the three measures of distance and frequency of occurance in each source.

1.1 Variables

The variables in the data (and some that are calculated in the script below) are described as follows:

“Set”: the cognate set the pair of comparisons belong to.

“Class”: the word class the set can appear as (and some binary variables representing the same information).

“NorseLexeme”, “EngLexeme”, “NorseForm”, “EngForm”: The lexemes and full forms for Norse and English terms.

“NorseFormDiagnostic”, “EngFormDiagnostic”: the relevant parts of the form that are diagnostic of the etymology.

“Alignment”, “FeatureAlignment”, “HistoricalAlignment”: multiple sequence alignment of the forms according to the three measures.

“RawDistance”, “NormDistance”, “RawFeatureDistance”, “NormFeatureDistance”, “RawHistoricalDistance” , “NormHistoricalDistance”: Raw and normed distances between

“NFreq…”, “EFreq…”: Frequencies of the Norse and English forms in each source.

“Alliteration”: only true if the source uses alliterative verse and the Norse form and the English form do *not* start with segments in the same alliterative category. That is, it is true if part of the decision about which form to use might be influenced by the need to alliterate. The alliterative texts include: Gawain, St Erkenwold, Wars of Alexander.

“totalNFreq”: The total Norse frequency across all sources.

“totalEFreq”: The total English frequency across all sources.

“NorseProp”: The proportion of total Norse frequency compared to total Norse Frequency + total English Frequency.

“NorseDiagnosticScore”: Whether or not the forms differ according to a specific segments that are characteristicly diagnostic of Norse etymology.

2 Load Libraries

```
library(openxlsx)
library(sjPlot)
library(lme4)
library(mgcv)
library(party)
library(ggplot2)
library(phangorn)
library(gridExtra)
library(GGally)
library(MuMIn)
library(brms)
library(ggeffects)
```

3 Load data

Load data created by the python program and convert variables to their proper type:

```
d = read.xlsx("../data/IntegrationDistances.xlsx",1)
# Ignore numerals in set name
d$Set = gsub("[0-9]","",d$Set)
d$Set = as.factor(d$Set)
d$EngLexeme = factor(d$EngLexeme)
d$ELen = nchar(d$EngForm)
d$NLen = nchar(d$NorseForm)

norseFrequencyColumns = c("NFreqFCPC","NFreqGawainPoet",
                          "NFreqGenAndEx","NFreqHavelok",
                          "NFreqMannyng","NFreqOrmulum",
                          'NFreqWarsAlexander',
                          "NFreqStErkenwald", "NFreqCursorMundi",
                          "NFreqLinc","NFreqNott","NFreqNorf","NFreqRolle")

englishFrequencyColumns = c("EFreqFCPC","EFreqGawainPoet",
                            "EFreqGenAndEx","EFreqHavelok",
                            "EFreqMannyng","EFreqOrmulum",
                            "EFreqWarsAlexander",
                            "EFreqStErkenwald", "EFreqCursorMundi",
                            "EFreqLinc","EFreqNott","EFreqNorf","EFreqRolle")
```

Convert frequencies to numeric type:

```
for(col in c(norseFrequencyColumns,englishFrequencyColumns)){
  d[,col] = as.numeric(d[,col])
}
```

Calculate the total frequency across all sources and the proportion of Norse forms compared to all forms:

```
d$totalNFreq = rowSums(d[,norseFrequencyColumns],na.rm = T)
d$totalEFreq = rowSums(d[,englishFrequencyColumns],na.rm = T)
d$NorseProp = d$totalNFreq/ rowSums(d[,c("totalNFreq","totalEFreq")],na.rm = T)

d = d[!is.na(d$NorseProp),]
```

Scale the distances to lie between 0 and 1:

```
d$NormDistance = as.numeric(d$NormDistance)
d$NormFeatureDistance = as.numeric(d$NormFeatureDistance)
d$NormHistoricalDistance = as.numeric(d$NormHistoricalDistance)
```

```
# Scale distances
normX = function(X){
  (X-min(X))/(max(X)-min(X))
}
d$NormDistance = normX(d$NormDistance)
d$NormFeatureDistance = normX(d$NormFeatureDistance)
d$NormHistoricalDistance = normX(d$NormHistoricalDistance)

d$NormDistance.rank =
  rank(d$NormDistance,ties.method = "max")
d$NormFeatureDistance.rank =
  rank(d$NormFeatureDistance,ties.method = "max")
d$NormHistoricalDistance.rank =
  rank(d$NormHistoricalDistance,ties.method = "max")
```

3.1 Examples

4 Descriptive statistics

Number of English forms: 135

Number of Norse forms: 127

Number of comparisons: 1638

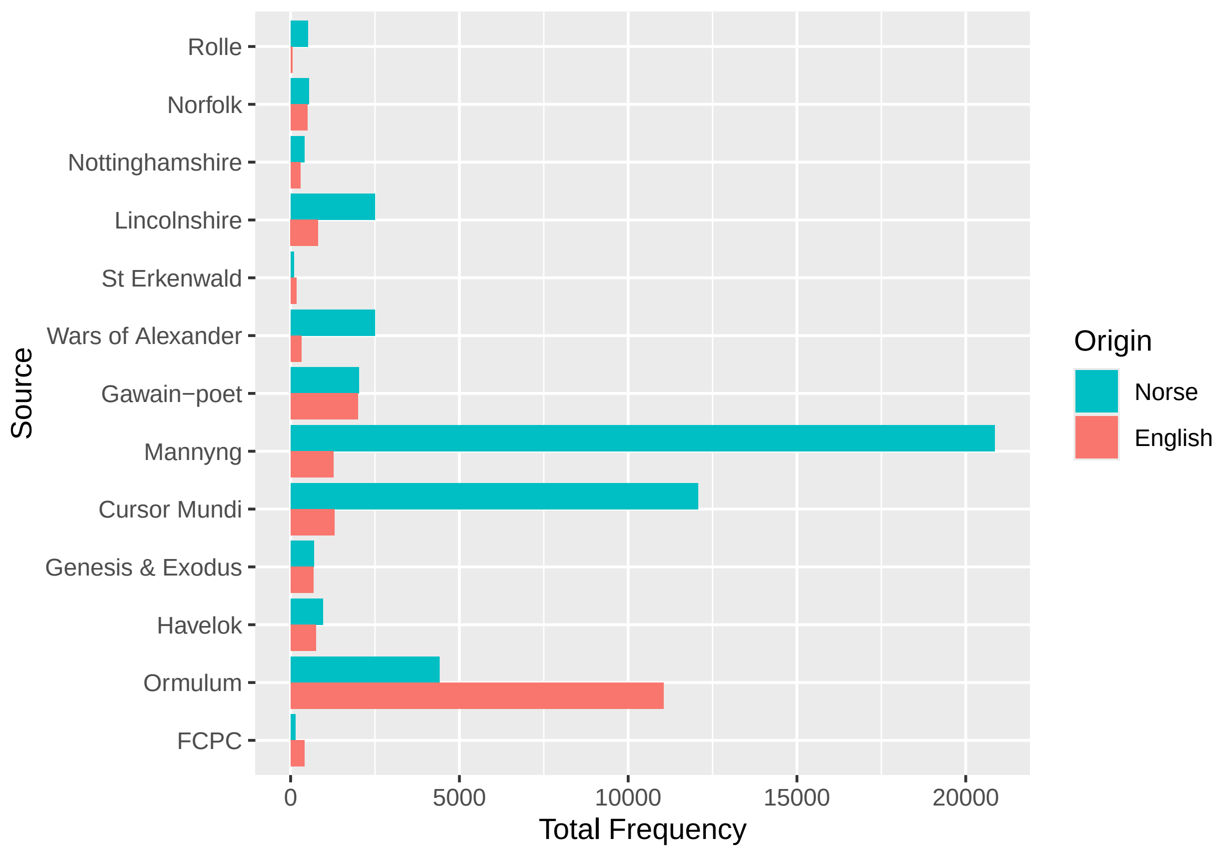
Number of sets: 67

Proportion of Norse and English terms (relative total frequency of each type):

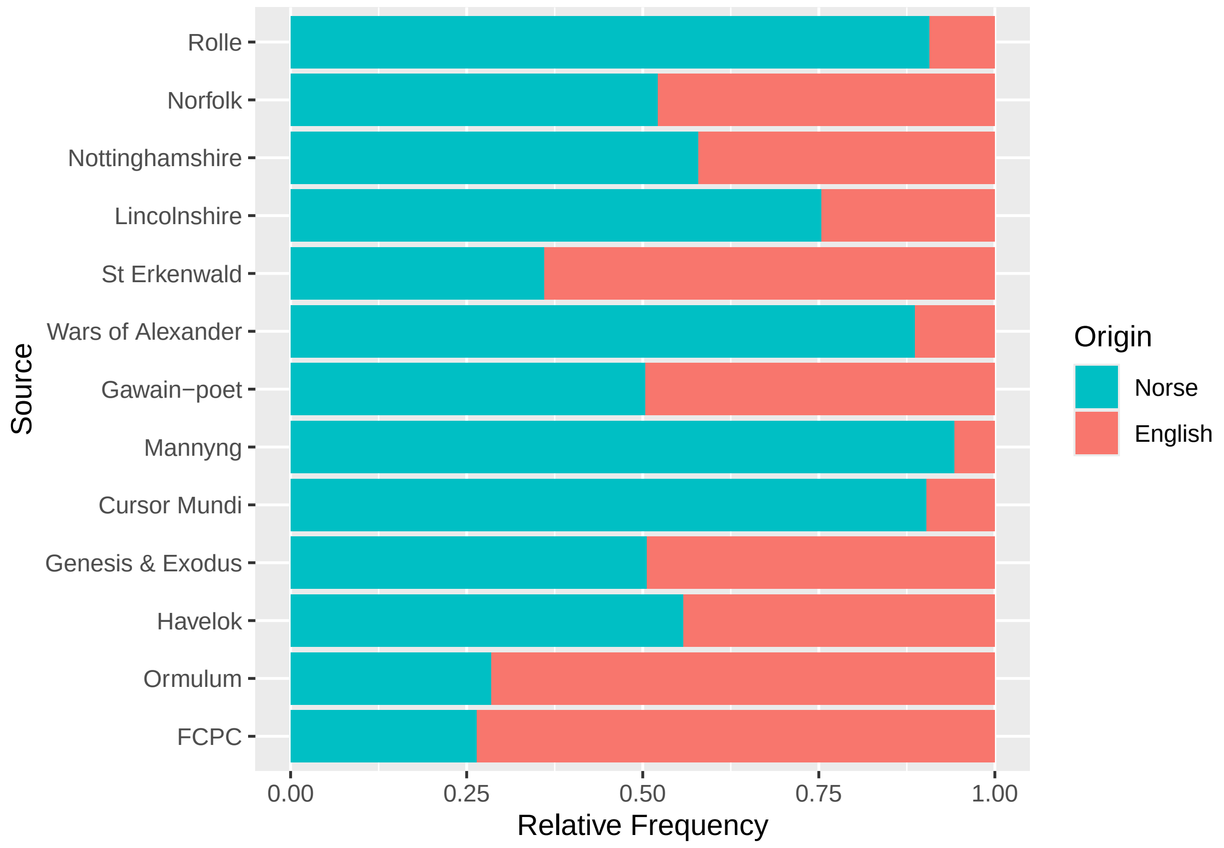
```
dx = rbind(
  data.frame(
    Lang = "Norse",
    Freq = colSums(d[,norseFrequencyColumns],na.rm = T),
    Source = c("FCPC","Gawain-poet","Genesis & Exodus","Havelok",
                "Mannyng", "Ormulum","Wars of Alexander",
                "St Erkenwald", "Cursor Mundi",
               "Lincolnshire","Nottinghamshire",
               "Norfolk", "Rolle")),
  data.frame(
    Lang = "English",
    Freq = colSums(d[,englishFrequencyColumns],na.rm = T),
    Source = c("FCPC","Gawain-poet","Genesis & Exodus","Havelok",
                "Mannyng", "Ormulum","Wars of Alexander",
                "St Erkenwald", "Cursor Mundi",
               "Lincolnshire","Nottinghamshire",
               "Norfolk", "Rolle")))

dx$Source = factor(dx$Source,
  levels=c("FCPC","Ormulum","Havelok",
                 "Genesis & Exodus",
                 "Cursor Mundi","Mannyng",
                 "Gawain-poet", "Wars of Alexander",
                 "St Erkenwald",
           "Lincolnshire","Nottinghamshire",
               "Norfolk", "Rolle"))

gRawFreq = ggplot(dx,aes(x=Source,y=Freq,fill=Lang)) +
  geom_bar(stat="identity",position = 'dodge') +
  ylab("Total Frequency") +
  scale_fill_discrete(breaks=c('Norse',"English"),
                      name = "Origin") +
  coord_flip()
gRawFreq
```



```
gPropFreq = ggplot(dx,aes(x=Source,y=Freq,fill=Lang)) +
  geom_bar(stat="identity",position = 'fill') +
  ylab("Relative Frequency") +
  scale_fill_discrete(breaks=c('Norse',"English"),
                      name = "Origin")+
  coord_flip()
gPropFreq
```



```
pdf("../results/GRawFreq.pdf",width=5,height=3.5)
gRawFreq
dev.off()
```

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

```
pdf("../results/GPropFreq.pdf",width=5,height=3.5)
gPropFreq
dev.off()
```

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

```
pdf("../results/GRawAndPropFreq.pdf",width=6,height=3)
  grid.arrange(gRawFreq+
                 theme(legend.position = "none"),
               gPropFreq +
                 theme(axis.text.y = element_blank(),
                       axis.title.y = element_blank()),
               ncol=2)
dev.off()
```

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

Correlations between distance measures:

```
cor.test(d$NormDistance,d$NormFeatureDistance)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d$NormDistance and d$NormFeatureDistance
## t = 94.868, df = 1636, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9120847 0.9270142
## sample estimates:
##      cor
## 0.919882
```

```
cor.test(d$NormDistance,d$NormHistoricalDistance)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d$NormDistance and d$NormHistoricalDistance
## t = 75.069, df = 1636, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8689625 0.8907967
## sample estimates:
##       cor
## 0.8803451
```

```
cor.test(d$NormFeatureDistance,d$NormHistoricalDistance)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d$NormFeatureDistance and d$NormHistoricalDistance
## t = 75.886, df = 1636, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8712788 0.8927493
## sample estimates:
##       cor
## 0.8824729
```

Function for extracting stats:

```
getStatReport = function(m0,m1,m2,m3,finalModel,outFile){
  modelComparison = as.data.frame(anova(m0,m1,m2,m3))
  modelComparison$pChi = round(modelComparison$`Pr(>Chisq)`,3)
  modelComparison$pChi[modelComparison$pChi==0] = "< 0.001"
  modelComparison$lldiff = NA
  modelComparison$lldiff[2:4] = diff(modelComparison$logLik)
  modelComparison = modelComparison[2:4,]
  modelComparison$Term = c("Linear","Quadratic","Cubic")

  coef = as.data.frame(summary(finalModel)$coefficients)
  rx = which(grepl("Norm",rownames(coef)))
  coef[rx,"Estimate"] = round(coef[rx,"Estimate"],3)
  coef[rx,"z value"] = round(coef[rx,"z value"],3)
  coef[,"Pr(>|z|)"] = round(coef[,"Pr(>|z|)"],3)
  coef[,"Pr(>|z|)"][coef[,"Pr(>|z|)"] ==0] = "< 0.001"

  modelComparison$Estimate = coef[rx,"Estimate"]
  modelComparison$z = coef[rx,"z value"]
  modelComparison$p = coef[rx,"Pr(>|z|)"]

  modelComparison = modelComparison[,
                                    c("Term","BIC","lldiff",
                                      "Chisq","Df","pChi",
                                      "Estimate","z","p")]
  mcx = paste(paste0(c("Linear: ","Quadratic: ","Cubic: "),
        "beta = ",coef[rx,"Estimate"],
        ", z = ", coef[rx,"z value"],
        ", Wald p = ", coef[rx,"Pr(>|z|)"],
        ", LLDiff = ",round(modelComparison$lldiff,1),
        ", df = ", modelComparison$Df,
        ", p = ",modelComparison$pChi),collapse="; ")
  mcx = gsub("= <","<",mcx)
  cat(mcx,file=outFile)

 # mx = rbind(c("","Model Comparison","","","","","Model Estimate","",""),
 #        names(modelComparison),
 #        modelComparison)

  modelComparison$BIC = round(modelComparison$BIC,1)
  modelComparison$lldiff = round(modelComparison$lldiff,1)
  modelComparison$Chisq = round(modelComparison$Chisq,1)
  modelComparison$Estimate = round(modelComparison$Estimate,2)

  write.csv(modelComparison,file=gsub("\\.txt",".csv",outFile))

  return(mcx)
}
```

5 Total frequency analysis

The analyses below predict the total frequency across all sources, using the orthographic form as the basis for observations.

5.1 Simple distance (total frequency)

We use nested model comparison to evaluate whether higher-order variables should be added (i.e. how non-linear the relationships is).

```
d$NormDistanceChosen = d$NormDistance
# Baseline model
m0 = glmer(cbind(totalNFreq,totalEFreq) ~
             1 + (1|Set) + (1|EngLexeme),
           data = d, family = "binomial")
# Add the distance measure
m1 = update(m0,~.+NormDistanceChosen)
# Add quadratic term
m2 = update(m1,~.+I(NormDistanceChosen^2))
# Add cubic term
m3 = update(m2,~.+I(NormDistanceChosen^3))
# Compare fit of models
anova(m0,m1,m2,m3)
```

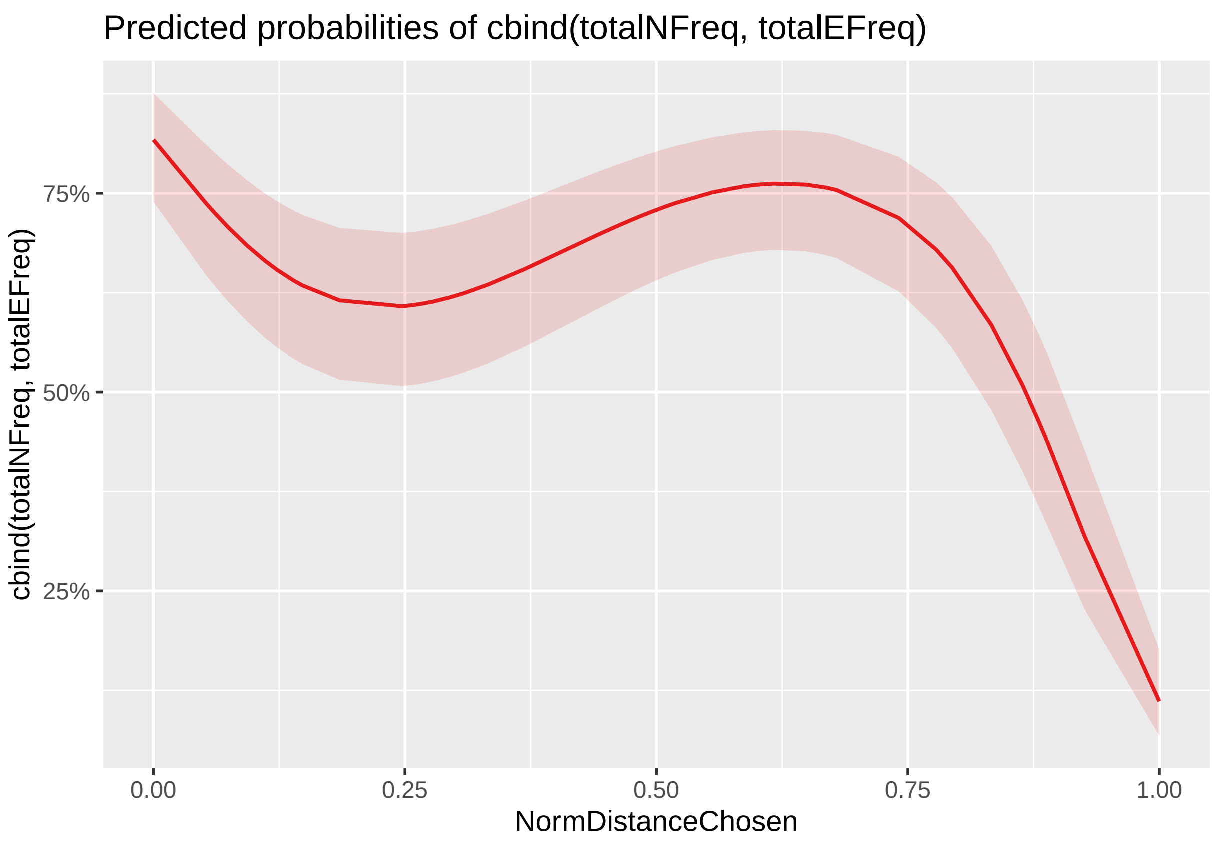
```
## Data: d
## Models:
## m0: cbind(totalNFreq, totalEFreq) ~ 1 + (1 | Set) + (1 | EngLexeme)
## m1: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen
## m2: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen + I(NormDist
## m3: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen + I(NormDist
##    npar   AIC   BIC logLik deviance    Chisq Df Pr(>Chisq)
## m0    3 32262 32278 -16128    32256
## m1    4 32264 32286 -16128    32256   0.0038  1     0.9511
## m2    5 32207 32234 -16098    32197  59.1556  1  1.457e-14 ***
## m3    6 31975 32007 -15981    31963 234.1472  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Summary of final model:

```
summary(m3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) +
##     NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDistanceChosen^3)
##    Data: d
##
##      AIC      BIC   logLik deviance df.resid
##  31974.6  32007.0 -15981.3  31962.6     1632
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -13.6620  -2.5875  -0.6251   0.7106  24.4508
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  EngLexeme (Intercept) 1.997    1.413
##  Set       (Intercept) 1.462    1.209
## Number of obs: 1638, groups:  EngLexeme, 135; Set, 67
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)                1.4975     0.2323   6.445 1.15e-10 ***
## NormDistanceChosen       -10.4393     0.9350 -11.165  < 2e-16 ***
## I(NormDistanceChosen^2)  30.8294     2.1940  14.052  < 2e-16 ***
## I(NormDistanceChosen^3) -23.9658     1.5108 -15.862  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) NrmDsC I(NDC^2
## NrmDstncChs -0.432
## I(NrmDsC^2)  0.384 -0.966
## I(NrmDsC^3) -0.342  0.904 -0.981
```

```
pSimpleTotal = plot_model(m3,'eff',
  terms="NormDistanceChosen[all]")
pSimpleTotal
```



Marginal represents the variance explained by the fixed effects. Conditional represents the variance explained by the entire model.

```
r.squaredGLMM(m3)
```

```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.

## Warning: the null model is correct only if all variables used by the original
## model remain unchanged.

##                    R2m       R2c
## theoretical 0.04430528 0.9783727
## delta       0.04404589 0.9726447
```

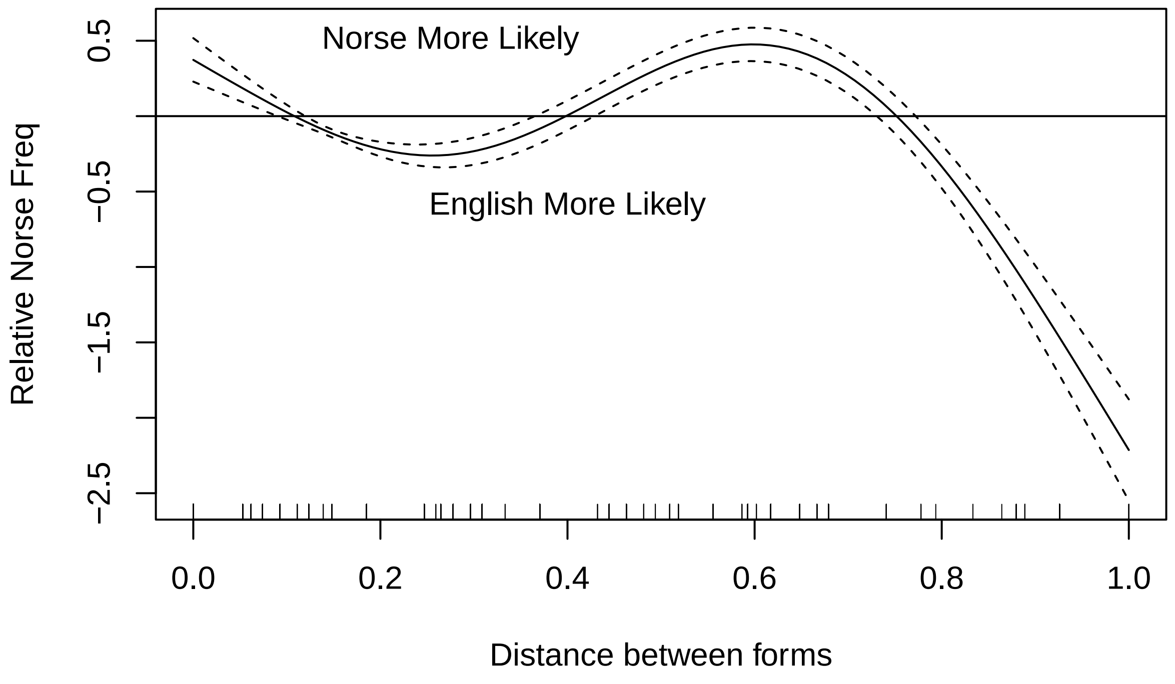
Statistics: (Linear: beta = -10.439, z = -11.165, Wald p < 0.001, LLDiff = 0, df = 1, p = 0.951; Quadratic: beta = 30.829, z = 14.052, Wald p < 0.001, LLDiff = 29.6, df = 1, p < 0.001; Cubic: beta = -23.966, z = -15.862, Wald p < 0.001, LLDiff = 117.1, df = 1, p < 0.001)

Same analysis using GAM with binomial distribution:

```
mGAM = gam(cbind(totalNFreq,totalEFreq) ~
             s(NormDistanceChosen,k=4) +
             s(Set,bs="re") +
             s(EngLexeme,bs="re"),
           data = d, family = "binomial")
summary(mGAM)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(totalNFreq, totalEFreq) ~ s(NormDistanceChosen, k = 4) +
##     s(Set, bs = "re") + s(EngLexeme, bs = "re")
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.6651     0.2292   2.902  0.00371 **
## ---
## 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(NormDistanceChosen)  2.998      3      250.5  <2e-16 ***
## s(Set)                44.361     66  1409276.0   0.361
## s(EngLexeme)          81.753    134   355114.5   0.545
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.438   Deviance explained = 45.9%
## UBRE = 16.108  Scale est. = 1         n = 1638
```

```
plot.gam(mGAM,
         ylab="Relative Norse Freq",
         xlab="Distance between forms",
         select = 1)
abline(h=0)
text(0.275,0.5,"Norse More Likely")
text(0.4,-0.6,"English More Likely")
```



The raw frequency of Norse forms is negatively correlated with distance:

```
mNorseFreq = glmer(totalNFreq ~ NormDistance +
                     (1|Set) + (1|NorseLexeme),
                   data = d, family = "poisson")
```

The distribution of Norse proportions is bimodal, with most terms having either low or high proportions. This isn't ideal for the binomial models above, so we also test the same model using a beta binomial distribution, which can fit bimodal binomial distributions. The result is very similar to the others:

```
d$totalAllFreq = d$totalNFreq + d$totalEFreq
mBinomBeta = brm(totalNFreq | trials(totalAllFreq) ~
               1 + NormDistanceChosen +
               I(NormDistanceChosen^2) +
               I(NormDistanceChosen^3) +
             (1|Set) + (1|EngLexeme),
           data = d, family = "beta_binomial")
```

```
## Compiling Stan program...

## Start sampling

##
## SAMPLING FOR MODEL '7404dd55f235b75d82269cea3d068515' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0.000564 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 5.64 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 1: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 1: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 1: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 1: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 1: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 1: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 1: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 1: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 70.7199 seconds (Warm-up)
## Chain 1:                64.0899 seconds (Sampling)
## Chain 1:                134.81 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL '7404dd55f235b75d82269cea3d068515' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 0.000462 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 4.62 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 2: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 2: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 2: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 2: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 2: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 2: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 2: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 2: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 2: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 2: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 2: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 2:
## Chain 2:  Elapsed Time: 73.5453 seconds (Warm-up)
## Chain 2:                68.7505 seconds (Sampling)
## Chain 2:                142.296 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL '7404dd55f235b75d82269cea3d068515' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 0.000463 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 4.63 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 3: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 3: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 3: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 3: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 3: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 3: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 3: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 3: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 3: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 3: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 3: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 3:
## Chain 3:  Elapsed Time: 66.5127 seconds (Warm-up)
## Chain 3:                62.0208 seconds (Sampling)
## Chain 3:                128.533 seconds (Total)
## Chain 3:
```

```
##
## SAMPLING FOR MODEL '7404dd55f235b75d82269cea3d068515' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 0.000457 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 4.57 seconds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
## Chain 4: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 4: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 4: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 4: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 4: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 4: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 4: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 4: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 4: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 4: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 4: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 4: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 4:
## Chain 4:  Elapsed Time: 73.2741 seconds (Warm-up)
## Chain 4:                57.0322 seconds (Sampling)
## Chain 4:                130.306 seconds (Total)
## Chain 4:
```

```
## Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior means and medians may
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#bulk-ess
```

```
## Warning: Tail Effective Samples Size (ESS) is too low, indicating posterior variances and tail qu
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#tail-ess
```

```
summary(mBinomBeta)
```

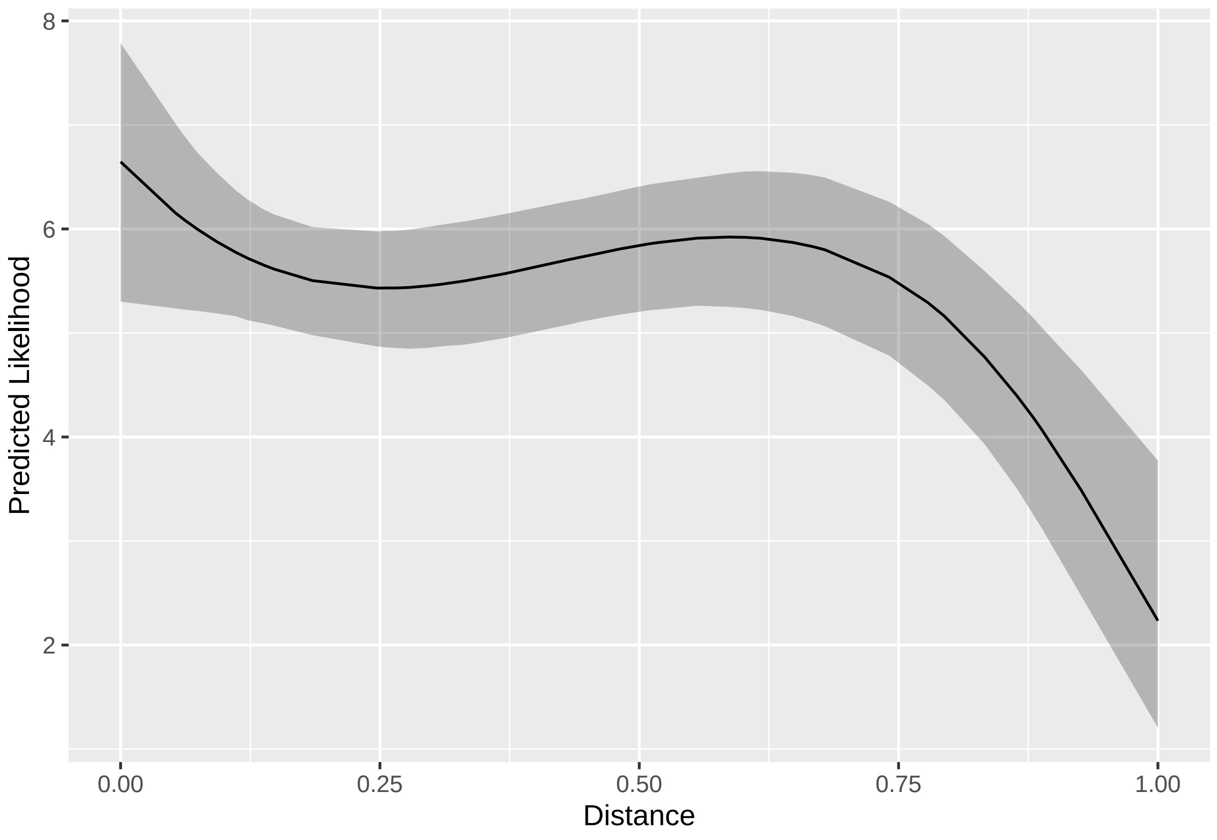
```
##  Family: beta_binomial
##   Links: mu = logit; phi = identity
## Formula: totalNFreq | trials(totalAllFreq) ~ 1 + NormDistanceChosen + I(NormDistanceChosen^2) + I
##    Data: d (Number of observations: 1638)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Group-Level Effects:
## ~EngLexeme (Number of levels: 135)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.69      0.09     0.53     0.87 1.01      410      968
##
## ~Set (Number of levels: 67)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.33      0.15     0.02     0.60 1.02      177      294
##
## Population-Level Effects:
##                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                 0.69      0.29     0.12     1.26 1.01      845
## NormDistanceChosen       -4.72      2.45    -9.58    -0.00 1.01      855
## INormDistanceChosenE2    13.32      5.61     2.49    24.34 1.00      900
## INormDistanceChosenE3   -10.53      3.76   -17.88    -3.21 1.00      978
##                       Tail_ESS
## Intercept                 1597
## NormDistanceChosen         1410
## INormDistanceChosenE2      1399
## INormDistanceChosenE3      1595
##
## Family Specific Parameters:
##     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi     2.00      0.08     1.85     2.16 1.00     3460     2591
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
pred = ggpredict(mBinomBeta,terms="NormDistanceChosen[all]")
```

```
## Note: uncertainty of error terms are not taken into account. Consider
##   setting `interval` to "prediction". This will call `posterior_predict()`
##   instead of `posterior_epred()`.
```

```
## Warning in checkMatrixPackageVersion(): Package version inconsistency detected.
## TMB was built with Matrix version 1.6.1
## Current Matrix version is 1.6.5
## Please re-install 'TMB' from source using install.packages('TMB', type = 'source') or ask CRAN fo
```

```
ggplot(pred,aes(x=x,y=predicted,ymin=conf.low,ymax=conf.high)) +
  geom_ribbon(alpha=0.3)+
  geom_line() +
  xlab("Distance") +
  ylab("Predicted Likelihood")
```



5.2 Feature-based distance (total frequency)

We use nested model comparison to evaluate whether higher-order variables should be added (i.e. how non-linear the relationships is).

```
d$NormDistanceChosen = d$NormFeatureDistance
# Baseline model
m0 = glmer(cbind(totalNFreq,totalEFreq) ~
             1 + (1|Set) + (1|EngLexeme),
           data = d, family = "binomial")
# Add the distance measure
m1 = update(m0,~.+NormDistanceChosen)
# Add quadratic term
m2 = update(m1,~.+I(NormDistanceChosen^2))
# Add cubic term
m3 = update(m2,~.+I(NormDistanceChosen^3))
# Compare fit of models
anova(m0,m1,m2,m3)
```

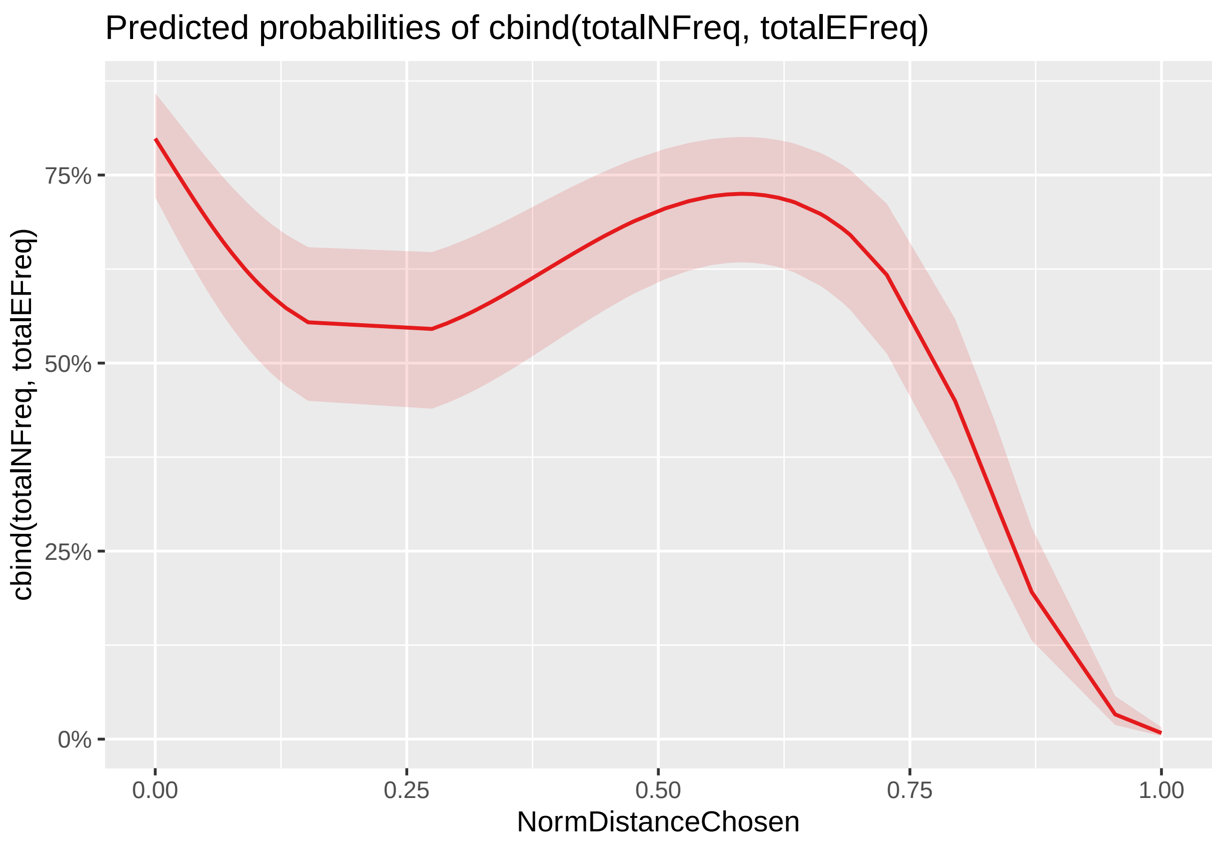
```
## Data: d
## Models:
## m0: cbind(totalNFreq, totalEFreq) ~ 1 + (1 | Set) + (1 | EngLexeme)
## m1: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen
## m2: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen + I(NormDist
## m3: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen + I(NormDist
##    npar   AIC   BIC logLik deviance   Chisq Df Pr(>Chisq)
## m0    3 32262 32278 -16128    32256
## m1    4 32247 32269 -16120    32239  16.464  1  4.958e-05 ***
## m2    5 32159 32186 -16074    32149  90.456  1  < 2.2e-16 ***
## m3    6 31856 31888 -15922    31844 305.264  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Summary of final model:

```
summary(m3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) +
##     NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDistanceChosen^3)
##    Data: d
##
##      AIC      BIC   logLik deviance df.resid
##  31855.8  31888.2 -15921.9  31843.8     1632
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -13.5687  -2.5875  -0.6362   0.7073  24.4503
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  EngLexeme (Intercept) 2.002    1.415
##  Set       (Intercept) 1.551    1.245
## Number of obs: 1638, groups:  EngLexeme, 135; Set, 67
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 1.3771     0.2192   6.282 3.33e-10 ***
## NormDistanceChosen        -13.1251     0.9665 -13.580  < 2e-16 ***
## I(NormDistanceChosen^2)  41.4022     2.6115  15.854  < 2e-16 ***
## I(NormDistanceChosen^3) -34.4563     1.9360 -17.797  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) NrmDsC I(NDC^2
## NrmDstncChs -0.264
## I(NrmDsC^2)  0.242 -0.976
## I(NrmDsC^3) -0.222  0.925 -0.983
```

```
pFeatureTotal = plot_model(m3,'eff',
  terms="NormDistanceChosen[all]")
pFeatureTotal
```



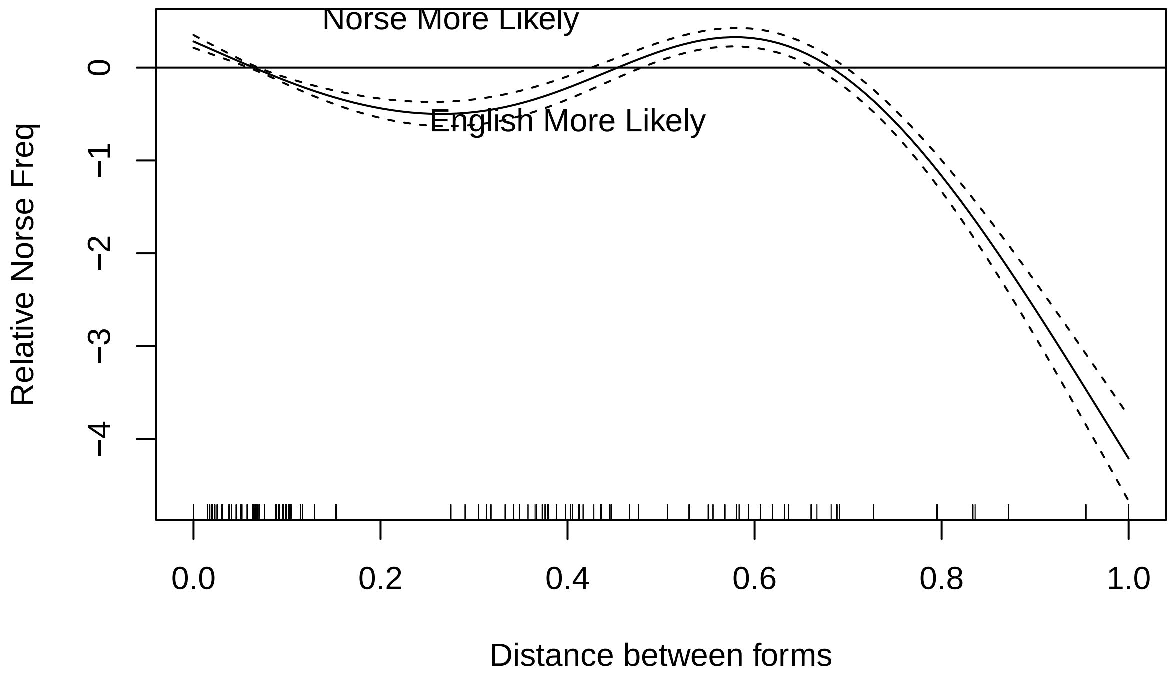
Statistics: (Linear: beta = -13.125, z = -13.58, Wald p < 0.001, LLDiff = 8.2, df = 1, p < 0.001; Quadratic: beta = 41.402, z = 15.854, Wald p < 0.001, LLDiff = 45.2, df = 1, p < 0.001; Cubic: beta = -34.456, z = -17.797, Wald p < 0.001, LLDiff = 152.6, df = 1, p < 0.001)

Same analysis using GAM with binomial distribution:

```
mGAM = gam(cbind(totalNFreq,totalEFreq) ~
             s(NormDistanceChosen,k=4) +
             s(Set,bs="re") +
             s(EngLexeme,bs="re"),
           data = d, family = "binomial")
summary(mGAM)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(totalNFreq, totalEFreq) ~ s(NormDistanceChosen, k = 4) +
##     s(Set, bs = "re") + s(EngLexeme, bs = "re")
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.6916     0.2334   2.964  0.00304 **
## ---
## 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(NormDistanceChosen)  2.999      3     348.8  <2e-16 ***
## s(Set)                45.288     66 1224049.3   0.399
## s(EngLexeme)          80.832    134  344925.2   0.644
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.44   Deviance explained = 46.1%
## UBRE = 16.045  Scale est. = 1         n = 1638
```

```
plot.gam(mGAM,
         ylab="Relative Norse Freq",
         xlab="Distance between forms",
         select = 1)
abline(h=0)
text(0.275,0.5,"Norse More Likely")
text(0.4,-0.6,"English More Likely")
```



5.3 Historical distance (total frequency)

We use nested model comparison to evaluate whether higher-order variables should be added (i.e. how non-linear the relationships is).

```
d$NormDistanceChosen = d$NormHistoricalDistance
# Baseline model
m0 = glmer(cbind(totalNFreq,totalEFreq) ~
             1 + (1|Set) + (1|EngLexeme),
           data = d, family = "binomial")
# Add the distance measure
m1 = update(m0,~.+NormDistanceChosen)
# Add quadratic term
m2 = update(m1,~.+I(NormDistanceChosen^2))
# Add cubic term
m3 = update(m2,~.+I(NormDistanceChosen^3))
# Compare fit of models
anova(m0,m1,m2,m3)
```

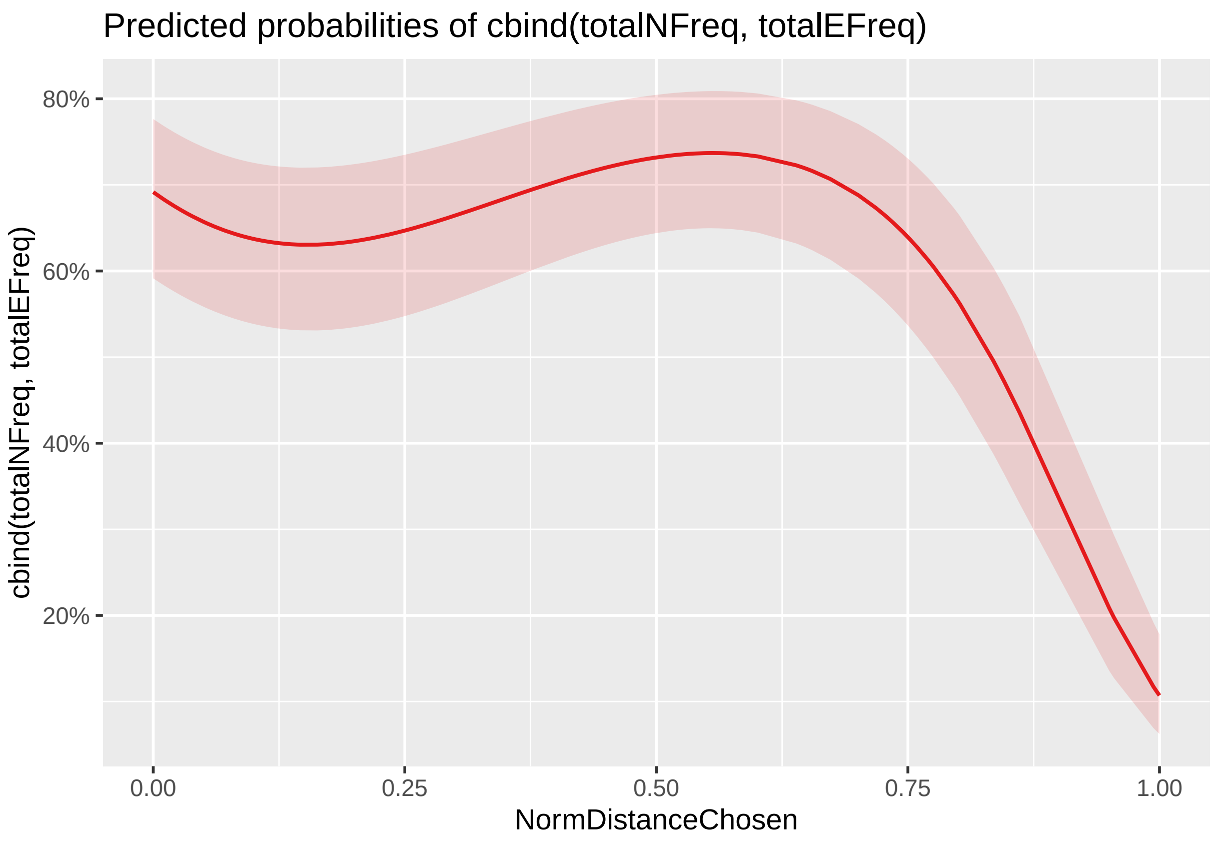
```
## Data: d
## Models:
## m0: cbind(totalNFreq, totalEFreq) ~ 1 + (1 | Set) + (1 | EngLexeme)
## m1: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen
## m2: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen + I(NormDist
## m3: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) + NormDistanceChosen + I(NormDist
##    npar   AIC   BIC logLik deviance    Chisq Df Pr(>Chisq)
## m0    3 32262 32278 -16128    32256
## m1    4 32263 32284 -16127    32255   1.3764  1     0.2407
## m2    5 32146 32173 -16068    32136 118.7880  1     <2e-16 ***
## m3    6 32080 32112 -16034    32068  67.9115  1     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Summary of final model:

```
summary(m3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(totalNFreq, totalEFreq) ~ (1 | Set) + (1 | EngLexeme) +
##     NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDistanceChosen^3)
##    Data: d
##
##      AIC      BIC   logLik deviance df.resid
##  32079.9  32112.3 -16033.9  32067.9     1632
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -13.6467  -2.5893  -0.6312   0.7375  24.4681
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  EngLexeme (Intercept) 1.976    1.406
##  Set       (Intercept) 1.486    1.219
## Number of obs: 1638, groups:  EngLexeme, 135; Set, 67
##
## Fixed effects:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)               0.8076     0.2234   3.616 0.000299 ***
## NormDistanceChosen       -3.9175     0.9838  -3.982 6.83e-05 ***
## I(NormDistanceChosen^2)  16.2533     2.5269   6.432 1.26e-10 ***
## I(NormDistanceChosen^3) -15.2648     1.7883  -8.536  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) NrmDsC I(NDC^2
## NrmDstncChs -0.350
## I(NrmDsC^2)  0.320 -0.978
## I(NrmDsC^3) -0.296  0.934 -0.985
```

```
pHistoricalTotal = plot_model(m3,'eff',
  terms="NormDistanceChosen[all]")
pHistoricalTotal
```



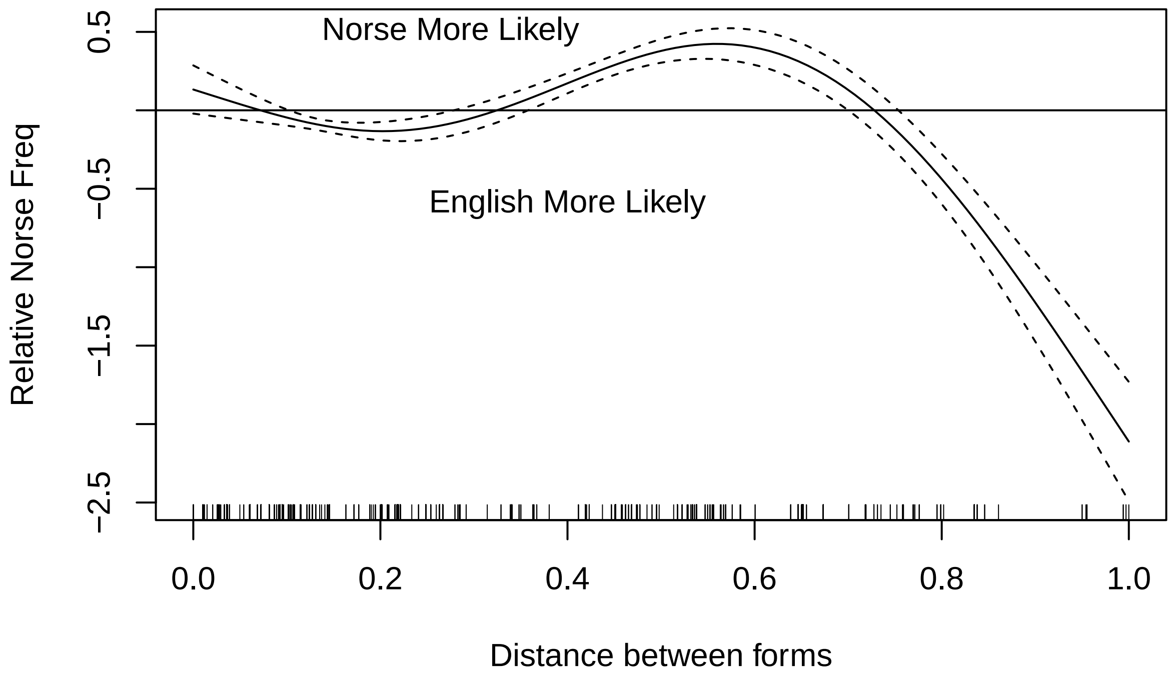
Statistics: (Linear: beta = -3.918, z = -3.982, Wald p < 0.001, LLDiff = 0.7, df = 1, p = 0.241; Quadratic: beta = 16.253, z = 6.432, Wald p < 0.001, LLDiff = 59.4, df = 1, p < 0.001; Cubic: beta = -15.265, z = -8.536, Wald p < 0.001, LLDiff = 34, df = 1, p < 0.001)

Same analysis using GAM with binomial distribution:

```
mGAM = gam(cbind(totalNFreq,totalEFreq) ~
             s(NormDistanceChosen,k=4) +
             s(Set,bs="re") +
             s(EngLexeme,bs="re"),
           data = d, family = "binomial")
summary(mGAM)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(totalNFreq, totalEFreq) ~ s(NormDistanceChosen, k = 4) +
##     s(Set, bs = "re") + s(EngLexeme, bs = "re")
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.5980     0.2378   2.514   0.0119 *
## ---
## 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(NormDistanceChosen)  2.998      3     163.6  <2e-16 ***
## s(Set)                45.968     66 698441.1  0.5322
## s(EngLexeme)          80.247    134 698557.1  0.0652 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.435   Deviance explained = 45.8%
## UBRE = 16.164  Scale est. = 1         n = 1638
```

```
plot.gam(mGAM,
         ylab="Relative Norse Freq",
         xlab="Distance between forms",
         select = 1)
abline(h=0)
text(0.275,0.5,"Norse More Likely")
text(0.4,-0.6,"English More Likely")
```

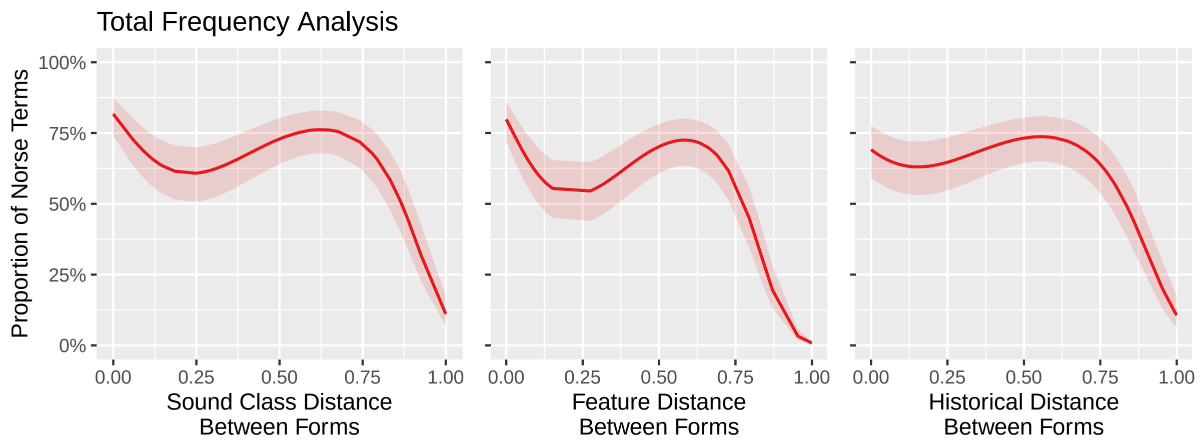


Summary of results for total frequency analyses:

```
bigPlot = grid.arrange(
             pSimpleTotal +
               ggtitle("Total Frequency Analysis") +
               coord_cartesian(ylim = c(0,1))+
               xlab("Sound Class Distance\nBetween Forms")+
               ylab("Proportion of Norse Terms"),
             pFeatureTotal+
               ggtitle("") +
               theme(axis.title.y = element_blank(),
                     axis.text.y=element_blank())+
               coord_cartesian(ylim = c(0,1))+
               xlab("Feature Distance\nBetween Forms"),
             pHistoricalTotal+
               ggtitle("") +
               theme(axis.title.y = element_blank(),
                     axis.text.y=element_blank())+
               coord_cartesian(ylim = c(0,1))+
               xlab("Historical Distance\nBetween Forms"),
             nrow=1,widths=c(1.3,1,1))
```

```
pdf("../results/BigEffectsPlot_totalFreq.pdf",width = 8,height=3)
  plot(bigPlot)
dev.off()
```

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



5.4 Exploratory analyses

5.4.1 Word Class

It is possible that lexical choices differ by word class. For example, verbs may be more resistant to integration. We test this by adding word class as a predictor. Since some word forms appear as several classes, we treat word class as a series of independent binary variables indicating the possibility or not of the word appearing as this class.

```
classes = unique(trimws(unlist(strsplit(unique(d$Class),"/"))))
classes = classes[!is.na(classes)]
classNames = paste0("Class.",gsub(" ",".",classes))
for(i in 1:length(classes)){
  d[,classNames[i]] = grepl(paste0("^",classes[i]),d$Class)
}
```

Build a null model with non-linear distance, as above:

```
d$NormDistanceChosen = d$NormDistance
mC0 = glmer(cbind(totalNFreq,totalEFreq) ~
             1 + NormDistanceChosen +
               I(NormDistanceChosen^2) +
               I(NormDistanceChosen^3) +
             (1|Set) + (1|EngLexeme),
           data = d, family = "binomial")
```

Adding the verb class variable does not improve the fit of the model:

```
mC1a = update(mC0,~.+Class.verb)
anova(mC0,mC1a)
```

```
## Data: d
## Models:
## mC0: cbind(totalNFreq, totalEFreq) ~ 1 + NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDis
## mC1a: cbind(totalNFreq, totalEFreq) ~ NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDistan
##      npar   AIC   BIC logLik deviance  Chisq Df Pr(>Chisq)
## mC0     6 31975 32007 -15981    31963
## mC1a    7 31977 32014 -15981    31963 0.0928  1     0.7607
```

Adding all other classes does not improve the fit of the model:

```
mC1b = update(mC0,~.+Class.adverb + Class.preposition + Class.noun +
               Class.numeral + Class.adjective + Class.verb +
               Class.indefinite.pronoun + Class.interjection)
```

```
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00689701 (tol = 0.002, component 1)
```

```
anova(mC0,mC1b)
```

```
## Data: d
## Models:
## mC0: cbind(totalNFreq, totalEFreq) ~ 1 + NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDis
## mC1b: cbind(totalNFreq, totalEFreq) ~ NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDistan
##      npar   AIC   BIC logLik deviance  Chisq Df Pr(>Chisq)
## mC0     6 31975 32007 -15981    31963
## mC1b   12 31980 32044 -15978    31956 7.0668  6     0.3147
```

```
summary(mC1b)
```

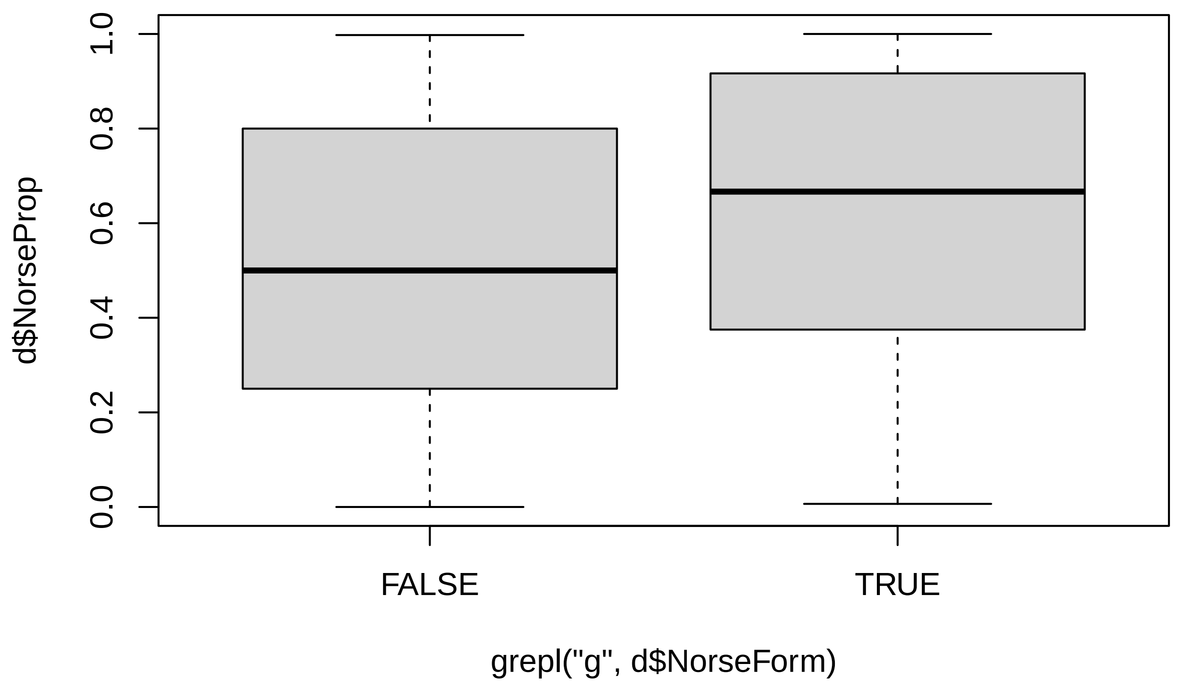
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## cbind(totalNFreq, totalEFreq) ~ NormDistanceChosen + I(NormDistanceChosen^2) +
##     I(NormDistanceChosen^3) + (1 | Set) + (1 | EngLexeme) + Class.adverb +
##     Class.preposition + Class.noun + Class.numeral + Class.adjective +
##     Class.verb + Class.indefinite.pronoun + Class.interjection
##    Data: d
##
##      AIC      BIC   logLik deviance df.resid
##  31979.6  32044.4 -15977.8  31955.6     1626
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -13.6715  -2.5875  -0.6247   0.7114  24.4498
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  EngLexeme (Intercept) 1.992    1.411
##  Set       (Intercept) 1.178    1.085
## Number of obs: 1638, groups:  EngLexeme, 135; Set, 67
##
## Fixed effects:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   1.2177     0.7815   1.558    0.119
## NormDistanceChosen          -10.4432     0.9922 -10.526   <2e-16 ***
## I(NormDistanceChosen^2)      30.8080     2.3382  13.176   <2e-16 ***
## I(NormDistanceChosen^3)     -23.9496     1.6074 -14.899   <2e-16 ***
## Class.adverbTRUE              0.9804     0.9147   1.072    0.284
## Class.nounTRUE                0.1828     0.8329   0.220    0.826
## Class.numeralTRUE             1.8335     1.1919   1.538    0.124
## Class.adjectiveTRUE          -0.4274     0.9183  -0.465    0.642
## Class.verbTRUE                0.1505     0.8427   0.179    0.858
## Class.indefinite.pronounTRUE   1.0948     1.6814   0.651    0.515
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) NrmDsC I(NDC^2 I(NDC^3 Clss.dvTRUE Clss.nnTRUE Clss.nmTRUE
## NrmDstncChs -0.129
## I(NrmDsC^2)  0.114 -0.969
## I(NrmDsC^3) -0.101  0.915 -0.983
## Clss.dvTRUE -0.833 -0.013  0.010  -0.008
## Clss.nnTRUE -0.917 -0.005  0.008  -0.009   0.781
## Clss.nmTRUE -0.636  0.009 -0.008   0.005   0.541       0.594
## Clss.djTRUE -0.831 -0.006  0.005  -0.005   0.708       0.785       0.539
## Clss.vrTRUE -0.861 -0.004  0.007  -0.007   0.732       0.805       0.557
## Clss.n.TRUE -0.454 -0.014  0.016  -0.019   0.388       0.427       0.296
##             Clss.djTRUE Clss.vTRUE
## NrmDstncChs
## I(NrmDsC^2)
## I(NrmDsC^3)
## Clss.dvTRUE
## Clss.nnTRUE
## Clss.nmTRUE
## Clss.djTRUE
## Clss.vrTRUE  0.729
## Clss.n.TRUE  0.387       0.400
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.00689701 (tol = 0.002, component 1)
```

5.4.2 Diagnostic consonants

Some Norse words have more salient diagnostic segments - they sound 'more Norse'. For example, the presence of Velar consonants (e.g. /g/ vs /j/, /sk/ vs post-alveolar fricative, /k/ vs post-alveolar affricate).

For example, the average Norse proportion is higher for Norse forms words with 'g':

```
boxplot(d$NorseProp ~ grepl("g",d$NorseForm))
```

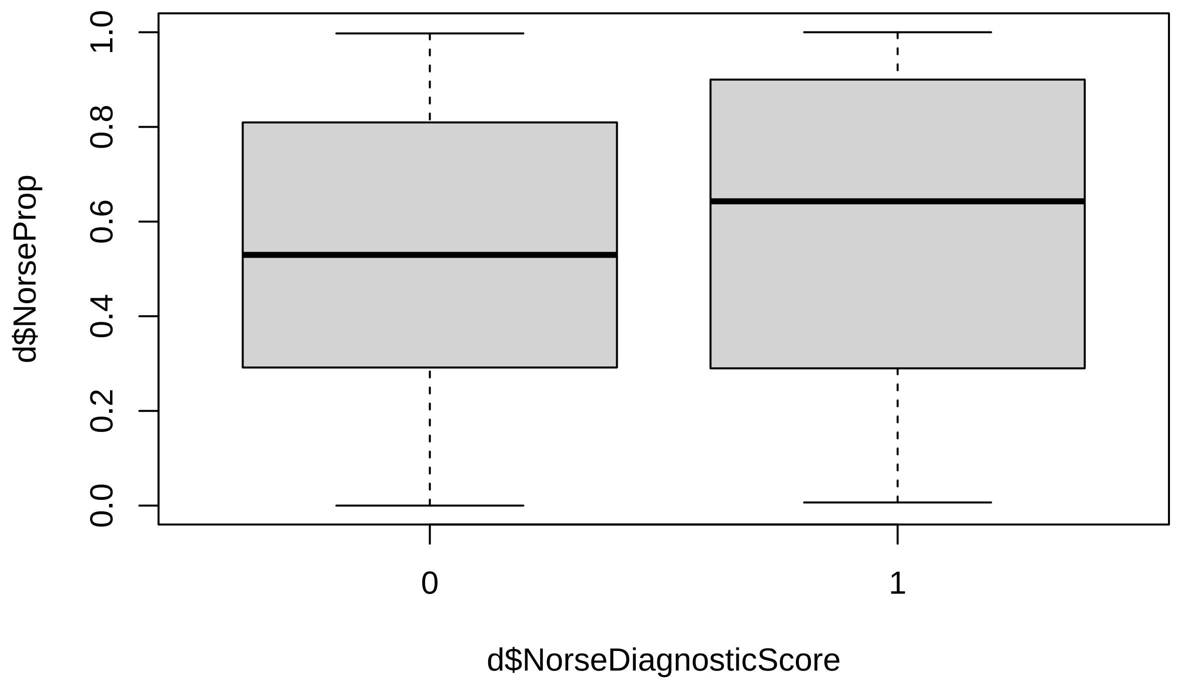


To test this systematically, we calculate a Norse Diagnostic Score: cases where these segments are diagnostic of the differences between Norse and English forms (the score is potentially more than one, but in our data there are only zero and one):

```
d$NorseDiagnosticScore =
  (grepl("g",d$NorseForm) & !grepl("g",d$EngForm))+
  (grepl(" ",d$NorseForm) & !grepl(" ",d$EngForm)) +
  (grepl("sk",d$NorseForm) & !grepl("sk",d$EngForm))+
  # (k in Norse vs   in English)
  (grepl("k",d$NorseForm) & grepl(" ",d$EngForm))

d$NorseDiagnosticScore = factor(d$NorseDiagnosticScore)

boxplot(d$NorseProp~ d$NorseDiagnosticScore)
```



```
t.test(d$NorseProp~ d$NorseDiagnosticScore)
```

```
##
##  Welch Two Sample t-test
##
## data:  d$NorseProp by d$NorseDiagnosticScore
## t = -2.2293, df = 1532.9, p-value = 0.02594
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -0.065524499 -0.004187601
## sample estimates:
## mean in group 0 mean in group 1
##       0.5501452       0.5850013
```

Adding the Norse Diagnostic Score to the model significantly improves the fit of the model. The model suggests that Norse forms which are more obviously Norse have a lower chance of being selected overall.

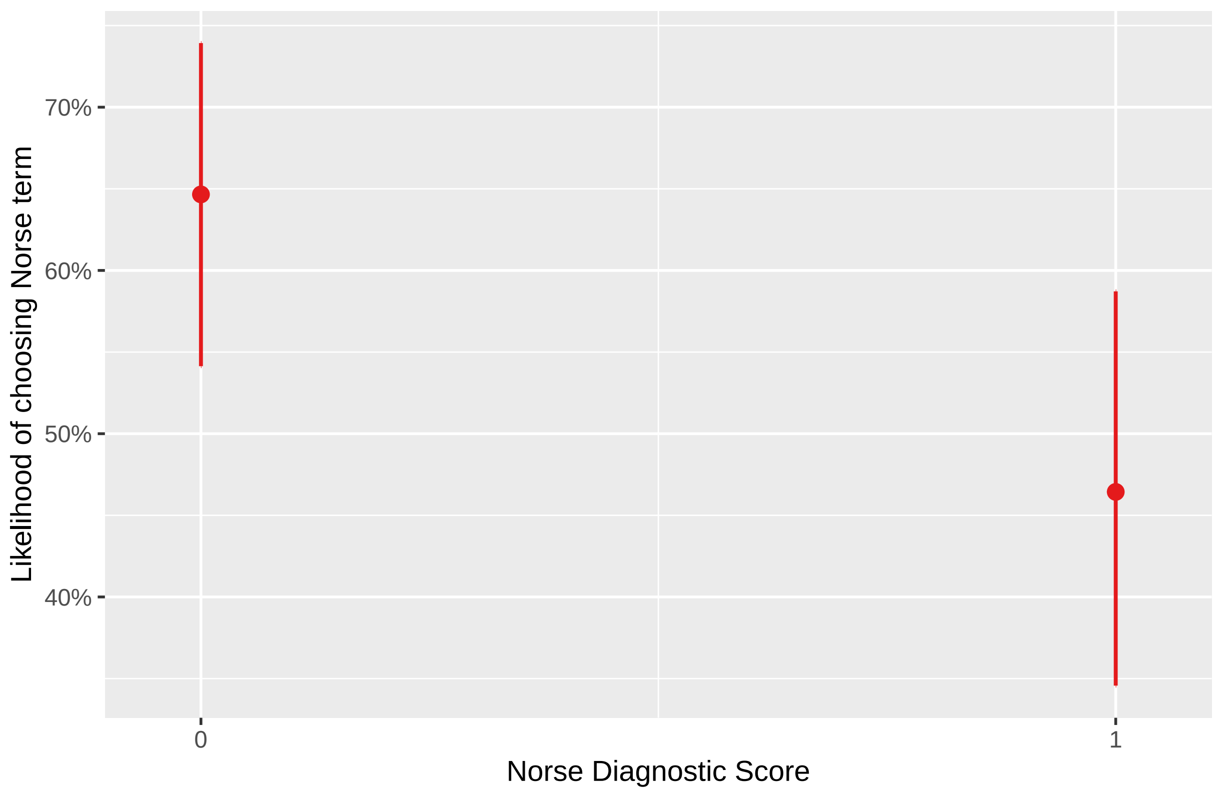
```
d$NormDistanceChosen = d$NormDistance
mD0 = glmer(cbind(totalNFreq,totalEFreq) ~
              1 + NormDistanceChosen +
                I(NormDistanceChosen^2) +
                I(NormDistanceChosen^3) +
              (1|Set) + (1|EngLexeme),
            data = d, family = "binomial")
mD1 = update(mD0, ~.+NorseDiagnosticScore)
anova(mD0,mD1)
```

```
## Data: d
## Models:
## mD0: cbind(totalNFreq, totalEFreq) ~ 1 + NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDis
## mD1: cbind(totalNFreq, totalEFreq) ~ NormDistanceChosen + I(NormDistanceChosen^2) + I(NormDistanc
##     npar   AIC   BIC logLik deviance  Chisq Df Pr(>Chisq)
## mD0    6 31975 32007 -15981    31963
## mD1    7 31954 31992 -15970    31940 22.871  1  1.732e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mD1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## cbind(totalNFreq, totalEFreq) ~ NormDistanceChosen + I(NormDistanceChosen^2) +
##     I(NormDistanceChosen^3) + (1 | Set) + (1 | EngLexeme) + NorseDiagnosticScore
##    Data: d
##
##      AIC      BIC   logLik deviance df.resid
##  31953.8  31991.6 -15969.9  31939.8     1631
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -13.6651  -2.5587  -0.6102   0.7161  24.4515
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  EngLexeme (Intercept) 2.024    1.423
##  Set       (Intercept) 1.774    1.332
## Number of obs: 1638, groups:  EngLexeme, 135; Set, 67
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)                1.6604     0.2476   6.705 2.01e-11 ***
## NormDistanceChosen       -10.3816     0.9876 -10.512  < 2e-16 ***
## I(NormDistanceChosen^2)   30.6307     2.3291  13.151  < 2e-16 ***
## I(NormDistanceChosen^3) -23.7685     1.6035 -14.823  < 2e-16 ***
## NorseDiagnosticScore1     -0.7469     0.1583  -4.717 2.39e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) NrmDsC I(NDC^2 I(NDC^3
## NrmDstncChs -0.422
## I(NrmDsC^2)  0.379 -0.969
## I(NrmDsC^3) -0.341  0.913 -0.983
## NrsDgnstcS1 -0.138 -0.010  0.011  -0.014
```

```r
plot_model(mD1,'eff', terms="NorseDiagnosticScore") +
  ylab("Likelihood of choosing Norse term") +
  xlab("Norse Diagnostic Score") +
  ggtitle("")
```

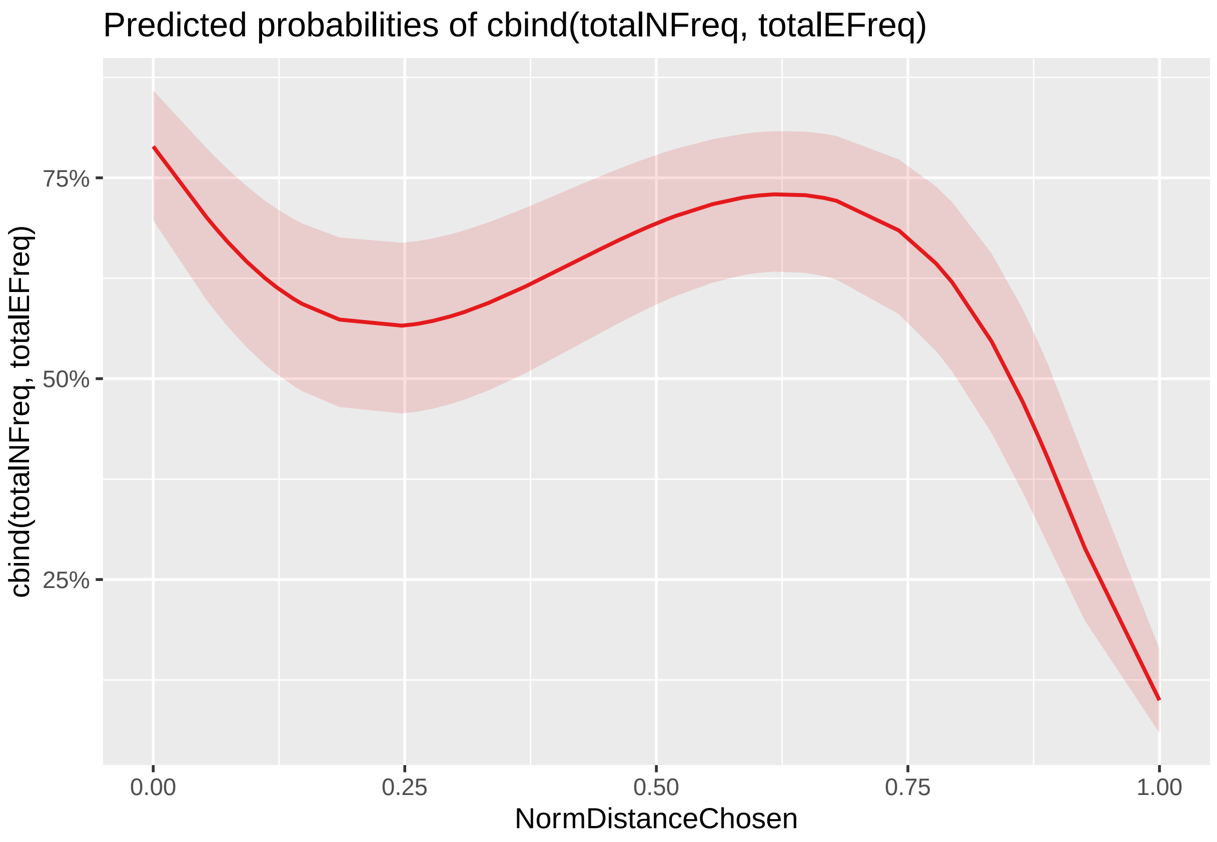


```
get_model_data(mD1,'eff', terms="NorseDiagnosticScore")
```

```
## # Predicted probabilities of cbind(totalNFreq, totalEFreq)
##
## NorseDiagnosticScore | Predicted |     95% CI | group_col
## ---------------------------------------------------------
##                    0 |      0.65 | 0.54, 0.74 |         1
##                    1 |      0.46 | 0.35, 0.59 |         1
```

The effect of form distance is unaffected:

```
plot_model(mD1,'eff',terms="NormDistanceChosen[all]")
```



6 Source-level frequency analysis

This analysis uses source-level observations: each observation is the frequency of a pair of forms within a particular source. This also lets us control for source-level features like the source itself as a random effect, the age of the source, and whether alliteration might affect decisions.

There may be multiple orthographic forms for each unique full form for comparison, so first, we collapse the data over unique pairs. We also restructure the data to be in 'long' format.

```
d2 = data.frame()
for(i in 1:length(englishFrequencyColumns)){
 dx = data.frame(
   Set = d$Set,
   EngForm = d$EngForm,
   NorseForm = d$NorseForm,
   NormDistance = d$NormDistance,
   NormFeatureDistance = d$NormFeatureDistance,
   NormHistoricalDistance = d$NormHistoricalDistance,
   NFreq = d[,norseFrequencyColumns[i]],
   EFreq = d[,englishFrequencyColumns[i]],
   Source = englishFrequencyColumns[i],
   Alliteration = d$Alliteration)
 dx = dx[rowSums(dx[,c("NFreq","EFreq")],na.rm = T)>0,]
 uforms = paste(dx$Set,dx$EngForm,dx$NorseForm)
 dx = data.frame(
   Set = tapply(dx$Set,uforms,head,n=1),
   EngForm = tapply(dx$EngForm,uforms,head,n=1),
   NorseForm = tapply(dx$NorseForm,uforms,head,n=1),
   NormDistance = tapply(dx$NormDistance,uforms,head,n=1),
   NormFeatureDistance = tapply(dx$NormFeatureDistance,uforms,head,n=1),
   NormHistoricalDistance = tapply(dx$NormHistoricalDistance,uforms,head,n=1),
   NFreq = tapply(dx$NFreq,uforms,sum,na.rm=T),
   EFreq = tapply(dx$EFreq,uforms,sum,na.rm=T),
   Source = englishFrequencyColumns[i],
   Alliteration = tapply(dx$Alliteration,uforms,head,n=1))
 d2 = rbind(d2,dx)
}

d2$Set = factor(d2$Set)
d2$Source = factor(d2$Source)

# Make a variable for each unique form within a set
d2$EngForm2 = paste(d2$Set,d2$EngForm)
d2$NorseForm2 = paste(d2$Set,d2$NorseForm)
d2$EngForm2 = factor(d2$EngForm2)

# Remove any cases with zero frequency
d2 = d2[!(d2$NFreq==0 & d2$EFreq==0),]

# Proportion of norse forms
d2$NProp = 100*(d2$NFreq/(d2$NFreq+d2$EFreq))
```

Modelling age is difficult, since exact dates are not known. It would be possible to model the date of publication as an ordinal variable, for example assuming FCPC > Ormulum > {Havelok, GenAndEx} > CursorMundi > {Mannyng, GawainPoet} > WarsAlexander > StErkenwald. However, the texts from the Corpus of Middle English span several centuries, and so are hard to place in this order. Instead, we simply use the century as an ordered category.

```
AgeCategories =
    c("EFreqFCPC"=12,
      "EFreqOrmulum"=12,
     "EFreqHavelok"=13,
     "EFreqGenAndEx" = 14,
     "EFreqCursorMundi" = 14,
     "EFreqGawainPoet" = 14,
     "EFreqStErkenwald" = 15,
     "EFreqMannyng" = 15,
     "EFreqWarsAlexander" = 15,
     "EFreqLinc"=15,
       "EFreqNott"=15,
       "EFreqNorf"=15,
       "EFreqRolle"=15)
```

```
d2$Age = AgeCategories[d2$Source]
d2$Age = factor(d2$Age,ordered=T)

contrasts(d2$Age) = contr.sum(length(unique(d2$Age)))

mean(d2$NFreq/(d2$NFreq+d2$EFreq))
```

```
## [1] 0.5579405
```

```
range(d2$NFreq/(d2$NFreq+d2$EFreq))
```

```
## [1] 0 1
```

```
mean(d2$NormDistance)
```

```
## [1] 0.3594087
```

Alliteration only applies to poetry sources: Gawain, St Erkenwold, and Wars of Alexander. So turn all others to ‘false’:

```
d2[!d2$Source %in%
     c("EFreqGawainPoet",
       "EFreqStErkenwald",
       "EFreqWarsAlexander",
       "EFreqLinc",
         "EFreqNott",
         "EFreqNorf",
         "EFreqRolle"),]$Alliteration = FALSE
d2$Alliteration = factor(d2$Alliteration)
```

```
gPairs = ggpairs(d2[,c("NormDistance","NormFeatureDistance",
              "NormHistoricalDistance","NProp")],
        columnLabels = c("Sound Class Distance",
                         "Feature Distance",
                         "Historical Distance",
                         "Freq (% Norse)"),
        rowLabels = c("Sound Class Distance",
                         "Feature Distance",
                         "Historical Distance",
                         "Freq (% Norse)"))

pdf("../results/GPairs.pdf",width=6,height=5.5)
  gPairs
dev.off()
```

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

6.1 Simple distance

Use a mixed effects model to predict the frequency of Norse and English forms by a random effect for cognate Set and Source. We add a main effect of age of source, then introduce the normalised distance measure along with its non-linear terms.

```
m0 = glmer(cbind(NFreq,EFreq) ~ Age + Alliteration +
              (1|Set) + (1|Source) +
             (1|EngForm2),
           data = d2, family = "binomial",
           glmerControl(optimizer = "bobyqa"))
# Add the distance measure
m1 = update(m0,~.+NormDistance)
# Add quadratic term
m2 = update(m1,~.+I(NormDistance^2))
# Add cubic term
m3 = update(m2,~.+I(NormDistance^3))
```

Compare fit of models:

```
anova(m0,m1,m2,m3)
```

```
## Data: d2
## Models:
## m0: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2)
## m1: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormDi
## m2: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormDi
## m3: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormDi
##    npar   AIC   BIC logLik deviance   Chisq Df Pr(>Chisq)
## m0    8 21104 21145 -10544    21088
## m1    9 20936 20981 -10459    20918 170.622  1  < 2.2e-16 ***
## m2   10 20875 20926 -10428    20855  62.509  1  2.652e-15 ***
## m3   11 20547 20602 -10262    20525 330.399  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

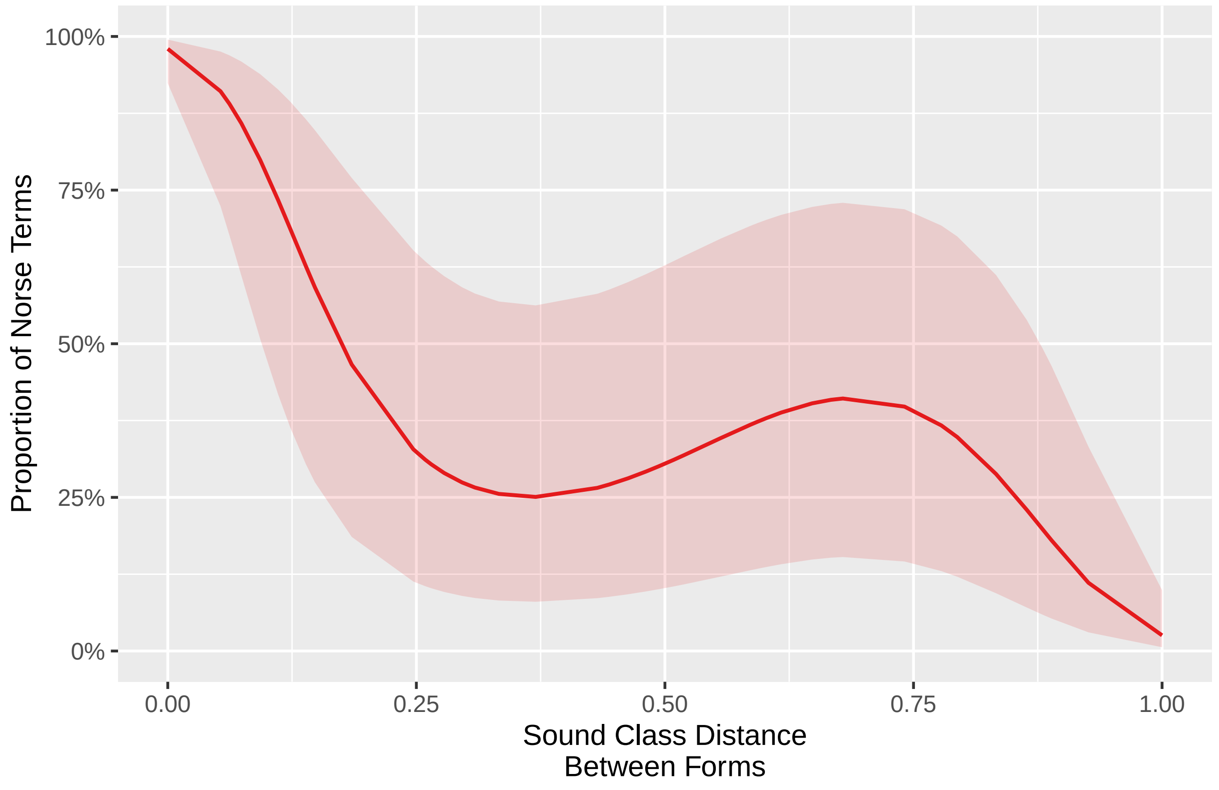
Summary of final model:

```
summary(m3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) +
##     (1 | EngForm2) + NormDistance + I(NormDistance^2) + I(NormDistance^3)
##    Data: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##  20546.6  20602.4 -10262.3  20524.6     1162
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -105.030   -1.362    0.114    1.127  175.531
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  EngForm2 (Intercept) 4.302    2.074
##  Set      (Intercept) 5.354    2.314
##  Source   (Intercept) 4.389    2.095
## Number of obs: 1173, groups:  EngForm2, 129; Set, 67; Source, 13
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         3.554398   0.834099   4.261 2.03e-05 ***
## Age1                1.062382   1.278355   0.831    0.406
## Age2               -1.281640   1.644782  -0.779    0.436
## Age3               -0.007456   1.124018  -0.007    0.995
## AlliterationTRUE    2.233356   0.071790  31.110  < 2e-16 ***
## NormDistance      -32.968226   1.575406 -20.927  < 2e-16 ***
## I(NormDistance^2)  68.761447   3.535850  19.447  < 2e-16 ***
## I(NormDistance^3) -43.320731   2.343141 -18.488  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Age1   Age2   Age3   AlTRUE NrmDst I(ND^2
## Age1         0.010
## Age2         0.398 -0.521
## Age3        -0.185 -0.260 -0.490
## AlltrtnTRUE -0.012  0.015 -0.010  0.000
## NormDistanc -0.211 -0.007  0.005  0.001 -0.026
## I(NrmDst^2)  0.189  0.007 -0.005  0.000  0.025 -0.968
## I(NrmDst^3) -0.169 -0.007  0.006  0.000 -0.026  0.908 -0.981
```

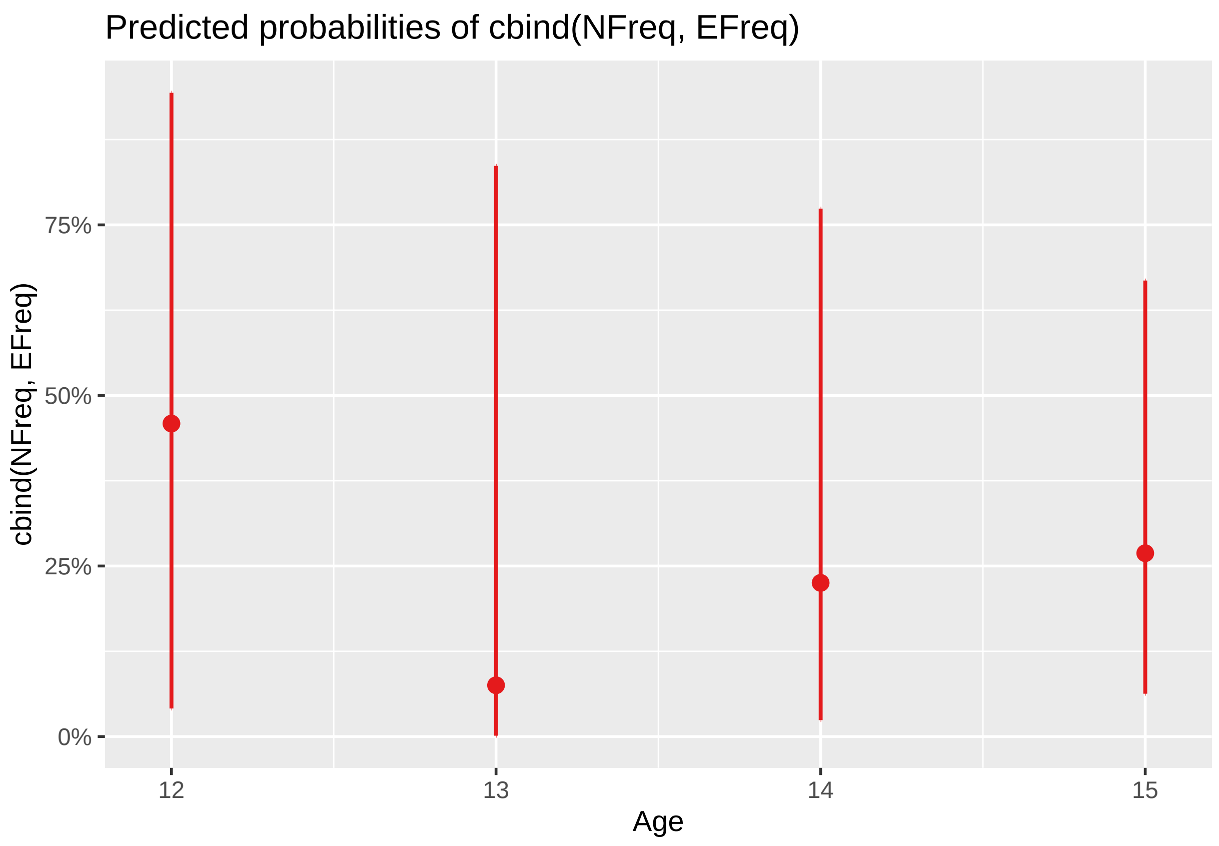
Norse frequency varies with distance. The plot below shows the marginal effects, holding discrete predictors constant at their proportions (not reference level):

```
pNormSimple =
  plot_model(m3,'eff', terms="NormDistance[all]") +
  xlab("Sound Class Distance\nBetween Forms") +
  ylab("Proportion of Norse Terms") +
  ggtitle("")+
    coord_cartesian(ylim=c(0,1))
pNormSimple
```

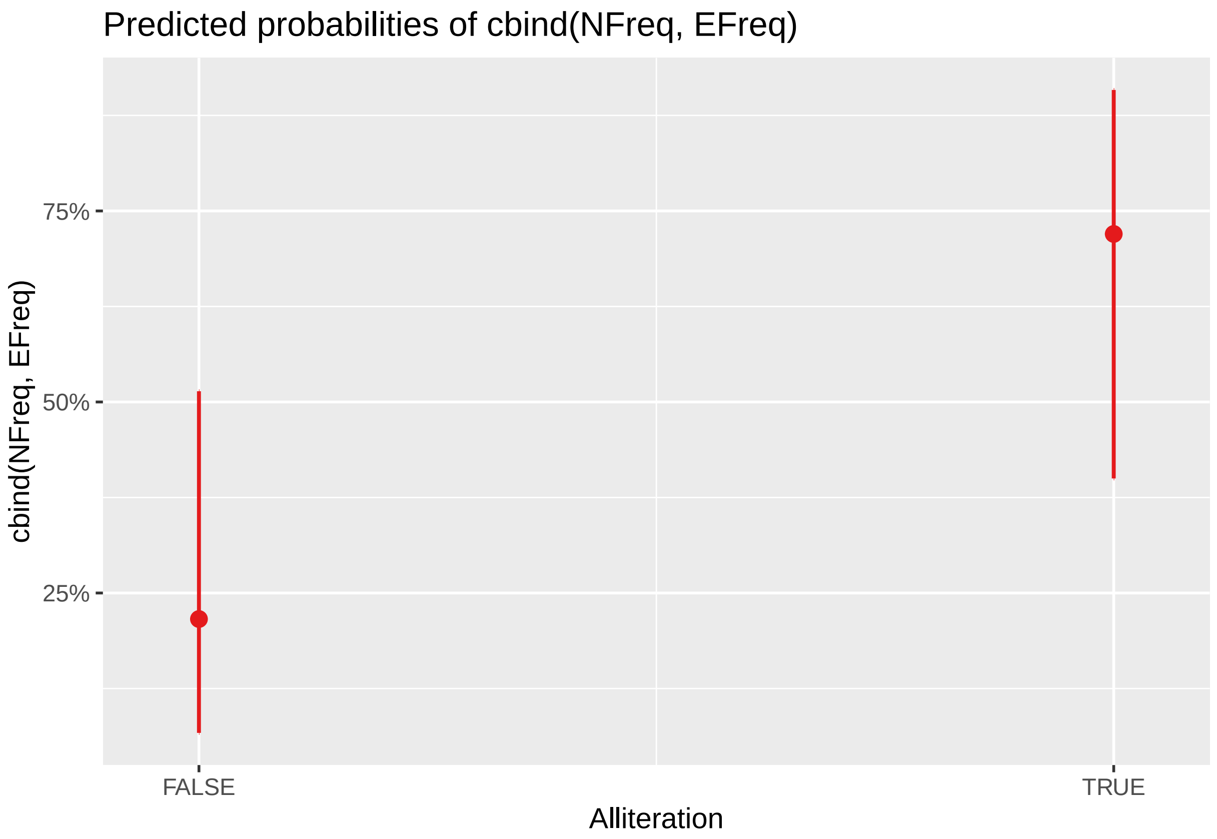


Effects over time and of alliteration:

```
plot_model(m3,'eff', terms="Age [all]")
```



```
plot_model(m3,'eff', terms="Alliteration")
```

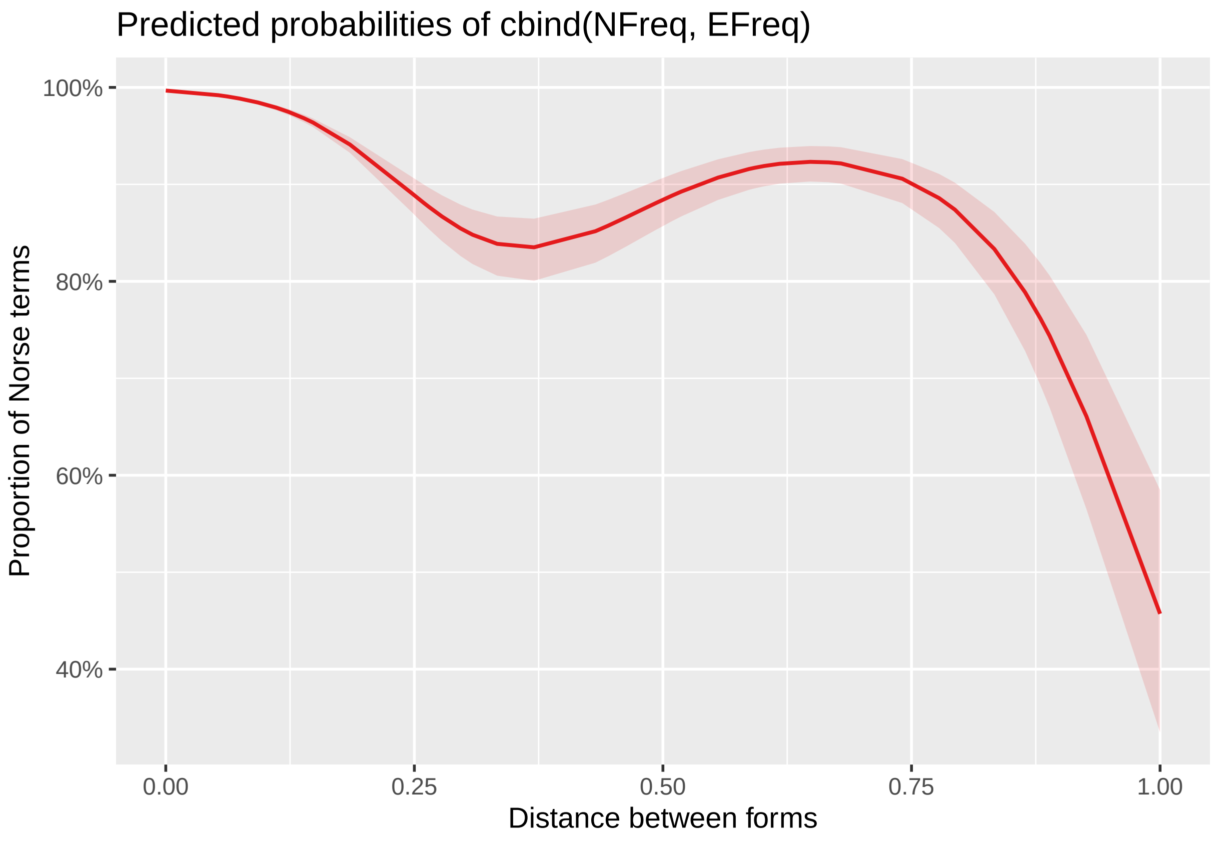


The GAM model seems a little different, showing a smaller effect at lower distances.

```
mGAM = gam(cbind(NFreq,EFreq) ~
             s(NormDistance,k=4) +
             s(Age,bs = "re") +
             s(Set,bs="re") +
             s(Source,bs="re")+
             s(EngForm2,bs="re"),
           data = d2, family = "binomial")
summary(mGAM)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(NFreq, EFreq) ~ s(NormDistance, k = 4) + s(Age, bs = "re") +
##     s(Set, bs = "re") + s(Source, bs = "re") + s(EngForm2, bs = "re")
##
## Parametric coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.001498   2.230288  -0.001    0.999
##
## Approximate significance of smooth terms:
##                     edf Ref.df    Chi.sq p-value
## s(NormDistance)  2.99967      3 4.539e+02 < 2e-16 ***
## s(Age)           0.03305      3 2.027e+03 0.99821
## s(Set)          49.04776     66 3.235e+07 0.10624
## s(Source)       11.96498     12 1.112e+07 < 2e-16 ***
## s(EngForm2)     72.08085    128 3.721e+07 0.00747 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.709   Deviance explained = 69.2%
## UBRE = 16.512  Scale est. = 1         n = 1173
```

```
plot_model(mGAM,"pred",terms="NormDistance") +
  ylab("Proportion of Norse terms") +
  xlab("Distance between forms")
```



Statistics for the simple measure:

(Linear: beta = -32.968, z = -20.927, Wald p < 0.001, LLDiff = 85.3, df = 1, p < 0.001; Quadratic: beta = 68.761, z = 19.447, Wald p < 0.001, LLDiff = 31.3, df = 1, p < 0.001; Cubic: beta = -43.321, z = -18.488, Wald p < 0.001, LLDiff = 165.2, df = 1, p < 0.001)

6.2 Feature-based distance

Same analysis as the simple distance above:

```
m0 = glmer(cbind(NFreq,EFreq) ~ Age + Alliteration
              + (1|Set) + (1|Source) +
             (1|EngForm2),
           data = d2, family = "binomial")
m1 = update(m0,~.+NormFeatureDistance)
m2 = update(m1,~.+I(NormFeatureDistance^2))
m3 = update(m2,~.+I(NormFeatureDistance^3))
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0469466 (tol = 0.002, component 1)
```

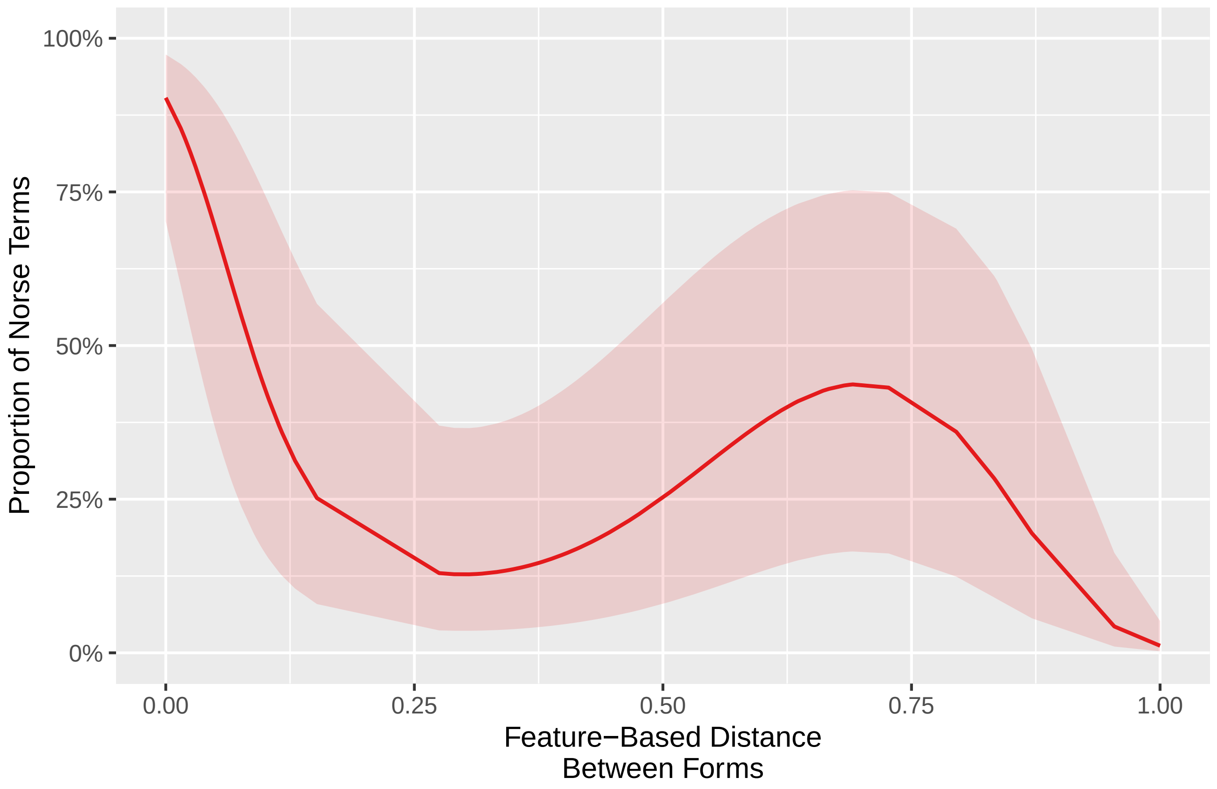
```
anova(m0,m1,m2,m3)
```

```
## Data: d2
## Models:
## m0: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2)
## m1: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormFe
## m2: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormFe
## m3: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormFe
##    npar   AIC   BIC logLik deviance   Chisq Df Pr(>Chisq)
## m0    8 21104 21145 -10544    21088
## m1    9 20901 20946 -10442    20883 205.280  1  < 2.2e-16 ***
## m2   10 20857 20907 -10418    20837  46.349  1  9.895e-12 ***
## m3   11 20582 20638 -10280    20560 276.202  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m3)
```

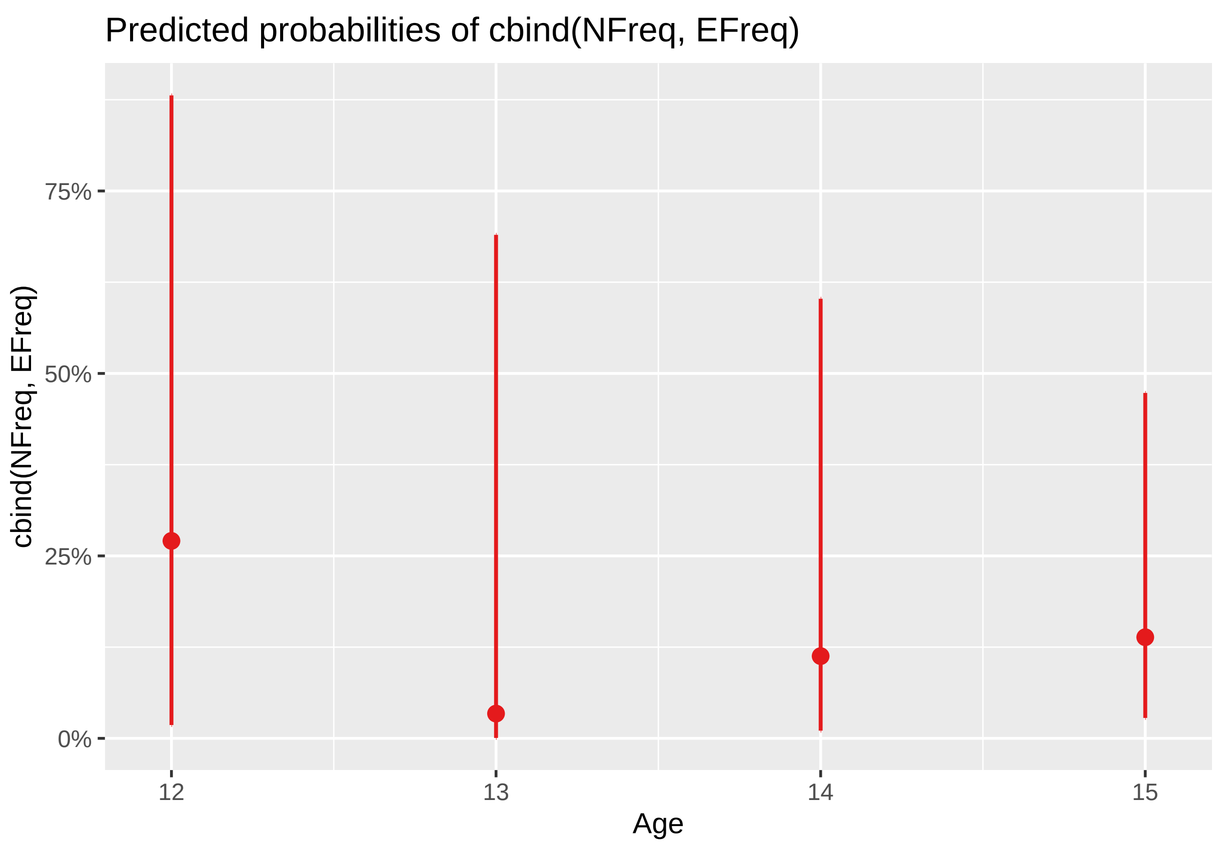
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) +
##     (1 | EngForm2) + NormFeatureDistance + I(NormFeatureDistance^2) +
##     I(NormFeatureDistance^3)
##    Data: d2
##
##      AIC      BIC   logLik deviance df.resid
##  20582.3  20638.1 -10280.2  20560.3     1162
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -102.933   -1.381    0.116    1.096  178.703
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  EngForm2 (Intercept) 4.740    2.177
##  Set      (Intercept) 5.840    2.417
##  Source   (Intercept) 4.365    2.089
## Number of obs: 1173, groups:  EngForm2, 129; Set, 67; Source, 13
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)               1.899237   0.829291   2.290    0.022 *
## Age1                      1.066301   1.278915   0.834    0.404
## Age2                     -1.291551   1.646010  -0.785    0.433
## Age3                     -0.005518   1.123471  -0.005    0.996
## AlliterationTRUE           2.251681   0.071937  31.301   <2e-16 ***
## NormFeatureDistance      -32.430222   1.781901 -18.200   <2e-16 ***
## I(NormFeatureDistance^2)  77.441357   4.551277  17.015   <2e-16 ***
## I(NormFeatureDistance^3) -51.690896   3.157168 -16.373   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Age1   Age2   Age3   AlTRUE NrmFtD I(NFD^2
## Age1          0.006
## Age2          0.404 -0.522
## Age3         -0.187 -0.259 -0.490
## AlltrtnTRUE -0.014  0.015 -0.010 -0.001
## NrmFtrDstnc -0.144  0.005 -0.017  0.011 -0.024
## I(NrmFtD^2)  0.135 -0.006  0.017 -0.011  0.026 -0.981
## I(NrmFtD^3) -0.125  0.006 -0.017  0.010 -0.028  0.934 -0.984
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0469466 (tol = 0.002, component 1)
```

```
pNormFeature =
  plot_model(m3,'eff', terms="NormFeatureDistance[all]")+
    xlab("Feature-Based Distance\nBetween Forms") +
    ylab("Proportion of Norse Terms") +
    ggtitle("")+
    coord_cartesian(ylim=c(0,1))
pNormFeature
```

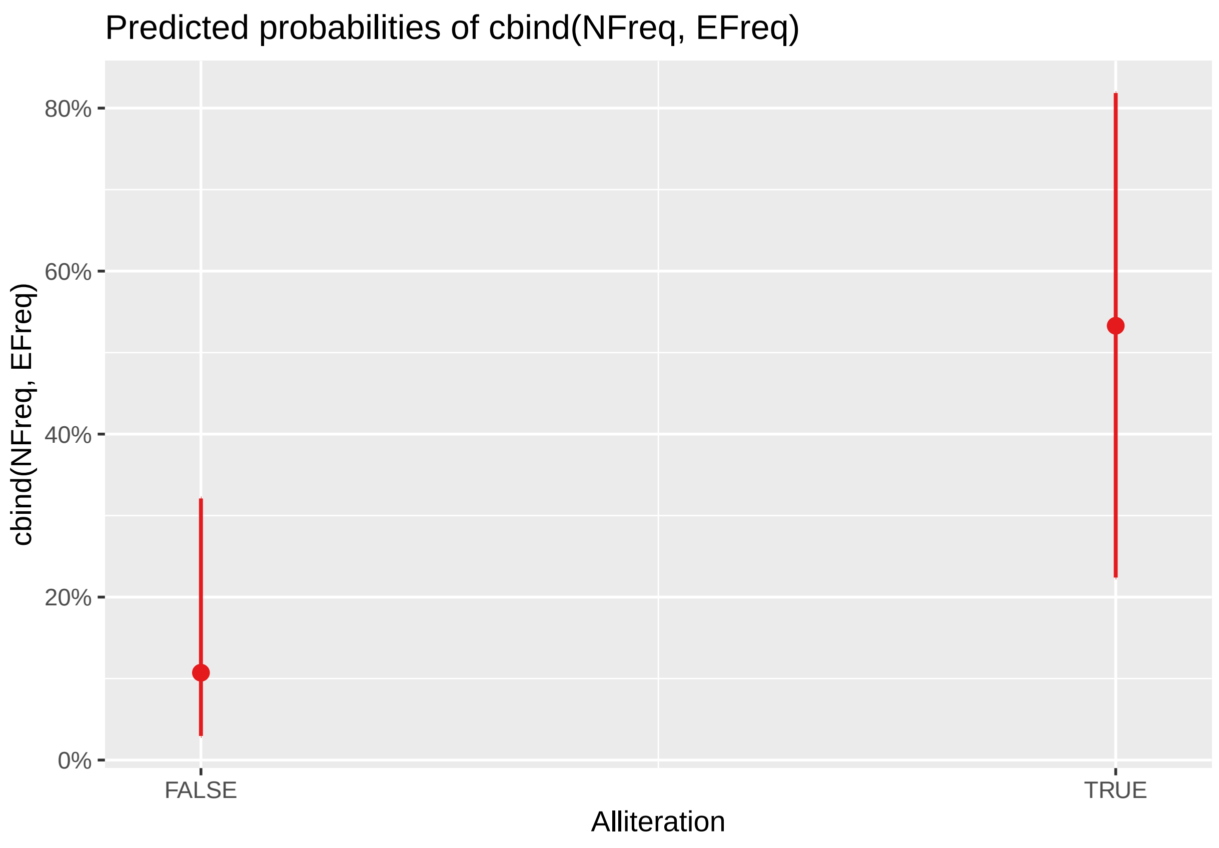


Effects over time and of alliteration:

```
plot_model(m3,'eff', terms="Age [all]")
```



```
plot_model(m3,'eff', terms="Alliteration")
```

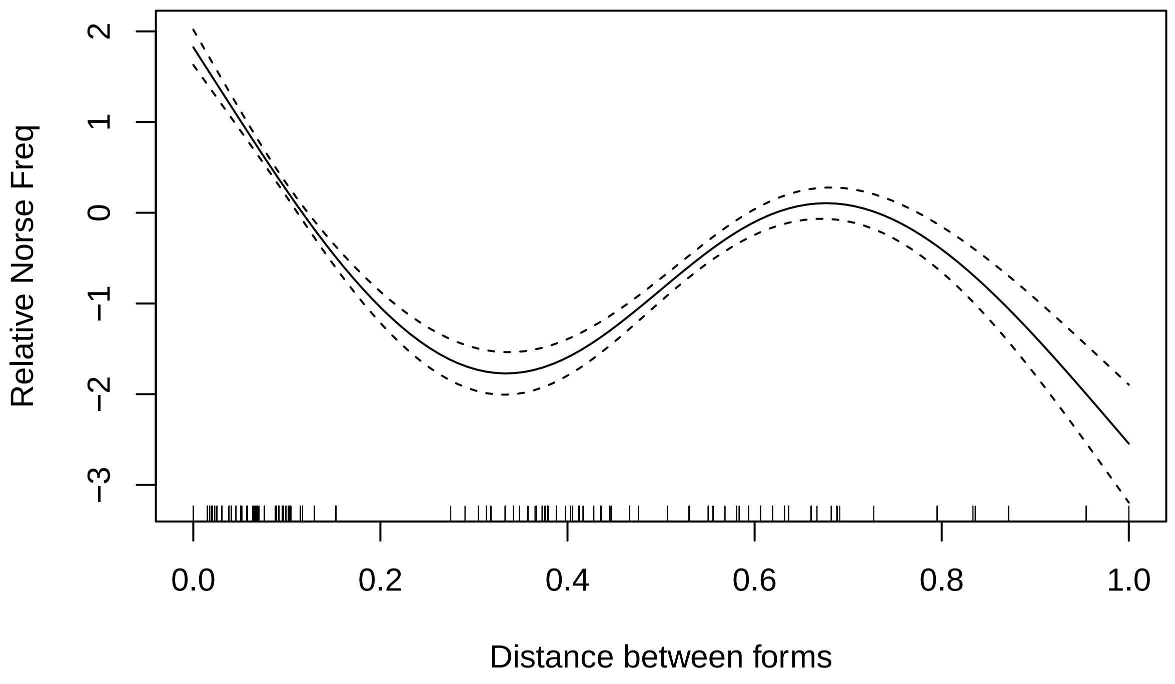


GAM model:

```
mGAM = gam(cbind(NFreq,EFreq) ~
             s(NormFeatureDistance,k=4) +
             s(Age,bs = "re") +
             s(Set,bs="re") +
             s(Source,bs="re")+
             s(EngForm2,bs="re"),
           data = d2, family = "binomial")
summary(mGAM)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(NFreq, EFreq) ~ s(NormFeatureDistance, k = 4) + s(Age,
##     bs = "re") + s(Set, bs = "re") + s(Source, bs = "re") + s(EngForm2,
##     bs = "re")
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.09027    2.81544   0.032    0.974
##
## Approximate significance of smooth terms:
##                             edf Ref.df    Chi.sq  p-value
## s(NormFeatureDistance)  2.99978      3 3.674e+02  < 2e-16 ***
## s(Age)                  0.04248      3 4.889e+03   0.9993
## s(Set)                 52.70122     66 7.617e+07   0.0244 *
## s(Source)              11.95629     12 1.658e+07 6.75e-05 ***
## s(EngForm2)            69.37364    128 2.384e+07   0.1411
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.711   Deviance explained = 69.1%
## UBRE = 16.565  Scale est. = 1         n = 1173
```

```
plot.gam(mGAM,
         ylab="Relative Norse Freq",
         xlab="Distance between forms",
         select = 1)
```



Linear: beta = -32.43, z = -18.2, Wald $p < 0.001$, LLDiff = 102.6, df = 1, $p < 0.001$; Quadratic: beta = 77.441, z = 17.015, Wald $p < 0.001$, LLDiff = 23.2, df = 1, $p < 0.001$; Cubic: beta = -51.691, z = -16.373, Wald $p < 0.001$, LLDiff = 138.1, df = 1, $p < 0.001$

6.3 Historical distance

Same analysis as the simple distance above:

```
m0 = glmer(cbind(NFreq,EFreq) ~ Age + Alliteration +
             (1|Set) + (1|Source) +
             (1|EngForm2),
           data = d2, family = "binomial",
           control=glmerControl(optimizer="bobyqa"))
m1 = update(m0,~.+NormHistoricalDistance)
m2 = update(m1,~.+I(NormHistoricalDistance^2),
            control=glmerControl(optimizer="bobyqa"))
m3 = update(m2,~.+I(NormHistoricalDistance^3),
            control=glmerControl(optimizer="bobyqa"))
anova(m0,m1,m2,m3)
```

```
## Data: d2
## Models:
## m0: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2)
## m1: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormHi
## m2: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormHi
## m3: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) + (1 | EngForm2) + NormHi
##    npar   AIC   BIC logLik deviance    Chisq Df Pr(>Chisq)
## m0    8 21104 21145 -10544    21088
## m1    9 20904 20949 -10443    20886 202.5263  1  < 2.2e-16 ***
## m2   10 20901 20952 -10441    20881   4.5342  1    0.03322 *
## m3   11 20879 20935 -10429    20857  23.9212  1  1.004e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

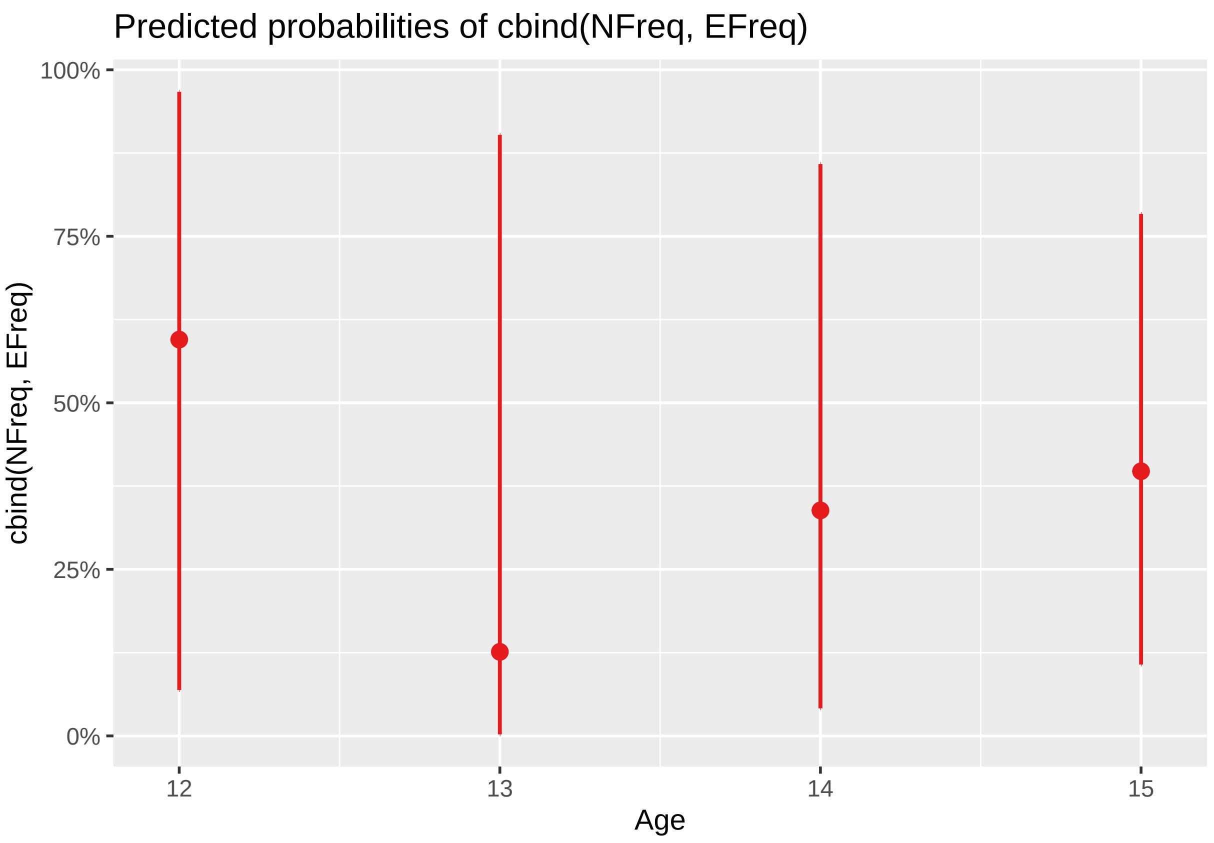
For this measure, the cubic term is marginal.

This is the cubic model:

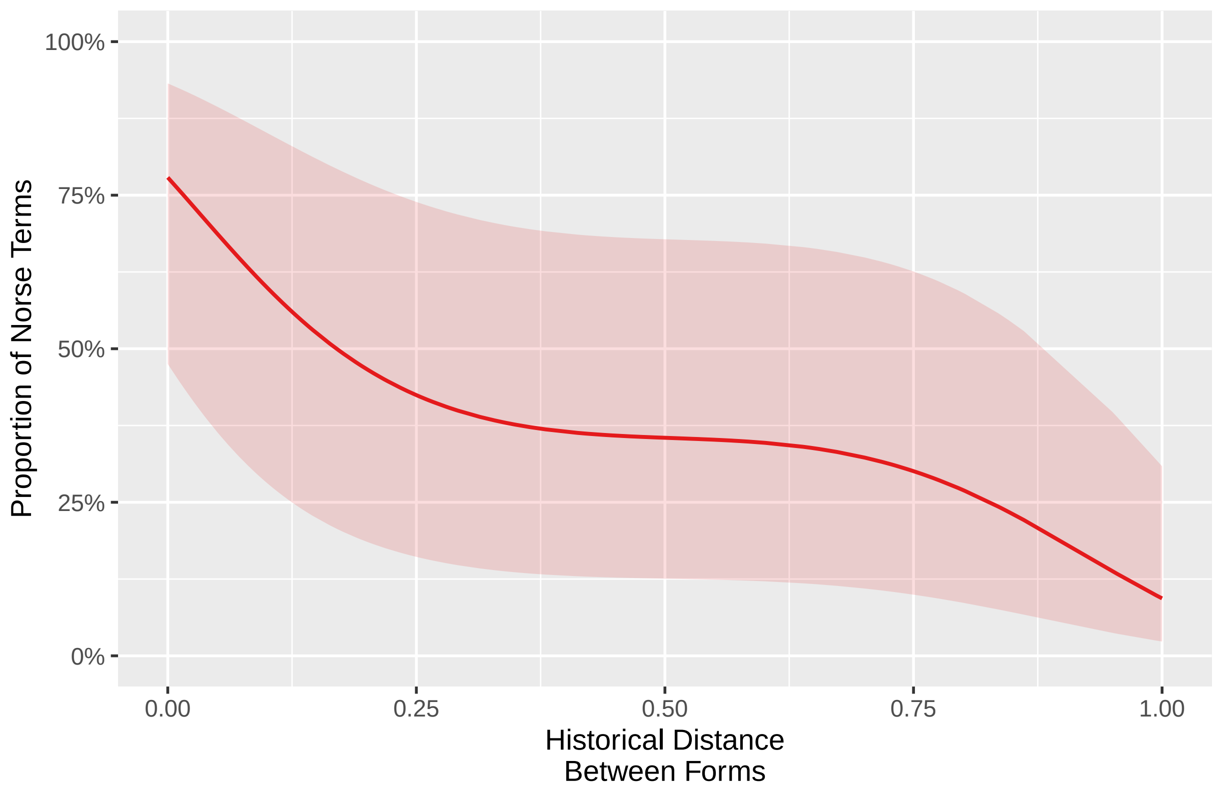
```
summary(m3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) +
##     (1 | EngForm2) + NormHistoricalDistance + I(NormHistoricalDistance^2) +
##     I(NormHistoricalDistance^3)
##    Data: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##  20879.2  20934.9 -10428.6  20857.2     1162
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -110.625   -1.325    0.118    1.129  171.595
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  EngForm2 (Intercept) 4.065    2.016
##  Set      (Intercept) 5.239    2.289
##  Source   (Intercept) 4.425    2.104
## Number of obs: 1173, groups:  EngForm2, 129; Set, 67; Source, 13
##
## Fixed effects:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  0.92307    0.82206   1.123    0.261
## Age1                         1.04395    1.28208   0.814    0.415
## Age2                        -1.27604    1.65242  -0.772    0.440
## Age3                        -0.01052    1.13003  -0.009    0.993
## AlliterationTRUE             2.24683    0.07204  31.190  < 2e-16 ***
## NormHistoricalDistance     -10.42926    1.41162  -7.388 1.49e-13 ***
## I(NormHistoricalDistance^2)  19.96760    3.64632   5.476 4.35e-08 ***
## I(NormHistoricalDistance^3) -13.06820    2.52493  -5.176 2.27e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Age1   Age2   Age3   AlTRUE NrmHsD I(NHD^2
## Age1         0.008
## Age2         0.407 -0.519
## Age3        -0.189 -0.260 -0.492
## AlltrtnTRUE -0.014  0.015 -0.010  0.000
## NrmHstrclDs -0.128  0.003 -0.001 -0.002 -0.025
## I(NrmHsD^2)  0.114 -0.003  0.001  0.002  0.031 -0.976
## I(NrmHsD^3) -0.104  0.002  0.000 -0.002 -0.040  0.929 -0.984
```

```
plot_model(m3,'eff', terms="Age [all]")
```



```
pNormHist =
  plot_model(m3,'eff', terms="NormHistoricalDistance[all]")+
    xlab("Historical Distance\nBetween Forms") +
    ylab("Proportion of Norse Terms") +
    ggtitle("")+
    coord_cartesian(ylim=c(0,1))
pNormHist
```

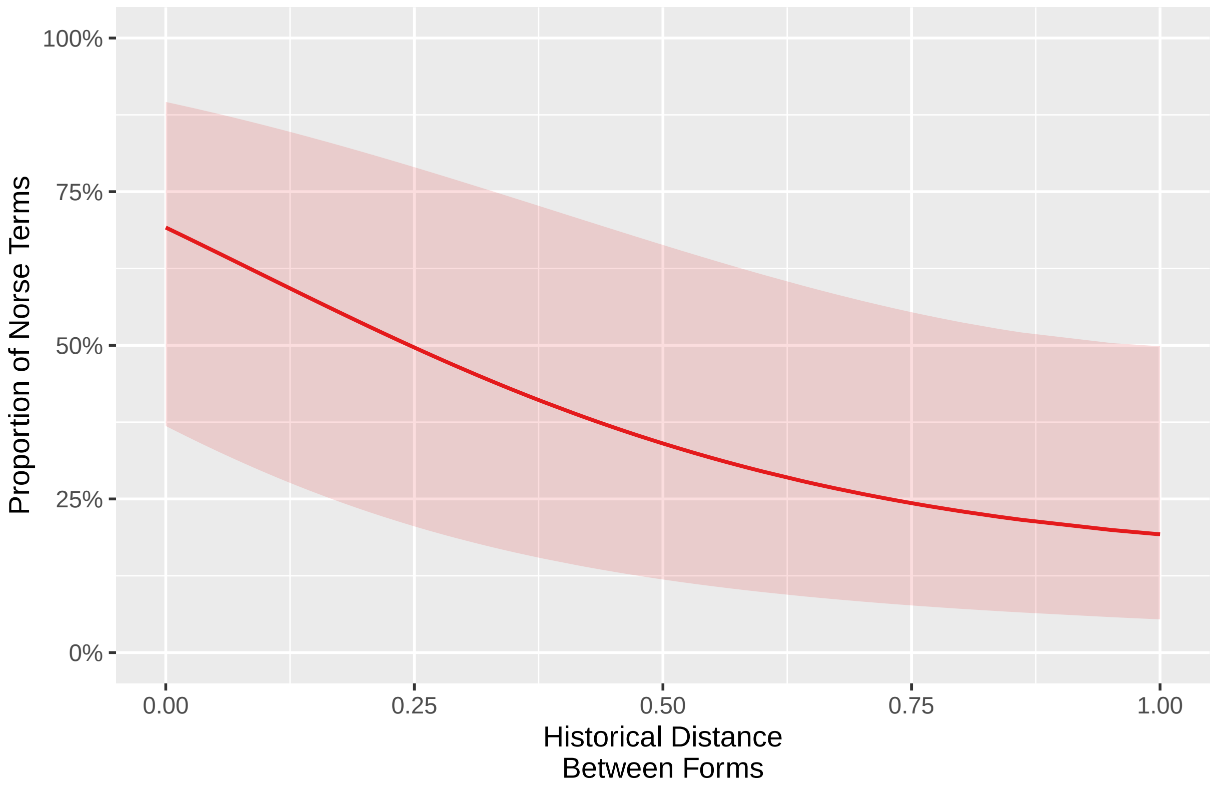


And for comparison, the quadratic model:

```
summary(m2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(NFreq, EFreq) ~ Age + Alliteration + (1 | Set) + (1 | Source) +
##     (1 | EngForm2) + NormHistoricalDistance + I(NormHistoricalDistance^2)
##    Data: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##  20901.1  20951.8 -10440.6  20881.1     1163
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -110.404   -1.347    0.116    1.150  171.447
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  EngForm2 (Intercept) 4.043    2.011
##  Set      (Intercept) 5.192    2.279
##  Source   (Intercept) 4.413    2.101
## Number of obs: 1173, groups:  EngForm2, 129; Set, 67; Source, 13
##
## Fixed effects:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   0.47469    0.81655   0.581   0.5610
## Age1                          1.03689    1.28216   0.809   0.4187
## Age2                         -1.26463    1.65211  -0.765   0.4440
## Age3                         -0.01151    1.12830  -0.010   0.9919
## AlliterationTRUE              2.23317    0.07193  31.047  < 2e-16 ***
## NormHistoricalDistance       -3.63796    0.52262  -6.961 3.38e-12 ***
## I(NormHistoricalDistance^2)  1.39642    0.65371   2.136   0.0327 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Age1   Age2   Age3   AlTRUE NrmHsD
## Age1         0.007
## Age2         0.410 -0.520
## Age3        -0.190 -0.259 -0.491
## AlltrtnTRUE -0.019  0.015 -0.010  0.000
## NrmHstrclDs -0.086  0.000 -0.001  0.000  0.037
## I(NrmHsD^2)  0.065 -0.001  0.001 -0.001 -0.053 -0.931
```

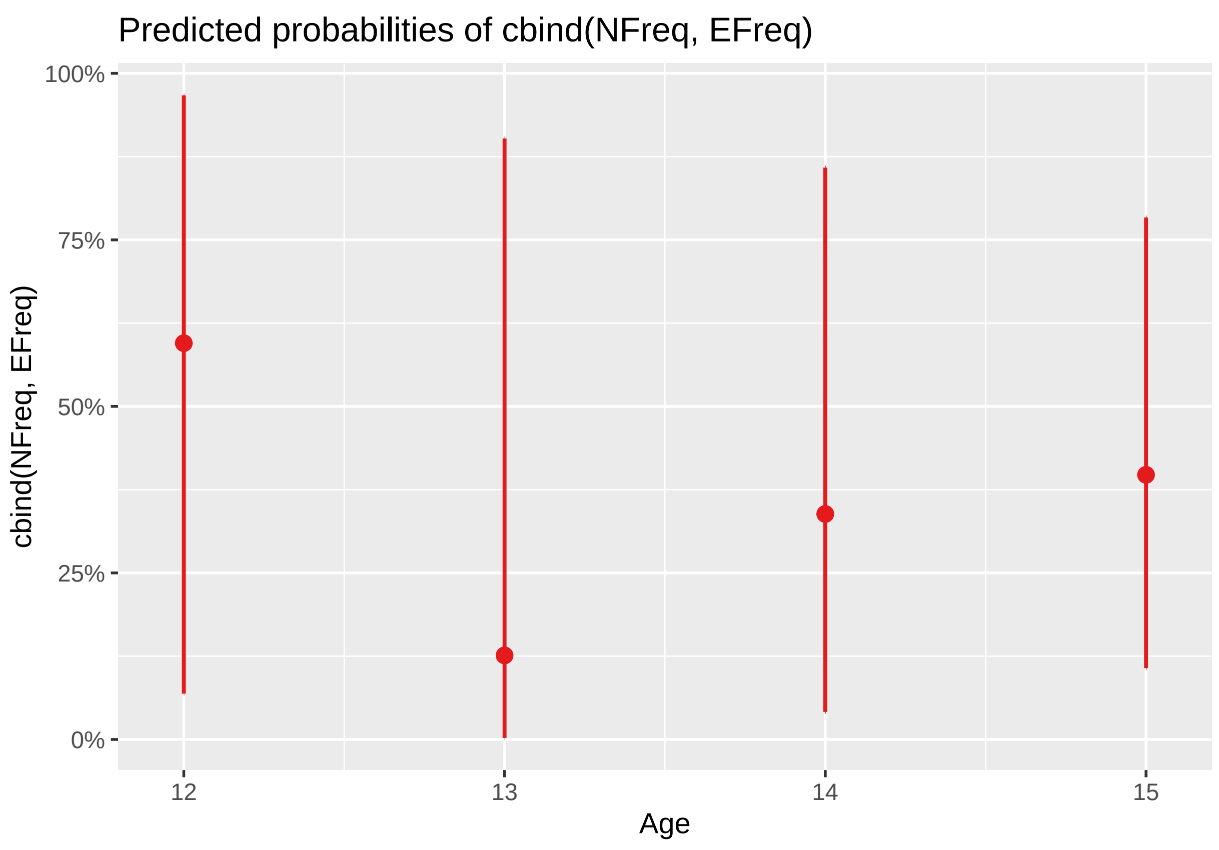
```
  plot_model(m2,'eff', terms="NormHistoricalDistance[all]")+
    xlab("Historical Distance\nBetween Forms") +
    ylab("Proportion of Norse Terms") +
    ggtitle("")+
    coord_cartesian(ylim=c(0,1))
```



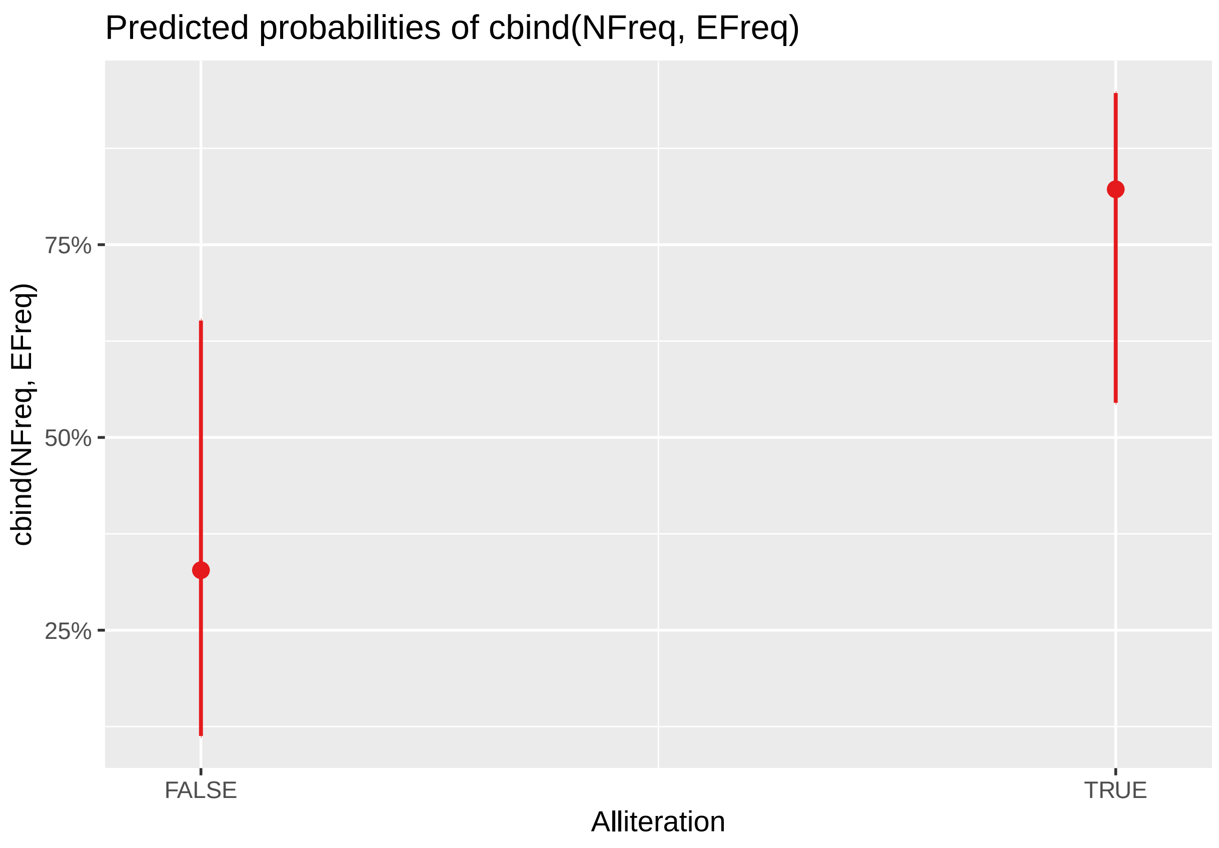
There is little qualitative difference, so for sake of easy comparison with the other results, we use the cubic model.

Effects over time and of alliteration:

```
plot_model(m3,'eff', terms="Age [all]")
```



```
plot_model(m3,'eff', terms="Alliteration")
```

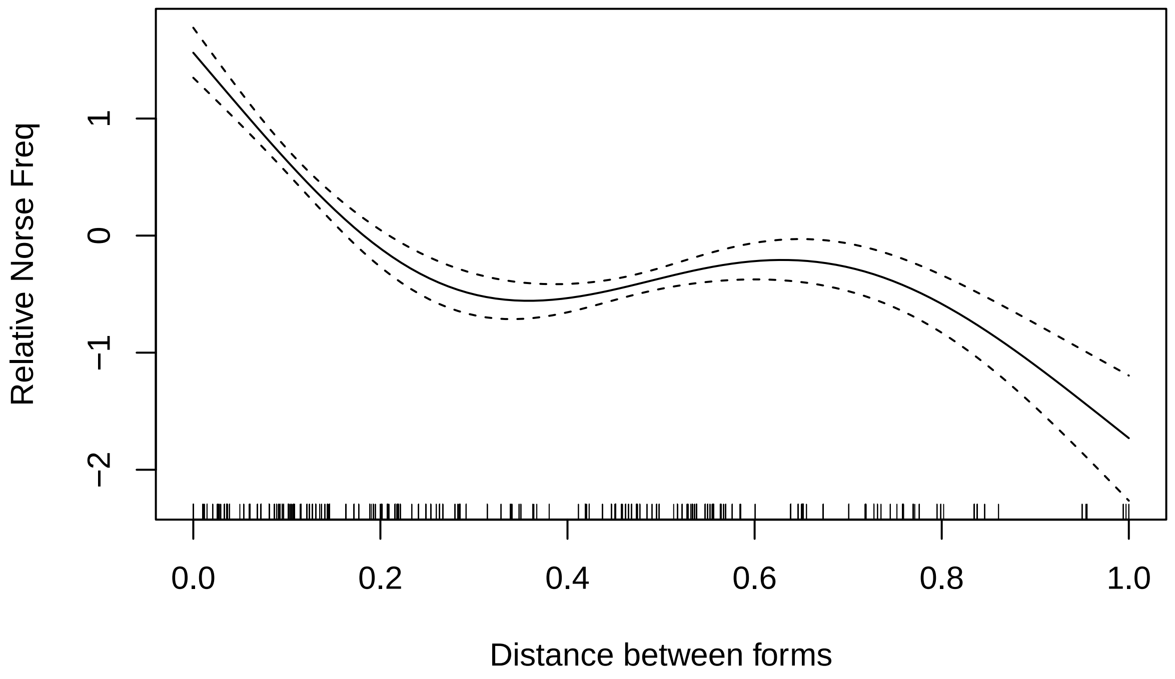


GAM model:

```
mGAM = gam(cbind(NFreq,EFreq) ~ Alliteration +
             s(NormHistoricalDistance,k=4) +
             s(Age,bs = "re") +
             s(Set,bs="re") +
             s(Source,bs="re")+
             s(EngForm2,bs="re"),
           data = d2, family = "binomial")
summary(mGAM)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(NFreq, EFreq) ~ Alliteration + s(NormHistoricalDistance,
##     k = 4) + s(Age, bs = "re") + s(Set, bs = "re") + s(Source,
##     bs = "re") + s(EngForm2, bs = "re")
##
## Parametric coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -0.35137    2.38755  -0.147    0.883
## AlliterationTRUE  2.24532    0.07209  31.144   <2e-16 ***
## ---
## 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(NormHistoricalDistance)  2.995951      3 2.472e+02  < 2e-16 ***
## s(Age)                     0.001067      3 1.164e+00 0.999276
## s(Set)                    47.845260     66 6.216e+07 0.000642 ***
## s(Source)                 11.996842     12 1.098e+07  < 2e-16 ***
## s(EngForm2)               72.914960    128 2.487e+07 0.001719 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.726   Deviance explained = 70.3%
## UBRE = 15.903  Scale est. = 1         n = 1173
```

```
plot.gam(mGAM,
         ylab="Relative Norse Freq",
         xlab="Distance between forms",
         select = 1)
```

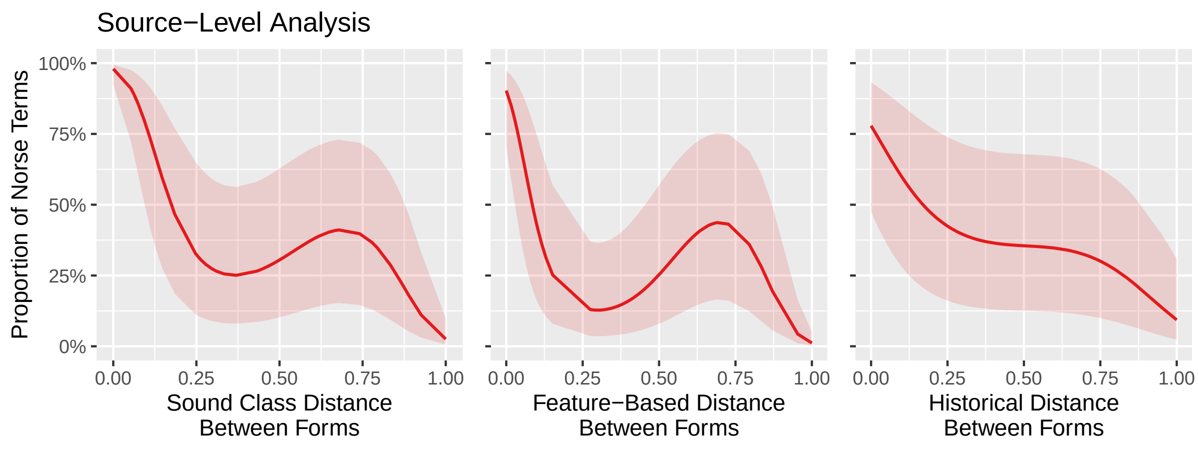


Linear: beta = -10.429, z = -7.388, Wald p < 0.001, LLDiff = 101.3, df = 1, p < 0.001; Quadratic: beta = 19.968, z = 5.476, Wald p < 0.001, LLDiff = 2.3, df = 1, p = 0.033; Cubic: beta = -13.068, z = -5.176, Wald p < 0.001, LLDiff = 12, df = 1, p < 0.001

```
bigPlot = grid.arrange(
       pNormSimple +
          ggtitle("Source-Level Analysis"),
       pNormFeature+
         ggtitle("") +
         theme(axis.title.y=element_blank(),
               axis.text.y=element_blank()),
       pNormHist+
         ggtitle("") +
         theme(axis.title.y=element_blank(),
               axis.text.y=element_blank()),
       nrow=1,widths=c(1.3,1,1))
```

```
pdf("../results/BigEffectsPlot.pdf",width = 8,height=3)
  plot(bigPlot)
dev.off()
```

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



```
tSimple = read.csv("../results/SimpleRes_totalFreq.csv",
                   stringsAsFactors = F)
tFeature = read.csv("../results/FeatureRes_totalFreq.csv",
                    stringsAsFactors = F)
tHistorical = read.csv("../results/HistoricalRes_totalFreq.csv",
                       stringsAsFactors = F)
sSimple = read.csv("../results/SimpleRes.csv",
                   stringsAsFactors = F)
sFeature = read.csv("../results/FeatureRes.csv",
                    stringsAsFactors = F)
sHistorical = read.csv("../results/HistoricalRes.csv",
                       stringsAsFactors = F)

res = rbind(tSimple,tFeature,tHistorical)
resNames = c(lldiff="Log Likelihood Difference",
             Chisq="Chi Squared",pChi="p")
resNames2 = names(res)
resNames2[resNames2 %in% names(resNames)] =
  resNames[resNames2[resNames2 %in% names(resNames)]]

res = res[,names(res)!="X"]
res = cbind(Measure=rep(c("Sound Class","Feature","Historical"),each=3), res)
res = rbind(c("","","Model Comparison","","","","",
              "Model Estimate","",""),
            resNames2,
            res)

write.table(res,file="../results/MainResults_totalFreq.csv",
            sep = ",",col.names = F,row.names = F,fileEncoding = "UTF-8")


res2 = res
res2[3:11,] = rbind(sSimple,sFeature,sHistorical)

write.table(res2,file="../results/MainResults_sourceLevel.csv",
            sep = ",",col.names = F,row.names = F,fileEncoding = "UTF-8")
```

7 Comparison between texts

Compare sources according to the difference in proportion of Norse terms for each set.

```r
g = read.xlsx("../data/SharedIntegrationOfCognatesData.xlsx",1)
g = g[g$Etymology %in% c("Norse","English"),]
# Ignore numerals in set name
g$Set = gsub("[0-9]","",g$Set)

nCols = names(g)[which(names(g)=="No..in.Ormulum"):which(names(g)=="Rolle")]
for(col in nCols){
  g[,col] = as.numeric(g[,col])
}
```

```
## Warning: NAs introduced by coercion

## Warning: NAs introduced by coercion

## Warning: NAs introduced by coercion
```

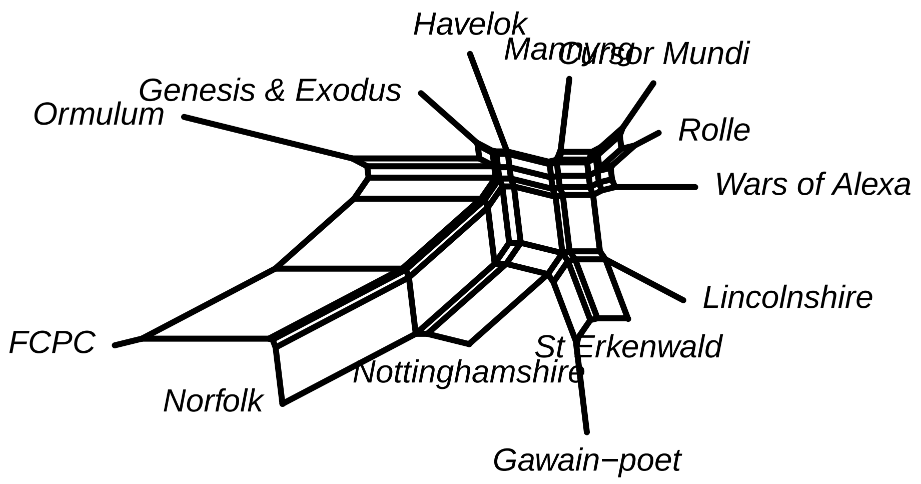
```r
allSets = unique(g$Set)
f = data.frame(Set = allSets)
fLog = data.frame(Set = allSets)
for(col in nCols){
  gN = g[g$Etymology == "Norse",]
  gE = g[g$Etymology == "English",]
  fNorse = tapply(gN[,col],gN$Set,sum)[allSets]
  fNorse[is.na(fNorse)] = 0
  fEng = tapply(gE[,col],gE$Set,sum)[allSets]
  fEng[is.na(fEng)] = 0
  f[,col] = fNorse / (fEng+fNorse)
  fLog[,col] = log10(1+fEng) - log10(1+fNorse)
}

nColsLabels = c("Ormulum","FCPC","Havelok","Genesis & Exodus",
                "Mannyng", "Gawain-poet","Wars of Alexander",
                "St Erkenwald","Cursor Mundi","Lincolnshire",
                "Nottinghamshire", "Norfolk","Rolle")

mat = matrix(NA,nrow=length(nCols),
             ncol = length(nCols))
rownames(mat) = nColsLabels
colnames(mat) = nColsLabels
matLog = matrix(NA,nrow=length(nCols),
                ncol = length(nCols))
rownames(matLog) = nColsLabels
colnames(matLog) = nColsLabels
for(i in 1:length(nCols)){
  iProp = f[,nCols[i]]
  iPropLog = fLog[,nCols[i]]
  for(j in 1:length(nCols)){
    jProp = f[,nCols[j]]
    jPropLog = fLog[,nCols[j]]

    diffs = abs(iProp-jProp)
    diffs = diffs[!is.nan(diffs)]
    diffs = diffs[!is.na(diffs)]
    mat[nColsLabels[i],nColsLabels[j]] = mean(diffs)
    diffsLog = abs(iPropLog - jPropLog)
    matLog[nColsLabels[i],nColsLabels[j]] = mean(diffsLog)
  }
}
```

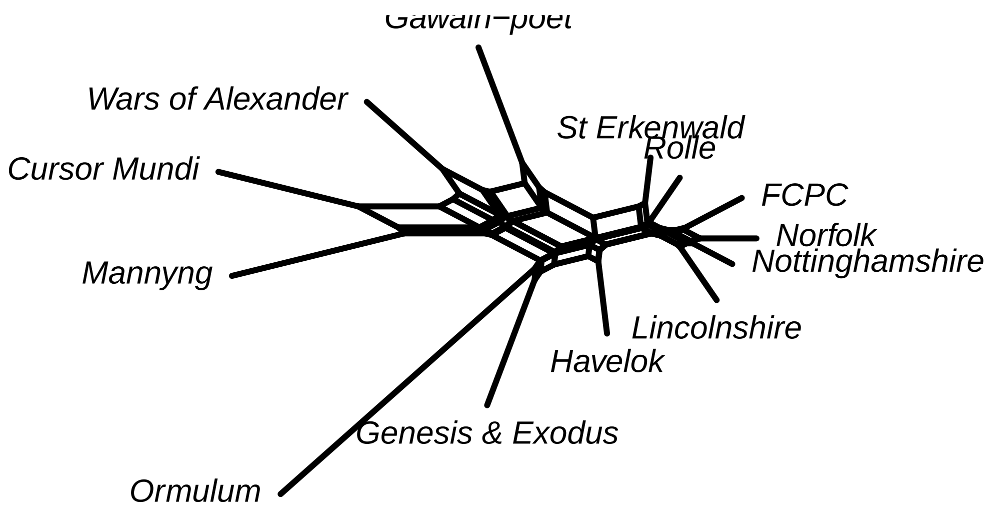
```
phy = neighborNet(mat)
plot(phy)
```



```
pdf("../results/NeighbourNet.pdf")
plot(phy)
dev.off()
```

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

```
phyLog = neighborNet(matLog)
plot(phyLog)
```



```
pdf("../results/NeighbourNet_Log.pdf")
plot(phyLog)
dev.off()
```

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