

A case for systematic sound symbolism in pragmatics: Supporting information

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Introduction

This is an analysis of an experiment into whether people can predict if an upcoming turn is a question or a statement, based on the previous turn type and the first phoneme of the target turn.

Participants listened to a series of audio samples. Each audio sample was made up of a *context* by speaker 1 (Statement or Initiating turn) and a *response* by speaker 2. The response was either no audio, a single segment [w] or a single segment other than [w].

Load libraries

```
library(lme4)
library(lattice)
library(gplots)
library(ggplot2)
library(sjPlot)
library(party)
library(Rmisc)
library(dplyr)
```

```
library("lme4")
library("optimx")
#library("nloptr")
```

Function for converting from logit scale

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

Load data

```
d = read.csv("../Data/Lab_Processed.csv")
```

Each row in the data is a single response from a participant to a single sample. The key variables are:

- *partID*: identifies participants
- *contextSample*: The name of the audio sample used for the context.
- *responseSample*: The name of the audio sample used for the response.
- *responsePhoneme*: The first segment of the response.
- *responseType*: Whether the first segment of the response came from a question or statement.
- *answer*: The participant's response to "Is the next turn a question?"

Make *answer* a binary variable.

```
d$answer = d$answer=="Yes"
d$lastAnswer = d$lastAnswer=="Yes"
```

Relevel response phoneme and context.

```
d$responsePhoneme = relevel(d$responsePhoneme, 'wh')
d$context = relevel(d$context, 'ST')
```

Center trial number, so that the intercept will reflect probabilities in the middle of the experiment.

```
d$trialNumber.center = d$trialNumber - 25
# Scale between -1 and 1
d$trialNumber.center = d$trialNumber.center /
  max(d$trialNumber.center)
```

Data exclusion

We exclude participant 13 because they took much longer than other participants.

```
d = d[as.character(d$partID)!="13",]
```

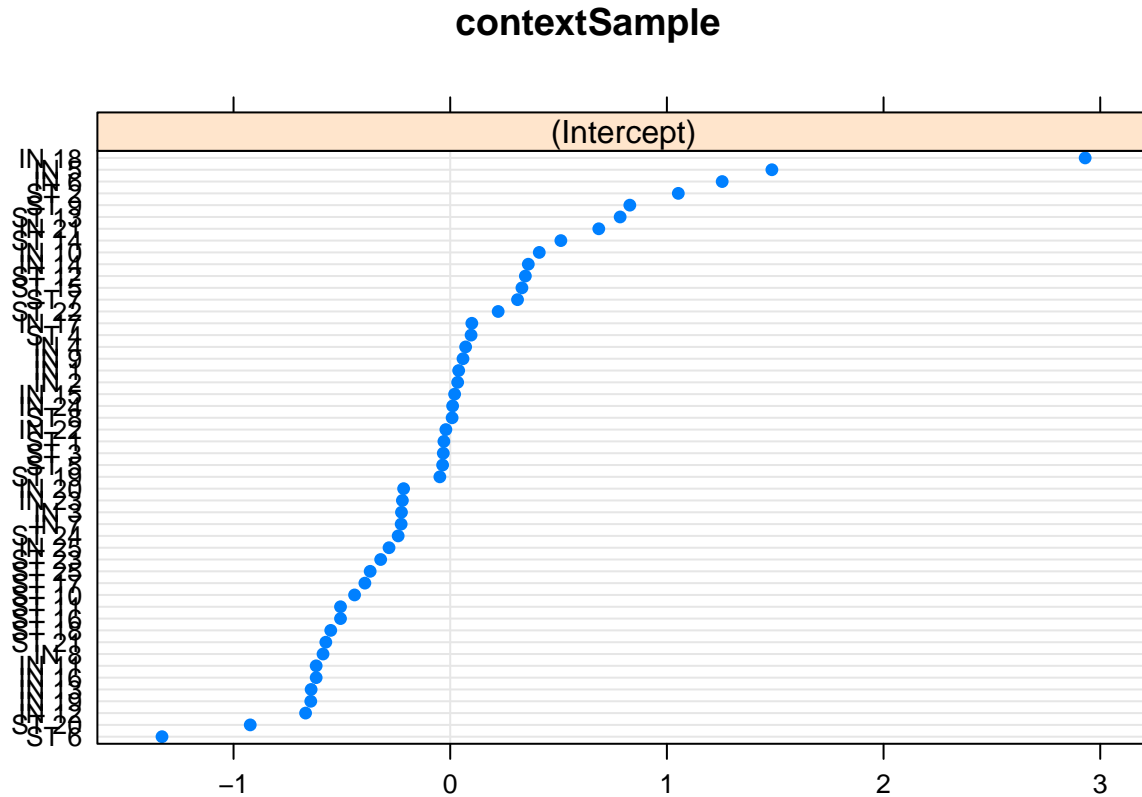
Are there any samples that look like outliers? Make a basic model:

```
m3 = glmer(
  answer ~ 1 + context + responsePhoneme +
    (1 | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
```

```
control = glmerControl(optimizer="bobyqa", optCtrl = list(maxfun=2e4))
)
```

Then look at the random effects.

```
dotplot(ranef(m3))[[2]]
```



The sample “IN 18” is an outlier. However, models have convergence problems when leaving it out.

The data has 1200 observations:

```
# Number of observations per participant
table(d$partID)
```

```
##
##  1  2  3  4  5  6  7  8  9 10 11 12 14 15 16 17 18 19 20 21 22 23 24 25
## 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50
```

```
table(d$context, d$responsePhoneme )
```

```
##
##      wh none other
## ST 240  120   240
## IN 240  120   240
```

Effects of block and trial

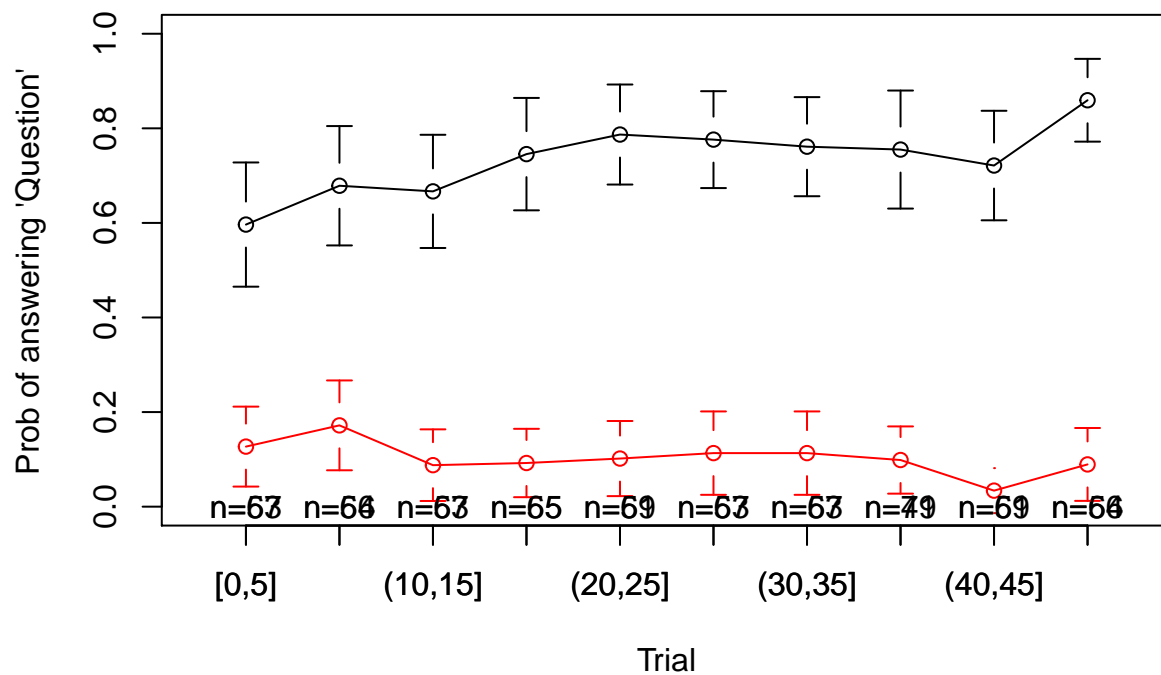
```
plotmeans(answer ~ cut(trialNumber,seq(0,50,length.out = 11), include.lowest = T),
  ylab = "Prob of answering 'Question'",
  xlab = 'Trial',
  data = d[d$context=="ST",],ylim=c(0,1),
  col = 1, barcol = 1)
plotmeans(answer ~ cut(trialNumber,seq(0,50,length.out = 11), include.lowest = T),
  ylab = "Prob of answering 'Question'",
  xlab = 'Trial',
  data = d[d$context=="IN",],ylim=c(0,1),
  col = 2, barcol = 2, add=T)
```

```
## Warning in arrows(x, li, x, pmax(y - gap, li), col = barcol, lwd = lwd, :
## zero-length arrow is of indeterminate angle and so skipped

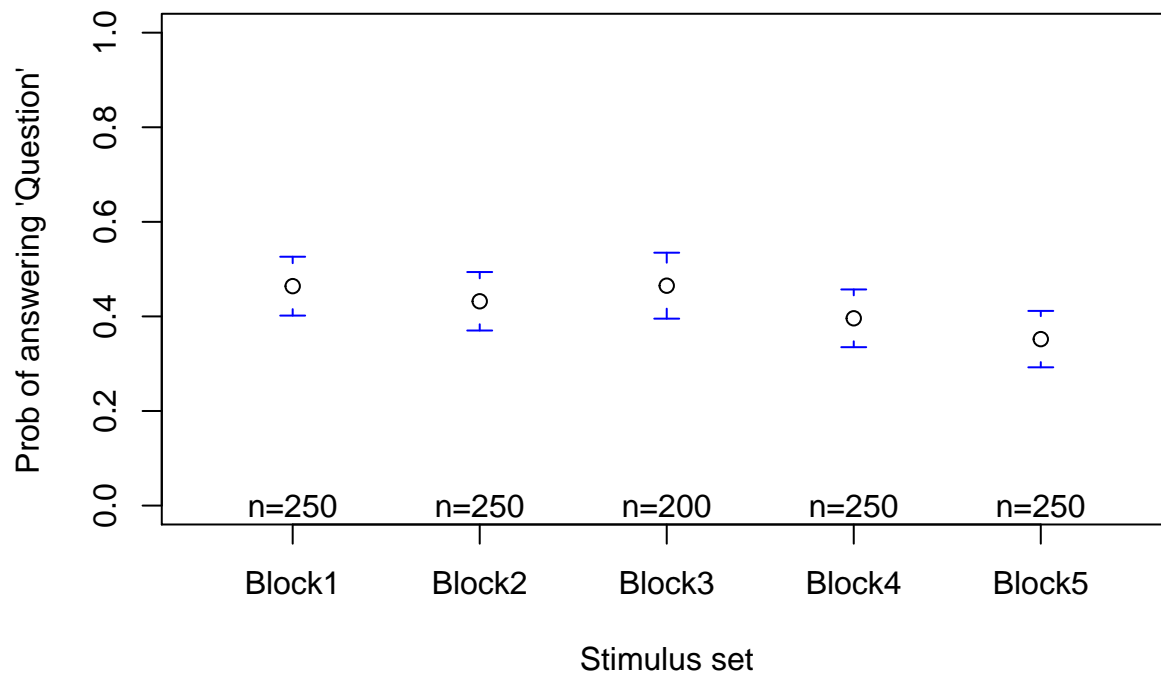
## Warning in arrows(x, ui, x, pmin(y + gap, ui), col = barcol, lwd = lwd, :
## zero-length arrow is of indeterminate angle and so skipped

## Warning in axis(1, at = 1:length(means), labels = legends, ...): "add" is
## not a graphical parameter

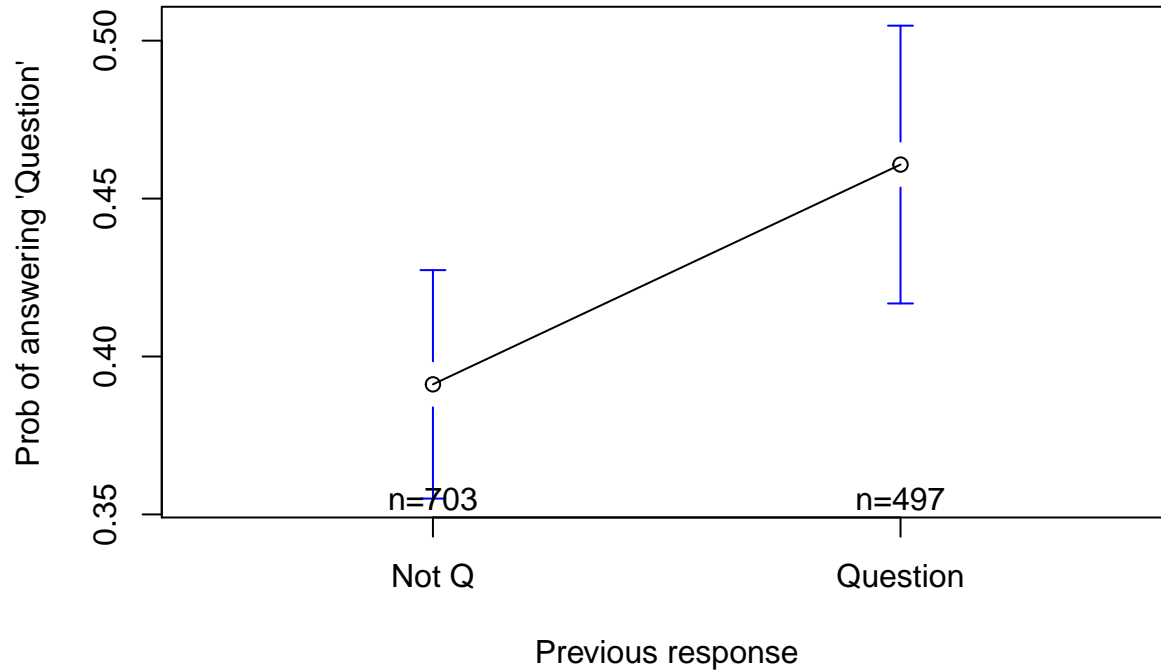
## Warning in plot.xy(xy.coords(x, y), type = type, ...): "add" is not a
## graphical parameter
```



```
plotmeans(d$answer ~ d$blockName,
  ylab = "Prob of answering 'Question'",
  xlab = 'Stimulus set',
  connect=F,
  ylim=c(0,1))
```



```
plotmeans(answer ~ lastAnswer,
  ylab = "Prob of answering 'Question'",
  xlab = "Previous response",
  legends = c("Not Q", "Question"),
  data = d)
```

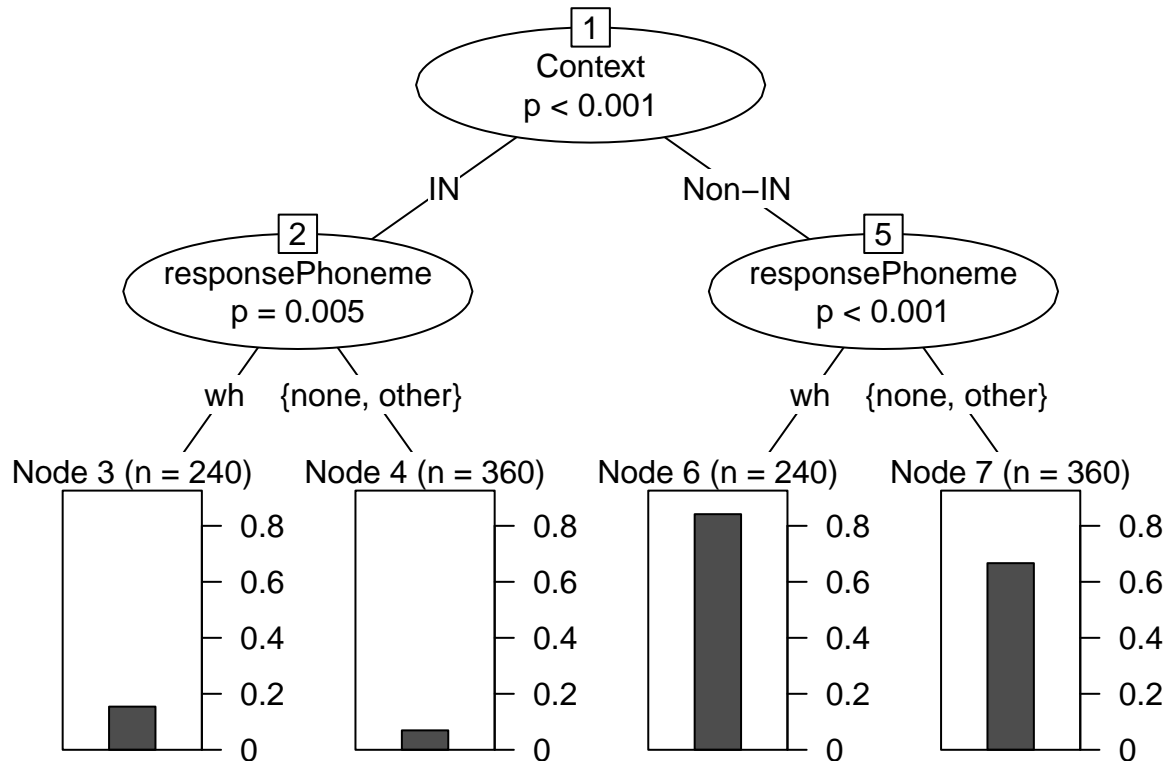


Decision tree

In order to get an idea of the structure of the data, we make a binary decision tree based on the data. We try to predict the participant's response by context and the type of turn the response was taken from.

```
d$Context = factor(d$context, labels = c("Non-IN", "IN"))

cx.simple = ctree(answer ~
  Context +
  responsePhoneme + responseType, data = d)
plot(cx.simple, terminal_panel=node_barplot(cx.simple))
```

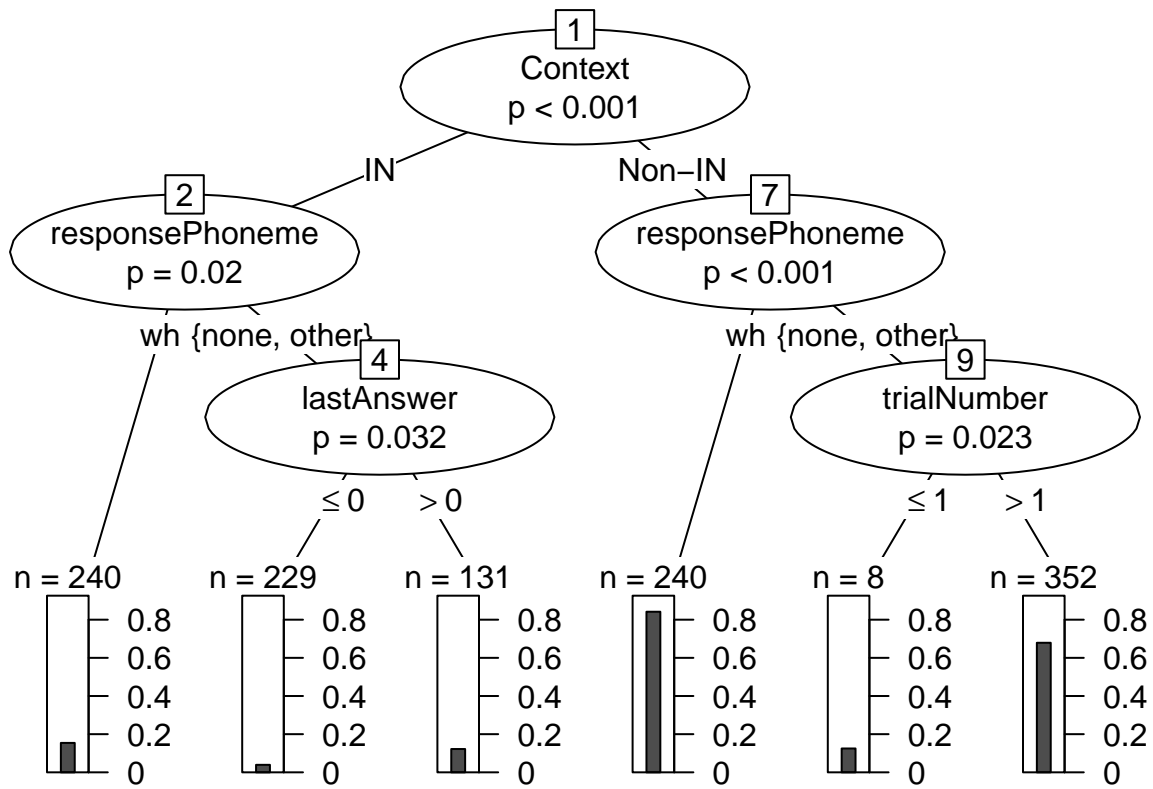


And here is a more detailed analysis:

```
cx = ctree(answer ~
  Context + responsePhoneme + responseType +
  Age + Sex + EnglishType +
  response.sex + context.sex +
  trialNumber + lastAnswer +
  blockName,
  data = d,
  controls = ctree_control(mincriterion = 0.95))
```

Plot the decision tree:

```
plot(cx, terminal_panel=node_barplot(cx, id=F))
```



Context is the most important factor, followed by first phoneme of the response.

Mixed effects models

Make a series of mixed effects models. We can fix this using the “nlminb” optimiser for both phases of the convergence and letting the algorithm run longer:

```
nlminbw <- lme4::nlminbwrap
gcontrol = glmerControl(optimizer="nlminbw",optCtrl = list(maxfun=2e4))
```

(Note that several convergence algorithms were tested, and the three best fitting solutions had essentially no differences in fixed effect estimates)

Random effects structure

We have a good idea of what the random effects structure should be, but first we check whether there are significant differences by participant etc.

```
mA0 = glmer(
  answer ~ 1 +
    (1 | partID),
  data = d,
  family = binomial,
  control = glmerControl(optimizer='bobyqa',optCtrl=list(maxfun=2e4))
)

mA0b = glmer(
  answer ~ 1 +
    (1 | blockName/partID) ,
  data = d,
  family = binomial,
  control = glmerControl(optimizer='bobyqa',optCtrl=list(maxfun=2e4))
)

ltrf = anova(mA0,mA0b)
ltrf
```

```
## Data: d
## Models:
## mA0: answer ~ 1 + (1 | partID)
## mA0b: answer ~ 1 + (1 | blockName/partID)
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mA0   2 1636.7 1646.9 -816.35  1632.7
## mA0b  3 1637.6 1652.8 -815.78  1631.6 1.1313    1    0.2875
```

There is no significant improvement in the model when taking stimulus set into account. Because it complicates the analysis, we'll leave it out.

```
## Mixed effect models summary
##
## ../results/lmerTests/lmerTestSummary.txt
```

```
mA1 = glmer(
  answer ~ 1 +
    (1 | partID) +
    (1 | contextSample),
  data = d,
  family = binomial,
```



```

    control = gcontrol
  )

mA2 = glmer(
  answer ~ 1 +
    (1 | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

mA3 = glmer(
  answer ~ 1 +
    (1 + context | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

mA4 = glmer(
  answer ~ 1 +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

ltrf2 = anova(mA0, mA1, mA2, mA3, mA4)
ltrf2

## Data: d
## Models:
## mA0: answer ~ 1 + (1 | partID)
## mA1: answer ~ 1 + (1 | partID) + (1 | contextSample)
## mA2: answer ~ 1 + (1 | partID) + (1 | contextSample) + (1 | responseSample)
## mA3: answer ~ 1 + (1 + context | partID) + (1 | contextSample) + (1 |
## mA3: responseSample)
## mA4: answer ~ 1 + (1 + context + responsePhoneme | partID) + (1 |
## mA4: contextSample) + (1 | responseSample)
##      Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## mA0  2 1636.7 1646.9 -816.35  1632.7
## mA1  3 1116.4 1131.7 -555.21  1110.4 522.281      1 < 2.2e-16 ***
## mA2  4 1094.7 1115.1 -543.37  1086.7 23.682      1 1.136e-06 ***
## mA3  6 1059.5 1090.0 -523.76  1047.5 39.222      2 3.041e-09 ***
## mA4 13 1054.1 1120.3 -514.06  1028.1 19.393      7 0.007041 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

All proposed random effects significantly improve the fit of the model, except for the random slope for responsePhoneme by participant.

Fixed effects

We are most interested in the effects of context and response type, but we need to check some other possible confounding variables.

Trial

```
m0 = glmer(
  answer ~ 1 +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)

trial = glmer(
  answer ~ 1 + trialNumber.center +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

trialQ = glmer(
  answer ~ 1 + trialNumber.center + I(trialNumber.center^2) +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

lttr = anova(m0,trial, trialQ)
lttr

## Data: d
## Models:
## m0: answer ~ 1 + (1 + context + responsePhoneme | partID) + (1 |
## m0: contextSample) + (1 | responseSample)
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial: partID) + (1 | contextSample) + (1 | responseSample)
## trialQ: answer ~ 1 + trialNumber.center + I(trialNumber.center^2) + (1 +
## trialQ: context + responsePhoneme | partID) + (1 | contextSample) +
## trialQ: (1 | responseSample)
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
```

```
## m0      13 1054.1 1120.3 -514.06 1028.1
## trial   14 1051.3 1122.6 -511.66 1023.3 4.796      1 0.02853 *
## trialQ  15 1052.5 1128.8 -511.23 1022.5 0.862      1 0.35318
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A significant effect of trial, but no significant quadratic term.

Previous answer

```
prevAns = glmer(
  answer ~ 1 + trialNumber.center + lastAnswer +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)
ltpa = anova(trial,prevAns)
ltpa

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## prevAns: answer ~ 1 + trialNumber.center + lastAnswer + (1 + context +
## prevAns:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trial      14 1051.3 1122.6 -511.66 1023.3
## prevAns    15 1051.6 1127.9 -510.80 1021.6 1.7284      1 0.1886
```

No significant effect of previous answer.

Sex of speakers in samples

```
contS = glmer(
  answer ~ 1 + trialNumber.center +
    context.sex +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)

respS = glmer(
  answer ~ 1 + trialNumber.center +
    context.sex + response.sex +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)
```

```

contXrespS = glmer(
  answer ~ 1 + trialNumber.center +
    context.sex * response.sex +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

ltsx = anova(trial, contS, respS, contXrespS)
ltsx

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## contS: answer ~ 1 + trialNumber.center + context.sex + (1 + context +
## contS:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## respS: answer ~ 1 + trialNumber.center + context.sex + response.sex +
## respS:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## respS:      (1 | responseSample)
## contXrespS: answer ~ 1 + trialNumber.center + context.sex * response.sex +
## contXrespS:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## contXrespS:      (1 | responseSample)
##
##           Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## trial      14 1051.3 1122.6 -511.66   1023.3
## contS      15 1051.8 1128.1 -510.90   1021.8 1.5291      1    0.2162
## respS      16 1053.8 1135.2 -510.89   1021.8 0.0194      1    0.8892
## contXrespS 17 1055.8 1142.3 -510.87   1021.8 0.0235      1    0.8783

```

No significant effects of the sex of the speakers in the samples.

Sex of participants

```

sex = glmer(
  answer ~ 1 + trialNumber.center + Sex +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)

ltsxp = anova(trial, sex)
ltsxp

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## sex: answer ~ 1 + trialNumber.center + Sex + (1 + context + responsePhoneme |

```

```
## sex:      partID) + (1 | contextSample) + (1 | responseSample)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trial 14 1051.3 1122.6 -511.66 1023.3
## sex    15 1053.3 1129.7 -511.65 1023.3 0.02      1      0.8874
```

No significant effect of the sex of the participant.

Age of participants

(doesn't converge with nlminb, so using bobyqa)

```
age = glmer(
  answer ~ 1 + trialNumber.center + Age +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = glmerControl(optimizer="bobyqa")
)
```

```
ltag = anova(trial,age)
ltag
```

```
## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## age: answer ~ 1 + trialNumber.center + Age + (1 + context + responsePhoneme |
## age:      partID) + (1 | contextSample) + (1 | responseSample)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trial 14 1051.3 1122.6 -511.66 1023.3
## age    15 1052.5 1128.9 -511.25 1022.5 0.8138      1      0.367
```

No significant effect of age of participant.

Type of English spoken

```
Etype = glmer(
  answer ~ 1 + trialNumber.center + EnglishType +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)
```

```
lten = anova(trial,Etype)
lten
```

```
## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## Etype: answer ~ 1 + trialNumber.center + EnglishType + (1 + context +
## Etype:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
```

```
## trial 14 1051.3 1122.6 -511.66 1023.3
## Etype 16 1053.2 1134.7 -510.61 1021.2 2.0944 2 0.3509
```

No significant effect of the type of English the participant speaks.

Effects of Context and Response

The only significant confounding variable is trial, so that forms the baseline.

```
context = glmer(
  answer ~ 1 + trialNumber.center +
    context +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)

rPhon = glmer(
  answer ~ 1 + trialNumber.center +
    context + responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

conXrPh = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

anova(trial, context, rPhon, conXrPh)

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## context: answer ~ 1 + trialNumber.center + context + (1 + context + responsePhoneme |
## context:      partID) + (1 | contextSample) + (1 | responseSample)
## rPhon: answer ~ 1 + trialNumber.center + context + responsePhoneme +
## rPhon:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## rPhon:      (1 | responseSample)
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
```

```
## conXrPh:      (1 | responseSample)
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## trial      14 1051.32 1122.6 -511.66  1023.32
## context    15 1007.58 1083.9 -488.79   977.58 45.742      1 1.349e-11 ***
## rPhon      17  997.75 1084.3 -481.88   963.75 13.828      2 0.0009938 ***
## conXrPh    19 1000.41 1097.1 -481.20   962.41  1.344      2 0.5106922
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction between Sex and responses

```
Sex = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    Sex +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)
```

```
SexXresp = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    Sex*responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)
```

```
SexXcon = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    Sex*responsePhoneme +
    Sex:context +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)
```

```
SxXcoXre = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    Sex*responsePhoneme*context +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
```

```

data = d,
family = binomial,
control = gcontrol
)

ltsxx = anova(conXrPh, Sex, SexXresp, SexXcon, SxXcoXre)
ltsxx

## Data: d
## Models:
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## conXrPh:      (1 | responseSample)
## Sex: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## Sex:      Sex + (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## Sex:      (1 | responseSample)
## SexXresp: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## SexXresp:      Sex * responsePhoneme + (1 + context + responsePhoneme |
## SexXresp:      partID) + (1 | contextSample) + (1 | responseSample)
## SexXcon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## SexXcon:      Sex * responsePhoneme + Sex:context + (1 + context + responsePhoneme |
## SexXcon:      partID) + (1 | contextSample) + (1 | responseSample)
## SxXcoXre: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## SxXcoXre:      Sex * responsePhoneme * context + (1 + context + responsePhoneme |
## SxXcoXre:      partID) + (1 | contextSample) + (1 | responseSample)
##           Df      AIC      BIC    logLik deviance  Chisq Chi Df Pr(>Chisq)
## conXrPh   19 1000.4 1097.1 -481.20   962.41
## Sex       20 1002.4 1104.2 -481.20   962.40 0.0049      1    0.9439
## SexXresp  22 1003.1 1115.1 -479.57   959.14 3.2639      2    0.1955
## SexXcon   23 1004.6 1121.7 -479.30   958.59 0.5471      1    0.4595
## SxXcoXre  25 1008.2 1135.5 -479.13   958.25 0.3400      2    0.8437

```

No effect by sex of participant.

Interaction with trial

```

trialXCon = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    trialNumber.center:context +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

trialXph = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    trialNumber.center:context +
    trialNumber.center:responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),

```



```

data = d,
family = binomial,
control = gcontrol
)

trXcoXph = glmer(
  answer ~ 1 + trialNumber.center *
    context * responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

lttrx = anova(conXrPh, trialXCon, trialXph, trXcoXph)
lttrx

## Data: d
## Models:
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## conXrPh:      (1 | responseSample)
## trialXCon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXCon:      trialNumber.center:context + (1 + context + responsePhoneme |
## trialXCon:      partID) + (1 | contextSample) + (1 | responseSample)
## trialXph: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXph:      trialNumber.center:context + trialNumber.center:responsePhoneme +
## trialXph:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## trialXph:      (1 | responseSample)
## trXcoXph: answer ~ 1 + trialNumber.center * context * responsePhoneme +
## trXcoXph:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## trXcoXph:      (1 | responseSample)
##
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## conXrPh  19 1000.41 1097.1 -481.20  962.41
## trialXCon 20  989.60 1091.4 -474.80  949.60 12.8092      1 0.0003449 ***
## trialXph  22  993.25 1105.2 -474.62  949.25  0.3540      2 0.8377824
## trXcoXph  24  996.63 1118.8 -474.32  948.63  0.6147      2 0.7353795
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Significant interaction between trial and context, but no reliable further interaction.

Effect of stimulus set

Below we adjust the random effects so that participants are nested within stimulus set (the variable *blockName*).

```
stimSet = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    trialNumber.center:context +
    (1 + context + responsePhoneme | blockName/partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)
```

```
anova(trialXCon, stimSet)
```

```
## Data: d
## Models:
## trialXCon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXCon:      trialNumber.center:context + (1 + context + responsePhoneme |
## trialXCon:      partID) + (1 | contextSample) + (1 | responseSample)
## stimSet: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## stimSet:      trialNumber.center:context + (1 + context + responsePhoneme |
## stimSet:      blockName/partID) + (1 | contextSample) + (1 | responseSample)
##           Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trialXCon 20  989.6 1091.4 -474.80   949.60
## stimSet   30 1002.3 1155.0 -471.16   942.32 7.2839   10    0.6984
```

There is no significant improvement in the model, and in any case the stimuli sets are counterbalanced experimentally, so we don't include it.

In any case, the qualitative results are the same, and the estimates are very similar, suggesting that stimulus set does not have an impact on the main findings.

```
cbind(without=fixef(trialXCon), withRForStimSet=fixef(stimSet))
```

	without	withRForStimSet
## (Intercept)	2.1405023	2.12652608
## trialNumber.center	0.7511443	0.77419202
## contextIN	-4.4088146	-4.37373392
## responsePhonemenone	-1.3028431	-1.27113955
## responsePhonemeother	-1.2297526	-1.21010008
## contextIN:responsePhonemenone	-0.4728529	-0.52928626
## contextIN:responsePhonemeother	0.2271069	0.03170117
## trialNumber.center:contextIN	-1.2321227	-1.25867272

Check /h/ phoneme samples

Only one stimuli set had a /h/ response phoneme, so we re-run the main analysis without those trials.

```
takeOutSet = d[d$response.first0=='h',]$setNum[1]
```

```
trialH = glmer(
  answer ~ 1 + trialNumber.center +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d[d$setNum != takeOutSet,],
  family = binomial,
  control = gcontrol
)
```

```
contextH = glmer(
  answer ~ 1 + trialNumber.center +
    context +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d[d$setNum != takeOutSet,],
  family = binomial,
  control = gcontrol
)
```

```
rPhonH = glmer(
  answer ~ 1 + trialNumber.center +
    context + responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d[d$setNum != takeOutSet,],
  family = binomial,
  control = gcontrol
)
```

```
conXrPhH = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    (1 + context + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d[d$setNum != takeOutSet,],
  family = binomial,
  control = gcontrol
)
```

```
trialXConH = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    trialNumber.center:context +
    (1 + context + responsePhoneme | partID) +
```

```

    (1 | contextSample) +
    (1 | responseSample),
  data = d[d$setNum != takeOutSet,],
  family = binomial,
  control = gcontrol
)

anova(trialH, contextH, rPhonH, conXrPhH, trialXConH)

## Data: d[d$setNum != takeOutSet, ]
## Models:
## trialH: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trialH:      partID) + (1 | contextSample) + (1 | responseSample)
## contextH: answer ~ 1 + trialNumber.center + context + (1 + context + responsePhoneme |
## contextH:      partID) + (1 | contextSample) + (1 | responseSample)
## rPhonH: answer ~ 1 + trialNumber.center + context + responsePhoneme +
## rPhonH:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## rPhonH:      (1 | responseSample)
## conXrPhH: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPhH:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## conXrPhH:      (1 | responseSample)
## trialXConH: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXConH:      trialNumber.center:context + (1 + context + responsePhoneme |
## trialXConH:      partID) + (1 | contextSample) + (1 | responseSample)
##
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## trialH      14 1022.03 1092.7 -497.02   994.03
## contextH     15  978.65 1054.4 -474.32   948.65 45.3814      1 1.622e-11
## rPhonH      17  969.63 1055.5 -467.82   935.63 13.0146      2 0.0014925
## conXrPhH    19  972.25 1068.2 -467.13   934.25  1.3801      2 0.5015480
## trialXConH  20  962.34 1063.3 -461.17   922.34 11.9158      1 0.0005566
##
## trialH
## contextH ***
## rPhonH **
## conXrPhH
## trialXConH ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
summary(trialXConH)$coef
```

```

##
##      Estimate Std. Error  z value
## (Intercept)      2.0887338  0.3635915  5.7447265
## trialNumber.center      0.7216970  0.2021668  3.5698089
## contextIN      -4.3725230  0.5135860 -8.5137119
## responsePhonemenone     -1.2261652  0.6124030 -2.0022194
## responsePhonemeother     -1.1943781  0.3375941 -3.5379117
## contextIN:responsePhonemenone    -0.4386208  0.6676415 -0.6569705
## contextIN:responsePhonemeother    0.2484692  0.4676457  0.5313193
## trialNumber.center:contextIN    -1.2000509  0.3534447 -3.3953006
##
##      Pr(>|z|)
## (Intercept)      9.206970e-09
## trialNumber.center      3.572417e-04
## contextIN      1.684522e-17

```

```
## responsePhonemenone      4.526114e-02
## responsePhonemeother     4.033049e-04
## contextIN:responsePhonemenone 5.111999e-01
## contextIN:responsePhonemeother 5.951976e-01
## trialNumber.center:contextIN 6.855328e-04
```

There are no qualitative differences when removing these trials.

Results

Model comparison

```
mainResults = anova(m0, trial, context, rPhon, conXrPh, trialXCon)
mainResults

## Data: d
## Models:
## m0: answer ~ 1 + (1 + context + responsePhoneme | partID) + (1 |
## m0:      contextSample) + (1 | responseSample)
## trial: answer ~ 1 + trialNumber.center + (1 + context + responsePhoneme |
## trial:      partID) + (1 | contextSample) + (1 | responseSample)
## context: answer ~ 1 + trialNumber.center + context + (1 + context + responsePhoneme |
## context:      partID) + (1 | contextSample) + (1 | responseSample)
## rPhon: answer ~ 1 + trialNumber.center + context + responsePhoneme +
## rPhon:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## rPhon:      (1 | responseSample)
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context + responsePhoneme | partID) + (1 | contextSample) +
## conXrPh:      (1 | responseSample)
## trialXCon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXCon:      trialNumber.center:context + (1 + context + responsePhoneme |
## trialXCon:      partID) + (1 | contextSample) + (1 | responseSample)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0      13 1054.12 1120.3 -514.06 1028.12
## trial    14 1051.32 1122.6 -511.66 1023.32  4.796      1 0.0285265 *
## context  15 1007.58 1083.9 -488.79  977.58 45.742      1 1.349e-11 ***
## rPhon    17  997.75 1084.3 -481.88  963.75 13.828      2 0.0009938 ***
## conXrPh  19 1000.41 1097.1 -481.20  962.41  1.344      2 0.5106922
## trialXCon 20  989.60 1091.4 -474.80  949.60 12.809      1 0.0003449 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effects

Model estimates:

```
finalModel = trialXCon
save(finalModel, file="../results/FinalModel.Rdat")
summary(finalModel)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialNumber.center:context + (1 + context + responsePhoneme |
## partID) + (1 | contextSample) + (1 | responseSample)
## Data: d
## Control: gcontrol
##
##      AIC      BIC   logLik deviance df.resid
##   989.6   1091.4   -474.8    949.6     1180
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.2698 -0.2894 -0.1330  0.4098  5.5016
##
## Random effects:
## Groups             Name                Variance Std.Dev. Corr
## responseSample (Intercept)            0.2651   0.5149
## contextSample  (Intercept)            1.0303   1.0150
## partID          (Intercept)            0.5637   0.7508
##                  contextIN             1.1434   1.0693   -0.67
##                  responsePhonemenone    0.4270   0.6535    0.34 -0.53
##                  responsePhonemeother  0.3828   0.6187   -0.45 -0.32  0.43
## Number of obs: 1200, groups:
## responseSample, 51; contextSample, 50; partID, 24
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.1405    0.3620   5.913 3.37e-09 ***
## trialNumber.center  0.7511    0.2008   3.740 0.000184 ***
## contextIN        -4.4088    0.5107  -8.632 < 2e-16 ***
## responsePhonemenone -1.3028    0.6326  -2.060 0.039440 *
## responsePhonemeother -1.2298    0.3389  -3.629 0.000285 ***
## contextIN:responsePhonemenone -0.4729    0.6773  -0.698 0.485085
## contextIN:responsePhonemeother  0.2271    0.4609   0.493 0.622169
## trialNumber.center:contextIN  -1.2321    0.3501  -3.519 0.000433 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) trlNm. cntxIN rspnsPhnmn rspnsPhnmt
## trlNmbr.cnt      0.107
## contextIN       -0.675 -0.093
## rspnsPhnmnn     -0.247 -0.027  0.128
## rspnsPhnmth     -0.593 -0.105  0.278  0.323
## cntxtIN:rspnsPhnmn 0.213  0.011 -0.279 -0.255   -0.221
```

```
## cntxtIN:rspnsPhnmt  0.264  0.045 -0.383 -0.150      -0.441
## trlNmbr.:IN        -0.071 -0.574  0.093  0.019      0.071
##                    cntxtIN:rspnsPhnmn cntxtIN:rspnsPhnmt
## trlNmbr.cnt
## contextIN
## rspnsPhnmnn
## rspnsPhnmth
## cntxtIN:rspnsPhnmn
## cntxtIN:rspnsPhnmt  0.333
## trlNmbr.:IN        0.012                0.033
```

Relevel the response phoneme to see other comparisons:

```
d2 = d
d2$responsePhoneme = relevel(d2$responsePhoneme,"other")
fm2 = update(finalModel, data=d2)
summary(fm2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: answer ~ 1 + trialNumber.center + context * responsePhoneme +
##          trialNumber.center:context + (1 + context + responsePhoneme |
##          partID) + (1 | contextSample) + (1 | responseSample)
## Data: d2
## Control: gcontrol
##
##          AIC          BIC    logLik deviance df.resid
##      989.6      1091.4    -474.8    949.6      1180
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.2698 -0.2894 -0.1330  0.4098  5.5015
##
## Random effects:
##  Groups      Name                Variance Std.Dev. Corr
##  responseSample (Intercept)      0.2651  0.5149
##  contextSample  (Intercept)      1.0302  1.0150
##  partID         (Intercept)      0.5273  0.7261
##              contextIN          1.1434  1.0693  -0.97
##              responsePhonemewh  0.3828  0.6187  -0.39  0.32
##              responsePhonemenone 0.4654  0.6822   0.34 -0.21  0.50
## Number of obs: 1200, groups:
## responseSample, 51; contextSample, 50; partID, 24
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.91078    0.31669   2.876 0.004028 **
## trialNumber.center  0.75116    0.20084   3.740 0.000184 ***
## contextIN        -4.18171    0.54110  -7.728 1.09e-14 ***
## responsePhonemewh  1.22977    0.33890   3.629 0.000285 ***
## responsePhonemenone -0.07309    0.61348  -0.119 0.905169
## contextIN:responsePhonemewh -0.22715    0.46086  -0.493 0.622101
## contextIN:responsePhonemenone -0.69994    0.68070  -1.028 0.303822
## trialNumber.center:contextIN -1.23213    0.35014  -3.519 0.000433 ***
```



```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) trlNm. cntxtIN rspnsPhnmw rspnsPhnmn
## trlNmbr.cnt      0.011
## contextIN        -0.592 -0.050
## rspnsPhnmwh      -0.392  0.105  0.113
## rspnsPhnmnn      -0.151  0.030  0.056  0.219
## cntxtIN:rspnsPhnmw  0.170 -0.045 -0.490 -0.441      -0.089
## cntxtIN:rspnsPhnmn  0.121 -0.019 -0.312 -0.079      -0.200
## trlNmbr.:IN       -0.006 -0.574  0.115 -0.071      -0.020
##              cntxtIN:rspnsPhnmw cntxtIN:rspnsPhnmn
## trlNmbr.cnt
## contextIN
## rspnsPhnmwh
## rspnsPhnmnn
## cntxtIN:rspnsPhnmw
## cntxtIN:rspnsPhnmn  0.346
## trlNmbr.:IN        -0.033          -0.010

write.csv(as.data.frame(summary(fm2)$coef),
          "../results/FinalModelCoefficients_relevel.csv")
```

Confidence intervals (through Wald method):

```
CI = confint(finalModel,parm="beta_", method="Wald")
cx = summary(finalModel)$coef
cx = cbind(cx[,1],CI,cx[,2:4])
cx2 = cx
for(i in 1:5){cx2[,i] = round(cx2[,i],3)}
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$estimate.odds = exp(cx2[,1])
cx2$estimate.odds.lower = exp(cx2[,2])
cx2$estimate.odds.upper = exp(cx2[,2])

cx2
```

	estimate.logit	2.5 %	97.5 %	Std. Error
## (Intercept)	2.141	1.431	2.850	0.362
## trialNumber.center	0.751	0.358	1.145	0.201
## contextIN	-4.409	-5.410	-3.408	0.511
## responsePhonemenone	-1.303	-2.543	-0.063	0.633
## responsePhonemeother	-1.230	-1.894	-0.566	0.339
## contextIN:responsePhonemenone	-0.473	-1.800	0.855	0.677
## contextIN:responsePhonemeother	0.227	-0.676	1.130	0.461
## trialNumber.center:contextIN	-1.232	-1.918	-0.546	0.350

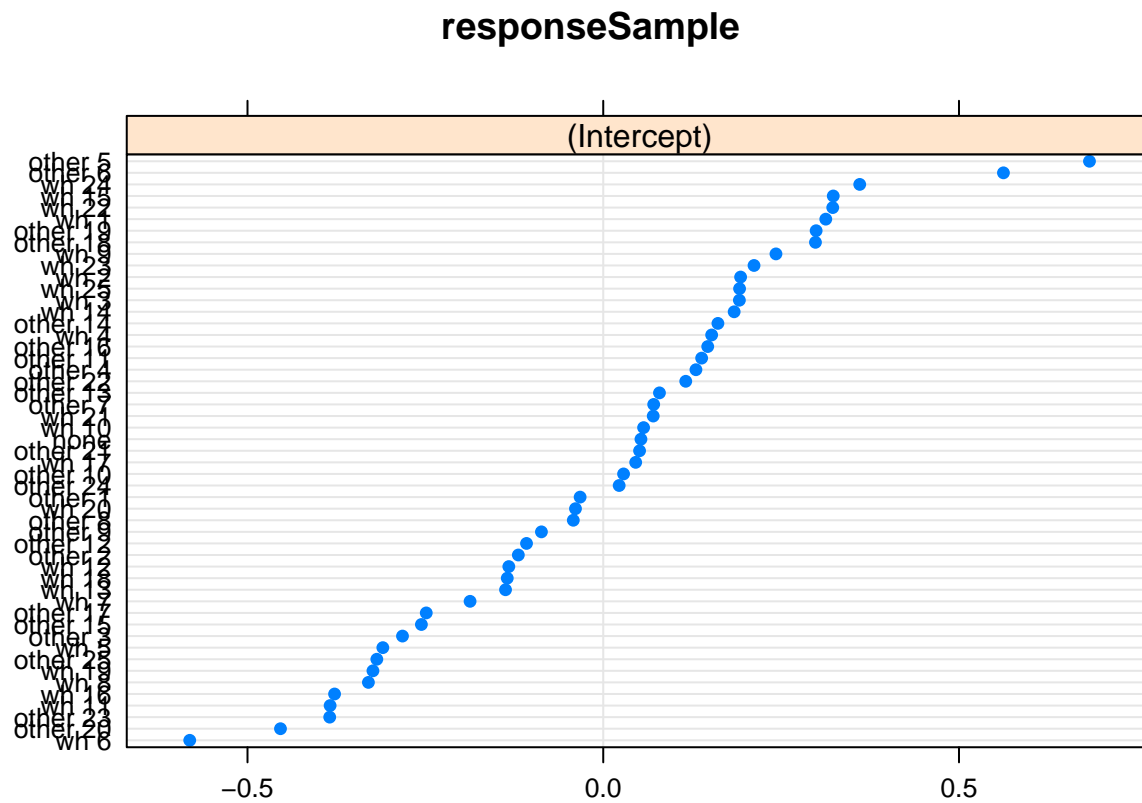
	z value	Pr(> z)	esimate.odds
## (Intercept)	5.913	3.366019e-09	8.50794132
## trialNumber.center	3.740	1.840016e-04	2.11911808
## contextIN	-8.632	6.007100e-18	0.01216734
## responsePhonemenone	-2.060	3.943976e-02	0.27171542
## responsePhonemeother	-3.629	2.848789e-04	0.29229258
## contextIN:responsePhonemenone	-0.698	4.850847e-01	0.62313007
## contextIN:responsePhonemeother	0.493	6.221693e-01	1.25482987

```
## trialNumber.center:contextIN    -3.519 4.333312e-04    0.29170858
##                                estimate.odd.lower estimate.odd.upper
## (Intercept)                     4.18287998      4.18287998
## trialNumber.center               1.43046562      1.43046562
## contextIN                        0.00447164      0.00447164
## responsePhonemenone              0.07863016      0.07863016
## responsePhonemeother             0.15046873      0.15046873
## contextIN:responsePhonemenone    0.16529889      0.16529889
## contextIN:responsePhonemeother   0.50864752      0.50864752
## trialNumber.center:contextIN     0.14690047      0.14690047
write.csv(cx, "../results/FinalModelCoefficients.csv")
```

Random effects

```
dotplot(ranef(finalModel))
```

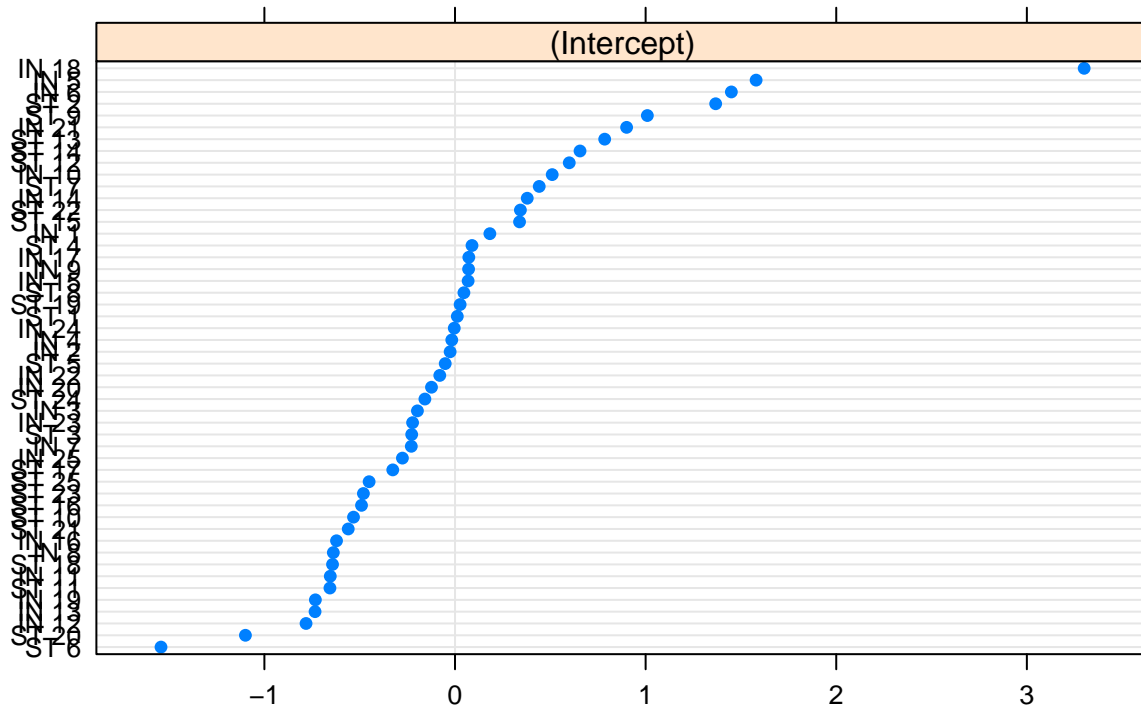
```
## $responseSample
```



```
##
```

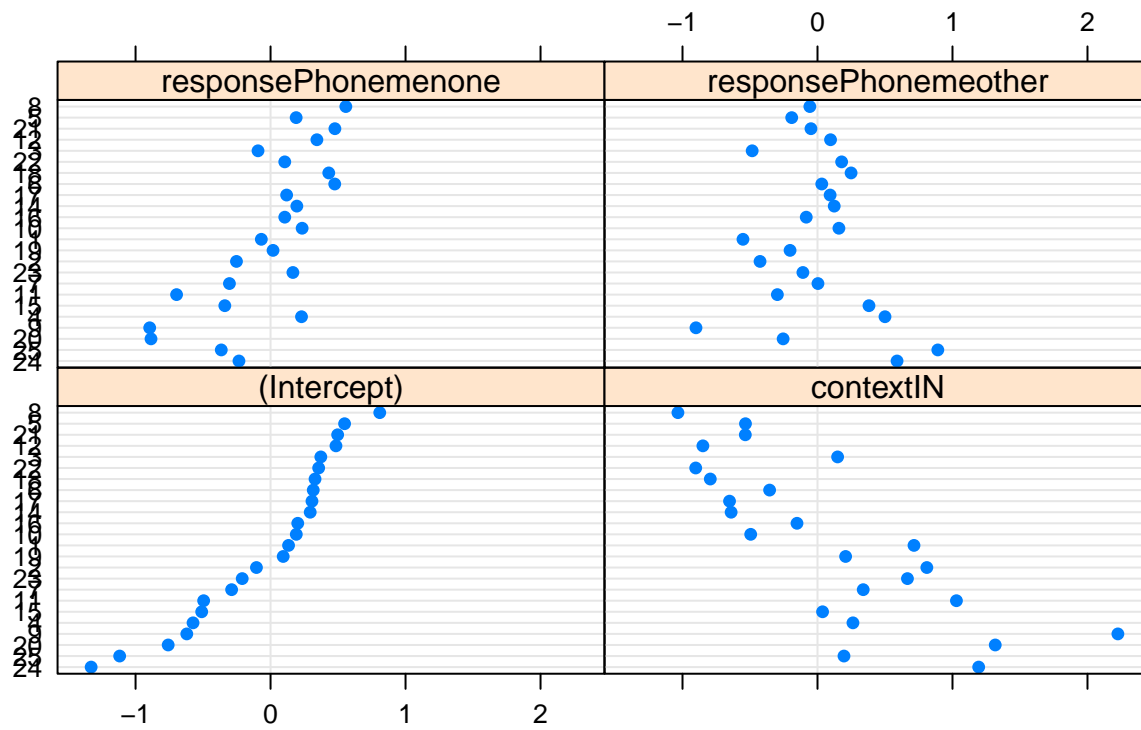
```
## $contextSample
```

contextSample



```
##
## $partID
```

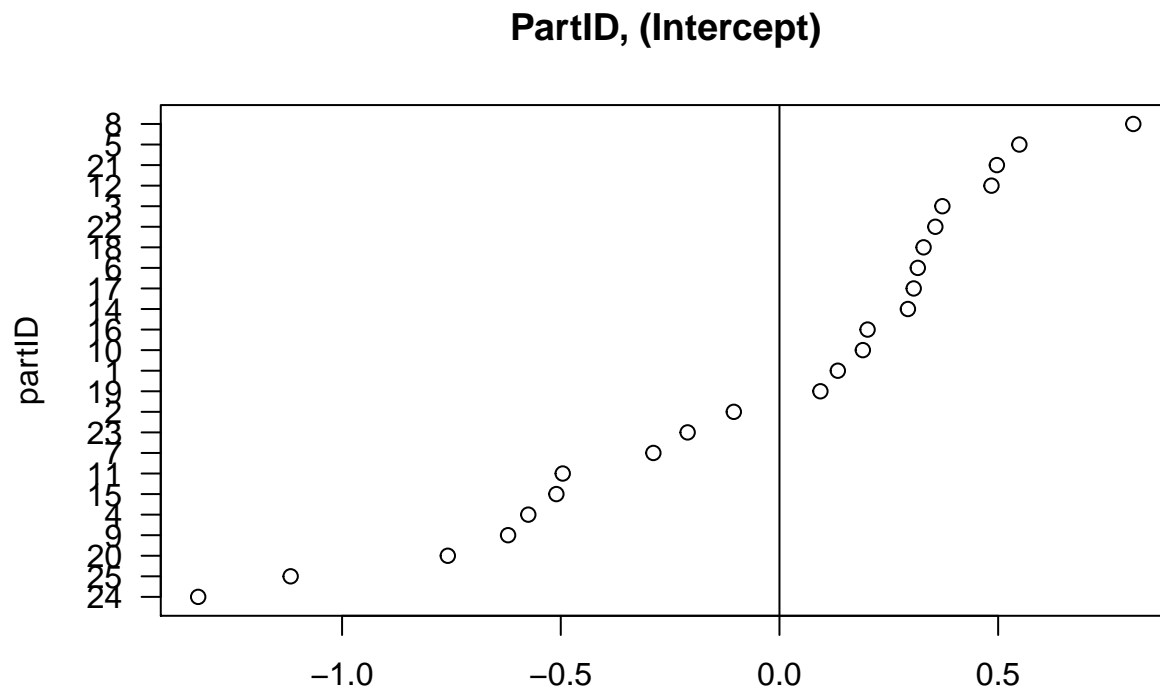
partID

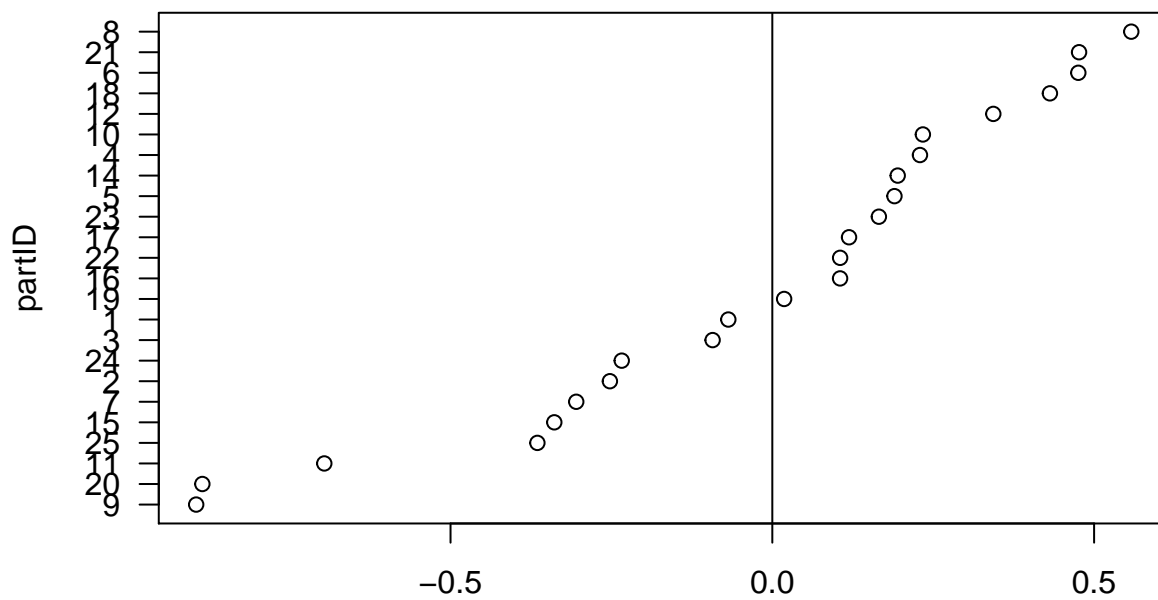
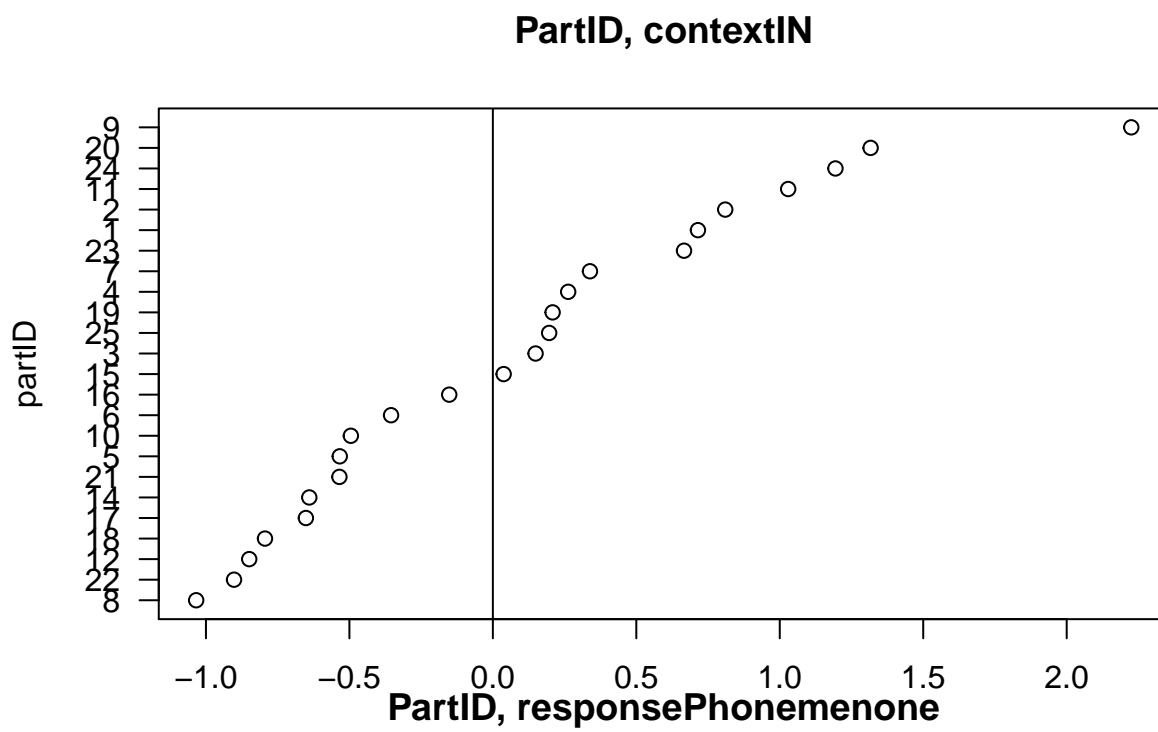


```

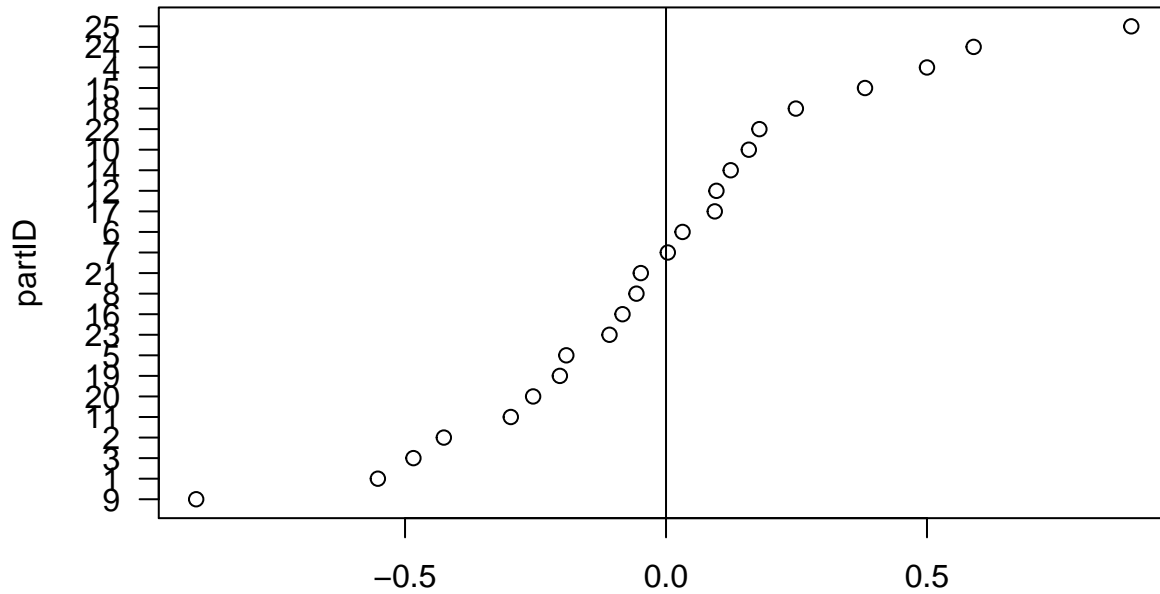
x = as.data.frame(ranef(finalModel)$partID)
rownames(x) = rownames(ranef(finalModel)$partID)
for(i in 1:ncol(x)){
  x = x[order(x[,i]),]
  plot(x[,i],1:nrow(x),
       main = paste("PartID,",colnames(x)[i]),
       yaxt='n',
       ylab='partID', xlab='')
  abline(v=0)
  axis(2,at=1:nrow(x),labels=rownames(x), las=2)
}

```



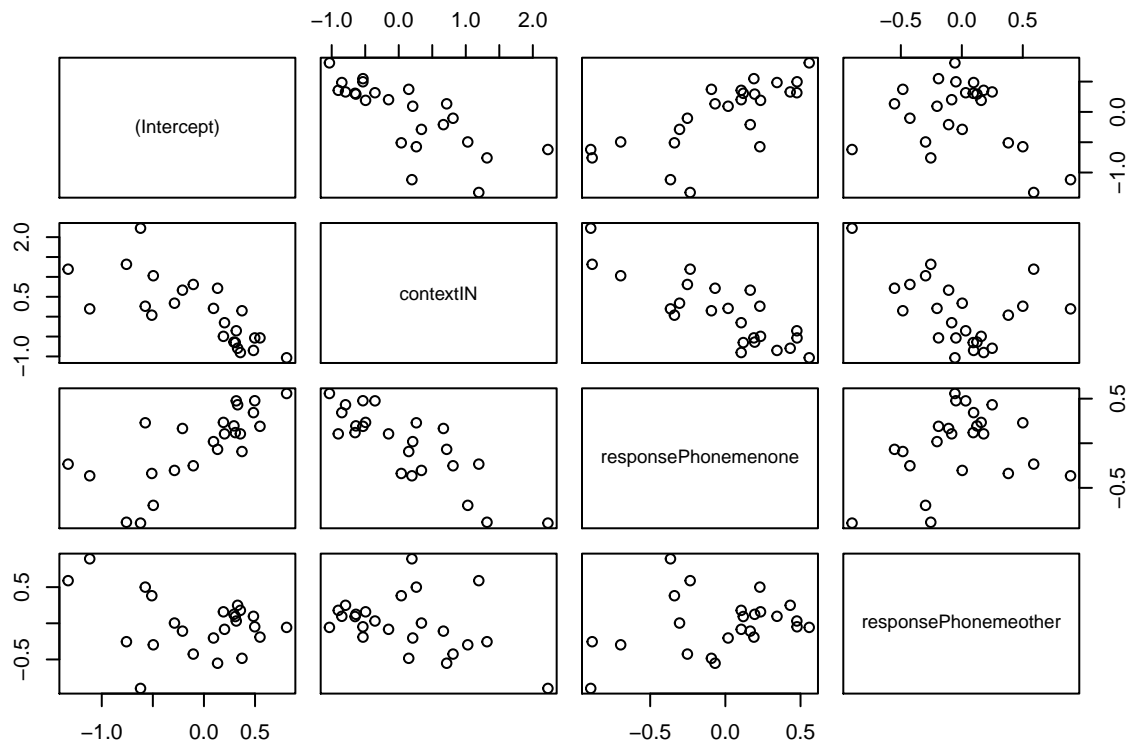


PartID, responsePhonemeother



Correlation between random effects for poarticipants:

```
plot(ranef(finalModel)$partID)
```



Summary

Here is a summary of the main results:

There was a significant main effect of context (log likelihood difference = 23 , df = 1 , Chi Squared = 45.74 , p = 1.3e-11).

There was a significant main effect of phoneme (log likelihood difference = 6.9 , df = 2 , Chi Squared = 13.83 , p = 0.00099).

There was no significant interaction between context and phoneme (log likelihood difference = 0.67 , df = 2 , Chi Squared = 1.34 , p = 0.51).

There was a significant main effect of trial (log likelihood difference = 2.4 , df = 1 , Chi Squared = 4.8 , p = 0.029).

Work out model estimates for probabilities in each condition:

```
newD = data.frame(context=c("IN","IN","IN","ST","ST","ST"),
  responsePhoneme = c("none","other","wh","none","other","wh"),
  trialNumber.center = c(0,0,0,0,0,0))
rownames(newD) = c("IN + none", "IN + other", "IN + wh",
  "ST + none", "ST + other", "ST + wh")
prx = predict(finalModel,re.form=NA,newdata=newD)

t(t(logit2per(prx)))
```

```
##           [,1]
## IN + none 0.01722517
## IN + other 0.03658105
## IN + wh   0.09378154
## ST + none 0.69797199
## ST + other 0.71315356
## ST + wh   0.89477791
```


Plots

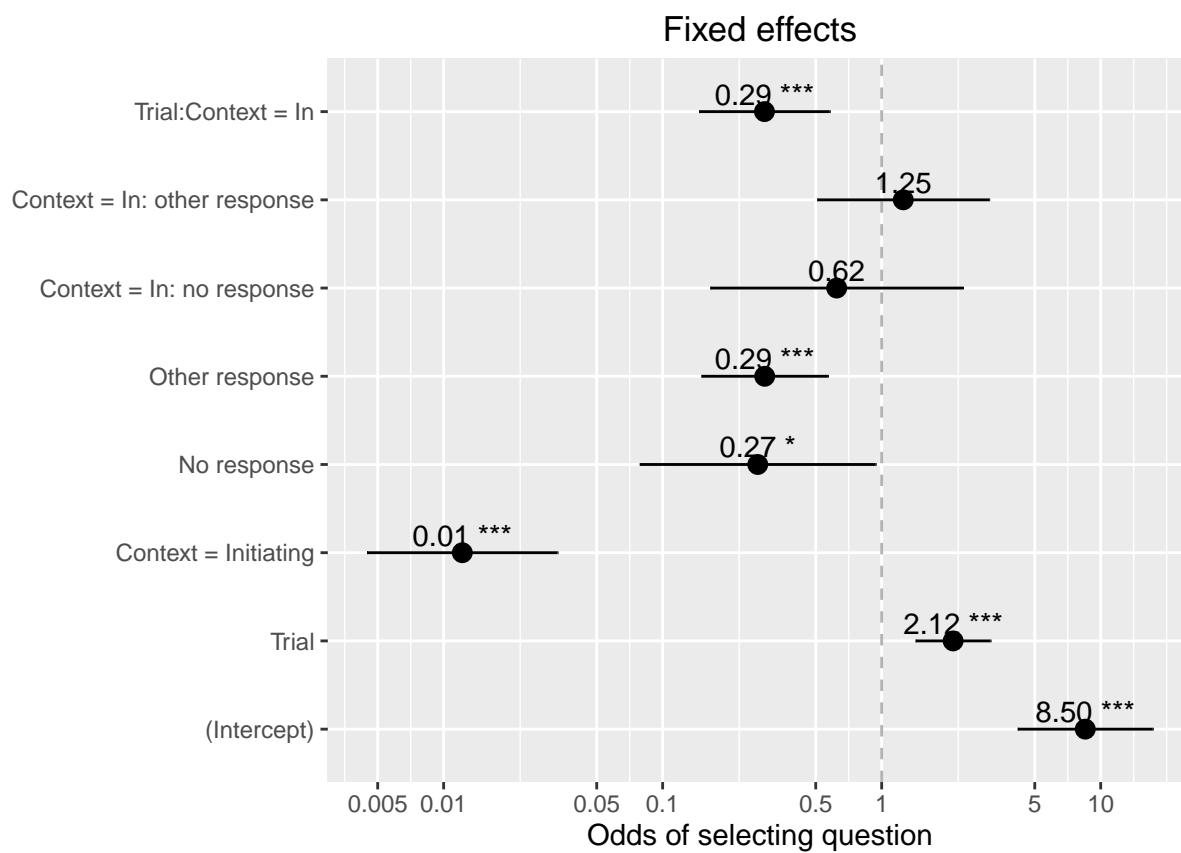
Fixed effects estimates:

```
feLabels = matrix(c(
  "(Intercept)"           , "Intercept"           , NA,
  "trialNumber.center", "Trial", NA,
  "contextST", "Context = Statement", "context",
  "contextIN", "Context = Initiating", "context",
  "responsePhonemenone", "No response", 'rPhon',
  "responsePhonemewh", "wh response", 'rPhon',
  "responsePhonemeother", "Other response", 'rPhon',
  "contextIN:responsePhonemenone", "Context = In: no response", "conXrPh",
  "contextIN:responsePhonemewh", "Context = In: wh response", "conXrPh",
  "contextIN:responsePhonemeother", "Context = In: other response", "conXrPh",
  "trialNumber.center:contextIN", "Trial:Context = In", 'trialXCon'
), ncol=3, byrow = T)

feLabels2 = as.vector(feLabels[match(names(fixef(finalModel)), feLabels[,1]), 2])

sjp.glmer(finalModel, 'fe',
  show.intercept = T,
  geom.colors = c(1,1),
  axis.title = "Odds of selecting question",
  y.offset = 0.2,
  axis.labels = feLabels2[2:length(feLabels2)]
)
```

Warning: Deprecated, use `tibble::rownames_to_column()` instead.



Raw data plots

```
d$responsePhoneme2 = relevel(relevel(d$responsePhoneme, 'other'), 'none')

sumStats = group_by(d, partID ,context,responsePhoneme2 ) %>%
  summarise(mean =mean(answer) )

sumStats2 = summarySE(sumStats, measurevar="mean", groupvars=c("context", "responsePhoneme2"))
sumStats2$upper = sumStats2$mean + sumStats2$ci
sumStats2$lower = sumStats2$mean - sumStats2$ci

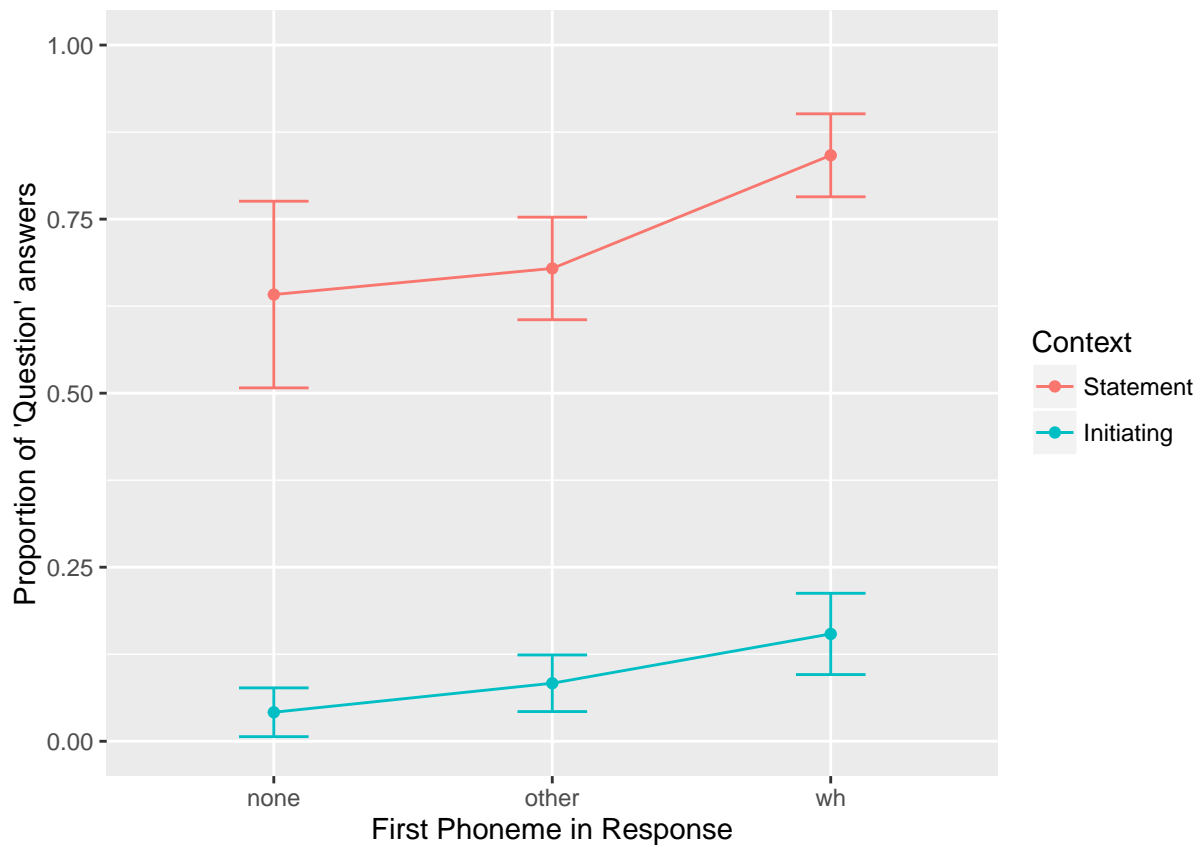
sumStats2
```

##	context	responsePhoneme2	N	mean	sd	se	ci
## 1	ST	none	24	0.64166667	0.31748559	0.06480648	0.13406241
## 2	ST	other	24	0.67916667	0.17440375	0.03560002	0.07364424
## 3	ST	wh	24	0.84166667	0.14116493	0.02881517	0.05960872
## 4	IN	none	24	0.04166667	0.08297022	0.01693623	0.03503525
## 5	IN	other	24	0.08333333	0.09630868	0.01965893	0.04066759
## 6	IN	wh	24	0.15416667	0.13824731	0.02821961	0.05837672
##	upper	lower					
## 1	0.77572907	0.507604259					
## 2	0.75281091	0.605522423					
## 3	0.90127539	0.782057946					
## 4	0.07670192	0.006631414					
## 5	0.12400092	0.042665743					
## 6	0.21254339	0.095789947					

```
dodge <- position_dodge(width=0.5)

main.plot <- ggplot(sumStats2,
  aes(x = responsePhoneme2, y = mean, colour=context)) +
  geom_point() + geom_line(aes(group=context)) +
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25) +
  xlab("First Phoneme in Response") +
  ylab("Proportion of 'Question' answers") +
  coord_cartesian(ylim=c(0,1)) +
  scale_color_discrete(breaks=c("ST", "IN"),
    labels=c("Statement", "Initiating"),
    name="Context")

main.plot
```

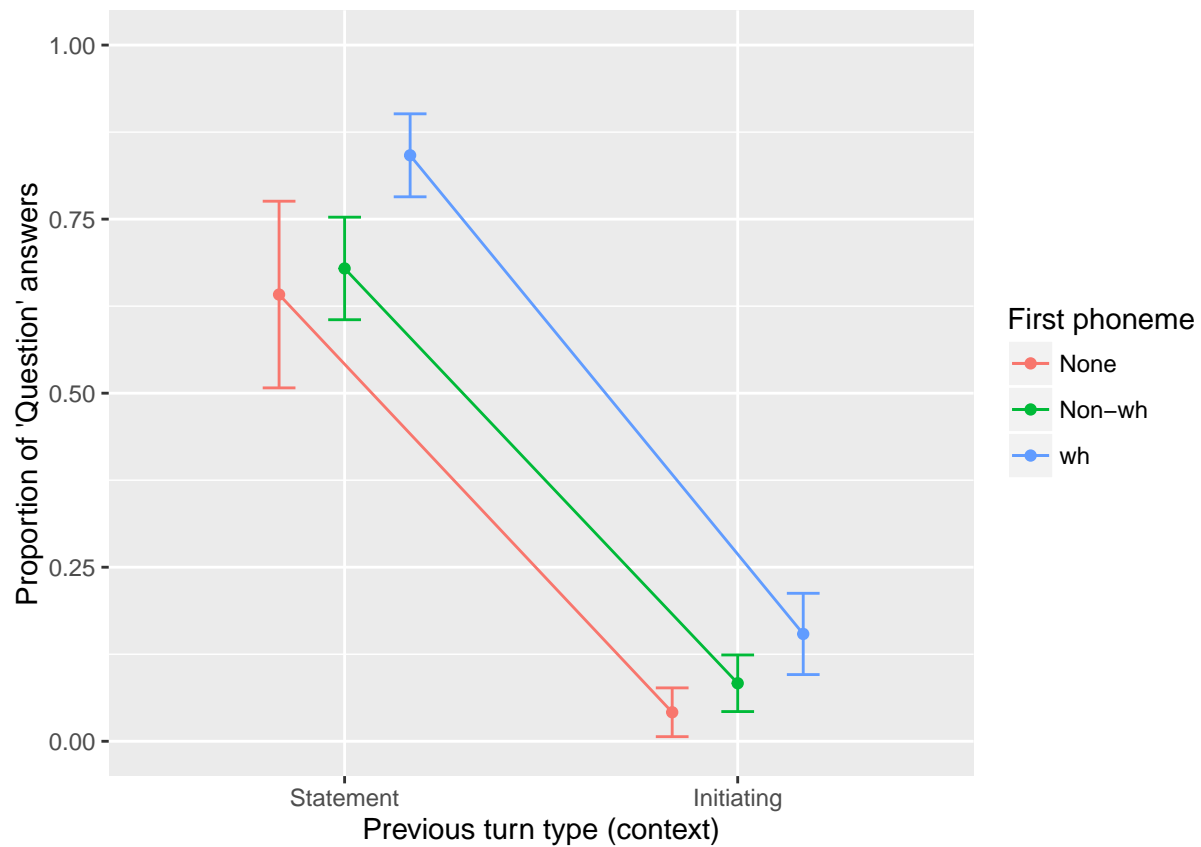


```
pdf("../results/graphs/PropQResponses_by_firstPhoneme_withPartCI.pdf",
     width = 4, height=3)
main.plot
dev.off()
```

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

```
main.plot2 <- ggplot(sumStats2,
  aes(x = context, y = mean, colour=responsePhoneme2)) +
  geom_point(position=dodge) + geom_line(aes(group=responsePhoneme2), position=dodge) +
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25, position=dodge) +
  xlab("Previous turn type (context)") +
  ylab("Proportion of 'Question' answers") +
  coord_cartesian(ylim=c(0,1)) +
  scale_color_discrete(breaks=c("none","other",'wh'),
    labels=c("None","Non-wh","wh"),
    name="First phoneme") +
  scale_x_discrete(breaks=c("ST", "IN"),
    labels=c("Statement", "Initiating"))

main.plot2
```



```
pdf("../results/graphs/PropQResponses_by_context_withPartCI.pdf",
     width = 4, height=3)
main.plot2
dev.off()
```

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

Predicting response type

```
d2 = d[d$responsePhoneme!="none",]

table(d2$answer,d2$responseType)

##
##      none other   Q
## FALSE    0   271 267
##  TRUE    0   209 213

d2$correct = "Correct"
d2$correct[!d2$answer & d2$responseType=="Q"] = "Incorrect"
d2$correct[d2$answer & d2$responseType=="other"] = "Incorrect"
# number of "correct" responses
table(d2$correct)

##
##   Correct Incorrect
##      484         476

m0T = glmer(answer ~ 1 + context*responsePhoneme +
            (1 + context | partID) +
            (1 | contextSample) +
            (1 | responseSample) ,
            data = d2,
            family = binomial,
            control=gcontrol)

respT = glmer(answer ~ 1 + context*responsePhoneme +
              responseType +
              (1 + context | partID) +
              (1 | contextSample) +
              (1 | responseSample) ,
              data = d2,
              family = binomial,
              control=gcontrol)

respTXco = glmer(answer ~ 1 + context*responsePhoneme +
                 responseType*context +
                 (1 + context | partID) +
                 (1 | contextSample) +
                 (1 | responseSample) ,
                 data = d2,
                 family = binomial,
                 control=gcontrol)

respTXrp = glmer(answer ~ 1 + context*responsePhoneme +
                 responseType*context +
                 + responseType: responsePhoneme +
                 (1 + context | partID) +
                 (1 | contextSample) +
                 (1 | responseSample) ,
                 data = d2,
                 family = binomial,
```

```

        control=gcontrol)

rTXcoXrp = glmer(answer ~ 1 + context*responsePhoneme +
                responseType*context *responsePhoneme +
                (1 + context | partID) +
                (1 | contextSample) +
                (1 | responseSample) ,
                data = d2,
                family = binomial,
                control=gcontrol)

anova(m0T, respT, respTXco, respTXrp, rTXcoXrp)

## Data: d2
## Models:
## m0T: answer ~ 1 + context * responsePhoneme + (1 + context | partID) +
## m0T:      (1 | contextSample) + (1 | responseSample)
## respT: answer ~ 1 + context * responsePhoneme + responseType + (1 +
## respT:      context | partID) + (1 | contextSample) + (1 | responseSample)
## respTXco: answer ~ 1 + context * responsePhoneme + responseType * context +
## respTXco:      (1 + context | partID) + (1 | contextSample) + (1 | responseSample)
## respTXrp: answer ~ 1 + context * responsePhoneme + responseType * context +
## respTXrp:      +responseType:responsePhoneme + (1 + context | partID) +
## respTXrp:      (1 | contextSample) + (1 | responseSample)
## rTXcoXrp: answer ~ 1 + context * responsePhoneme + responseType * context *
## rTXcoXrp:      responsePhoneme + (1 + context | partID) + (1 | contextSample) +
## rTXcoXrp:      (1 | responseSample)
##           Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0T         9 819.68 863.48 -400.84   801.68
## respT       10 821.57 870.24 -400.79   801.57 0.1050      1    0.7459
## respTXco    11 823.40 876.94 -400.70   801.40 0.1702      1    0.6800
## respTXrp    12 825.40 883.80 -400.70   801.40 0.0080      1    0.9288
## rTXcoXrp    13 826.31 889.58 -400.16   800.31 1.0823      1    0.2982

```

No effects of actual response type.

Note on different optimisers

The nlminb optimiser was used instead of the default bobyqa and Nelder-Mead optimisers. The default settings caused convergence problems for the model with the interaction between responsePhoneme and context, probably due to the lack of variation in some of the conditions. Several other optimisers were tried, and the main results remained qualitatively the same (main effect of context, main effect of responsePhoneme, no interaction).

For the conXrPh model above, 7 different optimiser settings were tried (following this approach), all but nlminbw produced convergence warnings. The optimisers returned very similar log likelihoods:

- Nelder_Mead -482.3682
- bobyqa -481.4402
- nloptwrap.NLOPT_LN_NELDERMEAD -481.2140
- nloptwrap.NLOPT_LN_BOBYQA -481.2140
- nmkbw -481.2042
- optimx.L-BFGS-B -481.2041
- nlminbw -481.2041

Below is a summary of the estimates for different fixed effects for different optimisers for the `conXrPh` model above. The estimates vary little between the runs.

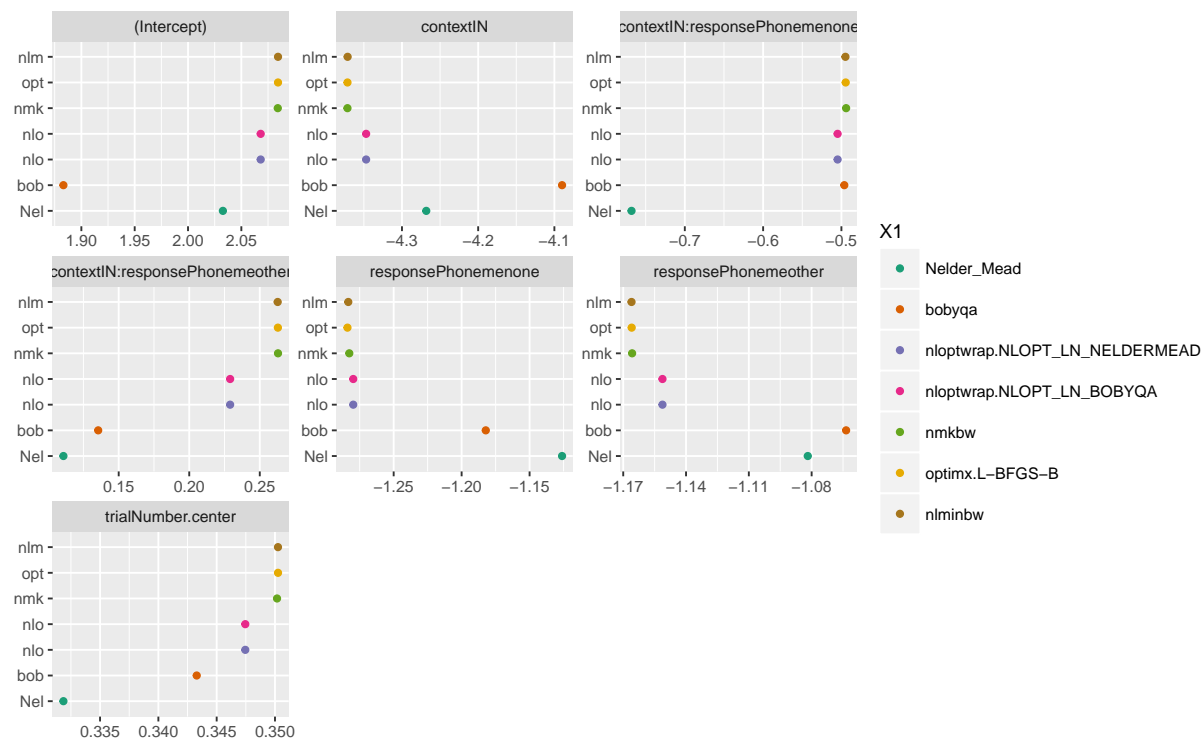


Figure 1: DifferentOptimizerResults