

# 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)
```

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, 'other')
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
```

## Data exclusion

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

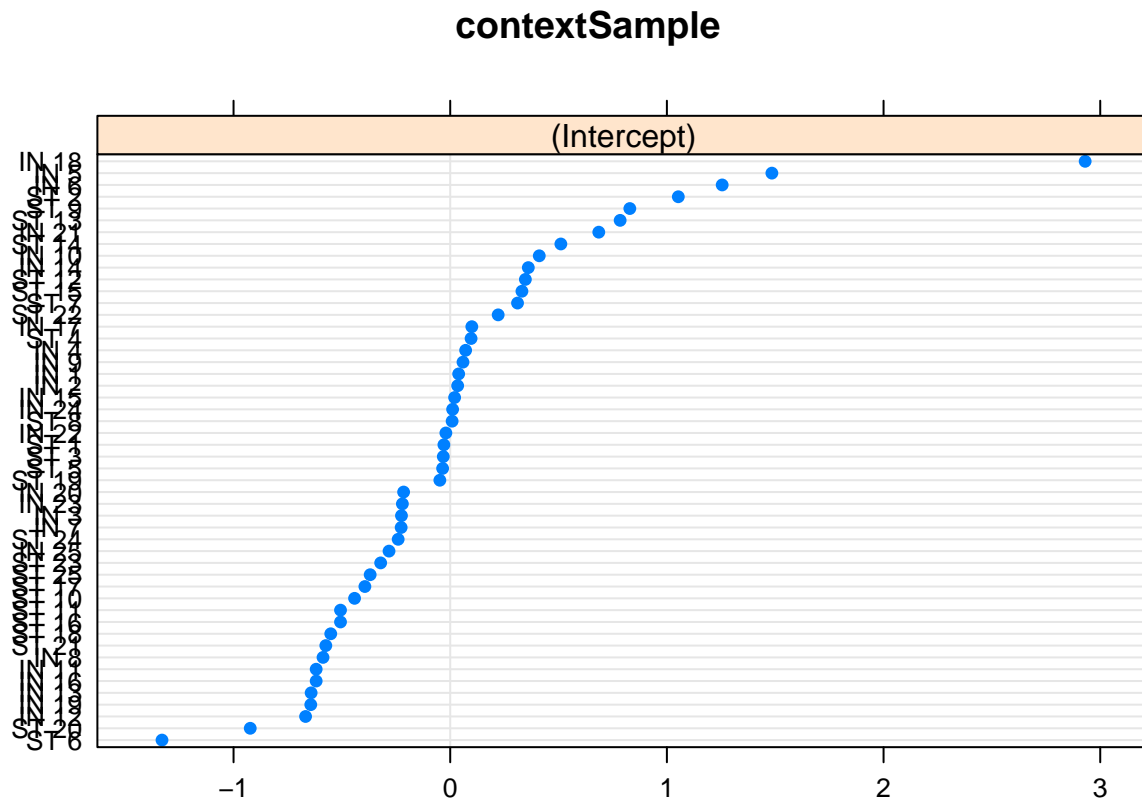
```
d = d[as.character(d$partID)!="13",]
```

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.

```
# Commented out - not run
#d = d[d$contextSample != 'IN 18',]
```

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 )
```

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

## Effects of block and trial

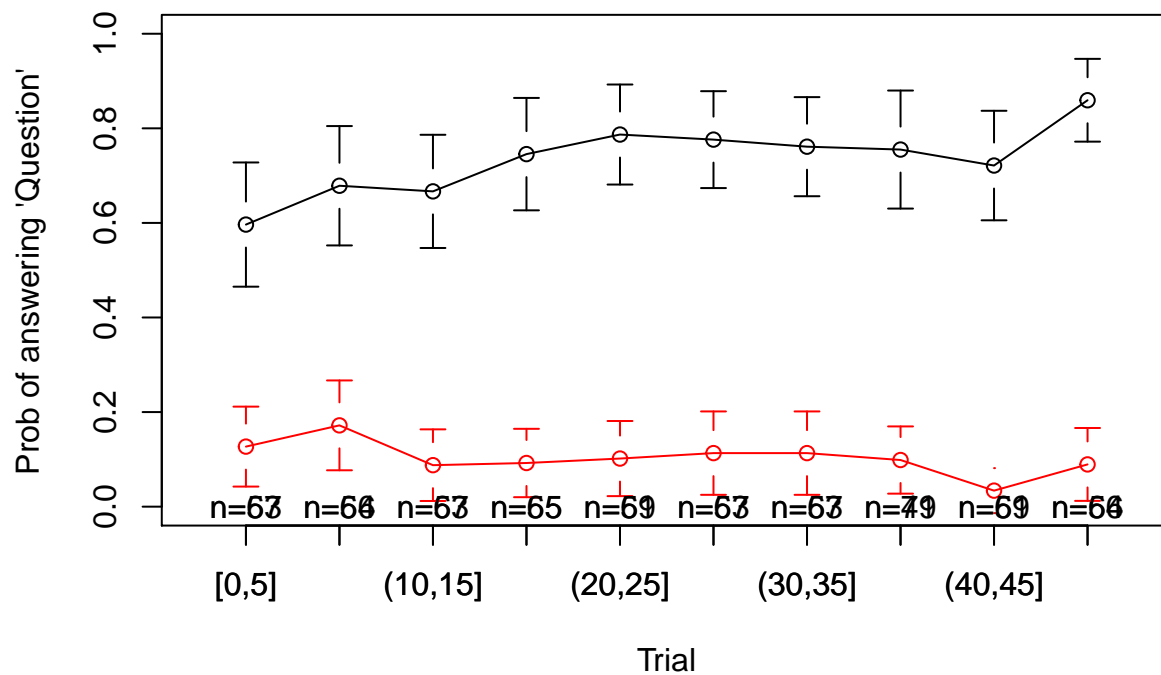
```
plotmeans(answer ~ cut(trialNumber,seq(0,50,length.out = 11), include.lowest = T),
  ylab = "Prob of answering 'Question'",
  xlab = 'Trial',
  data = d[d$context=="ST",],ylim=c(0,1),
  col = 1, barcol = 1)
plotmeans(answer ~ cut(trialNumber,seq(0,50,length.out = 11), include.lowest = T),
  ylab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

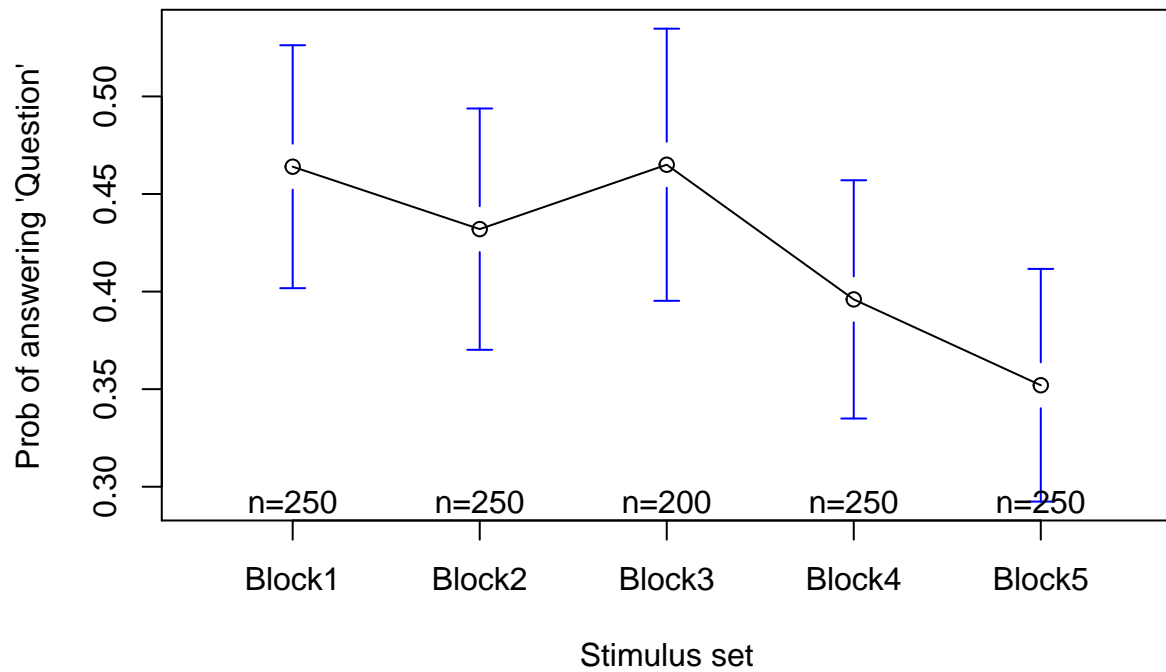
## Warning in arrows(x, ui, x, pmin(y + gap, ui), col = barcol, lwd = lwd, :
## zero-length arrow is of indeterminate angle and so skipped

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

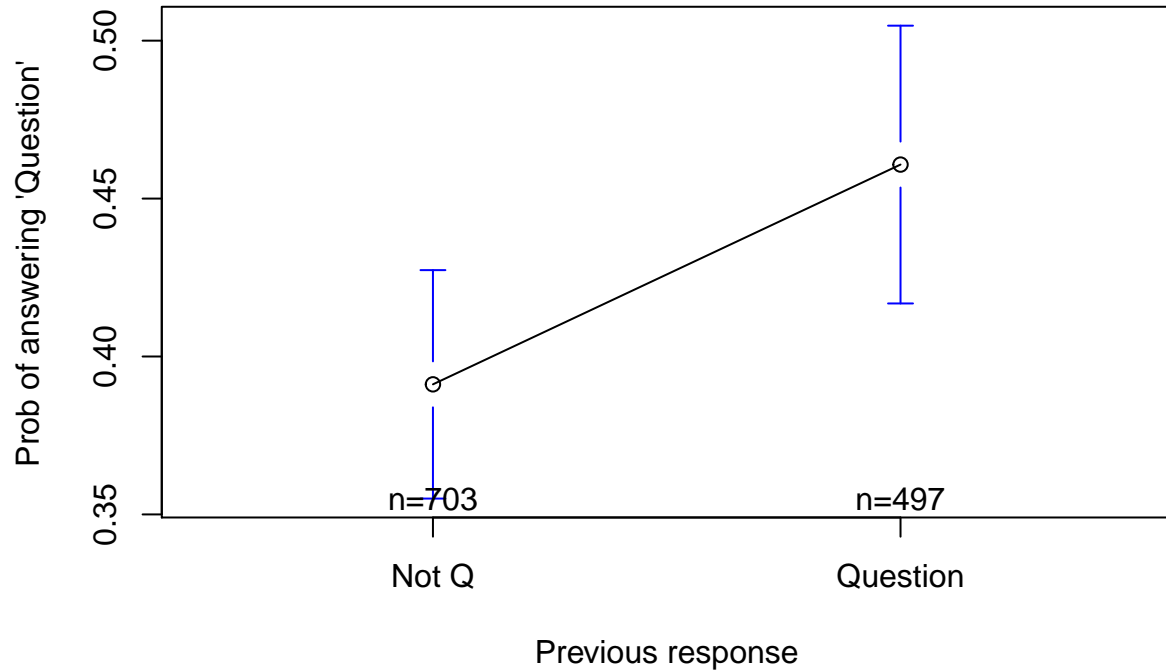
## Warning in plot.xy(xy.coords(x, y), type = type, ...): "add" is not a
## graphical parameter
```



```
plotmeans(d$answer ~ d$blockName,
  ylab = "Prob of answering 'Question'",
  xlab = 'Stimulus set')
```



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



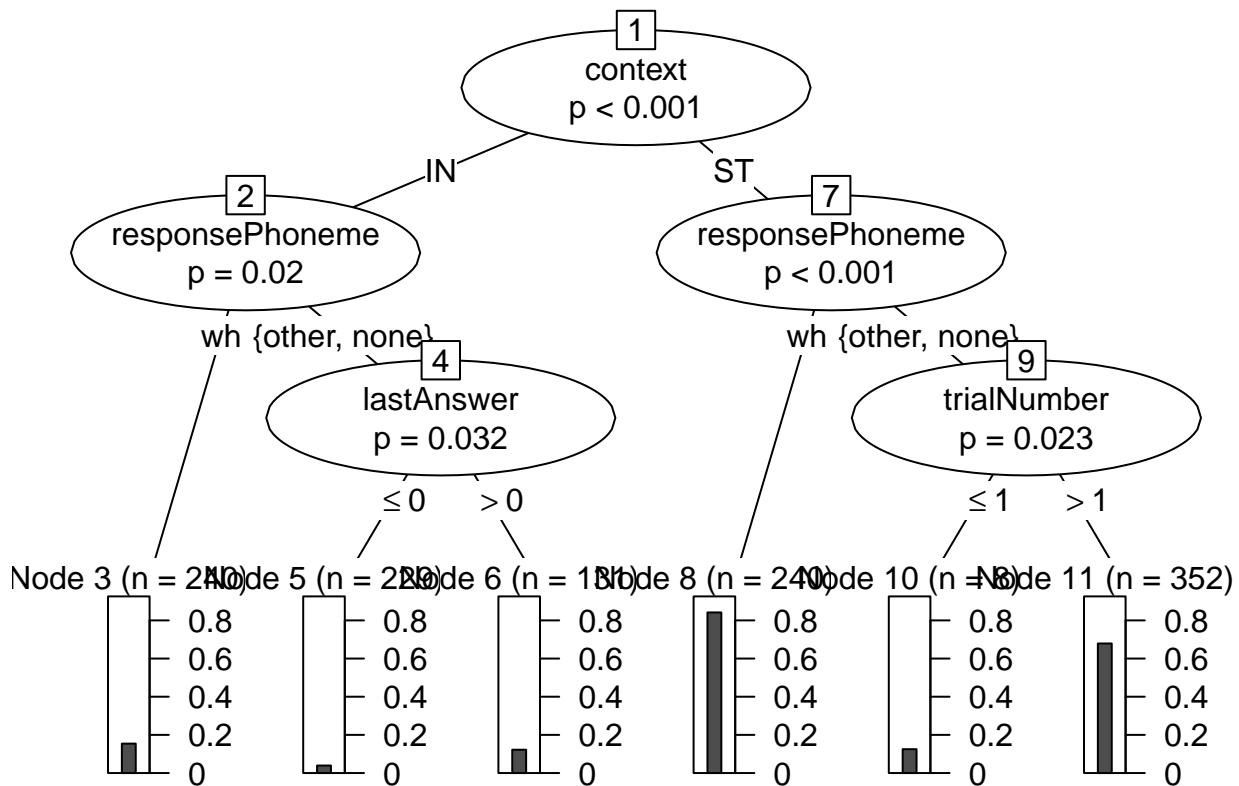
## Decision tree

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, the type of turn the response was taken from and the participants' age, sex and the type of English they speak (American, British, or other, which are the main groups).

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

Plot the decision tree:

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



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 “bobyqa” optimiser for both phases of the convergence and letting the algorithm run longer:

```
gcontrol = glmerControl(optimizer="bobyqa",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 = gcontrol
)

mA0b = glmer(
  answer ~ 1 +
    (1 | blockName/partID) ,
  data = d,
  family = binomial,
  control = gcontrol
)

anova(mA0,mA0b)
```

```
## 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.

```
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 | partID) +
    (0 + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

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

## 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 | partID) + (0 + responsePhoneme |
## mA4: partID) + (1 | 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  1110.4 522.2810      1 < 2.2e-16 ***
## mA2  4 1094.7 1115.1 -543.37  1086.7 23.6823      1 1.136e-06 ***
## mA3  6 1059.5 1090.0 -523.76  1047.5 39.2221      2 3.041e-09 ***
## mA4 12 1064.6 1125.7 -520.29  1040.6 6.9358      6 0.3268
## ---
## 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. Adding the correlation term between random effects slopes causes serious convergence issues, so we leave that out.



## 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 | partID) +
    (0 + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)

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

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

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.483631 (tol =
## 0.001, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable:
## - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?

anova(m0,trial, trialQ)

## Data: d
## Models:
## m0: answer ~ 1 + (1 + context | partID) + (0 + responsePhoneme |
## m0:      partID) + (1 | contextSample) + (1 | responseSample)
## trial: answer ~ 1 + trialNumber.center + (1 + context | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
```

```
## trialQ: answer ~ 1 + trialNumber.center + I(trialNumber.center^2) + (1 +
## trialQ:      context | partID) + (0 + responsePhoneme | partID) + (1 |
## trialQ:      contextSample) + (1 | responseSample)
##           Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0        12 1064.6 1125.7 -520.29  1040.6
## trial     13 1061.8 1128.0 -517.92  1035.8 4.7388      1 0.02949 *
## trialQ    14 1062.7 1134.0 -517.35  1034.7 1.1272      1 0.28837
## ---
## 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 | partID) +
    (0 + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample) ,
  data = d,
  family = binomial,
  control = gcontrol
)
anova(trial,prevAns)

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## prevAns: answer ~ 1 + trialNumber.center + lastAnswer + (1 + context |
## prevAns:      partID) + (0 + responsePhoneme | partID) + (1 | contextSample) +
## prevAns:      (1 | responseSample)
##           Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## trial     13 1061.8 1128.0 -517.92  1035.8
## prevAns    14 1062.1 1133.4 -517.06  1034.1 1.7211      1 0.1896
```

No significant effect of previous answer.

*Sex of speakers in samples*

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

respS = glmer(
  answer ~ 1 + trialNumber.center +
    context.sex + response.sex +
    (1 + context | partID) +
```

```

    (0 + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

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

anova(trial, contS, respS, contXrespS)

```

```

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## contS: answer ~ 1 + trialNumber.center + context.sex + (1 + context |
## contS:      partID) + (0 + responsePhoneme | partID) + (1 | contextSample) +
## contS:      (1 | responseSample)
## respS: answer ~ 1 + trialNumber.center + context.sex + response.sex +
## respS:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## respS:      (1 | contextSample) + (1 | responseSample)
## contXrespS: answer ~ 1 + trialNumber.center + context.sex * response.sex +
## contXrespS:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## contXrespS:      (1 | contextSample) + (1 | responseSample)
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trial      13 1061.8 1128.0 -517.92  1035.8
## contS      14 1062.5 1133.8 -517.27  1034.5 1.2964      1    0.2549
## respS      15 1064.5 1140.9 -517.27  1034.5 0.0044      1    0.9471
## contXrespS 16 1066.5 1147.9 -517.24  1034.5 0.0541      1    0.8160

```

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

#### *Sex of participants*

```

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

```

```
)

anova(trial,sex)

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## sex: answer ~ 1 + trialNumber.center + Sex + (1 + context | partID) +
## sex:      (0 + responsePhoneme | partID) + (1 | contextSample) + (1 |
## sex:      responseSample)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trial 13 1061.8 1128.0 -517.92  1035.8
## sex   14 1063.8 1135.1 -517.92  1035.8 0.0019      1      0.965
```

No significant effect of the sex of the participant.

*Type of English spoken*

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

anova(trial,Etype)

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## Etype: answer ~ 1 + trialNumber.center + EnglishType + (1 + context |
## Etype:      partID) + (0 + responsePhoneme | partID) + (1 | contextSample) +
## Etype:      (1 | responseSample)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## trial 13 1061.8 1128.0 -517.92  1035.8
## Etype 15 1064.0 1140.3 -516.99  1034.0 1.8605      2      0.3944
```

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

## Effects of Context and Response

The only significant confounding variable is trial.

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

```

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

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

conXrPh = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    (1 + context | partID) +
    (0 + 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 | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## context: answer ~ 1 + trialNumber.center + context + (1 + context | partID) +
## context:      (0 + responsePhoneme | partID) + (1 | contextSample) + (1 |
## context:      responseSample)
## rPhon: answer ~ 1 + trialNumber.center + context + responsePhoneme +
## rPhon:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## rPhon:      (1 | contextSample) + (1 | responseSample)
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## conXrPh:      (1 | contextSample) + (1 | responseSample)
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## trial   13 1061.84 1128.0 -517.92  1035.84
## context 14 1008.25 1079.5 -490.13   980.25 55.5831      1 8.959e-14 ***
## rPhon   16  997.04 1078.5 -482.52   965.04 15.2181      2 0.0004959 ***
## conXrPh 18  999.57 1091.2 -481.79   963.57  1.4601      2 0.4818731
## ---
## 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 | partID) +
    (0 + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

```

```

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

```

```

## Warning in optwrap(optimizer, devfun, start, rho$lower, control =
## control, : convergence code 1 from bobyqa: bobyqa -- maximum number of
## function evaluations exceeded

```

```

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.00729069 (tol =
## 0.001, component 1)

```

```

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

```

```

## Warning in optwrap(optimizer, devfun, start, rho$lower, control =
## control, : convergence code 1 from bobyqa: bobyqa -- maximum number of
## function evaluations exceeded

```

```

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.0525136 (tol =
## 0.001, component 1)

```

```

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

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 1 negative
## eigenvalues

```

```
anova(conXrPh, Sex, SexXresp, SexXcon, SxXcoXre)
```

```

## Data: d
## Models:
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## conXrPh:      (1 | contextSample) + (1 | responseSample)
## Sex: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## Sex:      Sex + (1 + context | partID) + (0 + responsePhoneme | partID) +
## Sex:      (1 | contextSample) + (1 | responseSample)
## SexXresp: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## SexXresp:      Sex * responsePhoneme + (1 + context | partID) + (0 + responsePhoneme |
## SexXresp:      partID) + (1 | contextSample) + (1 | responseSample)
## SexXcon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## SexXcon:      Sex * responsePhoneme + Sex:context + (1 + context | partID) +
## SexXcon:      (0 + responsePhoneme | partID) + (1 | contextSample) + (1 |
## SexXcon:      responseSample)
## SxXcoXre: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## SxXcoXre:      Sex * responsePhoneme * context + (1 + context | partID) +
## SxXcoXre:      (0 + responsePhoneme | partID) + (1 | contextSample) + (1 |
## SxXcoXre:      responseSample)
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## conXrPh  18  999.57 1091.2 -481.79  963.57
## Sex       19 1001.57 1098.3 -481.78  963.57 0.0075      1    0.9308
## SexXresp  21 1003.19 1110.1 -480.60  961.19 2.3762      2    0.3048
## SexXcon   22 1004.68 1116.7 -480.34  960.68 0.5081      1    0.4760
## SxXcoXre  24 1008.67 1130.8 -480.34  960.67 0.0110      2    0.9945

```

No effect by sex of participant.

*Interaction with trial*

```

trialXCon = glmer(
  answer ~ 1 + trialNumber.center +
    context * responsePhoneme +
    trialNumber.center:context +

```

```

    (1 + context | partID) +
    (0 + 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 | partID) +
    (0 + responsePhoneme | partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.100074 (tol =
## 0.001, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable:
## - Rescale variables?; Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?

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

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 1 negative
## eigenvalues

anova(conXrPh, trialXCon, trialXph, trXcoXph)

## Data: d
## Models:
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh: (1 + context | partID) + (0 + responsePhoneme | partID) +

```



```
## conXrPh:      (1 | contextSample) + (1 | responseSample)
## trialXCon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXCon:      trialNumber.center:context + (1 + context | partID) + (0 +
## trialXCon:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## trialXph: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXph:      trialNumber.center:context + trialNumber.center:responsePhoneme +
## trialXph:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## trialXph:      (1 | contextSample) + (1 | responseSample)
## trXcoXph: answer ~ 1 + trialNumber.center * context * responsePhoneme +
## trXcoXph:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## trXcoXph:      (1 | contextSample) + (1 | responseSample)
##           Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## conXrPh   18 999.57 1091.2 -481.79  963.57
## trialXCon 19 988.35 1085.1 -475.17  950.35 13.2258      1 0.0002761 ***
## trialXph  21 992.56 1099.5 -475.28  950.56  0.0000      2 1.0000000
## trXcoXph  23 995.74 1112.8 -474.87  949.74  0.8184      2 0.6641690
## ---
## 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 | blockName/partID) +
    (0 + responsePhoneme | blockName/partID) +
    (1 | contextSample) +
    (1 | responseSample),
  data = d,
  family = binomial,
  control = gcontrol
)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 2 negative
## eigenvalues
```

The model does not converge, so the statistics from this model are not reliable. However, we can see that the estimates are very similar, suggesting that stimulus set does not have an impact on the main findings.

```
cbind(fixef(trialXCon),fixef(stimSet))
```

```
##           [,1]      [,2]
## (Intercept) 0.90536774 0.84030513
## trialNumber.center 0.03032683 0.03100004
## contextIN -4.22329268 -4.13740165
## responsePhonemenone -0.07887023 -0.15382568
## responsePhonemewh 1.27449390 1.21339881
## contextIN:responsePhonemenone -0.72513923 -0.54375251
## contextIN:responsePhonemewh -0.20279030 -0.09272540
```

```
## trialNumber.center:contextIN -0.05001578 -0.05106231
```

## Results

Model comparison

```
anova(trial, context, rPhon, conXrPh, trialXCon)

## Data: d
## Models:
## trial: answer ~ 1 + trialNumber.center + (1 + context | partID) + (0 +
## trial:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## context: answer ~ 1 + trialNumber.center + context + (1 + context | partID) +
## context:      (0 + responsePhoneme | partID) + (1 | contextSample) + (1 |
## context:      responseSample)
## rPhon: answer ~ 1 + trialNumber.center + context + responsePhoneme +
## rPhon:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## rPhon:      (1 | contextSample) + (1 | responseSample)
## conXrPh: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## conXrPh:      (1 + context | partID) + (0 + responsePhoneme | partID) +
## conXrPh:      (1 | contextSample) + (1 | responseSample)
## trialXCon: answer ~ 1 + trialNumber.center + context * responsePhoneme +
## trialXCon:      trialNumber.center:context + (1 + context | partID) + (0 +
## trialXCon:      responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## trial      13 1061.84 1128.0 -517.92  1035.84
## context     14 1008.25 1079.5 -490.13   980.25 55.5831      1 8.959e-14 ***
## rPhon       16  997.04 1078.5 -482.52   965.04 15.2181      2 0.0004959 ***
## conXrPh     18  999.57 1091.2 -481.79   963.57  1.4601      2 0.4818731
## trialXCon   19  988.35 1085.1 -475.17   950.35 13.2258      1 0.0002761 ***
## ---
## 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 | partID) + (0 +
## responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## Data: d
## Control: gcontrol
##
##      AIC      BIC   logLik deviance df.resid
##   988.3   1085.1   -475.2   950.3     1181
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.4045 -0.2957 -0.1285  0.4105  5.8140
##
## Random effects:
## Groups             Name                Variance Std.Dev. Corr
## responseSample (Intercept)            0.26562  0.5154
## contextSample  (Intercept)            1.01699  1.0085
## partID         responsePhonemeother    0.07141  0.2672
##                responsePhonemenone     0.74191  0.8613    0.75
##                responsePhonemewh       0.30384  0.5512   -0.15  0.54
## partID.1       (Intercept)            0.41331  0.6429
##                contextIN              1.27770  1.1304   -1.00
## Number of obs: 1200, groups:
## responseSample, 51; contextSample, 50; partID, 24
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.905368   0.312674   2.896 0.003785 **
## trialNumber.center    0.030327   0.008026   3.778 0.000158 ***
## contextIN         -4.223293   0.547872  -7.709 1.27e-14 ***
## responsePhonemenone -0.078870   0.612708  -0.129 0.897576
## responsePhonemewh    1.274494   0.337000   3.782 0.000156 ***
## contextIN:responsePhonemenone -0.725139   0.678134  -1.069 0.284928
## contextIN:responsePhonemewh -0.202790   0.465950  -0.435 0.663403
## trialNumber.center:contextIN -0.050016   0.013995  -3.574 0.000352 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) trlNm. cntxIN rspnsPhnmn rspnsPhnmw
## trlNmbr.cnt      0.013
## contextIN       -0.584 -0.048
## rspnsPhnmnn     -0.166  0.030  0.074
## rspnsPhnmwh     -0.359  0.095  0.079  0.209
```

```
## cntxtIN:rspnsPhnmn  0.127 -0.019 -0.316 -0.205      -0.090
## cntxtIN:rspnsPhnmw  0.170 -0.043 -0.493 -0.087      -0.460
## trlNmbr.:IN        -0.008 -0.573  0.115 -0.019      -0.060
##                    cntxtIN:rspnsPhnmn cntxtIN:rspnsPhnmw
## trlNmbr.cnt
## contextIN
## rspnsPhnmnn
## rspnsPhnmwh
## cntxtIN:rspnsPhnmn
## cntxtIN:rspnsPhnmw  0.352
## trlNmbr.:IN        -0.015                -0.035
```

Relevel the response phoneme to see other comparisons:

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

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.0969101 (tol =
## 0.001, component 1)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable:
## - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

```
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 | partID) + (0 +
##          responsePhoneme | partID) + (1 | contextSample) + (1 | responseSample)
## Data: d2
## Control: gcontrol
##
##          AIC          BIC    logLik deviance df.resid
##        989.0      1085.7    -475.5    951.0      1181
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.2208 -0.3063 -0.1349  0.4201  5.7494
##
## Random effects:
## Groups          Name              Variance Std.Dev. Corr
## responseSample (Intercept)        0.24123  0.4912
## contextSample  (Intercept)        0.96034  0.9800
## partID         responsePhonemewh  0.23909  0.4890
##                responsePhonemeother 0.07491  0.2737  -0.21
##                responsePhonemenone  0.61250  0.7826   0.55  0.70
## partID.1       (Intercept)        0.40861  0.6392
##                contextIN          1.25136  1.1186  -1.00
## Number of obs: 1200, groups:
## responseSample, 51; contextSample, 50; partID, 24
##
```

```
## Fixed effects:
##
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.9728356  0.0009182   2148  <2e-16 ***
## trialNumber.center  0.0297555  0.0009962    30  <2e-16 ***
## contextIN        -4.0543846  0.0009182  -4415  <2e-16 ***
## responsePhonemeother -1.1932656  0.0009183  -1299  <2e-16 ***
## responsePhonemenone -1.2148679  0.0008959  -1356  <2e-16 ***
## contextIN:responsePhonemeother  0.0597451  0.0009183    65  <2e-16 ***
## contextIN:responsePhonemenone -0.5082153  0.0008675   -586  <2e-16 ***
## trialNumber.center:contextIN -0.0493559  0.0008677   -57  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##               (Intr) trlNm. cntxtIN rspnsPhnmt rspnsPhnmn
## trlNmbr.cnt      -0.218
## contextIN        -0.190 -0.218
## rspnsPhnmth       0.048 -0.218  0.048
## rspnsPhnmnn       0.000  0.000  0.000  0.000
## cntxtIN:rspnsPhnmt  0.048 -0.218  0.048 -0.190  0.000
## cntxtIN:rspnsPhnmn  0.000  0.000  0.000  0.000  0.000
## trlNmbr.:IN       0.002 -0.010  0.002  0.003  0.000
##
##               cntxtIN:rspnsPhnmt cntxtIN:rspnsPhnmn
## trlNmbr.cnt
## contextIN
## rspnsPhnmth
## rspnsPhnmnn
## cntxtIN:rspnsPhnmt
## cntxtIN:rspnsPhnmn  0.000
## trlNmbr.:IN       0.002  0.000
## convergence code: 0
## Model failed to converge with max|grad| = 0.0969101 (tol = 0.001, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
## - Rescale variables?
```

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
```

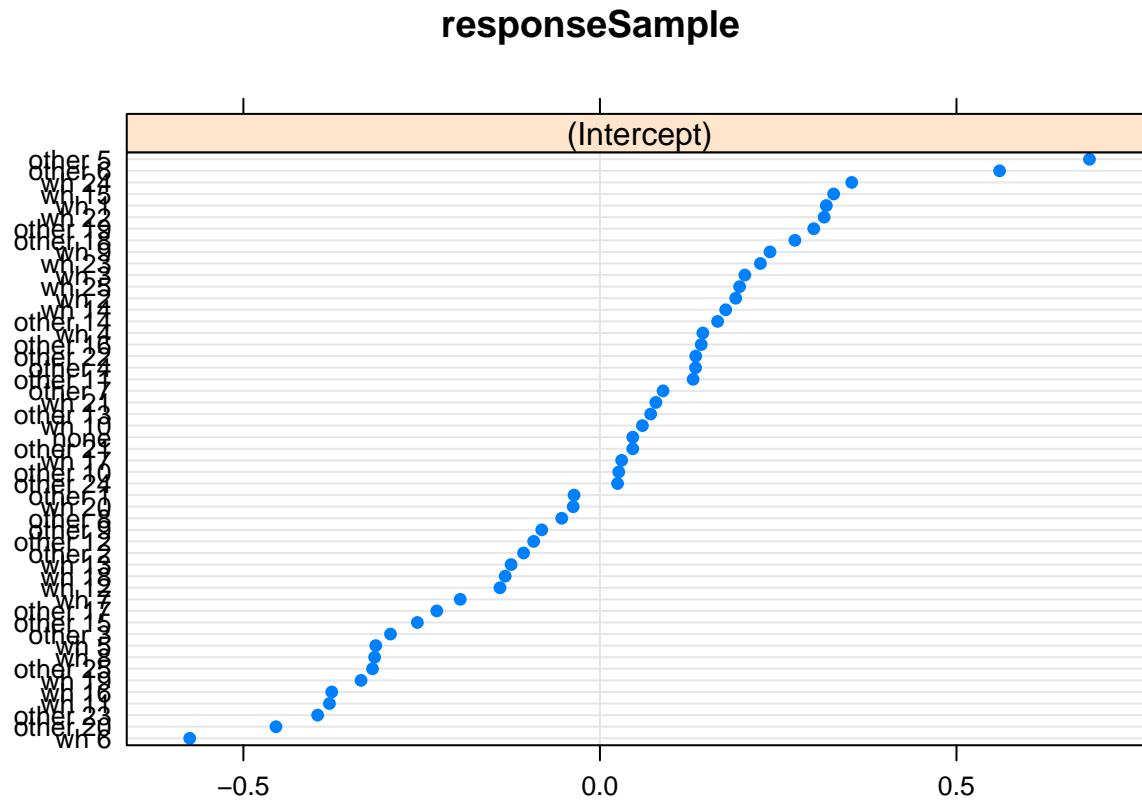
```
##               2.5 % 97.5 % Std. Error z value
## (Intercept)      0.905  0.293  1.518  0.313  2.896
## trialNumber.center  0.030  0.015  0.046  0.008  3.778
## contextIN        -4.223 -5.297 -3.149  0.548 -7.709
## responsePhonemenone -0.079 -1.280  1.122  0.613 -0.129
## responsePhonemewh   1.274  0.614  1.935  0.337  3.782
## contextIN:responsePhonemenone -0.725 -2.054  0.604  0.678 -1.069
## contextIN:responsePhonemewh -0.203 -1.116  0.710  0.466 -0.435
## trialNumber.center:contextIN -0.050 -0.077 -0.023  0.014 -3.574
```

```
##                                Pr(>|z|)
## (Intercept)                   3.784792e-03
## trialNumber.center            1.578562e-04
## contextIN                     1.272635e-14
## responsePhonemenone          8.975760e-01
## responsePhonemewh            1.556498e-04
## contextIN:responsePhonemenone 2.849278e-01
## contextIN:responsePhonemewh   6.634034e-01
## trialNumber.center:contextIN  3.518800e-04
write.csv(cx, "../results/FinalModelCoefficients.csv")
```

## Random effects

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

```
## $responseSample
```

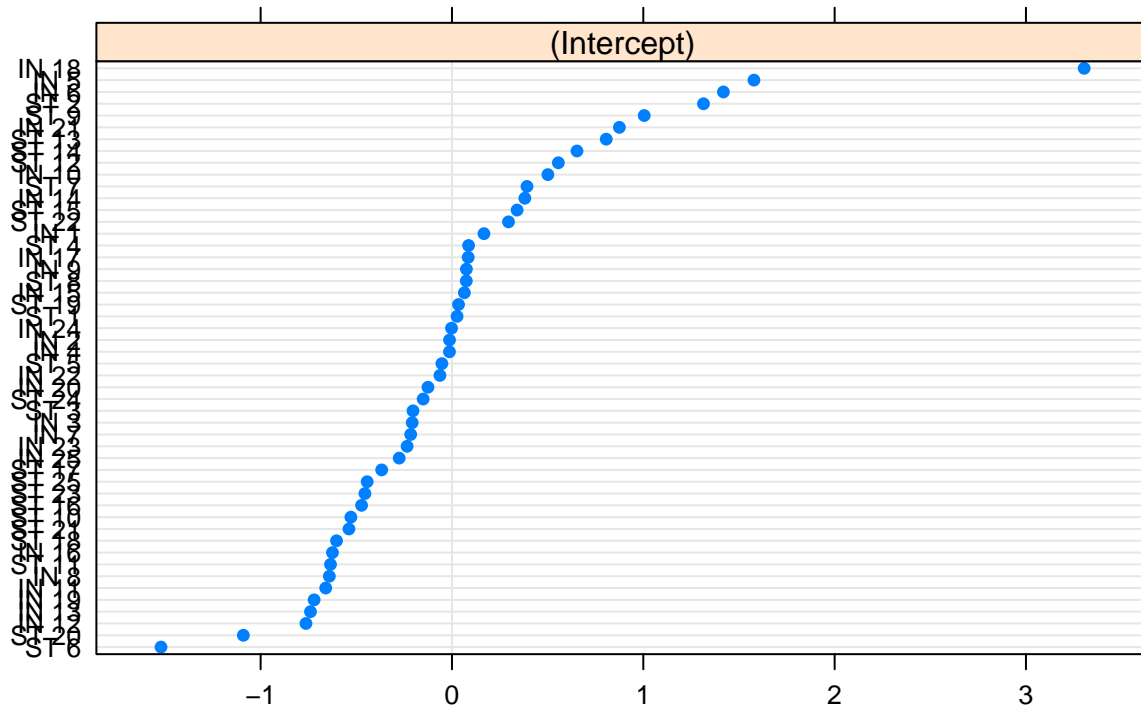


```
##
```

```
## $contextSample
```

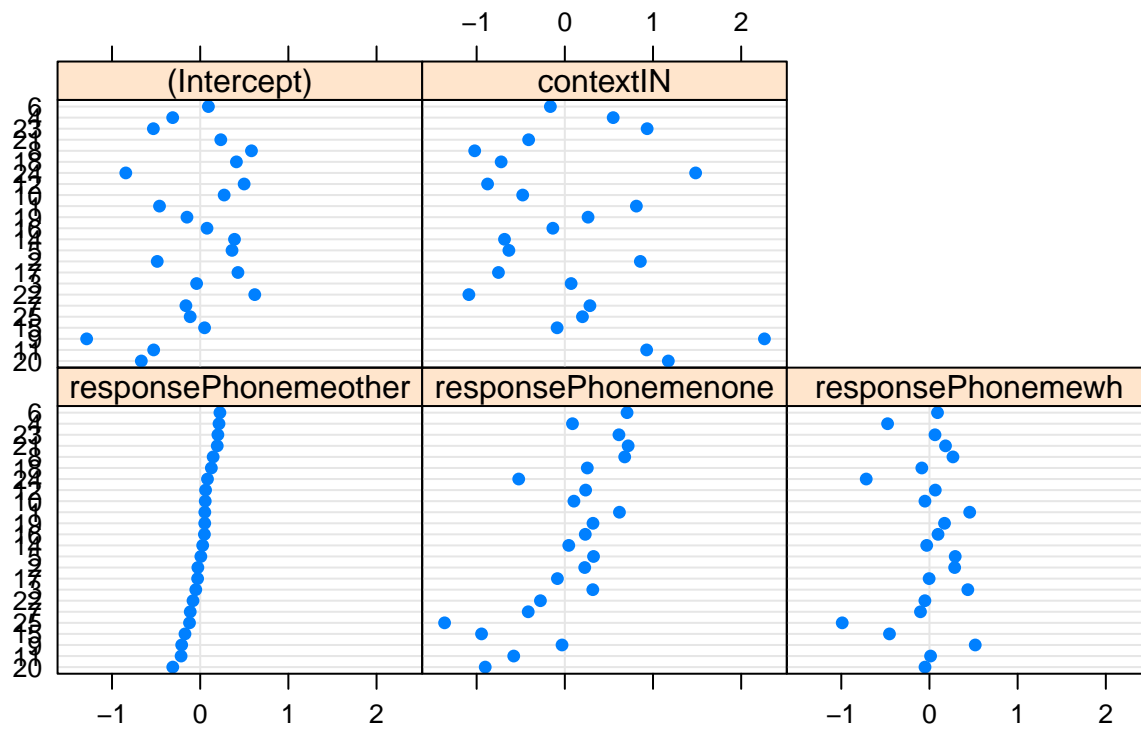


## contextSample



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

## partID



## Summary

Here is a summary of the main results:

There was a significant main effect of context ( log likelihood difference = 30 , df = 2 , Chi Squared = 60.32 , p = 8e-14 ).

There was a significant main effect of phoneme ( log likelihood difference = 7.6 , df = 2 , Chi Squared = 15.22 , p = 5e-04 ).

There was no significant interaction between context and phoneme ( log likelihood difference = 0.73 , df = 2 , Chi Squared = 1.46 , p = 0.48 ).

Work out model estimates for probabilities in each condition:

```
# prob of responding 'yes' when:
# Context = ST, other response
logit2per(fixef(finalModel)[1])[1]]

## [1] 0.7120513

# Context = ST, no response
logit2per(fixef(finalModel)[1] + fixef(finalModel)["responsePhonemenone"] )[[1]]

## [1] 0.6956138

# Context = ST, wh
logit2per(fixef(finalModel)[1] + fixef(finalModel)["responsePhonemewh"] )[[1]]

## [1] 0.8984264

# Context = IN, other response
logit2per(fixef(finalModel)[1] + fixef(finalModel)["contextIN"])[1]]

## [1] 0.03496135

# Context = IN, no response
logit2per(fixef(finalModel)[1] +
          fixef(finalModel)["contextIN"] +
          fixef(finalModel)["responsePhonemenone"])[1]]

## [1] 0.03239577

# Context = IN, wh
logit2per(fixef(finalModel)[1] +
          fixef(finalModel)["contextIN"] +
          fixef(finalModel)["responsePhonemewh"])[1]]

## [1] 0.1147178
```

## Plots

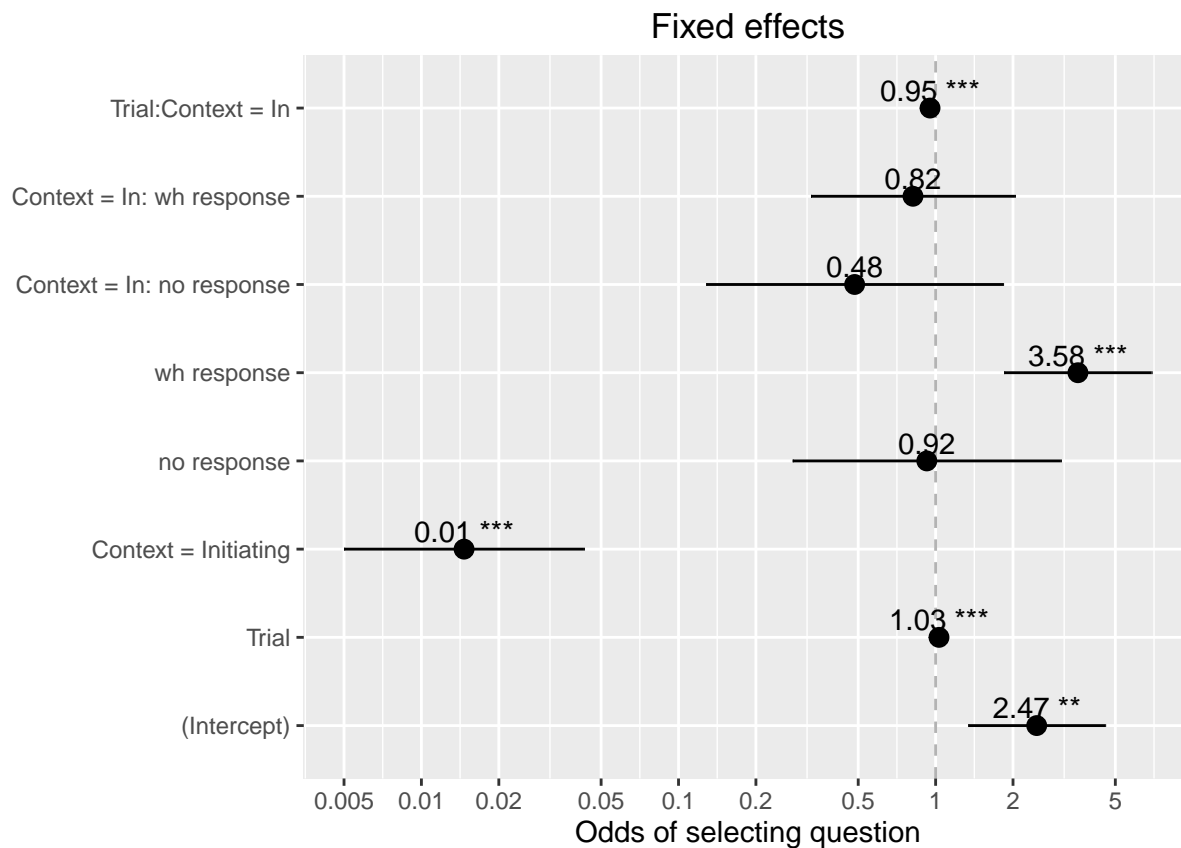
Fixed effects estimates:

```
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',
  "contextIN:responsePhonemenone", "Context = In: no response", "conXrPh",
  "contextIN:responsePhonemewh", "Context = In: wh 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$responsePhoneme = relevel(d$responsePhoneme, 'none')

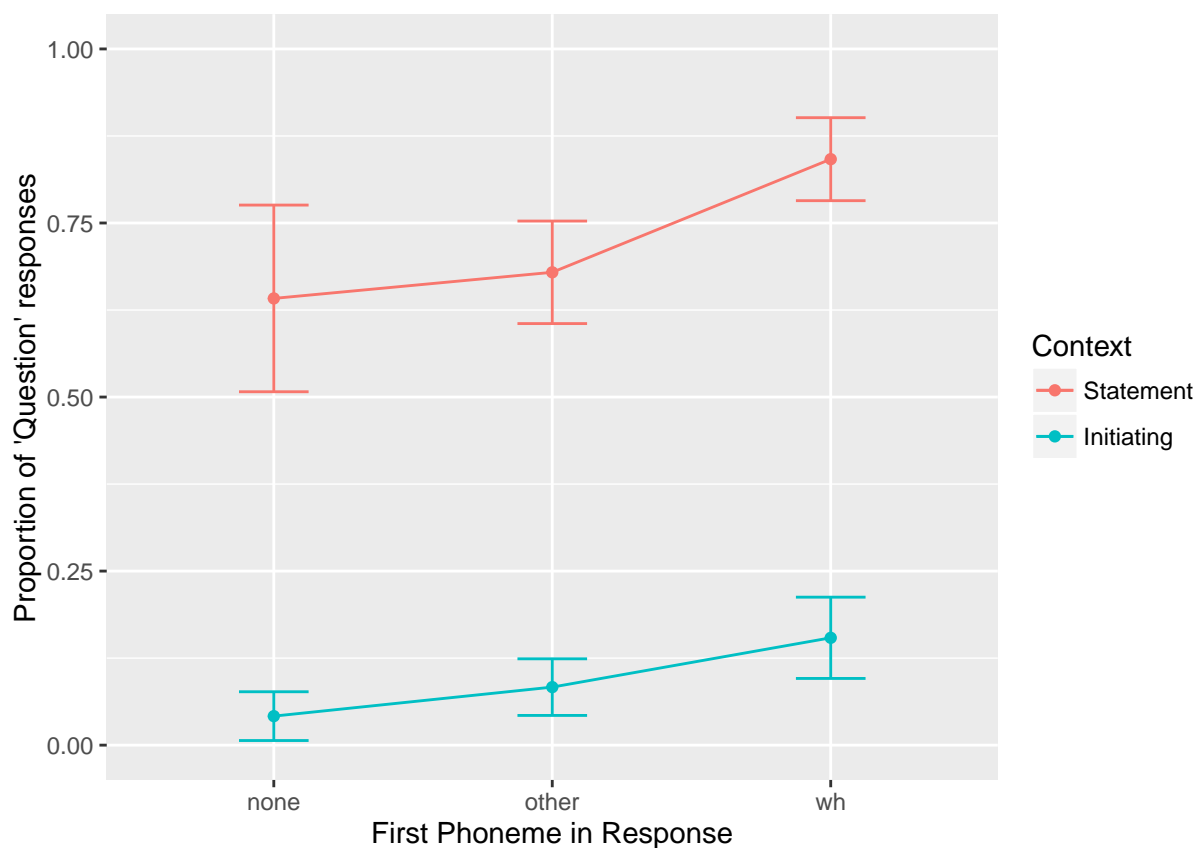
sumStats = group_by(d, partID ,context,responsePhoneme ) %>%
  summarise(mean =mean(answer))

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

dodge <- position_dodge(width=0.5)

main.plot <- ggplot(sumStats2,
  aes(x = responsePhoneme, 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' responses") +
  coord_cartesian(ylim=c(0,1)) +
  scale_color_discrete(breaks=c("ST","IN"),
    labels=c("Statement","Initiating"),
    name="Context")

main.plot
```



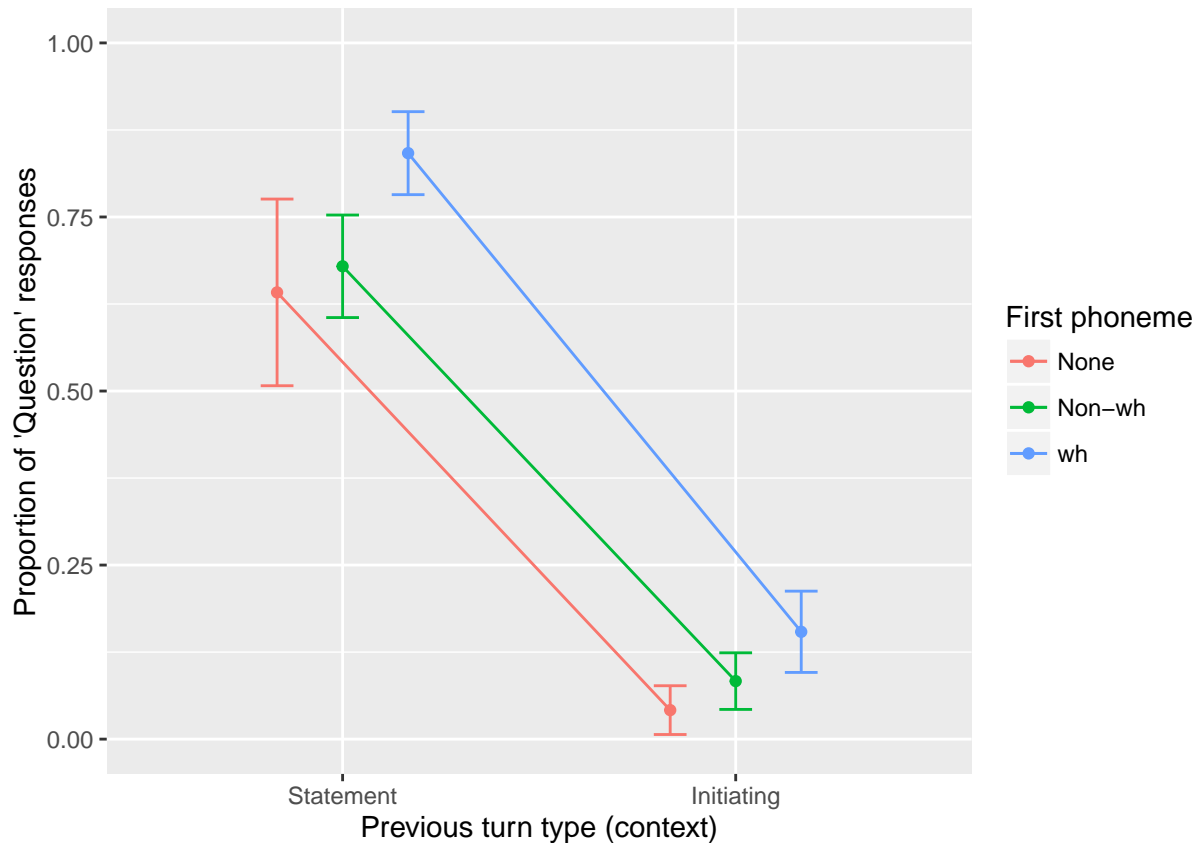
```
pdf("../results/graphs/PropQResponses_by_firstPhoneme_withPartCI.pdf",
     width = 4, height=3)
main.plot
dev.off()
```

```
## pdf
```

```
## 2
```

```
main.plot2 <- ggplot(sumStats2,
  aes(x = context, y = mean, colour=responsePhoneme)) +
  geom_point(position=dodge) + geom_line(aes(group=responsePhoneme), position=dodge) +
  geom_errorbar(aes(ymin=mean-ci, ymax=mean+ci), width=0.25, position=dodge) +
  xlab("Previous turn type (context)") +
  ylab("Proportion of 'Question' responses") +
  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