Supporting material: Analyses of silent gesture. Evolution of efficient encoding of meaning in the visual modality

Anita Slonimska, Asli Ozyurek, and Olga Capirci

Contents

Results   **34**

Load libraries

```r
library(reshape2)
library(plyr)
library(lme4)
library(lattice)
library(scales)
library(ggplot2)
library(sjPlot)
library(Rmisc)
library(dplyr)
library(nlme)
library(optimx)
library(magrittr)
library (sicegar)
library(lmerTest)
library(RColorBrewer)
library(devtools)
library(piecewiseSEM)
library(MuMIn)
library(dplyr)
library(tidyr)
library(minqa)
library(ggeffects)
library(partykit)
library(stringr)
```

Load data

```r
d = read.delim("masterfile_combined.txt")

MS = read.delim("masterfile_density_MS_silent.txt")


## look up frequencies for movement segments (MS)
MS$Movement_unit <- as.character(MS$Movement_unit)


MS$Movement_unit[MS$Movement_unit == "gesture"] <- "Gesture"
MS$Movement_unit[MS$Movement_unit == "body"] <- "Body"
MS$Movement_unit[MS$Movement_unit == "movement"] <- "Movement"

MS$Movement_unit <- as.factor(MS$Movement_unit)
table(MS$Movement_unit)
```

```
##
##      Body   Gesture Movement
##       270      2625      250
```

Convert variables to correct format

```
##homogenize trial entries by leaving only number of level, deleteing D

d$trial <- str_remove(d$trial, "D")

d$Animal_pair <- as.factor(d$Animal_pair)
d$Diff_level <- as.factor(d$Diff_level)
d$trial <- as.factor(d$trial)
d$length<- as.numeric(d$length)
d$simult_kinem <- as.numeric(d$simult_kinem)
d$one_info <- as.numeric(d$one_info)
d$two_info <- as.numeric(d$two_info)
d$three_info <- as.numeric(d$three_info)
d$four_info <- as.numeric(d$four_info)
d$PartID <- as.factor(d$PartID)
d$Age <- as.numeric(d$Age)
d$Sex <- as.factor(d$Sex)
d$Hand <- as.factor(d$Hand)
d$Group <- as.factor(d$Group)
```

```
### ONLY SILENT GESTURE DATA
#work with data which status is only silent_gesture

silent <- d[d$Group == "silent_gesture", ]
```

There were 23 particpants in silent gesture condition, each describing 30 trials (experimental stimuli).The resulting data has 647 data points. Missing data points (n=43) are due to incomplete productions, which were disregarded.

```
#Total number of observations
nrow(silent)
```

```
## [1] 647
```

```
# Number of observations per density level
table(silent$Diff_level)
```

```
##
##  D1  D2  D3  D4  D5
## 135 134 133 125 120
```

LENGTH OF ENCODING

Baseline model

Random effects

```
mA0 = glmer(
  length ~ 1 +
    (1 | PartID),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)

mA1 = glmer(
  length ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)

mA2 = glmer(
  length ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
## boundary (singular) fit: see ?isSingular
```

```
mA3 = glmer(
  length ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair) +
    (0 + Diff_level| PartID) ,
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
## boundary (singular) fit: see ?isSingular
```

Assess the best random structure for models that converge and with non-singular fit (following Barr et al, 2013). Recode into m0.

```
anova(mA0, mA1)
```

```
## Data: silent
## Models:
## mA0: length ~ 1 + (1 | PartID)
## mA1: length ~ 1 + (1 | PartID) + (1 | trial)
##      Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
```

4

```
## mA0  2 2649.4 2658.4 -1322.7    2645.4
## mA1  3 2557.5 2570.9 -1275.7    2551.5 93.969       1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
m0 = glmer(
  length ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

The best random structure includes random effects of participant and random effect of trial.

Fixed effects

```r
#Sex
mSex = glmer(
  length ~ 1 + Sex +
    (1 | PartID) +
    (1 | trial),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)

anova(m0,mSex) #no effect of Sex
```

```
## Data: silent
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mSex: length ~ 1 + Sex + (1 | PartID) + (1 | trial)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0     3 2557.5 2570.9 -1275.7   2551.5
## mSex   4 2557.9 2575.8 -1275.0   2549.9 1.5444      1     0.214
```

```r
#Handedness
mHand = glmer(
  length ~ 1 + Hand +
    (1 | PartID) +
    (1 | trial),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)

anova(m0,mHand) #no effect of handedness
```

```
## Data: silent
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
```

```
## mHand: length ~ 1 + Hand + (1 | PartID) + (1 | trial)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0     3 2557.5 2570.9 -1275.7   2551.5
## mHand  4 2559.5 2577.4 -1275.7   2551.5 0.0039      1     0.9503
```

```r
##Age
mAge = glmer(
  length ~ 1  +  Age +
    (1 | PartID) +
    (1 | trial),
  data = silent,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)

anova(m0, mAge) #no effect of age
```

```
## Data: silent
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mAge: length ~ 1 + Age + (1 | PartID) + (1 | trial)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0     3 2557.5 2570.9 -1275.7   2551.5
## mAge   4 2558.7 2576.6 -1275.3   2550.7 0.7913      1     0.3737
```

No fixed factors to include in baseline model

Effect of Density Level & Contrasts

We are interested in assessing differences between density levels in hierachical order. Glmer compares first level to all other levels. We use forward difference coding to specify contrasts between levels 1 & 2, 2 & 3, 3 & 4, 4 & 5.

```r
# Contrast Coding

# Create contrast matrix

library(codingMatrices)

constrast_matrix <- code_diff_forward(5, contrasts = TRUE, sparse = FALSE) #make a matrix with the cont

dimnames(constrast_matrix) <- list(c("D1","D2","D3", "D4","D5"), c("D1 VS D2","D2 VS D3","D3 VS D4","D4

contrasts(silent$Diff_level) <- constrast_matrix #define the contrasts above for your variable

# run model with Difficulty level

mDiff =glmer(
  length ~ 1 + Diff_level +
    (1 | PartID) +
    (1 | trial),
  data = silent,
```

```
    family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa'))
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(mDiff)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2495.1   2526.4  -1240.5   2481.1      640
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.1459 -0.4287 -0.1388  0.2266  4.4972
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  trial  (Intercept) 0.000000 0.00000
##  PartID (Intercept) 0.007662 0.08753
## Number of obs: 647, groups:  trial, 30; PartID, 23
##
## Fixed effects:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)         1.55650    0.02584  60.240  < 2e-16 ***
## Diff_levelD1 VS D2 -0.19786    0.06374  -3.104 0.001909 **
## Diff_levelD2 VS D3 -0.22669    0.05759  -3.936 8.28e-05 ***
## Diff_levelD3 VS D4 -0.06535    0.05435  -1.202 0.229246
## Diff_levelD4 VS D5 -0.18594    0.05244  -3.546 0.000392 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.047
## Dff_lD2VSD3  0.049 -0.501
## Dff_lD3VSD4  0.000  0.000 -0.473
## Dff_lD4VSD5  0.030  0.000  0.000 -0.517
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
anova(m0, mDiff)
```

```
## Data: silent
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
```

```
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0      3 2557.5 2570.9 -1275.7   2551.5
## mDiff   7 2495.1 2526.4 -1240.5   2481.1 70.413      4  1.857e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Singular fit driven by 0 variance in random effect of trial.

Check variance of trial in baseline model

```
dotplot(ranef(m0))$trial
```
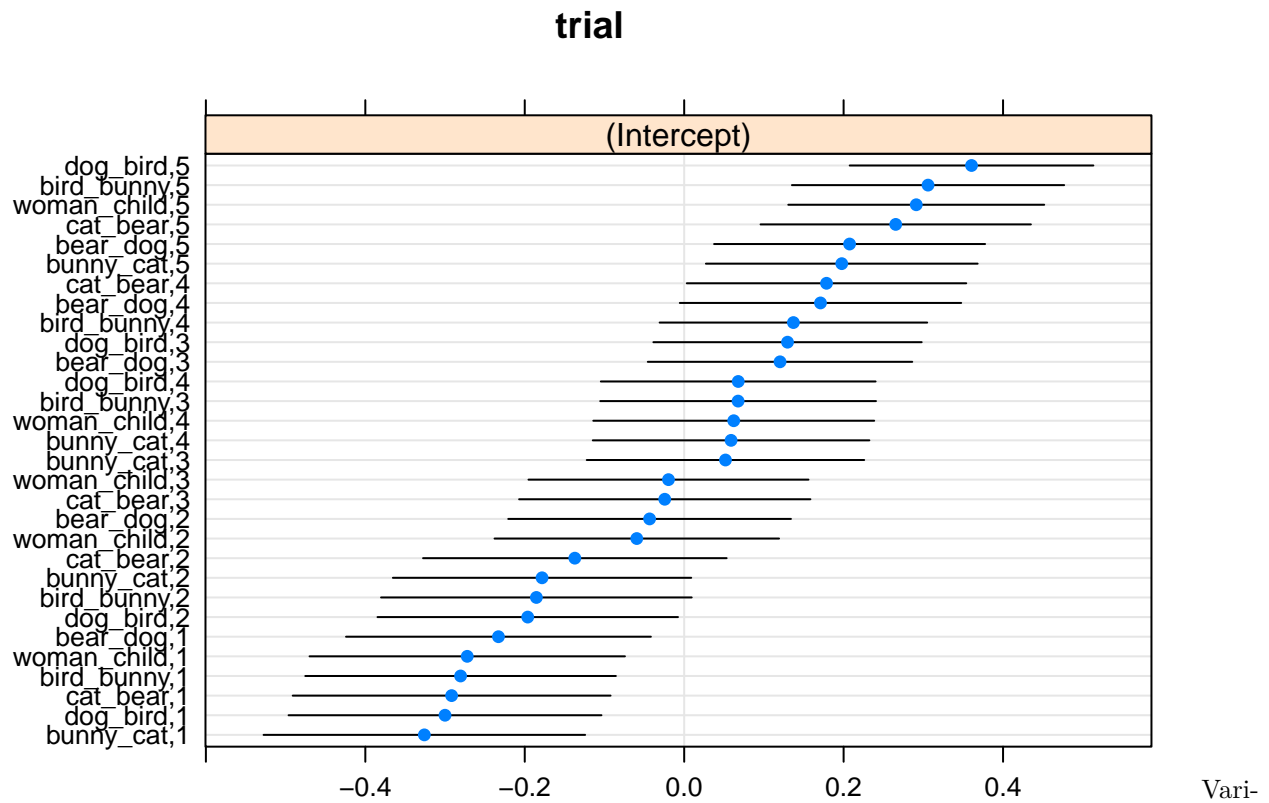

trial

Variance of trial in baseline model is clustered based on the density level (see final number that stands for each density level)

Check model if random effect of trial is left out:

```
mDiff_2 = glmer(
  length ~ 1 + Diff_level +
    (1 | PartID),
  data = silent,
   family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)

summary(mDiff_2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
```

```
##  Family: poisson  ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2493.1   2519.9  -1240.5   2481.1      641
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.1459 -0.4287 -0.1388  0.2266  4.4972
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.007662 0.08753
## Number of obs: 647, groups:  PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        1.55650    0.02584  60.241  < 2e-16 ***
## Diff_levelD1 VS D2 -0.19786    0.06374  -3.104 0.001909 **
## Diff_levelD2 VS D3 -0.22669    0.05759  -3.936 8.28e-05 ***
## Diff_levelD3 VS D4 -0.06535    0.05435  -1.202 0.229244
## Diff_levelD4 VS D5 -0.18594    0.05244  -3.546 0.000392 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.047
## Dff_lD2VSD3  0.049 -0.501
## Dff_lD3VSD4  0.000  0.000 -0.473
## Dff_lD4VSD5  0.030  0.000  0.000 -0.517
```

```r
anova(mDiff, mDiff_2) #no difference between models
```

```
## Data: silent
## Models:
## mDiff_2: length ~ 1 + Diff_level + (1 | PartID)
## mDiff: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##         Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## mDiff_2  6 2493.1 2519.9 -1240.5   2481.1
## mDiff    7 2495.1 2526.4 -1240.5   2481.1     0      1          1
```

Connclusion: Variance of trial in null model is driven by effect of density level nested within each trial. Once diff_level is accounted for in the model, trial no longer explains the varience. Given that results are not influenced by presence/absence of the random effect, we keep trial as random effect based on the initial design of the study.

Results

Model comparison

```
anova(m0, mDiff)
```

```
## Data: silent
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0      3 2557.5 2570.9 -1275.7   2551.5
## mDiff   7 2495.1 2526.4 -1240.5   2481.1 70.413      4  1.857e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effect

```
summary(mDiff)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2495.1   2526.4  -1240.5   2481.1      640
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.1459 -0.4287 -0.1388  0.2266  4.4972
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  trial  (Intercept) 0.000000 0.00000
##  PartID (Intercept) 0.007662 0.08753
## Number of obs: 647, groups:  trial, 30; PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        1.55650    0.02584  60.240  < 2e-16 ***
## Diff_levelD1 VS D2 -0.19786    0.06374  -3.104 0.001909 **
## Diff_levelD2 VS D3 -0.22669    0.05759  -3.936 8.28e-05 ***
## Diff_levelD3 VS D4 -0.06535    0.05435  -1.202 0.229246
## Diff_levelD4 VS D5 -0.18594    0.05244  -3.546 0.000392 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.047
## Dff_lD2VSD3  0.049 -0.501
## Dff_lD3VSD4  0.000  0.000 -0.473
## Dff_lD4VSD5  0.030  0.000  0.000 -0.517
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence intervals (Wald method)

```
CI = confint(mDiff,parm="beta_", method="Wald")
cx = summary(mDiff)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$esimate.linear = exp(cx2[,1])
cx2$esimate.linear.lower = exp(cx2[,2])
cx2$esimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2
```

```
##                   estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)                 1.56  1.51   1.61       0.03   60.24     0.00
## Diff_levelD1 VS D2         -0.20 -0.32  -0.07       0.06   -3.10     0.00
## Diff_levelD2 VS D3         -0.23 -0.34  -0.11       0.06   -3.94     0.00
## Diff_levelD3 VS D4         -0.07 -0.17   0.04       0.05   -1.20     0.23
## Diff_levelD4 VS D5         -0.19 -0.29  -0.08       0.05   -3.55     0.00
##                   esimate.linear esimate.linear.lower
## (Intercept)                 4.74                 4.51
## Diff_levelD1 VS D2          0.82                 0.72
## Diff_levelD2 VS D3          0.80                 0.71
## Diff_levelD3 VS D4          0.94                 0.84
## Diff_levelD4 VS D5          0.83                 0.75
##                   esimate.linear.upper
## (Intercept)                       4.99
## Diff_levelD1 VS D2                0.93
## Diff_levelD2 VS D3                0.89
## Diff_levelD3 VS D4                1.04
## Diff_levelD4 VS D5                0.92
```

Random effects
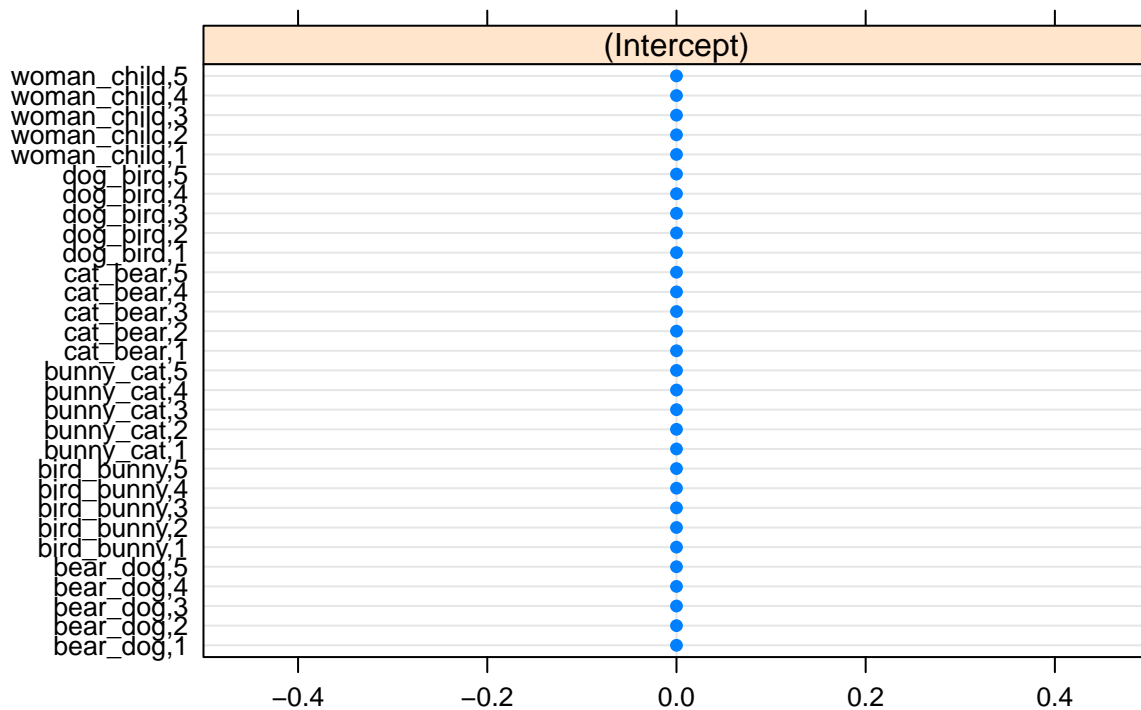
```
#Participant
dotplot(ranef(mDiff))$PartID
```

PartID


```
#Trial
dotplot(ranef(mDiff))$trial
```
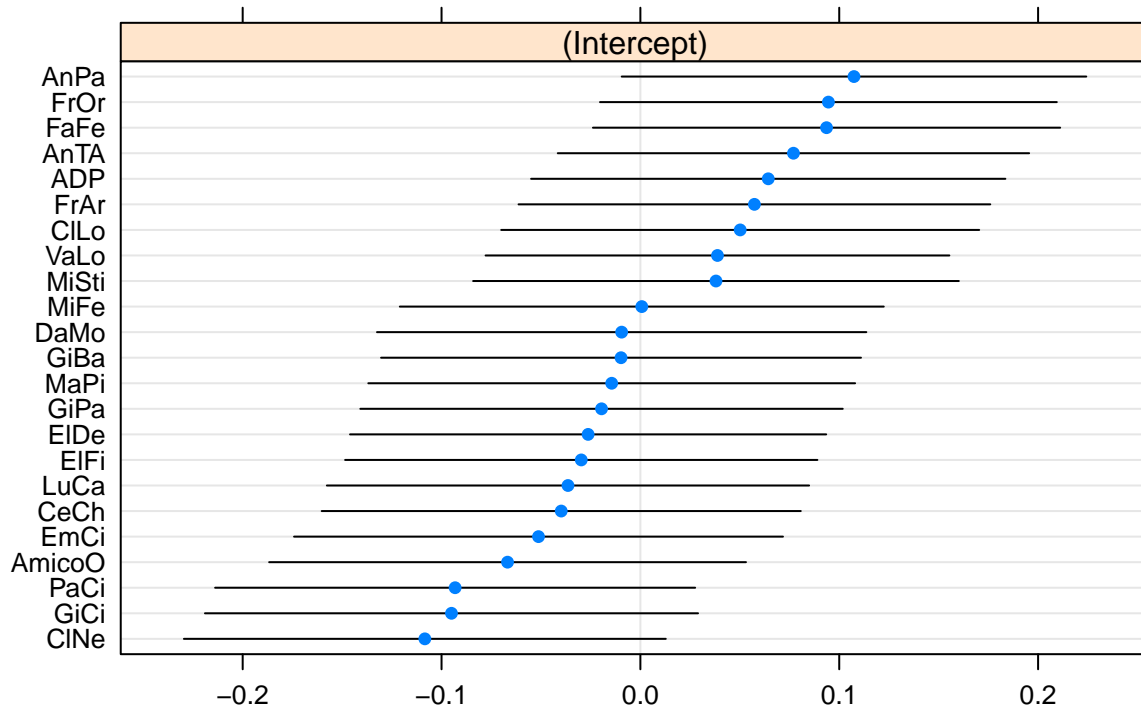
trial

Descriptive statistics of raw data

```
#Descriptive statistics
sumStats = group_by(silent, PartID , Diff_level ) %>%
  summarise(mean =mean(length) )

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

sumStats2$Diff_level <- as.character(sumStats2$Diff_level)

sumStats2$Diff_level[sumStats2$Diff_level == "D1"] <- "L1"
sumStats2$Diff_level[sumStats2$Diff_level == "D2"] <- "L2"
sumStats2$Diff_level[sumStats2$Diff_level == "D3"] <- "L3"
sumStats2$Diff_level[sumStats2$Diff_level == "D4"] <- "L4"
sumStats2$Diff_level[sumStats2$Diff_level == "D5"] <- "L5"

#Inspect statistics
sumStats2
```

```
##   Diff_level  N     mean        sd        se        ci    upper    lower
## 1         L1 23 3.334783 0.5958169 0.1242364 0.2576506 3.592433 3.077132
## 2         L2 23 4.063768 0.7439258 0.1551192 0.3216976 4.385466 3.742070
## 3         L3 23 5.105797 1.0862154 0.2264916 0.4697148 5.575512 4.636082
## 4         L4 23 5.399275 0.8884284 0.1852501 0.3841852 5.783461 5.015090
## 5         L5 23 6.560145 1.3660359 0.2848382 0.5907182 7.150863 5.969427
```

Plot for length

```
  main.plot.length <- ggplot(sumStats2,
                    aes(x = Diff_level, y = mean, group=1)) +
    geom_point(size=3, color= "dodgerblue4") + geom_line(color= "dodgerblue4") + theme(aspect.ratio = 9/
    geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25, color= "dodgerblue4") + xlab("Information
    ylab("Mean N of total MS per trial")  +
    theme(axis.text.y = element_text(colour="grey20",size=12,angle=90,hjust=.5,vjust=.5,face="plain"))+
    theme(axis.text.x = element_text(colour="grey20",size=12,hjust=.5,vjust=.5,face="plain")) +
    coord_cartesian(ylim=c(1,8))
  main.plot.length
```
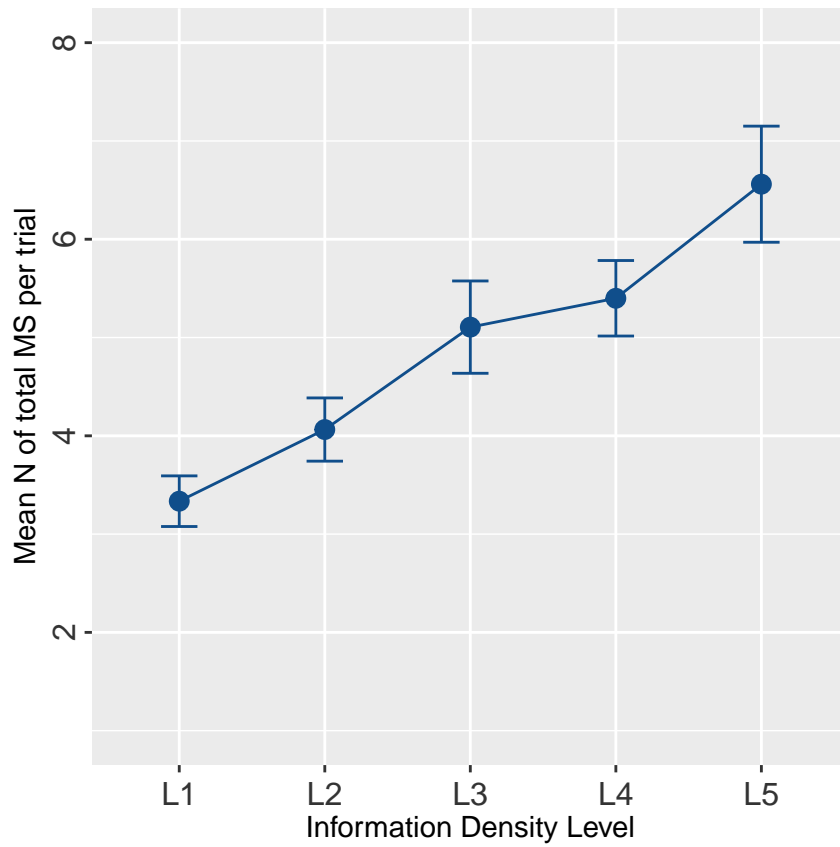
```
bold.text <- element_text( size = 13)
main.plot.length + theme(title = bold.text, axis.title = bold.text)
```
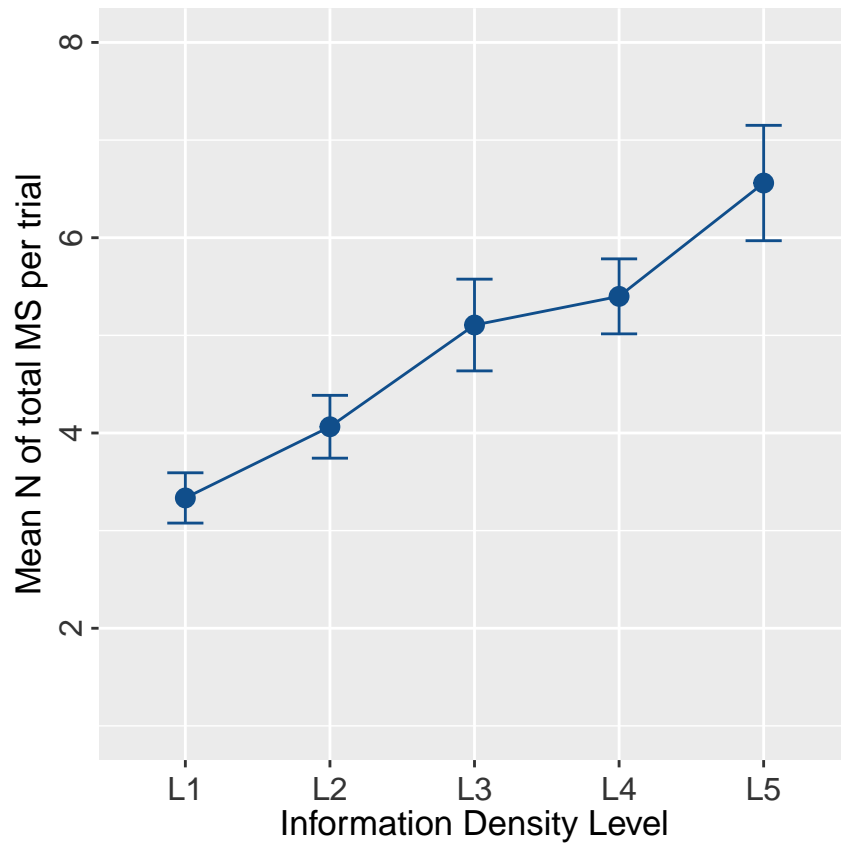
```
ggsave("plot_length.png")
```

```
## Saving 6.5 x 4.5 in image
```

KINEMATIC SIMULTANEITY

Baseline model

Random effects

```
mA0 = glmer(
  cbind(simult_kinem,one_info) ~ 1 +
    (1 | PartID),
  data = silent, family= "binomial",
      control = glmerControl(optimizer = 'bobyqa')
)

mA1 = glmer(
  cbind(simult_kinem,one_info) ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data = silent, family= "binomial",
      control = glmerControl(optimizer = 'bobyqa')
)
```

```
mA2 = glmer(
  cbind(simult_kinem,one_info) ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

```
## boundary (singular) fit: see ?isSingular
```

```
  mA3 = glmer(
  cbind(simult_kinem,one_info) ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair) +
    (1 + Diff_level| PartID) ,
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

```
## boundary (singular) fit: see ?isSingular
```

Assess the best random structure for models that converge and with non-singular fit (following Barr et al, 2013). Recode into m0.

```
anova(mA0, mA1)
```

```
## Data: silent
## Models:
## mA0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID)
## mA1: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
##     Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mA0  2 1671.4 1680.3 -833.69   1667.4
## mA1  3 1373.9 1387.3 -683.96   1367.9 299.45      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m0 = glmer(
  cbind(simult_kinem,one_info)  ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

Fixed effects

16

```
##Sex

mSex = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Sex +
    (1 | PartID) +
    (1 | trial),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)

anova(m0,mSex) #no significant effect of Sex
```

```
## Data: silent
## Models:
## m0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
## mSex: cbind(simult_kinem, one_info) ~ 1 + Sex + (1 | PartID) + (1 |
## mSex:      trial)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0     3 1373.9 1387.3 -683.96   1367.9
## mSex   4 1375.1 1393.0 -683.54   1367.1 0.8587      1     0.3541
```

```
##Handedness
mHand = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Hand +
    (1 | PartID) +
    (1 | trial),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)


anova(m0,mHand) #no significant effect of handedness
```

```
## Data: silent
## Models:
## m0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
## mHand: cbind(simult_kinem, one_info) ~ 1 + Hand + (1 | PartID) + (1 |
## mHand:      trial)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0      3 1373.9 1387.3 -683.96   1367.9
## mHand   4 1374.9 1392.8 -683.45   1366.9 1.0198      1     0.3126
```

```
##Age

mAge = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Age +
    (1 | PartID) +
    (1 | trial),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

```r
anova(m0, mAge) #no significant effect of age
```

```
## Data: silent
## Models:
## m0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
## mAge: cbind(simult_kinem, one_info) ~ 1 + Age + (1 | PartID) + (1 |
## mAge:     trial)
##     Df   AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## m0    3 1373.9 1387.3 -683.96   1367.9
## mAge  4 1375.6 1393.5 -683.82   1367.6 0.298      1     0.5852
```

```r
##Our baseline model is m0 as non of the other models were significantly better
```

Effect of Density Level & Contrasts

We are interested in assessing differences between density levels in hierachical order. Glmer compares first level to all other levels. We use forward difference coding to specify contrasts between levels 1 & 2, 2 & 3, 3 & 4, 4 & 5.

```r
# Contrast Coding

# Create contrast matrix

library(codingMatrices)

constrast_matrix <- code_diff_forward(5, contrasts = TRUE, sparse = FALSE) #make a matrix with the cont

dimnames(constrast_matrix) <- list(c("D1","D2","D3", "D4","D5"), c("D1 VS D2","D2 VS D3","D3 VS D4","D4

contrasts(silent$Diff_level) <- constrast_matrix #define the contrasts above for your variable

# run model with Difficulty level

mDiff = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Diff_level +
    (1 | PartID) +
    (1 | trial),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

```
## boundary (singular) fit: see ?isSingular
```

```r
anova(m0, mDiff)  #significant effect
```

```
## Data: silent
## Models:
## m0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
## mDiff:     (1 | trial)
```

```
##         Df     AIC     BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0      3 1373.9 1387.3 -683.96    1367.9
## mDiff   7 1259.5 1290.9 -622.78    1245.5 122.37      4  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
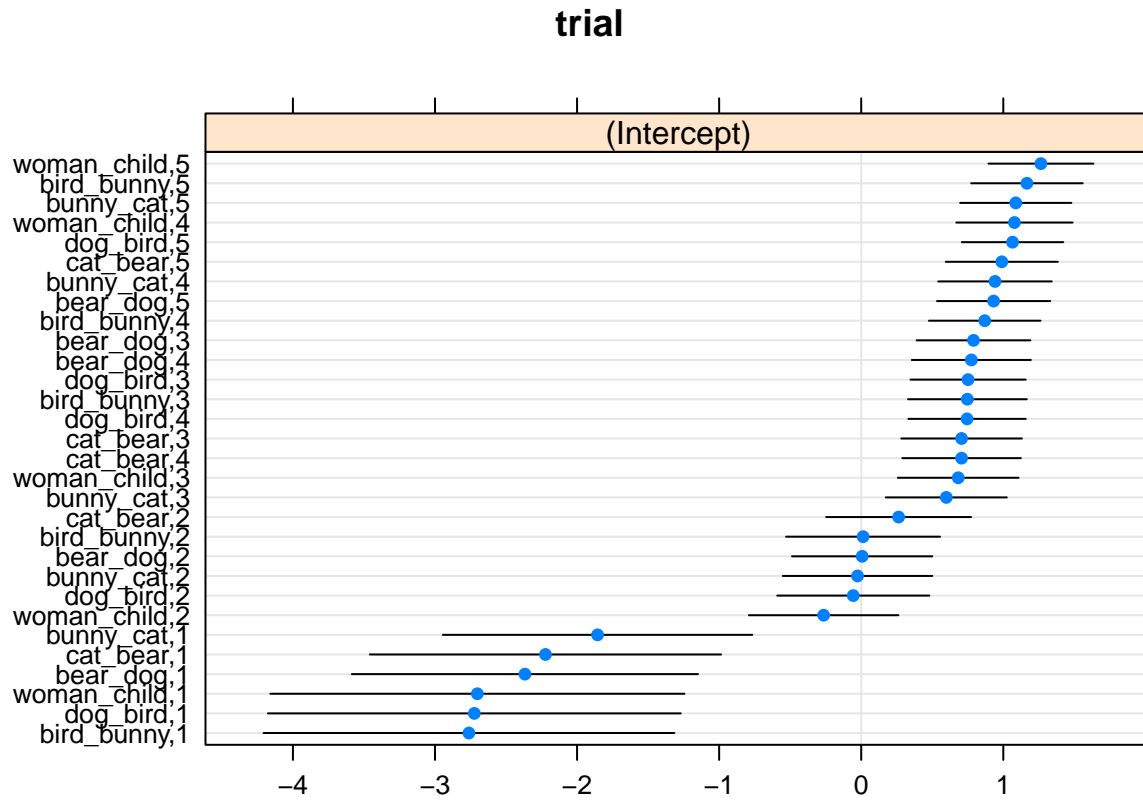
summary(mDiff)

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
##     (1 | trial)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   1259.6   1290.9   -622.8   1245.6      640
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9319 -0.2939 -0.1212  0.2781  5.9741
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  trial  (Intercept) 0.0000   0.0000
##  PartID (Intercept) 0.1499   0.3872
## Number of obs: 647, groups:  trial, 30; PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -1.4619     0.1335 -10.949  < 2e-16 ***
## Diff_levelD1 VS D2 -3.4463     0.5130  -6.718 1.84e-11 ***
## Diff_levelD2 VS D3 -0.7468     0.1335  -5.596 2.20e-08 ***
## Diff_levelD3 VS D4 -0.1424     0.1139  -1.250   0.2113
## Diff_levelD4 VS D5 -0.2361     0.1084  -2.178   0.0294 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.703
## Dff_lD2VSD3  0.053 -0.163
## Dff_lD3VSD4  0.005  0.000 -0.435
## Dff_lD4VSD5  0.014  0.000  0.002 -0.512
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

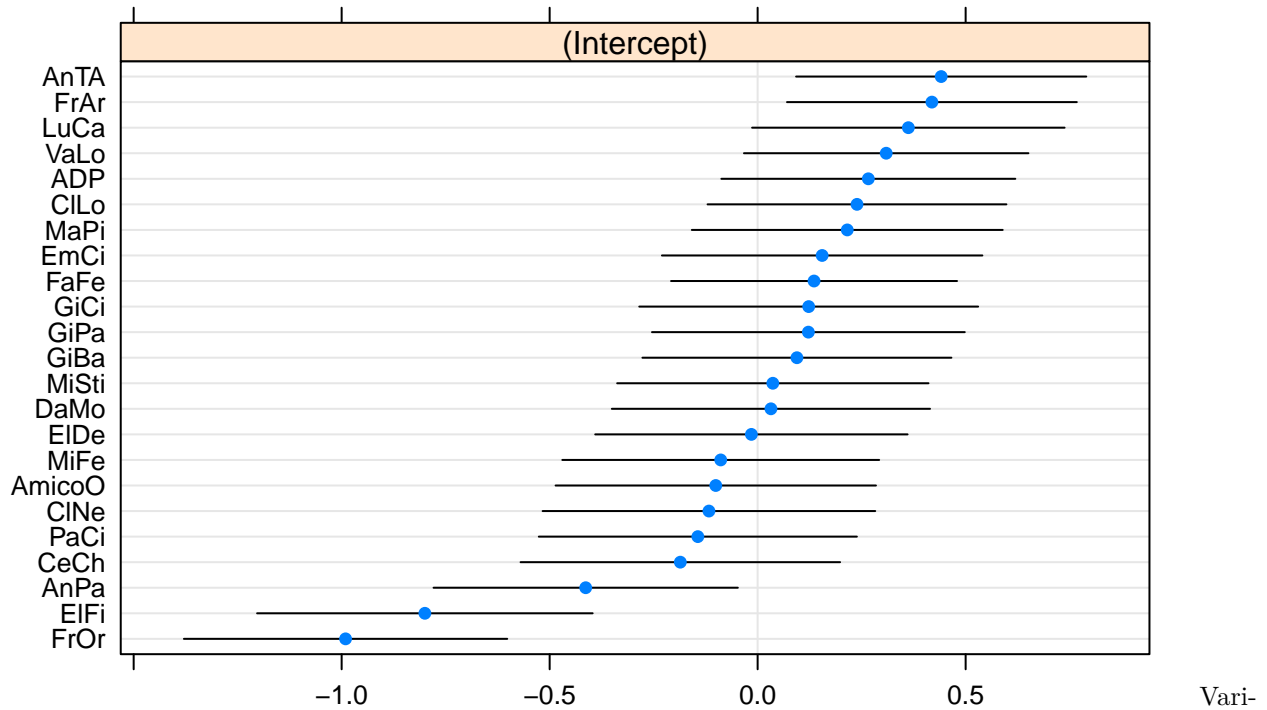Singular fit driven by 0 variance in random effect of trial.

Check variance of trial in baseline model

```
dotplot(ranef(m0))$trial
```

trial


```
dotplot(ranef(m0))$PartID
```

PartID

Variance of trial in baseline model is mainly clustered based on the density level (see final number that stands for each density level). Random effect of PartID seems normal.

Check whether model differs if random effect of trial is left out:

```
mDiff_2 = glmer(
  cbind(simult_kinem,one_info) ~ 1 + Diff_level +
    (1 | PartID),
  data = silent, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)


summary(mDiff_2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   1257.6   1284.4   -622.8   1245.6      641
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9319 -0.2939 -0.1212  0.2781  5.9741
##
## Random effects:
```

```
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.1499   0.3872
## Number of obs: 647, groups:  PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -1.4619     0.1335 -10.949  < 2e-16 ***
## Diff_levelD1 VS D2 -3.4463     0.5130  -6.718 1.84e-11 ***
## Diff_levelD2 VS D3 -0.7468     0.1335  -5.596 2.20e-08 ***
## Diff_levelD3 VS D4 -0.1424     0.1139  -1.250   0.2113
## Diff_levelD4 VS D5 -0.2361     0.1084  -2.178   0.0294 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.703
## Dff_lD2VSD3  0.053 -0.163
## Dff_lD3VSD4  0.005  0.000 -0.435
## Dff_lD4VSD5  0.014  0.000  0.002 -0.512
```

```r
anova(mDiff, mDiff_2)  #no difference between models
```

```
## Data: silent
## Models:
## mDiff_2: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID)
## mDiff: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
## mDiff:     (1 | trial)
##         Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## mDiff_2  6 1257.5 1284.4 -622.78   1245.5
## mDiff    7 1259.5 1290.9 -622.78   1245.5     0      1          1
```

Variance of trial in null model is driven by effect of density level nested within each trial. Once diff_level is accounted for in the model, trial no longer explains the variation. Given that results are not influenced by presence/absence of the random effect, we keep trial as random effect based on the initial design of the study.

Results

Model comparison

```r
anova(m0, mDiff)
```

```
## Data: silent
## Models:
## m0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
## mDiff:     (1 | trial)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0     3 1373.9 1387.3 -683.96   1367.9
```

```
## mDiff  7 1259.5 1290.9 -622.78    1245.5 122.37       4  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effect

```r
summary(mDiff)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
##     (1 | trial)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   1259.6   1290.9   -622.8   1245.6      640
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9319 -0.2939 -0.1212  0.2781  5.9741
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  trial  (Intercept) 0.0000   0.0000
##  PartID (Intercept) 0.1499   0.3872
## Number of obs: 647, groups:  trial, 30; PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -1.4619     0.1335 -10.949  < 2e-16 ***
## Diff_levelD1 VS D2 -3.4463     0.5130  -6.718 1.84e-11 ***
## Diff_levelD2 VS D3 -0.7468     0.1335  -5.596 2.20e-08 ***
## Diff_levelD3 VS D4 -0.1424     0.1139  -1.250   0.2113
## Diff_levelD4 VS D5 -0.2361     0.1084  -2.178   0.0294 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.703
## Dff_lD2VSD3  0.053 -0.163
## Dff_lD3VSD4  0.005  0.000 -0.435
## Dff_lD4VSD5  0.014  0.000  0.002 -0.512
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Get confidence intervals (Wald method)

```
CI = confint(mDiff,parm="beta_", method="Wald")
cx = summary(mDiff)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2 = round(cx2, digits = 2)
cx2
```

```
##                    estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)                 -1.46 -1.72  -1.20       0.13  -10.95     0.00
## Diff_levelD1 VS D2          -3.45 -4.45  -2.44       0.51   -6.72     0.00
## Diff_levelD2 VS D3          -0.75 -1.01  -0.49       0.13   -5.60     0.00
## Diff_levelD3 VS D4          -0.14 -0.37   0.08       0.11   -1.25     0.21
## Diff_levelD4 VS D5          -0.24 -0.45  -0.02       0.11   -2.18     0.03
```

Get probabilities for estimates in each level.

```
get_model_data(mDiff,"pred")
```

```
## $Diff_level
##
## # Predicted probabilities of cbind(simult_kinem, one_info)
## # x = Diff_level
##
##  x predicted std.error conf.low conf.high
## 1     0.008     0.134    0.006     0.011
## 2     0.210     0.614    0.074     0.470
## 3     0.359     0.194    0.277     0.451
## 4     0.393     0.176    0.314     0.477
## 5     0.450     0.173    0.368     0.535
##
## Adjusted for:
## * PartID = 0 (population-level)
## *  trial = 0 (population-level)


## Standard errors are on link-scale (untransformed).
```
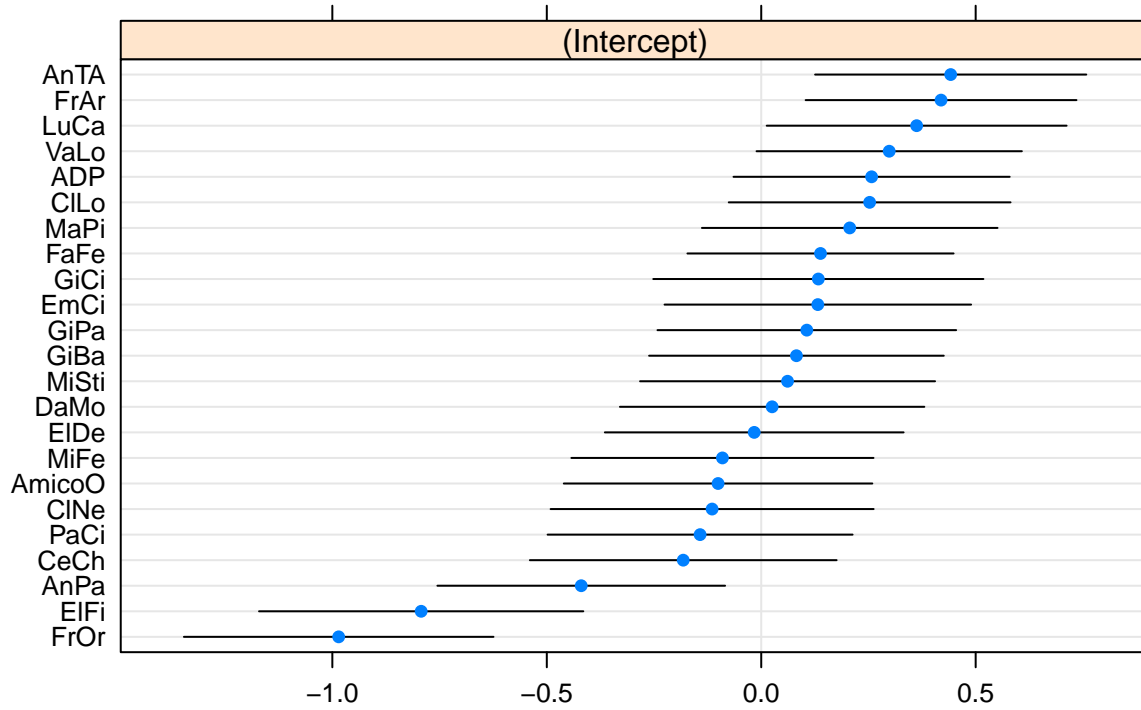
Random effects

```
#Participant
dotplot(ranef(mDiff))$PartID
```
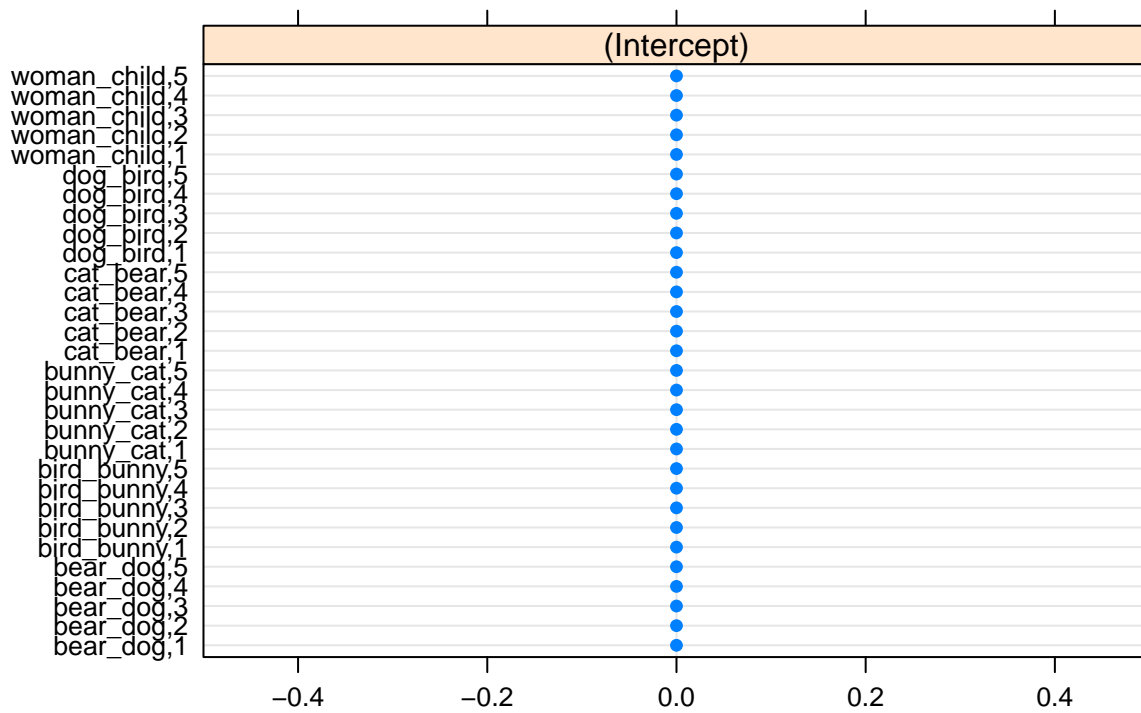
PartID


```
#Trial
dotplot(ranef(mDiff))$trial
```

trial

Descriptive statistics of raw data

```r
#Make new column with proportion of simultaneous MS versus total MS per trial.
silent$simult_prop <- (silent$simult_kinem/silent$length)

#Descriptive statistics
sumStats = group_by(silent, PartID , Diff_level ) %>%
  summarise(mean =mean(simult_prop) )

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

sumStats2$Diff_level <- as.character(sumStats2$Diff_level)

sumStats2$Diff_level[sumStats2$Diff_level == "D1"] <- "L1"
sumStats2$Diff_level[sumStats2$Diff_level == "D2"] <- "L2"
sumStats2$Diff_level[sumStats2$Diff_level == "D3"] <- "L3"
sumStats2$Diff_level[sumStats2$Diff_level == "D4"] <- "L4"
sumStats2$Diff_level[sumStats2$Diff_level == "D5"] <- "L5"

#Inspect statistics
sumStats2
```

```
##   Diff_level  N       mean         sd          se         ci      upper
## 1         L1 23 0.00731539 0.01931474 0.004027402 0.00835232 0.01566771
## 2         L2 23 0.21373361 0.09673663 0.020170981 0.04183205 0.25556566
## 3         L3 23 0.36387200 0.09102782 0.018980612 0.03936338 0.40323538
## 4         L4 23 0.40929967 0.12041682 0.025108644 0.05207214 0.46137181
## 5         L5 23 0.45507262 0.12007842 0.025038080 0.05192580 0.50699842
##        lower
## 1 -0.00103693
## 2  0.17190155
## 3  0.32450862
## 4  0.35722753
## 5  0.40314682
```

Plot for simultaneity

```
main.plot <- ggplot(sumStats2,
                    aes(x = Diff_level, y = mean)) +
  geom_bar(stat= "identity", width = 0.4, fill = "dodgerblue4") + theme(aspect.ratio = 9/9) +
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25) + xlab("Information Density Level") +
  ylab("Mean proportion of MS \n with simultaneous articulators") + coord_cartesian(ylim=c(0,1)) +
  theme(axis.text.y = element_text(colour="grey20",size=12,angle=90,hjust=.5,vjust=.5,face="plain"))+
  theme(axis.text.x = element_text(colour="grey20",size=12,hjust=.5,vjust=.5,face="plain"))

bold.text <- element_text( size = 13)

main.plot + theme(title = bold.text, axis.title = bold.text)
```
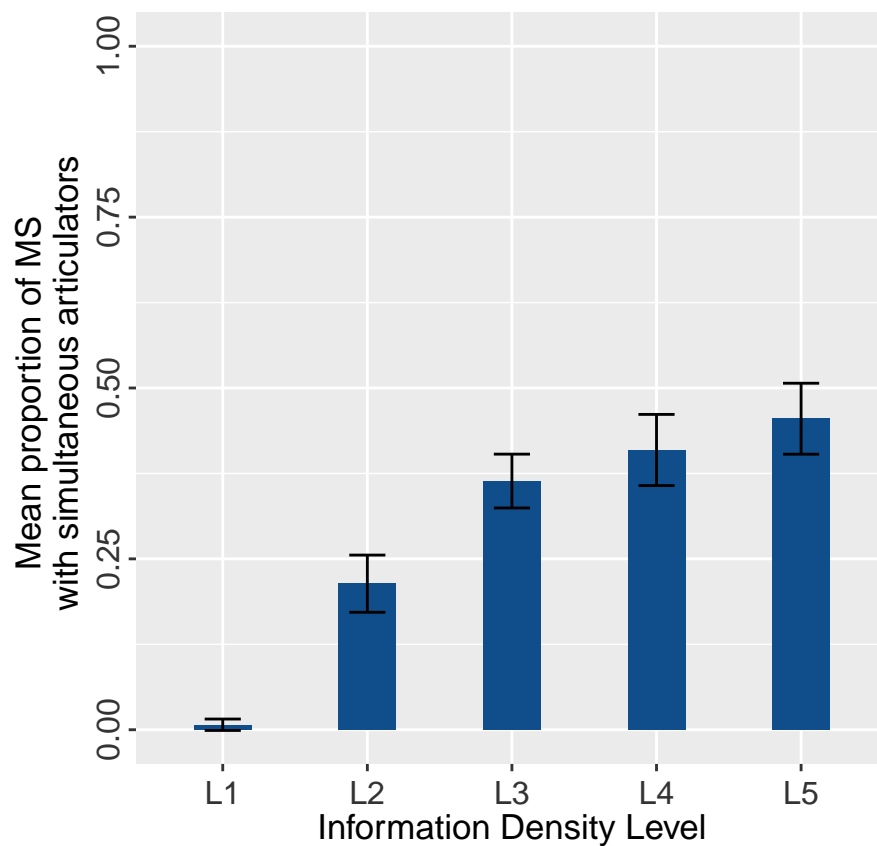


```
ggsave("plot_simultaneity.png")
```

```
## Saving 6.5 x 4.5 in image
```

DENSITY of SIMULTANEITY

Load data of density of simultaneity

```
d<- read.delim2("masterfile_density_combined.txt")
```

```
### ONLY SILENT GESTURE DATA
#work with data which status is only silent_gesture

silent <- d[d$Group == "silent_gesture", ]
```

There were 23 particpants each describing 30 trials (experimental stimuli). There were total of 3145 movement segments (MS) used.

```
#Total number of observations (movement segments produced)
sum(complete.cases(silent))
```

```
## [1] 3145
```

```
# Number of observations per density level
table(silent$Diff_level)
```

```
##
##   D1  D2  D3  D4  D5
## 449 534 677 702 783
```

```
# Number of observations per number of information units in a MS
table(silent$Info_n)
```

```
##
##     1    2    3    4
## 2149  727  262    7
```

```
# Number of observations per density level and N of info.units in a MS
table (silent$Diff_level,silent$Info_n )
```

```
##
##         1    2    3    4
##   D1  445    4    0    0
##   D2  417  113    4    0
##   D3  431  144   99    3
##   D4  423  246   33    0
##   D5  433  220  126    4
```

Baseline model

```
mSim2A0 = glmer(
  Info_n ~ 1 +
    (1 | PartID),
  data =  silent,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
```

```
)

mSim2A1 = glmer(
  Info_n ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data =  silent,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)


mSim2A2 = glmer(
  Info_n ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair),
  data =  silent,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
## boundary (singular) fit: see ?isSingular
```

Assess the best random structure for models that converge and with non-singular fit (following Barr et al, 2013). Recode into m0.

```
anova(mSim2A0, mSim2A1)
```

```
## Data: silent
## Models:
## mSim2A0: Info_n ~ 1 + (1 | PartID)
## mSim2A1: Info_n ~ 1 + (1 | PartID) + (1 | trial)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mSim2A0   2 7827.2 7839.3 -3911.6   7823.2
## mSim2A1   3 7796.6 7814.7 -3895.3   7790.6 32.631      1  1.114e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##Recode null model

m0 = glmer(
  Info_n ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data =  silent,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)
```

Fixed effects

```
##Sex

mSim2Sex = glmer(
  Info_n ~ 1 + Sex +
    (1 | PartID) +
    (1 | trial),
  data =  silent,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)

anova(m0,mSim2Sex)
```

```
## Data: silent
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mSim2Sex: Info_n ~ 1 + Sex + (1 | PartID) + (1 | trial)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0         3 7796.6 7814.7 -3895.3   7790.6
## mSim2Sex   4 7797.6 7821.8 -3894.8   7789.6 0.9559      1     0.3282
```

```
##Handedness
mSim2Hand = glmer(
  Info_n ~ 1 + Hand +
    (1 | PartID) +
    (1 | trial),
  data =  silent,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)
#model is not converging. no influence of age is expected, thus leaving this contorl out.



anova(m0,mSim2Hand)
```

```
## Data: silent
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mSim2Hand: Info_n ~ 1 + Hand + (1 | PartID) + (1 | trial)
##            Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## m0          3 7796.6 7814.7 -3895.3   7790.6
## mSim2Hand   4 7797.8 7822.0 -3894.9   7789.8 0.807      1      0.369
```

```
##Age

mSim2Age = glmer(
  Info_n ~ 1 + Age +
    (1 | PartID) +
    (1 | trial),
  data =  silent,
  family = "poisson",
```

```
    control = glmerControl(optimizer = 'bobyqa')
)
```

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

```r
anova(m0,mSim2Age)
```

```
## Data: silent
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mSim2Age: Info_n ~ 1 + Age + (1 | PartID) + (1 | trial)
##          Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## m0        3 7796.6 7814.7 -3895.3   7790.6
## mSim2Age  4 7798.6 7822.8 -3895.3   7790.6 8e-04      1     0.9768
```

Our baseline model is m0 as non of the other models were significantly better.

Effect of Density Level & Contrasts

We are interested in assessing differences between density levels in hierachical order. Glmer compares first
level to all other levels. We use forward difference coding to specify contrasts between levels 1 & 2, 2 & 3, 3
& 4, 4 & 5.

```r
# Contrast Coding
# Create contrast matrix

library(codingMatrices)

constrast_matrix <- code_diff_forward(5, contrasts = TRUE, sparse = FALSE) #make a matrix with the cont

dimnames(constrast_matrix) <- list(c("D1","D2","D3", "D4","D5"), c("D1 VS D2","D2 VS D3","D3 VS D4","D4

contrasts(silent$Diff_level) <- constrast_matrix #define the contrasts above for your variable (data=yo


mDiff = glmer(
  Info_n ~ 1 + Diff_level +
       (1 | PartID) +
       (1 | trial),
  data =  silent,
     family = "poisson",
     control = glmerControl(optimizer = 'bobyqa')
   )
```

```
## boundary (singular) fit: see ?isSingular
```

```r
anova(m0, mDiff)
```

```
## Data: silent
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0      3 7796.6 7814.7 -3895.3   7790.6
## mDiff   7 7737.4 7779.8 -3861.7   7723.4 67.188      4  8.898e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

summary(mDiff)

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##     Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##       AIC      BIC   logLik deviance df.resid
##    7737.4   7779.8  -3861.7   7723.4     3138
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.5458 -0.4060 -0.1979  0.3508  1.8885
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  trial  (Intercept) 0.000000 0.00000
##  PartID (Intercept) 0.002305 0.04801
## Number of obs: 3145, groups:  trial, 30; PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        0.29516    0.01900  15.537  < 2e-16 ***
## Diff_levelD1 VS D2 -0.19316    0.06116  -3.158  0.00159 **
## Diff_levelD2 VS D3 -0.21544    0.05004  -4.305 1.67e-05 ***
## Diff_levelD3 VS D4  0.05011    0.04431   1.131  0.25803
## Diff_levelD4 VS D5 -0.11535    0.04220  -2.733  0.00627 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.116
## Dff_lD2VSD3  0.117 -0.500
## Dff_lD3VSD4 -0.003  0.000 -0.439
## Dff_lD4VSD5  0.050 -0.001  0.001 -0.529
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```
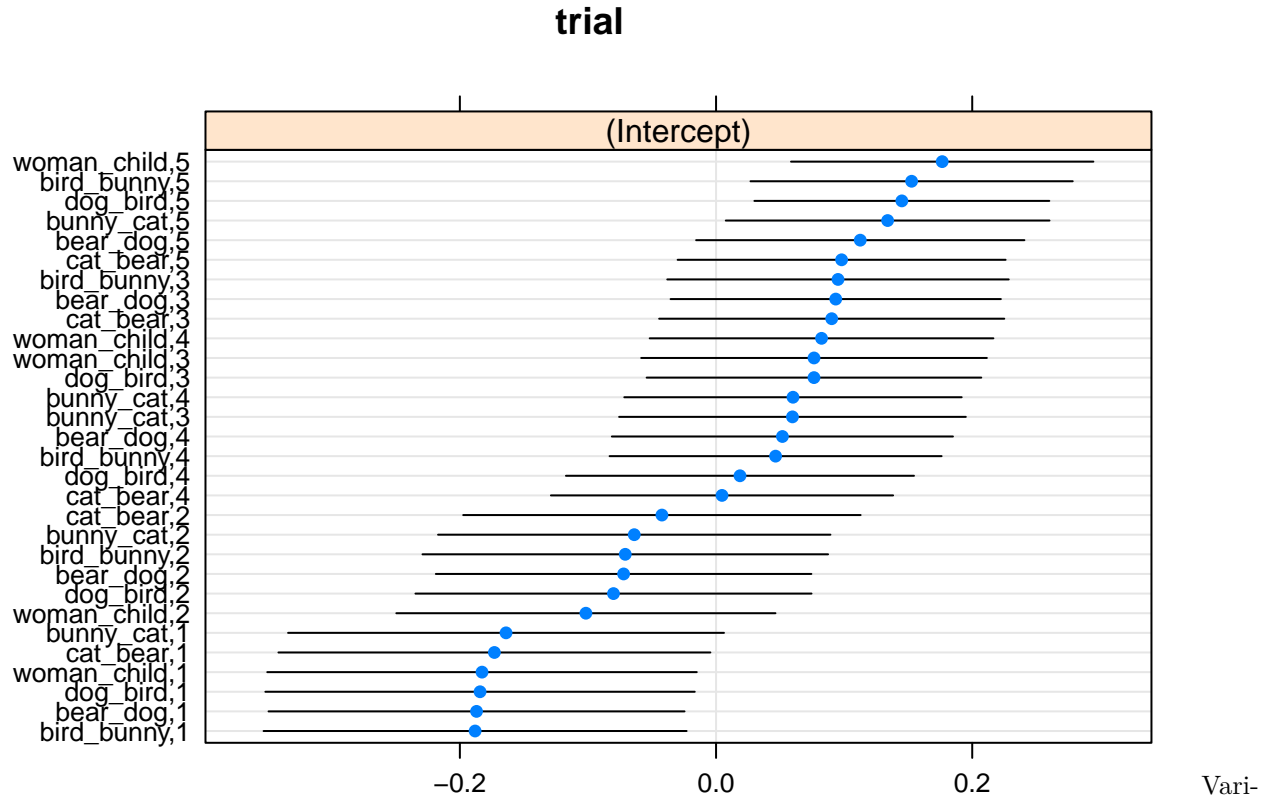
Singular fit driven by 0 variance in random effect of trial.

Check variance of trial in baseline model

```
dotplot(ranef(m0))$trial
```


trial

Vari-ance of trial in baseline model is mainly clustered based on the density level (see final number that stands for each density level)

##Check whether model differs if random effect of trial is left out:

```
mDiff_2 = glmer(
  cbind(Info_n) ~ 1 + Diff_level +
      (1 | PartID),
  data =  silent,
     family = "poisson",
     control = glmerControl(optimizer = 'bobyqa')
  )

summary(mDiff_2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: cbind(Info_n) ~ 1 + Diff_level + (1 | PartID)
##     Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   7735.4   7771.7  -3861.7   7723.4     3139
##
## Scaled residuals:
```

```
##     Min     1Q  Median      3Q     Max
## -0.5458 -0.4060 -0.1979  0.3508  1.8885
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.002305 0.04801
## Number of obs: 3145, groups:  PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        0.29516    0.01900  15.537  < 2e-16 ***
## Diff_levelD1 VS D2 -0.19316    0.06116  -3.158  0.00159 **
## Diff_levelD2 VS D3 -0.21544    0.05004  -4.305 1.67e-05 ***
## Diff_levelD3 VS D4  0.05011    0.04431   1.131  0.25802
## Diff_levelD4 VS D5 -0.11535    0.04220  -2.733  0.00627 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.116
## Dff_lD2VSD3  0.117 -0.500
## Dff_lD3VSD4 -0.003  0.000 -0.439
## Dff_lD4VSD5  0.050 -0.001  0.001 -0.529
```

```r
anova(mDiff, mDiff_2) #no difference between models
```

```
## Data: silent
## Models:
## mDiff_2: cbind(Info_n) ~ 1 + Diff_level + (1 | PartID)
## mDiff: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##         Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## mDiff_2  6 7735.4 7771.7 -3861.7   7723.4
## mDiff    7 7737.4 7779.8 -3861.7   7723.4     0      1          1
```

Variance of trial in null model is driven by effect of density level nested within each trial. Once diff_level is accounted for in the model, trial no longer explains the variation. Given that results are not influenced significantly by presence/absence of the random effect, we keep trial as random effect based on the initial design of the study.

Results

Model comparison

```r
anova(m0, mDiff)
```

```
## Data: silent
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
```

```
##         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0      3 7796.6 7814.7 -3895.3   7790.6
## mDiff   7 7737.4 7779.8 -3861.7   7723.4 67.188      4  8.898e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effect

```r
summary(mDiff)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
##    Data: silent
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   7737.4   7779.8  -3861.7   7723.4     3138
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.5458 -0.4060 -0.1979  0.3508  1.8885
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  trial  (Intercept) 0.000000 0.00000
##  PartID (Intercept) 0.002305 0.04801
## Number of obs: 3145, groups:  trial, 30; PartID, 23
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        0.29516    0.01900  15.537  < 2e-16 ***
## Diff_levelD1 VS D2 -0.19316    0.06116  -3.158  0.00159 **
## Diff_levelD2 VS D3 -0.21544    0.05004  -4.305 1.67e-05 ***
## Diff_levelD3 VS D4  0.05011    0.04431   1.131  0.25803
## Diff_levelD4 VS D5 -0.11535    0.04220  -2.733  0.00627 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD
## Dff_lD1VSD2  0.116
## Dff_lD2VSD3  0.117 -0.500
## Dff_lD3VSD4 -0.003  0.000 -0.439
## Dff_lD4VSD5  0.050 -0.001  0.001 -0.529
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence Intervals using Wald method

```
CI = confint(mDiff,parm="beta_", method="Wald")
cx = summary(mDiff)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$esimate.linear = exp(cx2[,1])
cx2$esimate.linear.lower = exp(cx2[,2])
cx2$esimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2
```

```
##                    estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)                  0.30  0.26   0.33       0.02   15.54     0.00
## Diff_levelD1 VS D2          -0.19 -0.31  -0.07       0.06   -3.16     0.00
## Diff_levelD2 VS D3          -0.22 -0.31  -0.12       0.05   -4.31     0.00
## Diff_levelD3 VS D4           0.05 -0.04   0.14       0.04    1.13     0.26
## Diff_levelD4 VS D5          -0.12 -0.20  -0.03       0.04   -2.73     0.01
##                    esimate.linear esimate.linear.lower
## (Intercept)                  1.34                 1.29
## Diff_levelD1 VS D2           0.82                 0.73
## Diff_levelD2 VS D3           0.81                 0.73
## Diff_levelD3 VS D4           1.05                 0.96
## Diff_levelD4 VS D5           0.89                 0.82
##                    esimate.linear.upper
## (Intercept)                        1.39
## Diff_levelD1 VS D2                 0.93
## Diff_levelD2 VS D3                 0.89
## Diff_levelD3 VS D4                 1.15
## Diff_levelD4 VS D5                 0.97
```

Plot for density of simultaneity

```
d.simult.plots =  silent[, c("trial", "Diff_level", "Info_n") ]

summary_info <- d.simult.plots %>%
  group_by(trial, Info_n) %>% summarize(count = n())

data_wide_info <- spread(summary_info, Info_n, count)

data_wide_info$Animal_pair <- sapply(strsplit(as.character(data_wide_info$trial),','), "[", 1)
data_wide_info$Diff_level <- sapply(strsplit(as.character(data_wide_info$trial),','), "[", 2)



names(data_wide_info)[names(data_wide_info) == "1"] <- "one_info"
names(data_wide_info)[names(data_wide_info) == "2"] <- "two_info"
names(data_wide_info)[names(data_wide_info) == "3"] <- "three_info"
names(data_wide_info)[names(data_wide_info) == "4"] <- "four_info"

data_wide_info[is.na(data_wide_info)] <- 0
```

```r
data_wide_info$total <- data_wide_info$one_info + data_wide_info$two_info + data_wide_info$three_info +
                        data_wide_info$four_info

data_wide_info$sim1 <- data_wide_info$one_info/data_wide_info$total
data_wide_info$sim2 <- data_wide_info$two_info/data_wide_info$total
data_wide_info$sim3 <- data_wide_info$three_info/data_wide_info$total
data_wide_info$sim4 <- data_wide_info$four_info/data_wide_info$total

plot_data <- data_wide_info[c("Diff_level", "sim1", "sim2", "sim3","sim4" )]

Plot.Units2 <- melt(plot_data , id=c("Diff_level"))


Plot.Units2$value <- as.numeric(as.character(Plot.Units2$value))

colnames(Plot.Units2)[colnames(Plot.Units2) == 'variable'] <- 'Units'
colnames(Plot.Units2)[colnames(Plot.Units2) == 'value'] <- 'proportion'

Plot.Units2$Units <- as.character(Plot.Units2$Units)

Plot.Units2$Units[Plot.Units2$Units == "sim1"] <- "1 information unit"
Plot.Units2$Units[Plot.Units2$Units == "sim2"] <- "2 simultaneous information units"
Plot.Units2$Units[Plot.Units2$Units == "sim3"] <- "3 simultaneous information units"
Plot.Units2$Units[Plot.Units2$Units == "sim4"] <- "4 simultaneous information units"

Plot.Units2$Diff_level[Plot.Units2$Diff_level == "1"] <- "L1"
Plot.Units2$Diff_level[Plot.Units2$Diff_level == "2"] <- "L2"
Plot.Units2$Diff_level[Plot.Units2$Diff_level == "3"] <- "L3"
Plot.Units2$Diff_level[Plot.Units2$Diff_level == "4"] <- "L4"
Plot.Units2$Diff_level[Plot.Units2$Diff_level == "5"] <- "L5"


Plot.Units2$Units <- factor(Plot.Units2$Units, levels = c("4 simultaneous information units",
                        "3 simultaneous information units", "2 simultaneous information units", "1 in

p <- ggplot(Plot.Units2,aes(x = Diff_level, y = proportion, fill = Units, width=0.5)) +
  geom_bar(position = "fill",stat = "identity")+ theme(aspect.ratio = 9/9) +
  theme(axis.text.y = element_text(colour="grey20",size=12,angle=90,hjust=.5,vjust=.5,face="plain"))+
  theme(axis.text.x = element_text(colour="grey20",size=12,hjust=.5,vjust=.5,face="plain"))+
  xlab("Information Density Level") +
  ylab("Mean prop. of MS containing specific number of  \n information units versus total N of MS ") +
  labs(fill = "Information units")

bold.text <- element_text( size = 14, colour = "black")
p+scale_fill_manual(values=c("navyblue","royalblue2","lightskyblue3", "gray81")) + theme(title = bold.te
```
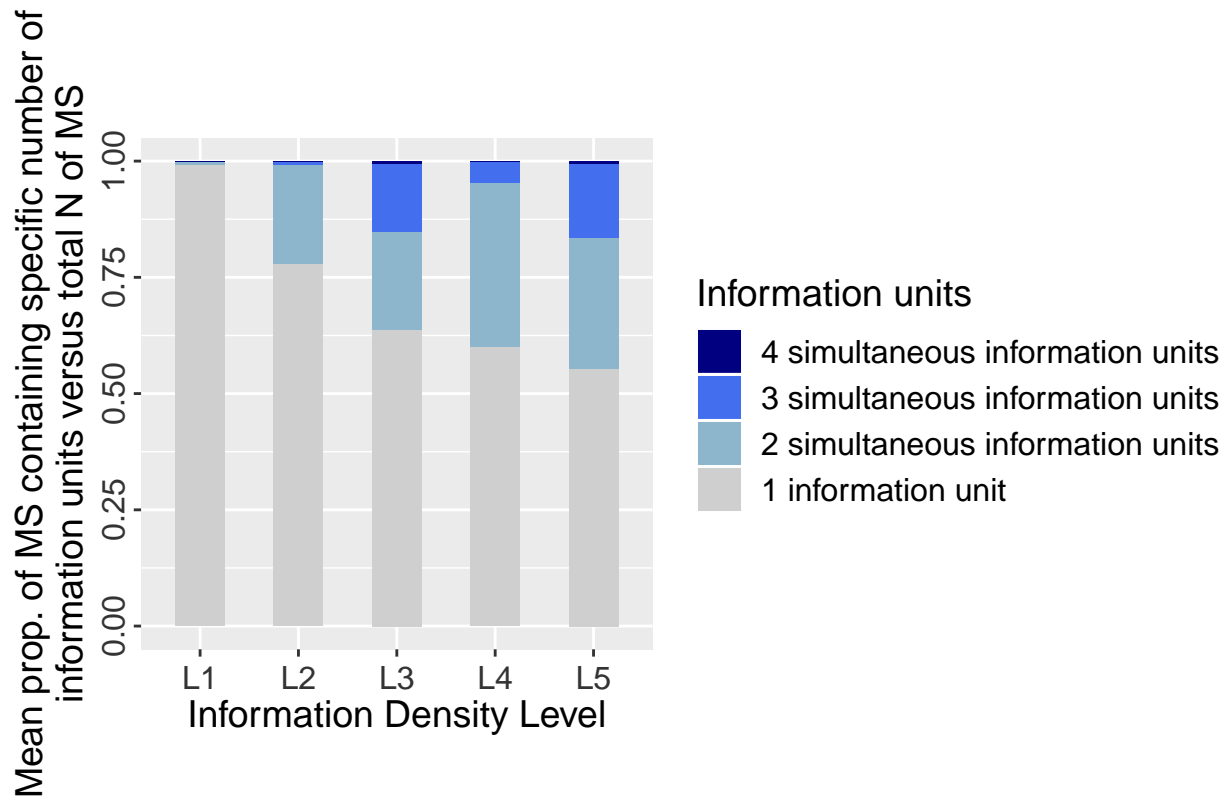
```
ggsave("plot_density.png")
```

```
## Saving 6.5 x 4.5 in image
```