Supporting Material: Analyses of silent gesture vs. sign language. Evolution of efficient encoding of meaning in the visual modality.

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Contents

Load libraries

```
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

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

Convert variables to correct format

```
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)

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

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

There were 46 particpants in total (23 in each condition - silent gesture/ sign) each describing 30 trials (experimental stimuli).The resulting data is based on 1325 experimental trials in total. Missing data points (n=55) are due to incomplete productions, which were disregarded.

```
# N of Participants

str(d$PartID)
```

```
##  Factor w/ 46 levels "a","ADP","AmicoO",..: 2 2 2 2 2 2 2 2 2 2 ...
```

```r
# Number of experimental groups
str(d$Group)
```

```
##  Factor w/ 2 levels "sign","silent_gesture": 2 2 2 2 2 2 2 2 2 2 ...
```

```r
#Total number of observations (experimental trials)
str(d$trial)
```

```
##  chr [1:1325] "bear_dog,1" "bear_dog,2" "bear_dog,3" "bear_dog,4" ...
```

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

```
##
## D1  D2  D3  D4  D5
## 273 268 271 260 253
```

LENGTH OF ENCODING

Baseline model

Random effects

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

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

mA2 = glmer(
  length ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair),
  data = d,
  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 = d,
  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: d
## Models:
## mA0: length ~ 1 + (1 | PartID)
## mA1: length ~ 1 + (1 | PartID) + (1 | trial)
##     Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mA0  2 5534.6 5544.9 -2765.3   5530.6
## mA1  3 5234.8 5250.4 -2614.4   5228.8 301.76      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

```
# Use forward difference coding to assess group effect
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(d$Diff_level) <- constrast_matrix #define the contrasts above for your variable (data=your da

print(contrasts(d$Diff_level))
```

```
##    D1 VS D2 D2 VS D3 D3 VS D4 D4 VS D5
## D1     0.8       0.6       0.4       0.2
## D2    -0.2       0.6       0.4       0.2
## D3    -0.2      -0.4       0.4       0.2
## D4    -0.2      -0.4      -0.6       0.2
## D5    -0.2      -0.4      -0.6      -0.8
```

Fixed effects

```r
## Effect of density level

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

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

```r
## Effect of Group


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

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

```r
## Interaction Density level x Group

mGroupDiff = glmer(
  length ~ 1 +  Diff_level*Group+
    (1 | PartID) +
    (1 | trial),
  data = d,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

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

```
anova(m0, mDiff, mGroup,  mGroupDiff)
```

```
## Data: d
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## mGroup: length ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
## mGroupDiff: length ~ 1 + Diff_level * Group + (1 | PartID) + (1 | trial)
##             Df    AIC    BIC  logLik deviance   Chisq Chi Df Pr(>Chisq)
## m0           3 5234.8 5250.4 -2614.4   5228.8
## mDiff        7 5147.0 5183.4 -2566.5   5133.0 95.7561      4    < 2e-16 ***
## mGroup       8 5143.9 5185.4 -2564.0   5127.9  5.1191      1    0.02366 *
## mGroupDiff  12 5149.8 5212.0 -2562.9   5125.8  2.1620      4    0.70599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
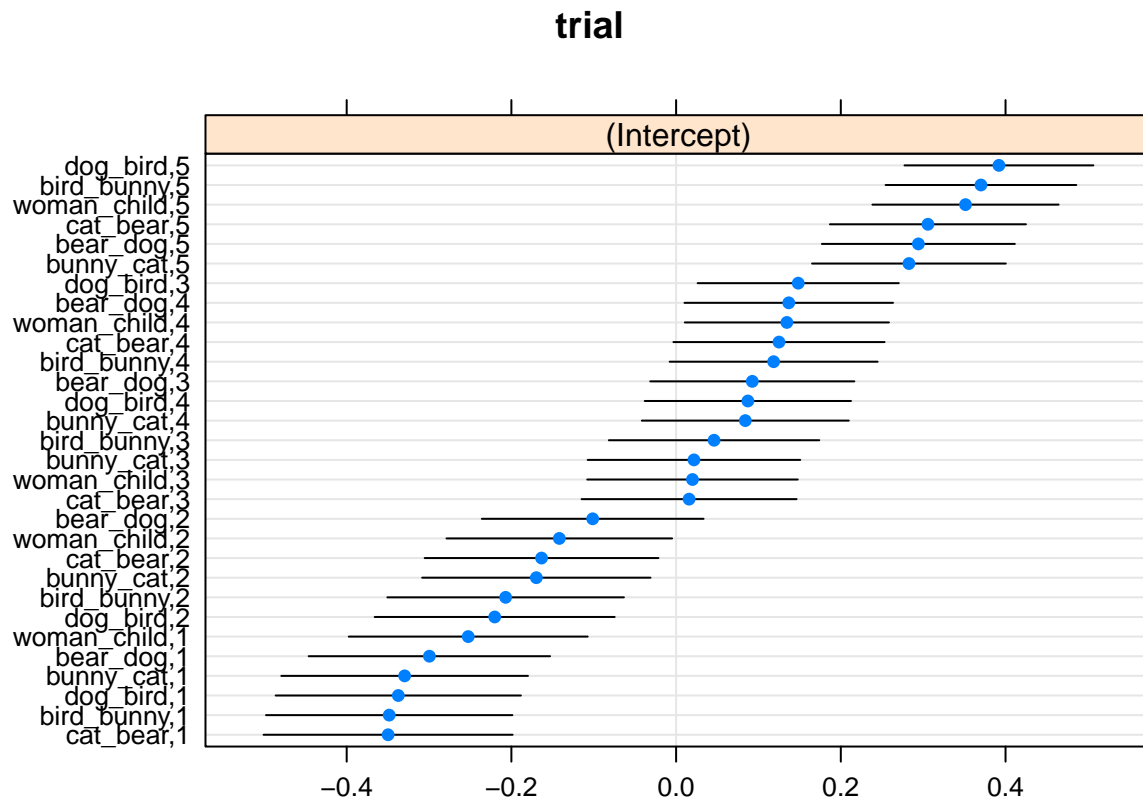
```
summary(mGroup)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: length ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
##    Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   5143.9   5185.4  -2564.0   5127.9     1317
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4479 -0.4024 -0.1068  0.2215  4.4195
##
## Random effects:
##  Groups Name        Variance  Std.Dev.
##  PartID (Intercept) 1.598e-02 1.264e-01
##  trial  (Intercept) 2.049e-16 1.431e-08
## Number of obs: 1325, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          1.65661    0.03130  52.935  < 2e-16 ***
## Diff_levelD1 VS D2  -0.17230    0.04387  -3.927 8.59e-05 ***
## Diff_levelD2 VS D3  -0.24349    0.03971  -6.131 8.73e-10 ***
## Diff_levelD3 VS D4  -0.05904    0.03696  -1.597   0.1102
## Diff_levelD4 VS D5  -0.23010    0.03505  -6.565 5.21e-11 ***
## Groupsilent_gesture -0.10395    0.04456  -2.333   0.0196 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD D_D4VD
## Dff_lD1VSD2  0.020
```

```
## Dff_lD2VSD3  0.034 -0.510
## Dff_lD3VSD4  0.004  0.000 -0.470
## Dff_lD4VSD5  0.024  0.000  0.000 -0.522
## Grpslnt_gst -0.696  0.002 -0.003 -0.004 -0.002
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Only main effect of Group improves the model. There is no interaction.

Check variance of trial in baseline model to assess single fit warning reasons

```
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). Variance of PartID appears normal. Singular fit driven by 0 variance in random effect of trial.

Model comparison without random effect of trial

```
## Baseline model


m02 = glmer(
  length ~ 1 + Diff_level +
    (1 | PartID),
  data = d,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)


## Effect of density level

mDiff2 = glmer(
  length ~ 1 + Diff_level +
    (1 | PartID),
  data = d,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
mGroup2 = glmer(
  length ~ 1 + Diff_level + Group +
    (1 | PartID),
  data = d,
family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
## Interaction Density level x Group
```

```
mGroupDiff2 = glmer(
  length ~ 1 +  Diff_level*Group+
    (1 | PartID),
  data = d,
  family= poisson(link = "log"),
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
anova(m02, mDiff2, mGroup2,  mGroupDiff2)
```

```
## Data: d
## Models:
## m02: length ~ 1 + Diff_level + (1 | PartID)
## mDiff2: length ~ 1 + Diff_level + (1 | PartID)
## mGroup2: length ~ 1 + Diff_level + Group + (1 | PartID)
## mGroupDiff2: length ~ 1 + Diff_level * Group + (1 | PartID)
##             Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m02          6 5145.0 5176.2 -2566.5   5133.0
## mDiff2       6 5145.0 5176.2 -2566.5   5133.0 0.0000      0    1.00000
## mGroup2      7 5141.9 5178.2 -2564.0   5127.9 5.1191      1    0.02366 *
## mGroupDiff2 11 5147.8 5204.8 -2562.9   5125.8 2.1620      4    0.70599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mGroup2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: length ~ 1 + Diff_level + Group + (1 | PartID)
##     Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   5141.9   5178.2  -2564.0   5127.9     1318
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -1.4479 -0.4024 -0.1068  0.2215  4.4195
##
## Random effects:
##  Groups Name          Variance Std.Dev.
##  PartID (Intercept) 0.01598  0.1264
## Number of obs: 1325, groups:  PartID, 46
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.65661    0.03130  52.935  < 2e-16 ***
## Diff_levelD1 VS D2   -0.17231    0.04387  -3.927 8.59e-05 ***
## Diff_levelD2 VS D3   -0.24349    0.03972  -6.131 8.73e-10 ***
## Diff_levelD3 VS D4   -0.05904    0.03696  -1.597   0.1102
## Diff_levelD4 VS D5   -0.23010    0.03505  -6.565 5.21e-11 ***
## Groupsilent_gesture  -0.10395    0.04456  -2.333   0.0196 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD D_D4VD
## Dff_lD1VSD2  0.020
## Dff_lD2VSD3  0.034 -0.510
## Dff_lD3VSD4  0.004  0.000 -0.470
## Dff_lD4VSD5  0.024  0.000  0.000 -0.522
## Grpslnt_gst -0.696  0.002 -0.003 -0.004 -0.002
```

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. Singular fit warning can be ignored.

Results

Model comparisons

```
anova(m0, mDiff, mGroup,  mGroupDiff)
```

```
## Data: d
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## mGroup: length ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
## mGroupDiff: length ~ 1 + Diff_level * Group + (1 | PartID) + (1 | trial)
##            Df    AIC    BIC  logLik deviance   Chisq Chi Df Pr(>Chisq)
## m0          3 5234.8 5250.4 -2614.4   5228.8
## mDiff       7 5147.0 5183.4 -2566.5   5133.0 95.7561      4    < 2e-16 ***
## mGroup      8 5143.9 5185.4 -2564.0   5127.9  5.1191      1    0.02366 *
## mGroupDiff 12 5149.8 5212.0 -2562.9   5125.8  2.1620      4    0.70599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effect

```
summary(mGroup)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson ( log )
## Formula: length ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
##     Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   5143.9   5185.4  -2564.0   5127.9     1317
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4479 -0.4024 -0.1068  0.2215  4.4195
##
## Random effects:
##  Groups Name        Variance  Std.Dev.
##  PartID (Intercept) 1.598e-02 1.264e-01
##  trial  (Intercept) 2.049e-16 1.431e-08
## Number of obs: 1325, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.65661    0.03130  52.935  < 2e-16 ***
## Diff_levelD1 VS D2   -0.17230    0.04387  -3.927 8.59e-05 ***
## Diff_levelD2 VS D3   -0.24349    0.03971  -6.131 8.73e-10 ***
## Diff_levelD3 VS D4   -0.05904    0.03696  -1.597   0.1102
## Diff_levelD4 VS D5   -0.23010    0.03505  -6.565 5.21e-11 ***
## Groupsilent_gesture  -0.10395    0.04456  -2.333   0.0196 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD D_D4VD
## Dff_lD1VSD2  0.020
## Dff_lD2VSD3  0.034 -0.510
## Dff_lD3VSD4  0.004  0.000 -0.470
## Dff_lD4VSD5  0.024  0.000  0.000 -0.522
## Grpslnt_gst -0.696  0.002 -0.003 -0.004 -0.002
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence intervals (Wald method)

```
CI = confint(mGroup,parm="beta_", method="Wald")
cx = summary(mGroup)$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
## (Intercept)                  1.66  1.60   1.72       0.03   52.93
## Diff_levelD1 VS D2          -0.17 -0.26  -0.09       0.04   -3.93
## Diff_levelD2 VS D3          -0.24 -0.32  -0.17       0.04   -6.13
## Diff_levelD3 VS D4          -0.06 -0.13   0.01       0.04   -1.60
## Diff_levelD4 VS D5          -0.23 -0.30  -0.16       0.04   -6.56
## Groupsilent_gesture         -0.10 -0.19  -0.02       0.04   -2.33
##                    Pr(>|z|) esimate.linear esimate.linear.lower
## (Intercept)            0.00           5.24                 4.93
## Diff_levelD1 VS D2     0.00           0.84                 0.77
## Diff_levelD2 VS D3     0.00           0.78                 0.73
## Diff_levelD3 VS D4     0.11           0.94                 0.88
## Diff_levelD4 VS D5     0.00           0.79                 0.74
## Groupsilent_gesture    0.02           0.90                 0.83
##                    esimate.linear.upper
## (Intercept)                        5.57
## Diff_levelD1 VS D2                 0.92
## Diff_levelD2 VS D3                 0.85
## Diff_levelD3 VS D4                 1.01
## Diff_levelD4 VS D5                 0.85
## Groupsilent_gesture                0.98
```
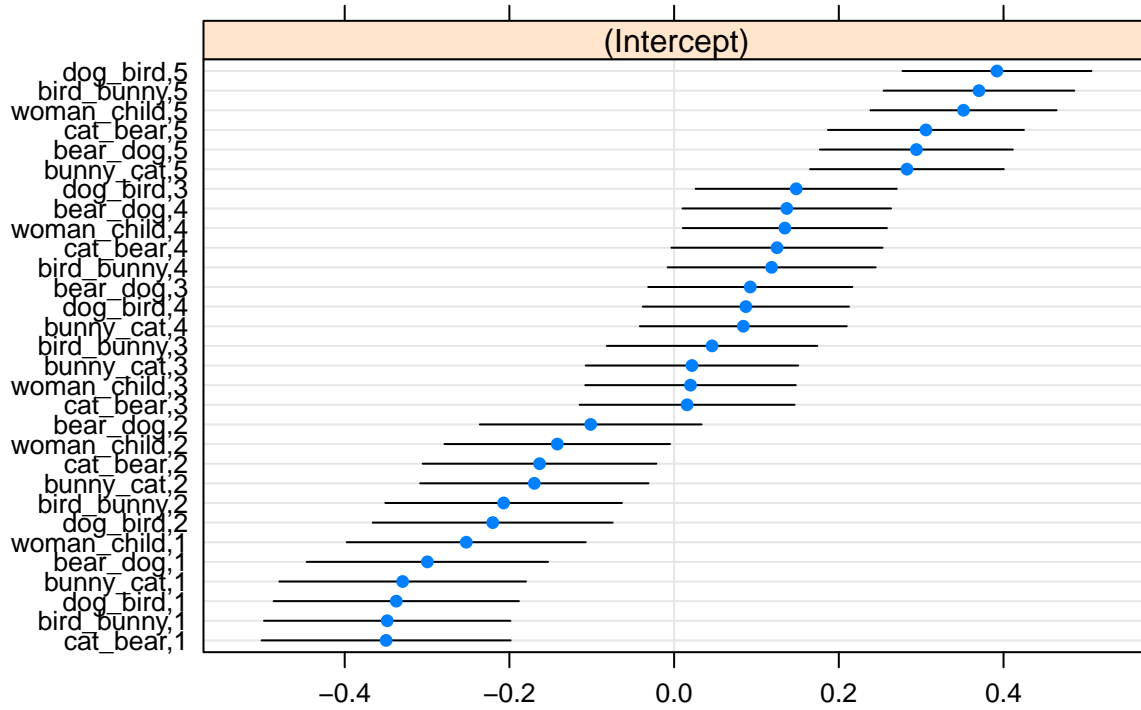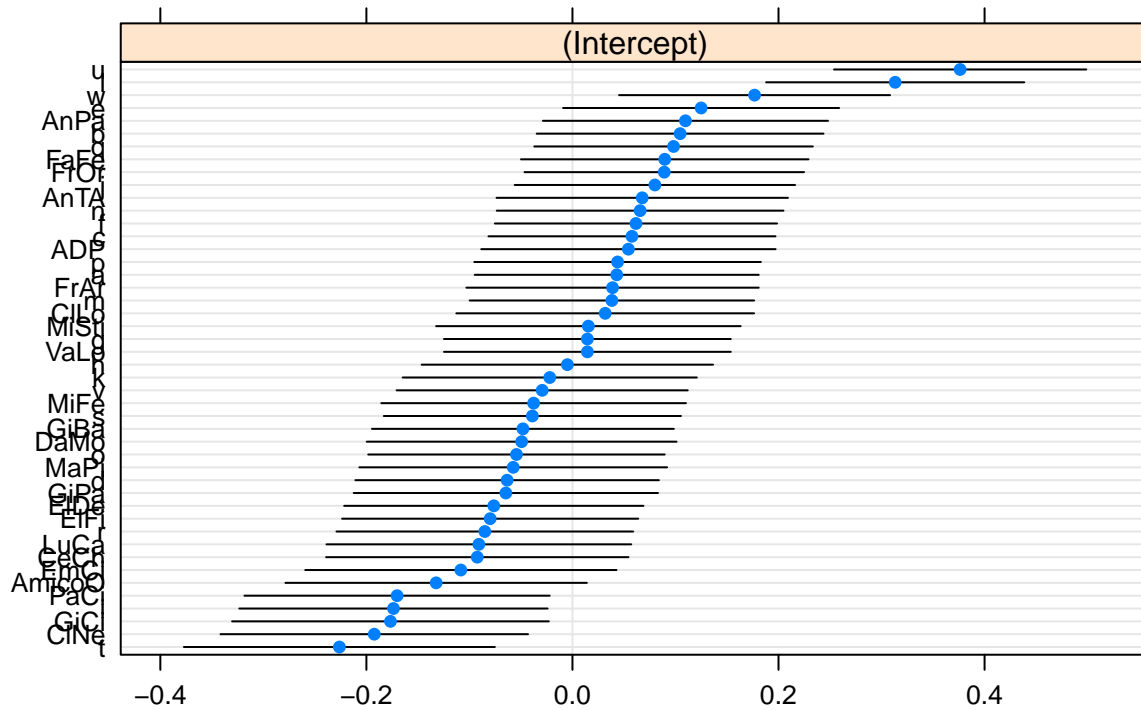
Random effects

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

trial


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

PartID

Plot - lenght

```
sumStats = group_by(d, PartID, Diff_level, Group ) %>%
  summarise(mean =mean(length))

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

#Inspect statistics
sumStats2
```

```
##    Diff_level         Group  N     mean        sd        se        ci
## 1          D1          sign 23 3.724638 1.0415711 0.2171826 0.4504091
## 2          D1 silent_gesture 23 3.334783 0.5958169 0.1242364 0.2576506
## 3          D2          sign 23 4.331884 0.7306755 0.1523564 0.3159678
## 4          D2 silent_gesture 23 4.063768 0.7439258 0.1551192 0.3216976
## 5          D3          sign 23 5.601449 1.1867738 0.2474595 0.5131995
## 6          D3 silent_gesture 23 5.105797 1.0862154 0.2264916 0.4697148
## 7          D4          sign 23 5.933333 1.3044988 0.2720068 0.5641076
## 8          D4 silent_gesture 23 5.399275 0.8884284 0.1852501 0.3841852
## 9          D5          sign 23 7.684058 1.6406721 0.3421038 0.7094798
## 10         D5 silent_gesture 23 6.560145 1.3660359 0.2848382 0.5907182
##        upper    lower
## 1   4.175047 3.274229
## 2   3.592433 3.077132
## 3   4.647852 4.015916
## 4   4.385466 3.742070
## 5   6.114649 5.088250
## 6   5.575512 4.636082
## 7   6.497441 5.369226
## 8   5.783461 5.015090
## 9   8.393538 6.974578
## 10  7.150863 5.969427
```

```
sumStats2$Group <- as.character(sumStats2$Group)

sumStats2$Group[sumStats2$Group == "sign"] <- "Signers"
sumStats2$Group[sumStats2$Group == "silent_gesture"] <- "Silent gesturers"

#Plot Lenght

main.plot <- ggplot(sumStats2,
                   aes(x = Diff_level, y = mean, colour=Group)) +
  geom_point(aes(shape=Group), size=3) + scale_shape_manual(values = c(17, 16)) + geom_line(aes(group=G:
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25) + xlab("Information Density level") +
  scale_x_discrete(labels=c("D1" = "L1", "D2" = "L2","D3" = "L3",
                            "D4" = "L4", "D5" = "L5"))+
  ylab("Mean N of total MS per trial")+
  coord_cartesian(ylim=c(1,8.5))

  bold.text <- element_text( size = 12)
main.plot+scale_color_manual(values=c("goldenrod2", "dodgerblue4")) + theme(title = bold.text, axis.tit]
```
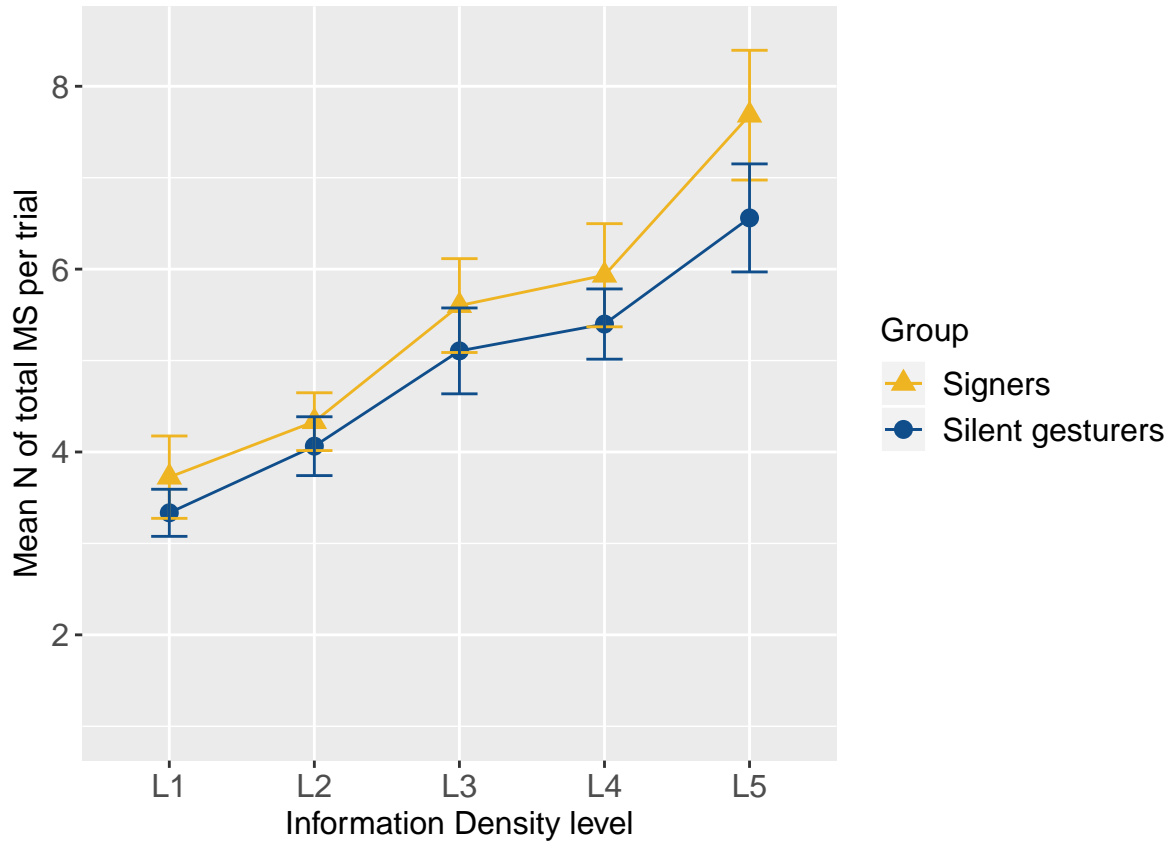
```
ggsave("plot_length_combined.png")
```

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

SIMULTANEITY

Baseline model

Random effects

```
## Baseline model

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

mA1 = glmer(
  cbind(simult_kinem,one_info) ~ 1 +
    (1 | PartID) +
    (1 | trial),
  data = d, family= "binomial",
```

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

mA2 = glmer(
  cbind(simult_kinem,one_info) ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair),
  data = d, 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 = d, 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: d
## 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 4012.4 4022.8 -2004.2   4008.4
## mA1  3 3078.5 3094.1 -1536.3   3072.5 935.86      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 = d, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

```r
# Use forward difference coding to assess group effect

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

print(contrasts(d$Diff_level))
```

```
##    D1 VS D2 D2 VS D3 D3 VS D4 D4 VS D5
## D1      0.8      0.6      0.4      0.2
## D2     -0.2      0.6      0.4      0.2
## D3     -0.2     -0.4      0.4      0.2
## D4     -0.2     -0.4     -0.6      0.2
## D5     -0.2     -0.4     -0.6     -0.8
```

Fixed effects

```r
## Effect of density level

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

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

```r
## Effect of group

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

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

```r
## Interaction of Density level X Group


mGroupDiff = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Diff_level*Group +
```

```
    (1 | PartID) +
    (1 | trial),
  data = d, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)
```

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

```
anova(m0, mDiff, mGroup, mGroupDiff)
```

```
## Data: d
## 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)
## mGroup: cbind(simult_kinem, one_info) ~ 1 + Diff_level + Group + (1 |
## mGroup:      PartID) + (1 | trial)
## mGroupDiff: cbind(simult_kinem, one_info) ~ 1 + Diff_level * Group + (1 |
## mGroupDiff:    PartID) + (1 | trial)
##             Df    AIC    BIC  logLik deviance    Chisq Chi Df Pr(>Chisq)
## m0           3 3078.5 3094.1 -1536.3   3072.5
## mDiff        7 2946.0 2982.3 -1466.0   2932.0 140.5686      4  < 2.2e-16
## mGroup       8 2910.1 2951.7 -1447.1   2894.1  37.8327      1  7.708e-10
## mGroupDiff  12 2908.8 2971.1 -1442.4   2884.8   9.3308      4    0.05334
##
## m0
## mDiff      ***
## mGroup     ***
## mGroupDiff .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mGroup)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + Group + (1 |
##     PartID) + (1 | trial)
##    Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2910.1   2951.6  -1447.1   2894.1     1317
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4987 -0.3828 -0.1662  0.3561  6.1450
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.1515   0.3892
```

```
##  trial  (Intercept) 0.0000    0.0000
## Number of obs: 1325, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -0.30819    0.09356  -3.294 0.000987 ***
## Diff_levelD1 VS D2  -2.70961    0.17956 -15.090  < 2e-16 ***
## Diff_levelD2 VS D3  -0.58293    0.08552  -6.816 9.34e-12 ***
## Diff_levelD3 VS D4  -0.10962    0.07750  -1.415 0.157214
## Diff_levelD4 VS D5  -0.28503    0.07396  -3.854 0.000116 ***
## Groupsilent_gesture -0.97554    0.12757  -7.647 2.05e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD D_D4VD
## Dff_lD1VSD2  0.271
## Dff_lD2VSD3  0.024 -0.275
## Dff_lD3VSD4  0.001  0.001 -0.457
## Dff_lD4VSD5  0.013  0.000  0.001 -0.516
## Grpslnt_gst -0.658  0.020  0.014  0.003  0.001
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

`summary(mGroupDiff)`

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level * Group + (1 |
##     PartID) + (1 | trial)
##    Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2908.8   2971.1  -1442.4   2884.8     1313
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4044 -0.4071 -0.1264  0.3663  5.9742
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.1514   0.389
##  trial  (Intercept) 0.0000   0.000
## Number of obs: 1325, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                                 Estimate Std. Error z value
## (Intercept)                     -0.27204    0.09382  -2.900
## Diff_levelD1 VS D2              -2.61022    0.19783 -13.194
## Diff_levelD2 VS D3              -0.46826    0.11275  -4.153
## Diff_levelD3 VS D4              -0.08059    0.10484  -0.769
## Diff_levelD4 VS D5              -0.32713    0.10038  -3.259
```

```
## Groupsilent_gesture                        -1.18997    0.16332  -7.286
## Diff_levelD1 VS D2:Groupsilent_gesture -0.83610    0.54976  -1.521
## Diff_levelD2 VS D3:Groupsilent_gesture -0.27864    0.17468  -1.595
## Diff_levelD3 VS D4:Groupsilent_gesture -0.06183    0.15483  -0.399
## Diff_levelD4 VS D5:Groupsilent_gesture  0.09093    0.14775   0.615
##                                         Pr(>|z|)
## (Intercept)                              0.00374 **
## Diff_levelD1 VS D2                       < 2e-16 ***
## Diff_levelD2 VS D3                       3.28e-05 ***
## Diff_levelD3 VS D4                       0.44207
## Diff_levelD4 VS D5                       0.00112 **
## Groupsilent_gesture                      3.19e-13 ***
## Diff_levelD1 VS D2:Groupsilent_gesture  0.12829
## Diff_levelD2 VS D3:Groupsilent_gesture  0.11068
## Diff_levelD3 VS D4:Groupsilent_gesture  0.68963
## Diff_levelD4 VS D5:Groupsilent_gesture  0.53827
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) Df_D1VSD2 Df_D2VSD3 Df_D3VSD4 Df_D4VSD5 Grpsl_
## Dff_lD1VSD2  0.268
## Dff_lD2VSD3  0.031 -0.320
## Dff_lD3VSD4  0.003  0.001    -0.468
## Dff_lD4VSD5  0.017  0.000     0.000    -0.516
## Grpslnt_gst -0.574 -0.154    -0.018    -0.002    -0.010
## D_D1VSD2:G_ -0.097 -0.360     0.115     0.000     0.000     0.592
## D_D2VSD3:G_ -0.020  0.207    -0.645     0.302     0.000     0.044
## D_D3VSD4:G_ -0.002  0.000     0.317    -0.677     0.350     0.004
## D_D4VSD5:G_ -0.012  0.000     0.000     0.351    -0.679     0.015
##             D_D1VSD2: D_D2VSD3: D_D3VSD4:
## Dff_lD1VSD2
## Dff_lD2VSD3
## Dff_lD3VSD4
## Dff_lD4VSD5
## Grpslnt_gst
## D_D1VSD2:G_
## D_D2VSD3:G_ -0.190
## D_D3VSD4:G_  0.000    -0.449
## D_D4VSD5:G_  0.000     0.001    -0.514
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```
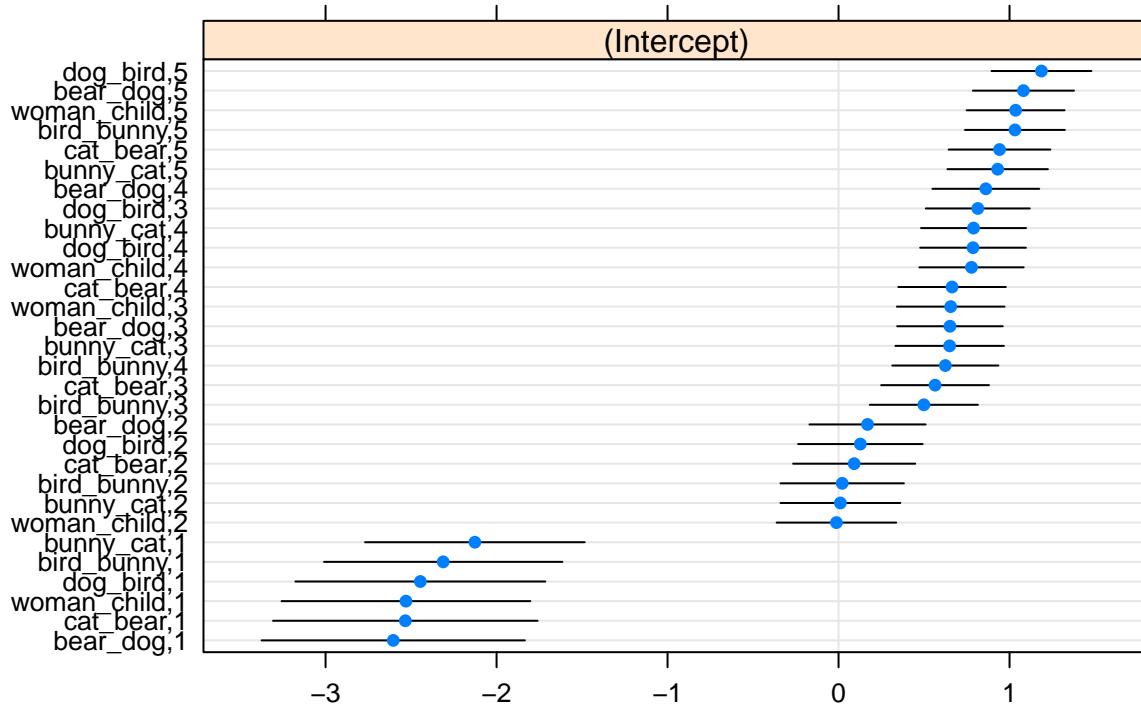
Only main effect of Group improves the model. There is no interaction.

Check variance of trial in baseline model to assess single fit warning reasons
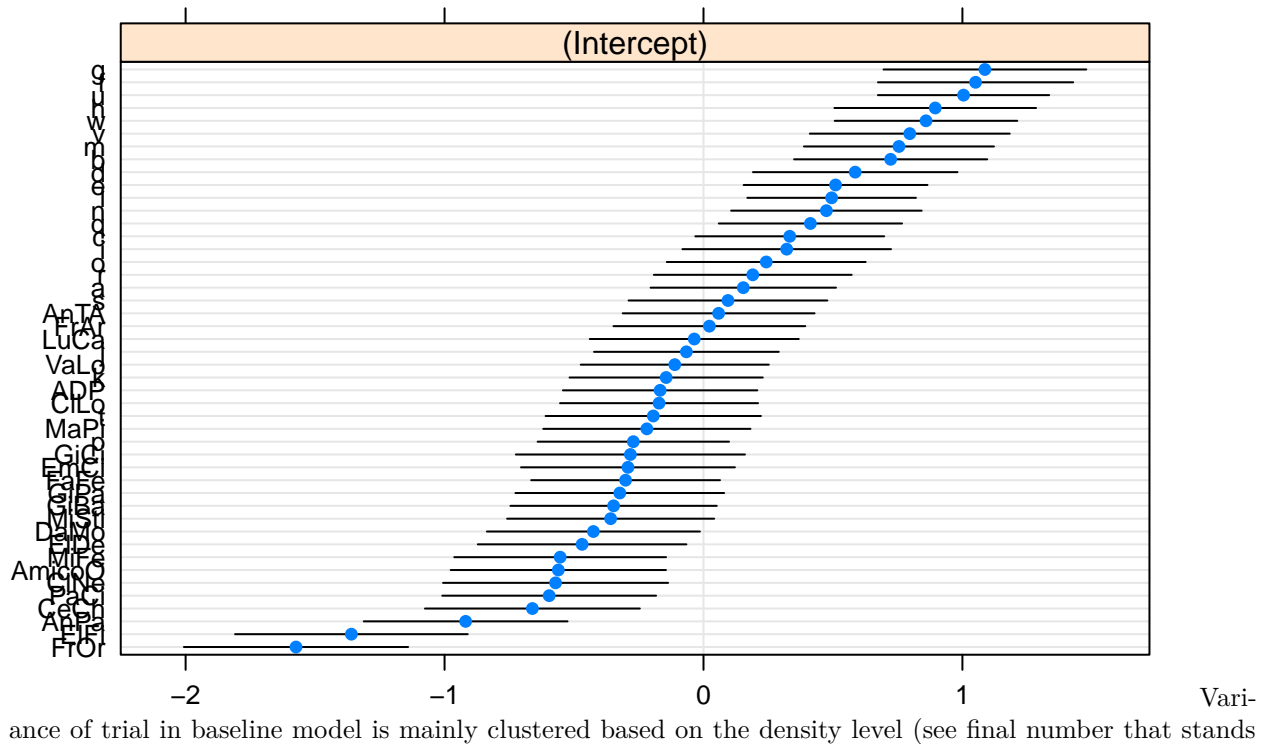
```
dotplot(ranef(m0))$trial
```

trial


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

PartID

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

for each density level). Variance of PartID appears normal. Singular fit driven by 0 variance in random effect of trial.

Model comparison without random effect of trial

```r
## Baseline model
  m02 = glmer(
  cbind(simult_kinem,one_info)  ~ 1 +
    (1 | PartID),
  data = d, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)

## Effect of density level

mDiff2 = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Diff_level +
    (1 | PartID),
  data = d, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)

## Effect of group

mGroup2 = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Diff_level + Group +
    (1 | PartID),
  data = d, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)

## Interaction of Density level X Group


mGroupDiff2 = glmer(
  cbind(simult_kinem,one_info)  ~ 1 + Diff_level*Group +
    (1 | PartID),
  data = d, family= "binomial",
    control = glmerControl(optimizer = 'bobyqa')
)

anova(m02, mDiff2, mGroup2, mGroupDiff2)
```

```
## Data: d
## Models:
## m02: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID)
## mDiff2: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID)
## mGroup2: cbind(simult_kinem, one_info) ~ 1 + Diff_level + Group + (1 |
## mGroup2:     PartID)
## mGroupDiff2: cbind(simult_kinem, one_info) ~ 1 + Diff_level * Group + (1 |
## mGroupDiff2:     PartID)
##             Df    AIC    BIC  logLik deviance    Chisq Chi Df Pr(>Chisq)
```

```
## m02          2 4012.4 4022.8 -2004.2   4008.4
## mDiff2       6 2944.0 2975.1 -1466.0   2932.0 1076.4299   4  < 2.2e-16
## mGroup2      7 2908.1 2944.5 -1447.1   2894.1   37.8327   1  7.708e-10
## mGroupDiff2 11 2906.8 2963.9 -1442.4   2884.8    9.3308   4    0.05334
##
## m02
## mDiff2      ***
## mGroup2     ***
## mGroupDiff2 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 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.Singular fit warning can be ignored.

Results

Model comparisons

```
anova(m0, mDiff, mGroup,  mGroupDiff)
```

```
## Data: d
## 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)
## mGroup: cbind(simult_kinem, one_info) ~ 1 + Diff_level + Group + (1 |
## mGroup:     PartID) + (1 | trial)
## mGroupDiff: cbind(simult_kinem, one_info) ~ 1 + Diff_level * Group + (1 |
## mGroupDiff:     PartID) + (1 | trial)
##            Df    AIC    BIC  logLik deviance   Chisq Chi Df Pr(>Chisq)
## m0          3 3078.5 3094.1 -1536.3   3072.5
## mDiff       7 2946.0 2982.3 -1466.0   2932.0 140.5686   4  < 2.2e-16
## mGroup      8 2910.1 2951.7 -1447.1   2894.1  37.8327   1  7.708e-10
## mGroupDiff 12 2908.8 2971.1 -1442.4   2884.8   9.3308   4    0.05334
##
## m0
## mDiff      ***
## mGroup     ***
## mGroupDiff .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effect

```
summary(mGroup)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + Group + (1 |
##     PartID) + (1 | trial)
##    Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2910.1   2951.6  -1447.1   2894.1     1317
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4987 -0.3828 -0.1662  0.3561  6.1450
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.1515   0.3892
##  trial  (Intercept) 0.0000   0.0000
## Number of obs: 1325, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.30819    0.09356  -3.294 0.000987 ***
## Diff_levelD1 VS D2   -2.70961    0.17956 -15.090  < 2e-16 ***
## Diff_levelD2 VS D3   -0.58293    0.08552  -6.816 9.34e-12 ***
## Diff_levelD3 VS D4   -0.10962    0.07750  -1.415 0.157214
## Diff_levelD4 VS D5   -0.28503    0.07396  -3.854 0.000116 ***
## Groupsilent_gesture  -0.97554    0.12757  -7.647 2.05e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) D_D1VD D_D2VD D_D3VD D_D4VD
## Dff_lD1VSD2  0.271
## Dff_lD2VSD3  0.024 -0.275
## Dff_lD3VSD4  0.001  0.001 -0.457
## Dff_lD4VSD5  0.013  0.000  0.001 -0.516
## Grpslnt_gst -0.658  0.020  0.014  0.003  0.001
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence intervals (Wald method)

```
CI = confint(mGroup,parm="beta_", method="Wald")
cx = summary(mGroup)$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
```

```
## (Intercept)                      -0.31 -0.49  -0.12      0.09   -3.29
## Diff_levelD1 VS D2               -2.71 -3.06  -2.36      0.18  -15.09
## Diff_levelD2 VS D3               -0.58 -0.75  -0.42      0.09   -6.82
## Diff_levelD3 VS D4               -0.11 -0.26   0.04      0.08   -1.41
## Diff_levelD4 VS D5               -0.29 -0.43  -0.14      0.07   -3.85
## Groupsilent_gesture              -0.98 -1.23  -0.73      0.13   -7.65
##                        Pr(>|z|)
## (Intercept)               0.00
## Diff_levelD1 VS D2        0.00
## Diff_levelD2 VS D3        0.00
## Diff_levelD3 VS D4        0.16
## Diff_levelD4 VS D5        0.00
## Groupsilent_gesture       0.00
```
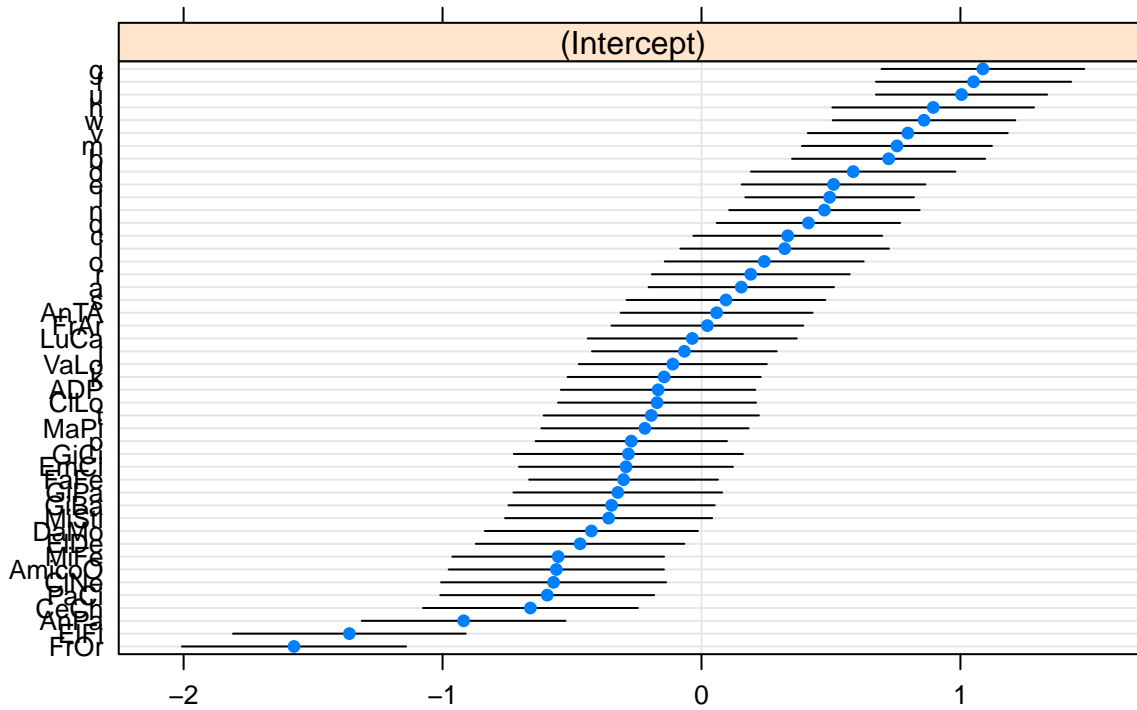
Random effects

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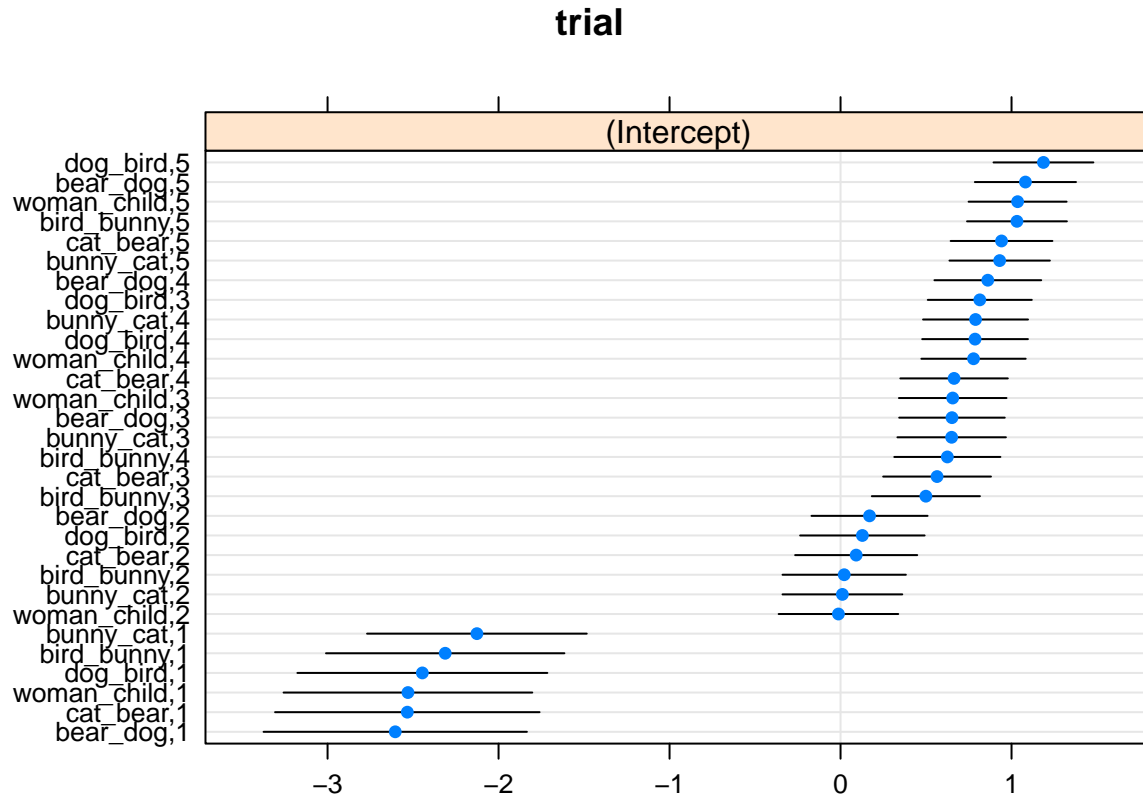

trial

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

PartID

Plot - Simultaneity

```r
#Make new column with proportion of simultaneous MS versus total MS per trial.

d$simult_prop <- (d$simult_kinem/d$length)

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


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


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

sumStats2$Group[sumStats2$Group == "sign"] <- "Signers"
sumStats2$Group[sumStats2$Group == "silent_gesture"] <- "Silent gesturers"

#Inspect statistics
sumStats2
```

```
##    Diff_level          Group  N       mean         sd          se
## 1          D1         Signers 23 0.05295031 0.06703657 0.013978092
## 2          D1 Silent gesturers 23 0.00731539 0.01931474 0.004027402
## 3          D2         Signers 23 0.46080745 0.15858962 0.033068222
```

```
## 4           D2 Silent gesturers 23 0.21373361 0.09673663 0.020170981
## 5           D3          Signers 23 0.57051153 0.11829986 0.024667226
## 6           D3 Silent gesturers 23 0.36387200 0.09102782 0.018980612
## 7           D4          Signers 23 0.60049041 0.10268607 0.021411527
## 8           D4 Silent gesturers 23 0.40929967 0.12041682 0.025108644
## 9           D5          Signers 23 0.66555714 0.10061023 0.020978684
## 10          D5 Silent gesturers 23 0.45507262 0.12007842 0.025038080
##           ci      upper      lower
## 1  0.02898879 0.08193910  0.02396152
## 2  0.00835232 0.01566771 -0.00103693
## 3  0.06857930 0.52938675  0.39222816
## 4  0.04183205 0.25556566  0.17190155
## 5  0.05115670 0.62166823  0.51935484
## 6  0.03936338 0.40323538  0.32450862
## 7  0.04440479 0.64489520  0.55608562
## 8  0.05207214 0.46137181  0.35722753
## 9  0.04350713 0.70906427  0.62205001
## 10 0.05192580 0.50699842  0.40314682
```

```r
#Plot SIMULTANEITY
main.plot <- ggplot(sumStats2,
                    aes(fill = Group, x = Diff_level, y = mean, fill= Group)) +
    geom_bar(position ='dodge', stat='identity') + theme(aspect.ratio = 9/9) +
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25, position=position_dodge(.9)) + xlab("Infor
scale_x_discrete(labels=c("D1" = "L1", "D2" = "L2","D3" = "L3",
                          "D4" = "L4", "D5" = "L5"))+
  ylab("Mean proportion of MS \n with simultaneous articulators") + coord_cartesian(ylim=c(0,1))
```

```
## Warning: Duplicated aesthetics after name standardisation: fill
```

```r
  bold.text <- element_text( size = 12)
main.plot+scale_fill_manual(values=c("goldenrod2", "dodgerblue4")) + theme(title = bold.text, axis.titl
```
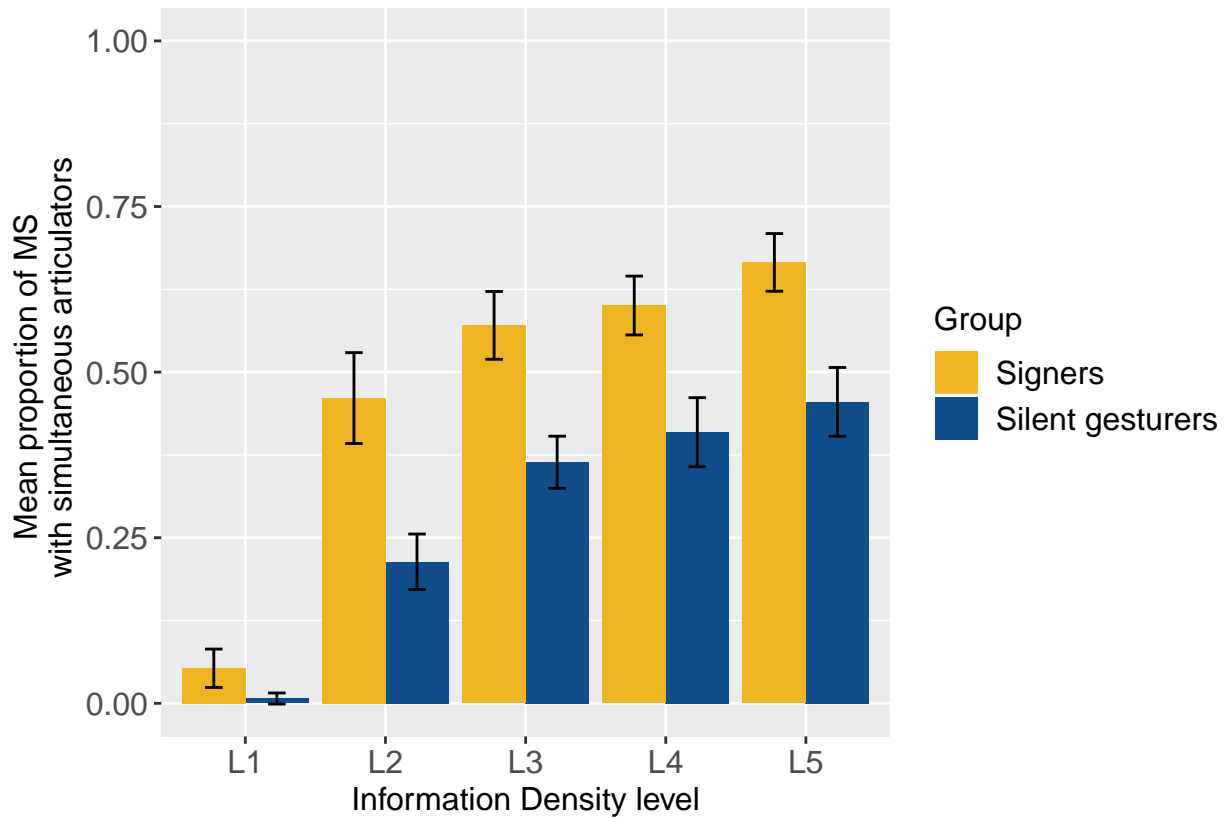
```
ggsave("plot_simultaneity_combined.png")
```

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

DENSITY OF SIMULTANEITY

Load data of density of simultaneity

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

There were 46 particpants each describing 30 trials (experimental stimuli). There were total of 6524 movement segments (MS) used.

```
# N of Participants
```

```
str(d$PartID)
```

```
##  Factor w/ 46 levels "a","ADP","AmicoO",..: 2 2 2 2 2 2 2 2 2 2 ...
```

```
#N of trials (experimental stimuli)
str(d$trial)
```

```
##  Factor w/ 30 levels "bear_dog,1","bear_dog,2",..: 19 19 19 19 19 28 28 28 28 28 ...
```

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

```
## [1] 6842
```

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

```
##
##    D1    D2    D3    D4    D5
##   963  1115  1450  1503  1811
```

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

```
##
##     1     2     3     4
##  3897  1952   884   109
```

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

```
## , ,  = sign
##
##
##        1    2    3    4
##   D1 480   34    0    0
##   D2 305  232   44    0
##   D3 319  261  192    1
##   D4 315  315  120   51
##   D5 329  383  266   50
##
## , ,  = silent_gesture
##
##
##        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

```r
mSim2A0 = glmer(
  Info_n ~ 1 +
    (1 | PartID),
  data =  d,
  family = "poisson",
```

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


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


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

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

```
mSim2A2 = glmer(
  Info_n ~ 1 +
    (1 | PartID) +
    (1 | trial) +
    (1 | Animal_pair) +
    (0 + Diff_level| PartID) ,
  data = d,
    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: d
## 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 18148 18162 -9072.2    18144
## mSim2A1  3 17928 17948 -8961.0    17922 222.42      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
##Recode null model

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

Fixed effects

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

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

```r
mGroup = glmer(
  Info_n ~ 1 + Diff_level + Group +
      (1 | PartID) +
      (1 | trial),
    data =  d,
    family = "poisson",
    control = glmerControl(optimizer = 'bobyqa')
  )
```

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

```r
mGroupDiff = glmer(
  Info_n ~ 1 + Diff_level*Group +
      (1 | PartID) +
      (1 | trial),
    data =  d,
    family = "poisson",
    control = glmerControl(optimizer = 'bobyqa')
  )
```

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

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

```
## Data: d
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## mGroup: Info_n ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
## mGroupDiff: Info_n ~ 1 + Diff_level * Group + (1 | PartID) + (1 | trial)
##            Df   AIC   BIC  logLik deviance    Chisq Chi Df Pr(>Chisq)
## m0          3 17928 17948 -8961.0    17922
## mDiff       7 17833 17881 -8909.7    17819 102.6930      4  < 2.2e-16 ***
## mGroup      8 17788 17842 -8885.7    17772  47.9099      1  4.463e-12 ***
## mGroupDiff 12 17787 17869 -8881.4    17763   8.5924      4    0.07213 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(mGroup)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Info_n ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
##    Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##  17787.5  17842.1  -8885.7  17771.5     6834
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -0.76702 -0.41795 -0.09405  0.35064  1.93803
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.001762 0.04197
##  trial  (Intercept) 0.000000 0.00000
## Number of obs: 6842, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.13074    0.03383   3.864 0.000112 ***
## Diff_levelD2         0.29670    0.04053   7.320 2.48e-13 ***
## Diff_levelD3         0.48583    0.03753  12.945  < 2e-16 ***
## Diff_levelD4         0.48000    0.03738  12.841  < 2e-16 ***
## Diff_levelD5         0.57304    0.03604  15.900  < 2e-16 ***
## Groupsilent_gesture -0.21244    0.02319  -9.163  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Dff_D2 Dff_D3 Dff_D4 Dff_D5
## Diff_levlD2 -0.727
## Diff_levlD3 -0.788  0.657
## Diff_levlD4 -0.791  0.660  0.713
## Diff_levlD5 -0.825  0.684  0.739  0.743
## Grpslnt_gst -0.302 -0.005  0.000  0.000  0.016
```

```
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Model comparison without random effect of trial

```r
m02 = glmer(
  Info_n ~ 1 + Diff_level +
        (1 | PartID),
      data =  d,
      family = "poisson",
      control = glmerControl(optimizer = 'bobyqa')
    )

mDiff2 = glmer(
  Info_n ~ 1 + Diff_level +
        (1 | PartID),
      data =  d,
      family = "poisson",
      control = glmerControl(optimizer = 'bobyqa')
    )


mGroup2 = glmer(
  Info_n ~ 1 + Diff_level + Group +
        (1 | PartID),
      data =  d,
      family = "poisson",
      control = glmerControl(optimizer = 'bobyqa')
    )

mGroupDiff2 = glmer(
  Info_n ~ 1 + Diff_level*Group +
        (1 | PartID),
      data =  d,
      family = "poisson",
      control = glmerControl(optimizer = 'bobyqa')
    )


anova(m02, mDiff2, mGroup2, mGroupDiff2)
```

```
## Data: d
## Models:
## m02: Info_n ~ 1 + Diff_level + (1 | PartID)
## mDiff2: Info_n ~ 1 + Diff_level + (1 | PartID)
## mGroup2: Info_n ~ 1 + Diff_level + Group + (1 | PartID)
## mGroupDiff2: Info_n ~ 1 + Diff_level * Group + (1 | PartID)
##             Df   AIC   BIC  logLik deviance   Chisq Chi Df Pr(>Chisq)
## m02          6 17831 17872 -8909.7    17819
## mDiff2       6 17831 17872 -8909.7    17819  0.0000      0    1.00000
## mGroup2      7 17786 17833 -8885.7    17772 47.9099      1  4.463e-12 ***
## mGroupDiff2 11 17785 17860 -8881.4    17763  8.5924      4    0.07213 .
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 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. Singular fit warning can be ignored.

Results

Model comparisons

```
anova(m0, mDiff, mGroup, mGroupDiff)
```

```
## Data: d
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mDiff: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## mGroup: Info_n ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
## mGroupDiff: Info_n ~ 1 + Diff_level * Group + (1 | PartID) + (1 | trial)
##             Df    AIC   BIC  logLik deviance    Chisq Chi Df Pr(>Chisq)
## m0           3 17928 17948 -8961.0    17922
## mDiff        7 17833 17881 -8909.7    17819 102.6930      4  < 2.2e-16 ***
## mGroup       8 17788 17842 -8885.7    17772  47.9099      1  4.463e-12 ***
## mGroupDiff  12 17787 17869 -8881.4    17763   8.5924      4    0.07213 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fixed effect

```
summary(mGroup)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Info_n ~ 1 + Diff_level + Group + (1 | PartID) + (1 | trial)
##    Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##  17787.5  17842.1  -8885.7  17771.5     6834
##
## Scaled residuals:
##     Min      1Q   Median      3Q      Max
## -0.76702 -0.41795 -0.09405  0.35064  1.93803
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  PartID (Intercept) 0.001762 0.04197
```

```
##  trial  (Intercept) 0.000000 0.00000
## Number of obs: 6842, groups:  PartID, 46; trial, 30
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          0.13074    0.03383   3.864 0.000112 ***
## Diff_levelD2         0.29670    0.04053   7.320 2.48e-13 ***
## Diff_levelD3         0.48583    0.03753  12.945  < 2e-16 ***
## Diff_levelD4         0.48000    0.03738  12.841  < 2e-16 ***
## Diff_levelD5         0.57304    0.03604  15.900  < 2e-16 ***
## Groupsilent_gesture -0.21244    0.02319  -9.163  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) Dff_D2 Dff_D3 Dff_D4 Dff_D5
## Diff_levlD2 -0.727
## Diff_levlD3 -0.788  0.657
## Diff_levlD4 -0.791  0.660  0.713
## Diff_levlD5 -0.825  0.684  0.739  0.743
## Grpslnt_gst -0.302 -0.005  0.000  0.000  0.016
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence Intervals using Wald method

```
CI = confint(mGroup,parm="beta_", method="Wald")
cx = summary(mGroup)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$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
## (Intercept)                   0.13  0.06   0.20       0.03    3.86
## Diff_levelD2                  0.30  0.22   0.38       0.04    7.32
## Diff_levelD3                  0.49  0.41   0.56       0.04   12.95
## Diff_levelD4                  0.48  0.41   0.55       0.04   12.84
## Diff_levelD5                  0.57  0.50   0.64       0.04   15.90
## Groupsilent_gesture          -0.21 -0.26  -0.17       0.02   -9.16
##                     Pr(>|z|) esimate.linear esimate.linear.lower
## (Intercept)                0           1.14                 1.07
## Diff_levelD2               0           1.35                 1.24
## Diff_levelD3               0           1.63                 1.51
## Diff_levelD4               0           1.62                 1.50
## Diff_levelD5               0           1.77                 1.65
## Groupsilent_gesture        0           0.81                 0.77
##                     esimate.linear.upper
## (Intercept)                         1.22
```
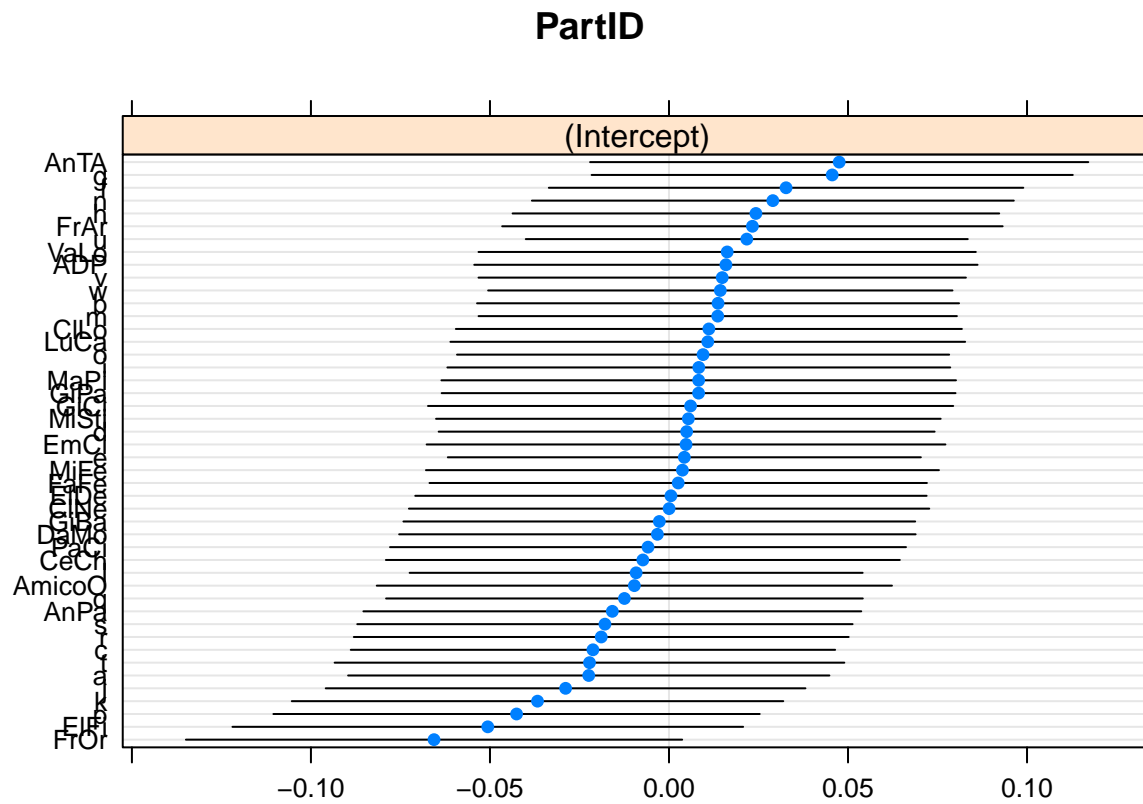
```
## Diff_levelD2                          1.46
## Diff_levelD3                          1.75
## Diff_levelD4                          1.74
## Diff_levelD5                          1.90
## Groupsilent_gesture                   0.85
```
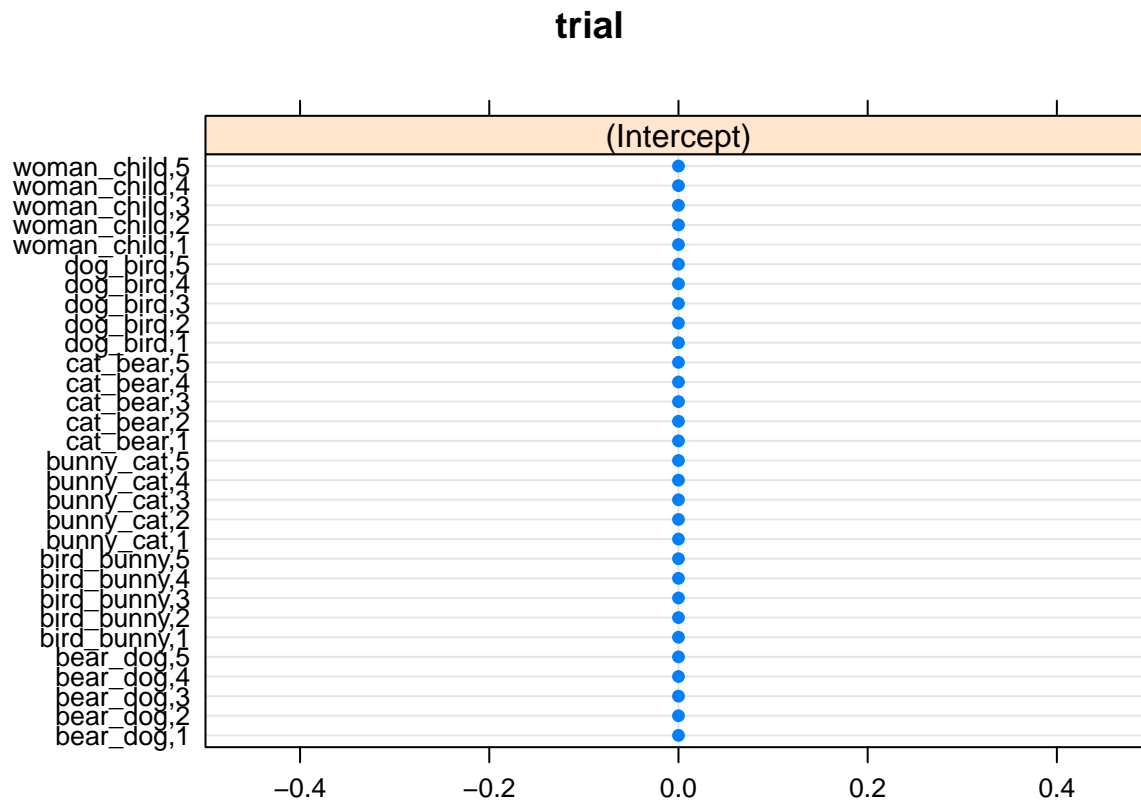
Random effects

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

PartID


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

trial

Plot - Density of simultaneity

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

summary_info <- d.simult.plots %>%
  group_by(trial, PartID, Info_n, Group) %>% 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

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


one_info <- data_wide_info[, c("Diff_level", "sim1", "Group", "PartID") ]
two_info <- data_wide_info[, c("Diff_level", "sim2", "Group", "PartID") ]
three_info <- data_wide_info[, c("Diff_level", "sim3", "Group", "PartID") ]
four_info <- data_wide_info[, c("Diff_level", "sim4", "Group", "PartID") ]


## One info
sumStats = group_by(one_info, PartID, Diff_level, Group ) %>%
  summarise(mean =mean(sim1))

sumStats2_one = summarySE(sumStats, measurevar="mean", groupvars=c("Diff_level", "Group"))
sumStats2$upper = sumStats2$mean + sumStats2$ci
sumStats2$lower = sumStats2$mean - sumStats2$ci

#Inspect statistics
sumStats2_one
```

```
##    Diff_level          Group  N      mean          sd          se
## 1           1           sign 23 0.9470497 0.06703657 0.013978092
## 2           1 silent_gesture 23 0.9926846 0.01931474 0.004027402
## 3           2           sign 23 0.5391925 0.15858962 0.033068222
## 4           2 silent_gesture 23 0.7859041 0.09626222 0.020072061
## 5           3           sign 23 0.4294885 0.11829986 0.024667226
## 6           3 silent_gesture 23 0.6409934 0.08357907 0.017427441
## 7           4           sign 23 0.3986814 0.10339868 0.021560115
## 8           4 silent_gesture 23 0.5990940 0.10940466 0.022812449
## 9           5           sign 23 0.3334284 0.09996444 0.020844026
## 10          5 silent_gesture 23 0.5446556 0.12011244 0.025045176
##            ci
## 1  0.02898879
## 2  0.00835232
## 3  0.06857930
## 4  0.04162691
## 5  0.05115670
## 6  0.03614230
## 7  0.04471294
## 8  0.04731012
## 9  0.04322786
## 10 0.05194052
```

```
## Two info
sumStats = group_by(two_info, PartID, Diff_level, Group ) %>%
  summarise(mean =mean(sim2))

sumStats2_two = summarySE(sumStats, measurevar="mean", groupvars=c("Diff_level", "Group"))
sumStats2$upper = sumStats2$mean + sumStats2$ci
sumStats2$lower = sumStats2$mean - sumStats2$ci

#Inspect statistics
sumStats2_two
```

```
##    Diff_level         Group  N       mean         sd          se
## 1           1          sign 23 0.05295031 0.06703657 0.013978092
## 2           1 silent_gesture 23 0.00731539 0.01931474 0.004027402
## 3           2          sign 23 0.39444444 0.13590943 0.028339075
## 4           2 silent_gesture 23 0.20854037 0.09258061 0.019304391
## 5           3          sign 23 0.31978716 0.08452085 0.017623816
## 6           3 silent_gesture 23 0.19653999 0.10150647 0.021165561
## 7           4          sign 23 0.38031495 0.11048628 0.023037983
## 8           4 silent_gesture 23 0.35753121 0.10671132 0.022250848
## 9           5          sign 23 0.34895680 0.10036781 0.020928135
## 10          5 silent_gesture 23 0.27855638 0.10278644 0.021432455
##            ci
## 1  0.02898879
## 2  0.00835232
## 3  0.05877165
## 4  0.04003486
## 5  0.03654956
## 6  0.04389469
## 7  0.04777785
## 8  0.04614543
## 9  0.04340229
## 10 0.04444819
```

```r
## Three info
sumStats = group_by(three_info, PartID, Diff_level, Group ) %>%
  summarise(mean =mean(sim3))

sumStats2_three = summarySE(sumStats, measurevar="mean", groupvars=c("Diff_level", "Group"))
sumStats2$upper = sumStats2$mean + sumStats2$ci
sumStats2$lower = sumStats2$mean - sumStats2$ci

#Inspect statistics
sumStats2_three
```

```
##    Diff_level         Group  N        mean         sd         se
## 1           1          sign 23 0.000000000 0.00000000 0.00000000
## 2           1 silent_gesture 23 0.000000000 0.00000000 0.00000000
## 3           2          sign 23 0.066363009 0.07921594 0.01651767
## 4           2 silent_gesture 23 0.005555556 0.02058352 0.00429196
## 5           3          sign 23 0.249516647 0.07428379 0.01548924
## 6           3 silent_gesture 23 0.160137399 0.09195317 0.01917356
## 7           4          sign 23 0.149107744 0.06481426 0.01351471
## 8           4 silent_gesture 23 0.043374741 0.05262023 0.01097208
## 9           5          sign 23 0.265266714 0.06710494 0.01399235
## 10          5 silent_gesture 23 0.171997318 0.07365598 0.01535833
##             ci
## 1  0.000000000
## 2  0.000000000
## 3  0.034255543
## 4  0.008900981
## 5  0.032122720
## 6  0.039763534
## 7  0.028027786
## 8  0.022754692
```

```
## 9  0.029018353
## 10 0.031851233
```

```r
## Four info
sumStats = group_by(four_info, PartID, Diff_level, Group ) %>%
  summarise(mean =mean(sim4))

sumStats2_four = summarySE(sumStats, measurevar="mean", groupvars=c("Diff_level", "Group"))
sumStats2$upper = sumStats2$mean + sumStats2$ci
sumStats2$lower = sumStats2$mean - sumStats2$ci

#Inspect statistics
sumStats2_four
```

```
##    Diff_level          Group  N       mean          sd          se
## 1           1           sign 23 0.000000000 0.000000000 0.000000000
## 2           1 silent_gesture 23 0.000000000 0.000000000 0.000000000
## 3           2           sign 23 0.000000000 0.000000000 0.000000000
## 4           2 silent_gesture 23 0.000000000 0.000000000 0.000000000
## 5           3           sign 23 0.001207729 0.005792067 0.001207729
## 6           3 silent_gesture 23 0.002329193 0.011170415 0.002329193
## 7           4           sign 23 0.071895874 0.043391142 0.009047679
## 8           4 silent_gesture 23 0.000000000 0.000000000 0.000000000
## 9           5           sign 23 0.052348123 0.041845722 0.008725436
## 10          5 silent_gesture 23 0.004790660 0.015946497 0.003325074
##            ci
## 1  0.000000000
## 2  0.000000000
## 3  0.000000000
## 4  0.000000000
## 5  0.002504678
## 6  0.004830450
## 7  0.018763737
## 8  0.000000000
## 9  0.018095447
## 10 0.006895782
```

```r
sumStats2_one$Info_n <- "Information units: 1"
sumStats2_two$Info_n <- "Information units: 2"
sumStats2_three$Info_n <- "Information units: 3"
sumStats2_four$Info_n <- "Information units: 4"

density <- rbind(sumStats2_one, sumStats2_two, sumStats2_three, sumStats2_four)


#Plot DENSITY


ggplot(density, aes(fill=Group, y=mean, x=Diff_level)) +
    geom_bar(position="dodge", stat="identity") +
    ggtitle("Density of simultaneity") +
    facet_wrap(~Info_n) +
    xlab("Information density level")
```

Density of simultaneity