

Supporting material: the role of iconicity and simultaneity for efficient communication

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Load libraries

```
setwd("~/Documents/PHD/Multireference_First_study/NEW_CODING/new_processing/Length_and_Simultaneity")

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)
```

Load data for length and simultaneity

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

Each row in the data is based on a single trial. The key variables are:

- PartID: identifies participants
- trial: the name of unique trial/experimental stimuli
- Diff_level: density level of the trial
- length: total number of movement segments (MS) produced for encoding each stimuli

- `simult_kinem`: total number of MS containing kinematically simultaneous articulators encoding distinct information units (2 information units or more)
- `one_info`: total number of MS without simultaneity (MS containing 1 information unit only)

Convert variables to correct format

```
#Format variables
d$PartID <- as.factor(d$PartID)
d$Age <- as.numeric(d$Age)
d$Sex <- as.factor(d$Sex)
d$Sign_since <- as.numeric(d$Sign_since)
d$Hand <- as.factor(d$Hand)
d$Animal_pair <- as.factor(d$Animal_pair)
d$Diff_level <- as.factor(d$Diff_level)
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$trial <- as.factor(d$trial)
```

There were 23 participants each describing 30 trials (experimental stimuli).The resulting data has 678 data points. Missing data points (n=12) are due to incomplete productions, which were disregarded.

```
# N of Participants
```

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

```
## Factor w/ 23 levels "a","b","c","d",...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
#N of trials (experimental stimuli)
```

```
str(d$trial)
```

```
## Factor w/ 30 levels "bear_dog,1","bear_dog,2",...: 1 2 3 4 5 6 7 8 9 10 ...
```

```
#Total number of observations
```

```
sum(complete.cases(d))
```

```
## [1] 678
```

```
# Number of observations per participant
```

```
table(d$PartID)
```

```
##
```

```
## a b c d e f g h i j k l m n o p q r s t u v w
## 30 28 29 28 30 30 30 29 29 30 29 30 30 29 29 29 30 30 29 30 30 30 30
```

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

```
##
## D1 D2 D3 D4 D5
## 138 134 138 135 133
```

LENGTH OF ENCODING

Baseline model

Random effects

```
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')
)
```

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

```
## 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 2880.0 2889.1 -1438.0  2876.0
## mA1  3 2731.2 2744.7 -1362.6  2725.2 150.89      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.

Fixed effects

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

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

```
## Data: d
## 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 2731.2 2744.7 -1362.6  2725.2
## mSex  4 2732.6 2750.7 -1362.3  2724.6 0.535      1    0.4645
```

```

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

anova(m0,mHand) #no effect of handedness

```

```

## Data: d
## 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 2731.2 2744.7 -1362.6  2725.2
## mHand  4 2733.1 2751.2 -1362.6  2725.1 0.0171     1    0.8961

```

```

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

anova(m0,mExp) #no effect of signing experience

```

```

## Data: d
## Models:
## m0: length ~ 1 + (1 | PartID) + (1 | trial)
## mExp: length ~ 1 + Sign_since + (1 | PartID) + (1 | trial)
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0     3 2731.2 2744.7 -1362.6  2725.2
## mExp   4 2733.1 2751.1 -1362.5  2725.1 0.0912     1    0.7627

```

```

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

anova(m0, mAge) #no effect of age

```

```
## Data: d
## 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 2731.2 2744.7 -1362.6  2725.2
## mAge  4 2731.5 2749.6 -1361.8  2723.5 1.633      1    0.2013
```

No fixed factors to include in baseline model

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
```

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

```
## Data: d
## 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 2731.2 2744.7 -1362.6  2725.2
## mDiff  7 2655.7 2687.3 -1320.8  2641.7 83.474      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: poisson ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 2655.7  2687.3 -1320.8  2641.7      671
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -1.4736 -0.3976 -0.0693  0.2851  3.8091
```

```

##
## Random effects:
## Groups Name      Variance Std.Dev.
## trial (Intercept) 0.00000  0.0000
## PartID (Intercept) 0.02335  0.1528
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.30310    0.05444  23.936 < 2e-16 ***
## Diff_levelD2  0.14923    0.06050   2.467  0.0136 *
## Diff_levelD3  0.40805    0.05686   7.177 7.15e-13 ***
## Diff_levelD4  0.46224    0.05649   8.182 2.79e-16 ***
## Diff_levelD5  0.72733    0.05400  13.470 < 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
## Diff_levlD2 -0.589
## Diff_levlD3 -0.627  0.564
## Diff_levlD4 -0.631  0.568  0.604
## Diff_levlD5 -0.660  0.594  0.632  0.637
## convergence code: 0
## boundary (singular) fit: see ?isSingular

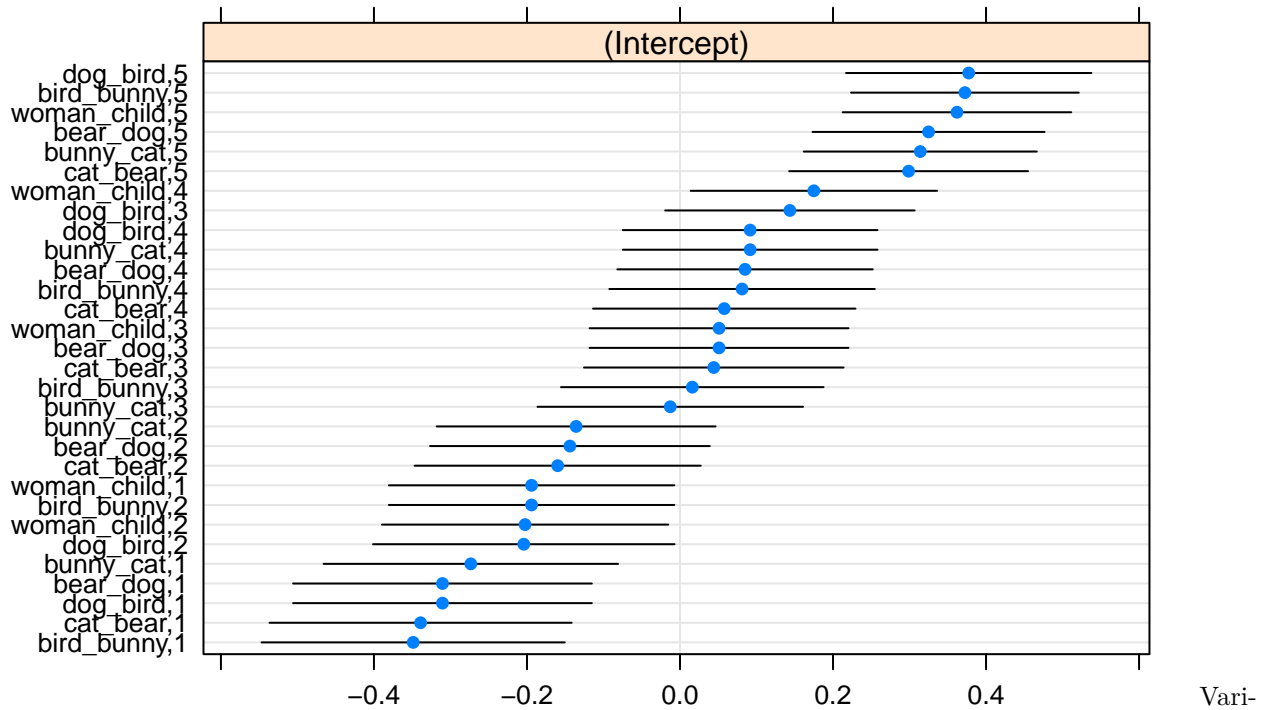
```

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

Check variance of trial in baseline model

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


trial



ance 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 = d,
  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: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 2653.7  2680.8 -1320.8  2641.7     672
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4736 -0.3976 -0.0693  0.2851  3.8091
##
```

```

## Random effects:
## Groups Name      Variance Std.Dev.
## PartID (Intercept) 0.02335  0.1528
## Number of obs: 678, groups: PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.30310    0.05444  23.936 < 2e-16 ***
## Diff_levelD2  0.14923    0.06050   2.467  0.0136 *
## Diff_levelD3  0.40806    0.05686   7.177 7.14e-13 ***
## Diff_levelD4  0.46224    0.05649   8.182 2.79e-16 ***
## Diff_levelD5  0.72733    0.05400  13.470 < 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
## Diff_levelD2 -0.589
## Diff_levelD3 -0.627  0.564
## Diff_levelD4 -0.631  0.568  0.604
## Diff_levelD5 -0.660  0.594  0.632  0.637

```

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

```

## Data: d
## 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 2653.7 2680.8 -1320.8  2641.7
## mDiff     7 2655.7 2687.3 -1320.8  2641.7    0    1    1

```

Conclusion: 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 variance. 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: d
## 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 2731.2 2744.7 -1362.6  2725.2
## mDiff     7 2655.7 2687.3 -1320.8  2641.7 83.474    4 < 2.2e-16 ***
## ---
## 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: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 2655.7 2687.3 -1320.8 2641.7      671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4736 -0.3976 -0.0693  0.2851  3.8091
##
## Random effects:
## Groups Name      Variance Std.Dev.
## trial (Intercept) 0.00000  0.0000
## PartID (Intercept) 0.02335  0.1528
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.30310    0.05444  23.936 < 2e-16 ***
## Diff_levelD2  0.14923    0.06050   2.467  0.0136 *
## Diff_levelD3  0.40805    0.05686   7.177 7.15e-13 ***
## Diff_levelD4  0.46224    0.05649   8.182 2.79e-16 ***
## Diff_levelD5  0.72733    0.05400  13.470 < 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
## Diff_levelD2 -0.589
## Diff_levelD3 -0.627  0.564
## Diff_levelD4 -0.631  0.568  0.604
## Diff_levelD5 -0.660  0.594  0.632  0.637
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence intervals (Wald method)

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

```

cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           1.30  1.20  1.41      0.05  23.94  0.00
## Diff_levelD2           0.15  0.03  0.27      0.06   2.47  0.01
## Diff_levelD3           0.41  0.30  0.52      0.06   7.18  0.00
## Diff_levelD4           0.46  0.35  0.57      0.06   8.18  0.00
## Diff_levelD5           0.73  0.62  0.83      0.05  13.47  0.00
##           estimate.linear estimate.linear.lower estimate.linear.upper
## (Intercept)           3.68                3.31                4.10
## Diff_levelD2           1.16                1.03                1.31
## Diff_levelD3           1.50                1.35                1.68
## Diff_levelD4           1.59                1.42                1.77
## Diff_levelD5           2.07                1.86                2.30

```

```

write.table(cx2, "results/FinalModelCoefficients_length.txt", sep="\t", row.names = F)

```

Contrasts

We are interested in assessing differences between density levels in hierarchical order. Glmer compares first level to all other levels. Accordingly, we relevel the order of the levels to attain desired contrasts.

Relevel Diff_level (D2 first) to compare level D2 to level D3.

```

d2 = d
d2$Diff_level = relevel(d2$Diff_level, "D2")
fm2 = update(mDiff, data=d2)

```

```

## boundary (singular) fit: see ?isSingular

```

```

summary(fm2)

```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## Data: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##           AIC      BIC  logLik deviance df.resid
##    2655.7    2687.3 -1320.8  2641.7     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4736 -0.3976 -0.0693  0.2851  3.8091
##
## Random effects:
##  Groups Name          Variance Std.Dev.

```

```

## trial (Intercept) 0.00000 0.0000
## PartID (Intercept) 0.02335 0.1528
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.45233    0.05237  27.732 < 2e-16 ***
## Diff_levelD1 -0.14923    0.06050  -2.467  0.0136 *
## Diff_levelD3  0.25882    0.05486   4.718 2.39e-06 ***
## Diff_levelD4  0.31300    0.05449   5.745 9.22e-09 ***
## Diff_levelD5  0.57809    0.05189  11.140 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) Dff_D1 Dff_D3 Dff_D4
## Diff_levelD1 -0.543
## Diff_levelD3 -0.599  0.518
## Diff_levelD4 -0.603  0.521  0.575
## Diff_levelD5 -0.633  0.547  0.604  0.608
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

```

CI = confint(fm2,param="beta_", method="Wald")
cx = summary(fm2)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$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)           1.45  1.35  1.55    0.05  27.73  0.00
## Diff_levelD1          -0.15 -0.27 -0.03    0.06  -2.47  0.01
## Diff_levelD3           0.26  0.15  0.37    0.05   4.72  0.00
## Diff_levelD4           0.31  0.21  0.42    0.05   5.74  0.00
## Diff_levelD5           0.58  0.48  0.68    0.05  11.14  0.00
##           esimate.linear esimate.linear.lower esimate.linear.upper
## (Intercept)           4.27                3.86                4.73
## Diff_levelD1           0.86                0.77                0.97
## Diff_levelD3           1.30                1.16                1.44
## Diff_levelD4           1.37                1.23                1.52
## Diff_levelD5           1.78                1.61                1.97

```

```

(cx2["Diff_levelD3",])

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD3           0.26  0.15  0.37    0.05   4.72  0
##           esimate.linear esimate.linear.lower esimate.linear.upper
## Diff_levelD3           1.3                1.16                1.44

```

```
write.table(cx2, "results/FinalModelCoefficients_relevel2_length.txt", sep="\t", row.names = F)
```

Relevel Diff_level (D3 first) to compare level D3 to level D4.

```
d3 = d
d3$Diff_level = relevel(d3$Diff_level, "D3")
fm3 = update(mDiff, data=d3)
```

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

```
summary(fm3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## Data: d3
## Control: glmerControl(optimizer = "bobyqa")
##
##           AIC      BIC   logLik deviance df.resid
##    2655.7    2687.3  -1320.8   2641.7     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4736 -0.3976 -0.0693  0.2851  3.8091
##
## Random effects:
## Groups Name      Variance Std.Dev.
## trial  (Intercept) 0.00000  0.0000
## PartID (Intercept) 0.02335  0.1528
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.71115    0.04810  35.578 < 2e-16 ***
## Diff_levelD1 -0.40806    0.05686  -7.177 7.14e-13 ***
## Diff_levelD2 -0.25882    0.05486  -4.718 2.39e-06 ***
## Diff_levelD4  0.05418    0.05041   1.075  0.282
## Diff_levelD5  0.31927    0.04759   6.708 1.97e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Dff_D1 Dff_D2 Dff_D4
## Diff_levlD1 -0.472
## Diff_levlD2 -0.489  0.414
## Diff_levlD4 -0.532  0.450  0.467
## Diff_levlD5 -0.564  0.477  0.494  0.538
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```

CI = confint(fm3,parm="beta_", method="Wald")
cx = summary(fm3)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$estimate.linear = exp(cx2[,1])
cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           1.71  1.62   1.81         0.05  35.58   0.00
## Diff_levelD1          -0.41 -0.52  -0.30         0.06  -7.18   0.00
## Diff_levelD2          -0.26 -0.37  -0.15         0.05  -4.72   0.00
## Diff_levelD4           0.05 -0.04   0.15         0.05   1.07   0.28
## Diff_levelD5           0.32  0.23   0.41         0.05   6.71   0.00
##           esimate.linear esimate.linear.lower esimate.linear.upper
## (Intercept)           5.54                   5.04                   6.08
## Diff_levelD1           0.66                   0.59                   0.74
## Diff_levelD2           0.77                   0.69                   0.86
## Diff_levelD4           1.06                   0.96                   1.17
## Diff_levelD5           1.38                   1.25                   1.51

```

```
(cx2["Diff_levelD4",])
```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD4           0.05 -0.04   0.15         0.05   1.07   0.28
##           esimate.linear esimate.linear.lower esimate.linear.upper
## Diff_levelD4           1.06                   0.96                   1.17

```

```
write.table(cx2, "results/FinalModelCoefficients_relevel3_length.txt", sep="\t", row.names = F)
```

Relevel Diff_level (D4 first) to compare level D4 to level D5.

```

d4 = d
d4$Diff_level = relevel(d4$Diff_level,"D4")
fm4 = update(mDiff, data=d4)

```

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

```
summary(fm4)
```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: length ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## Data: d4
## Control: glmerControl(optimizer = "bobyqa")

```

```

##
##      AIC      BIC   logLik deviance df.resid
##  2655.7   2687.3 -1320.8   2641.7     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4736 -0.3976 -0.0693  0.2851  3.8091
##
## Random effects:
##   Groups Name      Variance Std.Dev.
##   trial  (Intercept) 0.00000  0.0000
##   PartID (Intercept) 0.02335  0.1528
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.76533    0.04767  37.031 < 2e-16 ***
## Diff_levelD1 -0.46224    0.05649  -8.182 2.79e-16 ***
## Diff_levelD2 -0.31300    0.05449  -5.745 9.22e-09 ***
## Diff_levelD3 -0.05418    0.05041  -1.075  0.282
## Diff_levelD5  0.26509    0.04715   5.623 1.88e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Dff_D1 Dff_D2 Dff_D3
## Diff_levelD1 -0.464
## Diff_levelD2 -0.481  0.406
## Diff_levelD3 -0.520  0.439  0.455
## Diff_levelD5 -0.556  0.469  0.486  0.526
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

```

CI = confint(fm4,parm="beta_", method="Wald")
cx = summary(fm4)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$estimate.linear = exp(cx2[,1])
cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2

```

```

##              estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           1.77  1.67  1.86      0.05  37.03  0.00
## Diff_levelD1          -0.46 -0.57 -0.35      0.06  -8.18  0.00
## Diff_levelD2          -0.31 -0.42 -0.21      0.05  -5.74  0.00
## Diff_levelD3          -0.05 -0.15  0.04      0.05  -1.07  0.28
## Diff_levelD5           0.27  0.17  0.36      0.05   5.62  0.00
##              estimate.linear estimate.linear.lower estimate.linear.upper
## (Intercept)           5.84                    5.32                    6.42
## Diff_levelD1           0.63                    0.56                    0.70

```



```
## Diff_levelD2      0.73      0.66      0.81
## Diff_levelD3      0.95      0.86      1.05
## Diff_levelD5      1.30      1.19      1.43
```

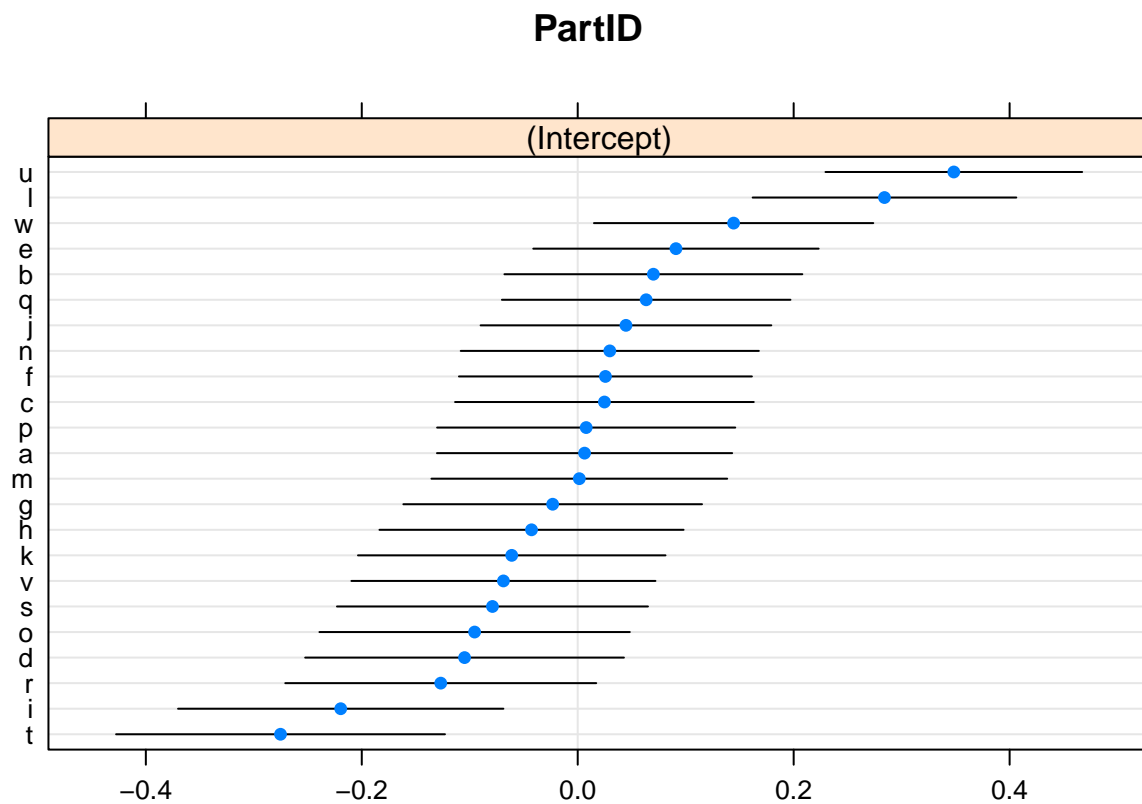
```
(cx2["Diff_levelD5",])
```

```
##          estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD5      0.27  0.17  0.36      0.05  5.62      0
##          estimate.linear estimate.linear.lower estimate.linear.upper
## Diff_levelD5      1.3      1.19      1.43
```

```
write.table(cx2, "results/FinalModelCoefficients_relevel4_length.txt", sep="\t", row.names = F)
```

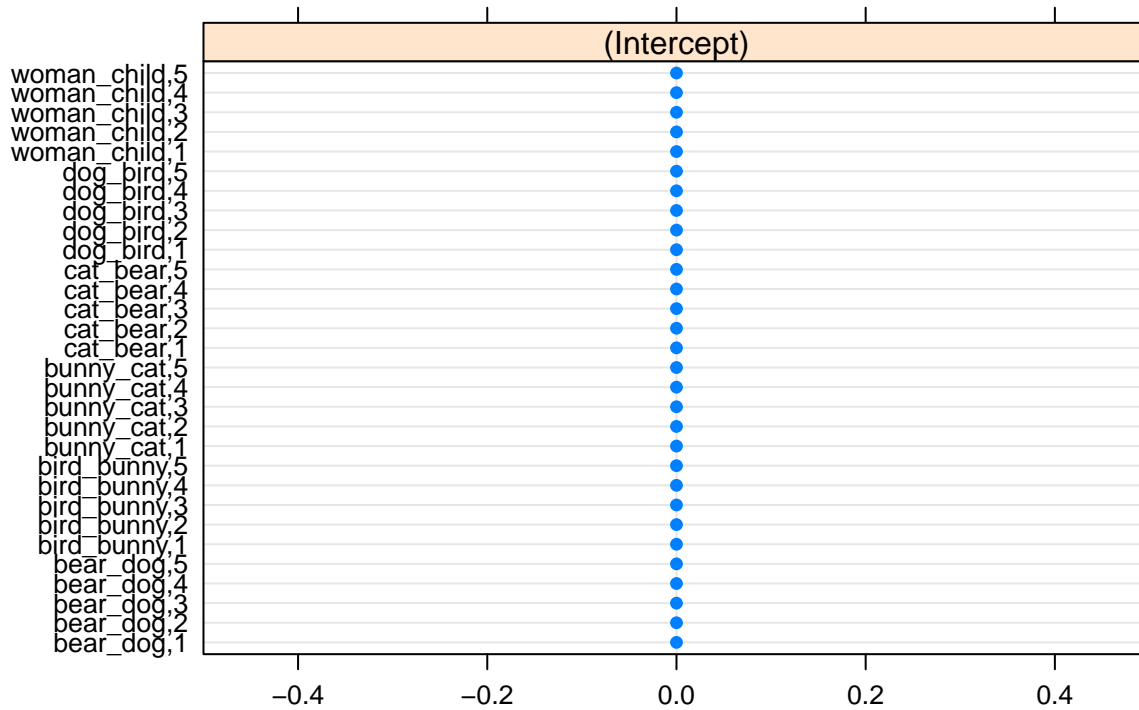
Random effects

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



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

trial



Descriptive statistics of raw data

```
#Descriptive statistics
sumStats = group_by(d, 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"

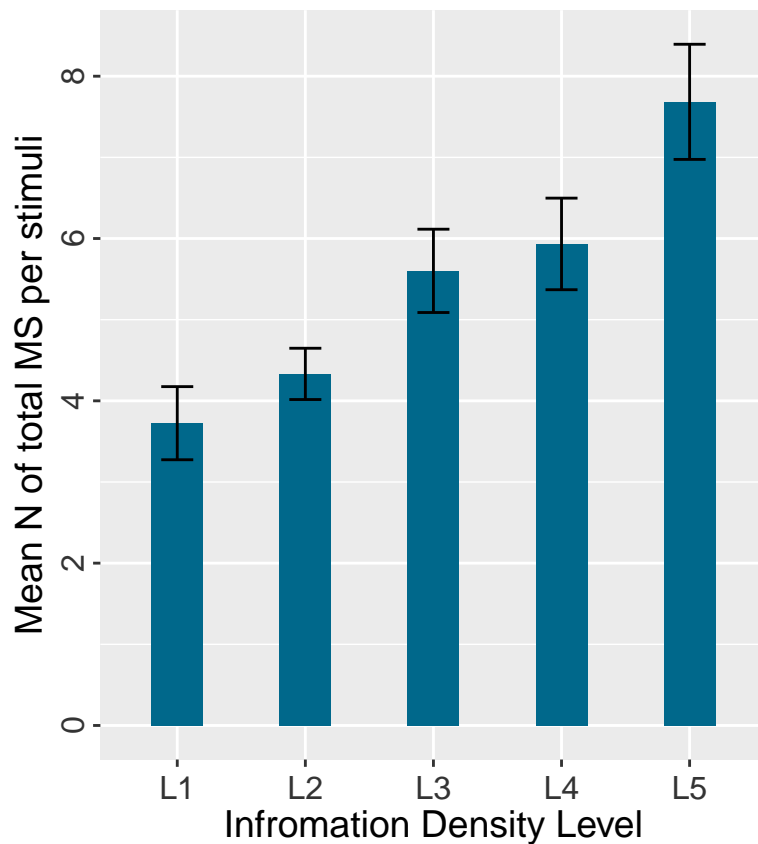
#Inspect statistics
sumStats2

##   Diff_level  N    mean      sd      se      ci    upper    lower
## 1          L1  23  3.724638  1.0415711  0.2171826  0.4504091  4.175047  3.274229
## 2          L2  23  4.331884  0.7306755  0.1523564  0.3159678  4.647852  4.015916
## 3          L3  23  5.601449  1.1867738  0.2474595  0.5131995  6.114649  5.088250
## 4          L4  23  5.933333  1.3044988  0.2720068  0.5641076  6.497441  5.369226
## 5          L5  23  7.684058  1.6406721  0.3421038  0.7094798  8.393538  6.974578
```

Plot for length

```
main.plot.length <- ggplot(sumStats2,
  aes(x = Diff_level, y = mean)) +
  geom_bar(stat= "identity", width = 0.4, fill = "deepskyblue4") + theme(aspect.ratio = 9/8) +
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25) + xlab("Infromation Density Level") +
  ylab("Mean N of total MS per stimuli") +
  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 = 14)
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

```

mAO = 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(mAO, mA1)
```

```

## Data: d
## Models:
## mAO: 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)
## mAO  2 2305.3 2314.4 -1150.7  2301.3
## mA1  3 1755.4 1769.0  -874.7  1749.4 551.93      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')
)
```

Fixed effects

```
##Sex

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

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

```
## Data: d
## 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 1755.4 1769.0 -874.70  1749.4
## mSex  4 1757.2 1775.2 -874.58  1749.2 0.2425    1    0.6224
```

```
##Handedness

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

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

```
## Data: d
## 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 1755.4 1769.0 -874.70  1749.4
## mHand  4 1757.0 1775.1 -874.51  1749.0 0.3895    1    0.5326
```

```
##Signing experience

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

anova(m0,mExp) #no significant effect of signing experience
```

```
## Data: d
## Models:
## m0: cbind(simult_kinem, one_info) ~ 1 + (1 | PartID) + (1 | trial)
## mExp: cbind(simult_kinem, one_info) ~ 1 + Sign_since + (1 | PartID) +
## mExp: (1 | trial)
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0    3 1755.4 1769.0 -874.70  1749.4
## mExp  4 1756.1 1774.2 -874.05  1748.1 1.3075    1  0.2529
```

```
##Age

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

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

```
## Data: d
## 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 1755.4 1769.0 -874.70  1749.4
## mAge  4 1757.3 1775.4 -874.66  1749.3 0.0785    1  0.7793
```

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

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
```

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

```
## 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)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0      3 1755.4 1769.0 -874.70  1749.4
## mDiff  7 1653.2 1684.9 -819.62  1639.2 110.16      4 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mDiff)
```

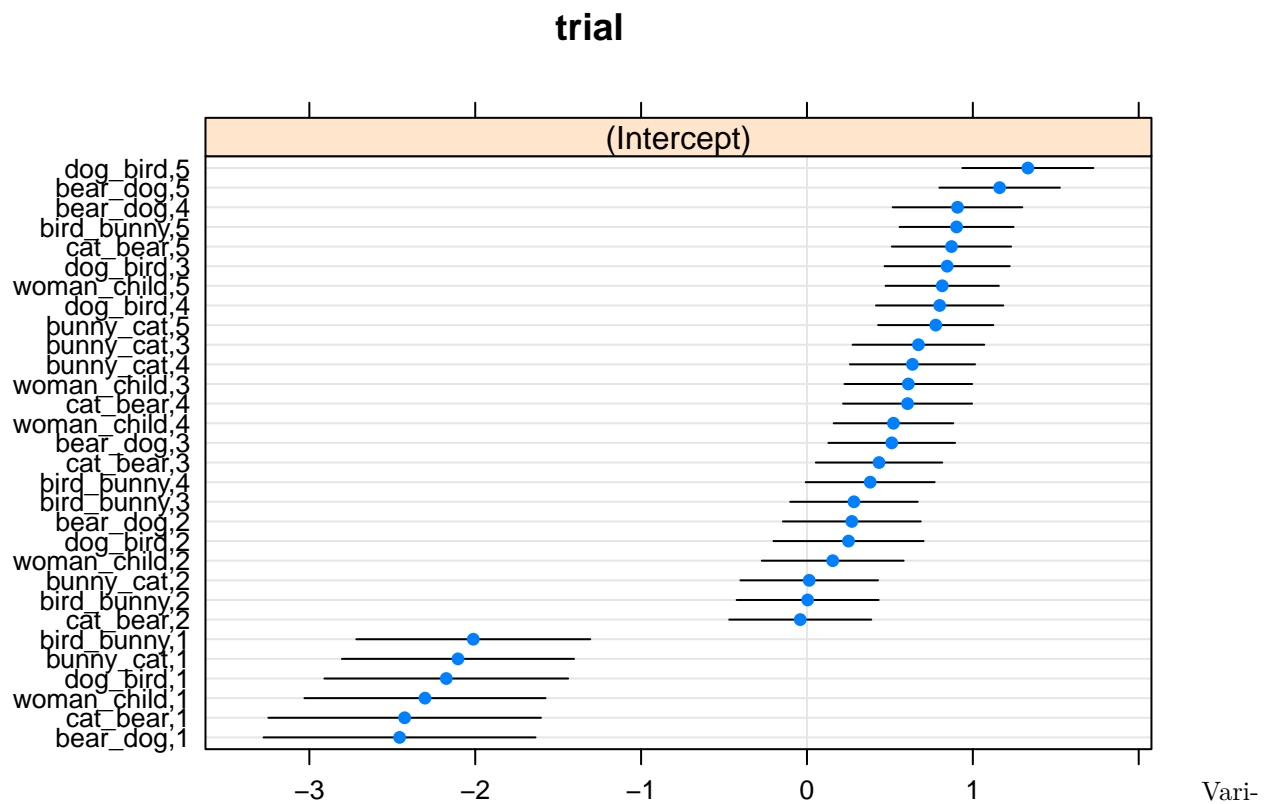
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
## (1 | trial)
## Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 1653.2  1684.9  -819.6  1639.2      671
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -2.4045 -0.4976 -0.1514  0.4839  5.5403
##
## Random effects:
## Groups Name          Variance Std.Dev.
## trial  (Intercept)  0.0000  0.0000
## PartID (Intercept)  0.1526  0.3907
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.7391    0.1969  -13.91  <2e-16 ***
## Diff_levelD2  2.6104    0.1979   13.19  <2e-16 ***
## Diff_levelD3  3.0787    0.1940   15.87  <2e-16 ***
## Diff_levelD4  3.1593    0.1939   16.30  <2e-16 ***
## Diff_levelD5  3.4864    0.1919   18.17  <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
## Diff_lev1D2 -0.822
## Diff_lev1D3 -0.840  0.835
## Diff_lev1D4 -0.842  0.836  0.854
## Diff_lev1D5 -0.851  0.844  0.863  0.865
## 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
```



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(simult_kinem,one_info) ~ 1 + Diff_level +
  (1 | PartID),
  data = d, 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: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 1651.2 1678.4 -819.6 1639.2    672
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4045 -0.4976 -0.1514  0.4839  5.5403
##
## Random effects:
## Groups Name          Variance Std.Dev.
## PartID (Intercept) 0.1526  0.3907
## Number of obs: 678, groups: PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.7391     0.1969  -13.91  <2e-16 ***
## Diff_levelD2  2.6104     0.1979   13.19  <2e-16 ***
## Diff_levelD3  3.0787     0.1940   15.87  <2e-16 ***
## Diff_levelD4  3.1593     0.1939   16.30  <2e-16 ***
## Diff_levelD5  3.4864     0.1919   18.17  <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
## Diff_levelD2 -0.822
## Diff_levelD3 -0.840  0.835
## Diff_levelD4 -0.842  0.836  0.854
## Diff_levelD5 -0.851  0.844  0.863  0.865

```

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

```

## Data: d
## 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 1651.2 1678.4 -819.62 1639.2
## mDiff    7 1653.2 1684.9 -819.62 1639.2    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

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

```
## 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)
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0     3 1755.4 1769.0 -874.70  1749.4
## mDiff  7 1653.2 1684.9 -819.62  1639.2 110.16     4 < 2.2e-16 ***
## ---
## 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: binomial ( logit )
## Formula: cbind(simult_kinem, one_info) ~ 1 + Diff_level + (1 | PartID) +
## (1 | trial)
## Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 1653.2  1684.9  -819.6  1639.2     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4045 -0.4976 -0.1514  0.4839  5.5403
##
## Random effects:
## Groups Name          Variance Std.Dev.
## trial  (Intercept)  0.0000   0.0000
## PartID (Intercept)  0.1526   0.3907
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.7391     0.1969  -13.91  <2e-16 ***
## Diff_levelD2  2.6104     0.1979   13.19  <2e-16 ***
## Diff_levelD3  3.0787     0.1940   15.87  <2e-16 ***
## Diff_levelD4  3.1593     0.1939   16.30  <2e-16 ***
## Diff_levelD5  3.4864     0.1919   18.17  <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
## Diff_levelD2 -0.822
## Diff_levelD3 -0.840  0.835
## Diff_levelD4 -0.842  0.836  0.854
## Diff_levelD5 -0.851  0.844  0.863  0.865
## 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)          -2.74 -3.12 -2.35      0.20 -13.91      0
## Diff_levelD2           2.61  2.22  3.00      0.20  13.19      0
## Diff_levelD3           3.08  2.70  3.46      0.19  15.87      0
## Diff_levelD4           3.16  2.78  3.54      0.19  16.30      0
## Diff_levelD5           3.49  3.11  3.86      0.19  18.17      0
```

```
write.table(cx2, "results/FinalModelCoefficients_simultaneity.txt", sep="\t", row.names = F)
```

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      0.061      0.197      0.042      0.087
## 2      0.468      0.118      0.411      0.525
## 3      0.584      0.110      0.531      0.636
## 4      0.604      0.110      0.551      0.654
## 5      0.679      0.106      0.632      0.722
##
## Adjusted for:
## * PartID = 0 (population-level)
## * trial = 0 (population-level)
##
## Standard errors are on link-scale (untransformed).
```

```
write.table(cx2, "results/FinalModel_probability_simultaneity.txt", sep="\t", row.names = F)
```

Contrasts

We are interested in assessing differences between density levels in hierarchical order. Glmer compares first level to all other levels. Accordingly, we relevel the order of the levels to attain desired contrasts.

Relevel Diff_level (D2 first) to compare level D2 to level D3.

```
d2 = d
d2$Diff_level = relevel(d2$Diff_level, "D2")
fm2 = update(mDiff, data=d2)
```

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

```
summary(fm2)
```

```
## 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: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 1653.2  1684.9  -819.6  1639.2     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4045 -0.4976 -0.1514  0.4839  5.5403
##
## Random effects:
## Groups Name          Variance Std.Dev.
## trial  (Intercept)  0.0000   0.0000
## PartID (Intercept)  0.1526   0.3907
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.1287    0.1176  -1.094   0.274
## Diff_levelD1 -2.6104    0.1979 -13.191 < 2e-16 ***
## Diff_levelD3  0.4683    0.1128  4.153 3.28e-05 ***
## Diff_levelD4  0.5489    0.1124  4.883 1.05e-06 ***
## Diff_levelD5  0.8761    0.1089  8.045 8.66e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Dff_D1 Dff_D3 Dff_D4
## Diff_levelD1 -0.305
## Diff_levelD3 -0.541  0.319
```

```
## Diff_levelD4 -0.543  0.320  0.566
## Diff_levelD5 -0.561  0.329  0.585  0.589
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
CI = confint(fm2,parm="beta_", method="Wald")
cx = summary(fm2)$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)          -0.13 -0.36  0.10          0.12  -1.09  0.27
## Diff_levelD1          -2.61 -3.00 -2.22          0.20 -13.19  0.00
## Diff_levelD3           0.47  0.25  0.69          0.11   4.15  0.00
## Diff_levelD4           0.55  0.33  0.77          0.11   4.88  0.00
## Diff_levelD5           0.88  0.66  1.09          0.11   8.04  0.00
```

```
(cx2["Diff_levelD3",])
```

```
##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD3           0.47  0.25  0.69          0.11   4.15  0
```

```
write.table(cx2, "results/FinalModelCoefficients__relevel2_simultaneity.txt", sep="\t", row.names = F)
```

Relevel Diff_level (D3 first) to compare level D3 to level D4.

```
d3 = d
d3$Diff_level = relevel(d3$Diff_level,"D3")
fm3 = update(mDiff, data=d3)
```

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

```
summary(fm3)
```

```
## 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: d3
## Control: glmerControl(optimizer = "bobyqa")
##
##           AIC           BIC    logLik deviance df.resid
##    1653.2    1684.9   -819.6  1639.2     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```

## -2.4045 -0.4976 -0.1514 0.4839 5.5403
##
## Random effects:
## Groups Name      Variance Std.Dev.
## trial (Intercept) 2.510e-15 5.010e-08
## PartID (Intercept) 1.526e-01 3.907e-01
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.3396     0.1105   3.074 0.00211 **
## Diff_levelD1 -3.0787     0.1940 -15.870 < 2e-16 ***
## Diff_levelD2 -0.4683     0.1128  -4.153 3.28e-05 ***
## Diff_levelD4  0.0806     0.1048   0.769 0.44204
## Diff_levelD5  0.4078     0.1010   4.037 5.41e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Dff_D1 Dff_D2 Dff_D4
## Diff_levelD1 -0.258
## Diff_levelD2 -0.445 0.256
## Diff_levelD4 -0.479 0.271 0.468
## Diff_levelD5 -0.497 0.281 0.485 0.525
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

```

CI = confint(fm3,parm="beta_", method="Wald")
cx = summary(fm3)$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)           0.34 0.12 0.56           0.11 3.07 0.00
## Diff_levelD1          -3.08 -3.46 -2.70           0.19 -15.87 0.00
## Diff_levelD2           -0.47 -0.69 -0.25           0.11 -4.15 0.00
## Diff_levelD4           0.08 -0.12 0.29           0.10 0.77 0.44
## Diff_levelD5           0.41 0.21 0.61           0.10 4.04 0.00

```

```

(cx2["Diff_levelD4",])

```

```

##              estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD4           0.08 -0.12 0.29           0.1 0.77 0.44

```

```

write.table(cx2, "results/FinalModelCoefficients__relevel3_simultaneity.txt", sep="\t", row.names = F)

```

Relevel Diff_level (D4 first) to compare level D4 to level D5.

```

d4 = d
d4$Diff_level = relevel(d4$Diff_level,"D4")
fm4 = update(mDiff, data=d4)

## boundary (singular) fit: see ?isSingular

summary(fm4)

## 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: d4
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 1653.2  1684.9  -819.6  1639.2     671
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4045 -0.4976 -0.1514  0.4839  5.5403
##
## Random effects:
##  Groups Name      Variance Std.Dev.
##  trial  (Intercept) 0.0000  0.0000
##  PartID (Intercept) 0.1526  0.3907
## Number of obs: 678, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.4202    0.1100   3.820 0.000134 ***
## Diff_levelD1  -3.1593    0.1939 -16.297 < 2e-16 ***
## Diff_levelD2  -0.5489    0.1124  -4.883 1.05e-06 ***
## Diff_levelD3  -0.0806    0.1048  -0.769 0.442036
## Diff_levelD5   0.3272    0.1004   3.259 0.001119 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Dff_D1 Dff_D2 Dff_D3
## Diff_levlD1 -0.256
## Diff_levlD2 -0.441  0.254
## Diff_levlD3 -0.472  0.269  0.463
## Diff_levlD5 -0.492  0.278  0.481  0.516
## convergence code: 0
## boundary (singular) fit: see ?isSingular

CI = confint(fm4,parm="beta_", method="Wald")
cx = summary(fm4)$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)           0.42  0.20  0.64         0.11   3.82   0.00
## Diff_levelD1          -3.16 -3.54 -2.78         0.19  -16.30  0.00
## Diff_levelD2           -0.55 -0.77 -0.33         0.11   -4.88  0.00
## Diff_levelD3           -0.08 -0.29  0.12         0.10   -0.77  0.44
## Diff_levelD5            0.33  0.13  0.52         0.10   3.26   0.00
```

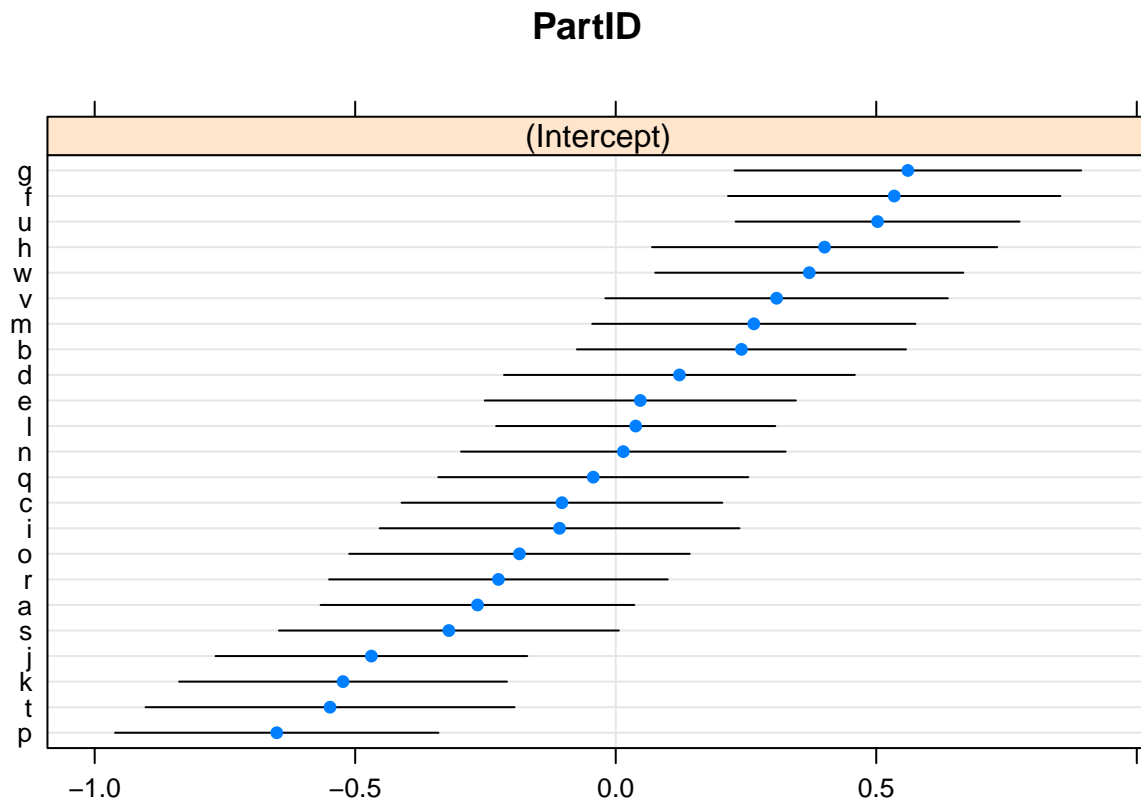
```
(cx2["Diff_levelD5",])
```

```
##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD5            0.33  0.13  0.52         0.1   3.26   0
```

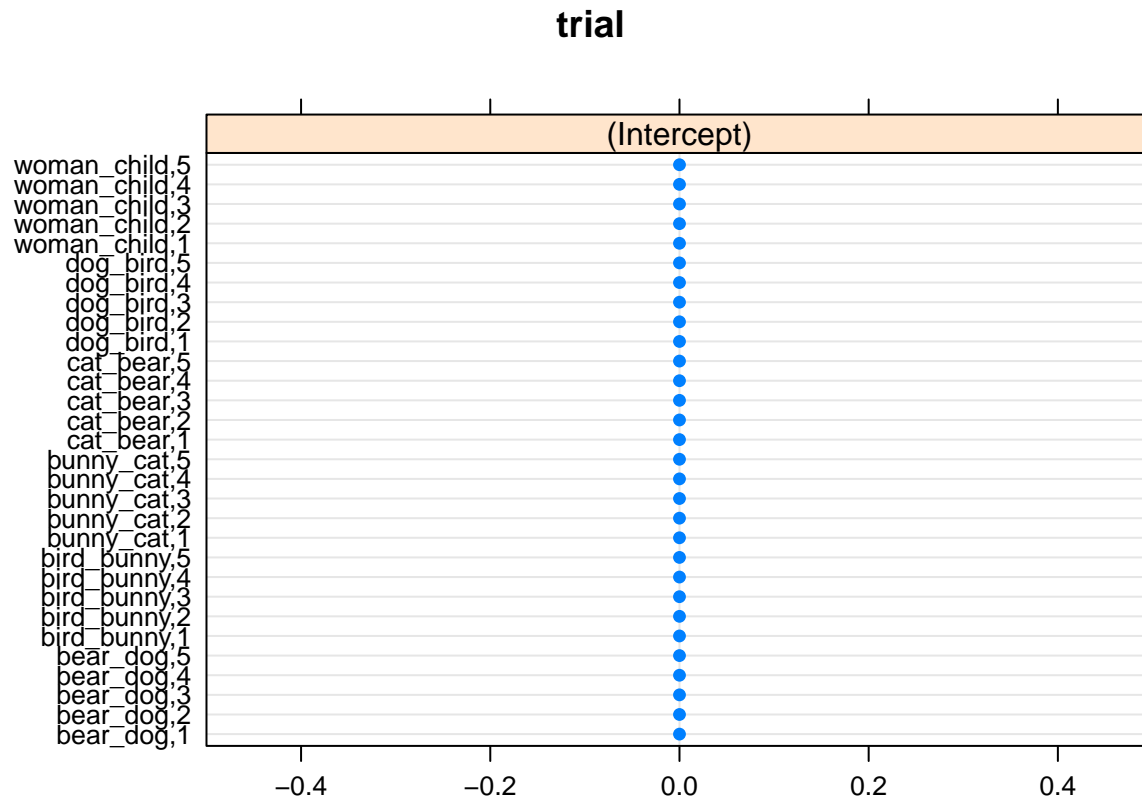
```
write.table(cx2, "results/FinalModelCoefficients__relevel4_simultaneity.txt", sep="\t", row.names = F)
```

Random effects

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




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



Descriptive statistics of raw data

```
#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 ) %>%
  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
```

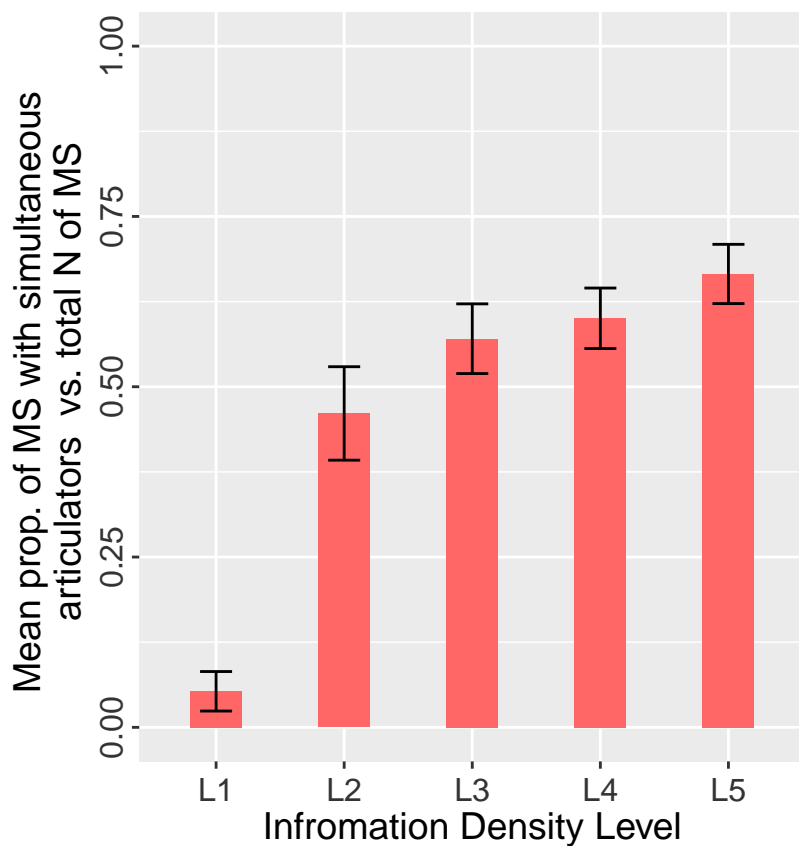
```
##   Diff_level  N      mean      sd      se      ci      upper
## 1          L1 23 0.05295031 0.06703657 0.01397809 0.02898879 0.0819391
## 2          L2 23 0.46080745 0.15858962 0.03306822 0.06857930 0.5293867
## 3          L3 23 0.57051153 0.11829986 0.02466723 0.05115670 0.6216682
## 4          L4 23 0.60049041 0.10268607 0.02141153 0.04440479 0.6448952
## 5          L5 23 0.66555714 0.10061023 0.02097868 0.04350713 0.7090643
##           lower
## 1 0.02396152
## 2 0.39222816
## 3 0.51935484
## 4 0.55608562
## 5 0.62205001
```

Plot for simultaneity

```
main.plot <- ggplot(sumStats2,
                    aes(x = Diff_level, y = mean)) +
  geom_bar(stat= "identity", width = 0.4, fill = "#FF6666") + theme(aspect.ratio = 9/8) +
  geom_errorbar(aes(ymax=mean+ci, ymin=mean-ci), width=0.25) + xlab("Infomation Density Level") +
  ylab("Mean prop. of MS with simultaneous \n articulators vs. total N of MS") + coord_cartesian(ylim=
  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 = 14)

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_sign_Anonym_density.txt")
```

Each row in the data is based on a single movement segment (MS) used by participant. The key variables are:

- PartID: identifies participants
- trial: the name of unique trial/experimental stimuli
- Diff_level: density level of the trial
- Info_n: total number of information units in a single MS

Baseline model

Random effects

```
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
```

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 10274 10286 -5135   10270
## mSim2A1   3 10134 10153 -5064   10128 141.95     1 < 2.2e-16 ***
## ---
## 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 = d,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)
```

Fixed effects

```
##Sex
```

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

```
anova(m0,mSim2Sex)
```

```
## Data: d
## 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 10134 10153 -5064.0   10128
## mSim2Sex     4 10136 10160 -5063.8   10128 0.485     1    0.4862
```

```
##Handedness
```

```
mSim2Hand = glmer(
  Info_n ~ 1 + Hand +
    (1 | PartID) +
    (1 | trial),
  data = d,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
anova(m0,mSim2Hand)
```

```
## Data: d
## 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 10134 10153 -5064.0   10128
## mSim2Hand   4 10135 10160 -5063.6   10127 0.7836     1    0.3761
```

```
##Signing experience
```

```
mSim2Exp = glmer(
  Info_n ~ 1 + Sign_since +
    (1 | PartID) +
    (1 | trial),
  data = d,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
)
```

```
anova(m0,mSim2Exp)
```

```
## Data: d
## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mSim2Exp: Info_n ~ 1 + Sign_since + (1 | PartID) + (1 | trial)
##           Df   AIC   BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0           3 10134 10153 -5064.0   10128
## mSim2Exp   4 10134 10159 -5063.3   10126 1.5719     1    0.2099
```

```
##Age
```

```
mSim2Age = glmer(
  Info_n ~ 1 + Age +
    (1 | PartID) +
    (1 | trial/MSnum),
  data = d,
  family = "poisson",
  control = glmerControl(optimizer = 'bobyqa')
) #model is not converging. no influence of age is expected, thus leaving this contorl out.
```

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

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

```
## Data: d
```

```

## Models:
## m0: Info_n ~ 1 + (1 | PartID) + (1 | trial)
## mSim2Age: Info_n ~ 1 + Age + (1 | PartID) + (1 | trial/MSnum)
##           Df   AIC   BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m0           3 10134 10153 -5064.0   10128
## mSim2Age    5 10018 10050 -5004.3   10008 119.53     2 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

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

Effect of density level

```

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

```

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

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

```

## Data: d
## 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 10134 10153 -5064.0   10128
## mDiff        7 10053 10097 -5019.7   10039 88.736     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: poisson ( log )
## Formula: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##           AIC       BIC   logLik deviance df.resid
## 10053.3 10096.8 -5019.7 10039.3     3690
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max

```

```

## -0.76704 -0.58312 -0.04078  0.33617  1.62187
##
## Random effects:
## Groups Name      Variance Std.Dev.
## trial (Intercept) 0.000000 0.00000
## PartID (Intercept) 0.001422 0.03771
## Number of obs: 3697, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.06215    0.04350   1.429   0.153
## Diff_levelD2  0.37505    0.05418   6.922 4.45e-12 ***
## Diff_levelD3  0.54532    0.05030  10.841 < 2e-16 ***
## Diff_levelD4  0.57030    0.04991  11.426 < 2e-16 ***
## Diff_levelD5  0.64751    0.04802  13.485 < 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
## Diff_levlD2 -0.775
## Diff_levlD3 -0.835  0.670
## Diff_levlD4 -0.842  0.675  0.728
## Diff_levlD5 -0.875  0.702  0.756  0.763
## convergence code: 0
## boundary (singular) fit: see ?isSingular

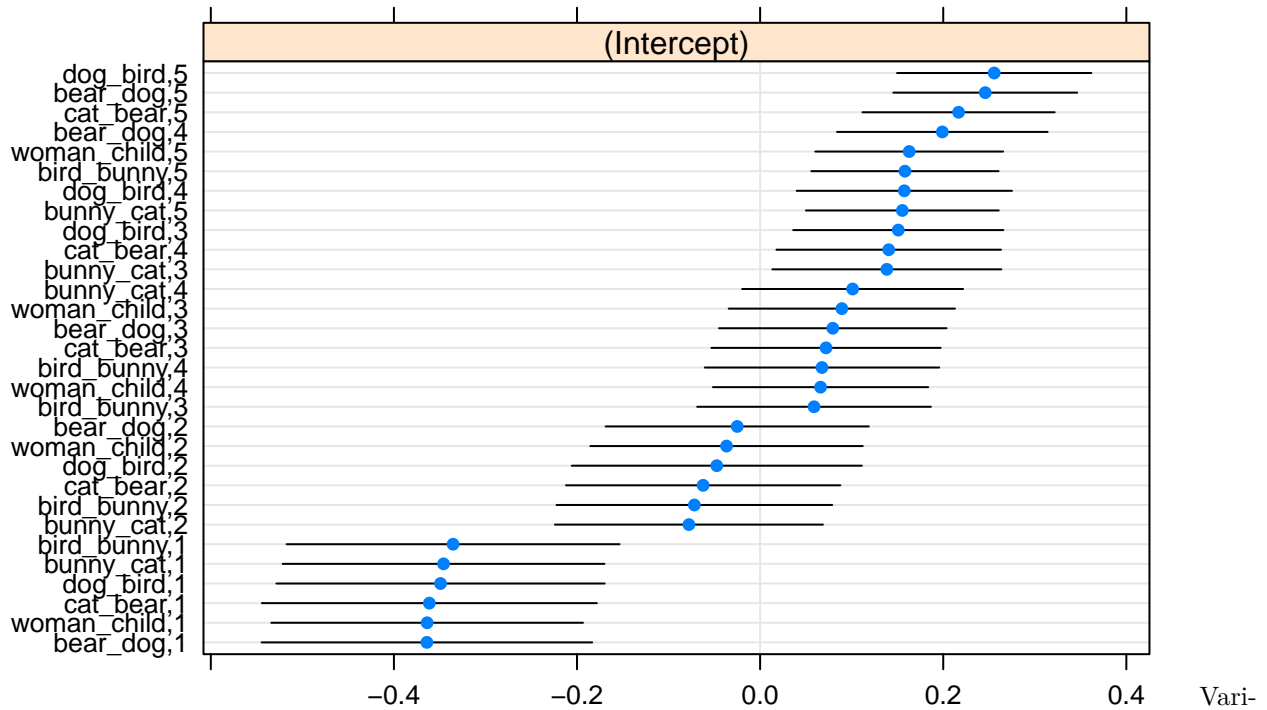
```

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

Check variance of trial in baseline model

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


trial



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 = d,
  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: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 10051.3 10088.6 -5019.7 10039.3    3691
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.76704 -0.58312 -0.04078  0.33617  1.62187
##
```

```

## Random effects:
## Groups Name      Variance Std.Dev.
## PartID (Intercept) 0.001422 0.03771
## Number of obs: 3697, groups: PartID, 23
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.06215    0.04350   1.429   0.153
## Diff_levelD2  0.37505    0.05418   6.922 4.44e-12 ***
## Diff_levelD3  0.54532    0.05030  10.842 < 2e-16 ***
## Diff_levelD4  0.57030    0.04991  11.427 < 2e-16 ***
## Diff_levelD5  0.64751    0.04801  13.486 < 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
## Diff_levelD2 -0.775
## Diff_levelD3 -0.835  0.670
## Diff_levelD4 -0.842  0.675  0.728
## Diff_levelD5 -0.875  0.702  0.756  0.763

```

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

```

## Data: d
## 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 10051 10089 -5019.7   10039
## mDiff     7 10053 10097 -5019.7   10039    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

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

```

## Data: d
## 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 10134 10153 -5064.0   10128
## mDiff     7 10053 10097 -5019.7   10039 88.736    4 < 2.2e-16 ***
## ---
## 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: Info_n ~ 1 + Diff_level + (1 | PartID) + (1 | trial)
## Data: d
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 10053.3 10096.8 -5019.7 10039.3    3690
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.76704 -0.58312 -0.04078  0.33617  1.62187
##
## Random effects:
## Groups Name          Variance Std.Dev.
## trial  (Intercept) 0.000000 0.00000
## PartID (Intercept) 0.001422 0.03771
## Number of obs: 3697, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.06215    0.04350   1.429    0.153
## Diff_levelD2 0.37505    0.05418   6.922 4.45e-12 ***
## Diff_levelD3 0.54532    0.05030  10.841 < 2e-16 ***
## Diff_levelD4 0.57030    0.04991  11.426 < 2e-16 ***
## Diff_levelD5 0.64751    0.04802  13.485 < 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
## Diff_levelD2 -0.775
## Diff_levelD3 -0.835  0.670
## Diff_levelD4 -0.842  0.675  0.728
## Diff_levelD5 -0.875  0.702  0.756  0.763
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Confidence Intervals using Wald method

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

```

cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           0.06 -0.02  0.15         0.04   1.43   0.15
## Diff_levelD2           0.38  0.27  0.48         0.05   6.92   0.00
## Diff_levelD3           0.55  0.45  0.64         0.05  10.84   0.00
## Diff_levelD4           0.57  0.47  0.67         0.05  11.43   0.00
## Diff_levelD5           0.65  0.55  0.74         0.05  13.49   0.00
##           estimate.linear estimate.linear.lower estimate.linear.upper
## (Intercept)           1.06                   0.98                   1.16
## Diff_levelD2           1.46                   1.31                   1.62
## Diff_levelD3           1.73                   1.56                   1.90
## Diff_levelD4           1.77                   1.60                   1.95
## Diff_levelD5           1.91                   1.74                   2.10

```

Contrasts

Relevel Diff_level (D2 first) to compare level D2 to level D3.

```

d2 = d
d2$Diff_level = relevel(d2$Diff_level, "D2")
fm2 = update(mDiff, data=d2)

```

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

```
summary(fm2)
```

```

## 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: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##           AIC          BIC    logLik deviance df.resid
## 10053.3 10096.8 -5019.7 10039.3    3690
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.76704 -0.58312 -0.04078  0.33616  1.62187
##
## Random effects:
## Groups Name          Variance Std.Dev.
## trial  (Intercept)  0.000000  0.00000
## PartID (Intercept)  0.001422  0.03771
## Number of obs: 3697, groups: trial, 30; PartID, 23
##
## Fixed effects:

```

```

##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.43720    0.03428  12.755 < 2e-16 ***
## Diff_levelD1 -0.37506    0.05418  -6.922 4.44e-12 ***
## Diff_levelD3  0.17026    0.04260   3.997 6.41e-05 ***
## Diff_levelD4  0.19525    0.04212   4.635 3.57e-06 ***
## Diff_levelD5  0.27245    0.03987   6.834 8.28e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) Dff_D1 Dff_D3 Dff_D4
## Diff_levelD1 -0.597
## Diff_levelD3 -0.760  0.481
## Diff_levelD4 -0.770  0.486  0.619
## Diff_levelD5 -0.813  0.514  0.654  0.662
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

```

CI = confint(fm2,parm="beta_", method="Wald")
cx = summary(fm2)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$estimate.linear = exp(cx2[,1])
cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           0.44  0.37  0.50          0.03  12.76      0
## Diff_levelD1          -0.38 -0.48 -0.27          0.05  -6.92      0
## Diff_levelD3           0.17  0.09  0.25          0.04   4.00      0
## Diff_levelD4           0.20  0.11  0.28          0.04   4.64      0
## Diff_levelD5           0.27  0.19  0.35          0.04   6.83      0
##           esimate.linear esimate.linear.lower esimate.linear.upper
## (Intercept)           1.55                   1.45                   1.66
## Diff_levelD1           0.69                   0.62                   0.76
## Diff_levelD3           1.19                   1.09                   1.29
## Diff_levelD4           1.22                   1.12                   1.32
## Diff_levelD5           1.31                   1.21                   1.42

```

```

(cx2["Diff_levelD3",])

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD3           0.17  0.09  0.25          0.04     4      0
##           esimate.linear esimate.linear.lower esimate.linear.upper
## Diff_levelD3           1.19                   1.09                   1.29

```

Relevel Diff_level (D3 first) to compare level D3 to level D4.

```
d3 = d
d3$Diff_level = relevel(d3$Diff_level,"D3")
fm3 = update(mDiff, data=d3)
```

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

```
summary(fm3)
```

```
## 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: d3
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 10053.3 10096.8 -5019.7 10039.3    3690
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.76704 -0.58312 -0.04078  0.33617  1.62187
##
## Random effects:
## Groups Name          Variance Std.Dev.
## trial  (Intercept)  0.000000 0.00000
## PartID (Intercept)  0.001422 0.03771
## Number of obs: 3697, groups: trial, 30; PartID, 23
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.60746    0.02773  21.909 < 2e-16 ***
## Diff_levelD1 -0.54532    0.05030 -10.842 < 2e-16 ***
## Diff_levelD2 -0.17026    0.04259  -3.997 6.41e-05 ***
## Diff_levelD4  0.02498    0.03698   0.676 0.49933
## Diff_levelD5  0.10219    0.03439   2.971 0.00297 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Dff_D1 Dff_D2 Dff_D4
## Diff_levelD1 -0.504
## Diff_levelD2 -0.596  0.329
## Diff_levelD4 -0.687  0.378  0.447
## Diff_levelD5 -0.738  0.407  0.480  0.554
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
CI = confint(fm3,parm="beta_", method="Wald")
cx = summary(fm3)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
```

```
names(cx2)[1] = "estimate.logit"
cx2$estimate.linear = exp(cx2[,1])
cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2
```

```
##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           0.61  0.55  0.66           0.03  21.91   0.0
## Diff_levelD1          -0.55 -0.64 -0.45           0.05 -10.84   0.0
## Diff_levelD2          -0.17 -0.25 -0.09           0.04  -4.00   0.0
## Diff_levelD4           0.02 -0.05  0.10           0.04   0.68   0.5
## Diff_levelD5           0.10  0.03  0.17           0.03   2.97   0.0
##           esimate.linear esimate.linear.lower esimate.linear.upper
## (Intercept)           1.84                   1.74                   1.94
## Diff_levelD1           0.58                   0.53                   0.64
## Diff_levelD2           0.84                   0.78                   0.92
## Diff_levelD4           1.03                   0.95                   1.10
## Diff_levelD5           1.11                   1.04                   1.18
```

```
(cx2["Diff_levelD4",])
```

```
##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## Diff_levelD4           0.02 -0.05  0.10           0.04   0.68   0.5
##           esimate.linear esimate.linear.lower esimate.linear.upper
## Diff_levelD4           1.03                   0.95                   1.1
```

Relevel Diff_level (D4 first) to compare level D4 to level D5.

```
d4 = d
d4$Diff_level = relevel(d4$Diff_level, "D4")
fm4 = update(mDiff, data=d4)
```

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

```
summary(fm4)
```

```
## 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: d4
## Control: glmerControl(optimizer = "bobyqa")
##
##           AIC           BIC    logLik deviance df.resid
## 10053.3 10096.8 -5019.7 10039.3    3690
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.76704 -0.58312 -0.04078  0.33617  1.62187
##
```

```

## Random effects:
## Groups Name      Variance Std.Dev.
## trial (Intercept) 0.000000 0.00000
## PartID (Intercept) 0.001422 0.03771
## Number of obs: 3697, groups: trial, 30; PartID, 23
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.63245    0.02696  23.456 < 2e-16 ***
## Diff_levelD1 -0.57030    0.04991 -11.427 < 2e-16 ***
## Diff_levelD2 -0.19525    0.04212  -4.635 3.57e-06 ***
## Diff_levelD3 -0.02498    0.03698  -0.676  0.4993
## Diff_levelD5  0.07721    0.03378   2.285  0.0223 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) Dff_D1 Dff_D2 Dff_D3
## Diff_levelD1 -0.493
## Diff_levelD2 -0.584  0.316
## Diff_levelD3 -0.665  0.360  0.426
## Diff_levelD5 -0.727  0.393  0.466  0.531
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

```

CI = confint(fm4,parm="beta_", method="Wald")
cx = summary(fm4)$coef
cx = cbind(cx[,1],CI, cx[,2:4])
cx2 = cx
cx2 = as.data.frame(cx2)
names(cx2)[1] = "estimate.logit"
cx2$estimate.linear = exp(cx2[,1])
cx2$estimate.linear.lower = exp(cx2[,2])
cx2$estimate.linear.upper = exp(cx2[,3])
cx2 = round(cx2, digits = 2)
cx2

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)
## (Intercept)           0.63  0.58  0.69          0.03  23.46  0.00
## Diff_levelD1          -0.57 -0.67 -0.47          0.05 -11.43  0.00
## Diff_levelD2          -0.20 -0.28 -0.11          0.04  -4.64  0.00
## Diff_levelD3          -0.02 -0.10  0.05          0.04  -0.68  0.50
## Diff_levelD5           0.08  0.01  0.14          0.03   2.29  0.02
##           esimate.linear esimate.linear.lower esimate.linear.upper
## (Intercept)           1.88                   1.79                   1.98
## Diff_levelD1           0.57                   0.51                   0.62
## Diff_levelD2           0.82                   0.76                   0.89
## Diff_levelD3           0.98                   0.91                   1.05
## Diff_levelD5           1.08                   1.01                   1.15

```

```

(cx2["Diff_levelD5",])

```

```

##           estimate.logit 2.5 % 97.5 % Std. Error z value Pr(>|z|)

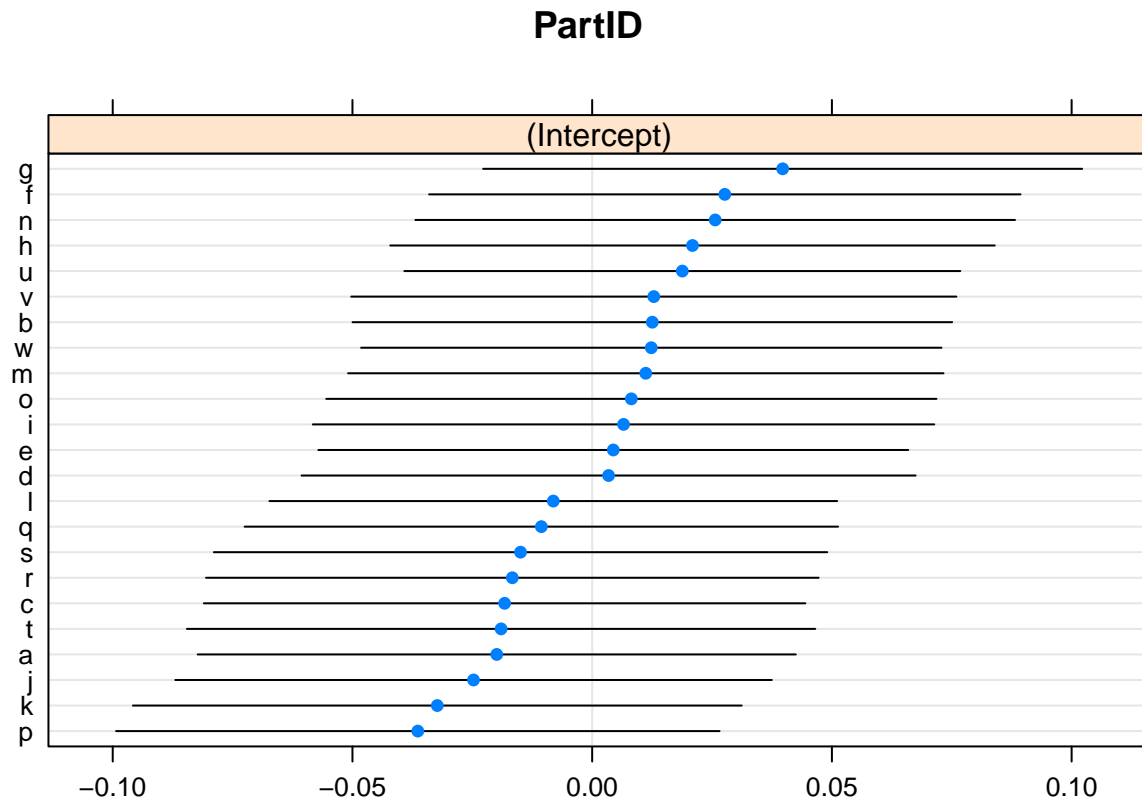
```



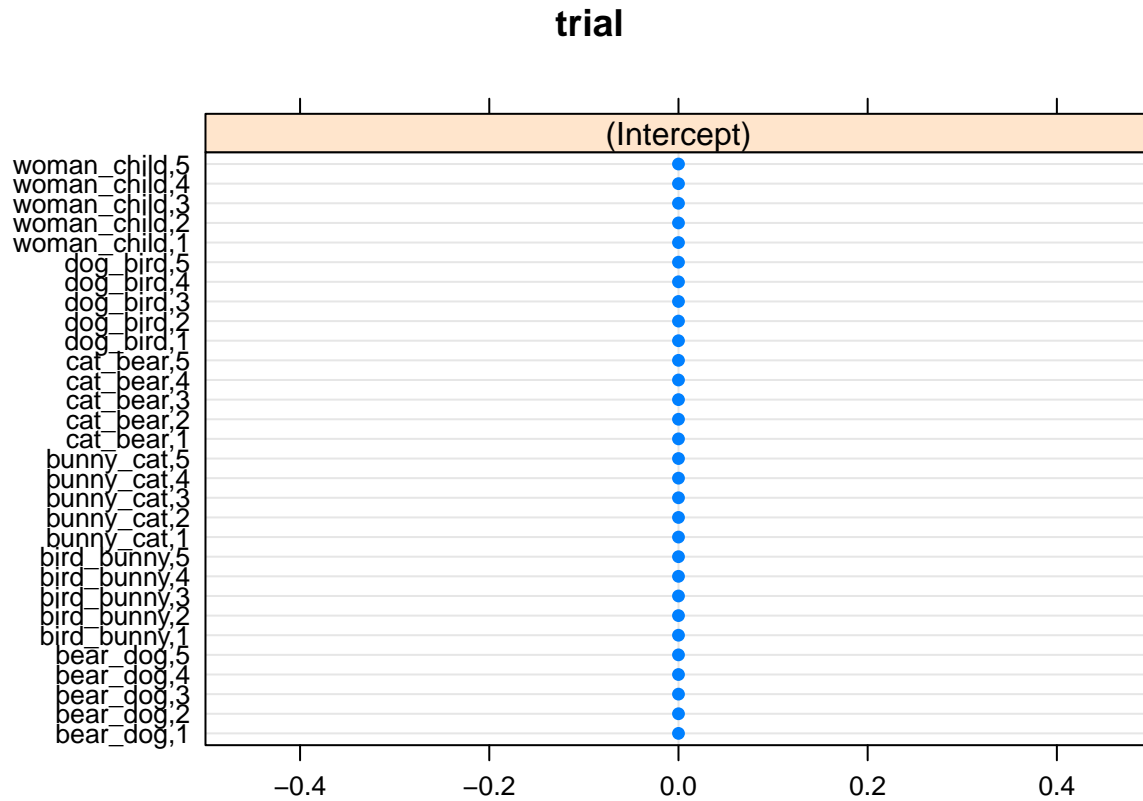
```
## Diff_levelD5      0.08  0.01  0.14      0.03  2.29  0.02
##      estimate.linear estimate.linear.lower estimate.linear.upper
## Diff_levelD5      1.08                1.01                1.15
```

Random effects

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



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



Descriptive statistics

There were 23 participants each describing 30 trials (experimental stimuli). There were total of 3697 movement segments (MS) used.

N of Participants

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

```
## Factor w/ 23 levels "a","b","c","d",...: 1 1 1 1 1 1 1 1 1 1 ...
```

#N of trials (experimental stimuli)

```
str(d$trial)
```

```
## Factor w/ 30 levels "bear_dog,1","bear_dog,2",...: 12 12 12 19 19 19 19 19 10 10 ...
```

#Total number of observations (movement segments produced)

```
sum(complete.cases(d))
```

```
## [1] 3697
```

Number of observations per participant

```
table(d$PartID)
```

```
##
##  a  b  c  d  e  f  g  h  i  j  k  l  m  n  o  p  q  r
## 163 162 159 133 181 167 157 149 117 171 144 227 162 160 139 159 175 137
##  s  t  u  v  w
## 139 111 244 148 193
```

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

```
##
##  D1  D2  D3  D4  D5
## 514 581 773 801 1028
```

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

```
##
##  1  2  3  4
## 1748 1225 622 102
```

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

```
##
##      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
```

Decision tree

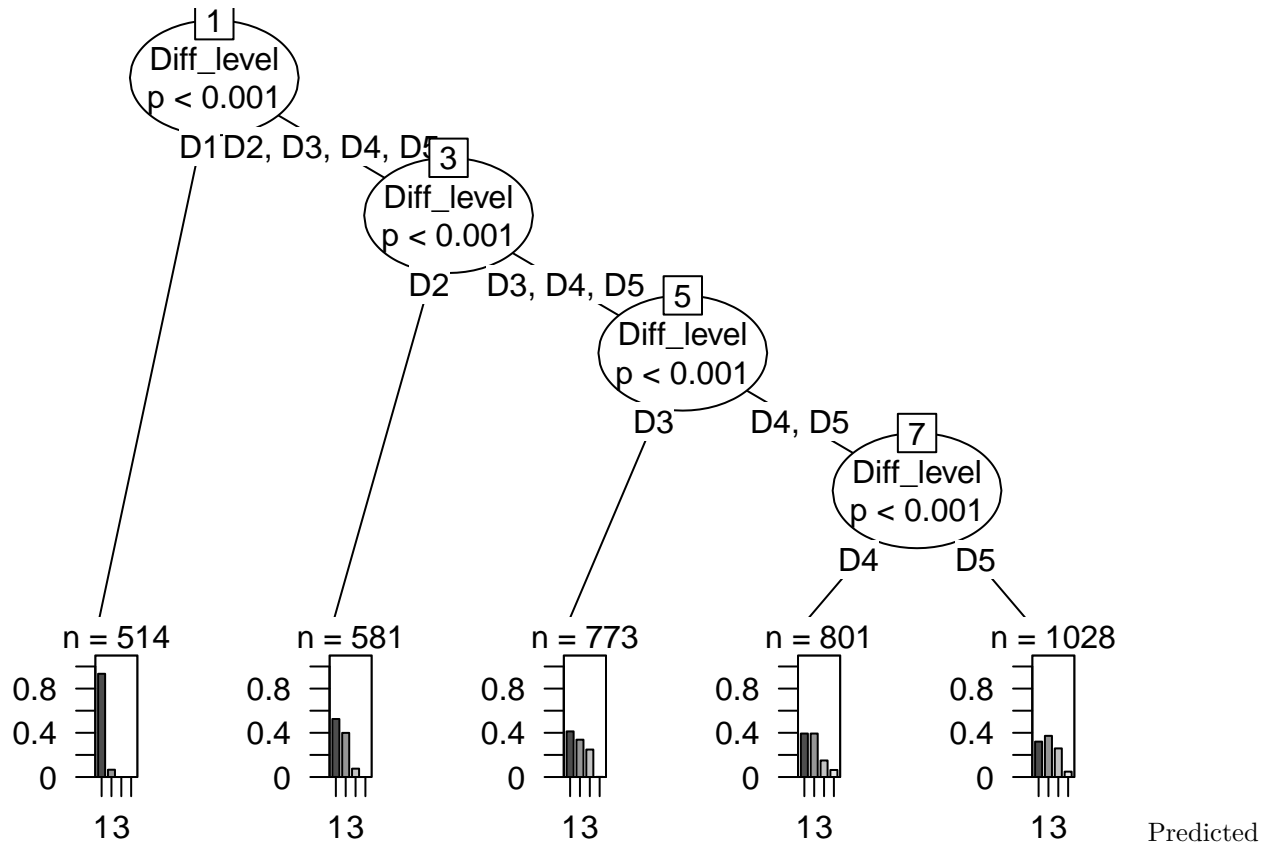
Make a decision tree assessing the fixed effect of density level to check predicted hypothesis that simultaneous information density in a MS would be clustered based on the density level

```
d$Info_n <- as.character(d$Info_n)
d$Info_n <- as.factor(d$Info_n)

#Predicting simultaneous info units based on density level

dec_tree_diff = ctree(Info_n ~
  Diff_level,
  data = d,)

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



hypothesis double confirmed. decision tree splits data, first clustering Level 1 and all other levels, then Level 2 and all other Levels, then Level 3 and remaining two densest levels. Finally, Levels 4 and 5 are split based on predicted information density units used. Overall pattern indicates that denser simultaneously encoded information is predicted in denser levels.

Plot for density of simultaneity

```
d.simult.plots <- d[, 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
```

```

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)

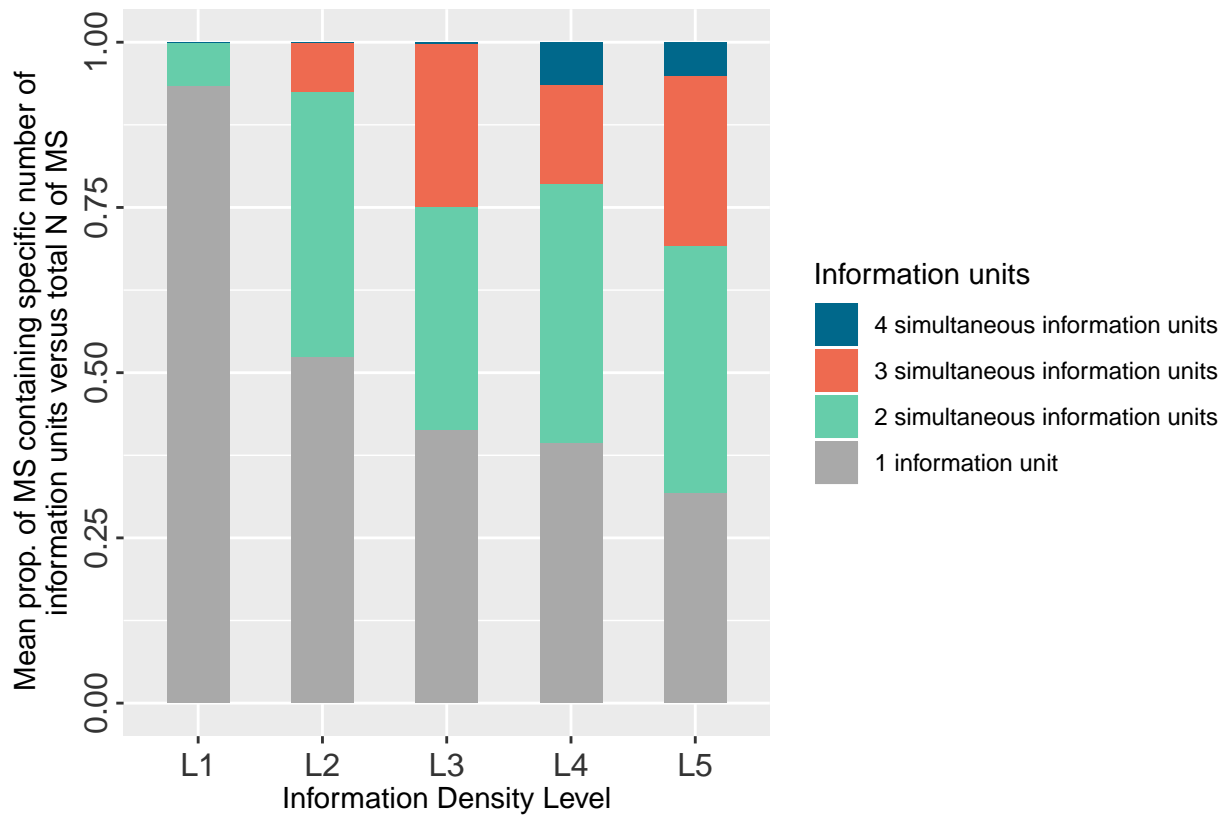
Plot.Units2$Units[Plot.Units2$Units == "sim1"] <- "1 information unit"
Plot.Units2$Units[Plot.Units2$Units == "sim2"] <- "2 simultaneous information units"
Plot.Units2$Units[Plot.Units2$Units == "sim3"] <- "3 simultaneous information units"
Plot.Units2$Units[Plot.Units2$Units == "sim4"] <- "4 simultaneous 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 = 9/8) +
  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")
p+scale_fill_manual(values=c("deepskyblue4", "coral2", "aquamarine3", "darkgray"))

```



```
bold.text <- element_text( size = 14, colour = "black")
ggsave("plot_density.png")
```

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

```
““
```