Colour experiment

Contents

Introduction

This analysis looks at the sign variants used in a colour naming game between signers of different sign languages meeting after 1 week of interaction and after 3 weeks of interaction. The data was collected by Kang Suk Byun.

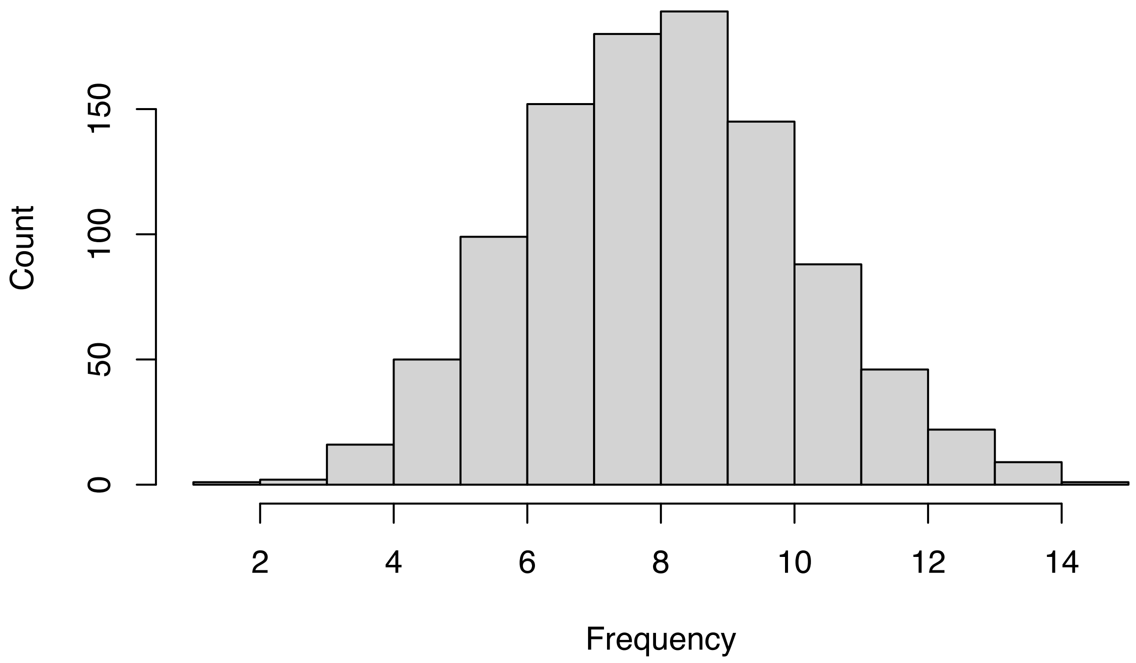
The analysis tries to predict the relative frequency of each variant within a colour category in week 3, based on measures from week 1.

Data

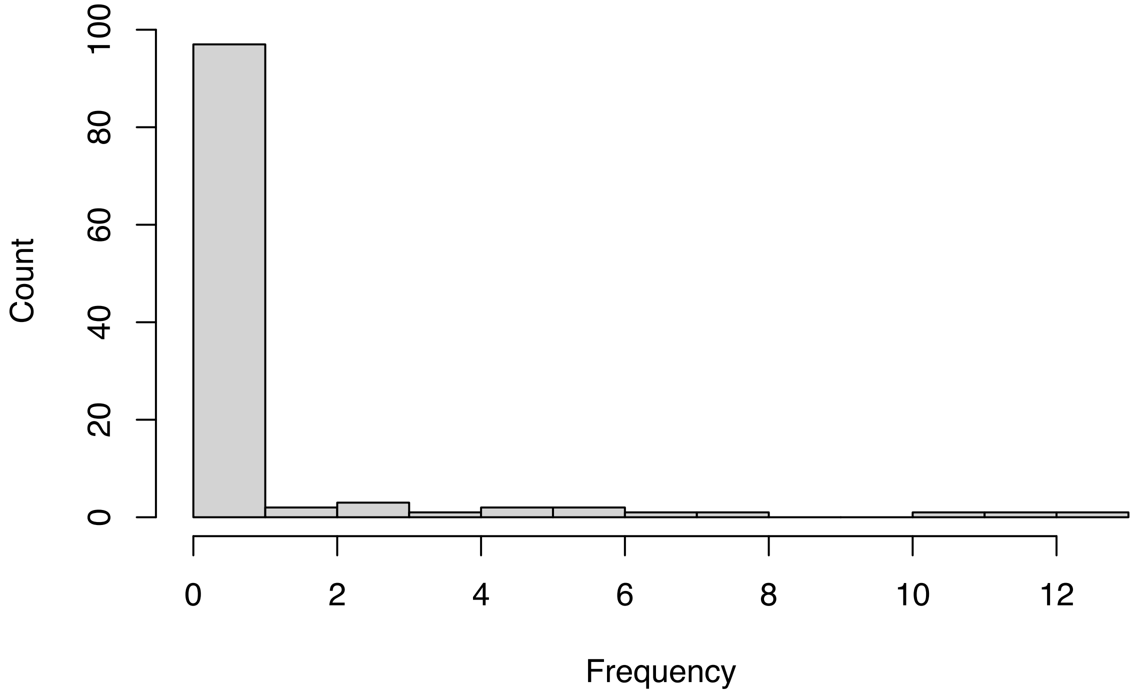
- colour: Code of the target colour
- colourName: English name of the target colour
- sign: label for the variant produced
- freq_week_1_total: Total number of occurances of the variant in the first week, across all colour contexts.
- freq_week_4_total: Total number of occurances of the variant in the final week, across all colour contexts.
- freq_week_1: Number of occurances of the variant used during the given target colour context in week 1.
- freq_week_4: Number of occurances of the variant used during the given target colour context in the final week.
- prop_week_1: Same as freq_week_1, but as a proportion of all variants used in the given colour context.
- prop_week_4: Same as freq_week_4, but as a proportion of all variants used in the given colour context.
- origin: The origin language of the sign. For many, identifying an origin is not possible, so is labelled "None"
- iconic: Old variable
- check: The number of times this variable was used in a checking turn.
- indexical: Is the variant non-indexical, indexical or indexical of the body?
- inventedBy: The name of the first signer to use this variant in the experiment.
- TryMarked: The number of times this sign was used in try-marking.
- Teach: The number of times this sign was explicitly taught.
- averageLength_week_1: Average time to produce the variant in milliseconds
- averageTrialLength_week_1: Average time for completing the trial for the given target colour.
- BodyAnchor: Is the variant body-anchored (redundant with 'indexical')

Poisson regression

This study uses a mixed effects regression model with poisson distributions. Most standard regression analyses assume that the values they are trying to model come from a normal distribution, like this:



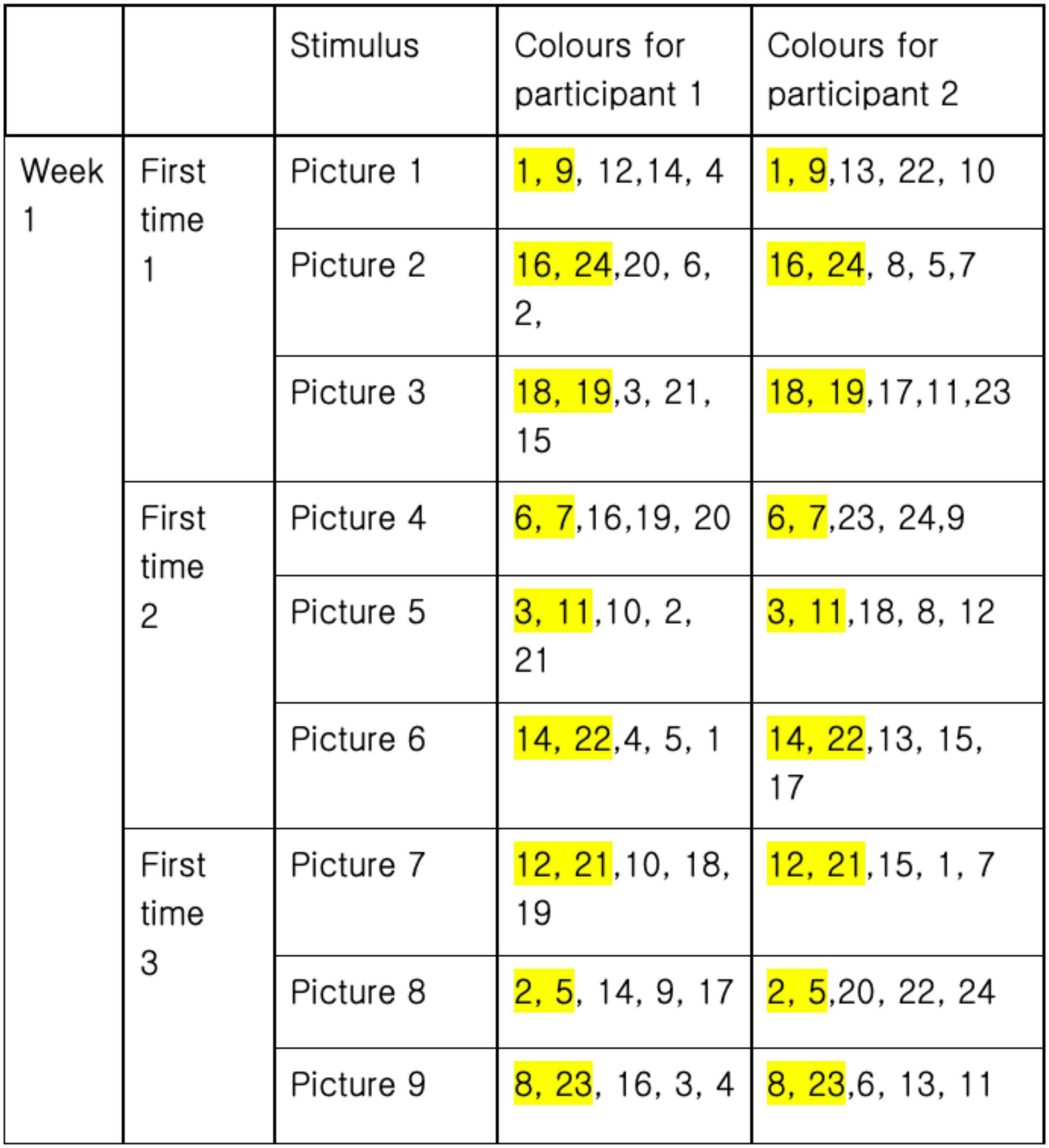
However, the main variable for this study is the frequency of sign variants, with a strong skew and many zero values:



Instead of using a normal distribution as the basis for the statistical model or transforming the data (which is difficult anyway because of the large number of zero counts), we can use a poisson distribution. This also has the advantage of only predicting whole, non-negative numbers, which makes sense for this data because a variant can't be used half a time or a negative number of times.

Stimuli

The table below summarises the colours used in each round, which we identified by giving each one a number. The numbers highlighted in yellow were the colours that were the same across both pictures. The table above gives an indication of the kind of planning that was carried out prior to the experiments to ensure robust organisation and reliable use of the materials. The actual table we used is much longer, encompassing all of the dates and rounds, but for the sake of brevity only the part related to the first week of data-gathering is shown here. The numbers in yellow, which indicate colours that were the same across both pictures, are also not repeated after that one use in the week; i.e. 1 and 9 do not appear after the first row. This was done to maximise discussion about as large a range of colours as possible.



		Stimulus	Colours for participant 1	Colours for participant 2
Week 1	First time 1	Picture 1	1, 9, 12,14, 4	1, 9,13, 22, 10
		Picture 2	16, 24,20, 6, 2,	16, 24, 8, 5,7
		Picture 3	18, 19,3, 21, 15	18, 19,17,11,23
	First time 2	Picture 4	6, 7,16,19, 20	6, 7,23, 24,9
		Picture 5	3, 11,10, 2, 21	3, 11,18, 8, 12
		Picture 6	14, 22,4, 5, 1	14, 22,13, 15, 17
	First time 3	Picture 7	12, 21,10, 18, 19	12, 21,15, 1, 7
		Picture 8	2, 5, 14, 9, 17	2, 5,20, 22, 24
		Picture 9	8, 23, 16, 3, 4	8, 23,6, 13, 11

Figure 1: Stimuli design

Load libraries

```
library(ggplot2)
library(lme4)
library(Rmisc)
library(dplyr)
library(sjPlot)
library(gridExtra)
library(REEMtree)
library(ggpubr)
```

Load data

```
variants = read.csv('../data/processedData/variants_summary.csv', stringsAsFactors = F)
```

There is only 1 variant for 'white'. Therefore, we remove it from this statistical analysis.

```
variants = variants[variants$colourName!='white',]
```

Some variants need to be removed:

```
variants = variants[!variants$sign %in%
            c("SAME",
              "DIFFERENT",
              "DO NOT UNDERSTAND",
              "UNDERSTAND",
              "ME",
              "YOU",
              "YES",
              "NOT",
              "SIGNING"),]
```

Transform some variables.

```
# The range of values for 'Teach' is very small:
table(variants$Teach)
```

```
##
##  0  1  2  3
## 88  6  1  2
```

```
# So we'll turn it into a binary category:
#  variants that were never taught and variants that were
variants$Teach = as.factor(variants$Teach >0)

# Similar for checking
variants$check.any = as.factor(variants$check>0)

variants$candidateUnderstanding.any = as.factor(variants$candidateUnderstanding>0)

variants$TO = c("No","Check")[as.numeric(variants$check.any=="TRUE")+1]
variants$TO[variants$candidateUnderstanding.any=="TRUE"] = "Candidate Understanding"

# Collapse checks and candidate understandings
variants$TO[variants$TO %in% c("Check","Candidate Understanding")] = "Yes"
```

```
variants$T0 = factor(variants$T0, levels = c("No","Yes"))

# ... and T-1

variants$T_minus_1.any = as.factor(variants$T_minus_1>0)

# Transform total frequency
variants$freq_week_1_total.logcenter =
  log(variants$freq_week_1_total + 1)
variants$freq_week_1_total.logcenter = scale(variants$freq_week_1_total.logcenter)

# cut TryMarking into two categories
variants$TryMarked.any = as.factor(variants$TryMarked>0)

# transform length

# One extreme value is scaled down to the next highest number
variants$averageLength_week_1[
  variants$averageLength_week_1>30000] =
  max(variants$averageLength_week_1[
    variants$averageLength_week_1<20000])

variants$averageLength_week_1.logcenter = log(variants$averageLength_week_1)
variants$averageLength_week_1.logcenter =
  scale(variants$averageLength_week_1.logcenter)

variants$indexical = as.factor(variants$indexical)

# Make inventedBy deviation coding
#  (deviation from the grand mean)
variants$inventedBy = as.factor(variants$inventedBy)
#contrasts(variants$inventedBy) = contr.sum(length(levels(variants$inventedBy)))


listofsigns = variants[,c("colourName","sign")]
write.csv(listofsigns,"../results/descriptive/ListOfVariants.csv", fileEncoding = 'utf-8')
```

LMER models

Each model predicts the frequency of a variant in week 4, with a random intercept by colourName. The random intercept allows some colours to have higher variant frequencies than others. This is useful because we know that signs for some colours are converged on quickly, making their frequencies within those colours potentially higher. In other words, the use of a particular variant to refer to a given colour is not entierly independent of the use of another variant to refer to the same colour.

Random slopes allow the strength of the effect of a factor to be different for each colour concept. Only indexicality is theoretically relevant here: it is possible that an indexical strategy, particularly body-indexical signs, would be more effective for some colours than others. For example, the body affords indexicality for black (hair) and red (tongue), but not green. We can check whether this is true by comparing a baseline model to one with a random slope for indexicality.

```
# Optimiser adjustments
gcontrol = control=glmerControl(
  optimizer = 'bobyqa',
  optCtrl = list(maxfun = 1000000))

m0 = glmer(freq_week_4 ~
             1
           + (1 | colourName) ,
           data=variants, family=poisson,
           control=gcontrol)

m1 = glmer(freq_week_4 ~
             1
           + (1 + indexical || colourName) ,
           data=variants, family=poisson,
           control=gcontrol)
```

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

```
anova(m0,m1)
```

```
## Data: variants
## Models:
## m0: freq_week_4 ~ 1 + (1 | colourName)
## m1: freq_week_4 ~ 1 + (1 + indexical || colourName)
##    npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## m0    2 375.66 380.81 -185.83   371.66
## m1    8 308.28 328.88 -146.14   292.28 79.383  6  4.791e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Indeed, a random slope for indexicality significantly improves the model. It is difficult to think of a theoretical reason why different colours would be affected differently for other variables. Given that random slopes make the model more complex, these are left out.

We begin with a null model and gradually add predictor variables, using model comparison to judge the significance of each variable.

```
# Null model
m0 = glmer(freq_week_4 ~
             1
           + (1 + indexical || colourName) ,
           data=variants, family=poisson,
           control=gcontrol)
```

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

```
mFrq = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

```
mLen = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=glmerControl(
               optimizer = 'bobyqa',
               optCtrl = list(maxfun = 10000000)))
```

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

```
# add indexicality
mIndx = glmer(freq_week_4 ~
                1 +
                freq_week_1_total.logcenter +
                averageLength_week_1.logcenter +
                indexical +
                (1 + indexical || colourName) ,
              data=variants, family=poisson,
              control=glmerControl(
                optimizer = c('Nelder_Mead'),
                optCtrl = list(maxfun = 100000000)))
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.0149663 (tol = 0.002, component 1)
```

```
# add whether the variant is explicitly taught
mTeach = glmer(freq_week_4 ~
                 1 +
                 freq_week_1_total.logcenter +
                 averageLength_week_1.logcenter +
                 indexical +
                 Teach +
                 (1 + indexical || colourName) ,
               data=variants, family=poisson,
               control=glmerControl(
                 optimizer = c('Nelder_Mead','bobyqa'),
                 optCtrl = list(maxfun = 10000000)))
```

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

```
mTry = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

```
mChk = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               TO +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

```
mTm1 = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               TO +
               T_minus_1.any +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=glmerControl(
                 optimizer = c('Nelder_Mead','bobyqa'),
                 optCtrl = list(maxfun = 10000000)))
```

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

```
mInv = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               TO +
               T_minus_1.any +
               inventedBy +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

Note that the model `mTm1` throws a convergence warning. It suggests that the estimates were still changing to some extent when the estimation process finished running. However, a more accurate estimation of the model graident shows that the model is actually converged suitably:

```
relgrad <- with(mTm1@optinfo$derivs,
                solve(Hessian,gradient))
max(abs(relgrad))
```

```
## [1] 5.614077e-06
```

Test some interactions:

```
mTOxF = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               T0 +
               T_minus_1.any +
               inventedBy +
               T0:freq_week_1_total.logcenter +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

```
mTchxF = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               T0 +
               T_minus_1.any +
               inventedBy +
               T0:freq_week_1_total.logcenter +
               Teach:freq_week_1_total.logcenter +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

```
mTryXF = glmer(freq_week_4 ~
               1 +
               freq_week_1_total.logcenter +
               averageLength_week_1.logcenter +
               indexical +
               Teach +
               TryMarked.any +
               T0 +
               T_minus_1.any +
               inventedBy +
               T0:freq_week_1_total.logcenter +
               Teach:freq_week_1_total.logcenter +
               TryMarked.any:freq_week_1_total.logcenter +
               (1 + indexical || colourName) ,
             data=variants, family=poisson,
             control=gcontrol)
```

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

Results

Model comparison test:

Results of the model comparison tests. In the output below, there is a summary of the structure of each model, then a table with titles “Df”, “AIC”, “BIC” etc. Each row represents an increasingly complex model, with each fixed effect being added one at a time. The statistics describe how much better the model fits the data compared to the model above. A significant result (low p-value) suggests that the fixed effect significantly improves the fit of the model, and therefore is a good predictor of frequency of variants in the first week.

```
modelComparisonResults =
  anova(m0,mFrq,mLen,mIndx,mTeach,mTry,mChk,
      mTm1,mInv,mT0xF,mTchxF, mTryXF)
modelComparisonResults
```

```
## Data: variants
## Models:
## m0: freq_week_4 ~ 1 + (1 + indexical || colourName)
## mFrq: freq_week_4 ~ 1 + freq_week_1_total.logcenter + (1 + indexical || colourName)
## mLen: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + (1 + indexical
## mIndx: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical +
## mTeach: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical +
## mTry: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical + Te
## mChk: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical + Te
## mTm1: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical + Te
## mInv: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical + Te
## mT0xF: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical + T
## mTchxF: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical +
## mTryXF: freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter + indexical +
##        npar    AIC    BIC   logLik deviance   Chisq Df Pr(>Chisq)
## m0        8 308.28 328.88 -146.141   292.28
## mFrq      9 252.04 275.21 -117.020   234.04 58.2425  1  2.317e-14 ***
## mLen     10 249.09 274.84 -114.546   229.09  4.9466  1  0.0261426 *
## mIndx    12 248.88 279.77 -112.439   224.88  4.2145  2  0.1215733
## mTeach   13 237.71 271.18 -105.853   211.71 13.1713  1  0.0002843 ***
## mTry     14 234.27 270.32 -103.136   206.27  5.4340  1  0.0197488 *
## mChk     15 214.50 253.12  -92.248   184.50 21.7768  1  3.063e-06 ***
## mTm1     16 211.88 253.07  -89.939   179.88  4.6172  1  0.0316528 *
## mInv     19 209.07 257.99  -85.535   171.07  8.8086  3  0.0319475 *
## mT0xF    20 189.28 240.78  -74.641   149.28 21.7882  1  3.045e-06 ***
## mTchxF   21 173.15 227.22  -65.577   131.15 18.1280  1  2.065e-05 ***
## mTryXF   22 152.79 209.43  -54.394   108.79 22.3668  1  2.252e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Choose a final model for the beta values.

```
finalModel = mTryXF
```

Write model comparison results to file:

```
mcr = as.data.frame(modelComparisonResults)
mcr$AIC = round(mcr$AIC,2)
mcr$BIC = round(mcr$BIC,2)
mcr$logLik = round(mcr$logLik,2)
mcr$deviance = round(mcr$deviance,2)
mcr$Chisq = round(mcr$Chisq,2)
mcr$Significance = ""
mcr$Significance[mcr$`Pr(>Chisq)`<0.05] = "*"
```

```r
mcr$p = mcr$`Pr(>Chisq)`
mcr$p = round(mcr$p,2)
mcr$p[mcr$p<0.001] = "< 0.001"

mcr = mcr[,c("AIC","BIC","logLik","Chisq",'Df','p',"Significance")]
names(mcr) = c("AIC","BIC","Log likelihood"," 2","Df",'p','')
mcr[is.na(mcr)] = ""

rownames(mcr) = c("Null model","Frequency","Length",
                  "Indexicality","Teach","Try-marking",
                  "T0","T-1",'Identity of first user',
                  "T0 x Frequency","T-1 x Frequency",
                  'Try-marking x Frequency')
write.csv(mcr,
          "../results/inferential/ModelComparisonResults.csv",
          row.names = T, fileEncoding = "utf-8")
```

Final model parameter summary

This show the estimates for all parameters in the model.

```
summary(finalModel)
```

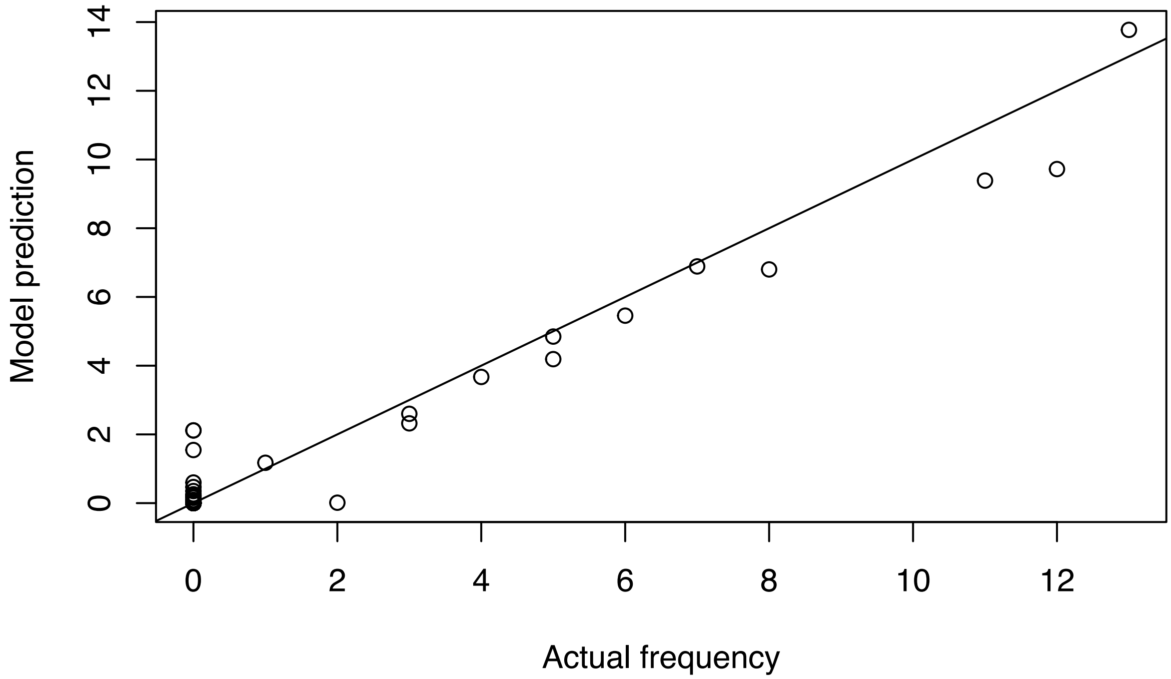
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## freq_week_4 ~ 1 + freq_week_1_total.logcenter + averageLength_week_1.logcenter +
##     indexical + Teach + TryMarked.any + T0 + T_minus_1.any +
##     inventedBy + T0:freq_week_1_total.logcenter + Teach:freq_week_1_total.logcenter +
##     TryMarked.any:freq_week_1_total.logcenter + (1 + indexical ||
##     colourName)
##    Data: variants
## Control: gcontrol
##
##      AIC      BIC   logLik deviance df.resid
##    152.8    209.4    -54.4    108.8       75
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4544 -0.0890 -0.0014  0.0000 18.2088
##
## Random effects:
##  Groups       Name              Variance Std.Dev. Corr
##  colourName   (Intercept)        0.00000 0.000
##  colourName.1 indexicalno       14.90386 3.861
##               indexicalyes       3.31863 1.822    -1.00
##               indexicalYes-body  0.09983 0.316     1.00 -1.00
## Number of obs: 97, groups:  colourName, 6
##
## Fixed effects:
##                                              Estimate Std. Error z value
## (Intercept)                                  -13.7285     4.1553  -3.304
## freq_week_1_total.logcenter                    7.1689     2.5202   2.845
## averageLength_week_1.logcenter                -1.0595     0.2555  -4.146
## indexicalyes                                  -1.7894     2.6629  -0.672
## indexicalYes-body                              0.7043     2.2258   0.316
## TeachTRUE                                     11.3216     2.6302   4.305
## TryMarked.anyTRUE                              1.3326     1.4854   0.897
## T0Yes                                         10.4168     2.8247   3.688
## T_minus_1.anyTRUE                             -2.2656     0.7723  -2.934
## inventedByIndonesia                           -3.0290     2.3089  -1.312
## inventedByJordan                               2.2129     0.7426   2.980
## inventedByNepal                                1.8396     0.7256   2.535
## freq_week_1_total.logcenter:T0Yes            -10.4990     3.0042  -3.495
## freq_week_1_total.logcenter:TeachTRUE         -9.6475     2.2786  -4.234
## freq_week_1_total.logcenter:TryMarked.anyTRUE   5.7483     1.7613   3.264
##                                              Pr(>|z|)
## (Intercept)                                  0.000954 ***
## freq_week_1_total.logcenter                  0.004446 **
## averageLength_week_1.logcenter               3.38e-05 ***
## indexicalyes                                 0.501601
## indexicalYes-body                          0.751665
## TeachTRUE                                  1.67e-05 ***
## TryMarked.anyTRUE                          0.369667
## TOYes                                      0.000226 ***
## T_minus_1.anyTRUE                          0.003349 **
## inventedByIndonesia                        0.189549
## inventedByJordan                           0.002881 **
## inventedByNepal                            0.011233 *
## freq_week_1_total.logcenter:TOYes          0.000474 ***
## freq_week_1_total.logcenter:TeachTRUE      2.30e-05 ***
## freq_week_1_total.logcenter:TryMarked.anyTRUE 0.001100 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

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

Check the predictions. Each point in the graph below is a variant. The actual frequency in the 3rd week is on the horizontal axis. Many have a frequency of 0: they don't appear. The model's predictions are shown on the vertical axis. The diagonal line is just a guide to show a perfect fit. Most of the points lie on this line, suggesting that the model has fit the data well.

```
plot(variants$freq_week_4, exp(predict(finalModel)),
     xlab="Actual frequency",
     ylab="Model prediction")
abline(0,1)
```



Here is a summary of whether a variant appeared or did not appear in the final week, and the model's predictions of whether they appeared or not:

```
##
##                          Not observed Observed
##   Predicted: Not observed           81        1
##   Predicted: Observed                3       12
```

These are the variants used in the final week:

```
variants[variants$freq_week_4>0,c("colourName","sign", 'freq_week_4')]
```

```
##    colourName                     sign freq_week_4
## 1         red            RED(FRONTLET)           3
## 2         red               RED(MOUTH)          11
## 6       brown IX:'BACK OF ONE'S HAND'           8
## 10      brown                   BOOGER           2
## 15      brown                 IX:WATCH           5
## 28      black                    BLACK          13
## 39      green              GREEN-CHEST          12
## 47      green                  CORRECT           5
## 48     yellow             YELLOW-CHEST           1
## 72     yellow                      SUN           4
## 74     yellow              YELLOW(ISL)           6
## 87       pink                   FLOWER           7
## 92       pink                IX:TONGUE           3
```

There were 13 variants that had a frequency of greater than 0 in the final week.

The model predicts 12 of these correctly, missing 1 variants (BOOGER).

The model predicts a further 3 variants should have been observed in the final week but were not observed in reality:

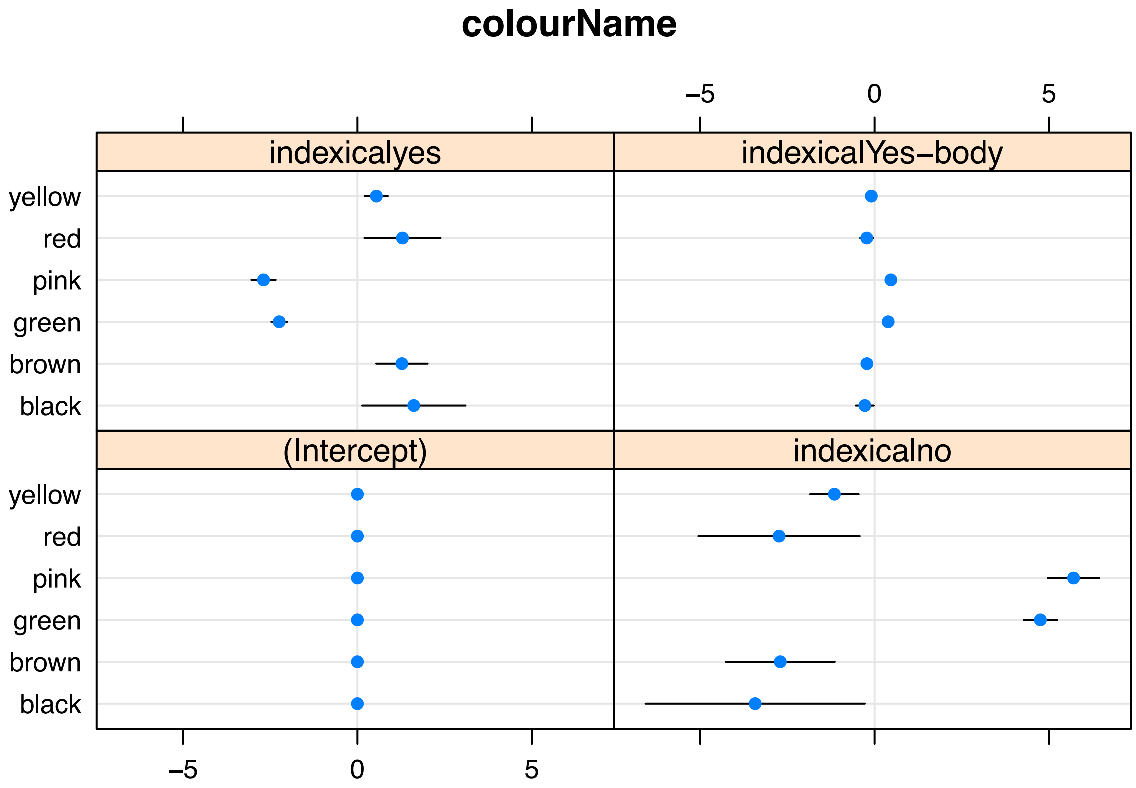
```
##    colourName      sign
## 5         red RED-BLOOD
## 7       brown      DARK
## 36      green GREEN-NSL
```

Random slopes results

We can plot the random slopes below:

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

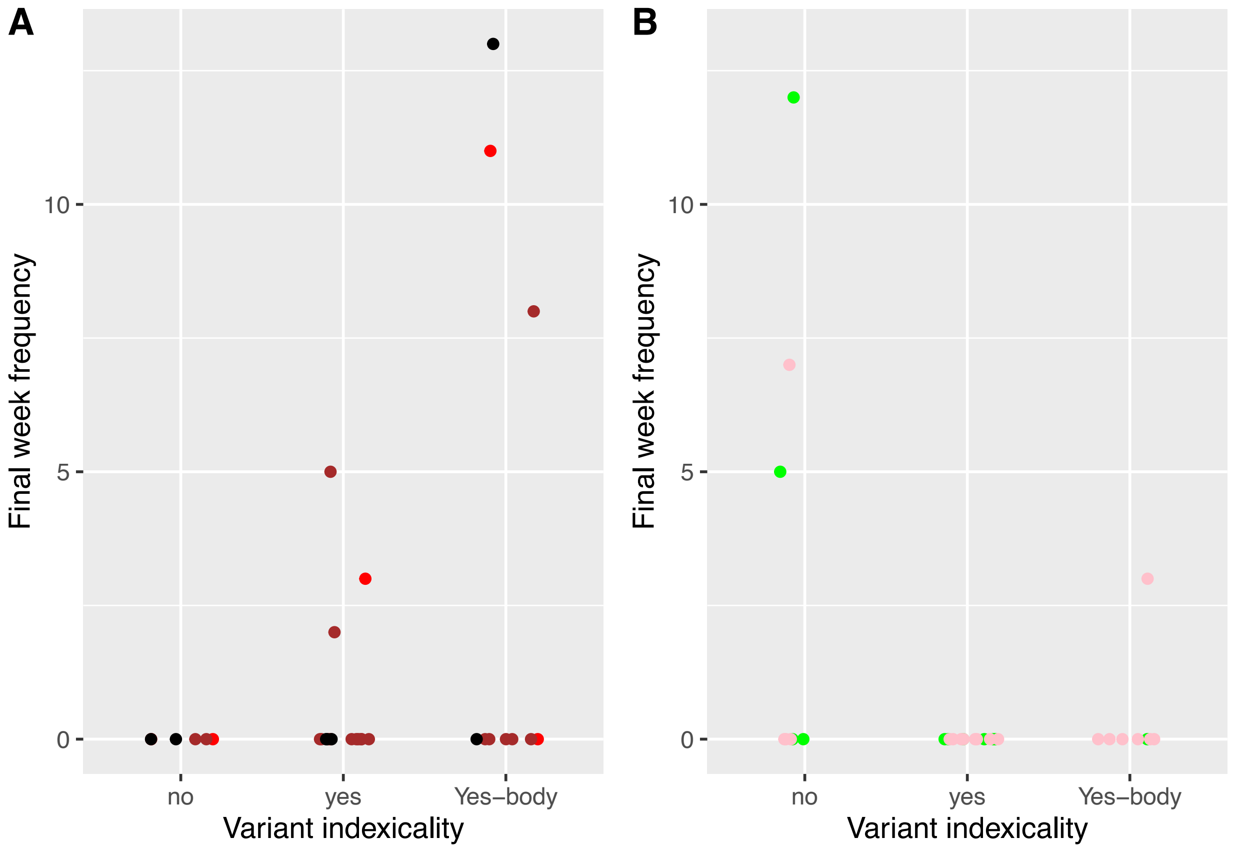
```
## $colourName
```



The effect of indexicality is stronger for red, brown, and black. It is weaker for pink and green.

```
indxRedBrownBlack = ggplot(variants[variants$colourName %in% c("red","brown","black"),],
       aes(x=indexical, y = freq_week_4,colour = colourName)) +
  geom_point(position = position_jitter(height = 0, width=0.2)) +
  scale_colour_manual(breaks=c("red","brown","black"), values = c("red","brown","black")) +
  theme(legend.position = 'none') +
  xlab("Variant indexicality") +
  ylab("Final week frequency")+
  coord_cartesian(ylim=c(0,13))
```

```
indxPinkGreen = ggplot(variants[variants$colourName %in% c("pink","green"),],
       aes(x=indexical, y = freq_week_4,colour = colourName)) +
  geom_point(position = position_jitter(height = 0, width=0.2)) +
  scale_colour_manual(breaks=c("pink","green"), values = c("pink","green")) +
  theme(legend.position = 'none') +
  xlab("Variant indexicality") +
  ylab("Final week frequency") +
  coord_cartesian(ylim=c(0,13))

indx = ggarrange(indxRedBrownBlack, indxPinkGreen, ncol=2, labels=c("A","B"))
indx
```



```
pdf("../results/descriptive/graphs/Indexicality_RedBrownBlack_GreenPink.pdf",
    width = 6,height=3)
indx
dev.off()
```

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

Check whether the coefficients are radically different with a full random effects structure:

```
finalModelFull = update(finalModel, ~. +
                          (0 + Teach + check.any +
                             T_minus_1.any + inventedBy || colourName),
                        control=gcontrol)
```

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

```
cor.test(fixef(finalModel), fixef(finalModelFull))
```

```
##
##  Pearson's product-moment correlation
##
## data:  fixef(finalModel) and fixef(finalModelFull)
## t = 5.625, df = 13, p-value = 8.269e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5795946 0.9461222
## sample estimates:
##       cor
## 0.8418948
```

The correlation is high, suggesting that the extra random slopes would not have a big effect on the results.

Summary

Here is a summary of the main results:

There was a significant main effect of frequency in week 1 (beta = 7.2 , log likelihood difference = 29 , df = , Chi Squared = 58.24 , p = 2.3e-14). More frequent forms in the first week were more likely to be more frequent in the final week.

There was a significant main effect of sign length (beta = -1.1 , log likelihood difference = 2.5 , df = , Chi Squared = 4.95 , p = 0.026). Shorter signs were more frequent in the final week.

There was no significant main effect of indexicality (beta = -1.8 , log likelihood difference = 2.1 , df = , Chi Squared = 4.21 , p = 0.12). (beta for body-indexical = 0.853).

There was a significant main effect of teaching (beta = 11 , log likelihood difference = 6.6 , df = , Chi Squared = 13.17 , p = 0.00028). Teaching increased the frequency of variants in the final week.

There was a significant main effect of try marking (beta = 1.3 , log likelihood difference = 2.7 , df = , Chi Squared = 5.43 , p = 0.02). Variants that were try marked more often were more frequent in the final week.

There was a significant main effect of of repair initiation (T0) (beta = 10 , log likelihood difference = 11 , df = , Chi Squared = 21.78 , p = 3.1e-06). Variants used in a repair initiation were more frequent in the final week.

There was a significant main effect of use in a problem source turn (T-1) (beta = -2.3 , log likelihood difference = 2.3 , df = , Chi Squared = 4.62 , p = 0.032).

There was a significant main effect of first user (inventedBy) (log likelihood difference = 4.4 , df = , Chi Squared = 8.81 , p = 0.032). Signs invented by the signer from Jordan and Nepal were more frequent in the final week.

There was a significant interaction between T0 and frequency (beta = -10 , log likelihood difference = 11 , df = , Chi Squared = 21.79 , p = 3e-06). The effect of appearing in a T0 sequence is stronger if the variant was more frequent in the first week.

There was a significant interaction between Teaching and frequency (log likelihood difference = 9.1 , df = , Chi Squared = 18.13 , p = 2.1e-05).. The effect of teaching was stronger if the variant was more frequent in the first week.

There was a significant interaction between Try marking and frequency (log likelihood difference = 11 , df = , Chi Squared = 22.37 , p = 2.3e-06).. The effect of try marking is stronger if the variant was more frequent in the first week.

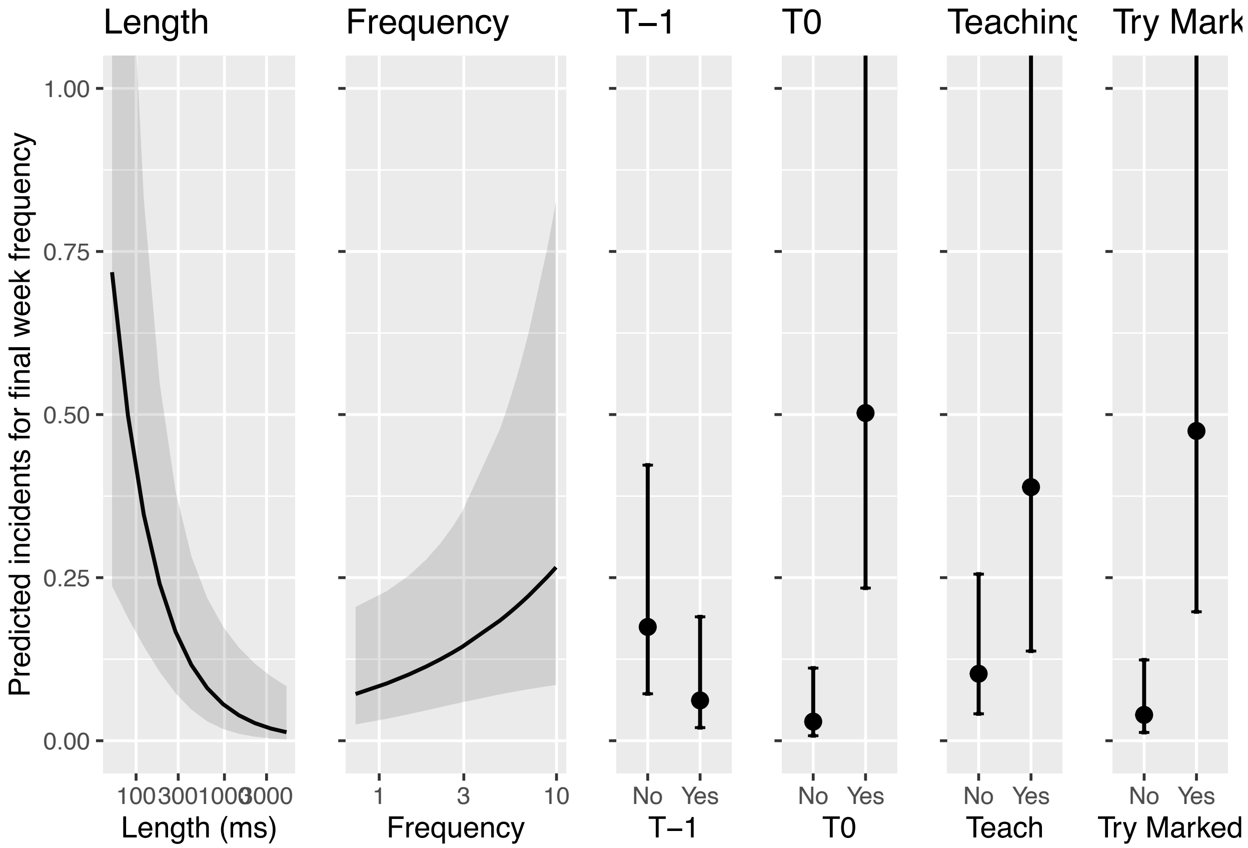
We also found some evidence that the effect of indexicality is more important for black and red, and less important for green and pink.

Graphs

Plot of the marginal effects of the predicted probabilities for each fixed effect:

```
x = plot_model(mInv, 'eff',
          vars=c('Teach',
                 'TryMarked.any',
                 'T0',
                 'freq_week_1_total.logcenter',
                 'averageLength_week_1.logcenter',
                 'T_minus_1.any'),
          facet.grid = F,
          prnt.plot = F,
          show.ci = T)

freqi = 1
leni = 2
t0i = 6
teachi = 4
tryi = 5
tm1i = 7

# Rescale frequency back to real values
freq.m = x[[freqi]]$data$x
x[[freqi]]$data$x =
  exp(freq.m*
  attr(variants$freq_week_1_total.logcenter, 'scaled:scale') +
  attr(variants$freq_week_1_total.logcenter, 'scaled:center') -1)

x[[freqi]]$labels$x = "Frequency"
x[[freqi]]$labels$title = "Frequency"

# Rescale length back to real values
len.m = x[[leni]]$data$x
x[[leni]]$data$x =
  exp(len.m*
  attr(variants$averageLength_week_1.logcenter, 'scaled:scale') +
  attr(variants$averageLength_week_1.logcenter, 'scaled:center') -1)

#x$plot.list[[1]]$labels$title = "Indexicality"
#x$plot.list[[1]]$scales$scales[[1]]$labels = c("No","Yes","Body")

x[[teachi]]$labels$title = "Teaching"
x[[teachi]]$scales$scales[[1]]$labels = c("No","Yes")
x[[teachi]]$coordinates$limits$x = c(0.5,2.5)

x[[tryi]]$labels$title = "Try Marked"
x[[tryi]]$scales$scales[[1]]$labels = c("No","Yes")
x[[tryi]]$coordinates$limits$x = c(0.5,2.5)

x[[t0i]]$labels$title = "T0"
x[[t0i]]$scales$scales[[1]]$labels = c("No","Yes")
x[[t0i]]$coordinates$limits$x = c(0.5,2.5)
```

```r
x[[tm1i]]$labels$title = "T-1"
x[[tm1i]]$scales$scales[[1]]$labels = c("No","Yes")
x[[tm1i]]$coordinates$limits$x = c(0.5,2.5)

x[[leni]]$labels$title = "Length"
for(i in 1:7){
  x[[i]]$coordinates$limits$y = c(0,1)
  if(i!=leni){
    x[[i]]$theme =
      list(
        panel.grid.minor.x = element_blank(),
        axis.text.y = element_blank(),
        axis.line.y=element_blank())
  } else{
    x[[i]]$theme = list(panel.grid.minor.x = element_blank())
  }
  x[[i]]$labels$y = element_blank()
}

x[[leni]]$labels$y = "Predicted incidents for final week frequency"
x[[leni]]$labels$x = "Length (ms)"
x[[tm1i]]$labels$x = "T-1"
x[[tryi]]$labels$x = "Try Marked"
#x[[tm1i]]$labels$y = "Predicted incidents for final week frequency"


grx = grid.arrange(
             x[[leni]]  + scale_x_log10(),
             x[[freqi]]  + scale_x_log10(),
             x[[tm1i]]+
               geom_point() +
               geom_errorbar(aes(ymin=conf.low,ymax=conf.high), width=0.2),
             x[[t0i]]+
               geom_point() +
               geom_errorbar(aes(ymin=conf.low,ymax=conf.high), width=0.2),
             x[[teachi]]+ geom_point()+
               geom_errorbar(aes(ymin=conf.low,ymax=conf.high), width=0.2),
             x[[tryi]]+ geom_point()+
               geom_errorbar(aes(ymin=conf.low,ymax=conf.high), width=0.2),
             widths=c(2.1,1.8,1.1,1.1,1.1,1.1))
```

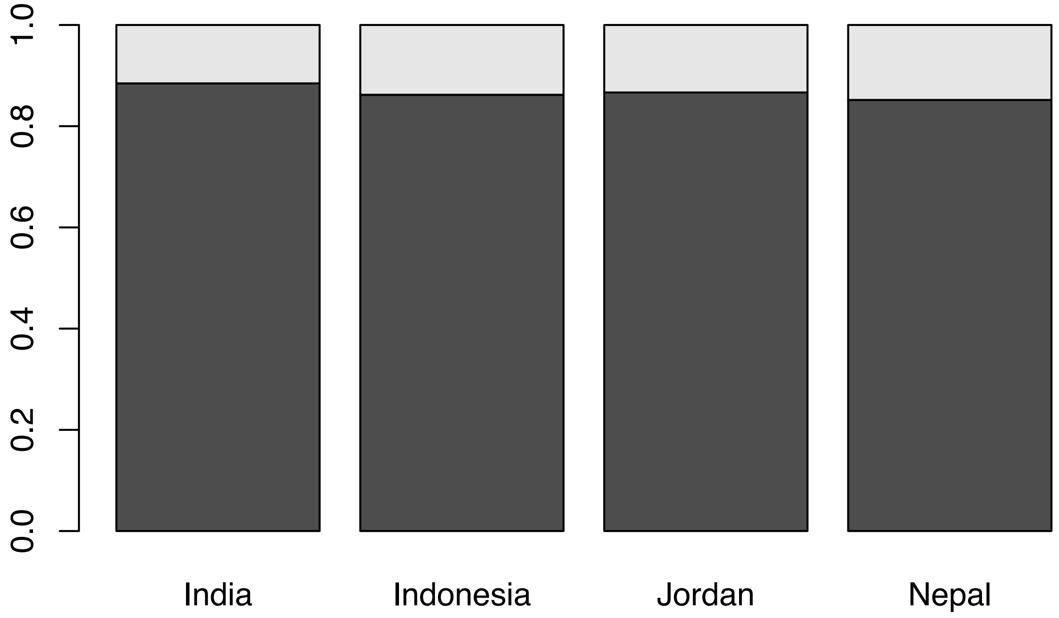


```
pdf("../results/descriptive/graphs/EffectsPlot.pdf", width=8.5, height=3.5)
plot(grx)
dev.off()
```

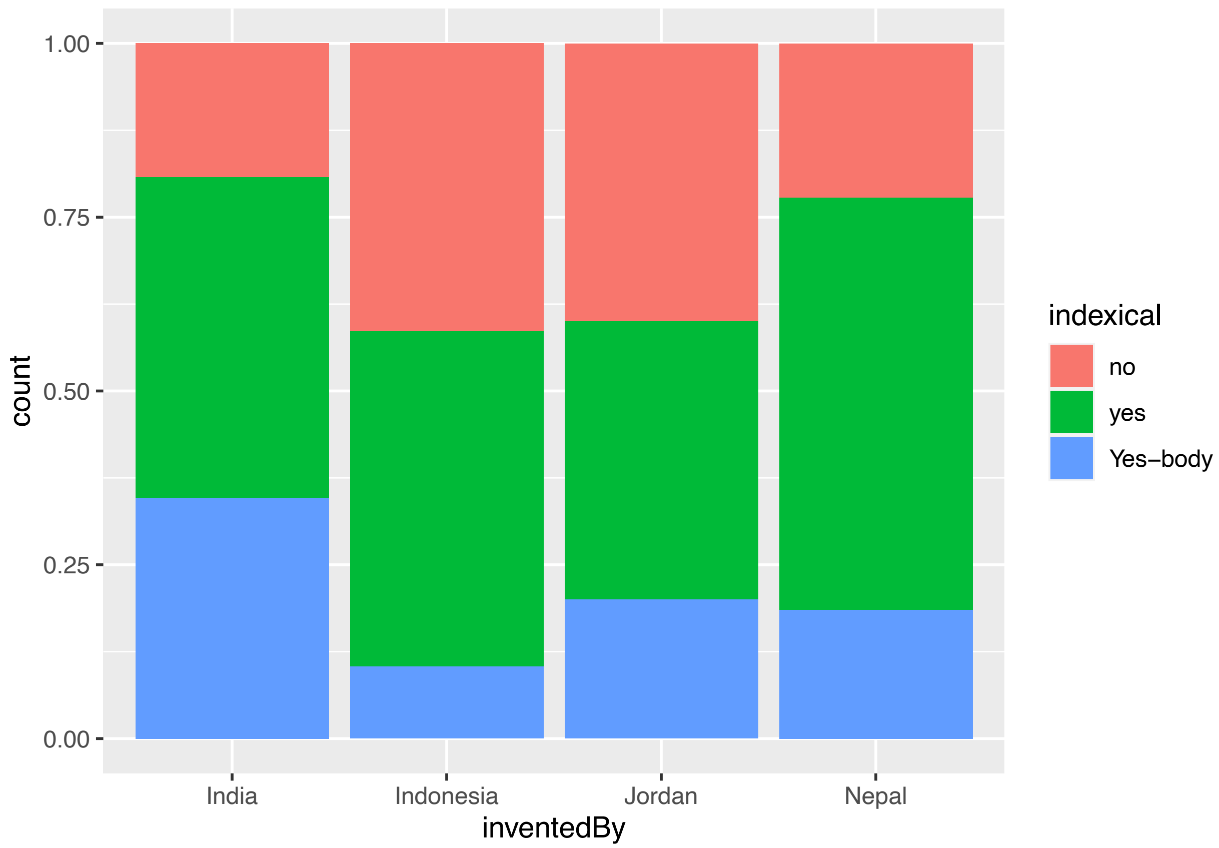
```
## pdf
##   2
```

Plot the average frequency in the final week for signs invented by each signer:

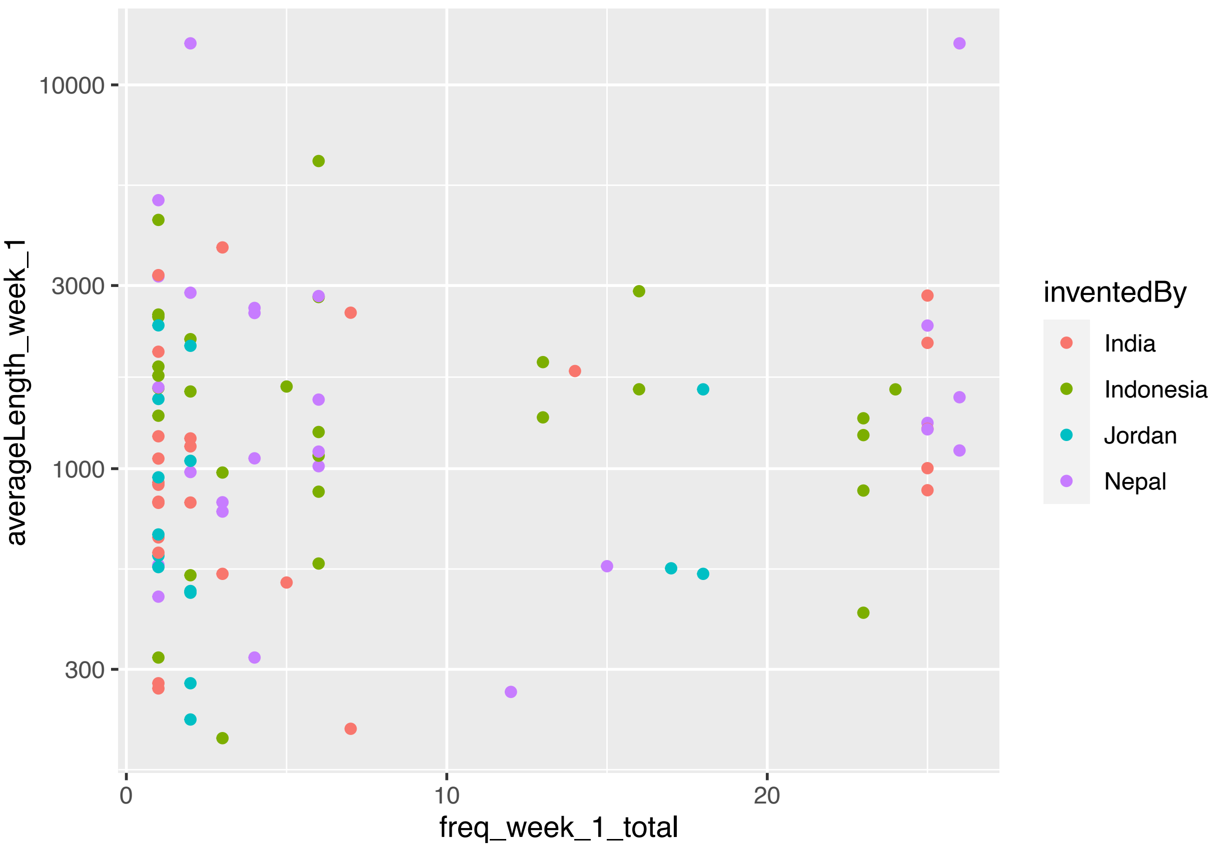
```
itx = prop.table(table(
  variants$inventedBy,
  variants$freq_week_4>0), margin=1)
barplot(t(itx))
```



```
ggplot(variants,
       aes(x=inventedBy, fill=indexical)) +
  geom_bar(position="fill")
```



```
ggplot(variants,
       aes(x=freq_week_1_total,
           y=averageLength_week_1,
           colour=inventedBy)) +
  geom_point() + scale_y_log10()
```


10000
3000
1000
300
averageLength_week_1
0
10
20
freq_week_1_total
inventedBy
India
Indonesia
Jordan
Nepal

Plot interactions between frequency and sequential variables. Here we're just visualising the rough relationship in the raw data in order to understand the direction of the interaction.

```r
variants$freq_week_1_total.cut = cut(variants$freq_week_1_total,
          breaks = quantile(variants$freq_week_1_total,
                            probs = c(0,1/3,2/3,1)),include.lowest = T,
          labels = c("low","medium","high"))
xi = variants %>% group_by(Teach, freq_week_1_total.cut) %>%
    summarise(freq_week_4 = mean(freq_week_4))
```

```
## `summarise()` has grouped output by 'Teach'. You can override using the `.groups` argument.
```

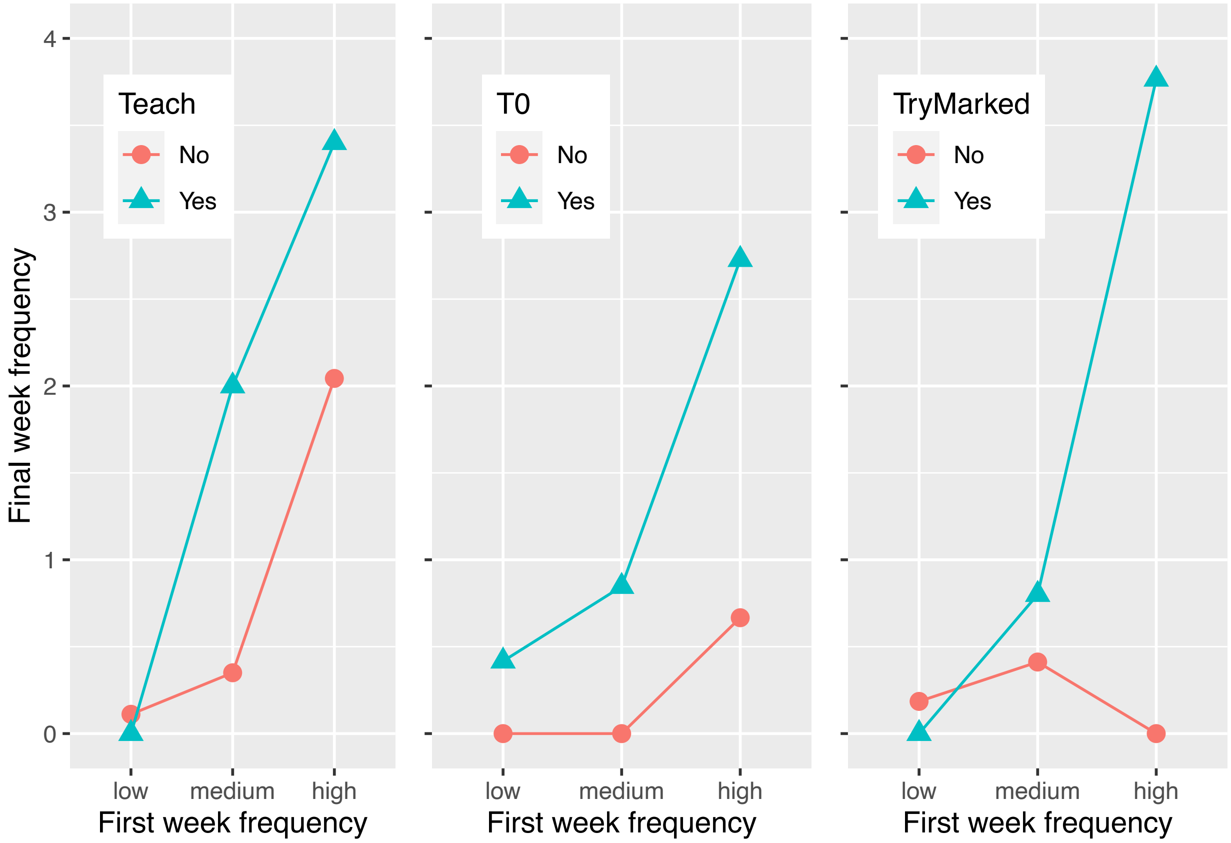
```r
int1 = ggplot(xi,aes(x=freq_week_1_total.cut,y=freq_week_4,group=Teach,colour=Teach,shape=Teach)) +
  geom_point(size=3) + geom_line() +
  ylab("Final week frequency") +
  xlab("First week frequency") +
  theme(legend.position = c(0.3,0.8)) +
  coord_cartesian(ylim=c(0,4)) +
  scale_colour_discrete(name = "Teach", labels = c("No", "Yes")) +
  scale_shape_discrete(name = "Teach", labels = c("No", "Yes"))

xi = variants %>% group_by(T0, freq_week_1_total.cut) %>%
    summarise(freq_week_4 = mean(freq_week_4))
```

```
## `summarise()` has grouped output by 'T0'. You can override using the `.groups` argument.
```

```r
int2 = ggplot(xi,aes(x=freq_week_1_total.cut,y=freq_week_4,group=T0,colour=T0,shape=T0)) +
  geom_point(size=3) + geom_line() +
  xlab("First week frequency") +
  theme(legend.position = c(0.3,0.8),
        axis.title.y = element_blank(),
        axis.text.y = element_blank()) +
  coord_cartesian(ylim=c(0,4))

xi = variants %>% group_by(TryMarked.any,freq_week_1_total.cut) %>%
    summarise(freq_week_4 = mean(freq_week_4))
```

```
## `summarise()` has grouped output by 'TryMarked.any'. You can override using the `.groups` argument.
```

```r
int3 = ggplot(xi,aes(x=freq_week_1_total.cut,y=freq_week_4,group=TryMarked.any,
              colour=TryMarked.any,shape=TryMarked.any)) +
  geom_point(size=3) + geom_line() +
  xlab("First week frequency") +
  theme(legend.position = c(0.3,0.8),
        axis.title.y = element_blank(),
        axis.text.y = element_blank()) +
  coord_cartesian(ylim=c(0,4)) +
  #labs(group="TryMarked",colour="TryMarked",shape="TryMarked")
  scale_colour_discrete(name = "TryMarked", labels = c("No", "Yes")) +
  scale_shape_discrete(name = "TryMarked", labels = c("No", "Yes"))

gx = grid.arrange(int1,int2,int3, layout_matrix=t(matrix(c(1,2,3))))
```



```
pdf("../results/descriptive/graphs/Interactions.pdf",
    width=6,height=3)
plot(gx)
dev.off()
```

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

```
gx
```

```
## TableGrob (1 x 3) "arrange": 3 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
```

Check model assumptions. The model is not good at predicting higher values and less common cases.

```
plot_model(finalModel, 'resid')
```

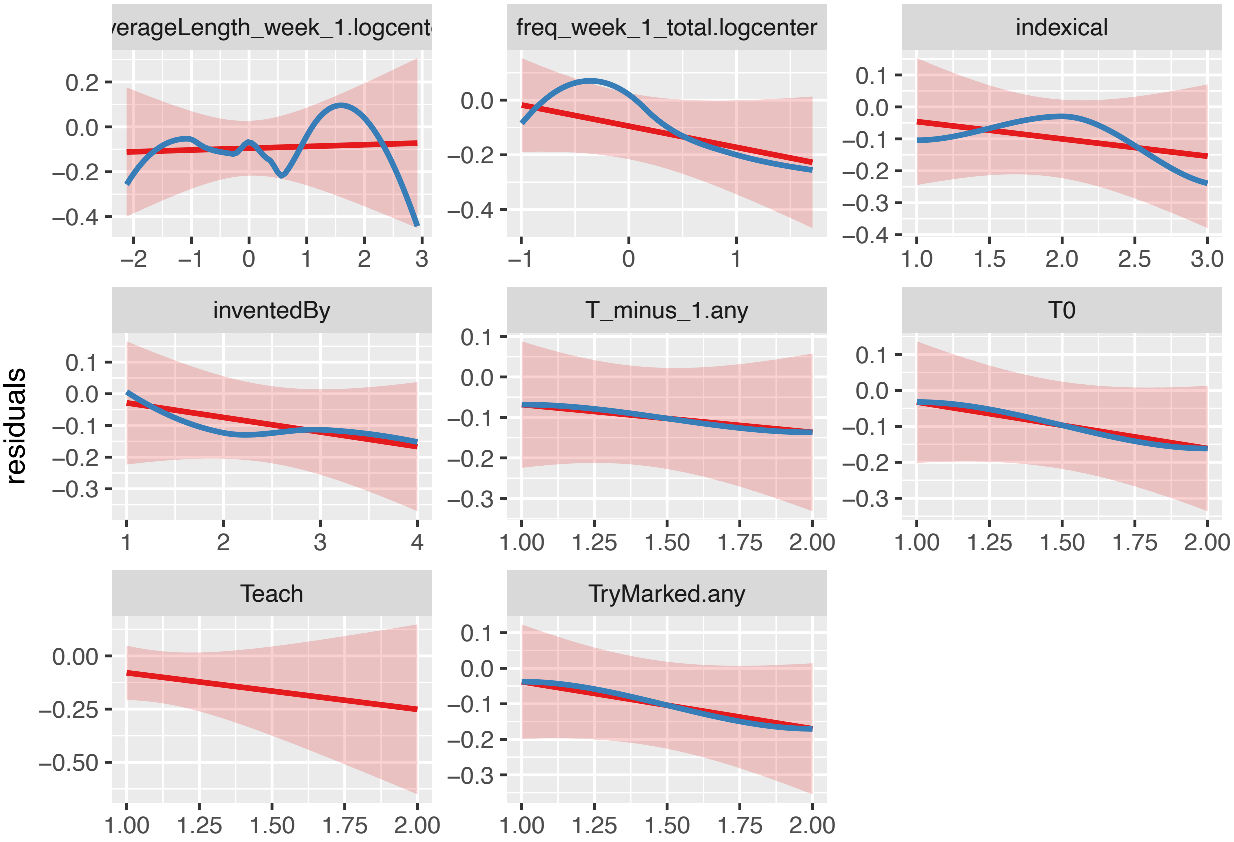
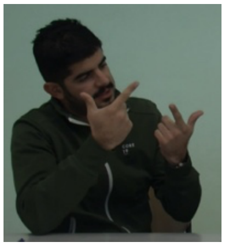
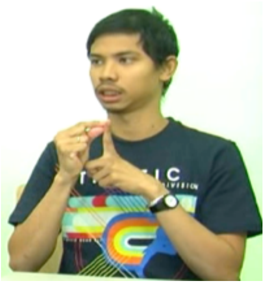
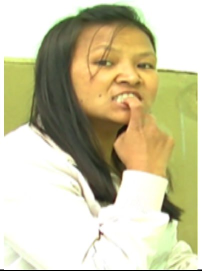
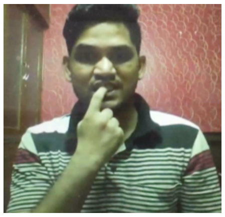
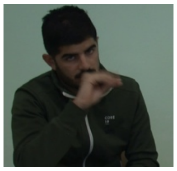
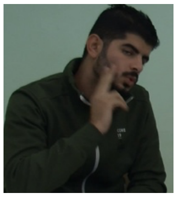
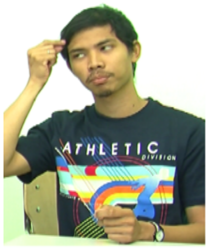
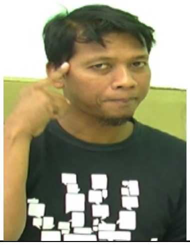
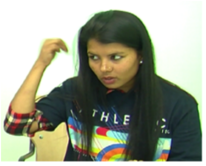
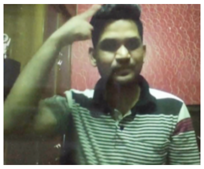
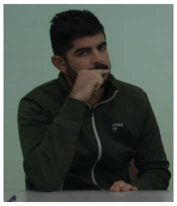
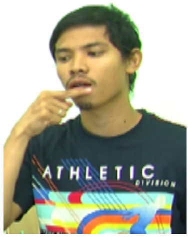
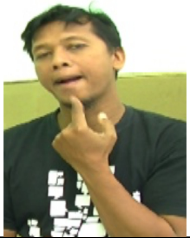
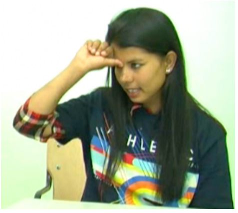
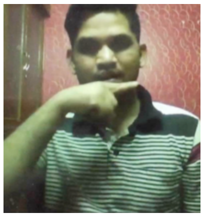
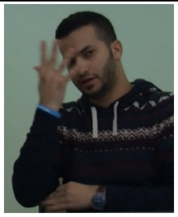
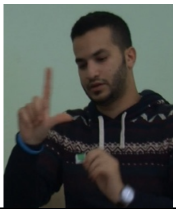
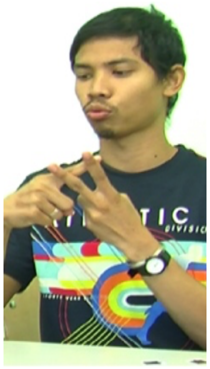
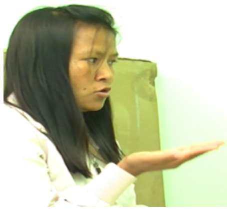
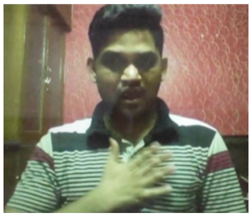
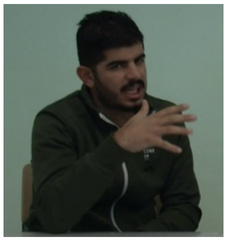
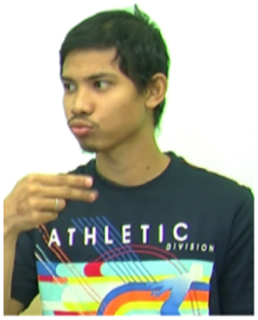
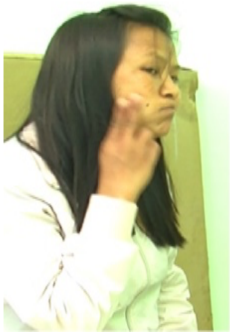
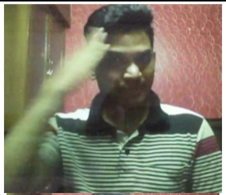
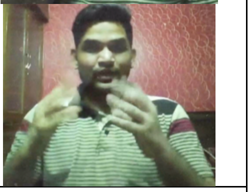
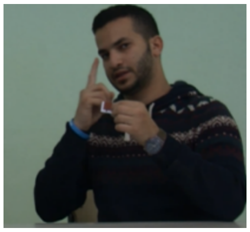
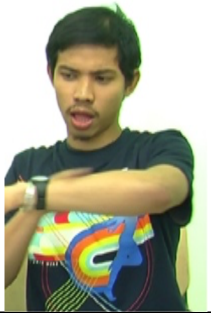
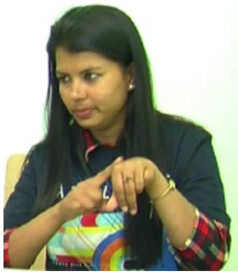
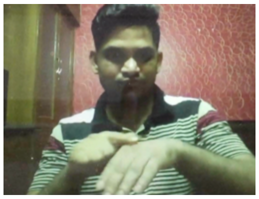
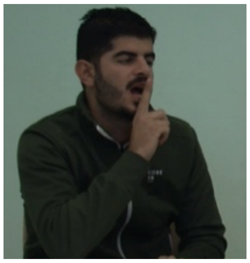


Table of established signs for colours in the different sign languages

Colour	Jordanian Sign Language	Indonesian Sign Language	Nepali Sign Language	Indian Sign Language
□				
⬛	 Variant 2: 	 Variant 2: 		
🟥		 Variant 2: 		

🟩	 Variant 2: 			
🟪				 
🟫				
🟨	 Variant 2: