Portfolio 7 - mixed effects

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```
#set working directory
setwd("~/Dropbox/Uni/2 semester/Ekseperimental Methods 2/R-code/Portfolio 7/portfo
lio_assignment_7_face_exp_data")

#Load packages
library(tidyverse)

library(lmerTest)

library(pastecs)

library(nlme)
```

Emotional faces experiment (response times)

This experiment was conducted during the fMRI laboratory days in 2016 and 2017. Participants responded to images of faces with button presses. The design was a 2x2x2 mixed effects experiment (color x emotion x frequency).

Hypotheses

The experiment had the following behavioral hypotheses:
H1: The index finger (blue) trials will lead to a shorter response time than middle finger (yellow) trials.
H2: Fearful faces will yield a shorter response time than neutral.
H3: Infrequent stimuli will yield longer responses time than frequent. This should surface as an interaction between color and frequency group.

Assignment tasks

Load data

```
#Load the data using the following code:
face_exp_2016 <- read.csv("face_exp_data_all_160310.csv", sep = ";")
face_exp_2017 <- read.csv("face_exp_all_logs_2017.csv", sep = ";")

#Bind the two datasets together
face_exp <- rbind(face_exp_2016, face_exp_2017)
```

1. Understanding the experiment

1.a.Comprehension question. Please explain which factor was between-participants and which were within- participants and why.

Frequency is a between-participant factor due to the fact that they were divided into two groups at the beginning as this factor does not change during the experiment.

Color and emotion are within-participant factors because those change within participants - so we have multiple data points from each participant.

1.b. What was the age range of the participants?

```
range(face_exp$age)

## [1] 19 27
```

2. Data exploring and preparation

```
#Make sure that factorial variables as marked as factors using as.factor()
sapply(face_exp, class) #check the current classes for the data set

##                rt duration_measured          scan.day               img
##         "numeric"         "numeric"          "factor"          "factor"
##          cond_emo         cond_blue                no            gender
##         "integer"         "integer"         "integer"          "factor"
##               age   duration_frames          response             onset
##         "integer"         "integer"          "factor"         "numeric"
##             key_t      delay_frames            offset              freq
##         "numeric"         "integer"         "numeric"          "factor"
##      correct_resp                ID         condition           scanner
##         "integer"          "factor"          "factor"          "factor"
##              year
##         "integer"

#Change classes
face_exp$freq <- as.factor(face_exp$freq)
face_exp$correct_resp <- as.factor(face_exp$correct_resp)
face_exp$cond_emo <- as.factor(face_exp$cond_emo)
face_exp$cond_blue <- as.factor(face_exp$cond_blue)
```

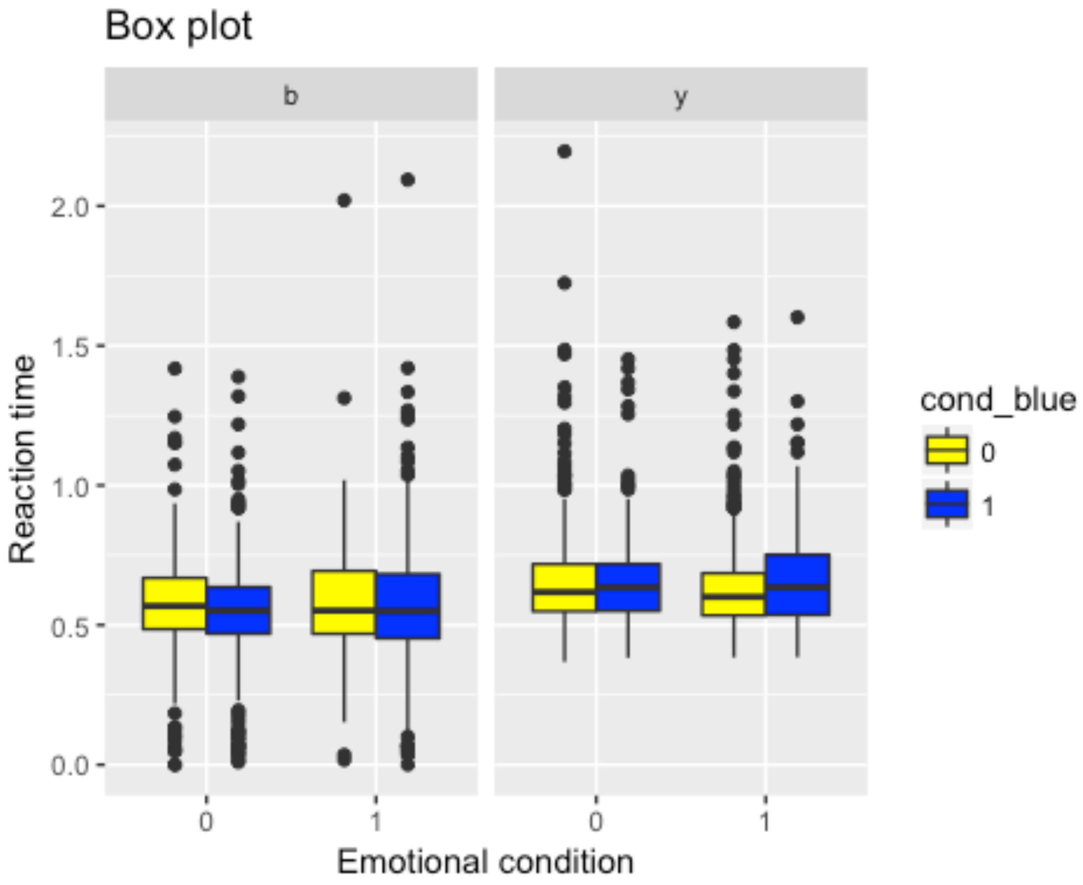
2.a

Make a box-plot of the data with RT on the y-axis and emotional condition on the x-axis. Make a box-plot for each of the color conditions by using “fill”. Use facet_wrap() to make two seperate graphs for each frequency group. Give the boxes colors that mathces the stimuli, eg. use " + scale_fill_manual(values=c(“yellow”,“blue”,“yellow”,“blue”,“yellow”,“blue”,“yellow”,“blue”))" .

```
#prepare plot
box_RT_emotional <- ggplot(face_exp, aes(x = cond_emo, y = rt, fill = cond_blue))+
                             geom_boxplot()+
                             facet_wrap(~freq)+
                             scale_fill_manual(values = c("yellow","blue", "yellow
", "blue", "yellow", "blue","yellow","blue")) + labs(title = "Box plot", x = "Emot
ional condition", y = "Reaction time")

#plot
box_RT_emotional

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```



2.b

Comprehension question: Explain why this plot shows that there is something wrong with the data.

A lot of the data points in the b frequency have a reaction time of zero, which seems impossible.

2.c

Make a subset of the data, including only correct responses.

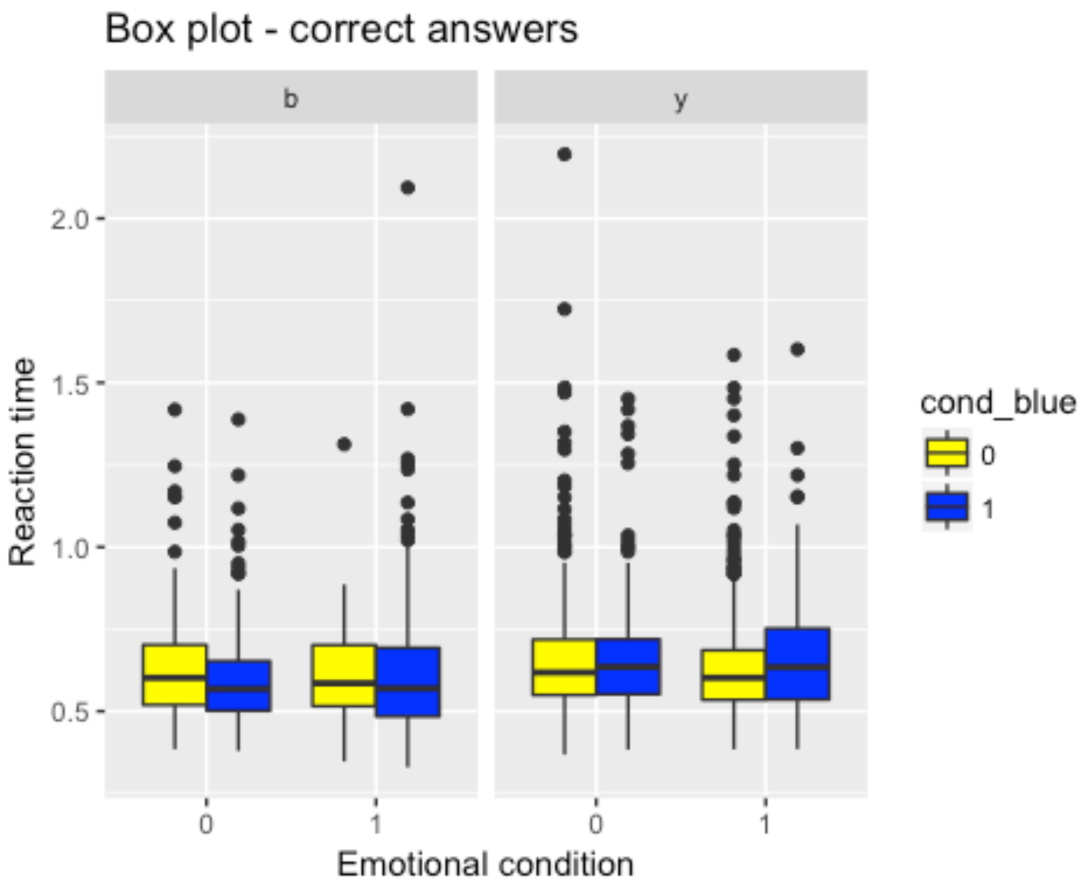
```
correct_response_df <- subset(face_exp, correct_resp == 1)
```

2.d

Make another boxplot similar to that in 2.a. Did it solve the observed problem?

```
#prepare plot
new_box_RT_emotional <- ggplot(correct_response_df, aes(x = cond_emo, y = rt, fill
= cond_blue))+
                              geom_boxplot()+
                              facet_wrap(~freq)+
                              scale_fill_manual(values = c("yellow","blue", "yellow
", "blue", "yellow", "blue","yellow","blue")) + labs(title = "Box plot - correct a
nswers", x = "Emotional condition", y = "Reaction time")

#plot
new_box_RT_emotional
```



This solved the observed problem

2.e

Use the by() function and stat.desc (in library(pastecs)) to get descriptive measures for the different conditions (e.g. see Field's book chapter 5.5.3.2.). Try to investigate the three hypotheses based on the descriptive statistics - would you expect any of the statistical analyses to be significant based on the descriptive stats?

```
by(data = correct_response_df$rt, INDICES = correct_response_df$cond_blue, FUN = s
tat.desc, basic = FALSE)

## correct_response_df$cond_blue: 0
##       median         mean      SE.mean CI.mean.0.95          var 
##  0.602198912  0.638994597  0.005035643  0.009879979  0.029465646 
##      std.dev     coef.var 
##  0.171655604  0.268633889 
## -------------------------------------------------------- 
## correct_response_df$cond_blue: 1
##       median         mean      SE.mean CI.mean.0.95          var 
##  0.600979187  0.624618041  0.005201635  0.010206873  0.028220459 
##      std.dev     coef.var 
##  0.167989462  0.268947502
```

```
by(data = correct_response_df$rt, INDICES = correct_response_df$cond_emo, FUN = st
at.desc, basic = FALSE)
```

```
## correct_response_df$cond_emo: 0
##       median         mean      SE.mean CI.mean.0.95          var 
##  0.602302368  0.635330286  0.005109437  0.010025273  0.028925827 
##      std.dev     coef.var 
##  0.170075945  0.267696895 
## -------------------------------------------------------- 
## correct_response_df$cond_emo: 1
##       median         mean      SE.mean CI.mean.0.95          var 
##  0.600937149  0.629026784  0.005133648  0.010072889  0.028910715 
##      std.dev     coef.var 
##  0.170031513  0.270308859
```

```
by(data = correct_response_df$rt, INDICES = correct_response_df$freq, FUN = stat.d
esc, basic = FALSE)
```

```
## correct_response_df$freq: b
##       median         mean      SE.mean CI.mean.0.95          var 
##  0.584016564  0.607400413  0.005415922  0.010629548  0.025988335 
##      std.dev     coef.var 
##  0.161208979  0.265408082 
## -------------------------------------------------------- 
## correct_response_df$freq: y
##       median         mean      SE.mean CI.mean.0.95          var 
##  0.617904615  0.648848804  0.004785901  0.009388815  0.030211495 
##      std.dev     coef.var 
##  0.173814541  0.267881422
```

```
by(correct_response_df$rt, list(correct_response_df$cond_blue, correct_response_df
$cond_emo, correct_response_df$freq), stat.desc, basic = FALSE)
```

```
## : 0
## : 0
## : b
##       median         mean      SE.mean CI.mean.0.95          var 
##   0.60159979   0.63615532   0.01432802   0.02833084   0.02853561 
##      std.dev     coef.var 
##   0.16892486   0.26554027 
## -------------------------------------------------------- 
## : 1
## : 0
## : b
##       median         mean      SE.mean CI.mean.0.95          var
##  0.568026462  0.590636005  0.007751537  0.015253260  0.018386415
##      std.dev     coef.var
##  0.135596515  0.229577123
## --------------------------------------------------------
## : 0
## : 1
## : b
##       median         mean      SE.mean CI.mean.0.95          var
##   0.58545942   0.60648383   0.01152153   0.02277728   0.01884989
##      std.dev     coef.var
##   0.13729490   0.22637850
## --------------------------------------------------------
## : 1
## : 1
## : b
##       median         mean      SE.mean CI.mean.0.95          var
##   0.56948924   0.61162493   0.01090179   0.02145425   0.03553585
##      std.dev     coef.var
##   0.18850956   0.30821105
## --------------------------------------------------------
## : 0
## : 0
## : y
##       median         mean      SE.mean CI.mean.0.95          var
##  0.618188695  0.654967004  0.008832336  0.017358700  0.034480489
##      std.dev     coef.var
##  0.185689226  0.283509284
## --------------------------------------------------------
## : 1
## : 0
## : y
##       median         mean      SE.mean CI.mean.0.95          var
##   0.63501408   0.65742232   0.01145482   0.02257523   0.02899807
##      std.dev     coef.var
##   0.17028819   0.25902404
## --------------------------------------------------------
## : 0
## : 1
## : y
##       median         mean      SE.mean CI.mean.0.95          var
##  0.601765221  0.634328046  0.007944025  0.015613146  0.027704205
##      std.dev     coef.var
##  0.166445803  0.262397042
## --------------------------------------------------------
## : 1
## : 1
## : y
##       median         mean      SE.mean CI.mean.0.95          var
##   0.63429340   0.65703139   0.01127530   0.02222371   0.02758775
##      std.dev     coef.var
##   0.16609561   0.25279707
```

Hypothesis 1: The mean reaction time for frequency blue is lower (0.61) than the mean for frequency y (0.65) which fits with the hypothesis 1.

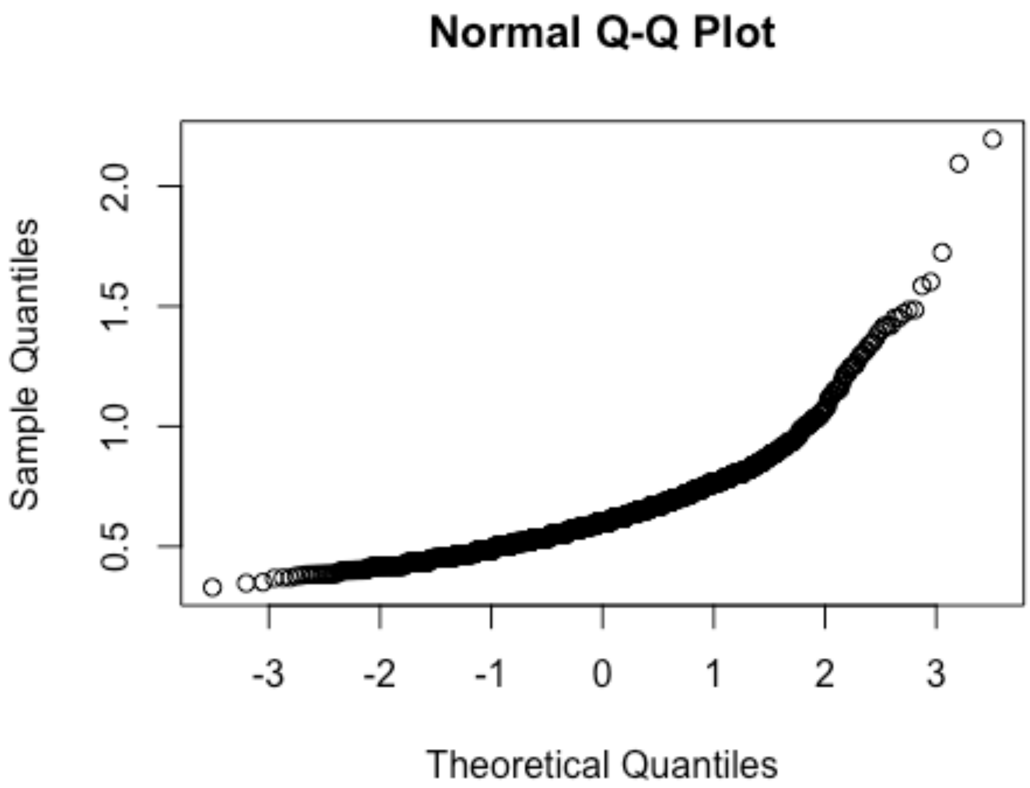
Hypothesis 2: The descriptive statistics for response time and emotional condition could also suggest that the fearful faces would lead to a shorter response time (0.63) compared to non-fearful (0.64)

Hypothesis 3: The descriptive statistics for response time and infrequent stimuli could suggest that our hypothesis is true due to the fact that when shown a blue neutral face in the blue frequency the response time is shorter (0.59) than when shown a yellow neutral face in the blue frequency (0.64)

2.f

Explore if the RT data is normally distributed using a qq-plot (e.g. qqnorm()).

```
qqnorm(correct_response_df$rt)
```



2.g

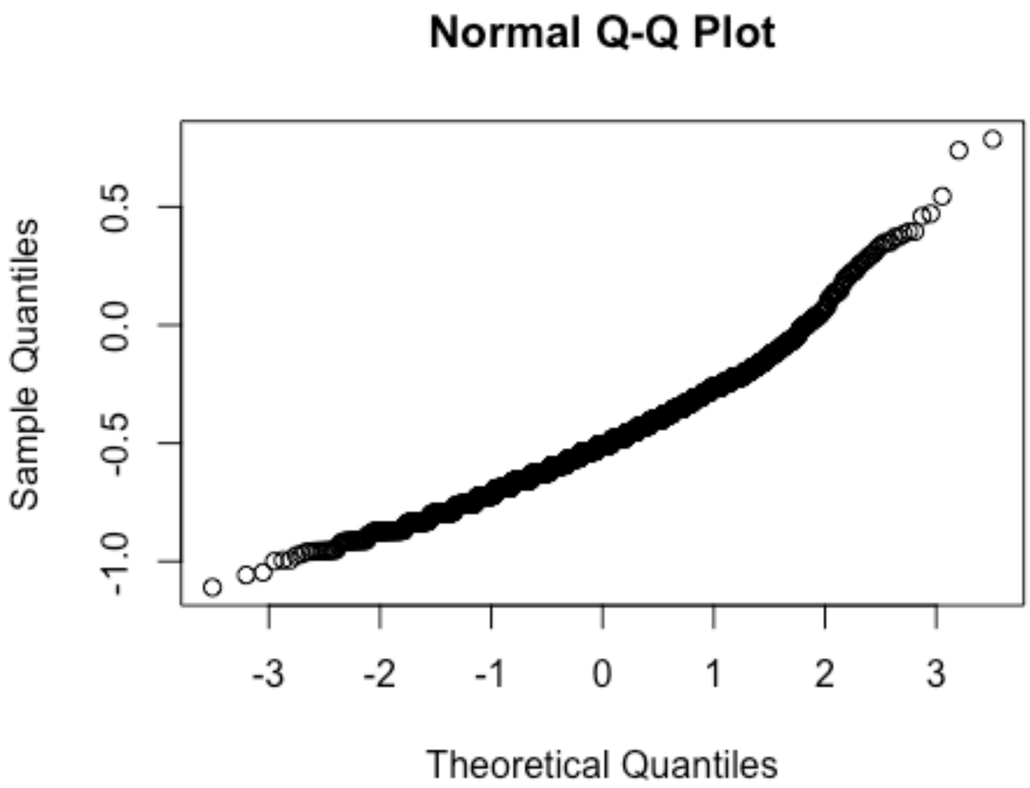
log-transform the RT data.

```
log_data <- mutate(correct_response_df, log_RT = log(correct_response_df$rt))
```

2.h

Use a qq-plot to explore if the transformed data appear more normal than the untransformed.

```
qqnorm(log_data$log_RT)
```



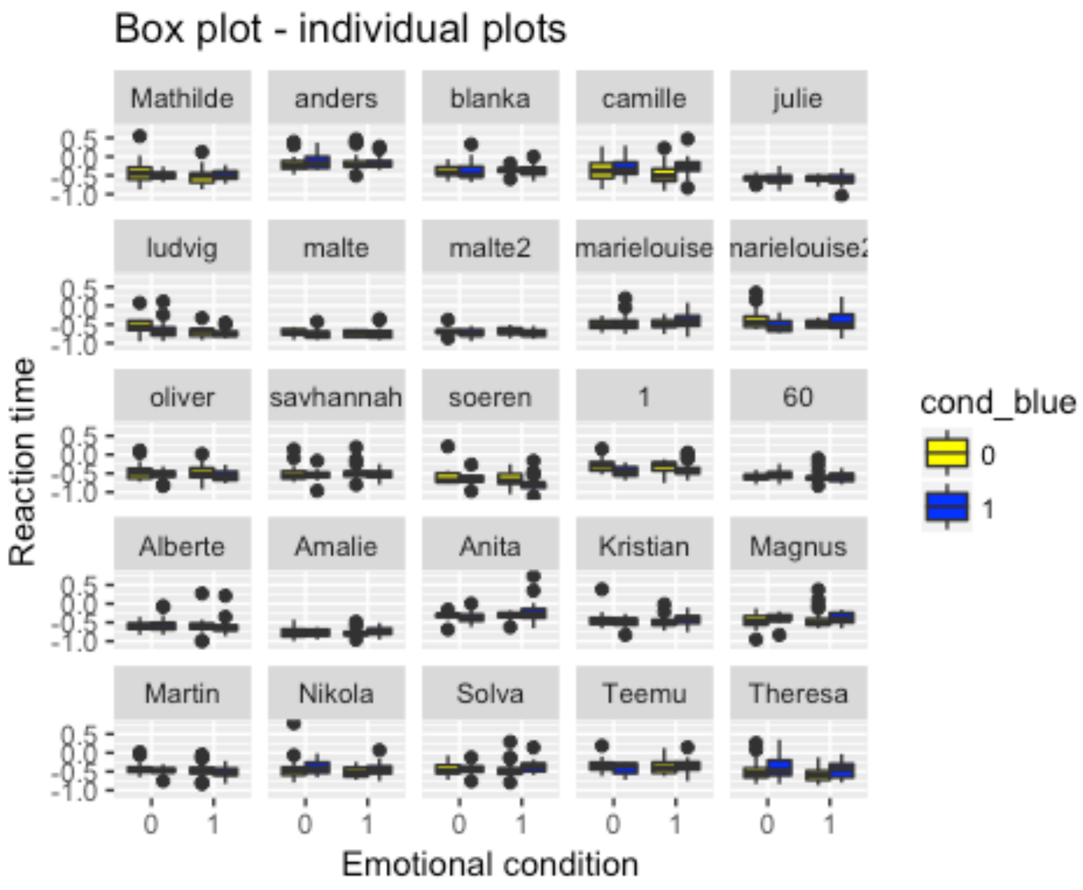
The transformed data seem more normally distributed than the untransformed

2.i

Make a plot that explores the response times for participants, individually, using a box-plot. Does anybody stick out as unusual?

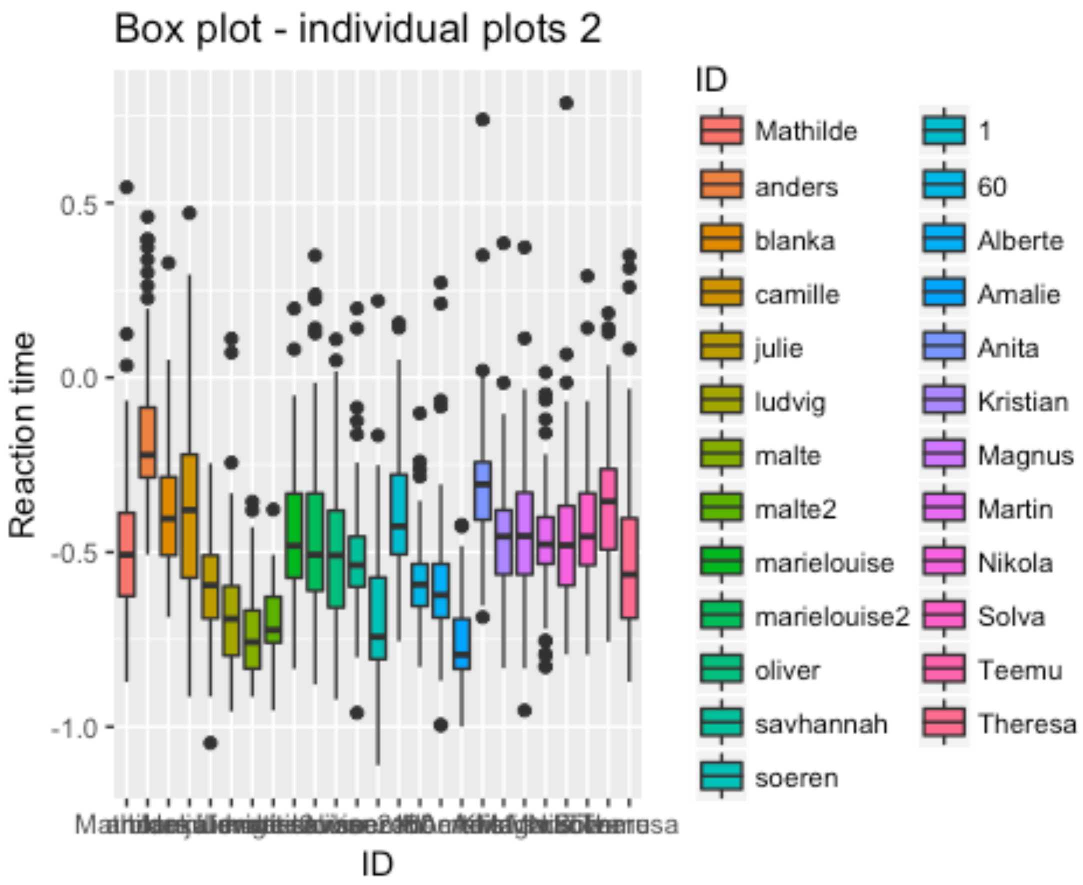
```
#prepare plot with facet wrap
individual_plot <- ggplot(log_data, aes(x = cond_emo, y = log_RT, fill = cond_blue
))+
                             geom_boxplot()+
                             facet_wrap(~ID)+
                             scale_fill_manual(values = c("yellow","blue", "yellow
", "blue", "yellow", "blue","yellow","blue")) + labs(title = "Box plot - individua
l plots", x = "Emotional condition", y = "Reaction time")

#plot
individual_plot
```



```
#plot with ID on the x-azis
individual_plot2 <- ggplot(log_data, aes(x = ID, y = log_RT, fill = ID))+
                              geom_boxplot()+
                              labs(title = "Box plot - individual plots 2", x = "ID
", y = "Reaction time")

#plot
individual_plot2
```



None of the participants stick out as unsual when only looking at the correct answers.

3. Data analysis

3.a

Make mixed effects model where you predict reaction time using the three factors as fixed effects, and include random intercepts for each participant (use "ID" from the log). Include 2-way and 3-way interactions as well. To do this use lme() from the "nlme" package, and use maximum-likelihood as estimation method(method = "ML").

```
model_1 <-lme(log_RT ~ cond_emo * cond_blue * freq, random = ~1|ID, data = log_dat
a, method = "ML")
```

3.b

Report the t-statistics using summary().

```
summary(model_1)
```

```
## Linear mixed-effects model fit by maximum likelihood
##  Data: log_data 
##         AIC       BIC   logLik
##   -921.7042 -864.7194 470.8521
## 
## Random effects:
##  Formula: ~1 | ID
##         (Intercept)  Residual
## StdDev:   0.1321929 0.1913286
## 
## Fixed effects: log_RT ~ cond_emo * cond_blue * freq 
##                                 Value  Std.Error   DF    t-value p-value
## (Intercept)                -0.5042037 0.04314318 2174 -11.686754  0.0000
## cond_emo1                  -0.0355707 0.02288740 2174  -1.554162  0.1203
## cond_blue1                 -0.0611733 0.01962203 2174  -3.117586  0.0018
## freqy                       0.0494312 0.05654396   23   0.874209  0.3910
## cond_emo1:cond_blue1        0.0546449 0.02769730 2174   1.972931  0.0486
## cond_emo1:freqy             0.0047882 0.02628060 2174   0.182193  0.8554
## cond_blue1:freqy            0.0668937 0.02518765 2174   2.655813  0.0080
## cond_emo1:cond_blue1:freqy -0.0224106 0.03563167 2174  -0.628952  0.5294
##  Correlation: 
##                            (Intr) cnd_m1 cnd_b1 freqy  cn_1:_1 cnd_m1:
## cond_emo1                  -0.268                                     
## cond_blue1                 -0.313  0.589                              
## freqy                      -0.763  0.205  0.239                       
## cond_emo1:cond_blue1        0.221 -0.826 -0.707 -0.169                
## cond_emo1:freqy             0.234 -0.871 -0.513 -0.234  0.719         
## cond_blue1:freqy            0.244 -0.459 -0.779 -0.245  0.551   0.525 
## cond_emo1:cond_blue1:freqy -0.172  0.642  0.550  0.172 -0.777  -0.737 
##                            cnd_b1:
## cond_emo1                         
## cond_blue1                        
## freqy                             
## cond_emo1:cond_blue1              
## cond_emo1:freqy                   
## cond_blue1:freqy                  
## cond_emo1:cond_blue1:freqy -0.706 
## 
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max 
## -2.79611058 -0.62288065 -0.09371291  0.45667751  6.44012772 
## 
## Number of Observations: 2205
## Number of Groups: 25
```

```
#Table with t-value and other relevant statistics
summary(model_1)$tTable
```

```
##                                   Value  Std.Error   DF     t-value
## (Intercept)                -0.504203732 0.04314318 2174 -11.6867539
## cond_emo1                  -0.035570719 0.02288740 2174  -1.5541618
## cond_blue1                 -0.061173345 0.01962203 2174  -3.1175855
## freqy                       0.049431215 0.05654396   23   0.8742087
## cond_emo1:cond_blue1        0.054644863 0.02769730 2174   1.9729314
## cond_emo1:freqy             0.004788152 0.02628060 2174   0.1821934
## cond_blue1:freqy            0.066893695 0.02518765 2174   2.6558134
## cond_emo1:cond_blue1:freqy -0.022410604 0.03563167 2174  -0.6289519
##                                 p-value
## (Intercept)                1.204048e-30
## cond_emo1                  1.202914e-01
## cond_blue1                 1.847250e-03
## freqy                      3.910418e-01
## cond_emo1:cond_blue1       4.862989e-02
## cond_emo1:freqy            8.554479e-01
## cond_blue1:freqy           7.969529e-03
## cond_emo1:cond_blue1:freqy 5.294466e-01
```

3.c

Report the F-statistics using anova() and type='sequential', which gives you type='I' analysis.

```
anova(model_1, type='sequential')
```

```
##                         numDF denDF  F-value p-value
## (Intercept)                 1  2174 346.6300  <.0001
## cond_emo                    1  2174   1.8854  0.1699
## cond_blue                   1  2174   0.0135  0.9076
## freq                        1    23   2.3160  0.1417
## cond_emo:cond_blue          1  2174   7.0788  0.0079
## cond_emo:freq               1  2174   0.1993  0.6553
## cond_blue:freq              1  2174   9.7558  0.0018
## cond_emo:cond_blue:freq     1  2174   0.3956  0.5294
```

3.d

Report the F-statistics using anova() and type='marginal'. Why might there be differences between results from 3.c and 3.d?

```
anova(model_1, type='marginal')
```

```
##                         numDF denDF   F-value p-value
## (Intercept)                 1  2174 136.58022  <.0001
## cond_emo                    1  2174   2.41542  0.1203
## cond_blue                   1  2174   9.71934  0.0018
## freq                          1    23   0.76424  0.3910
## cond_emo:cond_blue            1  2174   3.89246  0.0486
## cond_emo:freq                 1  2174   0.03319  0.8554
## cond_blue:freq                1  2174   7.05335  0.0080
## cond_emo:cond_blue:freq       1  2174   0.39558  0.5294
```

The F-statistics from 3.c uses a type I analysis, which means that the variance shared between the predictors will be attributed to the first predictor. In the type III (also called marginal) the interaction of predictors are taken into account.

3.e

Make a new model including a random slope from trial number ('no' in the log-file). Repeat 3.b. What does the inclusion of such a random slope model? Did it change the results?

```
model_2 <-lme(log_RT ~ cond_emo * cond_blue * freq, random = ~no|ID, data = log_da
ta, method = "ML")

#summarise model
summary(model_2)

## Linear mixed-effects model fit by maximum likelihood
##  Data: log_data 
##         AIC       BIC   logLik
##   -951.6366 -883.2548 487.8183
## 
## Random effects:
##  Formula: ~no | ID
##  Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev      Corr  
## (Intercept) 0.133853748 (Intr)
## no          0.001206009 -0.24 
## Residual    0.188433336       
## 
## Fixed effects: log_RT ~ cond_emo * cond_blue * freq 
##                                Value  Std.Error   DF    t-value p-value
## (Intercept)               -0.5161524 0.04265825 2174 -12.099711  0.0000
## cond_emo1                 -0.0354338 0.02260929 2174  -1.567224  0.1172
## cond_blue1                -0.0590149 0.01938506 2174  -3.044349  0.0024
## freqy                      0.0611364 0.05588388   23   1.093990  0.2853
## cond_emo1:cond_blue1       0.0567175 0.02735186 2174   2.073625  0.0382
## cond_emo1:freqy            0.0041543 0.02597105 2174   0.159960  0.8729
## cond_blue1:freqy           0.0640529 0.02489404 2174   2.573023  0.0101
## cond_emo1:cond_blue1:freqy -0.0272428 0.03521495 2174  -0.773613  0.4392
##  Correlation: 
##                            (Intr) cnd_m1 cnd_b1 freqy  cn_1:_1 cnd_m1:
## cond_emo1                  -0.267
## cond_blue1                 -0.316  0.587                            
## freqy                      -0.763  0.204  0.241                     
## cond_emo1:cond_blue1        0.222 -0.825 -0.706 -0.170              
## cond_emo1:freqy             0.232 -0.871 -0.511 -0.233  0.718       
## cond_blue1:freqy            0.246 -0.457 -0.779 -0.246  0.549   0.524
## cond_emo1:cond_blue1:freqy -0.173  0.641  0.548  0.174 -0.777  -0.736
##                            cnd_b1:
## cond_emo1                         
## cond_blue1                        
## freqy                             
## cond_emo1:cond_blue1              
## cond_emo1:freqy                   
## cond_blue1:freqy                  
## cond_emo1:cond_blue1:freqy -0.705 
## 
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max 
## -2.8498046 -0.6183224 -0.1120300  0.4594741  6.3231814 
## 
## Number of Observations: 2205
## Number of Groups: 25
```

Adding random slopes makes it possible to have different slopes for the different trial numbers. The inclusion of a random slope slightly improves the model.

3.f

Make a model comparison of model 3.a and 3.e using anova(). Did the inclusion of a random slope significantly improve the model?

```
#model comparison
anova(model_1, model_2)
```

```
##         Model df       AIC       BIC   logLik   Test  L.Ratio p-value
## model_1     1 10 -921.7042 -864.7194 470.8521                        
## model_2     2 12 -951.6366 -883.2548 487.8183 1 vs 2 33.93231  <.0001
```

Adding the trial number as random slope significantly improved the model p < .0001.

3.g

Response times are correlated in time which goes against the assumption of independence. It might therefore be an idea to model this by including a so-called auto-regressive component in the model (e.g. this is default in SPM analyses of fMRI-data). In lme(), this is done by adding the following to the model specification: “cor=corAR1(,form=~1|ID)”. Make a new model comparison. Does that have an effect?

```
#constructing model
newmodel_2 <-lme(log_RT ~ cond_emo * cond_blue * freq, random = ~no|ID, data = log
_data, method = "ML", cor=corAR1(,form=~1|ID))

#Summarise model
summary(newmodel_2)

## Linear mixed-effects model fit by maximum likelihood
##  Data: log_data
##         AIC       BIC   logLik
##   -979.5929 -905.5126 502.7964
##
## Random effects:
##  Formula: ~no | ID
##  Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev      Corr
## (Intercept) 0.132601160 (Intr)
## no          0.001138109 -0.216
## Residual    0.189247286
##
## Correlation Structure: AR(1)
##  Formula: ~1 | ID
##  Parameter estimate(s):
##       Phi
## 0.1280107
## Fixed effects: log_RT ~ cond_emo * cond_blue * freq
##                                 Value  Std.Error   DF    t-value p-value
## (Intercept)                -0.5148625 0.04262694 2174 -12.078338  0.0000
## cond_emo1                  -0.0380293 0.02219935 2174  -1.713083  0.0868
## cond_blue1                 -0.0567939 0.01900354 2174  -2.988596  0.0028
## freqy                       0.0648832 0.05587676   23   1.161184  0.2575
## cond_emo1:cond_blue1        0.0580627 0.02683977 2174   2.163310  0.0306
## cond_emo1:freqy             0.0029192 0.02552226 2174   0.114377  0.9089
## cond_blue1:freqy            0.0558958 0.02447713 2174   2.283593  0.0225
## cond_emo1:cond_blue1:freqy -0.0247166 0.03456095 2174  -0.715159  0.4746
##  Correlation:
##                            (Intr) cnd_m1 cnd_b1 freqy  cn_1:_1 cnd_m1:
## cond_emo1                  -0.262
## cond_blue1                 -0.309  0.583
## freqy                      -0.763  0.200  0.236
## cond_emo1:cond_blue1        0.217 -0.822 -0.705 -0.166
## cond_emo1:freqy             0.228 -0.870 -0.507 -0.229  0.715
## cond_blue1:freqy            0.240 -0.452 -0.776 -0.241  0.548   0.521
## cond_emo1:cond_blue1:freqy -0.169  0.638  0.548  0.171 -0.777  -0.734
##                            cnd_b1:
## cond_emo1
## cond_blue1
## freqy
## cond_emo1:cond_blue1
## cond_emo1:freqy
## cond_blue1:freqy
## cond_emo1:cond_blue1:freqy -0.706
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.8589689 -0.6186937 -0.1115944  0.4530465  6.2730827
##
## Number of Observations: 2205
## Number of Groups: 25
```

```
#model comparison
anova(model_2, newmodel_2)
```

```
##             Model df       AIC       BIC   logLik   Test L.Ratio p-value
## model_2         1 12 -951.6366 -883.2548 487.8183
## newmodel_2      2 13 -979.5929 -905.5126 502.7964 1 vs 2 29.9563  <.0001
```

Including the auto-regressive component significantly improved the model p < .0001

4. Results and interpretation

4.a

Comprehension question: If you were to report these results, which model would you use and why? Below are some ideas that you may want to consider:
Rule number 1: Report the first model you did.
Rule number 2: Report the most sensible model.
Rule number 3: Report the simplest model.
Rule number 4: Report the most extensive and complete model.

We chose the model called "newmodel_2", which is the more complex, but also the most complete model, because it does not violate the assumption of independency. It seems to be the more sensible model.

4.b

Throughout part 3 of this exercise we made several models to choose from. What is the problem of this strategy? (This is analogous to the motivation for using family-wise-error corrected p-values in the SPM analysis)

The problem of making to many models to choose from is that we run into the risk of just searching for results and then risk getting false positivs as we also see when not using a corrected p-value. On the other hand just conducting one model could risk overseeing relevant factors.

4.c

Write a few lines, briefly stating the results of the experiment in relation to the hypotheses, using the model you dicided upon in 4.a.

Hypothesis 1: We can see that the slope for cond_blue1 when the picture is blue is negative: -0.06, t(2174) = -2.99, p = 0.0028. This yields a shorter response time when the picture is blue compared to yellow, which means participants were faster when answering with the index finger (blue face). This mean we cannot reject this hypothesis. Because we see a significant interaction between condition blue and frequency we should in fact look at these results, because they overrules the main effect of cond_blue1, but when answering this hypothesis we just look at cond_blue1.

Hypothesis 2: We can see that the slope for cond_emo1 when the picture is emotional is negative: -0.04, t(2174) = -1.71, p = 0.0868, however the results are not significant, which means we should reject this hypothesis.

Hypothesis 3: To answer this hypothesis we look at the interaction between condition_blue and frequency. We can see that the slope when seeing a blue picture in frequency yellow is positive, which yields a longer reponse time with infrequent stimluli: 0.06, t(2174) = 2.28, p = 0.02. This means we cannot reject this hypothesis.