# Portfolio Assignment 7: Mixed effects

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## Deadline

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## Overview

This assignment contains two major parts:

A. Analyses of the behavioral data from an Emotional Face viewing experiment

B. Analyses of the reported experiences when eating amimo acids instead of breakfast (a tryptophan depletion study)

## A. 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).

#### Stimuli

Participants viewed 4 different stimuli:

blue neutral face

blue fearful face

yellow neutral face

yellow fearful face

Participants viewed a total of 96 stimuli, each displayed for 700 ms, with a mean interstimulus interval of 4100 ms.

#### Frequency manipulation

Participants were, without being told, divided into two "frequency" groups:

Group 1 recieved the blue/yellow stimuli in a 2:1 proportion (64:32)

Group 2 recieved the blue/yellow stimuli in a 1:2 proportion (32:64)

Both groups recieved the fearful and neutral faces at the same proportion (48:48)

###Responses

Participants responded to the colour of the stimuli:

blue face -> index finger response

yellow face -> middle finger response

### 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 A Tasks:

### 1. Understanding the experiment

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

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

### 1. Data exploring and preparation

Find the data on blackboard. Load the data using something like the following code:

```
face_exp_2016<- read.csv("~/Dropbox/fmri_data/face_exp_2016/face_exp_data_all_160310.csv", sep=";")
face_exp_2017<- read.csv("~/Dropbox/fmri_data/face_exp_2017/face_exp_data/face_exp_all_logs_2017.csv", s
#Binding the two datasets together
face_exp<-rbind(face_exp_2016,face_exp_2017)
#conditions are coded in the "cond_blue", "cond_emo" and "freq" variables
```

Make sure that factorial variables are coded as factors using the as.factor() function.

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”))" .

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

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

2.d.: Make another boxplot similar to that in 2.a. Did it solve 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?

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

2.g.: log-transform the RT data.

2.h.: Use a qq-plot to explore if the transformed data appear more normal 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?

### 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").

3.b.: Report the t-statistics using summary().

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

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

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?

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?

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?

### 4. Results and interpretion.

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.

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)

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..

## B. Tryptophan depletion study analysis

In this task you are going to analyze the data from a tryptohan depletion experiment. Students from the 2018 year in Cognitive Science at Aarhus University took part in a voluntary experiment where they were given a small portion (47 gram) of amino acids and ate that instead of breakfast. Half of the portions also contained 3 gram of tryptophan, an amino acid needed for serotonin production.

#### Dependent variable

Participants monitored their mood on a visual analog scale (VAS) with scores from 0 (your worst mood) to 100 (your best mood).

### Hypothesis 1

Being depleted of tryptophan is hypothesised to lead to alterations of mood.

### Groups

Particiants were free to choose not to take part, and the study thus consisted of three groups: - Tryptophan depleted - Tryptophan loaded - Controls

### Repeated measure

Mood rating was conducted at three time points:

- 6.55 (just before eating the amino acids)
- 7.05 (just after eating the amino acids)
- 12.00 (five hourse after eating the amino acids)

### Hypotheses 2 and 3

In addition to the tryptophan depletion effect, mood was hypothesised to be altered by

Hypothesis 2: forcing yourself to eat a nasty powder at 7.00, or

Hypothesis 3: becoming hungry at 12.00.

### Participants

Participants were given a participant number in the amino acid bag. This was to be used when reporting mood. 50 participants responded to the questionnaires. However, not everybody rated at all time-points and/or using consistent numbers. 43 participants were thus part of the final dataset, which was turned into long format.

## 5. Interpretation task

5.a. Find the data on Blackboard, load it and report figure and analysis using the code below.

5.b. Report and discuss the findings. What do they mean? How do they relate to the hypotheses?

```
#Load data
trypt_long<-read.csv(file='trypt_long.csv',header=TRUE,sep=",")
trypt_long$ID<-as.factor(trypt_long$ID)
trypt_long$time<-as.factor(trypt_long$time)

#use ggline to make nice line plot. Install ggpubr, if you haven't got it
library(ggpubr)
ggline(trypt_long, x = "time", y = "mood",col='Group',
       add = c("mean_se", "dodge"), palette = "jco")

library(lmerTest)
#Relevel to make the reference group "loaded"
trypt_long$Group<-relevel(trypt_long$Group,'loaded')
#Relevel to make the reference time "7.05"
```

```r
trypt_long$time<-relevel(trypt_long$time,'7.05')
#Make mixed effects model with Group and time as fixed effects and ID as random effect
trypt_model<-lmerTest::lmer(mood~Group*time+(1|ID), data = trypt_long)

#Get summary statistics
trypt_res<-summary(trypt_model)

#Apply Bonferroni correction for multiple comparisons to p-values (9 tests)
# and round a bit (5 decimals)
trypt_res$coefficients2<-matrix(round(c(trypt_res$coefficients,trypt_res$coefficients[,5]*9),
                                      digits=5),ncol=6)

#Add names to the new results matrix
colnames(trypt_res$coefficients2)<-c(colnames(trypt_res$coefficients),'p(bonf)')
rownames(trypt_res$coefficients2)<-c(rownames(trypt_res$coefficients))

#Show us what you've got
trypt_res$coefficients2

#Use library(emmeans) to get more comprehensible pairwise interactions (uncorrected for multiple compar
library(emmeans)
lsm = emmeans(trypt_model, ~Group*time)
contrast(lsm, interaction = "pairwise")
```

## Handing in the assignment

Use r_markdown in RStudio for your report. Submit report as a single pdf file. Include commented code and figures all the way from data import.

Submit report to Blackboard.