**Session 6: 2\_2 ANOVA.R**

(1) Another way to transform RT data is to use an inverse transform (i.e. 1/RT).

Take the RT data in Mydata, and create a new column with the inverse transformed data. Call this column InvRT  
   
Look at this data in a histogram and with quantile plots. Does it improve the distribution?

Mydata.corr$InvRT <- 1/Mydata.corr$RT

hist(Mydata.corr$InvRT)

qqnorm(Mydata.corr$InvRT)

qqline(Mydata.corr$InvRT)

(2) Create a boxplot of the inverse transformed RT data. From this, create a variable called ‘z’ that stores the outliers.

mybp <- boxplot(InvRT ~ SubNo, data=Mydata.corr)

z<-which(Mydata.corr$InvRT %in% mybp$out, arr.in=TRUE)

(3) Finally, create a column for these outliers called ‘OutInv’. In that column, mark all the rows which show outliers on the boxplot. Tip: pay attention to exactly where you need to change the original code.

Mydata.corr$OutInv<-rep("FALSE")

#loop to identify rows and put 'TRUE' for each outlier

for (i in 1:length(z))

{Mydata.corr$OutInv[z[i]]<-"TRUE"}

#make new column a factor/category

Mydata.corr$OutInv<-as.factor(Mydata.corr$OutInv)

head(Mydata.corr)

(4) Which participants have the most outliers for inverse transformed RT data?

Which participants have fewest outliers?   
How much data is removed if you take out outliers for inverse transformed data?

table(Mydata.corr$SubNo,Mydata.corr$OutInv)  
*Participant 5 and 20 have the most with 13  
Participant 2 has the least with 1*

temp<-filter(Mydata.corr,OutInv==FALSE)

1-dim(temp)/dim(Mydata.corr)  
*It is about 1.5%*

(5) Go back to Mydata.corr.a (this the data with errors and outliers removed).  
Extract summary data for each participant, with their mean RT for each level of HomLocation.   
Remember to rename the columns in your new set, so they are not called ‘variable’ and ‘value’  
What is the mean RT for the scalp location PZ? (across all subjects)

temp<-dcast(Mydata.corr.a, SubNo ~ HomLocation, value.var = "RT",

fun.aggregate = mean, na.rm = TRUE)

data.summary<-melt(temp, id.vars = "SubNo")

names(data.summary)[2:3]<-c("HomLocation","meanRT")

with(data.summary, tapply(meanRT, HomLocation, mean))

*PZ Mean RT = 443.14*

(6) Complete a 1-way repeated measures ANOVA for HomLocation.  
HomLocation was manipulated within subjects.  
Use the log of mean RT.  
Is there a significant main effect of HomLocation (scalp location)?

aov.1 <-aov(log(meanRT) ~ HomLocation + Error(SubNo/HomLocation), data.summary)

*No significant main effect (F(23,432) = 0.17, p>1)*

(7) Complete follow up pairwise t-tests. Use the Holm method to control for false positives.  
Is there a significant difference between scalp locations ATL and CZ?  
Is there a significant difference between scalp locations CP1.2 and F7.8

pairwise.t.test(log(data.summary$meanRT), data.summary$HomLocation, p.adjust.method="holm", paired=T)

*ATL and CZ: p = 0.00079 Yes  
CP1.2 and F7.8 = 0.01030 Yes*

(8) To look at the data, create a boxplot of the RTs by each HomLocation

par(mfrow=c(1,1))

boxplot(data.summary$meanRT ~ data.summary$HomLocation)

**Session 7: 2\_3 More on ANOVA.R**

(1) Complete an ANOVA analysis with Axes, TwitchFactor and Task (2x1 Mixed ANOVA).  
In this analysis, look for the interaction and main effects for Axes x TwitchFactor, but only look at the main effect for Task.  
Store the result of this analysis in ‘aov.4’  
What are the results?  
  
aov.4 <- aov(log(RT) ~ (Axes\*TwitchFactor) + Task

+ Error(SubNo/(Axes\*TwitchFactor)), data=Mydata.corr.a)

*Significant main effect of TwitchFactor  
Significant main effect of Task  
No effect of Axes  
No interaction between Axes and TwitchFactor*

(2) Complete an ANOVA analysis with TwitchFactor and Hemisphere.   
Look only at the interaction between these two variables.

Store the result of this analysis in ‘aov.4’  
Plot the interaction between these two variables  
What are the results? Use the plot to provide an interpretation (i.e. explain what the results mean)

aov.4 <- aov(log(RT) ~ TwitchFactor:Hemisphere

+ Error(SubNo/TwitchFactor), data=Mydata.corr.a)

*with(Mydata.corr.a, interaction.plot(TwitchFactor, Hemisphere, log(RT), fun = mean))*

*Significant interaction between TwitchFactor and Hemlabel*

*For the right hemisphere, not much difference between high and low twitches.  
For the left hemisphere, higher reaction times for High twitches, and shorter reaction times for Low twitches*

(3) Repeat the ANOVA above, with Axes, TwitchFactor and Task (2x1 Mixed ANOVA). Store it in ‘aov.4’  
Compare the output for this ANOVA with Type II and Type III sums of squares.  
Use contr.sum for the contrasts

aov.4 <- lm(log(RT) ~ (Axes\*TwitchFactor) + Task

+ Error(SubNo/(Axes\*TwitchFactor)), data=Mydata.corr.a,  
 contrasts = list(Axes = contr.sum, TwitchFactor = contr.sum)

(4) We want to look at the effects of Task and Hemisphere

These are both between subjects  
Look at the code from script 0\_Basic Statistics in R (line 101)  
and code on lines 225 and 229 of this script.

Write some code that completes a between subjects ANOVA using the RT data in Mydata.corr.a and tests Task and Hemisphere

ezANOVA(Mydata.corr.a, RT, wid = SubNo, between = .(Task,Hemisphere))

(5) Complete the same ANOVA but on the log(RT)  
Plot the data using interaction.plot.

What are the results?

Use ezStats to get the summary stats  
What is the mean RT for Left hemisphere in the Flanker task? (NB – left hemisphere is coded as 1)

ezANOVA(Mydata.corr.a, log(RT), wid = SubNo, between = .(Task,Hemisphere))

with(Mydata.corr.a, interaction.plot(Task, Hemisphere, log(RT), fun = mean))

ezStats(data= Mydata.corr.a,   
 dv = log(RT), wid = SubNo,

between = .(Task,Hemisphere))

*Significant effect of Task, no effect of Hemisphere and no interaction.*

*Mean RT for Left hemisphere in the Flanker task = 0.55 log(ms)*

(6) Complete a mixed ANOVA using the data Mydata.corr.a  
Test the effects of the variables Task (between subjects) and HomLocation (within subjects).  
Write code to complete this ANOVA using both ezANOVA Type 3 *and*   
the afex function aov\_car

*ezANOVA:*

mix.anova <- ezANOVA(data=Mydata.corr.a, dv = log(RT), wid = SubNo,

within = .(HomLocation),

between = .(Task),

type=3,

return\_aov = TRUE)

*afex aov\_car:*

mix.anova <- aov\_car(log(MeanRT) ~ (Task\*HomLocation) + Error(SubNo/(HomLocation)),

data= Mydata.corr.a, return = "aov")

(7) Use lsmeans to get the complete set of means for each cell in the design  
How many levels / conditions are there in HomLocation?   
How many total cells are there?  
Complete a post-hoc test to compare the mean RT for the ATL in the CRT task to CZ in the CRT task. What is the result?

ref1 <- lsmeans(mix.anova, c("Task", "HomLocation"))

unique(Mydata.corr.a$HomLocation)

unique(Mydata.corr.a $Task)

*There are 24 levels/conditions in HomLocation, and two levels of Task.   
This gives 48 cells.*

x<-rep(0,48)

x[3]<-1

x[11]<- -1

c\_list <- list("CRT.ATL - CRT.CZ" = x)

summary(contrast(ref1, c\_list), adjust = "holm") *OR*

summary(as.glht(contrast(ref1, c\_list)), test = adjusted("bonferroni"))

This comparison is significant

**Session 8: 3\_1 Introduction to LMMs.R**

(1) Build an LMM that includes fixed effects for Trial, main effects for Twitches and main effects and interactions between Task and Congruence and main effect of Twitches.  
Include random slopes for Twitches varying across Subjects, and random slopes for the effect of Congruence varying across Subjects. Include correlations between intercepts and slopes.  
Save this in lmer.4

lmer.4<-lmer(log(RT) ~ Trial + Twitches + (Task \* Congruence)

+ (1 + Twitches|SubNo) + (1+Congruence|SubNo), data = Mydata.corr.a)

(2) Plot the fixed effects from this model.

eff<-allEffects(lmer.4)

plot(allEffects(lmer.4))

(3) Use update( ) to compare this model to a model that does not include the interaction between Task and Congruence. Save this model in lmer.4.NoInt  
What is the result?  
  
lmer.4<-lmer(log(RT) ~ Trial + Twitches + (Task \* Congruence)

+ (1 + Twitches|SubNo) + (1+Congruence|SubNo), data = Mydata.corr.a)

lmer.4.NoInt <- update(lmer.2,.~.-Task:Congruence)

(4) Plot the random effects for Congruence varying across Subjects. Make sure you update the axes labels. (hint – modify code on lines 155-157)

lattice::xyplot(fitted(lmer.4) ~ Congruence|SubNo, data=Mydata.corr.a,

main="Congruence by Subject Random Effects",

ylab="Fitted log RT",xlab="Congruence")