

Ranging_Analyses_by_Clusters_on_Penlevel

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create table with Cluster Label and Variables

1. Read in Files

datafile of cluster label per hen based on distance matrices calculations using dtwclust for details see Codes "RCode.penXX.R":

2. merge files

3. exclude cluster 5, which is one HenID only

Penlevel Analysis

code given for pen 11 only ##### PEN 11

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```
library(lmerTest)
library(pbkrtest)
clus11.max.lmer <- lmer((Total_transitions) ~ mycl + (1|HenID), data=allhen11.df,REML=F)
summary(clus11.max.lmer)
anova(clus11.max.lmer)
clus11.min.lmer <- lmer((Total_transitions) ~ (1|HenID), data=allhen11.df, REML=F)
anova(clus11.max.lmer, clus11.min.lmer, test="F")
```

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```
library(multcomp)
summary(glht(clus11.max.lmer, linfct = mcp(mycl="Tukey")),test=adjusted("fdr"))
```

% fdr as p-value correction = forced discovery rate (Benjamin and Hochberg,1995)

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```
# Residuenanalysen #
par (mfrow= c (2, 2))
qqnorm (resid (clus11.max.lmer))
qqnorm (ranef (clus11.max.lmer) [['HenID']] [, 1])
scatter.smooth (fitted (clus11.max.lmer), resid (clus11.max.lmer))

# Random Analyse #
for (ranEF in names (ranef (clus11.max.lmer))) {
  qqnorm (ranef (clus11.max.lmer) [[ranEF]] [, 1])
}
```

% strong effect of heteroscedasticity ==> overall variance is forced to homos. but it should not affect the slope. % therefore the effect size won't change due to the strong heteroscedasticity % however, the p-values will be affected by the hetero ==> % therefore I tried not to use normal lmer, but robust lmer (Package: robustlmm) large parameter k values

(tuning parameter) yield more efficient, but less robust estimates, whereas smaller values yield more robust but less efficient estimates. A popular choice is to fix the asymptotic efficiency at 95% of the classic estimates ($k = 1.345$ for Huber function) (aus Paper: Koller 2016)

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```
library(robustlmm)
#install.packages("robustlmm")
#library(robustlmm)
clusl1.max.rlmer <- rlmer(Total_transitions ~ mycl + (1|HenID), data=allhen11.df, REML=F)
# clusl1.min.rlmer <- rlmer(Total_transitions ~ (1|HenID), data=allhen11.df, REML=F)
summary(clusl1.max.rlmer)
getME(clusl1.max.rlmer,"w_e") # getting all robustness weights for HenID

plot(clusl1.max.rlmer)
```

to get higher efficiency for the estimates will be achieved by tuning the parameter k

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```
clusl1.max.rlmer_tuned1 <- update(clusl1.max.rlmer, rho.sigma.e=psi2propII(smoothPsi, k=2.28))
plot(clusl1.max.rlmer_tuned1)
# with more than one random term:
# rsb <- list(psi2propII(smoothPsi),psi2propII(smoothPsi, k = 2.28))
# clusl1.max.rlmer_tuned2 <- update(clusl1.max.rlmer, rho.sigma.b=rsb)
```

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```
# comparison of robustness of different model fits, including non-robust lmer
compare(clusl1.max.lmer, clusl1.max.rlmer, clusl1.max.rlmer_tuned1, show.rho.functions = F)
```

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```
#effect size of model
1-var(residuals(clusl1.max.rlmer))/(var(model.response(model.frame(clusl1.max.rlmer))))
```

If understood correctly, based on the weighing there does not seem to be much of a difference despite of the heteroscedasticity in terms of the robustness of model fits, so I will stick to non-robust lmer. I did not manage to extract p-values with robust lmm, somehow not implemented and not extractable as with lmer. Therefore, I want to apply a bootstrap with 1000 Simulations using lmer: by parametric bootstrapping- that is, by simulating data from the fitted model, refitting the model with subset of data, and extracting the new estimated parameters (or any other quantities of interest). Therefore, I keep the results extracted from non-robust lmer mentioned above.

POISSON for Total_Transition

Because Total Transition refers to count data ==> POISSON

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```
clusl1.max.lmer <- glmer((Total_transitions) ~ mycl + (1|HenID), family=poisson,
data=allhen11.df)

clusl1.min.lmer <- glmer((Total_transitions) ~ (1|HenID), family=poisson, data=allhen11.df)
```

```
# Check for Overdispersion #
overdisp_fun <- function(model) {
  rdf <- df.residual(model)
  rp <- residuals(model,type="pearson")
  Pearson.chisq <- sum(rp^2)
  prat <- Pearson.chisq/rdf
  pval <- pchisq(Pearson.chisq, df=rdf, lower.tail=F)
  c(chisq=Pearson.chisq,ratio=prat, rdf=rdf, p=pval)
}
overdisp_fun(clus11.max.lmer)
```

Data is very overdispersed, therefore: negative binomial

[Hide](#)

```
clus11.max.lmer <- glmer.nb((Total_transitions) ~ mycl + (1|HenID), data=allhen11.df)
overdisp_fun(clus11.max.lmer)
```

with this approach: ratio is close to 1, so no overdispersion left

[Hide](#)

```
clus11.max.lmer <- glmer.nb((Total_transitions) ~ mycl + (1|HenID), data=allhen11.df)
clus11.min.lmer <- glmer.nb((Total_transitions) ~ (1|HenID), data=allhen11.df)
anova(clus11.max.lmer, clus11.min.lmer, test="F")
```

Modelling for Plotting

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```
library(boot)
pred.df <- expand.grid (mycl= c ("1","2","3","4","5"))
estim.Mod <- function (x) {
  predict (x, newdat= pred.df, re.form= NA)}
extract.ci <- function (x) {
  out <- data.frame (numeric (0), numeric (0), numeric (0))
  for (i in 1:length (x [['t0']])) {
    out <- rbind (out, c (x [['t0']] [i],
                        boot.ci (x, index= i, type= 'perc') [['percent']] [, 4:5]))
  }
  names (out) <- c ('estim', 'lo.ci', 'up.ci')
  out
}

# Boxplot with model estimations #
mod <-glmer.nb(Total_transitions ~ mycl +
              +(1 | HenID),
              REML= FALSE, data= allhen11.df)

mod.boot <- bootMer (mod, estim.Mod, nsim= 100, .progress= 'win')

##CI calculations #
mod.estim <- exp(extract.ci(mod.boot))
mod.estim
```

Plotting

Hide

```
library(Hmisc)
allhen11.df$mycl <- factor(allhen11.df$mycl,levels=c("4","3","2","1"))
par(mar=c(4,4,2,4))
boxplot((allhen11.df$Total_transitions)~allhen11.df$mycl
        , axes=F,las=1,ylab="number of transitions",xlab="",cex.lab=1.0, outline=F)
axis (2, seq(0, 120, 20), c ('0','20', '40', '60','80','100','120'), line= 0, las= 1,
cex.axis=1.0)
axis (1, at= c(1.0,2.0, 3.0, 4.0),
      labels = c("", "", "", ""),
      cex.axis = 1.3)

mtext (side =1, at = 0.2, "cluster", line = 1.2, cex=1.0)
mtext (side =1, at = 1, "1", line = 1.2, cex=1.0)
mtext (side =1, at = 2, "2", line = 1.2, cex=1.0)
mtext (side =1, at = 3, "3", line = 1.2, cex=1.0)
mtext (side =1, at = 4, "4", line = 1.2, cex=1.0)

segments(x0 = 0.56, x1 = 1.44, y0 = mod.estim [4:4, 'estim'], lwd = 3, lty= 1, col =
"firebrick")
segments(x0 = 0.56, x1 = 1.44, y0 = mod.estim [4:4, 'lo.ci'], lwd = 2, lty= 2, col =
"firebrick")
segments(x0 = 0.56, x1 = 1.44, y0 = mod.estim [4:4, 'up.ci'], lwd = 2, lty= 2, col =
"firebrick")

segments(x0 = 1.56, x1 = 2.44, y0 = mod.estim [3:3, 'estim'], lwd = 3, lty= 1, col =
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segments(x0 = 3.56, x1 = 4.44, y0 = mod.estim [1:1, 'estim'], lwd = 3, lty= 1, col =
"firebrick")
segments(x0 = 3.56, x1 = 4.44, y0 = mod.estim [1:1, 'lo.ci'], lwd = 2, lty= 2, col =
"firebrick")
segments(x0 = 3.56, x1 = 4.44, y0 = mod.estim [1:1, 'up.ci'], lwd = 2, lty= 2, col =
"firebrick")
```

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```
clus11.max.lmer <- lmer(total_time_IN ~ mycl + (1|HenID), data=allhen11.df, REML=F)
clus11_min.lmer <- lmer(total_time_IN ~ (1|HenID), data=allhen11.df, REML=F)
anova(clus11.max.lmer, clus11_min.lmer, test="F")
```

```
clus11.totIN.lmer <- PBmodcomp(clus11.max.lmer,clus11_min.lmer)
summary(clus11.totIN.lmer)
```

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```
library(multcomp)
summary(glht(clus11.max.lmer, linfct = mcp(mycl="Tukey")),test=adjusted("fdr"))
```

Hide

```
# Residuenanalysen #
par (mfrow= c (2, 2))
qqnorm (resid (clus11.max.lmer))
qqnorm (ranef (clus11.max.lmer) [['HenID']] [, 1])
scatter.smooth (fitted (clus11.max.lmer), resid (clus11.max.lmer))

# Random Analyse #
for (ranEF in names (ranef (clus11.max.lmer))) {
  qqnorm (ranef (clus11.max.lmer) [[ranEF]] [, 1])
}
```

Again issue with heteroscedasticity ==> check with robust rlmer how it is weighed.

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```
#install.packages("robustlmm")
#library(robustlmm)
clus11.max.rlmer <- rlmer(total_time_IN ~ mycl + (1|HenID), data=allhen11.df, REML=F)
summary(clus11.max.rlmer)
effect size of model
1-var(residuals(clus11.max.rlmer))/(var(model.response(model.frame(clus11.max.rlmer))))
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Modelling for Plotting

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```
library(boot)
pred.df <- expand.grid (mycl= c ("1","2","3","4","5"))
estim.Mod <- function (x) {
  predict (x, newdat= pred.df, re.form= NA)}
extract.ci <- function (x) {
  out <- data.frame (numeric (0), numeric (0), numeric (0))
  for (i in 1:length (x [['t0']])) {
    out <- rbind (out, c (x [['t0']] [i],
                        boot.ci (x, index= i, type= 'perc') [['percent']] [, 4:5]))
  }
  names (out) <- c ('estim', 'lo.ci', 'up.ci')
  out
}
```

```
mod <-lmer(total_time_IN ~ mycl +
           +(1 | HenID),
           REML= FALSE, data= allhen11.df)
```

```
mod.boot <- bootMer (mod, estim.Mod, nsim= 100, .progress= 'win')

mod.estim <- (extract.ci(mod.boot))

mod.estim
```

Plotting

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```
allhen11.df$mycl <- factor(allhen11.df$mycl,levels=c("4","3","2","1"))
par(mar=c(4,4,2,4))
boxplot((allhen11.df$total_time_IN)~allhen11.df$mycl
        , axes=F,las=1,ylab="duration spent indoors [min]",xlab="",cex.lab=1.0, outline=F)
axis (2, seq(0, 30240, 5040), c ('0','84', '168', '252','336','420','504'), line= 0, las= 1,
cex.axis=1.0)
axis (1, at= c(1.0,2.0, 3.0, 4.0),
      labels = c("", "", "", ""),
      cex.axis = 1.3)

mtext (side =1, at = 0.2, "cluster", line = 1.2, cex=1.0)

mtext (side =1, at = 1, "1", line = 1.2, cex=1.0)
mtext (side =1, at = 2, "2", line = 1.2, cex=1.0)
mtext (side =1, at = 3, "3", line = 1.2, cex=1.0)
mtext (side =1, at = 4, "4", line = 1.2, cex=1.0)

segments(x0 = 0.56, x1 = 1.44, y0 = mod.estim [4:4, 'estim'], lwd = 3, lty= 1, col =
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segments(x0 = 1.56, x1 = 2.44, y0 = mod.estim [3:3, 'lo.ci'], lwd = 2, lty= 2, col =
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segments(x0 = 1.56, x1 = 2.44, y0 = mod.estim [3:3, 'up.ci'], lwd = 2, lty= 2, col =
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"firebrick")
segments(x0 = 2.56, x1 = 3.44, y0 = mod.estim [2:2, 'lo.ci'], lwd = 2, lty= 2, col =
"firebrick")
segments(x0 = 2.56, x1 = 3.44, y0 = mod.estim [2:2, 'up.ci'], lwd = 2, lty= 2, col =
"firebrick")

segments(x0 = 3.56, x1 = 4.44, y0 = mod.estim [1:1, 'estim'], lwd = 3, lty= 1, col =
"firebrick")
segments(x0 = 3.56, x1 = 4.44, y0 = mod.estim [1:1, 'lo.ci'], lwd = 2, lty= 2, col =
"firebrick")
segments(x0 = 3.56, x1 = 4.44, y0 = mod.estim [1:1, 'up.ci'], lwd = 2, lty= 2, col =
"firebrick")
```