## set seed and path, load libraries

set.seed(123456)

path <- ("C:/Users/USER/jeewon")

setwd(path)

library(MASS)

library(lme4)

## number of replications

nrep= 5

## varying conditions (adapted from Matuschek et al.(2017))

# number of persons: 30, 50

# number of items per level: 10, 20

# fixed effect (b0): 2000

# fixed effect (b1): **0, 25, 50** ⇒ b1 고정효과는 3가지

# person random effect:

tau0(sd): 100

tau1(sd): 20

corr(tau0,tau1): 0.6

# item random effect(sd):

#[**omega1, omega2**]=[20,20], [20,60], **[20,100]**

# sigma(=sd(e)): 300

**## set parameters**

nperson=30;

nitem=10;

**b0=2000;**

b1=25;

tau0=100; tau1=20; r=0.6;

**omega1=20; omega2=100;**

sigma=300

S= matrix(c(tau0^2, r\*tau0\*tau1, r\*tau0\*tau1, tau1^2), nrow=2)

## design matrix

**#id**

j = rep(c(1:nperson), each=2\*nitem)

i = rep(c(1:(2\*nitem)), nperson)

**k1** <- rep(c(rep(1,nitem), rep(0,nitem)), nperson)

**k2** <- rep(c(rep**(0,**nitem), rep**(1,**nitem)), nperson)

**# fixed**

x0=1

**x1**= rep(c(rep(0, nitem), rep(1,nitem)), nperson)

###### spaces to save

ll<- numeric(0)

fixed<- numeric(0)

#### FOR LOOP

for (n in 1:nrep) {

# generate random effects

s = mvrnorm(nperson, mu=c(0,0), Sigma=S)

**w1** = rnorm(nitem, mean=0, **sd=omega1)**

**w2** = rnorm(nitem, mean=0, **sd=omega2)**

e = rnorm(nperson\*nitem\*2, mean=0, sd=sigma)

# person random

ss = rep(s[,1],each=2\*nitem)\*x0 + rep(s[,2],each=2\*nitem)\*x1

# item random

w= rep(c(w1,w2), nperson)

# y

y = (b0\*x0 + b1\*x1) + ss + w + e

## data frame

dat<- data.frame(j,i, k1, k2, **x0**, x1, ss,w,e,y)

**###### estimation**

m1 = **lmer**(y~1+x1+(1 + x1| **j**) + **(1|i)**, data=dat, REML=F)

m2 = **lmer**(y~1+x1+(1 + x1| **j**) + **(-1+k1|i)** **+** **(-1+k2|i),** data=dat, REML=F) **⇒ level-sepcific item**

**effect**

## several things to save

# b1

fixed1<- summary(m1)$coefficients[c(2,4)]

fixed2<- summary(m2)$coefficients[c(2,4)]

fixed\_n<-c(fixed1,fixed2)

fixed<- rbind(fixed,fixed\_n)

# log-likelihood

ll1<- summary(m1)$logLik

ll2<- summary(m2)$logLik

ll\_n<- c(ll1,ll2)

ll<- rbind(ll,ll\_n)

} ## END of FOR LOOP

## save files

# fixed effect

colnames(fixed) <- c("m1est","m1se","m2est","m2se")

write.table(fixed,file="**fixed\_nri.**txt",

sep="\t", row.names = F, col.names = T)

# log-likelihood

colnames(ll) <- c("m1ll","m2ll")

write.table(ll, file="**ll\_nri.**txt",

sep="\t", row.names = F, col.names = T)