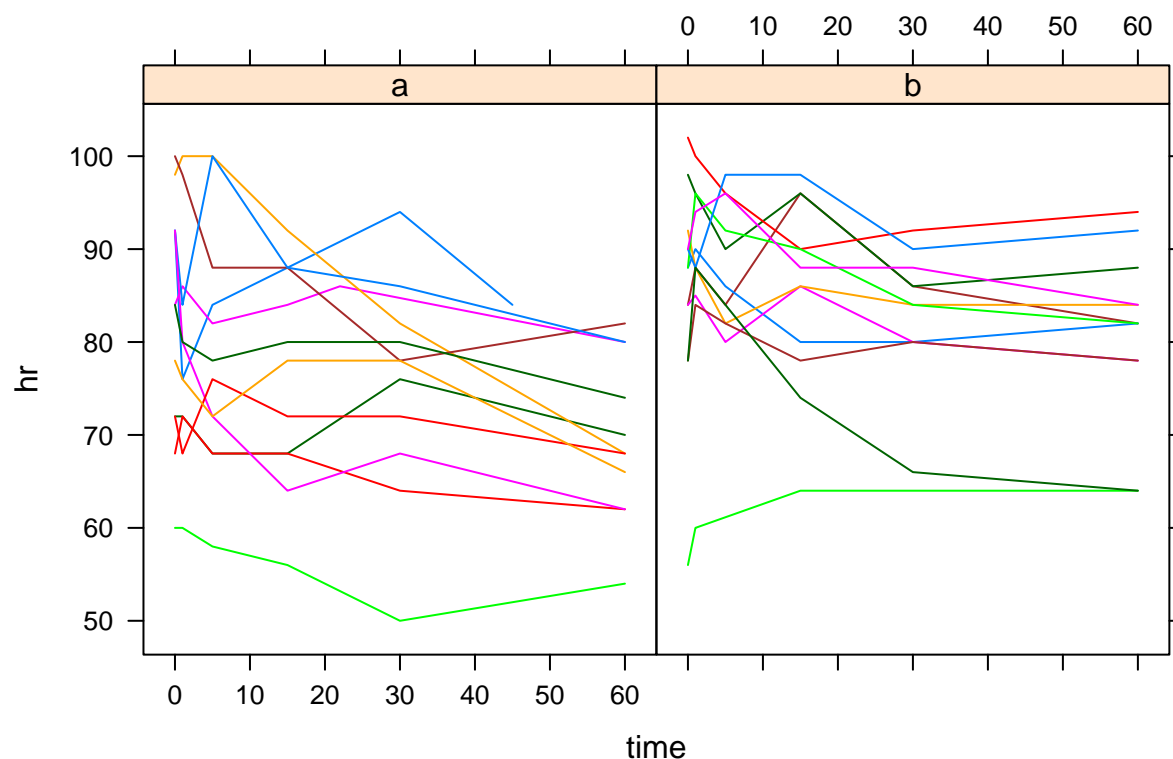


Complex Data - lab4

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```
hrunbalanced <- read.csv(file = "../data/hrunbalanced.csv", header = TRUE)
means <- tapply(hrunbalanced$hr, list(hrunbalanced$time, hrunbalanced$drug), mean)
xyplot(hr~time|factor(drug), type='l', groups=id, data=hrunbalanced, main = "Spaghetti plot of the heart rate over time in 2 groups")
```

Spaghetti plot of the heart rate over time in 2 groups



```
## Random intercept
fit.RandInt <- lme(hr ~ time*factor(drug),
  random=~1|id,
  data=hrunbalanced)
```

```
#Random slope
fit.RandSlp <- lme(hr ~ time*factor(drug),
  random=~1+time|id,
  data=hrunbalanced)
```

```
covar <- getVarCov(fit.RandSlp)
varCorr <- VarCorr(fit.RandSlp)
```

Task 1

Here we just perform proper computations, as in the task description. First we calculate the means.

```

#Calculating matrices (X,Z)
coefs <- fit.RandSlp$coefficients$fixed
coefs <- matrix(c(coefs[1], coefs[3], coefs[2], coefs[4]), ncol = 1)
ones <- matrix(rep(1,6), nrow=6)
zeros <- matrix(rep(0,6), nrow = 6)
tN <- matrix(c(0,1,5,15,30,60), nrow = 6)
t1 <- matrix(hrunbalanced$time[1:6], nrow = 6)
t2 <- matrix(hrunbalanced$time[7:12], nrow = 6)
t13 <- matrix(hrunbalanced$time[73:76], nrow = 4)
x1 <- cbind(ones,zeros,t1,zeros)
x2 <- cbind(ones,zeros, t2,zeros)
x13 <- cbind(ones[1:4,],ones[1:4,],t13,t13)
xNA <- cbind(ones, zeros, tN, zeros)
xNB <- cbind(ones, ones, tN, tN)
ZN <- cbind(ones,tN)
Z1 <- cbind(ones,t1)
Z2 <- cbind(ones, t2)
Z13 <- cbind(ones[1:4], t13)

#Calculating means
mA <- round(xNA%%coefs,1)
mB <- round(xNB%%coefs,1)
m1 <- round(x1%%coefs,1)
m2 <- round(x2%%coefs,1)
m13 <- rbind(round(x13%%coefs,1), c(NA), c(NA))
colnames(mA) <- c("Mean (drug A)")
colnames(mB) <- c("Mean (drug B)")
colnames(m1) <- c("Mean (obs. 1)")
colnames(m2) <- c("Mean (obs. 2)")
colnames(m13) <- c("Mean (obs. 13)")

kable(cbind(mA,m1,m2,mB,m13), format = "latex", booktabs=TRUE,
      caption = "Means") %>% kable_styling(latex_options="HOLD_position")

```

Table 1: Means

Mean (drug A)	Mean (obs. 1)	Mean (obs. 2)	Mean (drug B)	Mean (obs. 13)
80.5	80.5	80.5	86.6	86.6
80.3	80.3	80.3	86.5	86.5
79.7	79.7	79.7	86.1	85.0
78.0	78.0	78.0	85.0	80.2
75.6	75.6	76.9	83.4	NA
70.6	73.1	70.6	80.2	NA

And now we calculate the covariances:

```

getCov <- function(Z){
  Z%%covar%%t(Z) + as.numeric(varCorr[3,1])*diag(1,nrow = dim(Z)[1], ncol = dim(Z)[1])
}

#Calculating covariances
covZN <- round(getCov(ZN),1)
covZ1 <- round(getCov(Z1),1)

```

```

covZ2 <- round(getCov(Z2),1)
covZ13 <- round(getCov(Z13),1)
colnames(ZN) <- c("Cov. (standard)", "")
colnames(Z1) <- c("Cov. (obs. 1)", "")
colnames(Z2) <- c("Cov. (obs. 2)", "")
colnames(Z13) <- c("Cov. (obs. 13)", "")

kable(covZN, format = "latex", booktabs=TRUE,
      caption = "Cov. (standard)") %>% kable_styling(latex_options="HOLD_position")

```

Table 2: Cov. (standard)

132.2	112.5	110.0	103.7	94.3	75.5
112.5	130.9	109.4	103.3	94.0	75.5
110.0	109.4	126.2	101.5	92.9	75.9
103.7	103.3	101.5	116.0	90.2	76.7
94.3	94.0	92.9	90.2	105.1	77.9
75.5	75.5	75.9	76.7	77.9	99.4

```

kable(covZ1, format = "latex", booktabs=TRUE,
      caption = "Cov. (obs. 1)") %>% kable_styling(latex_options="HOLD_position")

```

Table 3: Cov. (obs. 1)

132.2	112.5	110.0	103.7	94.3	84.9
112.5	130.9	109.4	103.3	94.0	84.8
110.0	109.4	126.2	101.5	92.9	84.4
103.7	103.3	101.5	116.0	90.2	83.4
94.3	94.0	92.9	90.2	105.1	82.0
84.9	84.8	84.4	83.4	82.0	99.6

```

kable(covZ2, format = "latex", booktabs=TRUE,
      caption = "Cov. (obs. 2)") %>% kable_styling(latex_options="HOLD_position")

```

Table 4: Cov. (obs. 2)

132.2	112.5	110.0	103.7	99.3	75.5
112.5	130.9	109.4	103.3	99.0	75.5
110.0	109.4	126.2	101.5	97.5	75.9
103.7	103.3	101.5	116.0	93.8	76.7
99.3	99.0	97.5	93.8	110.2	77.3
75.5	75.5	75.9	76.7	77.3	99.4

```

kable(covZ13, format = "latex", booktabs=TRUE,
      caption = "Cov. (obs. 13)") %>% kable_styling(latex_options="HOLD_position")

```

Table 5: Cov. (obs. 13)

132.2	112.5	103.7	75.5
112.5	130.9	103.3	75.5
103.7	103.3	116.0	76.7
75.5	75.5	76.7	99.4

Task 2

```
## step one
coef.hr <- matrix(NA, ncol = 3, nrow = 0)
for (i in unique(hrunbalanced$id)) {
  model <- lm(hr~time, data = hrunbalanced, subset = id == i)
  model.drug <- unique(hrunbalanced[hrunbalanced$id == i, "drug"])
  coef.hr <- rbind(coef.hr, c(model.drug, coef(model)))
}
colnames(coef.hr) <- c("drug", "intercept", "slope")
coef.hr <- as.data.frame(coef.hr)
print(coef.hr)
```

```
##      drug intercept      slope
## 1      1  85.08455  0.078048780
## 2      1  84.80138 -0.066099604
## 3      1  70.78740  0.011492122
## 4      1  69.50324 -0.135310473
## 5      1 100.08156 -0.544949027
## 6      1  58.54853 -0.119740500
## 7      1  94.21909 -0.282113068
## 8      1  91.90646 -0.193141798
## 9      1  79.46728 -0.349582947
## 10     1  81.36336 -0.109731233
## 11     1  72.36206 -0.055607044
## 12     1  77.28650 -0.141612604
## 13     2  59.21327  0.094038623
## 14     2  87.84628 -0.063762743
## 15     2  86.53482 -0.118999073
## 16     2  83.98752 -0.098424467
## 17     2  95.09719 -0.149397590
## 18     2  97.64869 -0.107136237
## 19     2  87.35792 -0.073401297
## 20     2  92.06833 -0.183873957
## 21     2  80.93272 -0.050417053
## 22     2  92.79011 -0.006672845
## 23     2  92.85301 -0.154216867
## 24     2  82.25740 -0.356255792
```

```
## step two
hr.int <- lm(intercept~drug, data = coef.hr)
hr.slp <- lm(slope~drug, data=coef.hr)

sum.int <- summary(hr.int)
sum.slp <- summary(hr.slp)
```

```

sum.lme <- summary(fit.RandSlp)
print(sum.int)

##
## Call:
## lm(formula = intercept ~ drug, data = coef.hr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.3357  -4.6227   0.8607   6.2569  19.6306
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   74.353      7.055  10.539 4.61e-10 ***
## drug           6.098      4.462   1.367   0.186
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.93 on 22 degrees of freedom
## Multiple R-squared:  0.07825,    Adjusted R-squared:  0.03635
## F-statistic: 1.868 on 1 and 22 DF,  p-value: 0.1856
print(sum.slp)

##
## Call:
## lm(formula = slope ~ drug, data = coef.hr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.38592 -0.04489  0.02057  0.06470  0.23708
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.21235     0.09128  -2.326  0.0296 *
## drug          0.05332     0.05773   0.924  0.3657
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1414 on 22 degrees of freedom
## Multiple R-squared:  0.03732,    Adjusted R-squared: -0.006434
## F-statistic: 0.853 on 1 and 22 DF,  p-value: 0.3657
info.int <- round(sum.int$coefficients[,c(1,4)], 4)
info.slp <- round(sum.slp$coefficients[,c(1,4)], 4)
info.mixed <- round(summary(fit.RandSlp)$tTable[,c(1,5)], 4)

```

From above summaries we can clearly see that p-values for *drug* effect are greater than 0.05. Therefore, we conclude that neither the mean intercepts, nor the mean slopes differ significantly in the two groups.

Below we provide a table with coefficients' estimates and their p-values bot in Two-Stage and Mixed Effects analysis.

	Two-Stage	Mixed Effects
Intercept	74.353(0)	80.514(0)
Time	-0.2123(0.0296)	-0.1645(10^{-4})
Drug	6.098(0.1856)	6.0748(0.186)
Time*Drug	0.0533(0.3657)	0.0582(0.3041)

We can see that there are small differences both in estimates and the p-values when comparing these two models, however the interpretation didn't change - in both models only *time* and *intercept* are significant and they both indicate that the drug effect is not significant.