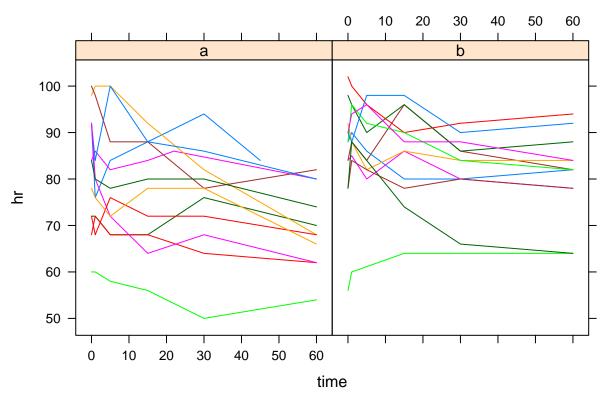
Complex Data - lab4

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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 :</pre>
```

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)</pre>
```

Task 1

```
coefs <- fit.RandSlp$coefficients$fixed
coefs <- matrix(c(coefs[1], coefs[3], coefs[2], coefs[4]), ncol = 1)</pre>
```

```
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, ones)
ZN <- cbind(ones,tN)
Z1 <- cbind(ones,t1)
Z2 <- cbind(ones, t2)
Z13 <- cbind(ones[1:4], t13)</pre>
```

Means:

Table 1: Means

Mean (drug A)	Mean (obs. 1)	Mean (obs. 2)	Mean (drug B)	Mean (obs. 13)
80.51400	80.51400	80.51400	86.64703	86.58879
80.34955	80.34955	80.34955	86.48257	86.48257
79.69173	79.69173	79.69173	85.82476	84.99553
78.04719	78.04719	78.04719	84.18022	80.21576
75.58038	75.58038	76.89601	81.71341	NA
70.64676	73.11357	70.64676	76.77979	NA

Covariances:

```
getCov <- function(Z){
    Z%*%covar%*%t(Z) + as.numeric(varCorr[3,1])*diag(1,nrow = dim(Z)[1], ncol = dim(Z)[1])
}
covZN <- getCov(ZN)
covZ1 <- getCov(Z1)
covZ2 <- getCov(Z2)
covZ13 <- getCov(Z13)
colnames(ZN) <- c("Cov. (standard)","")
colnames(Z1) <- c("Cov. (obs. 1)","")</pre>
```

Table 2: Cov. (standard)

132.15269	112.51142	109.99918	103.71859	94.29769	75.45591
112.51142	130.90842	109.43033	103.26816	94.02490	75.53839
109.99918	109.43033	126.16816	101.46645	92.93373	75.86828
103.71859	103.26816	101.46645	115.97541	90.20580	76.69301
94.29769	94.02490	92.93373	90.20580	105.12712	77.93011
75.45591	75.53839	75.86828	76.69301	77.93011	99.41753

Table 3: Cov. (obs. 1)

132.15269	112.51142	109.99918	103.71859	94.29769	84.87680
112.51142	130.90842	109.43033	103.26816	94.02490	84.78164
109.99918	109.43033	126.16816	101.46645	92.93373	84.40100
103.71859	103.26816	101.46645	115.97541	90.20580	83.44941
94.29769	94.02490	92.93373	90.20580	105.12712	82.02201
84.87680	84.78164	84.40100	83.44941	82.02201	99.60783

Table 4: Cov. (obs. 2)

132.15269	112.51142	109.99918	103.71859	99.32217	75.45591
112.51142	130.90842	109.43033	103.26816	98.95464	75.53839
109.99918	109.43033	126.16816	101.46645	97.48452	75.86828
103.71859	103.26816	101.46645	115.97541	93.80921	76.69301
99.32217	98.95464	97.48452	93.80921	110.24971	77.27033
75.45591	75.53839	75.86828	76.69301	77.27033	99.41753

Table 5: Cov. (obs. 13)

132.15269	112.51142	103.71859	75.45591
112.51142	130.90842	103.26816	75.53839
103.71859	103.26816	115.97541	76.69301
75.45591	75.53839	76.69301	99.41753

Task 2

```
## step one
coef.hr <- matrix(NA,ncol = 3, nrow = 0)</pre>
for (i in unique(hrunbalanced$id)) {
 model <- lm(hr~time, data = hrunbalanced, subset = id == i)</pre>
 model.drug <- unique(hrunbalanced[hrunbalanced$id == i, "drug"])</pre>
  coef.hr <- rbind(coef.hr, c(model.drug, coef(model)))</pre>
colnames(coef.hr) <- c("drug", "intercept", "slope")</pre>
coef.hr <- as.data.frame(coef.hr)</pre>
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
         1 79.46728 -0.349582947
## 9
## 10
         1 81.36336 -0.109731233
## 11
         1 72.36206 -0.055607044
## 12
         1 77.28650 -0.141612604
## 13
         2 59.21327 0.094038623
         2 87.84628 -0.063762743
## 14
## 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)</pre>
hr.slp <- lm(slope~drug, data=coef.hr)</pre>
sum.int <- summary(hr.int)</pre>
sum.slp <- summary(hr.slp)</pre>
```

```
sum.lme <- summary(fit.RandSlp)</pre>
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 ***
                 6.098
                                             0.186
                            4.462 1.367
## drug
## ---
## Signif. codes: 0 '***' 0.001 '**' 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
                 10
                     Median
                                   30
## -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)</pre>
info.mixed <- round(summary(fit.RandSlp)$tTable[,c(1,5)], 4)</pre>
```

	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)