Complex data - project

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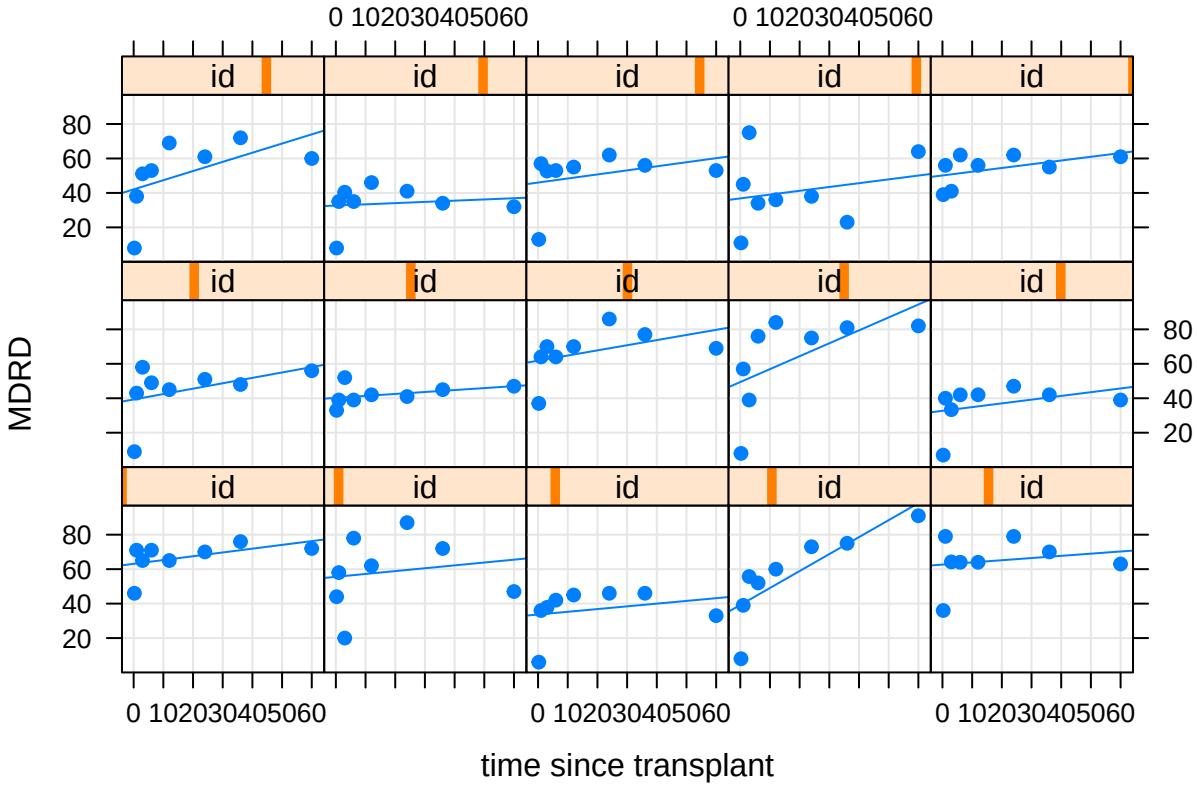
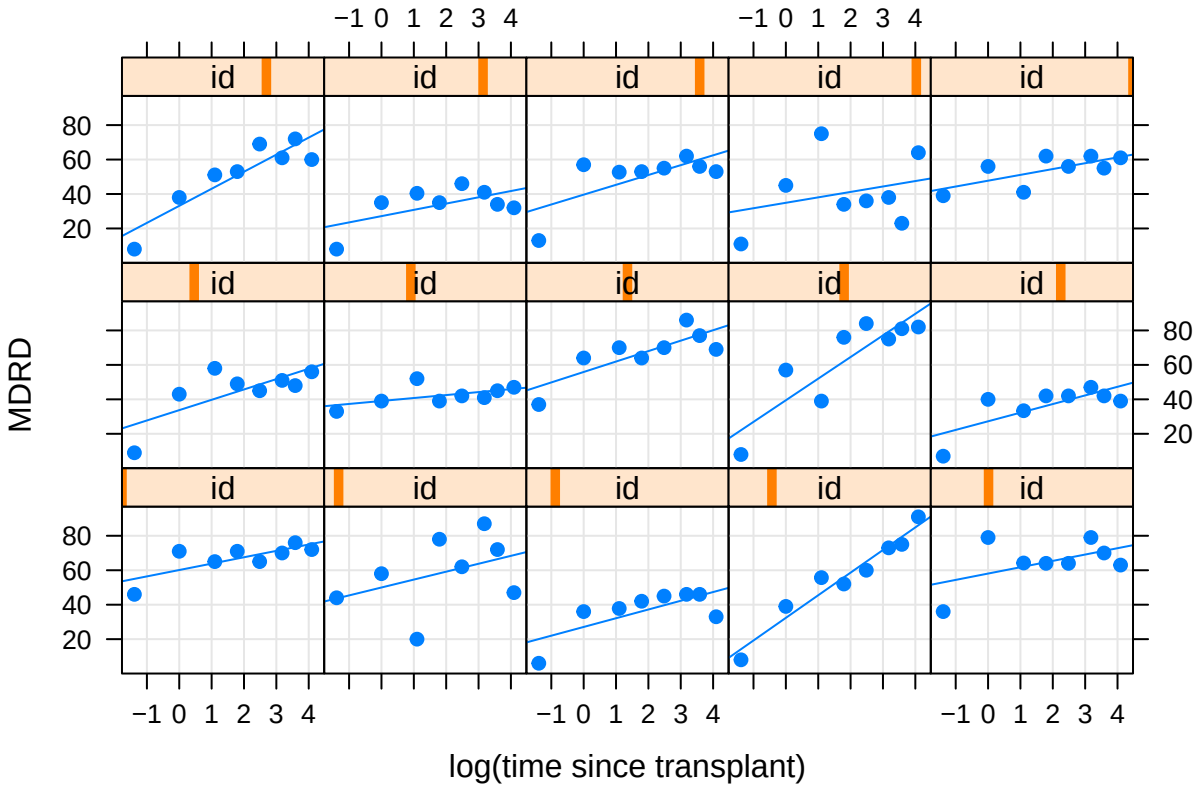
```
lkidney <- reshape(kidney, direction = "long", varying = list(9:16), v.names = c("MDRD"), times = c(1/4
lkidney$ltime <- log(lkidney$time)

lkidney.plot <- reshape(kidney[1:15,], direction = "long", varying = list(9:16), v.names = c("MDRD"), t
lkidney.plot$ltime <- log(lkidney.plot$time)

xyplot(MDRD ~ time | id, lkidney.plot, type=c("g","p","r"), xlab = "time since transplant", ylab = "MDR
```




```
xyplot(MDRD ~ ltime | id, lkidney.plot, type=c("g","p","r"), xlab = "log(time since transplant)", ylab =
```



Analiza bez efektów losowych (Stachu)

Analiza z efektami losowymi (Ania)

```
const.mixed.model <- lmer(MDRD~ltime+ (1|id),
                          data = lkidney, REML = FALSE)
summary(const.mixed.model)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: MDRD ~ ltime + (1 | id)
##    Data: lkidney
##
##      AIC      BIC   logLik deviance df.resid
##  22550.1  22573.7 -11271.1  22542.1     2668
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.7452 -0.4866  0.0206  0.5402  4.4121
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  id       (Intercept) 140.7    11.86
##  Residual             214.8    14.66
## Number of obs: 2672, groups:  id, 334
##
```

```
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  40.1081     0.7691   52.15
## ltime         4.5119     0.1614   27.95
##
## Correlation of Fixed Effects:
##       (Intr)
## ltime -0.390
```

```
lin.mixed.model <- lmer(MDRD~ltime+ (ltime|id),
                        data = lkidney, REML = FALSE)
print(summary(lin.mixed.model))
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: MDRD ~ ltime + (ltime | id)
##    Data: lkidney
##
##      AIC      BIC   logLik deviance df.resid
##  22445.1  22480.5 -11216.6  22433.1     2666
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.3317 -0.4637 -0.0046  0.4961  3.8846
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  id       (Intercept) 135.112  11.624
##           ltime         8.375   2.894   -0.16
##  Residual             185.263  13.611
## Number of obs: 2672, groups:  id, 334
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  40.1081     0.7425   54.02
## ltime         4.5119     0.2181   20.69
##
## Correlation of Fixed Effects:
##       (Intr)
## ltime -0.355
```

```
quadr.mixed.model <- lmer(MDRD~ltime + I(ltime^2) + (ltime + I(ltime^2)|id),
                        data = lkidney, REML = FALSE)
```

```
### nie dziala dla kwadratowego, bo nie zbiega odpowiednio szybko
#  quadr.mixed.model <- lme(MDRD~ltime + I(ltime^2),
#                           random = ~ltime + I(ltime^2)|factor(id),
#                           data = lkidney)
# summary(quadr.mixed.model)
```

```
anova(const.mixed.model,lin.mixed.model,quadr.mixed.model)
```

```
## Data: lkidney
## Models:
## const.mixed.model: MDRD ~ ltime + (1 | id)
## lin.mixed.model: MDRD ~ ltime + (ltime | id)
## quadr.mixed.model: MDRD ~ ltime + I(ltime^2) + (ltime + I(ltime^2) | id)
```

```
##                   Df   AIC   BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## const.mixed.model  4 22550 22574 -11271    22542
## lin.mixed.model    6 22445 22481 -11217    22433 108.96      2  < 2.2e-16
## quadr.mixed.model 10 22059 22118 -11020    22039 393.72      4  < 2.2e-16
##
## const.mixed.model
## lin.mixed.model   ***
## quadr.mixed.model ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
full.model <- lmer(MDRD~donor.age + recipient.age + therapy + diabetes + bpl.drugs + discrepancy.AB + di
summary(full.model)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## MDRD ~ donor.age + recipient.age + therapy + diabetes + bpl.drugs +
##     discrepancy.AB + discrepancy.DR + ltime + I(ltime^2) + (ltime +
##     I(ltime^2) | id)
##    Data: lkidney
##
##      AIC      BIC   logLik deviance df.resid
##  21983.1  22089.2 -10973.6  21947.1     2654
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.3697 -0.4479 -0.0326  0.4543  4.1356
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  id       (Intercept) 126.397  11.243
##           ltime        28.749   5.362   -0.01
##           I(ltime^2)    2.392   1.547   -0.25 -0.80
##  Residual             134.108  11.581
## Number of obs: 2672, groups:  id, 334
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)    68.80701    3.41005  20.178
## donor.age      -0.30158    0.05014  -6.015
## recipient.age  -0.14409    0.05866  -2.456
## therapycm      -1.41613    1.56778  -0.903
## therapytc      -4.75645    1.47247  -3.230
## diabetes        2.76100    1.48430   1.860
## bpl.drugs      -2.14935    0.54826  -3.920
## discrepancy.AB -0.79371    0.71056  -1.117
## discrepancy.DR -0.38099    1.15298  -0.330
## ltime           8.86844    0.38998  22.741
## I(ltime^2)     -1.54412    0.11580 -13.335
##
## Correlation of Fixed Effects:
##             (Intr) donr.g rcpnt. thrpyc thrpyt diabts bpl.dr dsc.AB dsc.DR
## donor.age   -0.331
## recipient.g -0.573 -0.219
## therapycm   -0.132 -0.145  0.114
```

```
## therapytc   -0.077 -0.268  0.135  0.399
## diabetes     0.139 -0.015 -0.244 -0.027 -0.004
## bpl.drugs   -0.231 -0.106 -0.065 -0.046 -0.104 -0.100
## dscrpncy.AB -0.399 -0.076  0.009 -0.002  0.046  0.004 -0.062
## dscrpncy.DR -0.264  0.010  0.023 -0.004 -0.069 -0.086  0.140 -0.058
## ltime       -0.007  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## I(ltime^2)  -0.053  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
##             ltime
## donor.age
## recipient.g
## therapycm
## therapytc
## diabetes
## bpl.drugs
## dscrpncy.AB
## dscrpncy.DR
## ltime
## I(ltime^2)  -0.829
```

```
anova(full.model)
```

```
## Analysis of Variance Table
##                 Df Sum Sq Mean Sq  F value
## donor.age        1   9696    9696  72.3003
## recipient.age    1    536     536   4.0003
## therapy          2   1736     868   6.4719
## diabetes         1    297     297   2.2152
## bpl.drugs        1   2124    2124  15.8391
## discrepancy.AB   1    174     174   1.2953
## discrepancy.DR   1     15      15   0.1092
## ltime            1  58576   58576 436.7797
## I(ltime^2)       1  23846   23846 177.8114
```