

SD2 - løsning til case 6

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Dette dokument indeholder supplerende kommentarer til filen **casesol6.pdf** og vedrører løsningen af case 6 lavet torsdag d. 16. marts 2017 i forbindelse med løsningen af case 6.

1. Indlæsning af data

```
data <- read.table(file = "../data/case6.txt", header = T)
head(data)
```

```
##   rotte uge    beh    vgt
## 1     1   1 Kontrol 4.0431
## 2     2   1 Kontrol 4.0943
## 3     3   1 Kontrol 3.9512
## 4     4   1 Kontrol 3.8918
## 5     5   1 Kontrol 4.0254
## 6     6   1 Kontrol 3.8286
```

```
data$rotte <- factor(data$rotte)
data$ugefac <- factor(data$uge)
```

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 3.3.2
```

```
## Loading tidyverse: ggplot2
## Loading tidyverse: tibble
## Loading tidyverse: tidyr
## Loading tidyverse: readr
## Loading tidyverse: purrr
## Loading tidyverse: dplyr
```

```
## Warning: package 'ggplot2' was built under R version 3.3.2
```

```
## Warning: package 'tibble' was built under R version 3.3.2
```

```
## Warning: package 'tidyr' was built under R version 3.3.2
```

```
## Warning: package 'readr' was built under R version 3.3.2
```

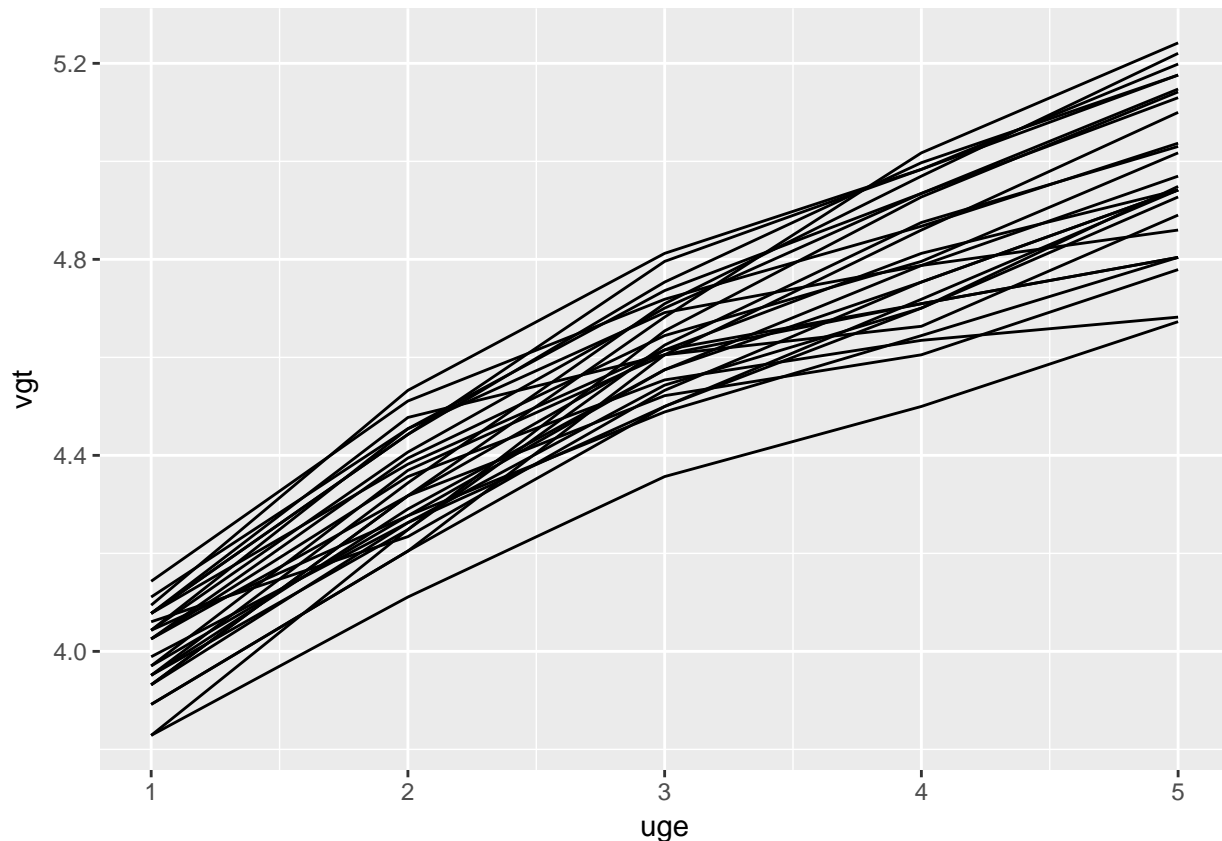
```
## Warning: package 'purrr' was built under R version 3.3.2
```

```
## Warning: package 'dplyr' was built under R version 3.3.2
```

```
## Conflicts with tidy packages -----
```

```
## filter(): dplyr, stats
## lag():    dplyr, stats
```

```
ggplot(data = data) + geom_line(aes(x = uge, y = vgt, group = rotte))
```



4.-5. Digglemodel

```
library(nlme)

## Warning: package 'nlme' was built under R version 3.3.2
##
## Attaching package: 'nlme'
## The following object is masked from 'package:dplyr':
##
## collapse
model0 <- lme(vgt ~ beh * ugefac, random = ~ 1 | rotte, data = data
, corr = corGaus(form = ~ uge | rotte, nugget = T), method = "ML")
```

7. Sammenligning af kontrol- og thyroxinrotter

Vi benytter en fremgangsmåde, hvor vi konstruerer en *ny* behandlingsfaktor med kun 2 niveauer, hvor rotter som har modtaget **kontrol**- og **thyroxin**-behandling kommer i samme grupper. Forskellige løsningsmetoder er angivet.

Løsning som anført i *hint*

```
data$nybeh <- rep(1, 135)
data$nybeh[data$beh == "Thiouracil"] = 2
data$nybeh <- factor(data$nybeh)
table(data$beh, data$nybeh)
```

```
##
##           1  2
## Kontrol    50  0
## Thiouracil  0 50
## Thyroxin   35  0
```

Løsning, der benytter samme ide som i *hint*, men hvor niveauerne kaldes TRUE og FALSE

```
data$nybeh2 <- (data$beh == "Thiouracil")
table(data$beh, data$nybeh2)
```

```
##
##           FALSE TRUE
## Kontrol      50    0
## Thiouracil   0   50
## Thyroxin     35    0
```

Løsning, hvor niveauerne af behandlingsfaktoren ændres manuelt

```
data$nybeh3 <- factor(data$beh)
levels(data$nybeh3)
```

```
## [1] "Kontrol"    "Thiouracil" "Thyroxin"
levels(data$nybeh3) <- c("KonThy", "Thiouracil", "KonThy")
table(data$beh, data$nybeh3)
```

```
##
##           KonThy Thiouracil
## Kontrol      50          0
## Thiouracil   0          50
## Thyroxin     35          0
```

Test for om grupperne **Kontrol** og **Thyroxin** kan slås sammen

```
modelny <- lme(vgt ~ nybeh3 * ugefac, random = ~ 1 | rotte, data = data
, corr = corGaus(form = ~ uge | rotte, nugget = T), method = "ML")
anova(modelny, model0)
```

```
##           Model df          AIC          BIC   logLik   Test  L.Ratio p-value
## modelny       1 14 -380.6785 -340.0046 204.3392
## model0        2 19 -380.5067 -325.3065 209.2533 1 vs 2 9.828194 0.0803
```

8. Forskelle til hver af de enkelte uger

Med lidt snilde kan man få R til en anvende en parametrisering af modellen **modelny** fra spørgsmål 7., så man direkte kan aflæse forskelle mellem grupperne til hver af de 5 uger. Bemærk i øvrigt, at modellen genfittes med **method == "REML"**.

```
modelny_refit <- lme(vgt ~ ugefac + nybeh3 : ugefac - 1, random = ~ 1 | rotte, data = data
, corr = corGaus(form = ~ uge | rotte, nugget = T), method = "REML")
summary(modelny_refit)
```

```

## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
##   -315.1069 -275.5105 171.5534
##
## Random effects:
## Formula: ~1 | rotte
##      (Intercept)  Residual
## StdDev:  0.05764853 0.07629465
##
## Correlation Structure: Gaussian spatial correlation
## Formula: ~uge | rotte
## Parameter estimate(s):
##      range      nugget
## 2.09802710 0.05500271
## Fixed effects: vgt ~ ugefac + nybeh3:ugefac - 1
##
##              Value Std.Error DF   t-value p-value
## ugefac1          3.997594 0.02319258 99 172.36522 0.0000
## ugefac2          4.343800 0.02319258 99 187.29267 0.0000
## ugefac3          4.654665 0.02319258 99 200.69630 0.0000
## ugefac4          4.870982 0.02319258 99 210.02331 0.0000
## ugefac5          5.079153 0.02319258 99 218.99906 0.0000
## ugefac1:nybeh3Thiouracil 0.000856 0.03810930 99   0.02246 0.9821
## ugefac2:nybeh3Thiouracil -0.014160 0.03810930 99  -0.37156 0.7110
## ugefac3:nybeh3Thiouracil -0.096115 0.03810930 99  -2.52208 0.0133
## ugefac4:nybeh3Thiouracil -0.189002 0.03810930 99  -4.95948 0.0000
## ugefac5:nybeh3Thiouracil -0.261223 0.03810930 99  -6.85457 0.0000
## Correlation:
##              ugefc1 ugefc2 ugefc3 ugefc4 ugefc5 ug1:3T ug2:3T
## ugefac2          0.843
## ugefac3          0.606 0.843
## ugefac4          0.441 0.606 0.843
## ugefac5          0.379 0.441 0.606 0.843
## ugefac1:nybeh3Thiouracil -0.609 -0.513 -0.369 -0.269 -0.231
## ugefac2:nybeh3Thiouracil -0.513 -0.609 -0.513 -0.369 -0.269 0.843
## ugefac3:nybeh3Thiouracil -0.369 -0.513 -0.609 -0.513 -0.369 0.606 0.843
## ugefac4:nybeh3Thiouracil -0.269 -0.369 -0.513 -0.609 -0.513 0.441 0.606
## ugefac5:nybeh3Thiouracil -0.231 -0.269 -0.369 -0.513 -0.609 0.379 0.441
##              ug3:3T ug4:3T
## ugefac2
## ugefac3
## ugefac4
## ugefac5
## ugefac1:nybeh3Thiouracil
## ugefac2:nybeh3Thiouracil
## ugefac3:nybeh3Thiouracil
## ugefac4:nybeh3Thiouracil 0.843
## ugefac5:nybeh3Thiouracil 0.606 0.843
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.77411498 -0.68094670 0.09841366 0.65444214 1.81956919
##
## Number of Observations: 135

```

```
## Number of Groups: 27
```

Heraf aflæses direkte, at **Thiouracil**-rotterne først ligger signifikant under rotter fra de øvrige to behandlingsgrupper fra uge 3 (-se på p-værdier for det relevante test).

8.-9. Løsning ved brug af estimable()

Neden for benyttes estimable til at besvare de spørgsmål der ønskes besvaret under punkt 8. og 9. Her benyttes ikke en *smart* parametrisering af modellerne.

```
modelny_refit2 <- lme(vgt ~ nybeh3 * ugefac, random = ~ 1 | rotte, data = data
, corr = corGaus(form = ~ uge | rotte, nugget = T), method = "REML")
summary(modelny_refit2)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC   logLik
## -315.1069 -275.5105 171.5534
##
## Random effects:
## Formula: ~1 | rotte
##      (Intercept)   Residual
## StdDev:  0.05764853 0.07629465
##
## Correlation Structure: Gaussian spatial correlation
## Formula: ~uge | rotte
## Parameter estimate(s):
##      range      nugget
## 2.09802710 0.05500271
## Fixed effects: vgt ~ nybeh3 * ugefac
##
##              Value Std.Error DF   t-value p-value
## (Intercept)      3.997594 0.02319258 100 172.36522 0.0000
## nybeh3Thiouracil      0.000856 0.03810930 25  0.02246 0.9823
## ugefac2      0.346206 0.01300701 100 26.61686 0.0000
## ugefac3      0.657071 0.02059099 100 31.91059 0.0000
## ugefac4      0.873388 0.02451637 100 35.62469 0.0000
## ugefac5      1.081559 0.02584054 100 41.85511 0.0000
## nybeh3Thiouracil:ugefac2 -0.015016 0.02137270 100 -0.70257 0.4840
## nybeh3Thiouracil:ugefac3 -0.096971 0.03383445 100 -2.86603 0.0051
## nybeh3Thiouracil:ugefac4 -0.189858 0.04028451 100 -4.71293 0.0000
## nybeh3Thiouracil:ugefac5 -0.262079 0.04246034 100 -6.17232 0.0000
## Correlation:
##              (Intr) nybh3T ugefc2 ugefc3 ugefc4 ugefc5 ny3T:2
## nybeh3Thiouracil      -0.609
## ugefac2      -0.280  0.171
## ugefac3      -0.444  0.270  0.792
## ugefac4      -0.529  0.322  0.543  0.848
## ugefac5      -0.557  0.339  0.351  0.627  0.868
## nybeh3Thiouracil:ugefac2  0.171 -0.280 -0.609 -0.482 -0.330 -0.214
## nybeh3Thiouracil:ugefac3  0.270 -0.444 -0.482 -0.609 -0.516 -0.382  0.792
## nybeh3Thiouracil:ugefac4  0.322 -0.529 -0.330 -0.516 -0.609 -0.528  0.543
## nybeh3Thiouracil:ugefac5  0.339 -0.557 -0.214 -0.382 -0.528 -0.609  0.351
##              ny3T:3 ny3T:4
## nybeh3Thiouracil
```

```

## ugefac2
## ugefac3
## ugefac4
## ugefac5
## nybeh3Thiouracil:ugefac2
## nybeh3Thiouracil:ugefac3
## nybeh3Thiouracil:ugefac4 0.848
## nybeh3Thiouracil:ugefac5 0.627 0.868
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.77411499 -0.68094671 0.09841366 0.65444213 1.81956919
##
## Number of Observations: 135
## Number of Groups: 27

thi1 <- c(1, 1, 0, 0, 0, 0, 0, 0, 0, 0)
thi2 <- c(1, 1, 1, 0, 0, 0, 1, 0, 0, 0)
thi3 <- c(1, 1, 0, 1, 0, 0, 0, 1, 0, 0)
thi4 <- c(1, 1, 0, 0, 1, 0, 0, 0, 1, 0)
thi5 <- c(1, 1, 0, 0, 0, 1, 0, 0, 0, 1)
kon1 <- c(1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
kon2 <- c(1, 0, 1, 0, 0, 0, 0, 0, 0, 0)
kon3 <- c(1, 0, 0, 1, 0, 0, 0, 0, 0, 0)
kon4 <- c(1, 0, 0, 0, 1, 0, 0, 0, 0, 0)
kon5 <- c(1, 0, 0, 0, 0, 1, 0, 0, 0, 0)
diff1 <- kon1 - thi1
diff2 <- kon2 - thi2
diff3 <- kon3 - thi3
diff4 <- kon4 - thi4
diff5 <- kon5 - thi5
kon_incr1_5 <- kon5 - kon1
thi_incr1_5 <- thi5 - thi1
diff_incr1_5 <- kon_incr1_5 - thi_incr1_5

est <- rbind(kon1, kon2, kon3, kon4, kon5
             , thi1, thi2, thi3, thi4, thi5
             , diff1, diff2, diff3, diff4, diff5
             , kon_incr1_5, thi_incr1_5, diff_incr1_5)
library(gmodels)
estimable(modelny_refit2, est, conf.int = 0.95)

## Warning in estimable.default(modelny_refit2, est, conf.int = 0.95): Degrees
## of freedom vary among parameters used to construct linear contrast(s):
## 6, 7, 8, 9, 10, 12, 13, 14, 15. Using the smallest df among the set of
## parameters.

##      Estimate Std. Error    t value  DF    Pr(>|t|)
## kon1      3.9975941176 0.02319258 172.36522463 100 0.000000e+00
## kon2      4.3438000000 0.02319258 187.29266672 100 0.000000e+00
## kon3      4.6546647059 0.02319258 200.69629482 100 0.000000e+00
## kon4      4.8709823529 0.02319258 210.02331470 100 0.000000e+00
## kon5      5.0791529412 0.02319258 218.99905590 100 0.000000e+00
## thi1      3.9984500000 0.03023942 132.22639611  25 0.000000e+00
## thi2      4.3296400000 0.03023942 143.17865514  25 0.000000e+00

```

```
## thi3      4.5585500000 0.03023942 150.74857457 25 0.000000e+00
## thi4      4.6819800000 0.03023942 154.83033227 25 0.000000e+00
## thi5      4.8179300000 0.03023942 159.32611903 25 0.000000e+00
## diff1     -0.0008558824 0.03810930 -0.02245862 25 9.822604e-01
## diff2      0.0141600000 0.03810930  0.37156288 25 7.133489e-01
## diff3      0.0961147059 0.03810930  2.52208031 25 1.840595e-02
## diff4      0.1890023529 0.03810930  4.95948157 25 4.139146e-05
## diff5      0.2612229412 0.03810930  6.85457267 25 3.481617e-07
## kon_incr1_5 1.0815588235 0.02584054 41.85511323 100 0.000000e+00
## thi_incr1_5 0.8194800000 0.03369195 24.32272752 100 0.000000e+00
## diff_incr1_5 0.2620788235 0.04246034  6.17231988 100 1.447625e-08
##           Lower.CI  Upper.CI
## kon1      3.95158070 4.04360753
## kon2      4.29778658 4.38981342
## kon3      4.60865129 4.70067812
## kon4      4.82496894 4.91699577
## kon5      5.03313952 5.12516636
## thi1      3.93617074 4.06072926
## thi2      4.26736074 4.39191926
## thi3      4.49627074 4.62082926
## thi4      4.61970074 4.74425926
## thi5      4.75565074 4.88020926
## diff1     -0.07934345 0.07763168
## diff2     -0.06432757 0.09264757
## diff3      0.01762714 0.17460227
## diff4      0.11051479 0.26748992
## diff5      0.18273538 0.33971051
## kon_incr1_5 1.03029192 1.13282572
## thi_incr1_5 0.75263614 0.88632386
## diff_incr1_5 0.17783871 0.34631894
```

10.

```
head(data)
```

```
##   rotte uge    beh    vgt ugefac nybeh nybeh2 nybeh3
## 1     1   1 Kontrol 4.0431      1     1 FALSE KonThy
## 2     2   1 Kontrol 4.0943      1     1 FALSE KonThy
## 3     3   1 Kontrol 3.9512      1     1 FALSE KonThy
## 4     4   1 Kontrol 3.8918      1     1 FALSE KonThy
## 5     5   1 Kontrol 4.0254      1     1 FALSE KonThy
## 6     6   1 Kontrol 3.8286      1     1 FALSE KonThy
```

```
data1 <- subset(data, uge == 1)
head(data1)
```

```
##   rotte uge    beh    vgt ugefac nybeh nybeh2 nybeh3
## 1     1   1 Kontrol 4.0431      1     1 FALSE KonThy
## 2     2   1 Kontrol 4.0943      1     1 FALSE KonThy
## 3     3   1 Kontrol 3.9512      1     1 FALSE KonThy
## 4     4   1 Kontrol 3.8918      1     1 FALSE KonThy
## 5     5   1 Kontrol 4.0254      1     1 FALSE KonThy
## 6     6   1 Kontrol 3.8286      1     1 FALSE KonThy
```

```
data5 <- subset(data, uge == 5)
head(data5)
```

```
##      rotte uge      beh      vgt ugefac nybeh nybeh2 nybeh3
## 109      1   5 Kontrol 5.1475      5      1 FALSE KonThy
## 110      2   5 Kontrol 5.1761      5      1 FALSE KonThy
## 111      3   5 Kontrol 5.2204      5      1 FALSE KonThy
## 112      4   5 Kontrol 5.0999      5      1 FALSE KonThy
## 113      5   5 Kontrol 5.0173      5      1 FALSE KonThy
## 114      6   5 Kontrol 5.0304      5      1 FALSE KonThy
```

```
data1$vg5 <- data5$vg5
data1$incr15 <- data1$vg5 - data1$vg
```

```
m1 <- lm(incr15 ~ beh, data = data1)
summary(m1)
```

```
##
## Call:
## lm(formula = incr15 ~ beh, data = data1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.19657 -0.08570  0.01393  0.08112  0.19032
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.09047    0.03523  30.951 < 2e-16 ***
## behThiouracil -0.27099    0.04983  -5.439 1.37e-05 ***
## behThyroxin   -0.02164    0.05490  -0.394  0.697
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1114 on 24 degrees of freedom
## Multiple R-squared:  0.5932, Adjusted R-squared:  0.5593
## F-statistic: 17.5 on 2 and 24 DF, p-value: 2.055e-05
```

```
m2 <- lm(incr15 ~ (beh == "Thiouracil"), data = data1)
summary(m2)
```

```
##
## Call:
## lm(formula = incr15 ~ (beh == "Thiouracil"), data = data1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.18766 -0.09041  0.01422  0.08112  0.19032
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.08156    0.02656  40.720 < 2e-16 ***
## beh == "Thiouracil"TRUE -0.26208    0.04364  -6.005 2.85e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```



```
## Residual standard error: 0.1095 on 25 degrees of freedom
## Multiple R-squared:  0.5906, Adjusted R-squared:  0.5742
## F-statistic: 36.06 on 1 and 25 DF,  p-value: 2.85e-06
```