

HS 16

vi indlæser data

```
pillbug <- read_table2("../pillbug.txt")
```

```
## Parsed with column specification:
## cols(
##   time = col_double(),
##   group = col_character()
## )
```

1

Eksperimentet lægger op til en etsidet variansanalyse, da vi kun undersøger en faktor, nemlig tid. De enkelte X'ier (bækebiderne) er uafhængige, og normalfordelte.

```
A <- model.matrix(~ pillbug$group -1)
A
```

```
##   pillbug$groupControl pillbug$groupLight pillbug$groupMoisture
## 1                    0                    1                    0
## 2                    0                    1                    0
## 3                    0                    1                    0
## 4                    0                    1                    0
## 5                    0                    1                    0
## 6                    0                    1                    0
## 7                    0                    1                    0
## 8                    0                    1                    0
## 9                    0                    1                    0
## 10                   0                    1                    0
## 11                   0                    1                    0
## 12                   0                    1                    0
## 13                   0                    1                    0
## 14                   0                    1                    0
## 15                   0                    1                    0
## 16                   0                    1                    0
## 17                   0                    1                    0
## 18                   0                    1                    0
## 19                   0                    1                    0
## 20                   0                    1                    0
## 21                   0                    0                    1
## 22                   0                    0                    1
## 23                   0                    0                    1
## 24                   0                    0                    1
## 25                   0                    0                    1
```

```

## 26          0          0          1
## 27          0          0          1
## 28          0          0          1
## 29          0          0          1
## 30          0          0          1
## 31          0          0          1
## 32          0          0          1
## 33          0          0          1
## 34          0          0          1
## 35          0          0          1
## 36          0          0          1
## 37          0          0          1
## 38          0          0          1
## 39          0          0          1
## 40          0          0          1
## 41          1          0          0
## 42          1          0          0
## 43          1          0          0
## 44          1          0          0
## 45          1          0          0
## 46          1          0          0
## 47          1          0          0
## 48          1          0          0
## 49          1          0          0
## 50          1          0          0
## 51          1          0          0
## 52          1          0          0
## 53          1          0          0
## 54          1          0          0
## 55          1          0          0
## 56          1          0          0
## 57          1          0          0
## 58          1          0          0
## 59          1          0          0
## 60          1          0          0
## attr("assign")
## [1] 1 1 1
## attr("contrasts")
## attr("contrasts")$'pillbug$group'
## [1] "contr.treatment"

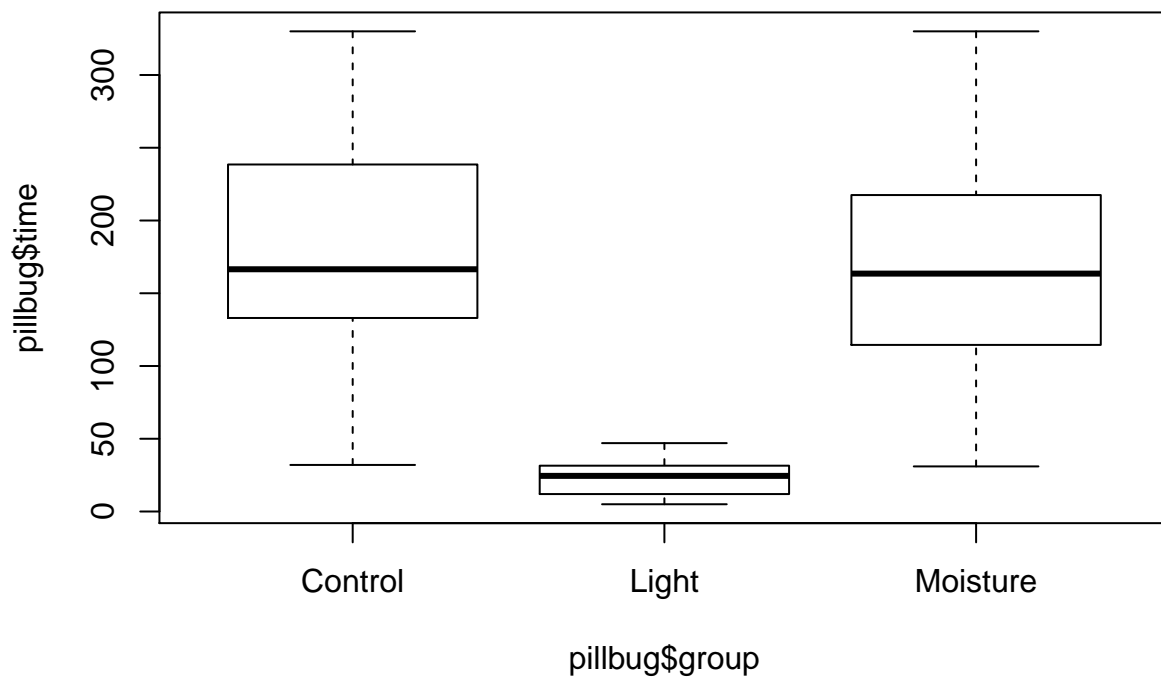
```

```
?model.matrix #finde ud af hvilke parametre der skal indgår i kommandoen
```

```
## starting httpd help server ... done
```

2

```
boxplot(pillbug$time ~ pillbug$group)
```

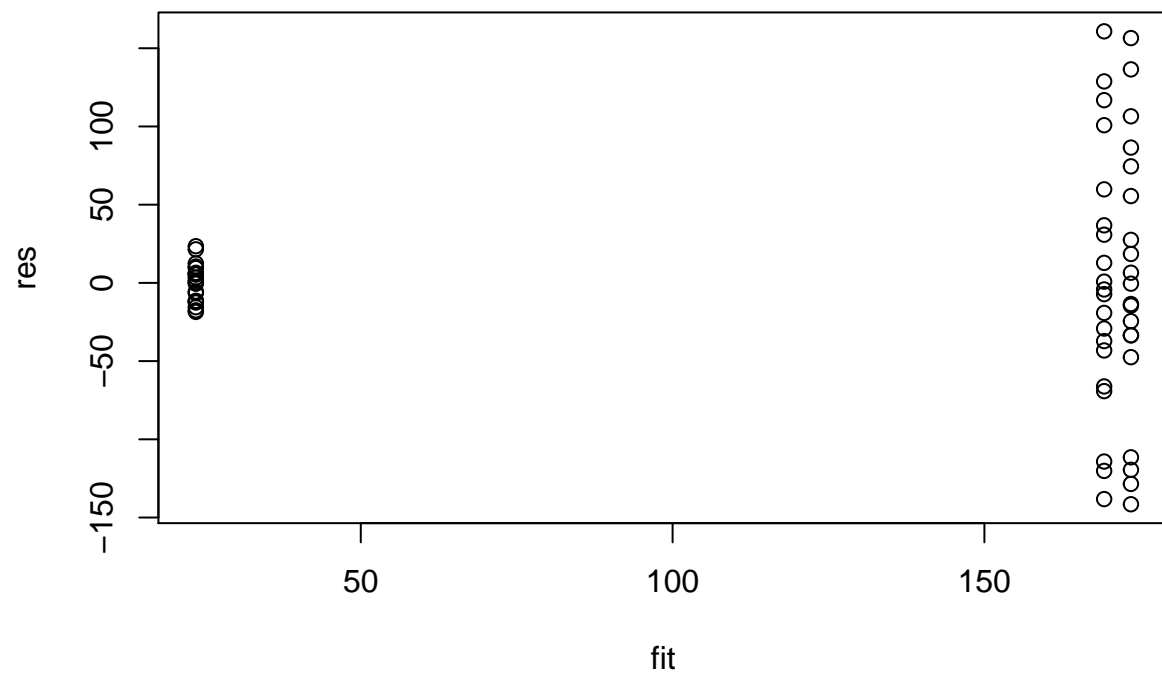


Vi ser at den mindste observerede værdi ligger knapt under 50 for kontrolgruppen...

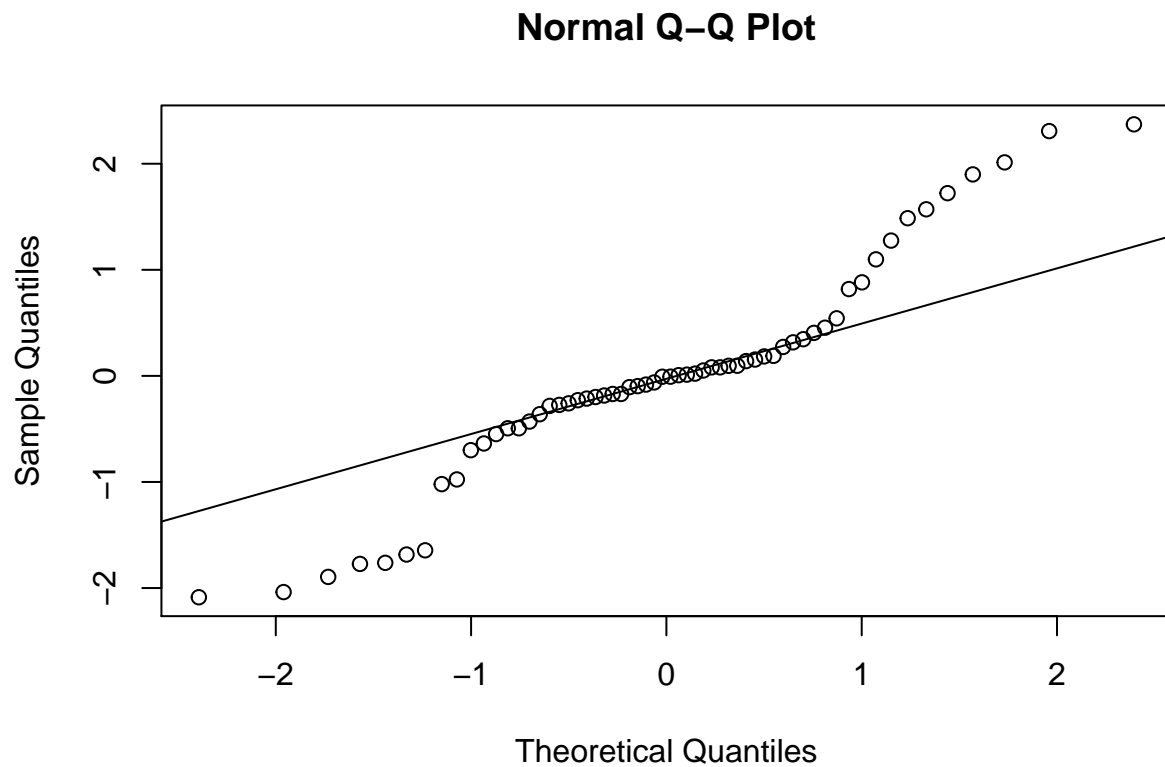
vi fitter modellen, for et sidet variansanalyse;

```
lm <- lm(pillbug$time ~ pillbug$group)
fit <- fitted(lm)
res <- residuals(lm)
rstad <- rstandard(lm)

plot(fit, res)
```



```
qqnorm(rstad)  
qqline(rstad)
```



vi finder at der ikke er varians homogenitet, da observationerne på venstre side har mindre varians end de to på højre siden (punkternes-linjes højde)

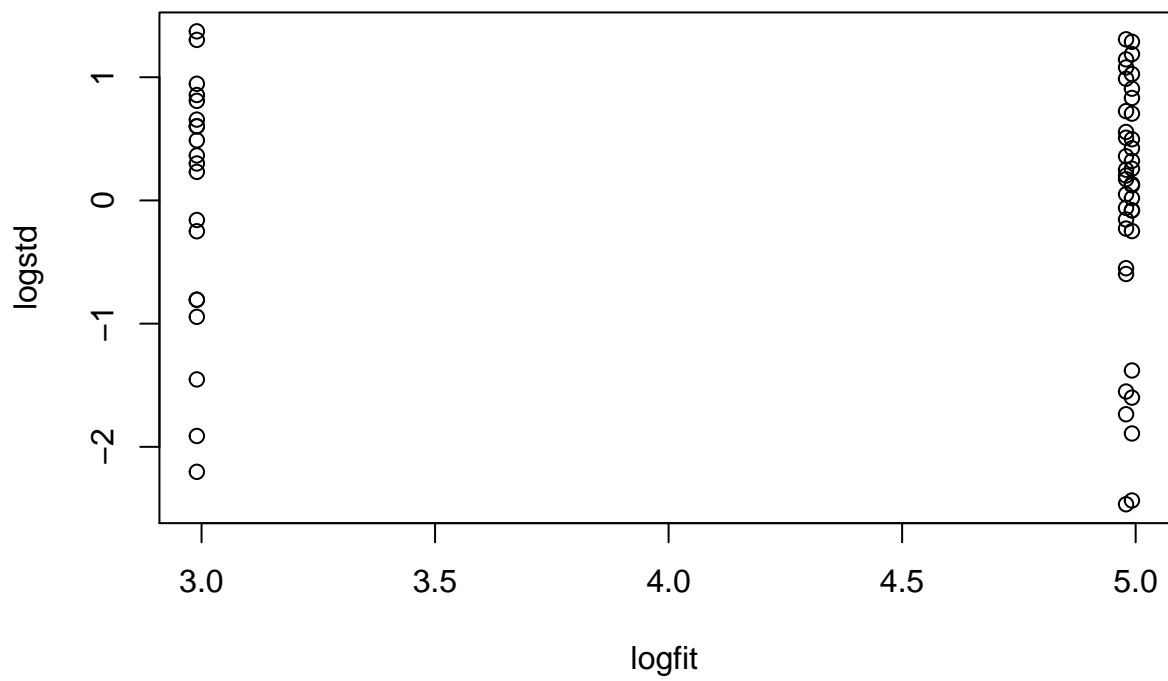
3

```
logtime <- log(pillbug$time)
```

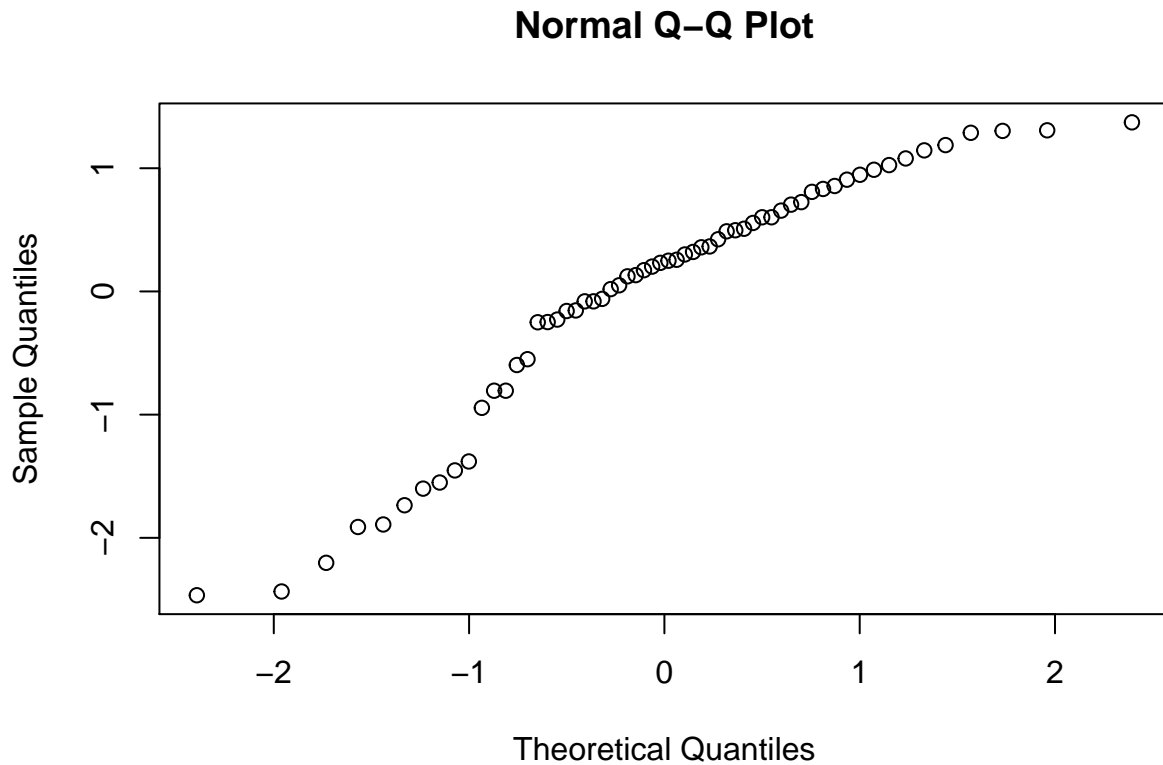
vi gentager

```
loglm <- lm(logtime~pillbug$group)
logfit <- fitted(loglm)
logstd <- rstandard(loglm)

plot(logfit, logstd)
```



```
qqnorm(logstd)
```



modellen ser mere fornuftigt ud.

det hjælper at log transformere, da

4

hypotesen er at middelværdien i de tre grupper er ens, vi bruger $\log(\text{tid})$, da vi i de forgående spørgsmål fandt at den opfylder varianshomogenitet og normalfordelingsantagelsen.

```
logModel0 <- lm(logtime ~ 1)
summary(logModel0)
```

```
##
## Call:
## lm(formula = logtime ~ 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7110 -0.8947  0.5158  0.8969  1.4786
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.3205     0.1472   29.36  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 1.14 on 59 degrees of freedom
```

```
anova(logModel0, loglm)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Model 1: logtime ~ 1
```

```
## Model 2: logtime ~ pillbug$group
```

```
##   Res.Df    RSS Df Sum of Sq    F    Pr(>F)
```

```
## 1      59 76.677
```

```
## 2      57 23.567  2    53.11 64.227 2.498e-15 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```