

Dexastudiet

PS

2023-10-03

Setup

```
##  
## Vedhæfter pakke: 'Hmisc'  
  
## De følgende objekter er maskerede fra 'package:base':  
##  
##     format.pval, units
```

Loading af pakker

Læs mere om pakkerne på CRAN, Google, etc.

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --  
## v dplyr      1.1.3      v readr      2.1.4  
## v forcats    1.0.0      v stringr   1.5.0  
## v ggplot2    3.4.3      v tibble    3.2.1  
## v lubridate  1.9.2      v tidyr     1.3.0  
## v purrr      1.0.2  
## -- Conflicts ----- tidyverse_conflicts() --  
## x dplyr::between()      masks data.table::between()  
## x dplyr::filter()       masks stats::filter()  
## x dplyr::first()        masks data.table::first()  
## x lubridate::hour()     masks data.table::hour()  
## x lubridate::isoweek()  masks data.table::isoweek()  
## x dplyr::lag()          masks stats::lag()  
## x dplyr::last()         masks data.table::last()  
## x lubridate::mday()     masks data.table::mday()  
## x lubridate::minute()   masks data.table::minute()  
## x lubridate::month()    masks data.table::month()  
## x lubridate::quarter()  masks data.table::quarter()  
## x lubridate::second()   masks data.table::second()  
## x dplyr::src()          masks Hmisc::src()  
## x dplyr::summarize()     masks Hmisc::summarize()  
## x purrr::transpose()    masks data.table::transpose()  
## x lubridate::wday()     masks data.table::wday()  
## x lubridate::week()     masks data.table::week()  
## x lubridate::yday()     masks data.table::yday()  
## x lubridate::year()     masks data.table::year()  
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
## Indlæser krævet pakke: prodlim
##
##
## Vedhæfter pakke: 'cowplot'
##
##
## Det følgende objekt er maskeret fra 'package:lubridate':
##
##     stamp
##
##
## Vedhæfter pakke: 'DescTools'
##
##
## Det følgende objekt er maskeret fra 'package:data.table':
##
##     %like%
##
##
## De følgende objekter er maskerede fra 'package:Hmisc':
##
##     %nin%, Label, Mean, Quantile
```

Loading af data

Data er udtrækket fra redcap. Først køres en separat fil fra RedCap der importerer data og sætte den op. Herefter skal data loades og sorteres så den bliver nemmer at arbejde med (små bogstaver i alle variable) samt patienterne skal sorteres i grupper.

```
patientdata <- setDT(data)
patientdata <- patientdata %>%
  rename_all(tolower)

#Fjerner ekskluderede patienter:
patientdata <- patientdata %>%
  filter(patientdata$pt_ekskluderet ==0)

#Grupperer alle patienter i 0(kontrol gruppen), 1(dexa gruppen) og 2(mellem gruppen)
patientdata$group <- ifelse(patientdata$record_id<33,0,ifelse(patientdata$record_id>55,1,2))

#Fjerner patienter fra mellemgruppen:
patientdata <- patientdata %>%
  filter(patientdata$group<2)
```

Herefter har vi den rigtige population tilbage, 37 patienter i alt, 20 i kontrol gruppen og 17 i dexa gruppen.

Data kurering

Nogle variable er tekst. Disse konverteres til tal, så vi kan lave beregninger på dem.

```

patientdata$pn_morfin_1 <- as.numeric(patientdata$pn_morfin_1)
patientdata$administreret_pn_morfin_iv_1 <- as.numeric(patientdata$administreret_pn_morfin_iv_1)
patientdata$record_id <- as.numeric(patientdata$record_id)
patientdata$tid_fuld_mob <- as.numeric(patientdata$tid_fuld_mob)
patientdata$patientdata$vas_mob_1 <- as.numeric(patientdata$patientdata$vas_mob_1)

```

Derudover laves nogle af tiderne til det rigtige format

```

patientdata$tid_til_dr_nfjernelse <- as.POSIXct(patientdata$tid_til_dr_nfjernelse, format = "%Y-%m-%d %H:%M", tz = "CET")
patientdata$knivtid_slut <- as.POSIXct(patientdata$knivtid_slut, format = "%Y-%m-%d %H:%M", tz = "CET")
patientdata$tid_smertegennebrud <- as.POSIXct(patientdata$tid_smertegennebrud, format = "%Y-%m-%d %H:%M", tz = "CET")

```

Ikke mobiliserede patienter laves fra vas 11 om til NA

```

patientdata$vas_mob_1 <- ifelse(patientdata$vas_mob_1==11,NA,patientdata$vas_mob_1)
patientdata$vas_mob_1_2 <- ifelse(patientdata$vas_mob_1_2==11,NA,patientdata$vas_mob_1_2)

```

Beregning af variable

MME

Først laves missing om til 0 for alle opioiderne. Dette for at kunne regne med dem.

```

patientdata <- patientdata %>%
  mutate(pn_morfin_1 = ifelse(is.na(pn_morfin_1), 0, pn_morfin_1),
         pn_morfin_1_2 = ifelse(is.na(pn_morfin_1_2), 0, pn_morfin_1_2),
         pn_morfin_1_3 = ifelse(is.na(pn_morfin_1_3), 0, pn_morfin_1_3),
         pn_morfin_1_4 = ifelse(is.na(pn_morfin_1_4), 0, pn_morfin_1_4),
         administreret_pn_morfin_iv_1 = ifelse(is.na(administreret_pn_morfin_iv_1), 0, administreret_pn_morfin_iv_1),
         administreret_pn_morfin_iv_1_2 = ifelse(is.na(administreret_pn_morfin_iv_1_2), 0, administreret_pn_morfin_iv_1_2),
         administreret_pn_morfin_iv_1_3 = ifelse(is.na(administreret_pn_morfin_iv_1_3), 0, administreret_pn_morfin_iv_1_3),
         administreret_pn_morfin_iv_1_4 = ifelse(is.na(administreret_pn_morfin_iv_1_4), 0, administreret_pn_morfin_iv_1_4),
         pn_ketogan_1 = ifelse(is.na(pn_ketogan_1), 0, pn_ketogan_1),
         pn_ketogan_1_2 = ifelse(is.na(pn_ketogan_1_2), 0, pn_ketogan_1_2),
         pn_ketogan_1_3 = ifelse(is.na(pn_ketogan_1_3), 0, pn_ketogan_1_3),
         pn_ketogan_1_4 = ifelse(is.na(pn_ketogan_1_4), 0, pn_ketogan_1_4),
         pn_fentanyl_1 = ifelse(is.na(pn_fentanyl_1), 0, pn_fentanyl_1),
         pn_fentanyl_1_2 = ifelse(is.na(pn_fentanyl_1_2), 0, pn_fentanyl_1_2),
         pn_fentanyl_1_3 = ifelse(is.na(pn_fentanyl_1_3), 0, pn_fentanyl_1_3),
         pn_fentanyl_1_4 = ifelse(is.na(pn_fentanyl_1_4), 0, pn_fentanyl_1_4))

```

Herefter kan de enkelte tidspunkters opioid forbrug summeres. Faktorerne der ganges med kommer fra artiklen.

```

patientdata$mme_t0 <- patientdata$pn_morfin_1*1+patientdata$administreret_pn_morfin_iv_1*3+patientdata$pn_ketogan_1*1+patientdata$pn_fentanyl_1*1
patientdata$mme_t12 <- patientdata$pn_morfin_1_2*1+patientdata$administreret_pn_morfin_iv_1_2*3+patientdata$pn_ketogan_1_2*1+patientdata$pn_fentanyl_1_2*1
patientdata$mme_t24 <- patientdata$pn_morfin_1_3*1+patientdata$administreret_pn_morfin_iv_1_3*3+patientdata$pn_ketogan_1_3*1+patientdata$pn_fentanyl_1_3*1
patientdata$mme_t36 <- patientdata$pn_morfin_1_4*1+patientdata$administreret_pn_morfin_iv_1_4*3+patientdata$pn_ketogan_1_4*1+patientdata$pn_fentanyl_1_4*1

```

Da vi gerne vil kigge på opioid det første døgn lægges nu t0 og t12 sammen

```
patientdata$opioid_24h <- rowSums(patientdata[,c("mme_t0", "mme_t12")], na.rm = TRUE)
```

BMI

```
patientdata$bmi <- patientdata$kg/(patientdata$h_jde/100*patientdata$h_jde/100)
```

Nyreskade

Nyreskade beregnes af to omgange. Først laves de der er noteret som over 90 om til et tal (90). Derefter grupperes efter deres nyefunktion.

```
patientdata$gfr <- ifelse(patientdata$gfr==">90", 90, patientdata$gfr)
patientdata$kidney <- ifelse(patientdata$gfr>60, "Normal", ifelse(patientdata$gfr>=30, "Mild KF", ifelse
```

Ketorolac

Dosis er noteret, men vi er mere interesseret om de får eller ej, da dosis er meget behandler afhængig.

```
patientdata$ketorolac.factor <- ifelse(patientdata$iop_toradol>0, "Yes", "No")
```

Tider

Tider regnes fra tidspunkt til differencen mellem slutning af operation og eventet. Der er nogle der ikke får opioid. Deres tid sættes til 24 timer.

```
patientdata$drain_removal <- difftime(patientdata$tid_til_dr_nfjernelse, patientdata$knivtid_slut, units = "h")
patientdata$breakthrough <- difftime(patientdata$tid_smertegennebrud, patientdata$knivtid_slut, units = "h")
patientdata$breakthrough <- ifelse(is.na(patientdata$breakthrough), 24, patientdata$breakthrough)
```

Bupivacain

Regnes fra kategorisk til numerisk dosis

```
patientdata$bupidose <- ifelse(patientdata$lokalan_konc==1, 100, ifelse(patientdata$lokalan_konc==2, 200,
```

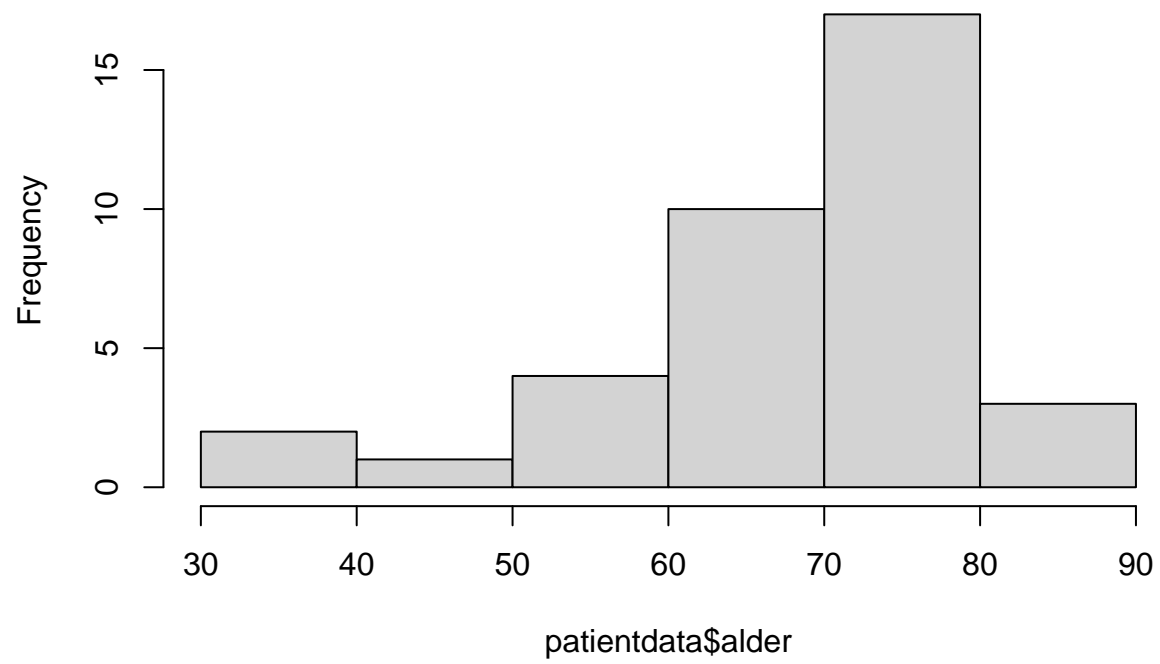
Normalitets test

Der laves normalitetstest på alle variable på nær faktorer da disse ikke kan være normalfordelte. Der er tale om: - operationsside - operationstype - diabetes_mellitus - kidneyfunktion - ketorolac - asa

Der laves histogrammer for visualiseringens skyld

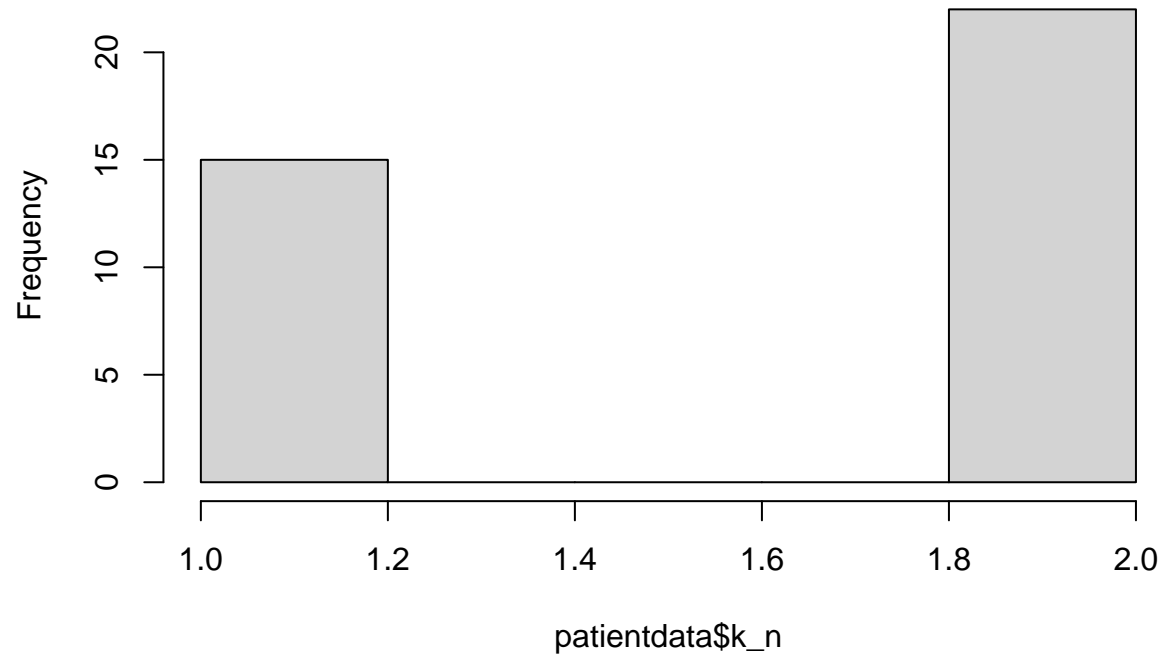
```
hist(patientdata$alder)
```

Histogram of patientdata\$alder



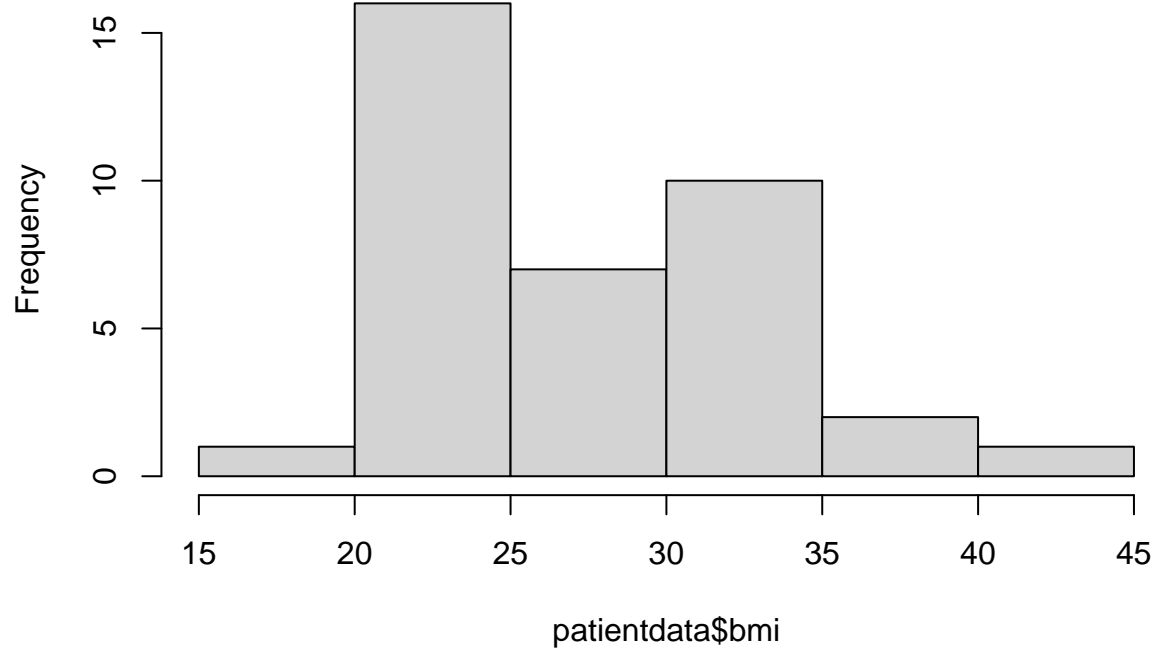
```
hist(patientdata$k_n)
```

Histogram of patientdata\$k_n



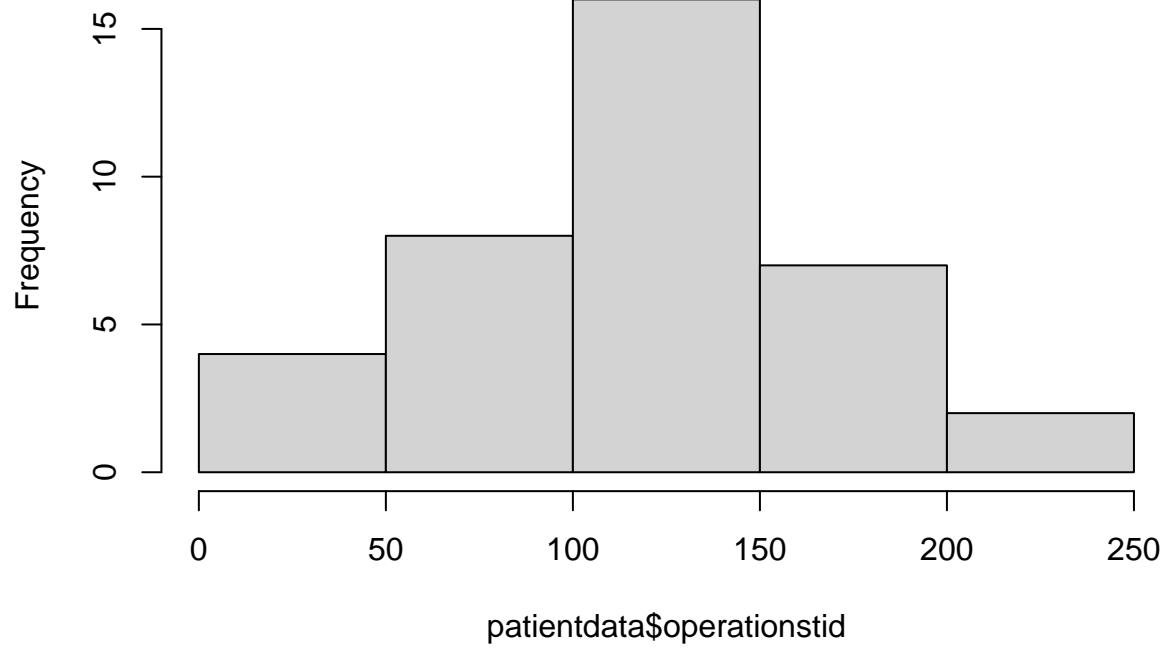
```
hist(patientdata$bmi)
```

Histogram of patientdata\$bmi



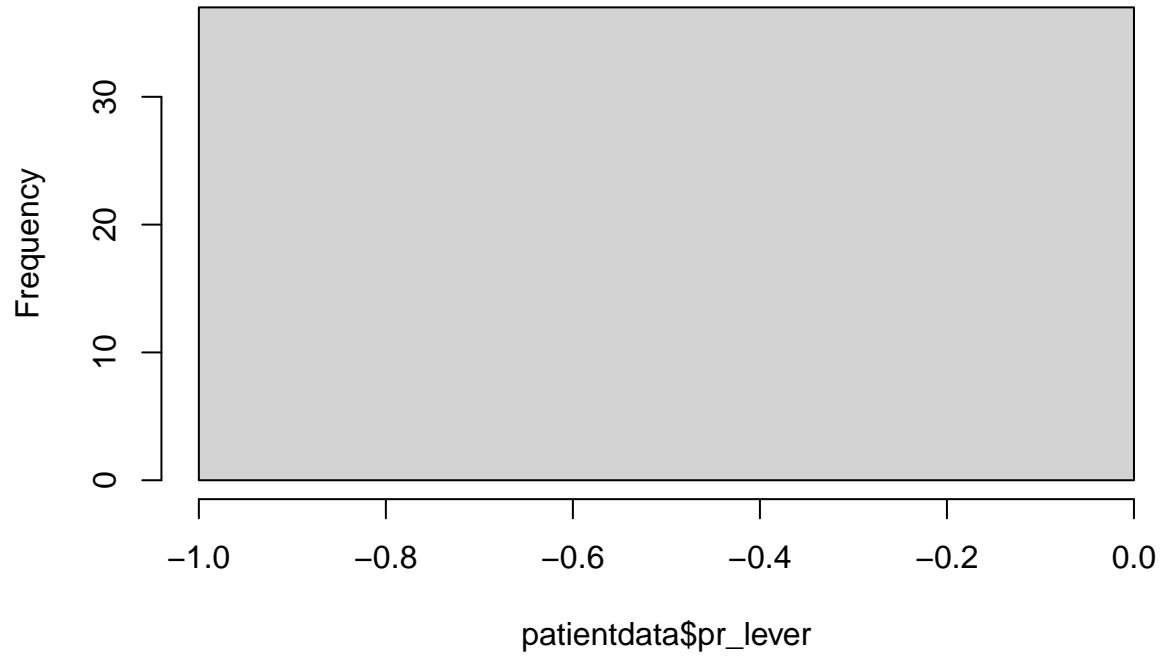
```
hist(patientdata$operationstid)
```

Histogram of patientdata\$operationstid



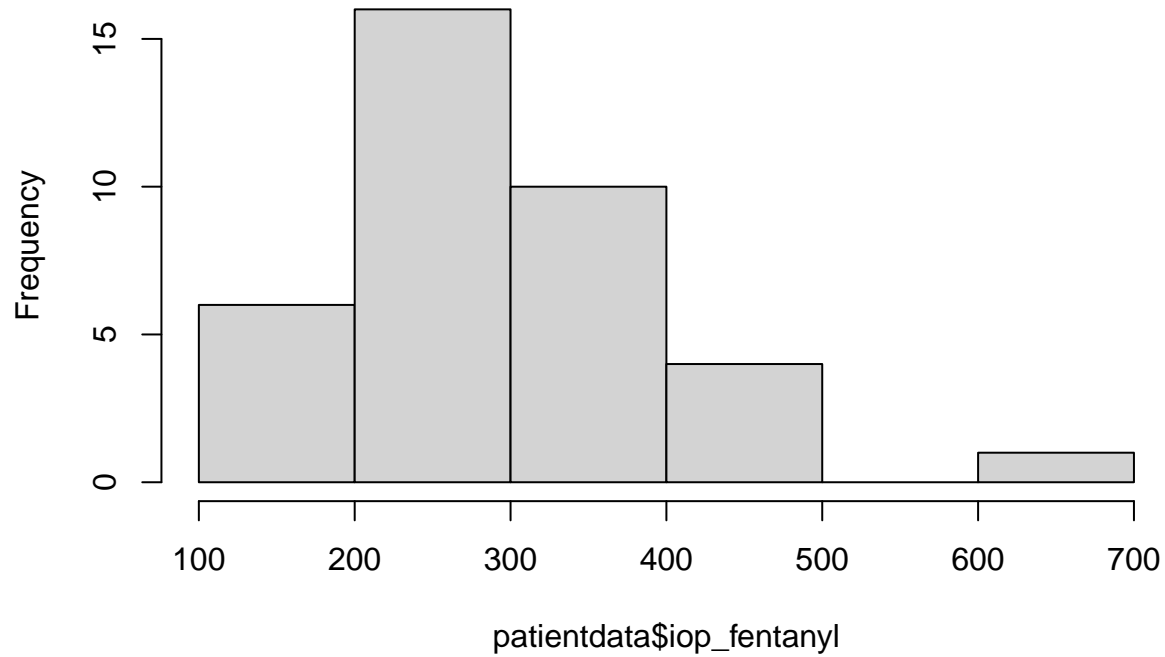
```
hist(patientdata$pr_lever)
```


Histogram of patientdata\$pr_lever



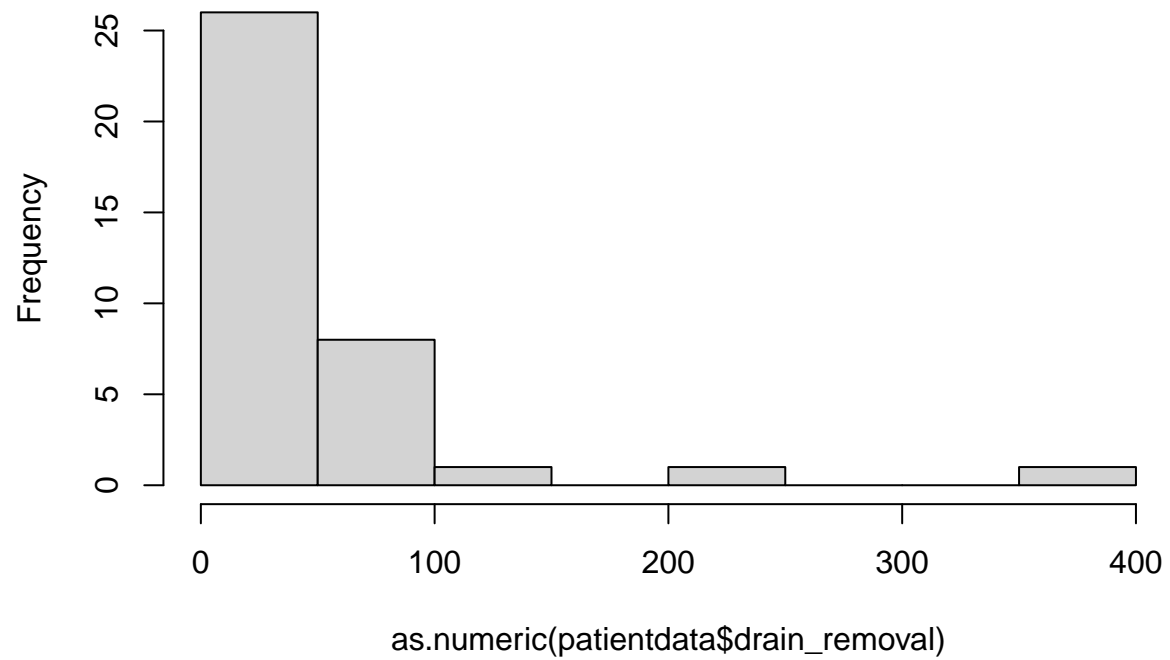
```
hist(patientdata$iop_fentanyl)
```

Histogram of patientdata\$iop_fentanyl



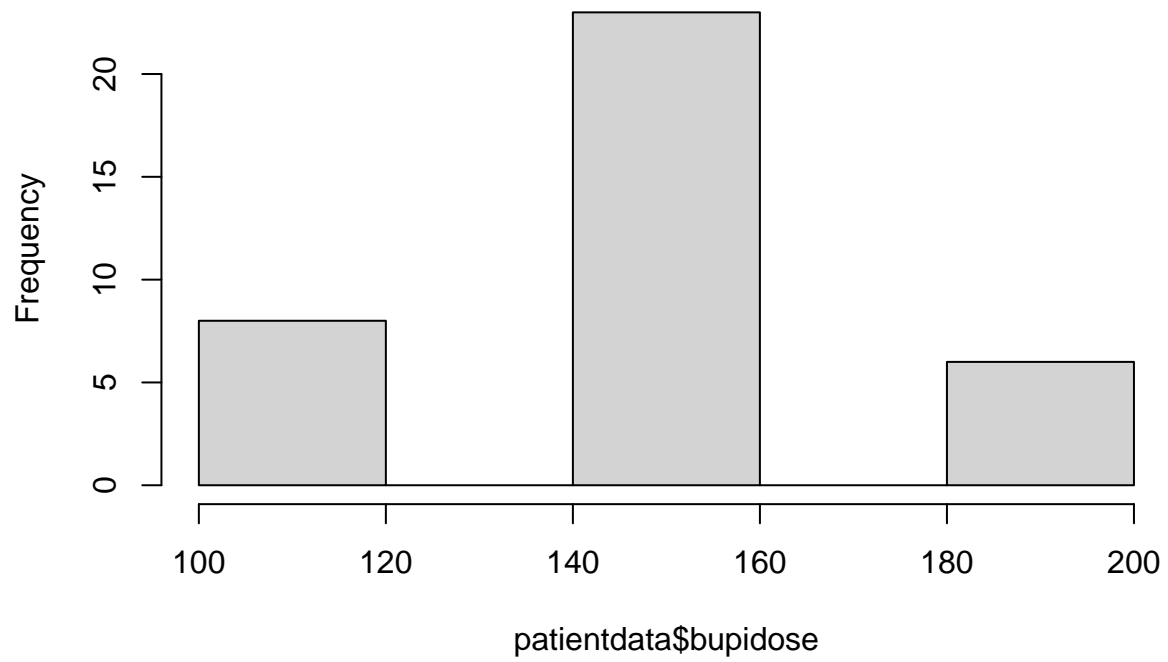
```
hist(as.numeric(patientdata$drain_removal))
```

Histogram of as.numeric(patientdata\$drain_removal)



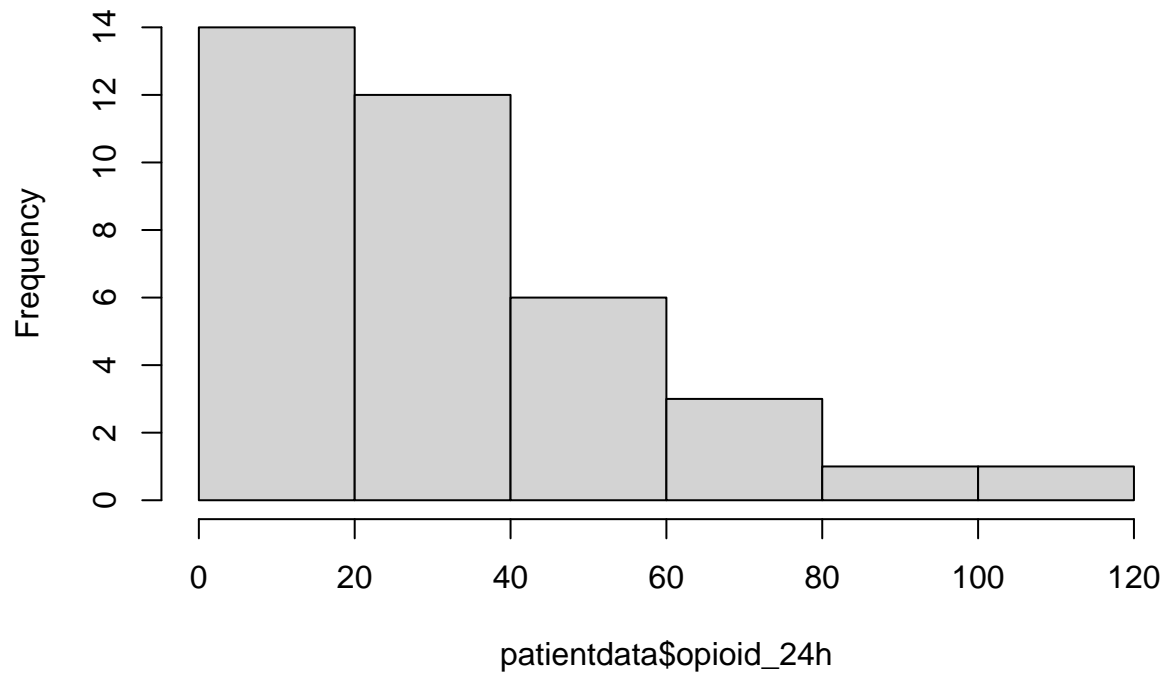
```
hist(patientdata$bupidose)
```

Histogram of patientdata\$bupidose



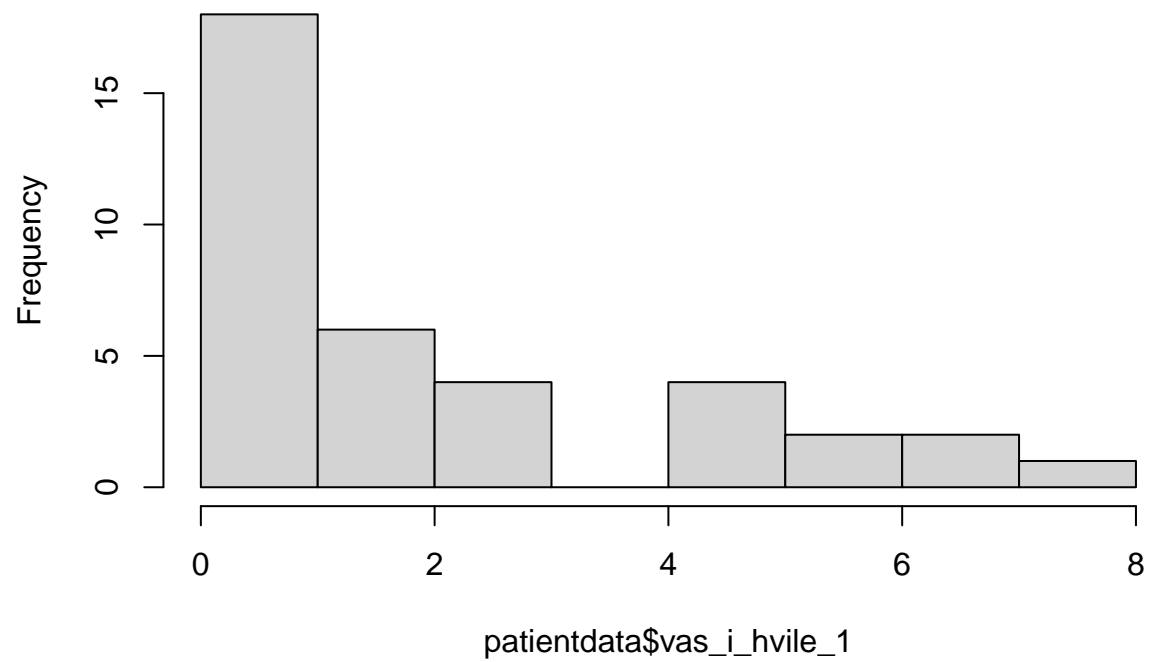
```
hist(patientdata$opioid_24h)
```

Histogram of patientdata\$opioid_24h



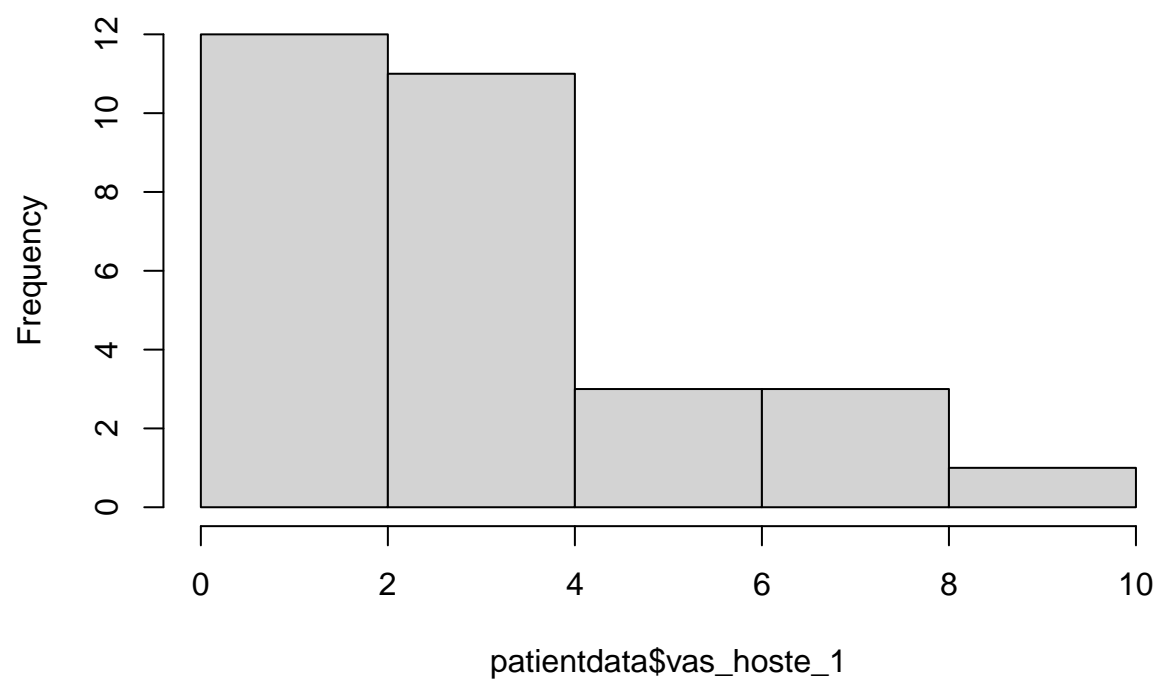
```
hist(patientdata$vas_i_hvile_1)
```

Histogram of patientdata\$vas_i_hvile_1



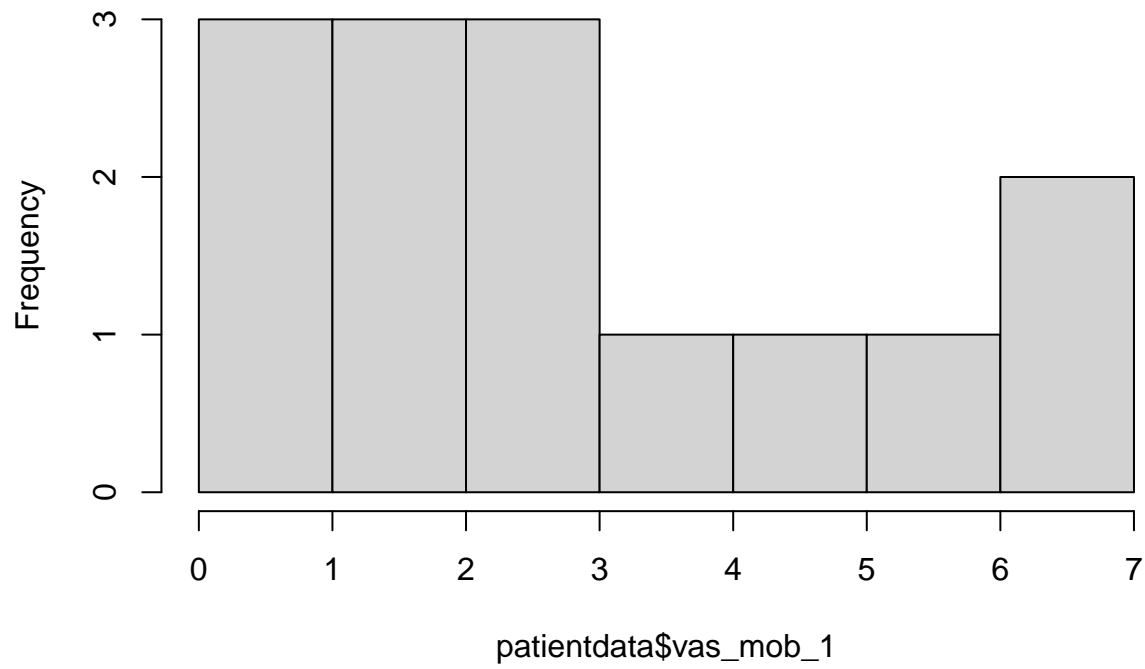
```
hist(patientdata$vas_hoste_1)
```

Histogram of patientdata\$vas_hoste_1



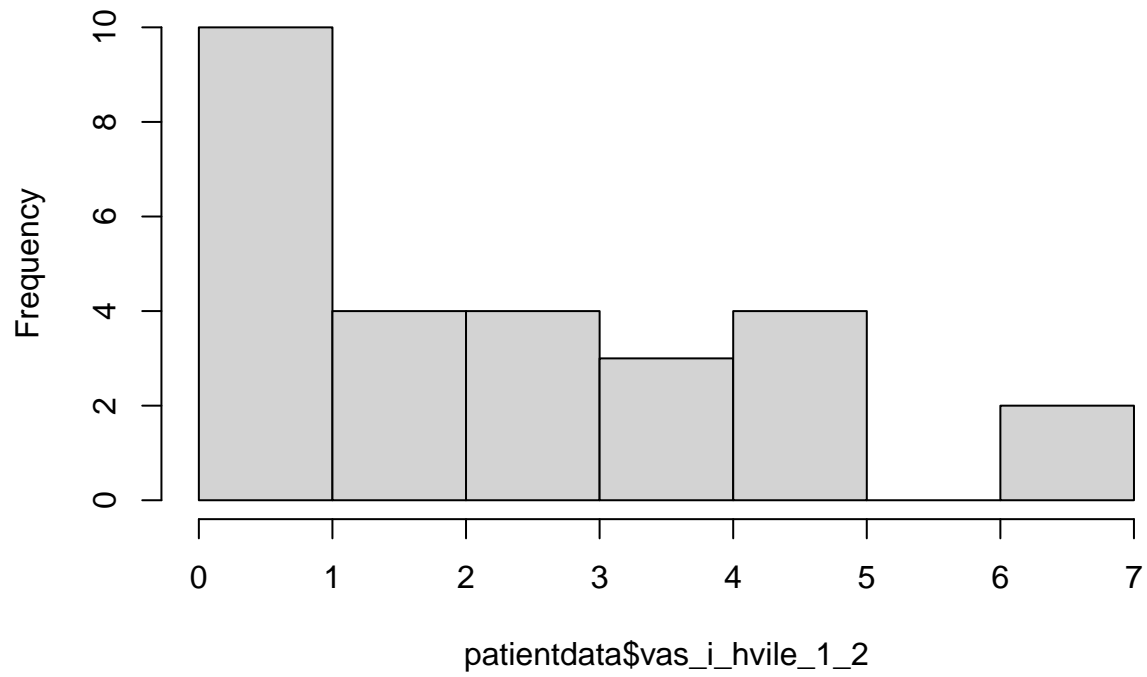
```
hist(patientdata$vas_mob_1)
```

Histogram of patientdata\$vas_mob_1



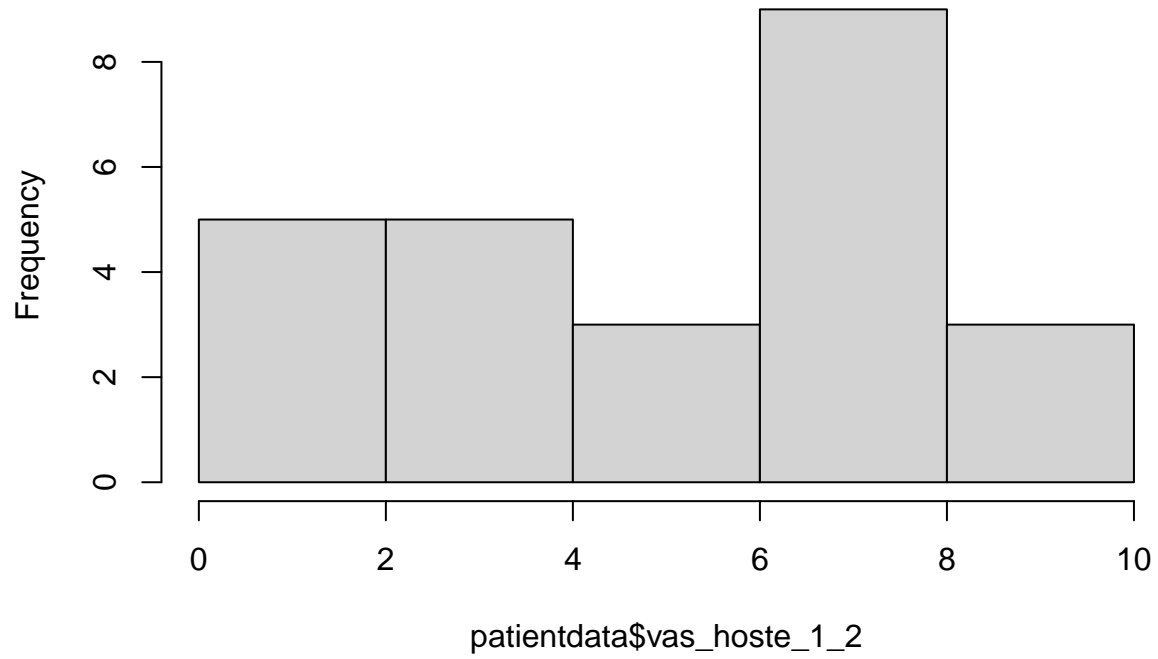
```
hist(patientdata$vas_i_hvile_1_2)
```


Histogram of patientdata\$vas_i_hvile_1_2



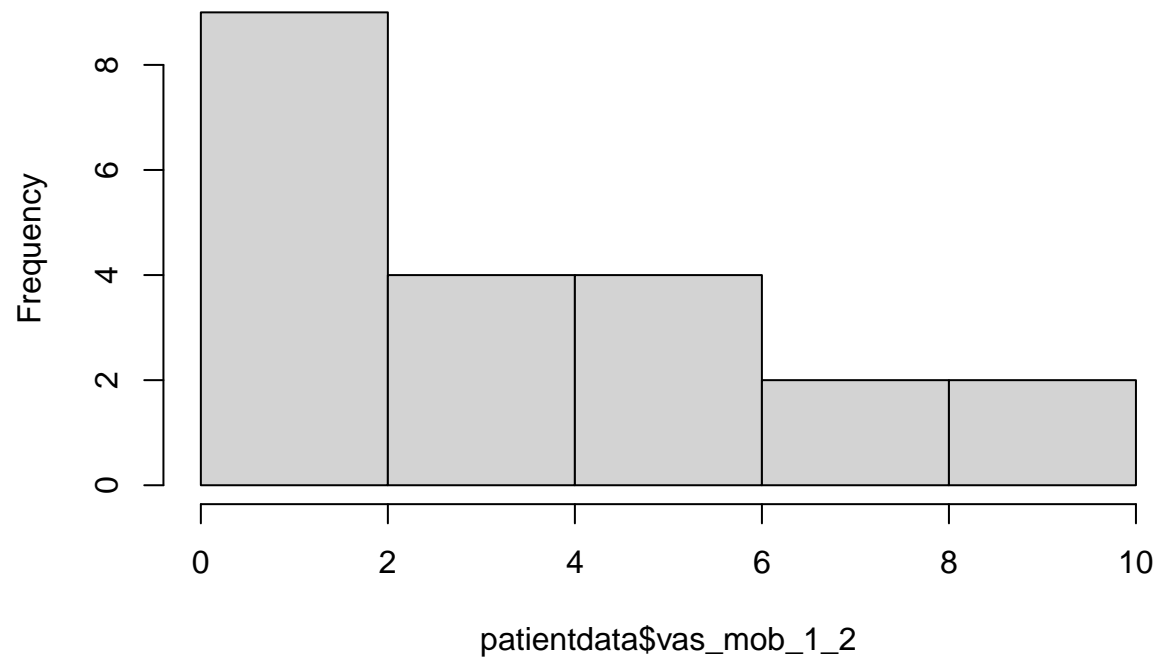
```
hist(patientdata$vas_hvile_1_2)
```

Histogram of patientdata\$vas_hoste_1_2



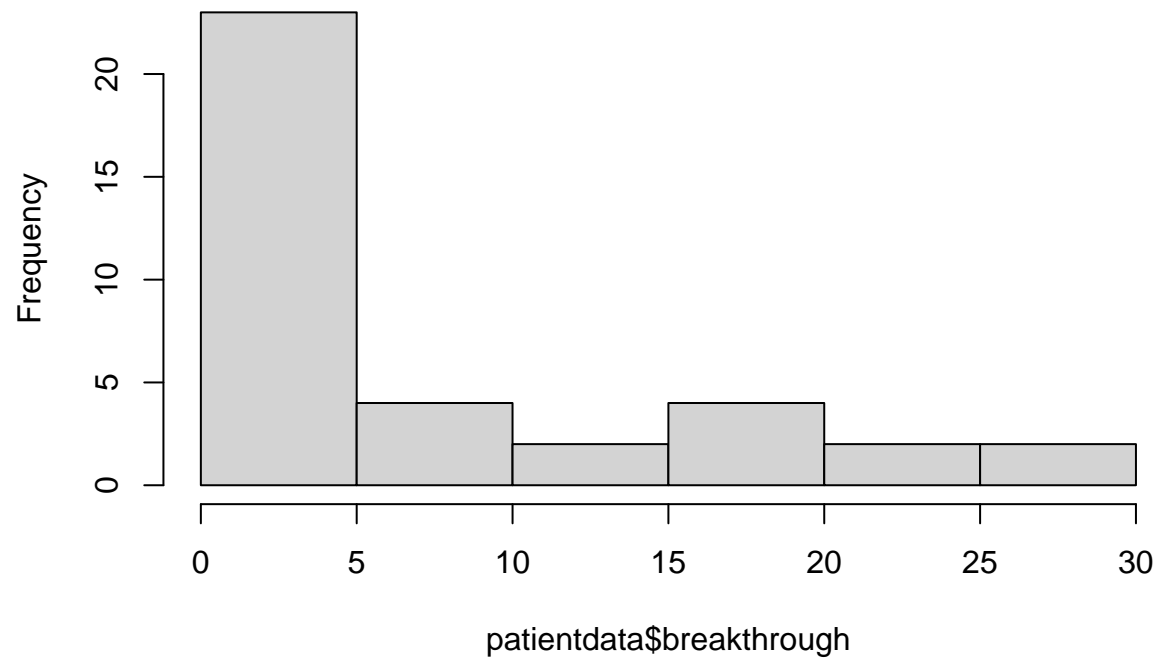
```
hist(patientdata$vas_mob_1_2)
```

Histogram of patientdata\$vas_mob_1_2



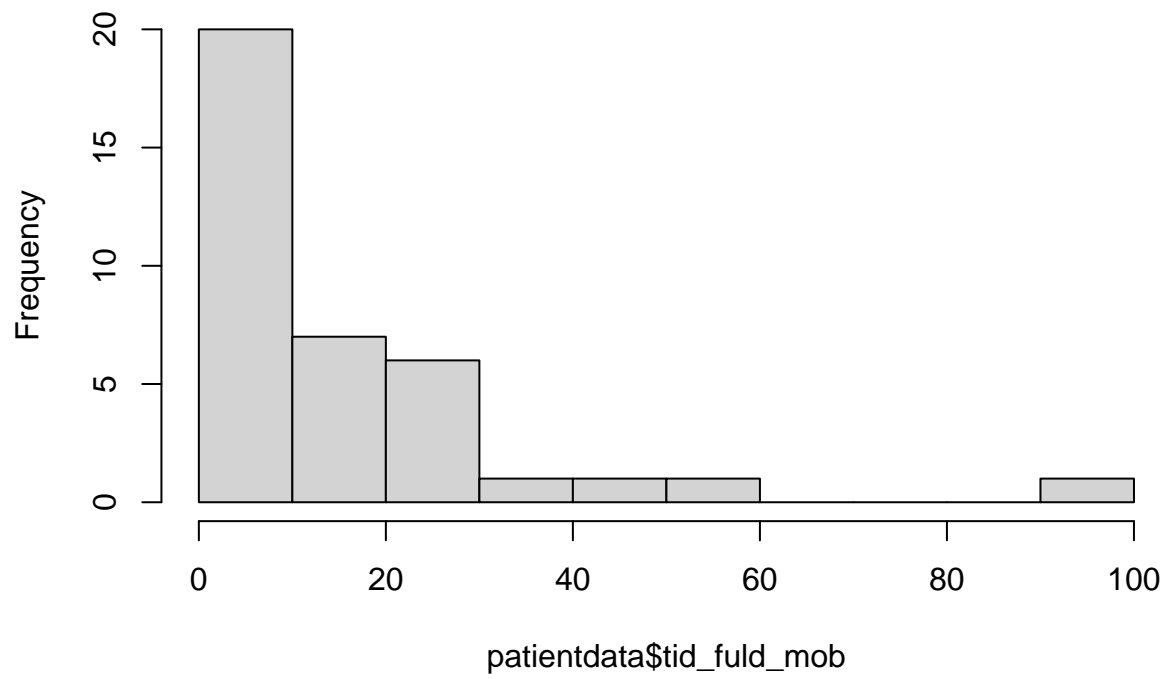
```
hist(patientdata$breakthrough)
```

Histogram of patientdata\$breakthrough



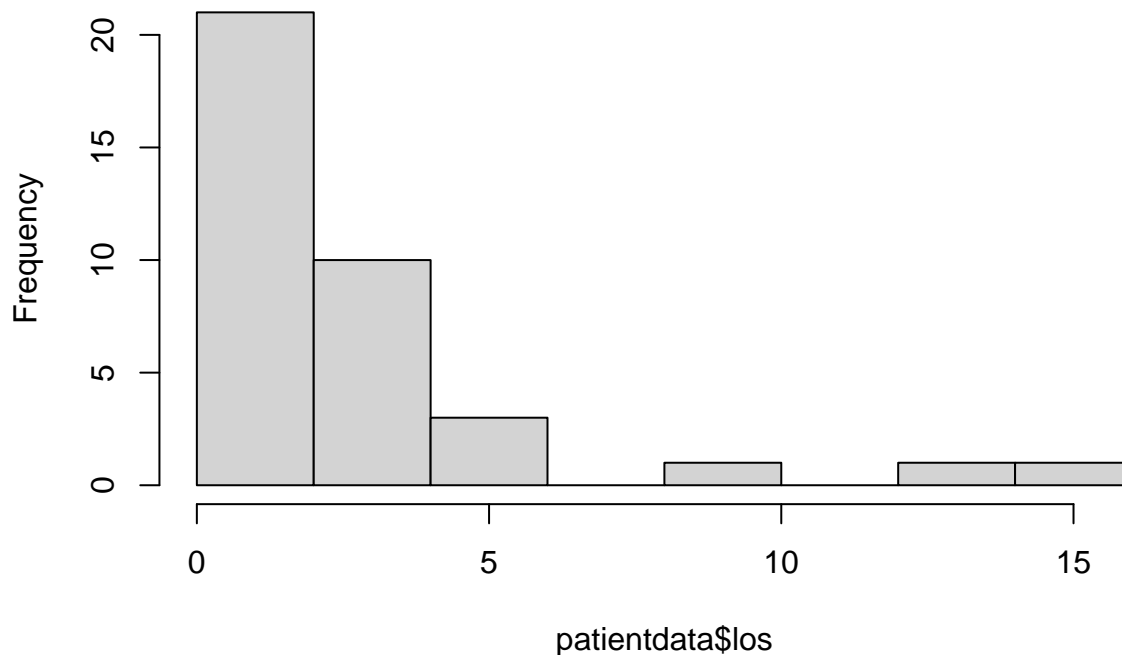
```
hist(patientdata$tid_fuld_mob)
```

Histogram of patientdata\$tid_fuld_mob



```
hist(patientdata$los)
```

Histogram of patientdata\$los



Herefter testes de alle for normalitet med shapiro wilks test. Fraset leverskade, da der ingen var

```
shapiro.test(patientdata$alder) #Ej
```

```
##
## Shapiro-Wilk normality test
##
## data:  patientdata$alder
## W = 0.89134, p-value = 0.001708
```

```
shapiro.test(patientdata$k_n) #Ej
```

```
##
## Shapiro-Wilk normality test
##
## data:  patientdata$k_n
## W = 0.62433, p-value = 1.641e-08
```

```
shapiro.test(patientdata$bmi) #Ej
```

```
##
## Shapiro-Wilk normality test
##
## data:  patientdata$bmi
## W = 0.93375, p-value = 0.0293
```

```
shapiro.test(patientdata$operationstid) #Normalfordelt
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$operationstid  
## W = 0.97491, p-value = 0.5567
```

```
shapiro.test(patientdata$iop_fentanyl) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$iop_fentanyl  
## W = 0.93913, p-value = 0.04328
```

```
shapiro.test(as.numeric(patientdata$drain_removal)) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: as.numeric(patientdata$drain_removal)  
## W = 0.53987, p-value = 1.336e-09
```

```
shapiro.test(patientdata$bupidose) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$bupidose  
## W = 0.77501, p-value = 4.254e-06
```

```
shapiro.test(patientdata$opioid_24h) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$opioid_24h  
## W = 0.88512, p-value = 0.001167
```

```
shapiro.test(patientdata$vas_i_hvile_1) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$vas_i_hvile_1  
## W = 0.82854, p-value = 5.161e-05
```

```
shapiro.test(patientdata$vas_hoste_1) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$vas_hoste_1  
## W = 0.92173, p-value = 0.02975
```

```
shapiro.test(patientdata$vas_mob_1) #"normalfordelt" se fordeling
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$vas_mob_1  
## W = 0.92779, p-value = 0.284
```

```
shapiro.test(patientdata$vas_i_hvile_1_2) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$vas_i_hvile_1_2  
## W = 0.91681, p-value = 0.03311
```

```
shapiro.test(patientdata$vas_hoste_1_2) #"normalfordelt" se fordeling
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$vas_hoste_1_2  
## W = 0.94524, p-value = 0.1954
```

```
shapiro.test(patientdata$vas_mob_1_2) #"normalfordelt" se fordeling
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$vas_mob_1_2  
## W = 0.93242, p-value = 0.1539
```

```
shapiro.test(patientdata$breakthrough) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$breakthrough  
## W = 0.74526, p-value = 1.226e-06
```



```
shapiro.test(patientdata$tid_fuld_mob) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$tid_fuld_mob  
## W = 0.67145, p-value = 7.811e-08
```

```
shapiro.test(patientdata$los) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: patientdata$los  
## W = 0.63481, p-value = 2.295e-08
```

De variable der var normalfordelte var: - operationstid - vas_mob_1 - vas_hoste_1_2 - vas_mob_1_2

opdeling af datasæt

Til nogle beregninger er det nemmere at have datasættet i to. Derfor deles det i før og efter

```
foer <- patientdata  
foer <- foer %>%  
  filter(group==0)  
efter <- patientdata  
efter <- efter %>%  
  filter(group==1)
```

Data behandling

Tabel 1 og 2 genereres. Tabel 1 laves både som resultatet af normalitets test og som anført allerede i artiklen

```
tabell1_1 <- univariateTable(data=patientdata,group~alder+k_n+bmi+asa.factor+operationstid+operationsside  
summary(tabell1_1)
```

##	Variable	Level	group = 0 (n=20)
## 1	alder	mean (sd)	71.5 (8)
## 2	k_n	1	10 (50.0)
## 3		2	10 (50.0)
## 4	bmi	mean (sd)	26.2 (4.8)
## 5	asa.factor	1	0 (0.0)
## 6		2	10 (50.0)
## 7		3	9 (45.0)
## 8		4	1 (5.0)
## 9	operationstid	mean (sd)	137 (41.6)
## 10	operationsside.factor	Venstre	9 (45.0)
## 11		Højre	11 (55.0)
## 12	operationstype.factor	Lobektomi	8 (40.0)

```

## 13                      Segmentresektion          2 (10.0)
## 14                      Kileresektion             10 (50.0)
## 15                      Bilobektomi                0 (0.0)
## 16 diabetes_mellitus.factor      Nej              19 (95.0)
## 17                      Ja                        1 (5.0)
## 18          pr_lever              0              20 (100.0)
## 19          kidney              Normal            16 (80.0)
## 20                      Mild KF                   4 (20.0)
## 21                      Severe KF                 0 (0.0)
## 22          iop_fentanyl    median [iqr]         300 [250, 400]
## 23          ketorolac.factor      No              11 (55.0)
## 24                      Yes                       9 (45.0)
## 25          drain_removal    median [iqr]        23.8 [21.9, 47.4]
## 26          bupidose         median [iqr]        150 [137.5, 150.0]
##      group = 1 (n=17)      Total (n=37) p-value
## 1      65.1 (14.8)          68.6 (11.9) 0.09503
## 2      5 (29.4)            15 (40.5)
## 3      12 (70.6)           22 (59.5) 0.34968
## 4      29.2 (5.9)          27.6 (5.5) 0.08601
## 5      0 (0.0)             0 (0.0)
## 6      5 (29.4)            15 (40.5)
## 7      12 (70.6)           21 (56.8)
## 8      0 (0.0)             1 (2.7)      NA
## 9      100.6 (52)          120.3 (49.6) 0.01801
## 10     10 (58.8)           19 (51.4)
## 11     7 (41.2)            18 (48.6) 0.61118
## 12     7 (41.2)            15 (40.5)
## 13     0 (0.0)             2 (5.4)
## 14     10 (58.8)           20 (54.1)
## 15     0 (0.0)             0 (0.0)      NA
## 16     15 (88.2)           34 (91.9)
## 17     2 (11.8)            3 (8.1) 0.88314
## 18     17 (100.0)          37 (100.0) 0.62187
## 19     13 (76.5)           29 (78.4)
## 20     3 (17.6)            7 (18.9)
## 21     1 (5.9)             1 (2.7) 0.54390
## 22     300 [250, 350]      300 [250, 350] 0.42137
## 23     6 (35.3)            17 (45.9)
## 24     11 (64.7)           20 (54.1) 0.38557
## 25     46.5 [22.9, 70.9]   40.2 [22.3, 53.5] 0.34478
## 26     150 [150, 150]      150 [150, 150] 0.62131

```

```

tabel1_2<- univariateTable(data=patientdata,group~Q(alder)+k_n+Q(bmi)+asa.factor+operationstid+operation
summary(tabel1_2)

```

```

##      Variable      Level  group = 0 (n=20)
## 1      alder    median [iqr]      73 [64, 78]
## 2      k_n      1              10 (50.0)
## 3      2              10 (50.0)
## 4      bmi    median [iqr]      24.7 [23.3, 28.7]
## 5      asa.factor      1              0 (0.0)
## 6      2              10 (50.0)
## 7      3              9 (45.0)
## 8      4              1 (5.0)

```

```

## 9          operationstid      mean (sd)      137 (41.6)
## 10 operationsside.factor      Venstre       9 (45.0)
## 11          HÅ,jre           11 (55.0)
## 12 operationstype.factor      Lobektomi      8 (40.0)
## 13          Segmentresektion  2 (10.0)
## 14          Kileresektion     10 (50.0)
## 15          Bilobektomi       0 (0.0)
## 16 diabetes_mellitus.factor    Nej         19 (95.0)
## 17          Ja               1 (5.0)
## 18          pr_lever          0          20 (100.0)
## 19          kidney           Normal        16 (80.0)
## 20          Mild KF          4 (20.0)
## 21          Severe KF        0 (0.0)
## 22          iop_fentanyl     median [iqr]    300 [250, 400]
## 23          ketorolac.factor    No         11 (55.0)
## 24          Yes              9 (45.0)
## 25          drain_removal     median [iqr]    23.8 [21.9, 47.4]
## 26          bupidose         median [iqr]    150 [137.5, 150.0]
##      group = 1 (n=17)      Total (n=37) p-value
## 1          70 [57, 78]      71 [64, 78] 0.25849
## 2          5 (29.4)         15 (40.5)
## 3          12 (70.6)        22 (59.5) 0.34968
## 4 29.1 [24.8, 32.8] 26.1 [23.7, 32.0] 0.11302
## 5          0 (0.0)          0 (0.0)
## 6          5 (29.4)         15 (40.5)
## 7          12 (70.6)        21 (56.8)
## 8          0 (0.0)          1 (2.7)      NA
## 9          100.6 (52)        120.3 (49.6) 0.01801
## 10         10 (58.8)         19 (51.4)
## 11         7 (41.2)          18 (48.6) 0.61118
## 12         7 (41.2)          15 (40.5)
## 13         0 (0.0)           2 (5.4)
## 14         10 (58.8)         20 (54.1)
## 15         0 (0.0)           0 (0.0)      NA
## 16         15 (88.2)         34 (91.9)
## 17         2 (11.8)          3 (8.1) 0.88314
## 18         17 (100.0)        37 (100.0) 0.62187
## 19         13 (76.5)         29 (78.4)
## 20         3 (17.6)          7 (18.9)
## 21         1 (5.9)           1 (2.7) 0.54390
## 22        300 [250, 350]     300 [250, 350] 0.42137
## 23         6 (35.3)          17 (45.9)
## 24         11 (64.7)         20 (54.1) 0.38557
## 25 46.5 [22.9, 70.9] 40.2 [22.3, 53.5] 0.34478
## 26        150 [150, 150]     150 [150, 150] 0.62131

```

```

tabel2 <- univariateTable(data=patientdata, group ~Q(opiod_24h)+Q(vas_i_hvile_1)+Q(vas_hoste_1)+vas_mol
summary(tabel2)

```

```

##      Variable      Level group = 0 (n=20) group = 1 (n=17)
## 1      opiod_24h median [iqr]    30 [21.9, 48.1]    10 [ 5, 35]
## 2      vas_i_hvile_1 median [iqr]    3 [0.0, 5.2]     0 [0, 2]
## 3      vas_hoste_1 median [iqr]    3.5 [2.2, 5.5]    2 [1.5, 3.0]
## 4                      missing      2              5

```

```
## 5      vas_mob_1      mean (sd)          3.5 (2.1)          2.7 (3.1)
## 6              missing                    9              14
## 7  vas_i_hvile_1_2 median [iqr]      2.5 [1.0, 4.2]      2 [0.5, 3.5]
## 8              missing                    4              6
## 9      vas_hoste_1_2 mean (sd)          5.9 (3.1)          4.5 (2.8)
## 10             missing                    5              7
## 11      vas_mob_1_2 mean (sd)          3.9 (2.7)          3.5 (3.2)
## 12             missing                    9              7
## 13 breakthrough median [iqr]      1.5 [0.8, 4.2] 5.5 [ 1.5, 15.7]
## 14 tid_fuld_mob median [iqr] 19.5 [ 8.0, 25.6]      5 [ 5, 10]
## 15      los median [iqr]          2 [1.0, 4.2]          2 [2, 4]
##      Total (n=37)  p-value
## 1  27.5 [10.0, 42.5] 0.0390646
## 2      2 [0, 3] 0.0135197
## 3      3 [2, 4] 0.1027427
## 4          7
## 5      3.3 (2.2) 0.5986918
## 6          23
## 7      2 [1, 4] 0.7265480
## 8          10
## 9      5.3 (3) 0.2589178
## 10         12
## 11      3.7 (2.9) 0.7509974
## 12         16
## 13  2 [ 1.2, 10.7] 0.0352719
## 14  8.5 [ 5, 21] 0.0005539
## 15      2 [2, 4] 0.7062717
```

Confidens intervaller

Beregnes for de fire normalfordelte variable samt bupi (grundet ønske fra reviewer)

```
# Bupi
aggregate(patientdata$bupidose, list(patientdata$group), FUN=mean)
```

```
##   Group.1  x
## 1      0 145
## 2      1 150
```

```
modell1 <- lm(bupidose ~ 1, foer)
confint(modell1, level=0.95)
```

```
##              2.5 %   97.5 %
## (Intercept) 130.0066 159.9934
```

```
modell2 <- lm(bupidose ~ 1, efter)
confint(modell2, level=0.95)
```

```
##              2.5 %   97.5 %
## (Intercept) 134.2574 165.7426
```

```
hist(patientdata$bupidose)
```



```
shapiro.test(patientdata$bupidose)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  patientdata$bupidose  
## W = 0.77501, p-value = 4.254e-06
```

```
#ttest bupi  
t.test(foer$bupidose,after$bupidose)
```

```
##  
##  Welch Two Sample t-test  
##  
## data:  foer$bupidose and after$bupidose  
## t = -0.48459, df = 34.485, p-value = 0.631  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
##  -25.958  15.958  
## sample estimates:  
## mean of x mean of y  
##      145      150
```

```

### Operationstid
aggregate(patientdata$operationstid, list(patientdata$group), FUN=mean)

##      Group.1      x
## 1          0 137.0000
## 2          1 100.5882

model1 <- lm(operationstid ~ 1, foer)
confint(model1, level=0.95)

##              2.5 %   97.5 %
## (Intercept) 117.519 156.481

model2 <- lm(operationstid ~ 1, efter)
confint(model2, level=0.95)

##              2.5 %   97.5 %
## (Intercept)  73.843 127.3335

### VAS mob 1
mean(foer$vas_mob_1[!is.na(foer$vas_mob_1)])

## [1] 3.454545

mean(etter$vas_mob_1[!is.na(etter$vas_mob_1)])

## [1] 2.666667

model1 <- lm(vas_mob_1 ~ 1, foer[!is.na(foer$vas_mob_1)], na.action = na.exclude)
confint(model1, level=0.95)

##              2.5 %   97.5 %
## (Intercept)  2.033748 4.875343

model2 <- lm(vas_mob_1 ~ 1, etter[!is.na(etter$vas_mob_1)], na.action = na.exclude)
confint(model2, level=0.95)

##              2.5 %   97.5 %
## (Intercept) -4.922499 10.25583

### vas host2
mean(foer$vas_hoste_1_2[!is.na(foer$vas_hoste_1_2)])

## [1] 5.866667

mean(etter$vas_hoste_1_2[!is.na(etter$vas_hoste_1_2)])

## [1] 4.5

```

```
model1 <- lm(vas_hoste_1_2 ~ 1, foer[!is.na(foer$vas_hoste_1_2)],na.action = na.exclude)
confint(model1, level=0.95)
```

```
##                2.5 %    97.5 %
## (Intercept) 4.155098 7.578235
```

```
model2 <- lm(vas_hoste_1_2 ~ 1, efter[!is.na(etter$vas_hoste_1_2)],na.action = na.exclude)
confint(model2, level=0.95)
```

```
##                2.5 %    97.5 %
## (Intercept) 2.526456 6.473544
```

```
### vas mob 2
mean(foer$vas_mob_1_2[!is.na(foer$vas_mob_1_2)])
```

```
## [1] 3.909091
```

```
mean(etter$vas_mob_1_2[!is.na(etter$vas_mob_1_2)])
```

```
## [1] 3.5
```

```
model1 <- lm(vas_mob_1_2 ~ 1, foer[!is.na(foer$vas_mob_1_2)],na.action = na.exclude)
confint(model1, level=0.95)
```

```
##                2.5 %    97.5 %
## (Intercept) 2.120146 5.698035
```

```
model2 <- lm(vas_mob_1_2 ~ 1, efter[!is.na(etter$vas_mob_1_2)],na.action = na.exclude)
confint(model2, level=0.95)
```

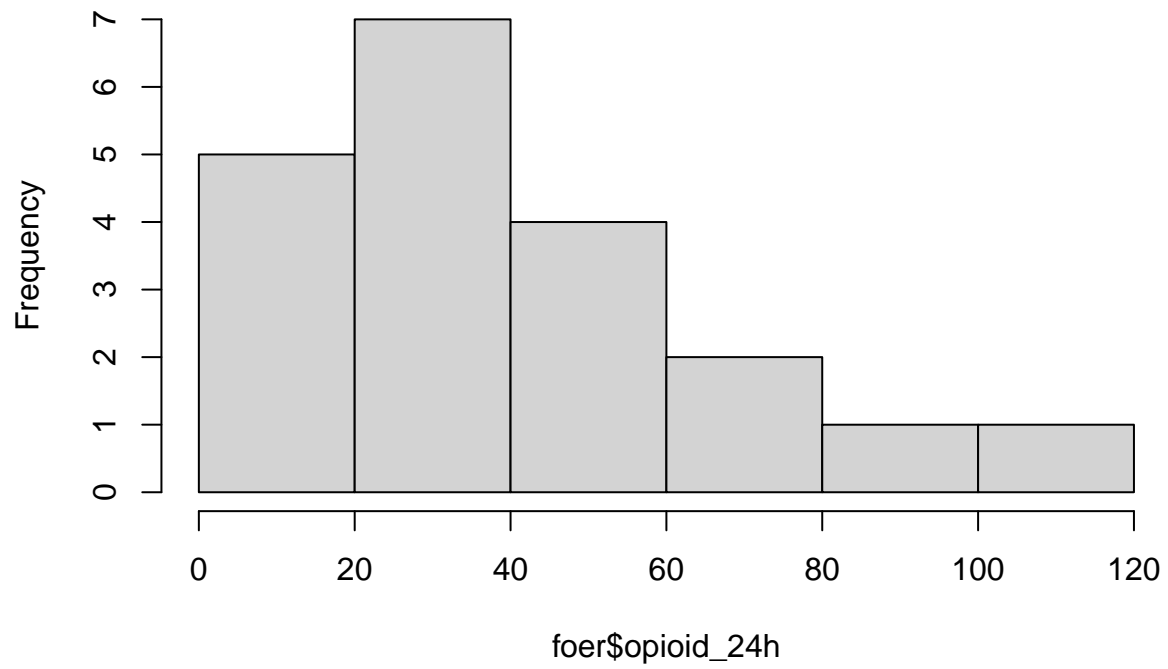
```
##                2.5 %    97.5 %
## (Intercept) 1.181979 5.818021
```

REVEIWERENS KOMMENTARER

For at undersøge de variable han var særligt interesseret i laves normalitetstest på opioid og tid til pn opioid fordelt i grupper

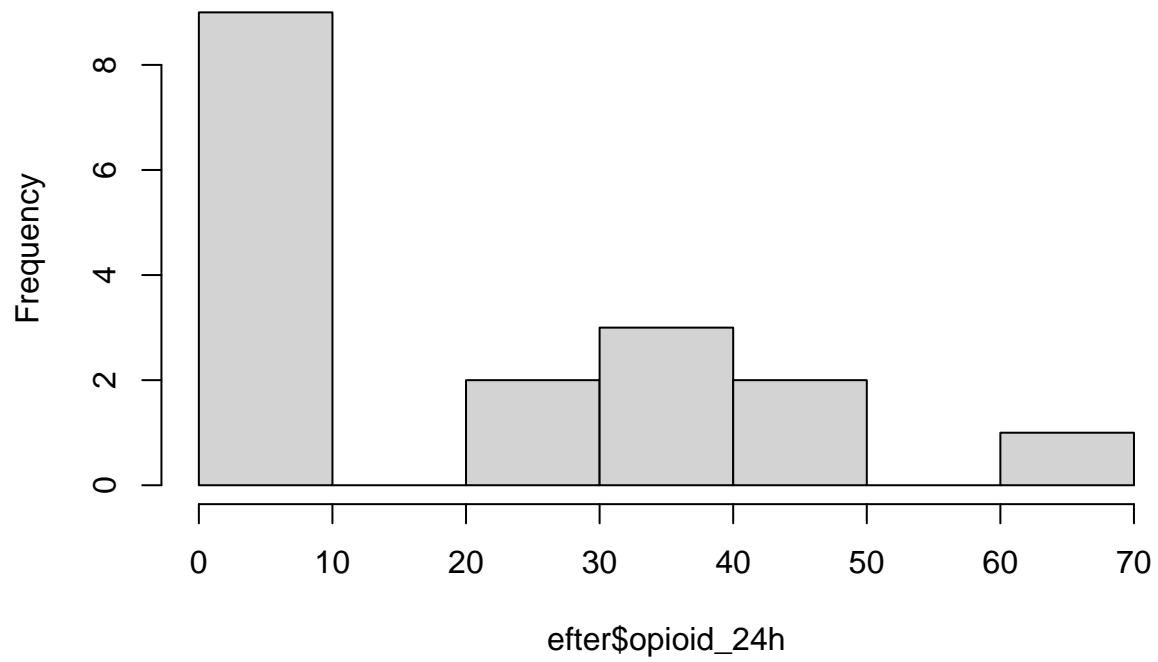
```
hist(foer$opioid_24h)
```

Histogram of foer\$opioid_24h



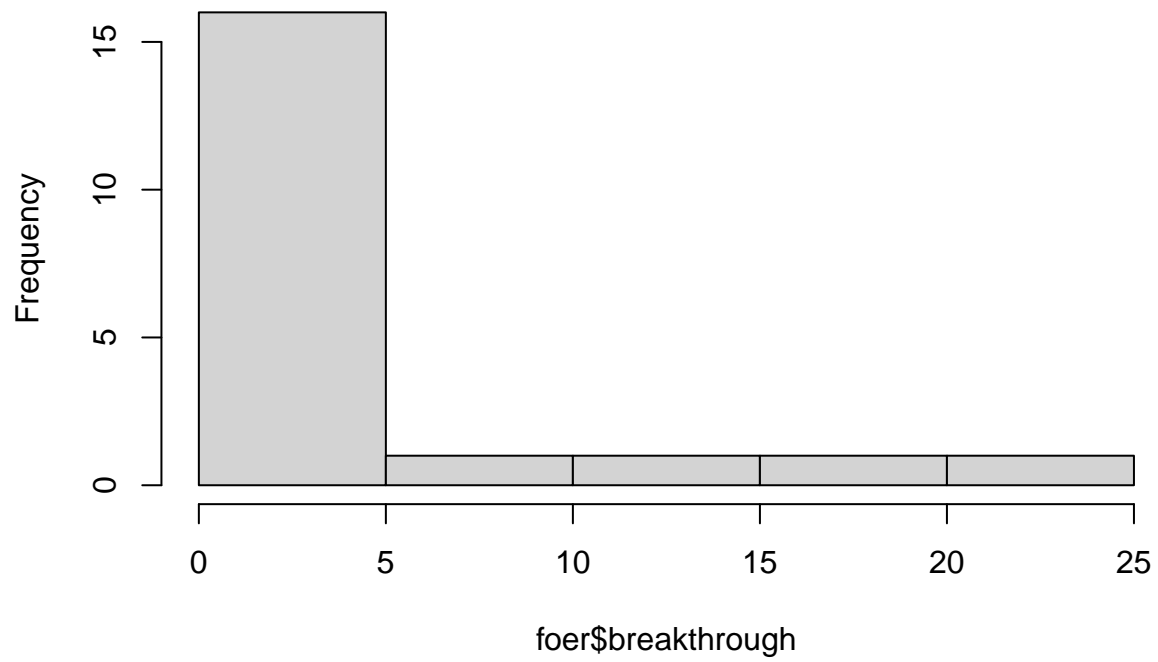
```
hist(after$opioid_24h)
```


Histogram of efter\$opioid_24h



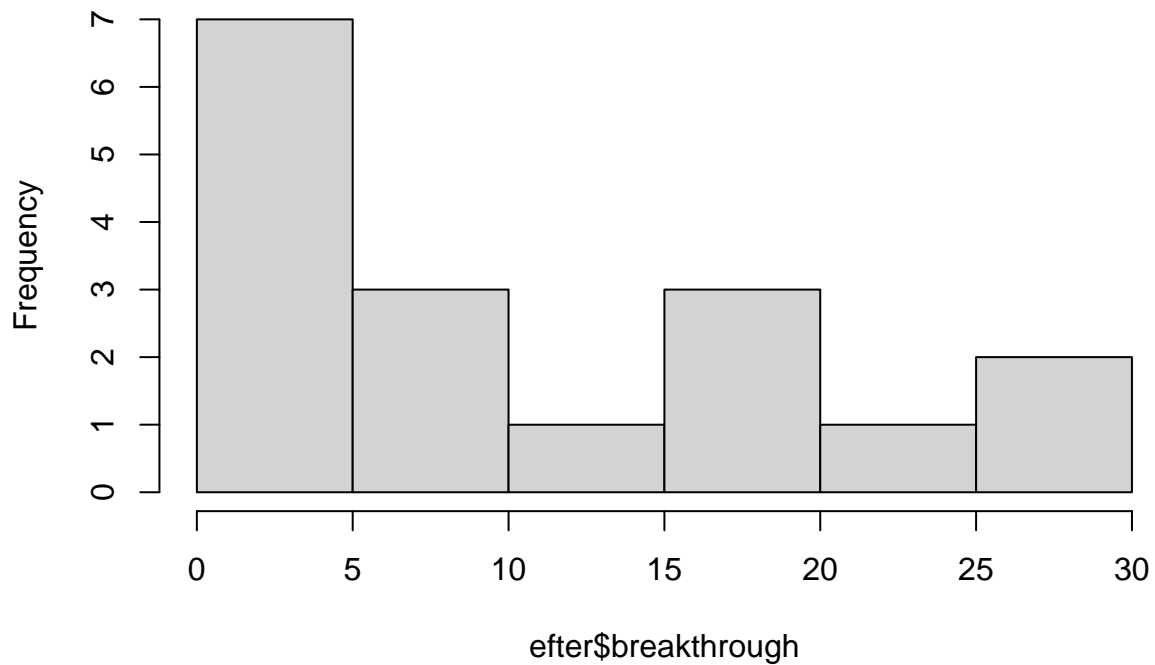
```
hist(foer$breakthrough)
```

Histogram of foer\$breakthrough



```
hist(after$breakthrough)
```

Histogram of after\$breakthrough



```
shapiro.test(foer$opioid_24h) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data:  foer$opioid_24h  
## W = 0.88636, p-value = 0.02307
```

```
shapiro.test(after$opioid_24h) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data:  after$opioid_24h  
## W = 0.89146, p-value = 0.04899
```

```
shapiro.test(foer$breakthrough) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data:  foer$breakthrough  
## W = 0.61643, p-value = 4.378e-06
```

```
shapiro.test(after$breakthrough) #Ej
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: after$breakthrough  
## W = 0.85516, p-value = 0.01287
```

TESTS

Til sidst testes om data her stemmer overens med noget af det fra stata.

Henter data fra stata

```
statafile4 <- read_dta("statadata4.dta") #Til opioid  
statafile5 <- read_dta("statadata5.dta") #Til tid til første opioid
```

Tilføjer de to kolonner til patientdata for sammenligning

```
patientdata <- left_join(patientdata, statafile4 %>% select(record_id, T12), by= "record_id")  
patientdata <- left_join(patientdata, statafile5 %>% select(record_id, smerte_tid), by= "record_id")
```

Ser om de giver det samme:

```
test1 <- univariateTable(data=patientdata,group~Q(T12)+Q(opioid_24h))  
summary(test1) # DET PASSER MED DE NYE TAL!
```

```
##      Variable      Level group = 0 (n=20) group = 1 (n=17)      Total (n=37)  
## 1      T12 median [iqr] 30 [21.9, 48.1]      10 [ 5, 35] 27.5 [10.0, 42.5]  
## 2 opioid_24h median [iqr] 30 [21.9, 48.1]      10 [ 5, 35] 27.5 [10.0, 42.5]  
##    p-value  
## 1 0.04206  
## 2 0.03906
```

```
patientdata$forskel_tid <- patientdata$smerte_tid-patientdata$breakthrough  
test2 <- univariateTable(data=patientdata,group~smerte_tid+Q(breakthrough))  
summary(test2) #DET PASSER MED DE NYE TAL!
```

```
##      Variable      Level group = 0 (n=20) group = 1 (n=17)      Total (n=37)  
## 1  smerte_tid  mean (sd)      4.1 (6.2)      9.8 (9.3)      6.7 (8.2)  
## 2 breakthrough median [iqr] 1.5 [0.8, 4.2] 5.5 [ 1.5, 15.7] 2 [ 1.2, 10.7]  
##    p-value  
## 1 0.02580  
## 2 0.03527
```