

# Patient flowchart and chi<sup>2</sup> tests

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## Import

```
dta_all<-read.csv("/Volumes/Data/depression/dep_dataset.csv")
```

## Defining patients to include for analysis

Only including cases with complete pase\_0 and MDI at 1 & 6 months

```
dta<-dta_all[!is.na(dta_all$pase_0),]  
# !is.na(dta$mdi_1)!is.na(dta$mdi_6)
```

## Backup

```
dta_b<-dta
```

## Sammentællinger

```
summary(cbind(is.na(dta_all[,c("pase_0", "mdi_1", "mdi_1_enr", "mdi_6_newobs", "mdi_6_newobs_enr")])),  
         both_missing=is.na(dta$mdi_1)&is.na(dta$mdi_6_newobs),  
         either_missing=is.na(dta$mdi_1)|is.na(dta$mdi_6_newobs)))
```

```
## Warning in cbind(is.na(dta_all[, c("pase_0", "mdi_1", "mdi_1_enr",  
## "mdi_6_newobs", : number of rows of result is not a multiple of vector length  
## (arg 2)
```

```
##   pase_0           mdi_1           mdi_1_enr           mdi_6_newobs  
## Mode :logical   Mode :logical   Mode :logical   Mode :logical  
## FALSE:625      FALSE:550      FALSE:559      FALSE:505  
## TRUE :17        TRUE :92        TRUE :83        TRUE :137  
## mdi_6_newobs_enr both_missing   either_missing  
## Mode :logical   Mode :logical   Mode :logical  
## FALSE:514      FALSE:576      FALSE:497  
## TRUE :128        TRUE :66        TRUE :145
```

```
suppressWarnings(summary(cbind(all_particip=dta_all$mors_180=="yes",
  all_pase0=dta$mors_180=="yes",
  all_mdi_1=!is.na(dta$mdi_1)&dta$mors_180=="yes"))) # Antal der dør
```

```
## all_particip    all_pase0      all_mdi_1
## Mode :logical  Mode :logical  Mode :logical
## FALSE:614     FALSE:619     FALSE:637
## TRUE :28      TRUE :23      TRUE :5
```

```
table(dta$pase_0_bin,factor(dta$mors_180)) # Antal der dør, stratificeret efter PASE gruppe
```

```
##
##           no yes
## higher 306  6
## lower  296 17
```

```
# summary(factor(dta$mors_v1))
# summary(factor(dta$mors_v16)) # OBS medregnet er 2 dødsfald, der ikke har MDI 1.
```

## Flow

### 1 month

Shows counts of all patients with missing MDI 1 scores.

```
source("/Volumes/Data/depression/function_flow.R") # Home made flow function
show(flow_prog(df=dta[dta$excluded_1%in%c("ex_1","mi_1","ca_1"),],
  sngl=c("mors_v1","drop1"),
  sngl_keep=c("no","yes"),
  mltp=c("open_treat","wants_out","side_effect","side_effect2")))
```

```
## $'nrow of provided data frame'
## [1] 71
##
## $mors_v1
##   mors_v1
## no      65
## yes     6
##
## $drop1
##   drop1
## no     22
## yes    43
##
## $'open_treat_for_drop1==yes'
##   open_treat
## no          43
##
## $'wants_out_for_drop1==yes'
```

```
##      wants_out
## no           2
## yes          41
##
## $'side_effect_for_drop1==yes'
##      side_effect
## no           39
## yes           4
##
## $'side_effect2_for_drop1==yes'
##      side_effect2
## no           41
## yes           2
```

```
# v1<-dta$rnumb[dta$excluded_1%in%c("ex_1","mi_1")]
```

Same overview, but vectorised

```
summary(factor(dta$excluded_1))
```

```
## ca_1 dt_1 en_1 ex_1 mi_1
##  16 545   9  49   6
```

```
# dt_1 are organic data, en_1 are enriched, ex_1 are excluded, mi_1 were missing,
# ca_1 were missing at 1 month, but held data at 6 months, and thus carried along.
```

## 6 months

Shows counts of all patients with missing MDI 6 scores.

```
show(flow_prog(df=dta[is.na(dta$mdi_6_newobs_enr)&dta$excluded_6%in%c("ex_6"),], #
  sngl=c("mors_v16","drop16"),
  sngl_keep=c("no","yes"),
  mltp=c("open_treat","wants_out","side_effect","side_effect2")))
```

```
## $'nrow of provided data frame'
## [1] 62
##
## $mors_v16
##      mors_v16
## no           60
## yes           2
##
## $drop16
##      drop16
## no           55
## yes           5
##
## $'open_treat_for_drop16==yes'
##      open_treat
## no             5
```

```
##
## $'wants_out_for_drop16==yes'
##   wants_out
## no         1
## yes        4
##
## $'side_effect_for_drop16==yes'
##   side_effect
## no          4
## yes         1
##
## $'side_effect2_for_drop16==yes'
##   side_effect2
## no          4
## yes         1
```

```
# v2<-dta$rnumb[is.na(dta$mdi_6_newobs_enr)&dta$excluded_1%in%c("ca_1","dt_1")]
```

```
summary(factor(dta$excluded_6))
```

```
## dt_6 en_6 ex_6 mi_6
## 499   9  62  55
```

```
# dt_6 are organic data, en_6 are enriched, ex_6 are excluded, mi_6 were excluded at 1 month.
# At 6 month 118 are excluded due to any cause
# Due to later inclusion of ca_1 patients, the sum of patients excluded at 6 months is 71+62-16=117
```

This flow counts all patients dying or dropping out early after 1 month. Some have a recorded MDI at dropout. This is just to give a perspective on data.

```
show(flow_frog(df=dta, #
              sngl=c("mors_v16","drop16"),
              sngl_keep=c("no","yes"),
              mltp=c("open_treat","wants_out","side_effect","side_effect2")))
```

```
## $'nrow of provided data frame'
## [1] 625
##
## $mors_v16
##   mors_v16
## no       617
## yes       8
##
## $drop16
##   drop16
## no     544
## yes    73
##
## $'open_treat_for_drop16==yes'
##   open_treat
## no         28
## yes        45
```

```
##
## $'wants_out_for_drop16==yes'
##   wants_out
## no         53
## yes        20
##
## $'side_effect_for_drop16==yes'
##   side_effect
## no         59
## yes        14
##
## $'side_effect2_for_drop16==yes'
##   side_effect2
## no         61
## yes        12
```

```
# v2<-dta$rnumb[is.na(dta$mdi_6_newobs_enr)&dta$excluded_1%in%c("ca_1","dt_1")]
```

```
summary(as.numeric(dta$inc_time[dta$drop16=="yes"]))
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   39.0   82.5   110.0   125.1   170.0   471.0
```

## Chi<sup>2</sup> tests

```
source("/Volumes/Data/depression/function_chi_test_sum.R")
ex_lst<-list()
ex_var<-c("mdi_1_enr","rtreat","pase_0_bin")
for (i in 2:3){
  ex_lst <- append(ex_lst,chi_test_sum(a=is.na(dta[,ex_var[1]]),
                                     b=dta[,ex_var[i]],
                                     aname=ex_var[1],
                                     bname=ex_var[i]))
}
```

```
# ex_var<-c("open_treat","rtreat","pase_0_bin")
# for (i in 2:3){
#   ex_lst <- append(ex_lst,
#                   chi_test_sum(a=dta[,ex_var[1]],
#                               b=dta[,ex_var[i]],
#                               aname=ex_var[1],
#                               bname=ex_var[i]))
# }
```

```
## Target ud grundet for lave tal
```

```
ex_var<-c("mdi_1_enr","rtreat","pase_0_bin")
for (i in 2:3){
  ex_lst <- append(ex_lst,
                  chi_test_sum(a=is.na(dta$mdi_6_newobs_enr)&!is.na(dta$mdi_1_enr),
```

```

        b=dta[,ex_var[i]],
        aname="Excluded at 6 months",
        bname=ex_var[i]))
}
for (i in 2:3){
  ex_lst <- append(ex_lst,
                   chi_test_sum(a=is.na(dta$mdi_6_newobs_enr),
                                b=dta[,ex_var[i]],
                                aname="Total unavailable at 6 months",
                                bname=ex_var[i]))
}

```

```

# ex_var<-c("open_treat","rtreat","pase_0_bin")
# for (i in 2:3){
#   ex_lst <- append(ex_lst,
#                    chi_test_sum(a=dta[,ex_var[1]],
#                                  b=dta[,ex_var[i]],
#                                  aname=ex_var[1],
#                                  bname=ex_var[i]))
# }
show(ex_lst)

```

```

## $'observed, mdi_1_enr vs rtreat'
##      Active Placebo
## FALSE      264      290
## TRUE       45      26
##
## $'pval^'
## [1] 0.01781914
##
## $'observed, mdi_1_enr vs pase_0_bin'
##      higher lower
## FALSE      286      268
## TRUE       26      45
##
## $'pval^'
## [1] 0.0241552
##
## $'observed, Excluded at 6 months vs rtreat'
##      Active Placebo
## FALSE      286      277
## TRUE       23      39
##
## $'pval^'
## [1] 0.05557436
##
## $'observed, Excluded at 6 months vs pase_0_bin'
##      higher lower
## FALSE      288      275
## TRUE       24      38
##
## $'pval^'
## [1] 0.08429996

```

```
##
## $'observed, Total unavailable at 6 months vs rtreat'
##      Active Placebo
## FALSE      247      261
## TRUE        62       55
##
## $'pval^'
## [1] 0.4534395
##
## $'observed, Total unavailable at 6 months vs pase_0_bin'
##      higher lower
## FALSE      268      240
## TRUE        44       73
##
## $'pval^'
## [1] 0.004343526
```