

# Data export and wrangling

Andreas Gammelgaard Damsbo

Knitted: 06 January, 2022

## Contents

<b>Variables</b>	<b>2</b>
New additions and formatting . . . . .	2
Formatting . . . . .	3
<b>Cleaning MDI scores</b>	<b>3</b>
Step 1 . . . . .	3
Step 2 . . . . .	4
Step 3 . . . . .	4
Step 4 . . . . .	5
Step 5 . . . . .	5
<b>Visit delay</b>	<b>5</b>
<b>newobs definition - DEPRECATED</b>	<b>5</b>
<b>Drops</b>	<b>6</b>
<b>Enriching</b>	<b>7</b>
<b>Main Dataset export</b>	<b>8</b>

```
library(haven)
library(plyr)
library(dplyr)
library(reshape2)
```

```
dta<-read.csv("/Volumes/Data/exercise/source/background.csv",
             na.strings = c("NA",""),colClasses = "character")
# dta_b<-dta
```

## Variables

List of variables included in dataset

```
dput(names(dta))
```

```
## c("cpr", "rnumb", "rdate", "rtreat", "compliant", "wants_out",  
## "side_effect", "open_treat", "side_effect2", "eos_done", "protocol",  
## "enddate", "eos_early", "mors_d", "mors_p", "inc_time", "completed",  
## "mors_180", "intention_t", "who5_score_0", "who5_score_1", "who5_score_6",  
## "who5_cut_0", "who5_cut_1", "who5_cut_6", "sdmt_1_c", "sdmt_6_c",  
## "mmse_6", "mmse_single", "mmse_range", "mmse_severity", "mmse_clin",  
## "cprdash", "debut_time", "deb_adm", "time_diff", "nihss_0", "mrs_0",  
## "mrs_1", "mrs_6", "visit_1", "visit_6", "mrs_0_cut2", "mrs_1_cut2",  
## "mrs_6_cut2", "mrs_0_cut1", "mrs_1_cut1", "mrs_6_cut1", "mrs_0_cut0",  
## "mrs_1_cut0", "mrs_6_cut0", "dob", "age", "sex", "pase_0_date",  
## "pase_0", "pase_6_date", "pase_6", "pase_0_q", "pase_0_m", "pase_6_q",  
## "pase_06_q", "pase_6_m", "pase_time", "mdi_1", "mdi_6", "mfi_gen_1",  
## "mfi_phys_1", "mfi_act_1", "mfi_mot_1", "mfi_men_1", "mfi_gen_bin_1",  
## "mfi_phys_bin_1", "mfi_act_bin_1", "mfi_mot_bin_1", "mfi_men_bin_1",  
## "mfi_gen_6", "mfi_phys_6", "mfi_act_6", "mfi_mot_6", "mfi_men_6",  
## "mfi_gen_bin_6", "mfi_phys_bin_6", "mfi_act_bin_6", "mfi_mot_bin_6",  
## "mfi_men_bin_6", "diabetes", "hypertension", "claud", "pad",  
## "height", "weight", "weight_est", "afl", "smoker", "alc", "civil",  
## "bolig", "ami", "tci", "thrombolysis", "thrombechtomy", "dap_nihss",  
## "dap_nihss_24", "smoke_ever", "nihss_c", "nihss_clin5", "rep_any",  
## "vasc_dis", "age_std", "nihss_std", "pase_0_std", "est_weight",  
## "bmi", "bmi_cut", "pase_change", "pase_qfall", "pase_dcln", "pase_drop",  
## "pase_extreme", "pase_0_q_n", "pase_06_q_n", "delta_pase", "pase_change_num"  
## )
```

## New additions and formatting

```
dta$mors_delay<-difftime(as.Date(dta$mors_d),as.Date(dta$rdate),units = "days")  
dta$mors_v1<-factor(ifelse(dta$mors_delay<=38&  
                          (dta$mors_delay-as.numeric(dta$inc_time))<=1,  
                          "yes","no"))  
# Tæller som død hvis død inden 38 dage og dødsdato og EOS ligger indenfor 1 døgn.  
dta$mors_v1[is.na(dta$mors_v1)]<-"no"
```

```
dta$mors_v16<-factor(ifelse(dta$mors_v1=="no"&  
                          (dta$mors_delay-as.numeric(dta$inc_time))<=1,  
                          "yes","no"))  
# Tæller som død mellem 1 til 6 mdr, hvis ikke død inden 1 mdr,  
# og dødsdato og EOS ligger indenfor 1 døgn.  
dta$mors_v16[is.na(dta$mors_v16)]<-"no"
```

PASE score dichotomisation at median score.

```
dta$pass_0<-as.numeric(dta$pass_0)
dta$pass_0_bin<-cut(dta$pass_0,
                    c(min(dta$pass_0,na.rm = T),median(dta$pass_0,na.rm = T),
                      max(dta$pass_0,na.rm = T)),include.lowest = T,
                    labels = c("lower","higher"))
quantile(dta$pass_0,na.rm = T)
```

```
##      0%      25%      50%      75%     100%
##  0.00  76.40 132.50 197.00 574.26
```

## Formatting

```
dta$inc_time<-as.numeric(dta$inc_time)
```

## Cleaning MDI scores

The following contains a serious bit of data wrangling. Reasons are the occasional recording of visit 1 data at 6 months due to LOCF approach. Additionally some patients have data recorded at 6 months, but later end date has been defined as prior to the visit 6. Additionally the definition of when to define a MDI recording as 1 month or 6 months have added a bit of extra work..

This work should be applied for all endpoint data. If needed, a general script or function should be written.

Steps used for the correction:

1. If the inc\_time is 38 days or less MDI 6 scores are moved to MDI 1 and visit 6 is defined as visit 1.
2. If both visit 1 and 6 dates are NA, use enddate as visit 1 date. This is the case if patients were excluded early.
3. If visit 6 is recorded later than enddate, use enddate instead. MDI 6 score is dropped.
4. If visit delay is 7 days or less, and inclusion time is more than 38, MDI 1 is moved to MDI 6 and dropped. If MDI 1 and 6 are different both are kept. Enddate is moved to visit 6 date.
5. Defining the visit 6 date as same as enddate if visit delay is <7.

```
summary(inc196<-dta$inc_time>196)
```

```
##      Mode  FALSE   TRUE
## logical    612    30
```

```
dt1<-dta[inc196,c("rnumb","rdate","visit_1","visit_6","enddate","inc_time","mdi_1","mdi_6","mors_delay")]
```

## Step 1

```
summary(inc38<-dta$inc_time<=38)
```

```
##      Mode  FALSE   TRUE
## logical    549    93
```

```

dt1<-dta[inc38,c("rnumb","rdate","visit_1","visit_6","inc_time","mdi_1","mdi_6")]
dta$visit_1<-ifelse(inc38&!is.na(dta$visit_6),dta$visit_6,dta$visit_1)
dta$mdi_1<-ifelse(inc38&is.na(dta$mdi_1),dta$mdi_6,dta$mdi_1)
dta$mdi_6[inc38]<-NA
dta$visit_6[inc38]<-NA
# If the inc_time is 38 days or less MDI 6 scores are moved to MDI 1 and visit 6 is defined as visit 1.
# LOCF correction.

```

## Step 2

```
summary(na16enddate<-is.na(dta$visit_1)&is.na(dta$visit_6))
```

```
##      Mode  FALSE   TRUE
## logical    570    72
```

```

dt2<-dta[na16enddate,c("rnumb","rdate","visit_1","visit_6","inc_time","mdi_1","mdi_6")]
dta$visit_1<-ifelse(na16enddate,dta$enddate,dta$visit_1)
# If both visit 1 and 6 dates are NA, use enddate as visit 1 date. This is the case if patients were ex

```

## Step 3

```
summary(late61<-as.Date(dta$visit_6)>as.Date(dta$enddate)&difftime(as.Date(dta$visit_6),as.Date(dta$end
```

```
##      Mode  FALSE   TRUE   NA's
## logical    537     2    103
```

```
summary(late62<-as.Date(dta$visit_6)>as.Date(dta$enddate)&difftime(as.Date(dta$visit_6),as.Date(dta$end
```

```
##      Mode  FALSE   TRUE   NA's
## logical    530     9    103
```

```

late61[is.na(late61)]<-FALSE
late62[is.na(late62)]<-FALSE

# dt5<-dta[late61,c("rnumb","rdate","visit_1","visit_6","enddate","inc_time","mdi_1","mdi_6")]
# dt6<-dta[late62,c("rnumb","rdate","visit_1","visit_6","enddate","inc_time","mdi_1","mdi_6")]

dta$visit_6<-ifelse(late61,dta$enddate,dta$visit_6)
dta$visit_6<-ifelse(late62,dta$enddate,dta$visit_6)
dta$mdi_6[late62]<-NA
# If visit 6 is recorded later than enddate, use enddate instead
# A group of patients have visit 6 and MDI 6 recorded, but enddate is before visit 6 data.
# After manual lookups, this is likely due to some patients coming for visit 6, but the
# interviewer later realizing, that the patients should have been excluded earlier on.
# Due to this, patients with enddate more than 1 day (leaving room for simple recording errors) prior t
# Patients with 1 day difference the enddate is moved to visit 6 date.

```

## Step 4

```
summary(locflatedata<-difftime(as.Date(dta$visit_6),as.Date(dta$visit_1))<=7|is.na(dta$visit_1))&dta$inc_t
```

```
##      Mode  FALSE   TRUE   NA's  
## logical    620    12    10
```

```
locflatedata[is.na(locflatedata)]<-FALSE
```

```
dt2<-dta[locflatedata,c("rnumb","rdate","visit_1","visit_6","inc_time","mdi_1","mdi_6")]
```

```
dta$mdi_6<-ifelse(locflatedata&is.na(dta$mdi_6),dta$mdi_1,dta$mdi_6)
```

```
dta$mdi_1[locflatedata&dta$mdi_1==dta$mdi_6]<-NA
```

```
dta$visit_1[locflatedata&is.na(dta$mdi_1)]<-NA
```

```
dta$visit_6<-ifelse(locflatedata,dta$enddate,dta$visit_6)
```

```
# If visit delay is 7 days or less, and inclusion time is more than 38, MDI 1 is moved to MDI 6 and drops
```

## Step 5

```
summary(samein6date<-difftime(as.Date(dta$visit_6),as.Date(dta$visit_1),units = "days")<7)
```

```
##      Mode  FALSE   TRUE   NA's  
## logical    527     1    114
```

```
samein6date[is.na(samein6date)]<-FALSE
```

```
# dt5<-dta[samein6date,c("rnumb","rdate","visit_1","visit_6","enddate","inc_time","mdi_1","mdi_6",drops
```

```
dta$visit_6<-ifelse(samein6date,dta$enddate,dta$visit_6)
```

```
# Defining the visit 6 date as same as enddate if visit delay is <7.
```

## Visit delay

```
dta$visit_delay<-difftime(as.Date(dta$visit_6),as.Date(dta$visit_1),units = "days")
```

```
# Final calculation of days between visits
```

```
summary(as.numeric(dta$visit_delay))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's  
##      13.0  145.0  152.0  143.6  155.0  286.0   114
```

## newobs definition - DEPRECATED

The definition of a truly new observation is a recorded score at least 7 days after the first score. This was relevant prior to the work of redefining time points for scoring.

```
dta$mdi_6_newobs<-dta$mdi_6
# The newobs variable is later used, but is obsolete due to the previous change in definitions. The pre

# dta$mdi_6_166<-ifelse(dta$inc_time>166,NA,dta$mdi_6)
# dta$mdi_6_80<-ifelse(dta$inc_time>80,NA,dta$mdi_6)
# dta$mdi_6_protocol<-ifelse(dta$protocol=="2",NA,ifelse(is.na(dta$mdi_6),dta$mdi_1,dta$mdi_6))
# dta$mdi_6_locf<-ifelse(is.na(dta$mdi_6),dta$mdi_1,dta$mdi_6)
```

## Drops

Streamlining drop out data to avoid NA's.

```
drops<-c("side_effect2","side_effect","wants_out","open_treat")
for (i in drops) {
  dta[i]<-ifelse(dta[i]=="1. Ja","yes","no")
  dta[i][is.na(dta[i])]<- "no"
}
```

Defining a common all cause drop variable

```
dta$drop<-ifelse(dta$side_effect2=="yes"|dta$side_effect=="yes"|dta$wants_out=="yes"|dta$open_treat=="y
```

Defining drop before or at day 38 (Following protocol design) as drop before 1 month and drop after day 38 as drop between 1 and 6 months

```
cut_line<-38
dta$inc_time<-as.numeric(dta$inc_time)
dta$drop1<-ifelse(dta$drop=="yes"&dta$inc_time<=cut_line,"yes","no")
summary(factor(dta$drop1))
```

```
## no yes
## 568 74
```

```
# dt3<-dta[,c("rnumb","rdate","visit_1","visit_6","inc_time","mdi_1","mdi_6","mdi_6_newobs","drop1","dr
```

```
dta$drop16<-ifelse(dta$drop=="yes"&dta$inc_time>cut_line,"yes","no")
summary(factor(dta$drop16))
```

```
## no yes
## 567 75
```

```
summary(factor(dta$drop))
```

```
## no yes
## 493 149
```

```
# dtf<-dta[dta$drop1=="yes",c("mdi_6_newobs","inc_time")]
# dtf<-dta[,c("mdi_1","mdi_6_newobs","inc_time","drop","drop1","drop16")]
```

## Enriching

With patients excluded due to open treatment need and defining populations to include/exclude

```
summary(sel_enr_1<-dta$open_treat=="yes"&is.na(dta$mdi_1)&dta$drop1=="yes")
```

```
## open_treat
## Mode :logical
## FALSE:633
## TRUE :9
```

```
dta$mdi_1_enr<-ifelse(sel_enr_1,21,dta$mdi_1) # Per agreement, patients excluded due to open treatment
```

Vectorising ex/inclusions at 1 month, to keep patients with data or with later data.

```
summary(dta$excluded_1<-factor(case_when(dta$mors_v1=="yes" |
                                         is.na(dta$mdi_1_enr)&
                                         dta$drop1=="yes"~"ex_1", # Excluded
                                         is.na(dta$mdi_1_enr)&!is.na(dta$mdi_6_newobs)~"ca_1", # Missing, but carried t
                                         is.na(dta$mdi_1_enr)~"mi_1", # Missing,
                                         is.na(dta$mdi_1)&!is.na(dta$mdi_1_enr)~"en_1",
                                         TRUE ~ "dt_1"))) # Data available
```

```
## ca_1 dt_1 en_1 ex_1 mi_1
## 17 550 9 55 11
```

```
summary(sel_enr_6<-dta$open_treat=="yes"&dta$drop16=="yes"&is.na(dta$mdi_6_newobs)&dta$excluded_1%in%c(
```

```
## open_treat
## Mode :logical
## FALSE:633
## TRUE :9
```

```
# Entries to be enriched are entries with need for open treatment after 1 month, with missing mdi_6_new
```

```
dta$mdi_6_newobs_enr<-as.numeric(ifelse(sel_enr_6,21,dta$mdi_6_newobs)) # Per agreement, patients excl
```

```
summary(dta$excluded_6<-factor(case_when(is.na(dta$mdi_6_newobs_enr)&dta$excluded_1%in%c("ca_1","dt_1",
                                             is.na(dta$mdi_6_newobs_enr)~"mi_6", # Missing data due to excl
                                             is.na(dta$mdi_6_newobs)&!is.na(dta$mdi_6_newobs_enr)~"en_6", #
                                             dta$excluded_1%in%c("ca_1","dt_1")~"dt_6" # Organic data avail
                                             ))) # Data available
```

```
## dt_6 en_6 ex_6 mi_6
## 505 9 62 66
```

```
# dtf<-cbind(dta[,c("rnumb", "mdi_1", "mdi_6_newobs", "inc_time", "drop", "drop1", "drop16", "mdi_1_enr", "mdi_1_
#
# summary(dtf %>% filter(excluded==TRUE))
```

## Main Dataset export

```
variable_namebits<-c("rnumb", "rtreat", "age", "sex",
                    "bmi",
                    "smoke_ever",
                    "civil",
                    "diabetes",
                    "hypertension",
                    "pad",
                    "afl",
                    "ami",
                    "tci",
                    "nihss_0",
                    "thrombolysis",
                    "thrombechtomy",
                    "rep_any",
                    "pase_0",
                    "pase_6",
                    "mrs_0", "mrs_1", "mrs_6",
#                    "who5_score",
                    "mdi",
#                    "ham_score_1", "ham_score_6",
                    "mors",
                    "drop",
                    "wants_out",
                    "side_effect",
                    "open_treat",
                    "side_effect2",
                    "excluded",
                    "protocol", "eos_early", "inc_time",
                    "rdate", "visit", "enddate"
                    )
```

```
export<-dta %>% select(contains(variable_namebits))
```

```
write.csv(export, "/Volumes/Data/depression/dep_dataset.csv", row.names = FALSE)
```