model.rmd

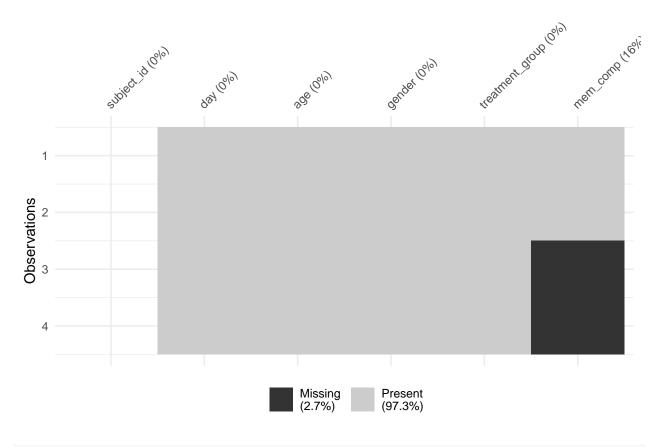
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2024-03-20

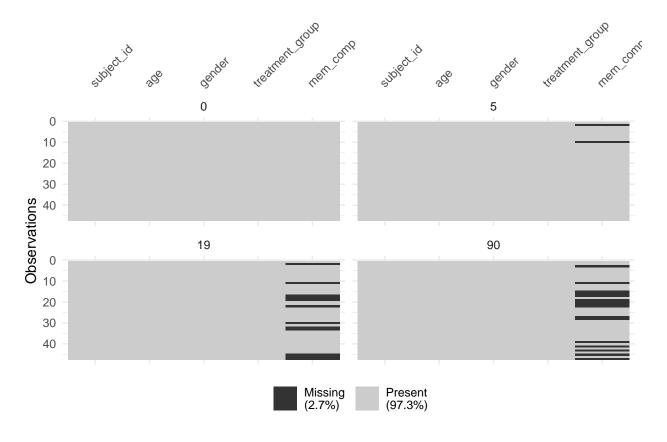
```
library(mice)
## Attaching package: 'mice'
## The following object is masked from 'package:stats':
##
##
       filter
## The following objects are masked from 'package:base':
##
##
       cbind, rbind
library(tidyr)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
library(visdat)
library(naniar)
library(ggplot2)
data <- read.csv("data.csv") %>%
  janitor::clean_names()
# pre-processing: expand design matrix and fill in NAs
full_data <- data %>%
  complete(day,
           nesting(subject_id, treatment_group)) %>%
```

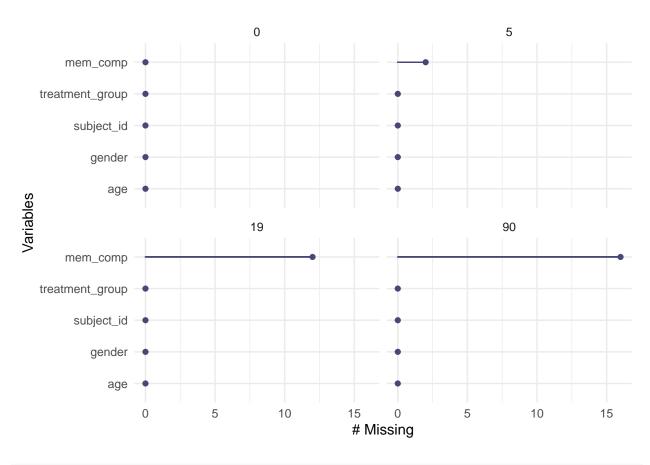
```
relocate(day, .after = subject_id) %>%
relocate(treatment_group, .after = gender) %>%
group_by(subject_id) %>%
fill(age, gender, .direction = "downup") %>%
arrange(subject_id, day)
```

vis_miss(full_data)



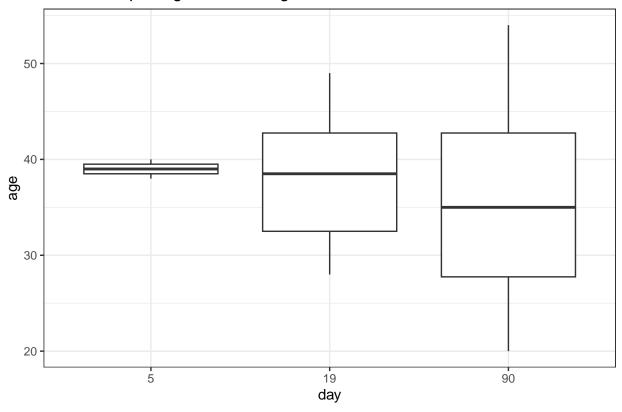
vis_miss(full_data, facet = day)





```
full_data %>% filter(is.na(mem_comp)) %>%
    ggplot(aes(x=as.factor(day)))+
    geom_boxplot(aes(y=age))+
    theme_bw()+
    xlab("day")+
    ggtitle("Relationship of age and missing values")
```

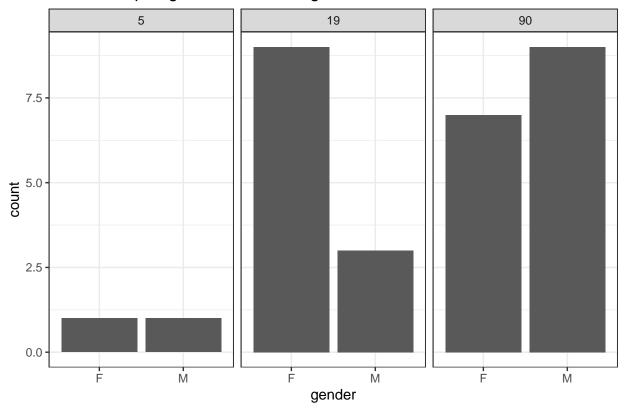
Relationship of age and missing values



```
full_data %>% filter(is.na(mem_comp)) %>%
   ggplot()+
   geom_bar(aes(x=gender, stat = "count"))+
   facet_wrap(day~.)+
   theme_bw()+
   xlab("gender")+
   ggtitle("Relationship of gender and missing values")
```

```
## Warning in geom_bar(aes(x = gender, stat = "count")): Ignoring unknown
## aesthetics: stat
```

Relationship of gender and missing values



```
# assume MAR
# multiple imputations
imputed_data <- mice::mice(data = full_data, m = 6, seed =2024, print = FALSE)</pre>
```

Warning: Number of logged events: 2

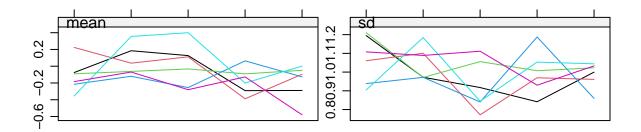
imputed_data

```
## Class: mids
## Number of multiple imputations: 6
## Imputation methods:
##
       subject_id
                                               age
                                                            gender treatment_group
##
##
         mem_comp
             "pmm"
##
## PredictorMatrix:
                   subject_id day age gender treatment_group mem_comp
## subject_id
                            0
                                           0
                                                           0
## day
                            1
                                0
                                    1
                                           0
                                                           0
                                                                    1
## age
                                1
                                                                    1
                                                           0
## gender
                            1
                                    1
                                           0
                                                                    1
                                1
## treatment_group
                                    1
                                           0
                                                           0
                                                                    1
## mem_comp
                                    1
                            1
## Number of logged events: 2
##
     it im dep
                  meth
                                    out
```

```
## 1 0 0 constant gender
## 2 0 0 constant treatment_group
```

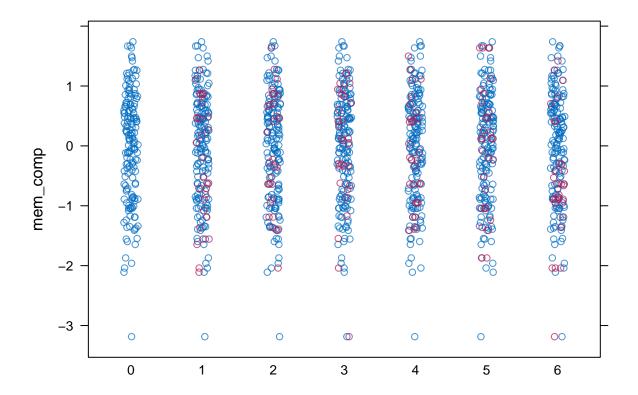
```
# used pmm method
```

```
# check convergence
plot(imputed_data)
```



Iteration

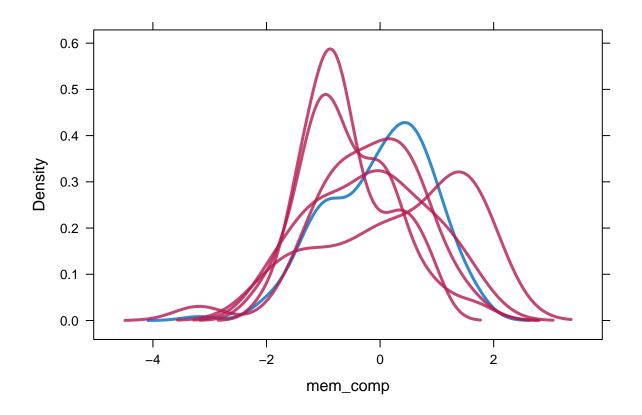
```
# check if imputed data makes sense (ie. in a reasonable bound)
# red is imputed, blue is observed
mice::stripplot(imputed_data, mem_comp)
```



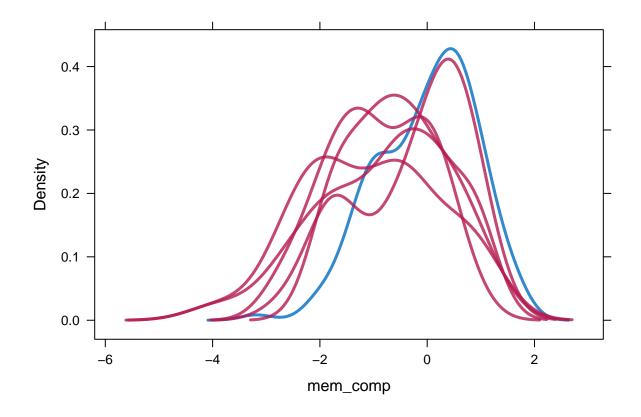
```
# fit model to each imputed datasets
# pool coef estimates and standard errors to create 95% CIs
# sensitivity analysis for each data missing assumptions
# mcar - fit data with completers data
# mnar - fill na's with different delta --> fit model --> CI's
# Create a delta vector that represent the following adjustment values for mmHg: 0 for MAR, and -0.7, -
delta \leftarrow c(0, -0.7, -0.2, 0.2, 0.7)
imp.all <- vector("list", length(delta))</pre>
post <- imputed_data$post</pre>
for (i in 1:length(delta)){
  d <- delta[i]
  cmd <- paste("imp[[j]][,i] <- imp[[j]][,i] +", d)</pre>
  post["mem_comp"] <- cmd</pre>
  imp <- mice::mice(full_data, post = post, seed = i, print = FALSE)</pre>
  imp.all[[i]] <- imp</pre>
## Warning: Number of logged events: 2
```

Warning: Number of logged events: 2

```
## Warning: Number of logged events: 2
## Warning: Number of logged events: 2
## Warning: Number of logged events: 2
## imputation with no adjustment (delta = 0)
densityplot(imp.all[[1]], lwd = 3)
```



```
# imputation with adjustment (delta = -0.7)
densityplot(imp.all[[2]], lwd = 3)
```



imputation with adjustment (delta = 0.7)
densityplot(imp.all[[5]], lwd = 3)

