

model.rmd

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```
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
```

```
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)
```

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

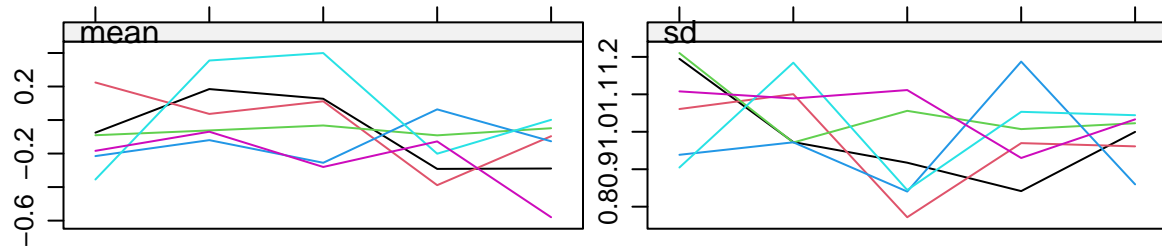
```
## Warning: Number of logged events: 2
```

```
imputed_data
```

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

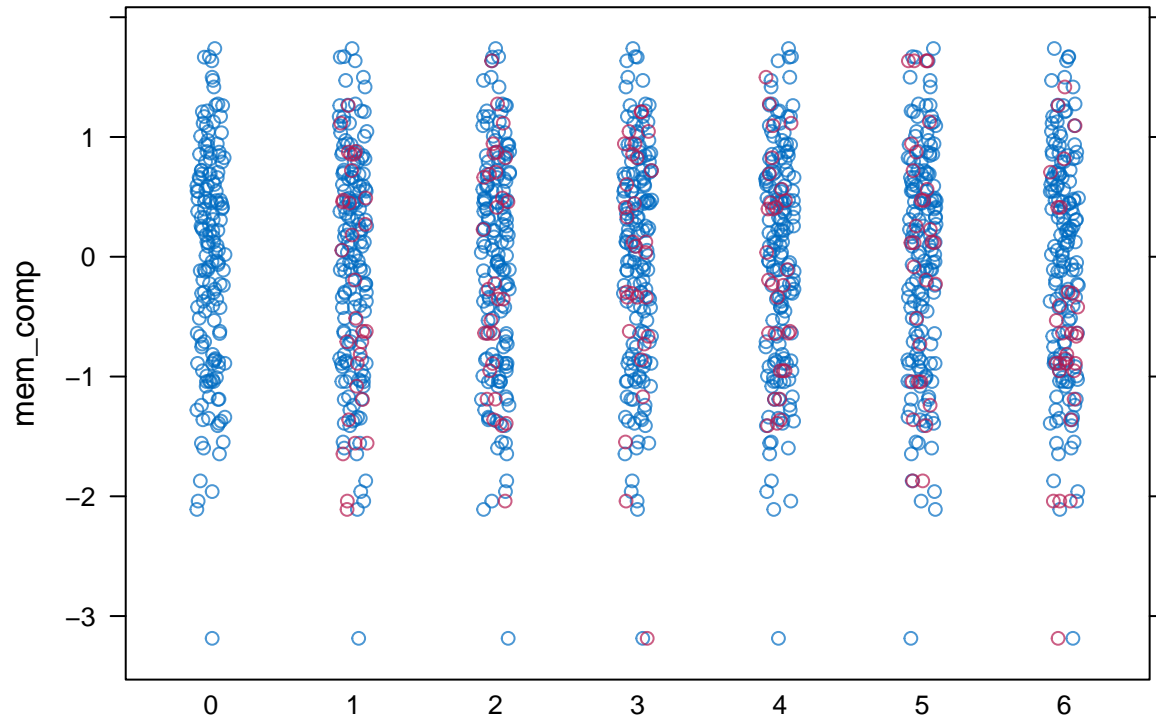
```
# used pmm method
```

```
# 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
```

```
# mmnr - 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 <- c(0, -0.7, -0.2, 0.2, 0.7 )
```

```
imp.all <- vector("list", length(delta))  
post <- imputed_data$post  
for (i in 1:length(delta)){  
  d <- delta[i]  
  cmd <- paste("imp[[j]][,i] <- imp[[j]][,i] +", d)  
  post["mem_comp"] <- cmd  
  imp <- mice::mice(full_data, post = post, seed = i, print = FALSE)  
  imp.all[[i]] <- imp  
}
```

```
## Warning: Number of logged events: 2
```

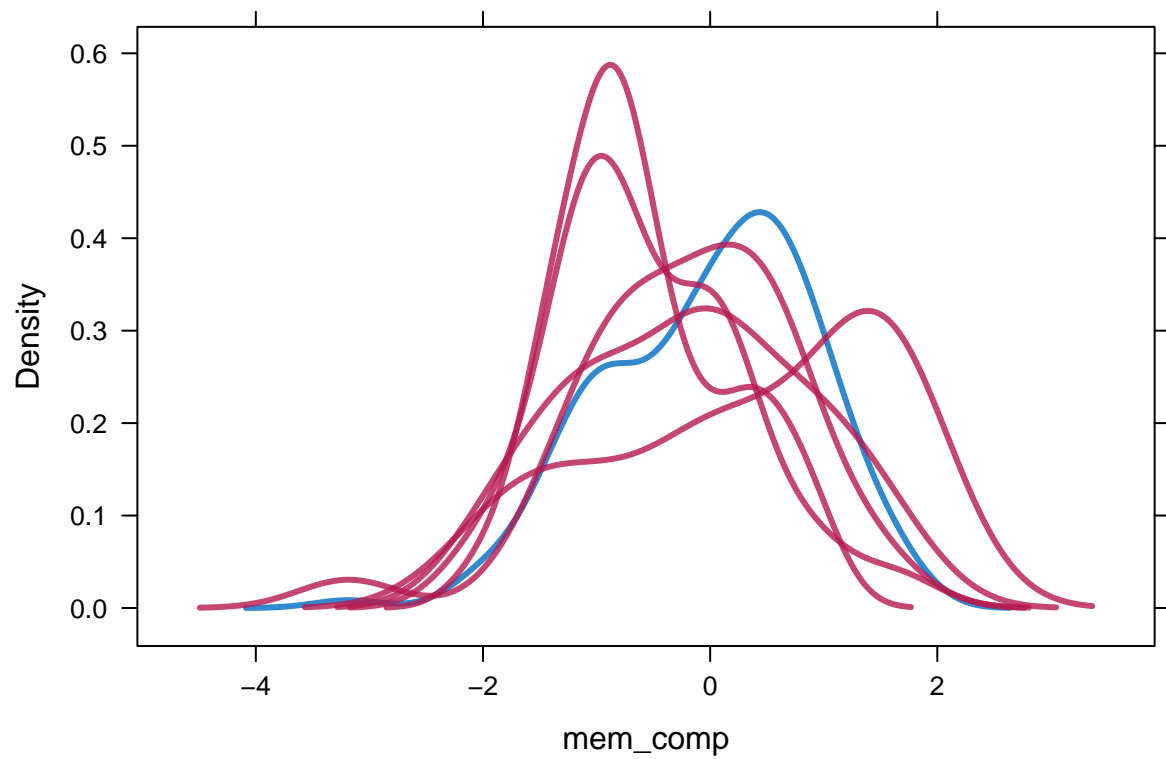
```
## Warning: Number of logged events: 2
```

```
## Warning: Number of logged events: 2
```

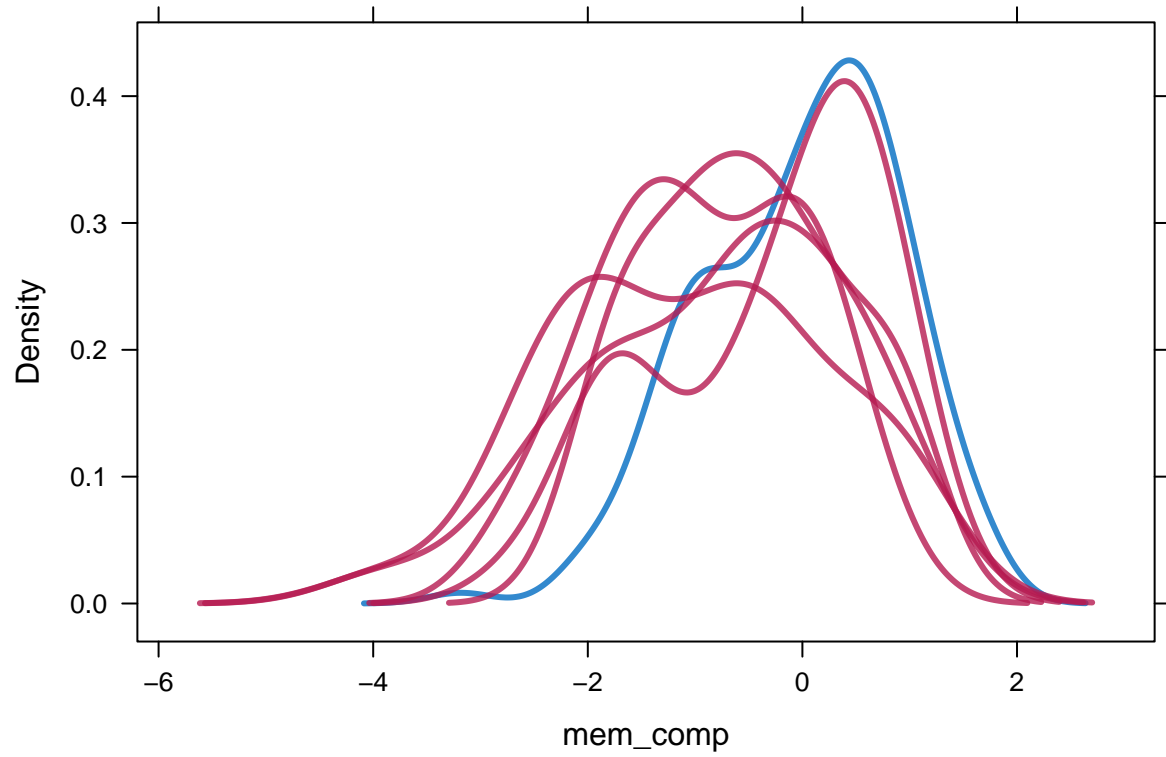
```
## Warning: Number of logged events: 2
```

```
## 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)
```

