4.2_Mice_imputation_field.rmd

Fay

2022-11-01

field

Load libraries

```
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)
```

```
## Warning: package 'tidyr' was built under R version 4.2.1
```

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.2.1

## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --

## v ggplot2 3.3.6      v dplyr   1.0.10
## v tibble  3.1.8      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## v purrr   0.3.5

## Warning: package 'tibble' was built under R version 4.2.1

## Warning: package 'readr' was built under R version 4.2.1
```

```
## Warning: package 'purrr' was built under R version 4.2.1

## Warning: package 'dplyr' was built under R version 4.2.1

## Warning: package 'stringr' was built under R version 4.2.1

## Warning: package 'forcats' was built under R version 4.2.1

## -- Conflicts --------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks mice::filter(), stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(VIM)
```

```
## Warning: package 'VIM' was built under R version 4.2.1

## Loading required package: colorspace
## Loading required package: grid
## VIM is ready to use.
##
## Suggestions and bug-reports can be submitted at: https://github.com/statistikat/VIM/issues
##
## Attaching package: 'VIM'
##
## The following object is masked from 'package:datasets':
##
##     sleep
```

```
library(fitdistrplus)
```

```
## Loading required package: MASS

## Warning: package 'MASS' was built under R version 4.2.1

##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
##
## Loading required package: survival

## Warning: package 'survival' was built under R version 4.2.1
```

```
library(fitur)
```

```
## Warning: package 'fitur' was built under R version 4.2.1
```

```
##
## Attaching package: 'fitur'
##
## The following object is masked from 'package:purrr':
##
##     rdunif
```

```
library(visdat)
```

Load data

Import data

```
hm <- read.csv("output_data/MICE.csv")
```

```
# Vectors for selecting genes

#Lab genes
# The measurements of IL.12 and IRG6 are done with an other assay and will
#ignore for now
Gene_lab   <- c("IFNy", "CXCR3", "IL.6", "IL.13", "IL.10",
                "IL1RN","CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",
                "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",
                "TICAM1", "TNF") #"IL.12", "IRG6")

Genes_wild   <- c("IFNy", "CXCR3", "IL.6", "IL.13", "IL.10",
                  "IL1RN","CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",
                  "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",
                  "TICAM1", "TNF") #, "IL.12", "IRG6")

Facs_lab <- c("CD4", "Treg", "Div_Treg", "Treg17", "Th1",
                    "Div_Th1", "Th17", "Div_Th17", "CD8", "Act_CD8",
                    "Div_Act_CD8", "IFNy_CD4", "IFNy_CD8","Treg_prop",
                    "IL17A_CD4")

Facs_wild <- c( "Treg", "CD4", "Treg17", "Th1", "Th17", "CD8",
                     "Act_CD8", "IFNy_CD4", "IL17A_CD4", "IFNy_CD8")
```

Field data imputation

Genes

```
# field samples
field <- hm %>%  filter(origin == "Field")

gf_field <- field %>%
```

```
  dplyr::select(all_of(c(Genes_wild)))

vis_dat(gf_field)
```

```
## Warning: `gather_()` was deprecated in tidyr 1.2.0.
## i Please use `gather()` instead.
## i The deprecated feature was likely used in the visdat package.
##   Please report the issue at <https://github.com/ropensci/visdat/issues>.
```


```
#remove rows with only nas
gf_field <- gf_field[,colSums(is.na(gf_field))<nrow(gf_field)]

#remove colums with only nas
gf_field <- gf_field[rowSums(is.na(gf_field)) != ncol(gf_field), ]


#select same rows in the first table
field_genes <- field[row.names(gf_field), ]


#remove wrongly normalized genes
field <- field %>%
  dplyr::select(-ends_with("_N"))

# really removing empty columns
```

```r
field_genes <- field_genes %>%
  discard(~all(is.na(.) | . ==""))



# looking at patterns of nas
#pattern_na <-as.data.frame(md.pattern(field_genes))

#sapply(field, function(x) sum(is.na(x)))

#select the relevant columns to use for the imputation
field_genes <- field_genes %>%
  dplyr::select(c(Mouse_ID, MC.Eimeria, delta_ct_cewe_MminusE, Sex, Longitude, Latitude,
                  Year, mtBamH, YNPAR, X332, X347, X65, Tsx, Btk, Syap1, Es1,
                  Gpd1, Idh1, Mpi, Np, Sod1, Es1C, Gpd1C, Idh1C, NpC, Sod1C,
                  HI_NLoci,  Spleen, Trichuris_muris, Mastophorus_muris,
                  Catenotaenia_pusilla, Status,
                  Heterakis_sp, N_oocysts_sq1,
                  N_oocysts_sq2, N_oocysts_sq3, N_oocysts_sq4, N_oocysts_sq5,
                  N_oocysts_sq6, N_oocysts_sq7, N_oocysts_sq8, Region,
                  Body_Length, Fleas, Tail_Length, eimeriaSpecies, Ct.Eimeria,
                  Ct.Mus, ILWE_Crypto_Ct, Aspiculuris_sp, Syphacia_sp, Taenia_sp,
                  Hymenolepis_sp, FEC_Eim_Ct,
                  all_of(Genes_wild)))

#had to remove as they were disturbing the imputation: Worms_presence, MC.Eimeria.FEC,  Heligmosomoides

#vis_miss(field)


# The frequency distribution of the missing cases per variable can be obtained
# as:
init <- mice(field_genes, maxit = 0)
```

```
## Warning: Number of logged events: 24
```

```r
#we want to impute only the specific variables
meth <- init$method

# m=5 refers to the number of imputed datasets. Five is the default value.
igf <- mice(field_genes, m = 5, seed = 500) # method = meth,
```

```
##
##  iter imp variable
##   1   1  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   1   2  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   1   3  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   1   4  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   1   5  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   2   1  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   2   2  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   2   3  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
```

```
##   2   4  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   2   5  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   3   1  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   3   2  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   3   3  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   3   4  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   3   5  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   4   1  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   4   2  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   4   3  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   4   4  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   4   5  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   5   1  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   5   2  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   5   3  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   5   4  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts
##   5   5  MC.Eimeria  delta_ct_cewe_MminusE  HI_NLoci  Spleen  N_oocysts_sq1  N_oocysts_sq2  N_oocysts

## Warning: Number of logged events: 568
```

```
summary(igf)
```

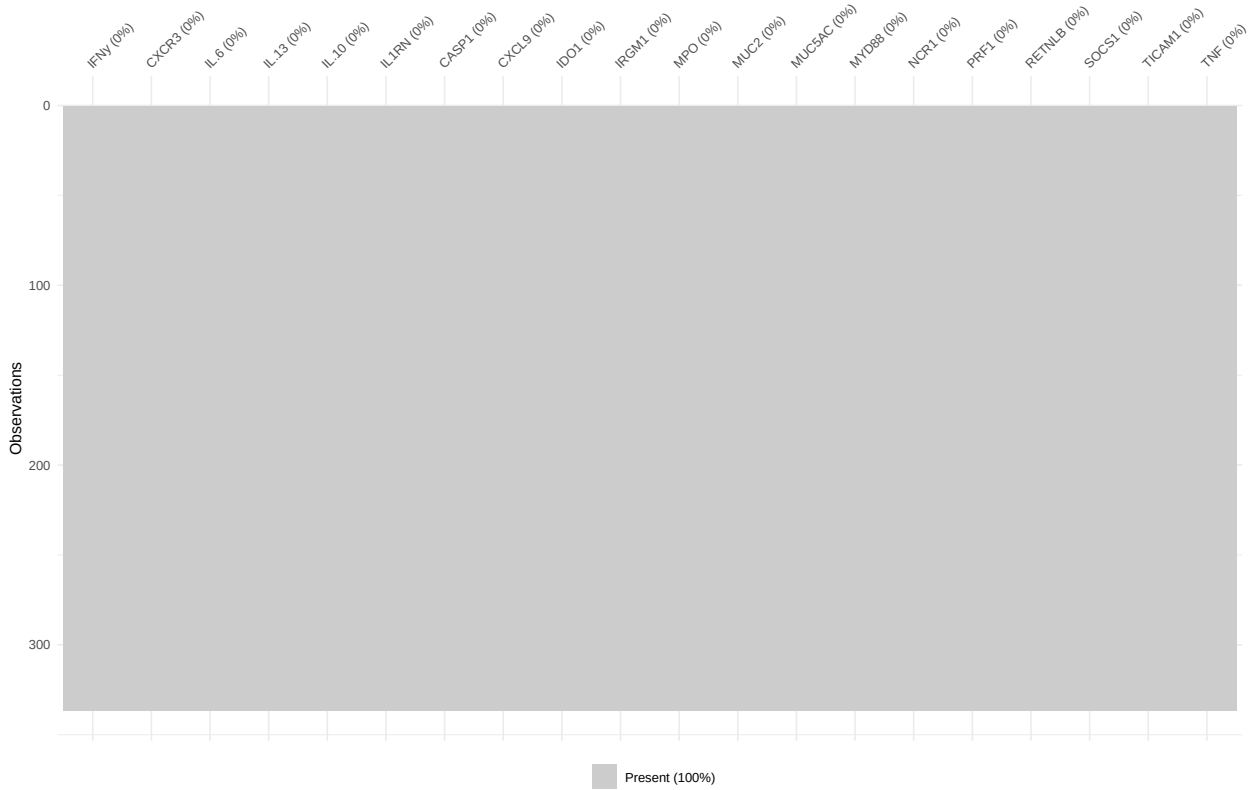
```
## Class: mids
## Number of multiple imputations:  5
## Imputation methods:
##              Mouse_ID            MC.Eimeria delta_ct_cewe_MminusE
##                    ""             "logreg"                 "pmm"
##                   Sex             Longitude              Latitude
##                    ""                    ""                    ""
##                  Year               mtBamH                 YNPAR
##                    ""                    ""                    ""
##                 X332                 X347                   X65
##                    ""                    ""                    ""
##                  Tsx                  Btk                 Syap1
##                    ""                    ""                    ""
##                  Es1                 Gpd1                  Idh1
##                    ""                    ""                    ""
##                  Mpi                   Np                  Sod1
##                    ""                    ""                    ""
##                Es1C                Gpd1C                 Idh1C
##                    ""                    ""                    ""
##                  NpC                Sod1C              HI_NLoci
##                    ""                    ""                 "pmm"
##               Spleen       Trichuris_muris     Mastophorus_muris
##                "pmm"                    ""                    ""
##  Catenotaenia_pusilla                Status          Heterakis_sp
##                    ""                    ""                    ""
##         N_oocysts_sq1         N_oocysts_sq2         N_oocysts_sq3
##                 "pmm"                 "pmm"                 "pmm"
##         N_oocysts_sq4         N_oocysts_sq5         N_oocysts_sq6
##                 "pmm"                 "pmm"                 "pmm"
##         N_oocysts_sq7         N_oocysts_sq8                Region
##                 "pmm"                 "pmm"                    ""
```

```
##           Body_Length                 Fleas           Tail_Length
##                 "pmm"              "logreg"                 "pmm"
##        eimeriaSpecies            Ct.Eimeria                Ct.Mus
##                    ""                 "pmm"                 "pmm"
##        ILWE_Crypto_Ct        Aspiculuris_sp           Syphacia_sp
##                 "pmm"                    ""                    ""
##             Taenia_sp        Hymenolepis_sp            FEC_Eim_Ct
##                    ""                    ""                 "pmm"
##                  IFNy                CXCR3                  IL.6
##                 "pmm"                 "pmm"                 "pmm"
##                IL.13                IL.10                 IL1RN
##                 "pmm"                 "pmm"                 "pmm"
##                CASP1                CXCL9                  IDO1
##                 "pmm"                 "pmm"                 "pmm"
##                IRGM1                  MPO                  MUC2
##                 "pmm"                 "pmm"                 "pmm"
##               MUC5AC                MYD88                  NCR1
##                 "pmm"                 "pmm"                 "pmm"
##                 PRF1               RETNLB                 SOCS1
##                 "pmm"                 "pmm"                 "pmm"
##               TICAM1                  TNF
##                 "pmm"                 "pmm"
## PredictorMatrix:
##                       Mouse_ID MC.Eimeria delta_ct_cewe_MminusE Sex Longitude
## Mouse_ID                     0          1                     1   0         1
## MC.Eimeria                   0          0                     1   0         1
## delta_ct_cewe_MminusE        0          1                     0   0         1
## Sex                          0          1                     1   0         1
## Longitude                    0          1                     1   0         0
## Latitude                     0          1                     1   0         1
##                       Latitude Year mtBamH YNPAR X332 X347 X65 Tsx Btk Syap1
## Mouse_ID                     1    1      0     0    0    0   0   0   0     0
## MC.Eimeria                   1    1      0     0    0    0   0   0   0     0
## delta_ct_cewe_MminusE        1    1      0     0    0    0   0   0   0     0
## Sex                          1    1      0     0    0    0   0   0   0     0
## Longitude                    1    1      0     0    0    0   0   0   0     0
## Latitude                     0    1      0     0    0    0   0   0   0     0
##                       Es1 Gpd1 Idh1 Mpi Np Sod1 Es1C Gpd1C Idh1C NpC Sod1C
## Mouse_ID                0    0    0   0  0    0    0     0     0   0     0
## MC.Eimeria              0    0    0   0  0    0    0     0     0   0     0
## delta_ct_cewe_MminusE   0    0    0   0  0    0    0     0     0   0     0
## Sex                     0    0    0   0  0    0    0     0     0   0     0
## Longitude               0    0    0   0  0    0    0     0     0   0     0
## Latitude                0    0    0   0  0    0    0     0     0   0     0
##                       HI_NLoci Spleen Trichuris_muris Mastophorus_muris
## Mouse_ID                     1      1               1                 1
## MC.Eimeria                   1      1               1                 1
## delta_ct_cewe_MminusE        1      1               1                 1
## Sex                          1      1               1                 1
## Longitude                    1      1               1                 1
## Latitude                     1      1               1                 1
##                       Catenotaenia_pusilla Status Heterakis_sp N_oocysts_sq1
## Mouse_ID                                 1      0            1             1
## MC.Eimeria                               1      0            1             1
```

```
## delta_ct_cewe_MminusE                   1      0            1             1
## Sex                                     1      0            1             1
## Longitude                               1      0            1             1
## Latitude                                1      0            1             1
##                       N_oocysts_sq2 N_oocysts_sq3 N_oocysts_sq4 N_oocysts_sq5
## Mouse_ID                          1             1             1             1
## MC.Eimeria                        1             1             1             1
## delta_ct_cewe_MminusE             1             1             1             1
## Sex                               1             1             1             1
## Longitude                         1             1             1             1
## Latitude                          1             1             1             1
##                       N_oocysts_sq6 N_oocysts_sq7 N_oocysts_sq8 Region
## Mouse_ID                          1             1             1      0
## MC.Eimeria                        1             1             1      0
## delta_ct_cewe_MminusE             1             1             1      0
## Sex                               1             1             1      0
## Longitude                         1             1             1      0
## Latitude                          1             1             1      0
##                       Body_Length Fleas Tail_Length eimeriaSpecies Ct.Eimeria
## Mouse_ID                        1     1           1              0          1
## MC.Eimeria                      1     1           1              0          1
## delta_ct_cewe_MminusE           1     1           1              0          1
## Sex                             1     1           1              0          1
## Longitude                       1     1           1              0          1
## Latitude                        1     1           1              0          1
##                       Ct.Mus ILWE_Crypto_Ct Aspiculuris_sp Syphacia_sp
## Mouse_ID                   1              1              1           1
## MC.Eimeria                 1              1              1           1
## delta_ct_cewe_MminusE      1              1              1           1
## Sex                        1              1              1           1
## Longitude                  1              1              1           1
## Latitude                   1              1              1           1
##                       Taenia_sp Hymenolepis_sp FEC_Eim_Ct IFNy CXCR3 IL.6 IL.13
## Mouse_ID                      1              1          1    1     1    1     1
## MC.Eimeria                    1              1          1    1     1    1     1
## delta_ct_cewe_MminusE         1              1          1    1     1    1     1
## Sex                           1              1          1    1     1    1     1
## Longitude                     1              1          1    1     1    1     1
## Latitude                      1              1          1    1     1    1     1
##                       IL.10 IL1RN CASP1 CXCL9 IDO1 IRGM1 MPO MUC2 MUC5AC MYD88
## Mouse_ID                  1     1     1     1    1     1   1    1      1     1
## MC.Eimeria                1     1     1     1    1     1   1    1      1     1
## delta_ct_cewe_MminusE     1     1     1     1    1     1   1    1      1     1
## Sex                       1     1     1     1    1     1   1    1      1     1
## Longitude                 1     1     1     1    1     1   1    1      1     1
## Latitude                  1     1     1     1    1     1   1    1      1     1
##                       NCR1 PRF1 RETNLB SOCS1 TICAM1 TNF
## Mouse_ID                 1    1      1     1      1   1
## MC.Eimeria               1    1      1     1      1   1
## delta_ct_cewe_MminusE    1    1      1     1      1   1
## Sex                      1    1      1     1      1   1
## Longitude                1    1      1     1      1   1
## Latitude                 1    1      1     1      1   1
## Number of logged events:  568
```

```
##   it im dep     meth      out
## 1  0  0     constant Mouse_ID
## 2  0  0     constant      Sex
## 3  0  0     constant   mtBamH
## 4  0  0     constant    YNPAR
## 5  0  0     constant     X332
## 6  0  0     constant     X347
```

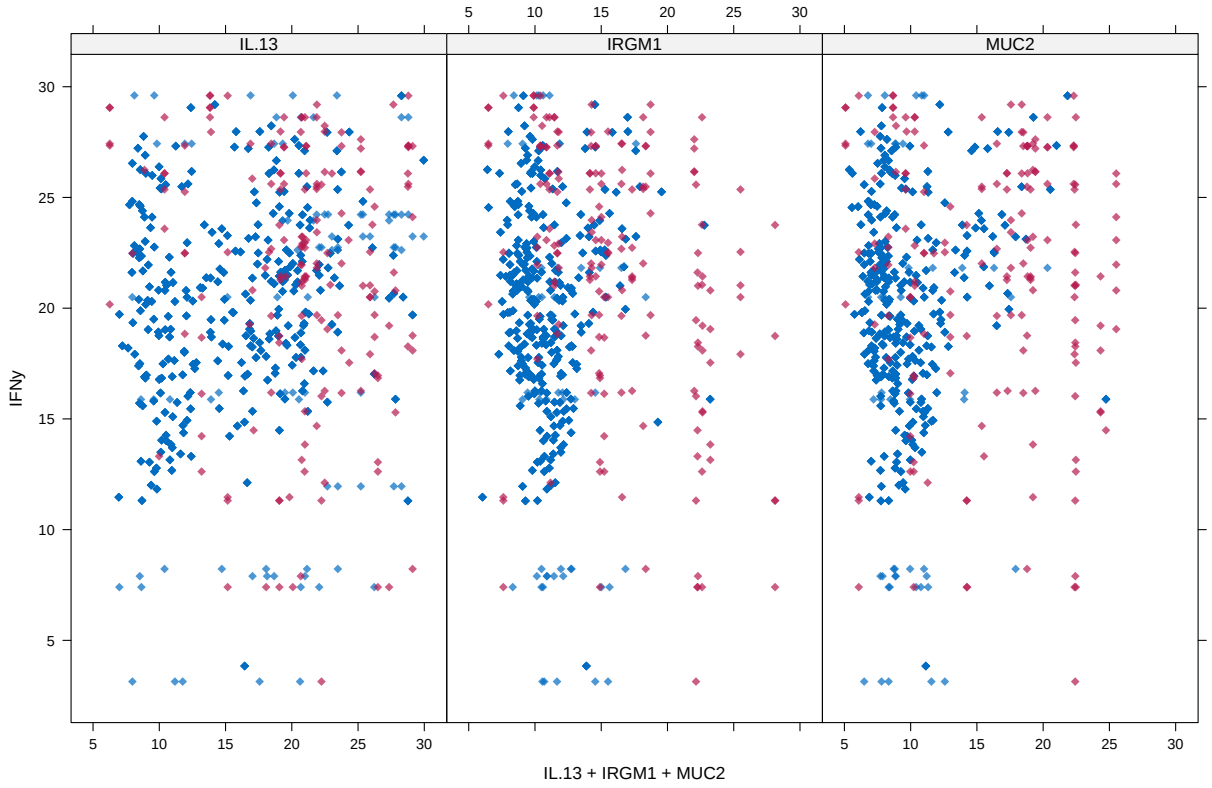
```
# to check each column with imputed data
## igf$imp$IFNy

#Now we can get back the completed dataset using the complete()
complete_field <- complete(igf, 1)


#sapply(complete_field, function(x) sum(is.na(x)))


# select the required columns
imp_field <- complete_field %>%
  dplyr::select(all_of(Genes_wild))

#visualize missingness
vis_miss(imp_field)
```



```
#add an ending to the imputed columns
colnames(imp_field) <- paste(colnames(imp_field), "imp", sep = "_")

#now join it to the full data set of the laboratory infections
field_genes <- cbind(field_genes, imp_field)


Genes_wild_imp <- paste(Genes_wild, "imp", sep = "_")


field_genes <- field_genes %>%
  dplyr::select(c(Mouse_ID, all_of(Genes_wild_imp)))


# join the now imputed columns to the field
field <- field %>%
  left_join(field_genes, by = "Mouse_ID")
```

Let's compare the distributions of original and imputed data using a some useful plots.First of all we can use a scatterplot and plot Ozone against all the other variables. Let's first plot the variables for which we have few missing values.

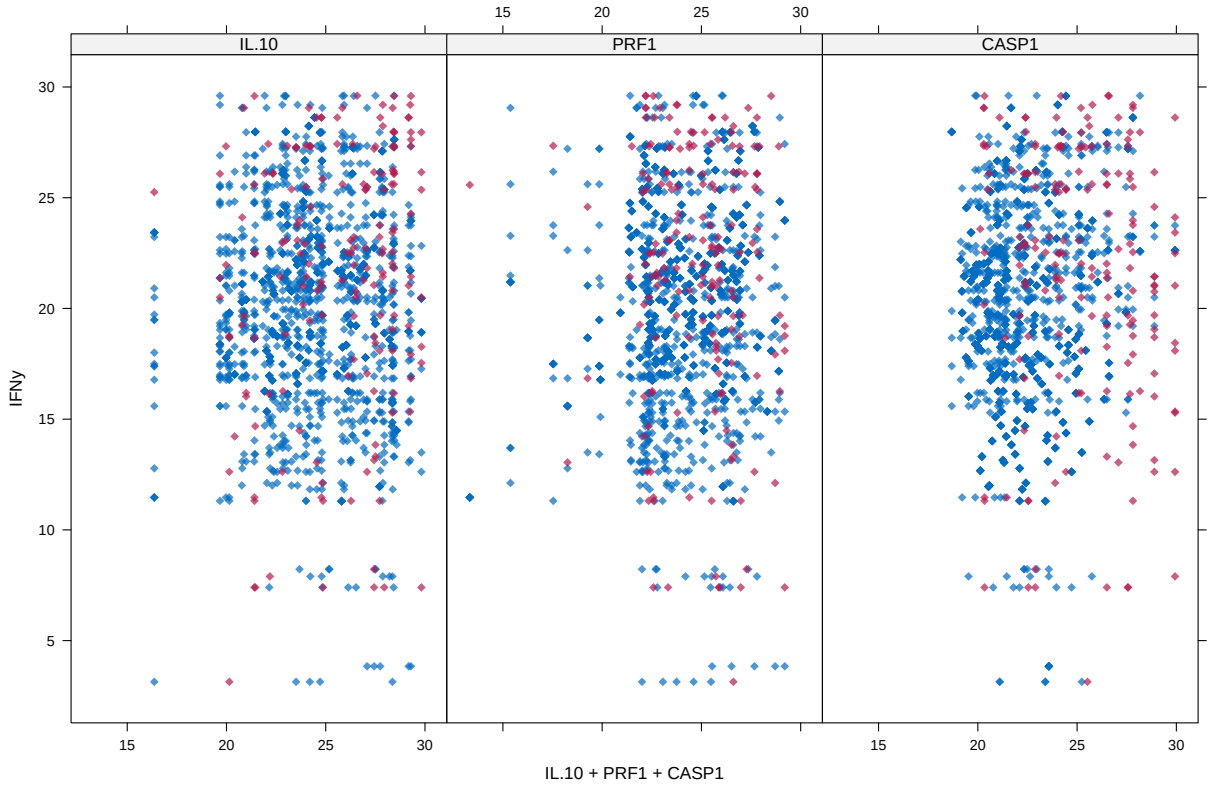
```
xyplot(igf, IFNy ~ IL.13 + IRGM1 + MUC2, pch=18,cex=1)
```



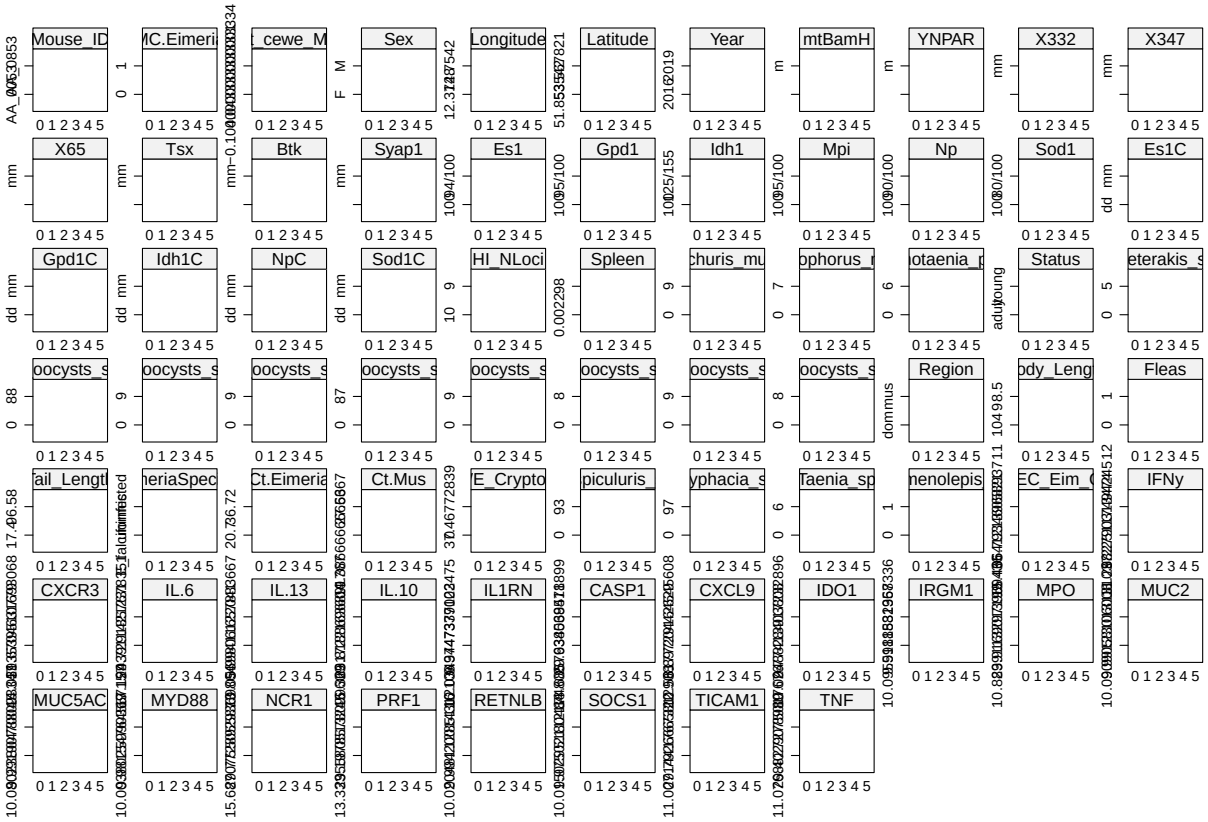
What we would like to see is that the shape of the magenta points (imputed) matches the shape of the blue ones (observed). The matching shape tells us that the imputed values are indeed "plausible values".

Now let's plot the variables with many missing data points.

```
xyplot(igf,IFNy ~ IL.10 + PRF1 + CASP1, pch=18,cex=1)
```




```
stripplot(igf, pch = 20, cex = 1.2)
```



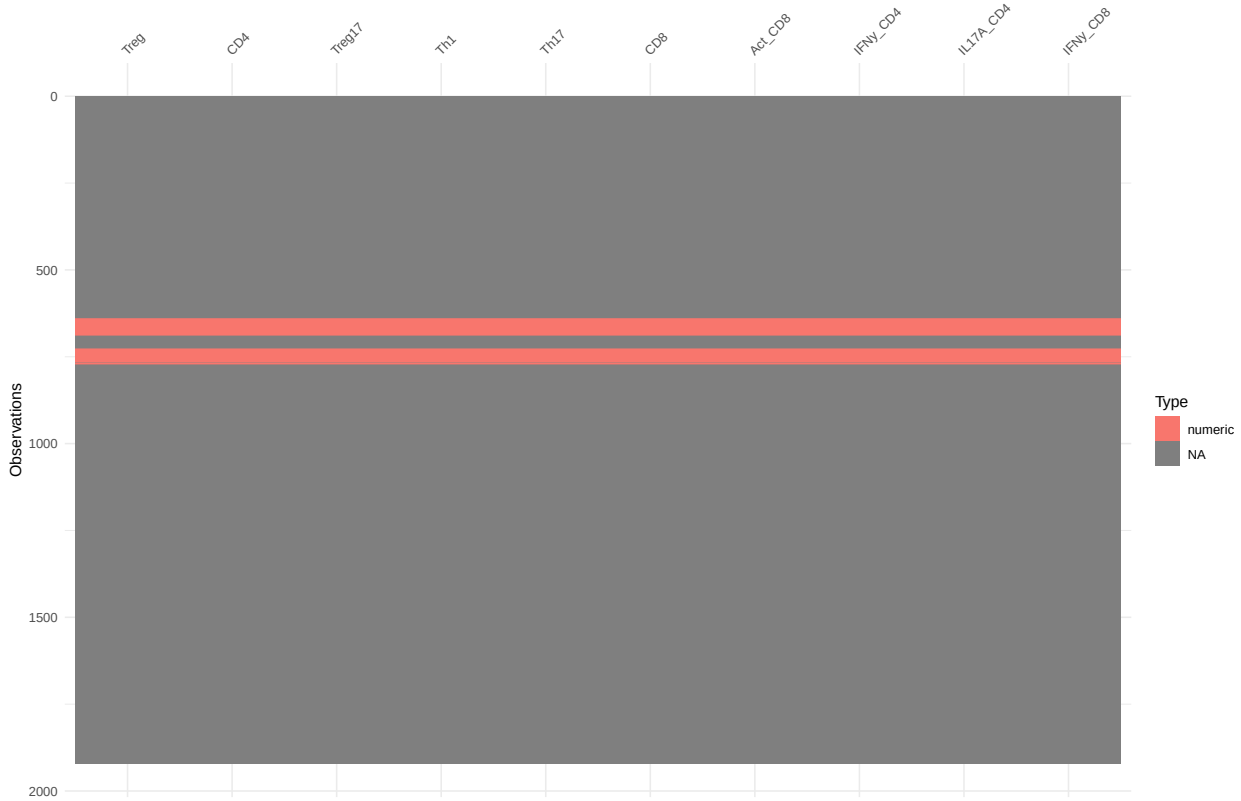

```
#densityplot(igf)
```

The density of the imputed data for each imputed dataset is showed in magenta while the density of the observed data is showed in blue. Again, under our previous assumptions we expect the distributions to be similar.

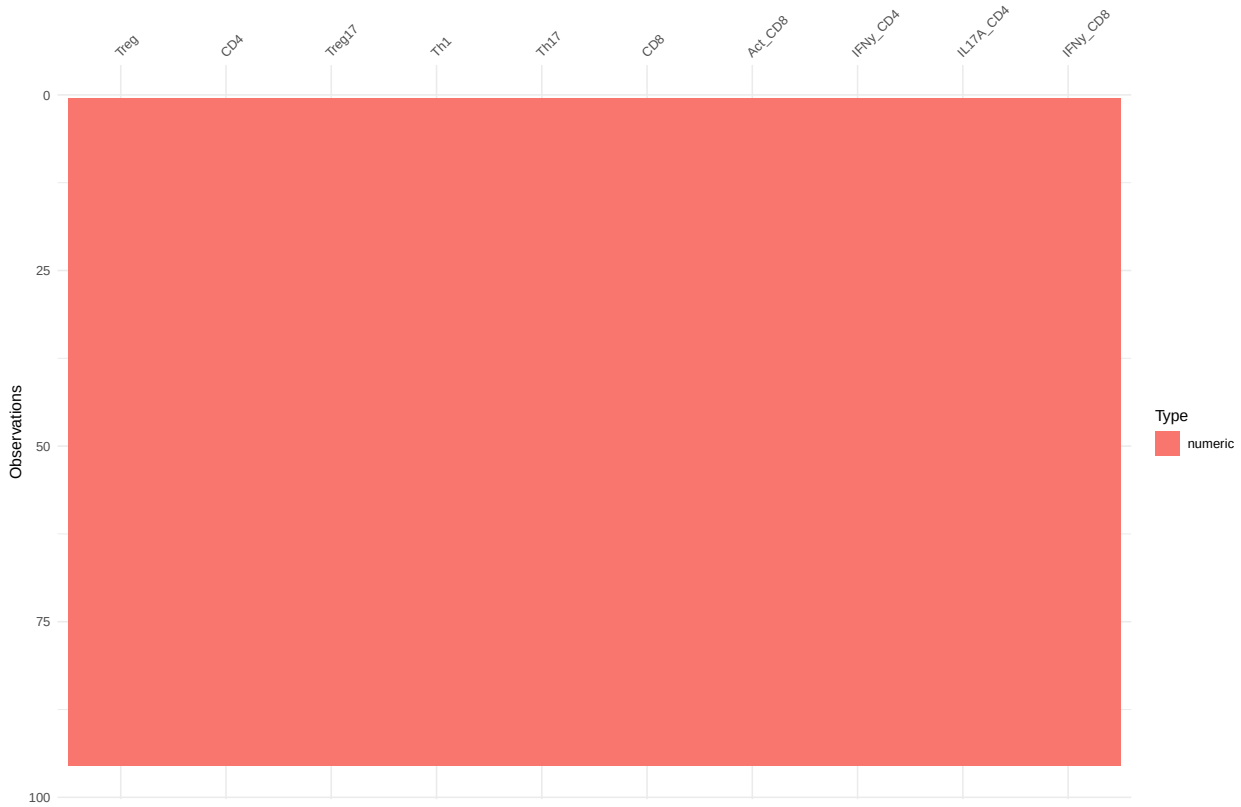
Another useful visual take on the distributions can be obtained using the stripplot() function that shows the distributions of the variables as individual points

FACS

```
gf_field <- field %>%
  dplyr::select(all_of(c(Facs_wild)))

vis_dat(gf_field)
```




```
#remove rows with only nas
gf_field <- gf_field[,colSums(is.na(gf_field))<nrow(gf_field)]

#remove colums with only nas
gf_field <- gf_field[rowSums(is.na(gf_field)) != ncol(gf_field), ]


#select same rows in the first table
field_facs <- field[row.names(gf_field), ]


# really removing empty columns
field_facs <- field_facs %>%
  discard(~all(is.na(.) | . ==""))

vis_dat(gf_field)
```



We have no need to impute the facs data, as nothing is missing from the 95 samples

Just add here the lab data and join the two tables

```
lab <- read.csv("output_data/Lab_imputed.csv")

# join the genes and facs data
imputed_mice <- lab %>%
  full_join(field, by = intersect(colnames(lab), colnames(field)))

 ##save the imputed data
write.csv(imputed_mice, "output_data/imputed_mice.csv", row.names = FALSE)
```