first_lesson

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Data

For this work we used the dataset **Stroke Prediction Dataset** retrieved from Kaggle.

We used the dataset to predict whether a patient is likely to get stroke based on the input parameters like gender, age, various diseases, and smoking status. Each row in the data provides relavant information about the patient.

Below the information about the attributes:

1. id: unique identifier
2. gender: "Male", "Female" or "Other"
3. age: age of the patient
4. hypertension: 0 if the patient doesn't have hypertension, 1 if the patient has hypertension
5. heart_disease: 0 if the patient doesn't have any heart diseases, 1 if the patient has a heart disease
6. ever_married: "No" or "Yes"
7. work_type: "children", "Govt_jov", "Never_worked", "Private" or "Self-employed"
8. Residence_type: "Rural" or "Urban"
9. avg_glucose_level: average glucose level in blood
10. bmi: body mass index
11. smoking_status: "formerly smoked", "never smoked", "smokes" or "Unknown"*
12. stroke: 1 if the patient had a stroke or 0 if not

*Note: "Unknown" in smoking_status means that the information is unavailable for this patient

Load the dataset

Set the current directory as working directory and load the dataset.

```
setwd(dirname(rstudioapi::getSourceEditorContext()$path))

source("../utils/plots.R")
source("../utils/data_analysis.R")
dataset = read.csv("stroke.csv")
str(dataset)
```

```
## 'data.frame':    5110 obs. of  12 variables:
##  $ id               : int  9046 51676 31112 60182 1665 56669 53882 10434 27419 60491 ...
##  $ gender           : chr  "Male" "Female" "Male" "Female" ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : int  0 0 0 0 1 0 1 0 0 0 ...
##  $ heart_disease    : int  1 0 1 0 0 0 1 0 0 0 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Self-employed" "Private" "Private" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Rural" "Urban" ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : chr  "36.6" "N/A" "32.5" "34.4" ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "never smoked" "smokes" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

Data Preparation

We converted the categorical variables in factors.

```
dataset$id = NULL

dataset$gender = factor(dataset$gender)
dataset$hypertension = factor(dataset$hypertension, levels = c(0,1), labels = c("No", "Yes"))
dataset$heart_disease = factor(dataset$heart_disease, levels = c(0,1), labels = c("No", "Yes"))
dataset$ever_married = factor(dataset$ever_married)
dataset$work_type = factor(dataset$work_type)
dataset$residence_type = factor(dataset$Residence_type)
dataset$Residence_type = NULL
dataset$smoking_status = factor(dataset$smoking_status)
dataset$stroke = factor(dataset$stroke, levels = c(0,1), labels = c("No", "Yes"))
dataset$bmi = as.numeric(dataset$bmi)
```

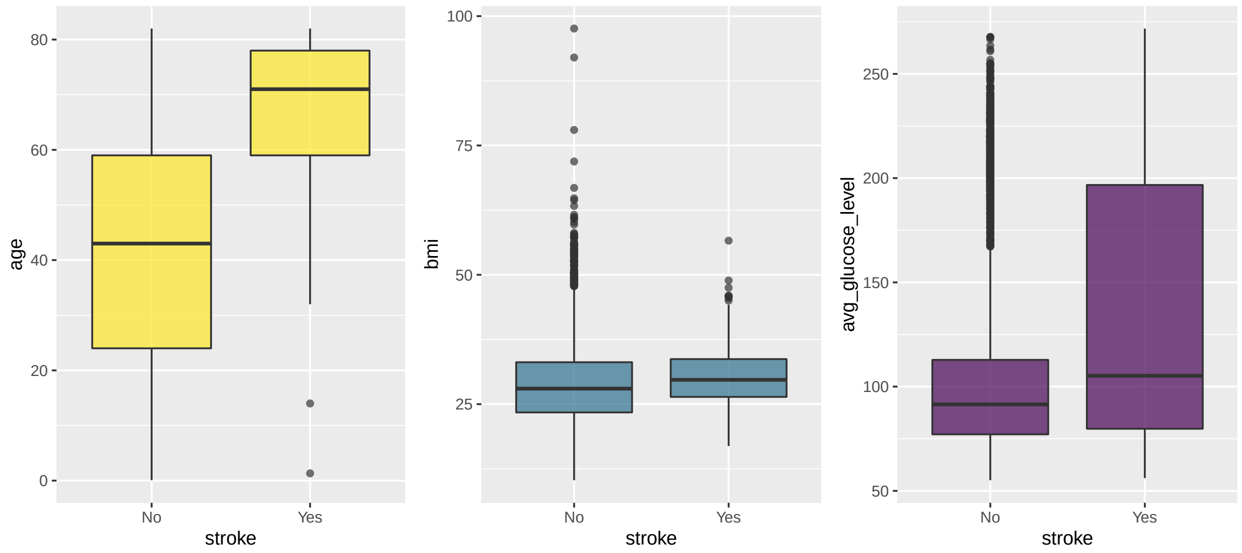
```
str(dataset)
```

```
## ’data.frame':    5110 obs. of  11 variables:
##  $ gender           : Factor w/ 3 levels "Female","Male",..: 2 1 2 1 1 2 2 1 1 1 ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : Factor w/ 2 levels "No","Yes": 1 1 1 1 2 1 2 1 1 1 ...
##  $ heart_disease    : Factor w/ 2 levels "No","Yes": 2 1 2 1 1 1 2 1 1 1 ...
##  $ ever_married     : Factor w/ 2 levels "No","Yes": 2 2 2 2 2 2 2 1 2 2 ...
##  $ work_type        : Factor w/ 5 levels "children","Govt_job",..: 4 5 4 4 5 4 4 4 4 4 ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : num  36.6 NA 32.5 34.4 24 29 27.4 22.8 NA 24.2 ...
##  $ smoking_status   : Factor w/ 4 levels "formerly smoked",..: 1 2 2 3 2 1 2 2 4 4 ...
##  $ stroke           : Factor w/ 2 levels "No","Yes": 2 2 2 2 2 2 2 2 2 2 ...
##  $ residence_type   : Factor w/ 2 levels "Rural","Urban": 2 1 1 2 1 2 1 2 1 2 ...
```

Data Visualization

Boxplots to visualize the stroke status in association with **age**, **bmi** and **glucose level**.

```
grid.arrange(ggplot(dataset, aes(x=stroke ,y=age)) +
              geom_boxplot(fill= "#FDE725FF", alpha= 0.7),
            ggplot(dataset, aes(x=stroke, y=bmi))+
              geom_boxplot(fill= "#2D708EFF", alpha= 0.7),
            ggplot(dataset, aes(x=stroke, y=avg_glucose_level))+
              geom_boxplot(fill= "#440154FF", alpha= 0.7),
            ncol=3)
```

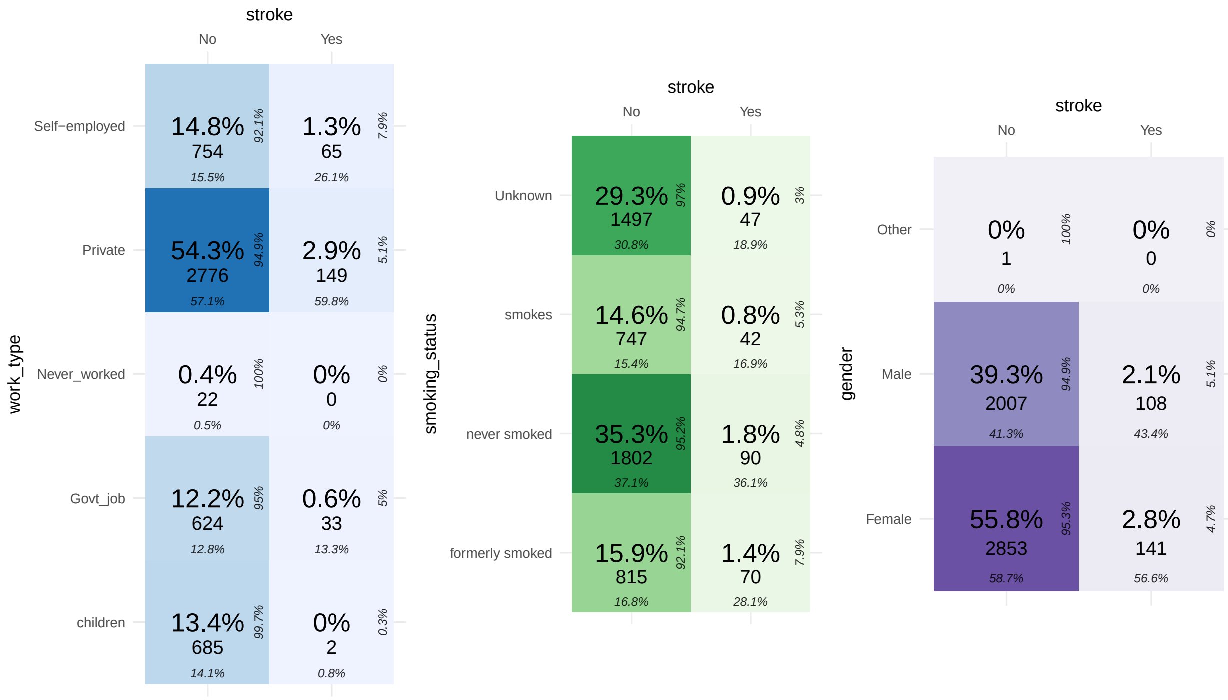


1. **Age** there is a relation with age: older people are more likely to have a stroke
2. **Bmi** there is no evident relation between stroke and bmi
3. **Averagre glucose level** the higher the level of glucose, the higher the relation with stroke

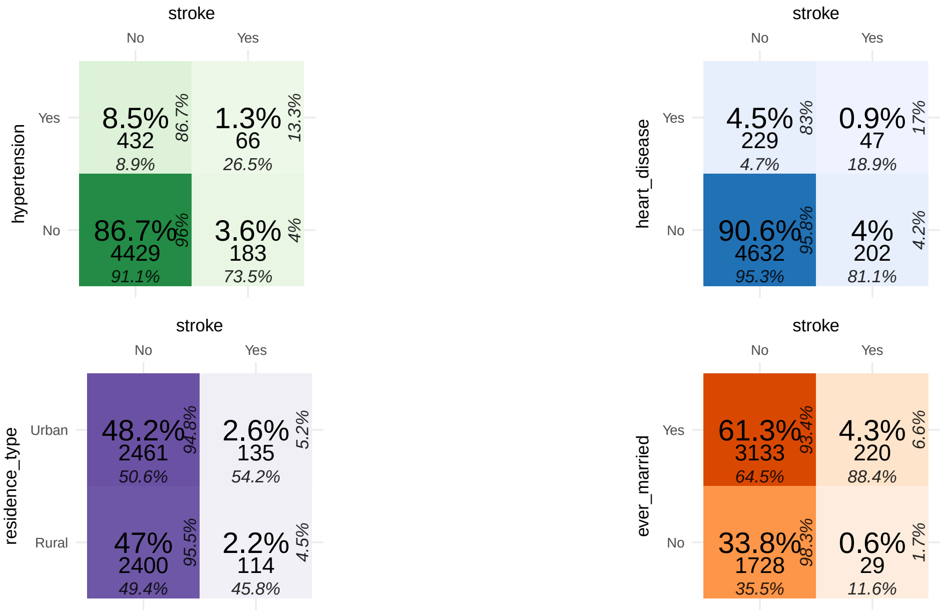
Then we built some matrices to show the relationship between stroke and some **categorical variables** that have different levels.

```
source("../utils/plots.R")
#,fig.height=12

grid.arrange(factors_plot(tidy(table(dataset %>% select(stroke,work_type))), palette='Blues',
                          font_count_size=4, font_normalized_size=5.1, font_percentages_size=2.5,
                          font_categories_size=10),
            factors_plot(tidy(table(dataset %>% select(stroke,smoking_status))), palette='Greens',
                          font_count_size=4, font_normalized_size=5.1, font_percentages_size=2.5,
                          font_categories_size=10),
            factors_plot(tidy(table(dataset %>% select(stroke,gender))), palette='Purples',
                          font_count_size=4, font_normalized_size=5.1, font_percentages_size=2.5,
                          font_categories_size=10),
            ncol=3, nrow=1)
```

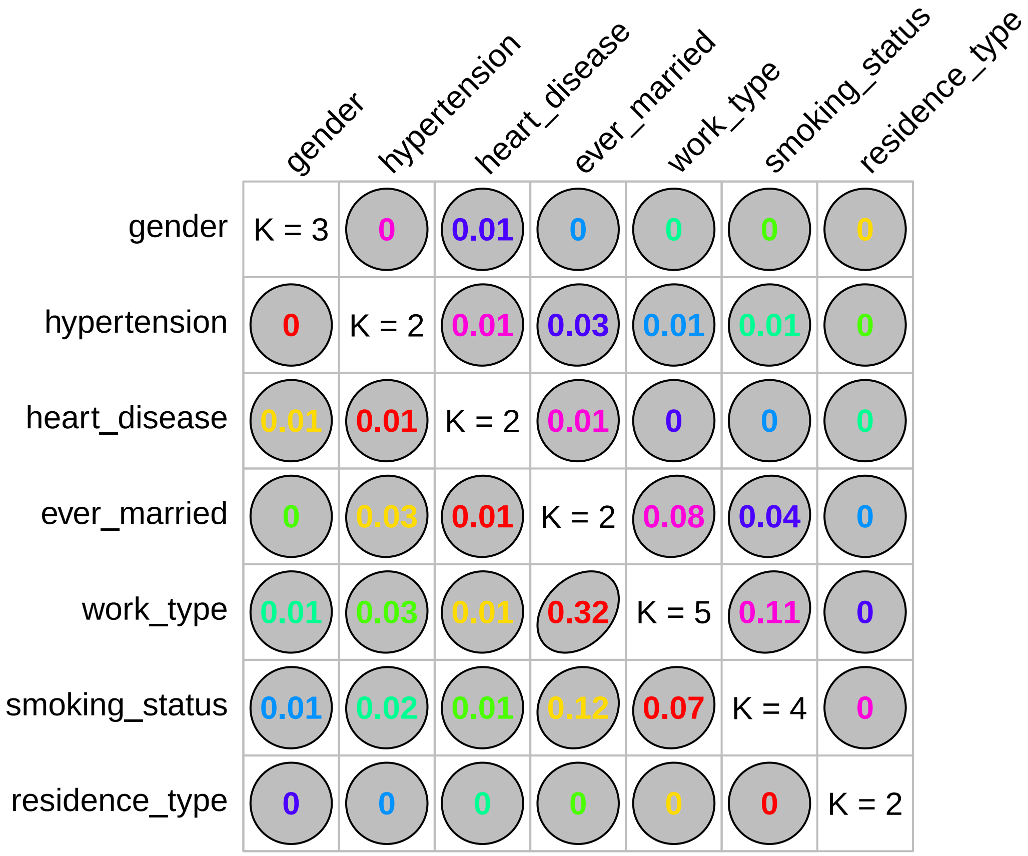


```
grid.arrange(factors_plot(tidy(table(dataset %>% select(stroke,hypertension))), palette='Greens',
                          font_count_size=4.5, font_normalized_size=6, font_percentages_size=3.5,
                          font_categories_size=10),
             factors_plot(tidy(table(dataset %>% select(stroke,heart_disease))), palette='Blues',
                          font_count_size=4.5, font_normalized_size=6, font_percentages_size=3.5,
                          font_categories_size=10),
             factors_plot(tidy(table(dataset %>% select(stroke,residence_type))), palette='Purples',
                          font_count_size=4.5, font_normalized_size=6, font_percentages_size=3.5,
                          font_categories_size=10),
             factors_plot(tidy(table(dataset %>% select(stroke,ever_married))), palette='Oranges',
                          font_count_size=4.5, font_normalized_size=6, font_percentages_size=3.5,
                          font_categories_size=10),
             ncol=2, nrow=2)
```



After we built some plots to show the **qualitative** and **quantitative** correlation.

```
qualitative_vars = c('gender', 'hypertension', 'heart_disease', 'ever_married',
                     'work_type', 'smoking_status', 'residence_type')
plot(GKtauDataframe(dataset %>% select(all_of(qualitative_vars))))
```



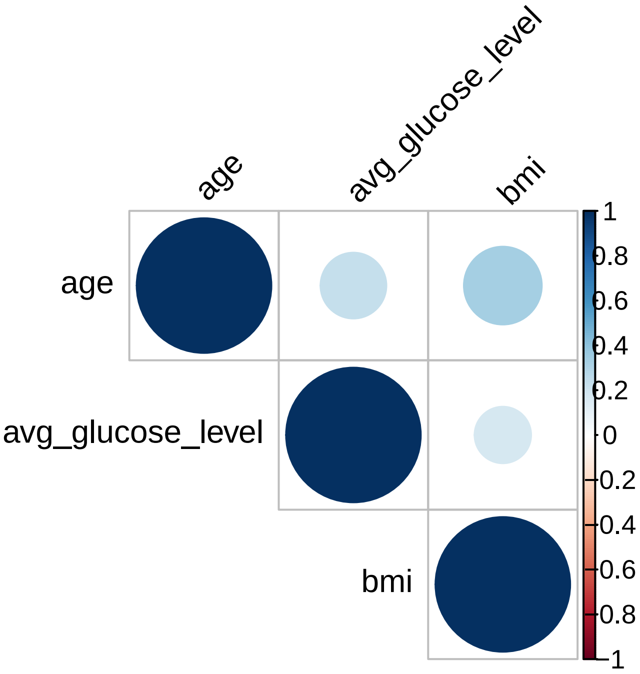
	gender	hypertension	heart_disease	ever_married	work_type	smoking_status	residence_type
gender	K = 3	0	0.01	0	0	0	0
hypertension	0	K = 2	0.01	0.03	0.01	0.01	0
heart_disease	0.01	0.01	K = 2	0.01	0	0	0
ever_married	0	0.03	0.01	K = 2	0.08	0.04	0
work_type	0.01	0.03	0.01	0.32	K = 5	0.11	0
smoking_status	0.01	0.02	0.01	0.12	0.07	K = 4	0
residence_type	0	0	0	0	0	0	K = 2

```
# TODO find a way to plot table and image side-by-side

quantitative_vars = c('age', 'avg_glucose_level', 'bmi')

corr <- rcorr(as.matrix(dataset %>% select(all_of(quantitative_vars))))

corrplot(corr$r, type = "upper", tl.col = "black", tl.srt = 45)
```



```
#flattenCorrMatrix(corr$r, corr$P)
```

Data Manipulation

In order to facilitate our work, we removed the level “other” from the variable gender and the level “never_worked” from the variable work_type, since they are not relevant for the analysis.

```
# rm gender "other"
dataset$gender <- as.character(dataset$gender)
stroke <- dataset[dataset$gender == "Male" | dataset$gender == "Female",]
stroke$gender <- as.factor(stroke$gender)

# rm "Never_worked"
dataset$work_type <- as.character(dataset$work_type)
stroke <- dataset[!dataset$work_type == "Never_worked",]
stroke$work_type <- as.factor(stroke$work_type)
```

We removed the NA values from the **bmi** variable. In order to replace them, we predicted their values using a fitted tree.

```
stroke <- as_tibble(stroke)
sum(is.na(stroke$bmi))
```

```
## [1] 201
```

```
missing_index <- which(is.na(stroke$bmi))
X <- stroke[missing_index,]
train_v <- stroke[-c(missing_index),]

tree = caret::train(bmi ~ .,
                    data=train_v,
                    method="rpart",
                    trControl = trainControl(method = "cv"))

bmi_pred <- predict(tree, newdata = X)

stroke[missing_index,"bmi"] <- bmi_pred
sum(is.na(stroke$bmi))
```

```
## [1] 0
```

```
sum(is.na(stroke))
```

```
## [1] 0
```

```
# check for other NAs
for (i in 1:11) {
  print(which(is.na(stroke[,i])))
}
```

```
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
## integer(0)
```

```
# clean Glob_Env
rm(train_v,X,tree, bmi_pred,i,missing_index)
```

Divide in training and test set

```
set.seed(42)
stroke <- as.data.frame(stroke)
for (i in 1:11) {
  levels(stroke[,i]) <- make.names(c(levels(stroke[,i])))
}

split_train_test <- createDataPartition(y = stroke$stroke, p=0.5, list = F)
train <- stroke[split_train_test,]
test <-  stroke[-split_train_test,]
```

SMOTE algorithm

Since our dataset has a problem of under sampling, we used the SMOTE algorithm to create synthetic new data.

```
# new smote algo
```

Logistic Regression

```
Logit <- glm(stroke~., data=train, family = binomial(link = "logit"))
summary(Logit)
```

```
##
## Call:
## glm(formula = stroke ~ ., family = binomial(link = "logit"),
##     data = train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.24055  -0.32175  -0.16709  -0.08114   3.03598
##
## Coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)               -2.039e+01  5.667e+02  -0.036   0.9713
## genderMale                  2.056e-01  1.993e-01   1.031   0.3023
## genderOther                -1.452e+01  1.075e+04  -0.001   0.9989
## age                         7.149e-02  8.197e-03   8.721   <2e-16 ***
## hypertensionYes             5.664e-01  2.223e-01   2.548   0.0108 *
## heart_diseaseYes            3.453e-01  2.671e-01   1.293   0.1960
## ever_marriedYes            -1.706e-01  3.134e-01  -0.544   0.5863
## work_typeGovt_job           1.236e+01  5.667e+02   0.022   0.9826
## work_typePrivate            1.286e+01  5.667e+02   0.023   0.9819
## work_typeSelf.employed      1.251e+01  5.667e+02   0.022   0.9824
## avg_glucose_level           2.993e-03  1.706e-03   1.755   0.0793 .
## bmi                         8.237e-03  1.596e-02   0.516   0.6058
## smoking_statusnever.smoked -1.453e-01  2.462e-01  -0.590   0.5550
## smoking_statussmokes        3.513e-01  2.904e-01   1.210   0.2265
## smoking_statusUnknown      -2.820e-01  3.120e-01  -0.904   0.3660
## residence_typeUrban        -1.380e-02  1.965e-01  -0.070   0.9440
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 997.15  on 2544  degrees of freedom
## Residual deviance: 782.80  on 2529  degrees of freedom
## AIC: 814.8
##
## Number of Fisher Scoring iterations: 18
```

As we can see, the only significant variables are **age** and **hypertension**, that have both an high positive impact on the increase of the logit probability.

Also about the **smoking status** we can see, as expected, that it has a positive impact and a negatie one when the individual has never smoked.

```
# TODO clean code and stuff

# data Preprocessing, Econding with OneHotEncoding ------------------------------
#
#dummy <- dummyVars(" ~ gender + work_type + smoking_status + ever_married + Residence_type", data=stro
#newdata <- data.frame(predict(dummy, newdata = stroke))
#a <- stroke[,2:4]
#b <- stroke[,8:9]
#dt <- cbind(a, b, newdata, stroke['stroke'])
#dt <- as_tibble(dt)
#
#y <- stroke['stroke']
```

```
# Fill missing bmi data w/ tree prediction
# TODO keep this way? should we just remove them?
#
# missing_index <-which(is.na(dataset$bmi))
#
# train_set <- dataset[-c(missing_index),]
#
# tree = caret::train(bmi ~ .,
#                     data=train_set,
#                      method="rpart",
#                      trControl = trainControl(method = "cv"))
# predicted_bmi <- predict(tree, newdata = dataset[missing_index,])
#
# #######################
# # What? Why?
# # x <- mean(bmi_pred)
# # bmi_pred[202] <- x
# #######################
#
# dataset[missing_index,"bmi"] <- predicted_bmi
#
# dataset = na.omit(dataset)
#
# # Check quantitative correlation is under control w/ new data
# TODO side by side :)
#
# new_corr <- rcorr(as.matrix(dataset %>% select(all_of(quantitative_vars))))
# flattenCorrMatrix(new_corr$r, new_corr$P)
#
# grid.arrange(corrplot(corr$r,    type = "upper", tl.col = "black", tl.srt = 45),
#             corrplot(new_corr$r, type = "upper", tl.col = "black", tl.srt = 45),
#             ncol=2, nrow=1)
```

```
# Solve the under sampling problem with SMOTE algho to create synth new data

# dataset <- as.data.frame(lapply(dataset, as.factor)) # What? Why?
#
# trainSplit <- DMwR::SMOTE(stroke ~ ., dt, perc.over = 2000, perc.under=10)
#
# dt_synth<- rbind(trainSplit,dt)
#
#
# dt_synth$work_type.Never_worked <- NULL # Again, but why :D
#
# dt_synth$avg_glucose_level <- as.numeric(dt_synth$avg_glucose_level)
# dt_synth$bmi <- as.numeric(dt_synth$bmi)
# dt_synth$age <- as.numeric(dt_synth$age)

# TODO Show some stats of new dataset
```

```
 # TODO recheck correlations, maybe w/ function to plot both side-by-side
```

```
 # TODO add models/predictions
```