

# Final EDA

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```
library(tidyverse)
library(summarytools)
library(corrplot)
library(caret)
library(vip)
library(rpart.plot)
library(ranger)
library(gridExtra)
```

## 1 Data Import

```
# import data
load("./recovery.RData")

set.seed(3196)
lts.dat <- dat[sample(1:10000, 2000),]
set.seed(2575)
lincole.dat <- dat[sample(1:10000, 2000),]
set.seed(5509)
amy.dat <- dat[sample(1:10000, 2000),]

dat1 <- lts.dat %>%
  merge(lincole.dat, all = TRUE) %>%
  na.omit() %>%
  select(-id) %>%
  mutate(
    gender = as.factor(gender),
    race = as.factor(race),
    smoking = as.factor(smoking),
    hypertension = as.factor(hypertension),
    diabetes = as.factor(diabetes),
    vaccine = as.factor(vaccine),
    severity = as.factor(severity),
    study = as.factor(study))

dat2 <- lts.dat %>%
  merge(amy.dat, all = TRUE) %>%
  na.omit() %>%
  select(-id) %>%
  mutate(
    gender = as.factor(gender),
    race = as.factor(race),
    smoking = as.factor(smoking),
    hypertension = as.factor(hypertension),
    diabetes = as.factor(diabetes),
    vaccine = as.factor(vaccine),
    severity = as.factor(severity),
    study = as.factor(study))

dat3 <- lincole.dat %>%
  merge(amy.dat, all = TRUE) %>%
  na.omit() %>%
```

```

select(-id) %>%
mutate(
  gender = as.factor(gender),
  race = as.factor(race),
  smoking = as.factor(smoking),
  hypertension = as.factor(hypertension),
  diabetes = as.factor(diabetes),
  vaccine = as.factor(vaccine),
  severity = as.factor(severity),
  study = as.factor(study))

dat <- dat1
summary(dat)

```

##	age	gender	race	smoking	height	weight
##	Min. :45.00	0:1842	1:2372	0:2223	Min. :151.2	Min. : 56.70
##	1st Qu.:57.00	1:1781	2: 172	1:1034	1st Qu.:166.2	1st Qu.: 75.40
##	Median :60.00		3: 716	2: 366	Median :170.2	Median : 80.20
##	Mean :60.06		4: 363		Mean :170.2	Mean : 80.13
##	3rd Qu.:63.00				3rd Qu.:174.2	3rd Qu.: 84.80
##	Max. :77.00				Max. :188.6	Max. :103.40
##	bmi	hypertension	diabetes	SBP	LDL	vaccine
##	Min. :19.70	0:1891	0:3065	Min. :102.0	Min. : 28.0	0:1469
##	1st Qu.:25.80	1:1732	1: 558	1st Qu.:125.0	1st Qu.: 97.0	1:2154
##	Median :27.60			Median :130.0	Median :110.0	
##	Mean :27.73			Mean :130.2	Mean :110.5	
##	3rd Qu.:29.40			3rd Qu.:136.0	3rd Qu.:124.0	
##	Max. :39.80			Max. :158.0	Max. :174.0	
##	severity	study	recovery_time			
##	0:3289	A: 728	Min. : 3.00			
##	1: 334	B:2171	1st Qu.: 28.00			
##		C: 724	Median : 38.00			
##			Mean : 42.87			
##			3rd Qu.: 49.00			
##			Max. :365.00			

```

bin.dat <- dat %>%
  mutate(recovery_time = ifelse(recovery_time > 30, "gt30", "lt30")) %>%
  mutate(recovery_time = factor(recovery_time, levels = c("lt30", "gt30")))

```

```

summary(bin.dat)

```

##	age	gender	race	smoking	height	weight
##	Min. :45.00	0:1842	1:2372	0:2223	Min. :151.2	Min. : 56.70
##	1st Qu.:57.00	1:1781	2: 172	1:1034	1st Qu.:166.2	1st Qu.: 75.40
##	Median :60.00		3: 716	2: 366	Median :170.2	Median : 80.20
##	Mean :60.06		4: 363		Mean :170.2	Mean : 80.13
##	3rd Qu.:63.00				3rd Qu.:174.2	3rd Qu.: 84.80
##	Max. :77.00				Max. :188.6	Max. :103.40
##	bmi	hypertension	diabetes	SBP	LDL	vaccine
##	Min. :19.70	0:1891	0:3065	Min. :102.0	Min. : 28.0	0:1469
##	1st Qu.:25.80	1:1732	1: 558	1st Qu.:125.0	1st Qu.: 97.0	1:2154
##	Median :27.60			Median :130.0	Median :110.0	
##	Mean :27.73			Mean :130.2	Mean :110.5	

```
## 3rd Qu.:29.40          3rd Qu.:136.0  3rd Qu.:124.0
## Max.    :39.80          Max.    :158.0  Max.    :174.0
## severity study  recovery_time
## 0:3289  A: 728  lt30:1102
## 1: 334  B:2171  gt30:2521
##          C: 724
##
##
##
```

## 2 Data partition

```
# data partition
dat.matrix <- model.matrix(recovery_time ~ ., dat)[ , -1]

set.seed(2023)
trainRows <- createDataPartition(y = dat$recovery_time, p = 0.8, list = FALSE)

train.dat <- dat[trainRows,]
train.bin.dat <- bin.dat[trainRows,]

train.dat.matrix <- model.matrix(~., train.dat)[ , -1]
train.bin.dat.matrix <- train.dat.matrix %>%
  as.data.frame() %>%
  mutate(recovery_time = ifelse(recovery_time > 30, "gt30", "lt30")) %>%
  mutate(recovery_time = factor(recovery_time, levels = c("lt30", "gt30")))

train.x <- dat.matrix[trainRows,]
train.y <- dat$recovery_time[trainRows]
train.bin.y <- bin.dat$recovery_time[trainRows]

test.x <- dat.matrix[-trainRows,]
test.y <- dat$recovery_time[-trainRows]
test.bin.y <- bin.dat$recovery_time[-trainRows]
```

## 3 Exploratory analysis and data visualization

```
# data summary
st_options(plain.ascii = FALSE,
            style = "rmarkdown",
            dfSummary.silent = TRUE,
            footnote = NA,
            subtitle.emphasis = FALSE)
dfSummary(train.dat)
```

### 3.0.1 Data Frame Summary

```
train.dat
Dimensions: 2900 x 15
Duplicates: 0
```

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Valid	Missing
1	age [numeric]	Mean (sd) : 60.1 (4.5) min < med < max: 45 < 60 < 77 IQR (CV) : 6 (0.1)	33 distinct values	: : .: .: .:	2900 (100.0%)	0 (0.0%)
2	gender [factor]	1. 0 2. 1	1468 (50.6%) 1432 (49.4%)	IIIIIIII IIIIIIII	2900 (100.0%)	0 (0.0%)
3	race [factor]	1. 1 2. 2 3. 3 4. 4	1909 (65.8%) 132 ( 4.6%) 568 (19.6%) 291 (10.0%)	IIIIIIIIII III II	2900 (100.0%)	0 (0.0%)
4	smoking [factor]	1. 0 2. 1 3. 2	1763 (60.8%) 845 (29.1%) 292 (10.1%)	IIIIIIIIII IIII II	2900 (100.0%)	0 (0.0%)
5	height [numeric]	Mean (sd) : 170.2 (6) min < med < max: 151.2 < 170.1 < 188.6 IQR (CV) : 8 (0)	312 distinct values	: : .: .: .:	2900 (100.0%)	0 (0.0%)
6	weight [numeric]	Mean (sd) : 80.2 (7) min < med < max: 57.1 < 80.3 < 103.4 IQR (CV) : 9.5 (0.1)	361 distinct values	: : .: .: .:	2900 (100.0%)	0 (0.0%)
7	bmi [numeric]	Mean (sd) : 27.8 (2.7) min < med < max: 19.7 < 27.7 < 39.8 IQR (CV) : 3.6 (0.1)	160 distinct values	: : .: .: .:	2900 (100.0%)	0 (0.0%)
8	hypertension [factor]	1. 0 2. 1	1514 (52.2%) 1386 (47.8%)	IIIIIIII IIIIIIII	2900 (100.0%)	0 (0.0%)
9	diabetes [factor]	1. 0 2. 1	2446 (84.3%) 454 (15.7%)	IIIIIIIIIIII III	2900 (100.0%)	0 (0.0%)
10	SBP [numeric]	Mean (sd) : 130.2 (8.1) min < med < max: 104 < 130 < 158 IQR (CV) : 11 (0.1)	54 distinct values	: : .: .: .:	2900 (100.0%)	0 (0.0%)
11	LDL [numeric]	Mean (sd) : 110.3 (19.9) min < med < max: 32 < 110 < 174 IQR (CV) : 27 (0.2)	116 distinct values	: : .: .: .:	2900 (100.0%)	0 (0.0%)
12	vaccine [factor]	1. 0 2. 1	1192 (41.1%) 1708 (58.9%)	IIIIII IIIIIIIIII	2900 (100.0%)	0 (0.0%)
13	severity [factor]	1. 0 2. 1	2619 (90.3%) 281 ( 9.7%)	IIIIIIIIIIIIII I	2900 (100.0%)	0 (0.0%)
14	study [factor]	1. A 2. B 3. C	580 (20.0%) 1750 (60.3%) 570 (19.7%)	III IIIIIIIIII III	2900 (100.0%)	0 (0.0%)

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Valid	Missing
15	recovery_time [numeric]	Mean (sd) : 43 (30.5) min < med < max: 3 < 38 < 365 IQR (CV) : 21 (0.7)	144 distinct values	: : : : : : : : : .	2900 (100.0%)	0 (0.0%)

```
skimr::skim_without_charts(train.dat)
```

Table 2: Data summary

Name	train.dat
Number of rows	2900
Number of columns	15
Column type frequency:	
factor	8
numeric	7
Group variables	None

**Variable type: factor**

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
gender	0	1	FALSE	2	0: 1468, 1: 1432
race	0	1	FALSE	4	1: 1909, 3: 568, 4: 291, 2: 132
smoking	0	1	FALSE	3	0: 1763, 1: 845, 2: 292
hypertension	0	1	FALSE	2	0: 1514, 1: 1386
diabetes	0	1	FALSE	2	0: 2446, 1: 454
vaccine	0	1	FALSE	2	1: 1708, 0: 1192
severity	0	1	FALSE	2	0: 2619, 1: 281
study	0	1	FALSE	3	B: 1750, A: 580, C: 570

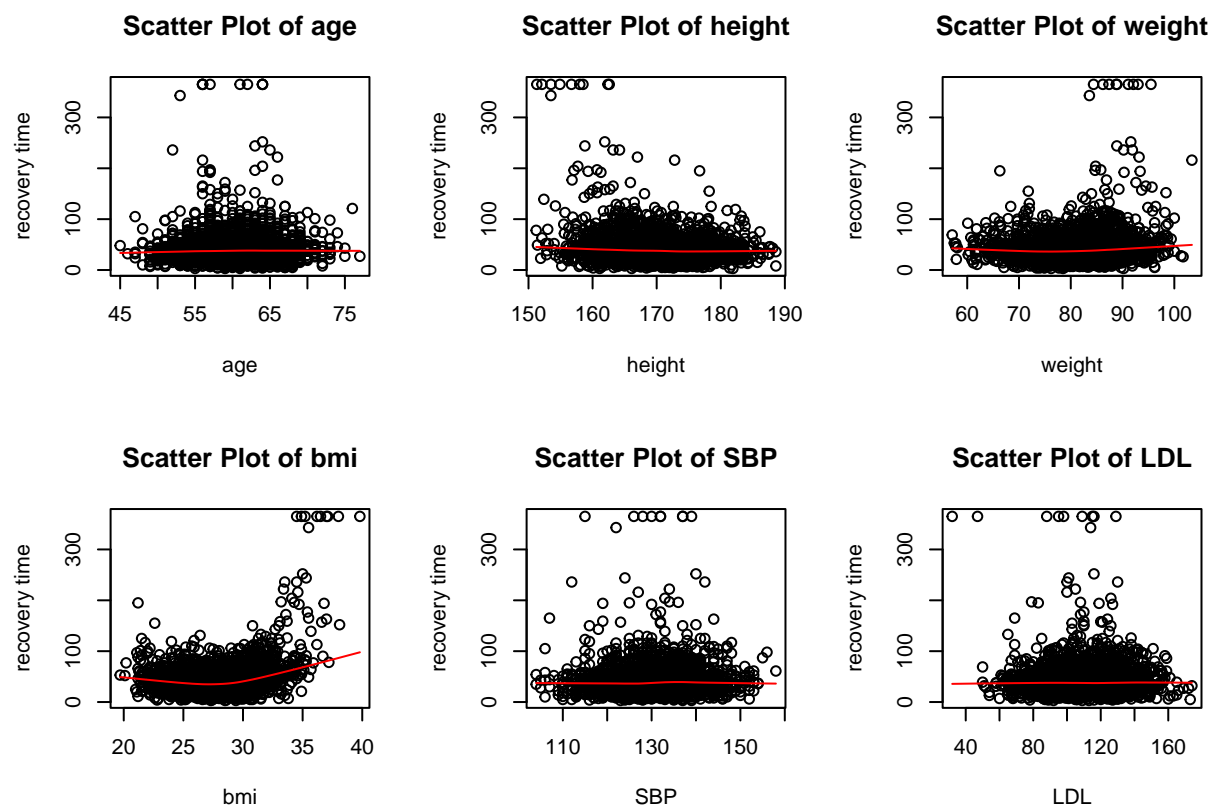
**Variable type: numeric**

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
age	0	1	60.07	4.51	45.0	57.0	60.00	63.0	77.0
height	0	1	170.17	6.04	151.2	166.1	170.15	174.1	188.6
weight	0	1	80.20	7.00	57.1	75.4	80.30	84.9	103.4
bmi	0	1	27.76	2.73	19.7	25.9	27.70	29.5	39.8
SBP	0	1	130.19	8.08	104.0	125.0	130.00	136.0	158.0
LDL	0	1	110.27	19.87	32.0	97.0	110.00	124.0	174.0
recovery_time	0	1	43.02	30.51	3.0	28.0	38.00	49.0	365.0

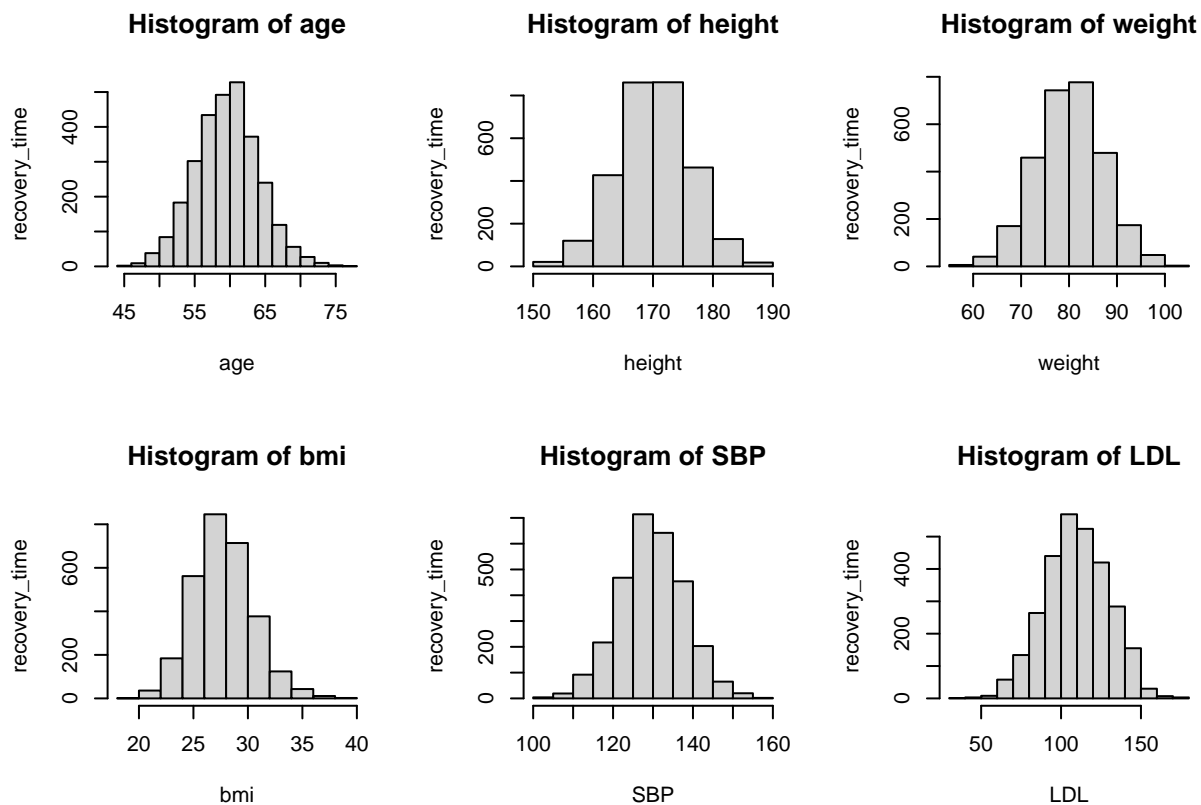
```
# EDA
```

```
cts_var = c("age", "height", "weight", "bmi", "SBP", "LDL")
fct_var = c("gender", "race", "smoking", "hypertension", "diabetes", "vaccine", "severity", "study")
```

```
# scatter plot of continuous predictors
par(mfrow=c(2, 3))
for (i in 1:length(cts_var)){
  var = cts_var[i]
  plot(recovery_time~train.dat[,var],
       data = train.dat,
       ylab = "recovery time",
       xlab = var,
       main = str_c("Scatter Plot of ", var))
  lines(stats::lowess(train.dat[,var], train.dat$recovery_time), col = "red", type = "l")
}
```

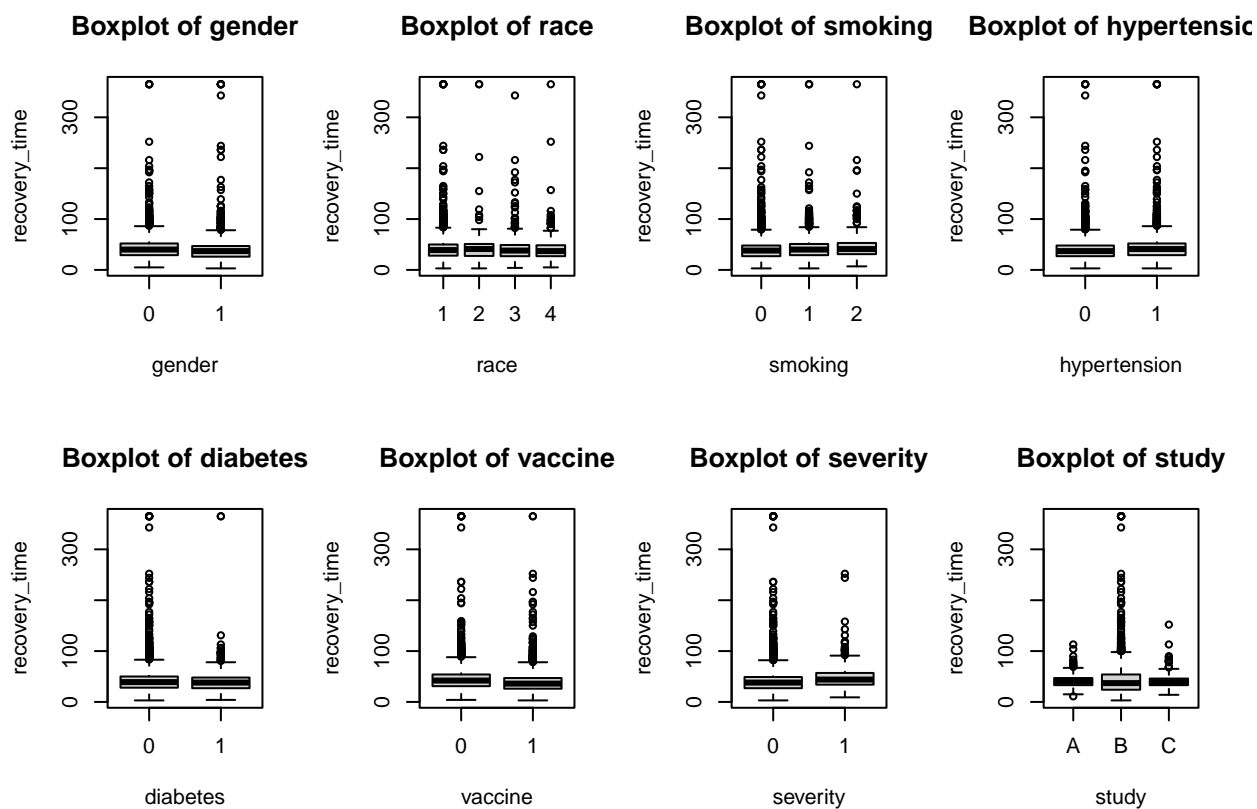


```
for (i in 1:length(cts_var)){
  var = cts_var[i]
  hist(train.dat[,var],
       ylab = "recovery_time",
       xlab = var,
       main = str_c("Histogram of ", var))
}
```



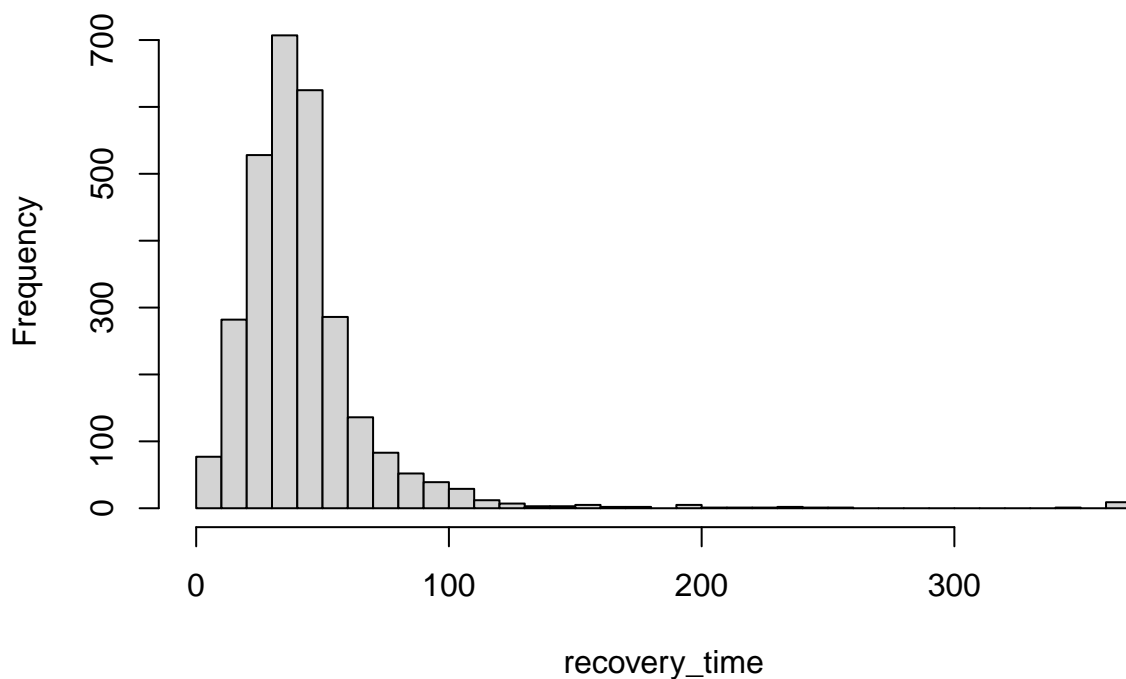
```
# boxplot of categorical predictors
par(mfrow=c(2, 4))
for (i in 1:length(fct_var)){
  var = fct_var[i]
  plot(recovery_time~train.dat[,var],
       data = train.dat,
       ylab = "recovery_time",
       xlab = var,
       main = str_c("Boxplot of ", var))
}
```





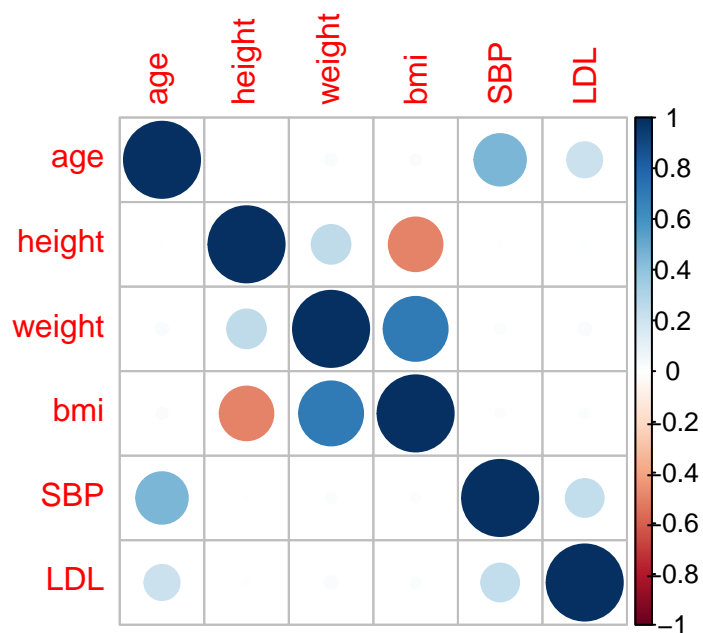
```
# histogram of response
par(mfrow=c(1, 1))
hist(train.dat$recovery_time,
      breaks = 50,
      main = "Histogram of recovery_time",
      xlab = "recovery_time")
```

## Histogram of recovery\_time



```
# correlation
par(mfrow=c(1, 1))
corrplot(cor(train.dat[,cts_var]), method = "circle", type = "full",
          title = "Correlation plot of continuous variables",
          mar = c(2, 2, 4, 2))
```

## Correlation plot of continuous variables



```
train.bin.dat
Dimensions: 2900 x 15
Duplicates: 0
```

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Valid	Missing
1	age [numeric]	Mean (sd) : 60.1 (4.5) min < med < max: 45 < 60 < 77 IQR (CV) : 6 (0.1)	33 distinct values	: : .: .: .: : .	2900 (100.0%)	0 (0.0%)
2	gender [factor]	1. 0 2. 1	1468 (50.6%) 1432 (49.4%)	IIIIIIIIII IIIIIIIIII	2900 (100.0%)	0 (0.0%)
3	race [factor]	1. 1 2. 2 3. 3 4. 4	1909 (65.8%) 132 ( 4.6%) 568 (19.6%) 291 (10.0%)	IIIIIIIIIIIIII III II	2900 (100.0%)	0 (0.0%)
4	smoking [factor]	1. 0 2. 1 3. 2	1763 (60.8%) 845 (29.1%) 292 (10.1%)	IIIIIIIIIIIIII IIIII II	2900 (100.0%)	0 (0.0%)
5	height [numeric]	Mean (sd) : 170.2 (6) min < med < max: 151.2 < 170.1 < 188.6 IQR (CV) : 8 (0)	312 distinct values	: : : : .: : . .: : : .: : : .	2900 (100.0%)	0 (0.0%)
6	weight [numeric]	Mean (sd) : 80.2 (7) min < med < max: 57.1 < 80.3 < 103.4 IQR (CV) : 9.5 (0.1)	361 distinct values	. : . : : .: : : .: : : . .: : : : .	2900 (100.0%)	0 (0.0%)
7	bmi [numeric]	Mean (sd) : 27.8 (2.7) min < med < max: 19.7 < 27.7 < 39.8 IQR (CV) : 3.6 (0.1)	160 distinct values	: : : : .: : . .: : : .: : : : .	2900 (100.0%)	0 (0.0%)
8	hypertension [factor]	1. 0 2. 1	1514 (52.2%) 1386 (47.8%)	IIIIIIIIII IIIIIIIIII	2900 (100.0%)	0 (0.0%)
9	diabetes [factor]	1. 0 2. 1	2446 (84.3%) 454 (15.7%)	IIIIIIIIIIIIIIIIII III	2900 (100.0%)	0 (0.0%)

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Valid	Missing
10	SBP [numeric]	Mean (sd) : 130.2 (8.1) min < med < max: 104 < 130 < 158 IQR (CV) : 11 (0.1)	54 distinct values	: :. :.:. :.:. .:.:.:	2900 (100.0%)	0 (0.0%)
11	LDL [numeric]	Mean (sd) : 110.3 (19.9) min < med < max: 32 < 110 < 174 IQR (CV) : 27 (0.2)	116 distinct values	.: :. :. :. .:.:.:	2900 (100.0%)	0 (0.0%)
12	vaccine [factor]	1. 0 2. 1	1192 (41.1%) 1708 (58.9%)	IIIIII IIIIIIII	2900 (100.0%)	0 (0.0%)
13	severity [factor]	1. 0 2. 1	2619 (90.3%) 281 ( 9.7%)	IIIIIIIIIIII I	2900 (100.0%)	0 (0.0%)
14	study [factor]	1. A 2. B 3. C	580 (20.0%) 1750 (60.3%) 570 (19.7%)	III IIIIIIII III	2900 (100.0%)	0 (0.0%)
15	recovery_time [factor]	1. lt30 2. gt30	887 (30.6%) 2013 (69.4%)	IIII IIIIIIII	2900 (100.0%)	0 (0.0%)

```
skimr::skim_without_charts(train.bin.dat)
```

Table 6: Data summary

Name	train.bin.dat
Number of rows	2900
Number of columns	15
Column type frequency:	
factor	9
numeric	6
Group variables	None

**Variable type: factor**

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
gender	0	1	FALSE	2	0: 1468, 1: 1432
race	0	1	FALSE	4	1: 1909, 3: 568, 4: 291, 2: 132
smoking	0	1	FALSE	3	0: 1763, 1: 845, 2: 292
hypertension	0	1	FALSE	2	0: 1514, 1: 1386
diabetes	0	1	FALSE	2	0: 2446, 1: 454
vaccine	0	1	FALSE	2	1: 1708, 0: 1192
severity	0	1	FALSE	2	0: 2619, 1: 281
study	0	1	FALSE	3	B: 1750, A: 580, C: 570
recovery_time	0	1	FALSE	2	gt3: 2013, lt3: 887

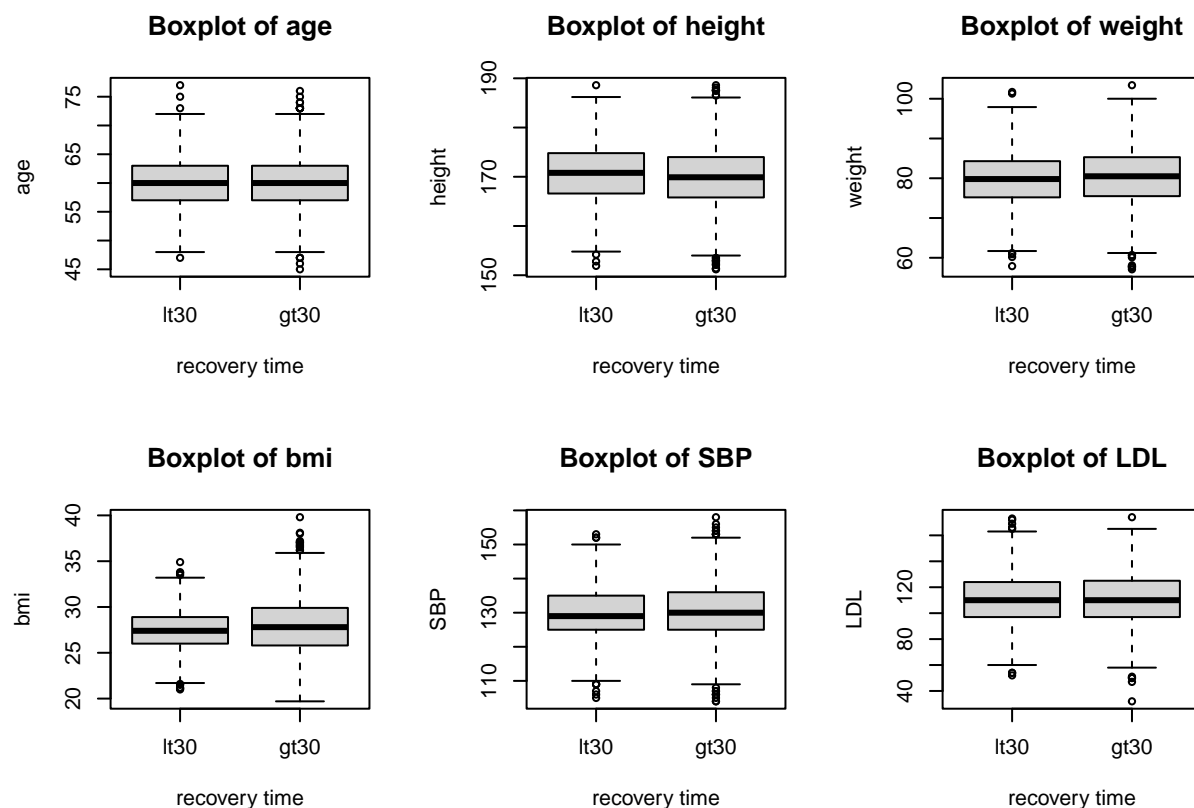
**Variable type: numeric**

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
age	0	1	60.07	4.51	45.0	57.0	60.00	63.0	77.0
height	0	1	170.17	6.04	151.2	166.1	170.15	174.1	188.6
weight	0	1	80.20	7.00	57.1	75.4	80.30	84.9	103.4
bmi	0	1	27.76	2.73	19.7	25.9	27.70	29.5	39.8
SBP	0	1	130.19	8.08	104.0	125.0	130.00	136.0	158.0
LDL	0	1	110.27	19.87	32.0	97.0	110.00	124.0	174.0

```
# EDA
```

```
# boxplot of continuous predictors
```

```
par(mfrow=c(2, 3))
for (i in 1:length(cts_var)){
  var = cts_var[i]
  boxplot(train.bin.dat[,var]~recovery_time,
    data = train.bin.dat,
    xlab = "recovery time",
    ylab = var,
    main = str_c("Boxplot of ", var))
}
```



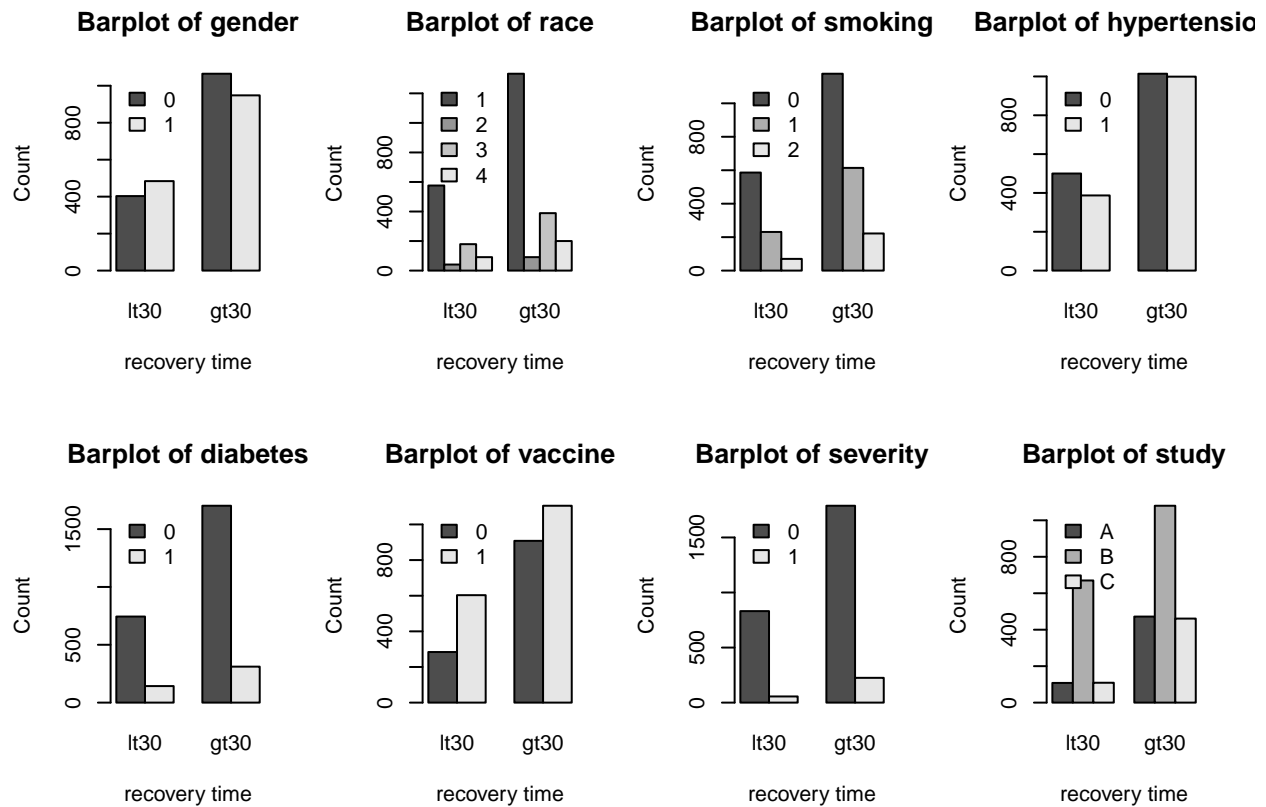
```
# barplot of categorical predictors
```

```
par(mfrow=c(2, 4))
for (i in 1:length(fct_var)){
  var <- fct_var[i]
  counts <- table(train.bin.dat[,var], train.bin.y)
  barplot(counts, beside = TRUE, legend.text = TRUE,
```

```

xlab = "recovery time",
ylab = "Count",
main = str_c("Barplot of ", var),
args.legend = list(bty = 'n', x = 'topleft'))
}

```



```

# barplot of response
par(mfrow=c(1, 1))
counts <- table(train.bin.y)
barplot(counts,
  xlab = "recovery time",
  ylab = "Count",
  main = "Barplot of binary recovery_time")

```

