P8106_primary_EDA

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Contents

Import and data manipulation

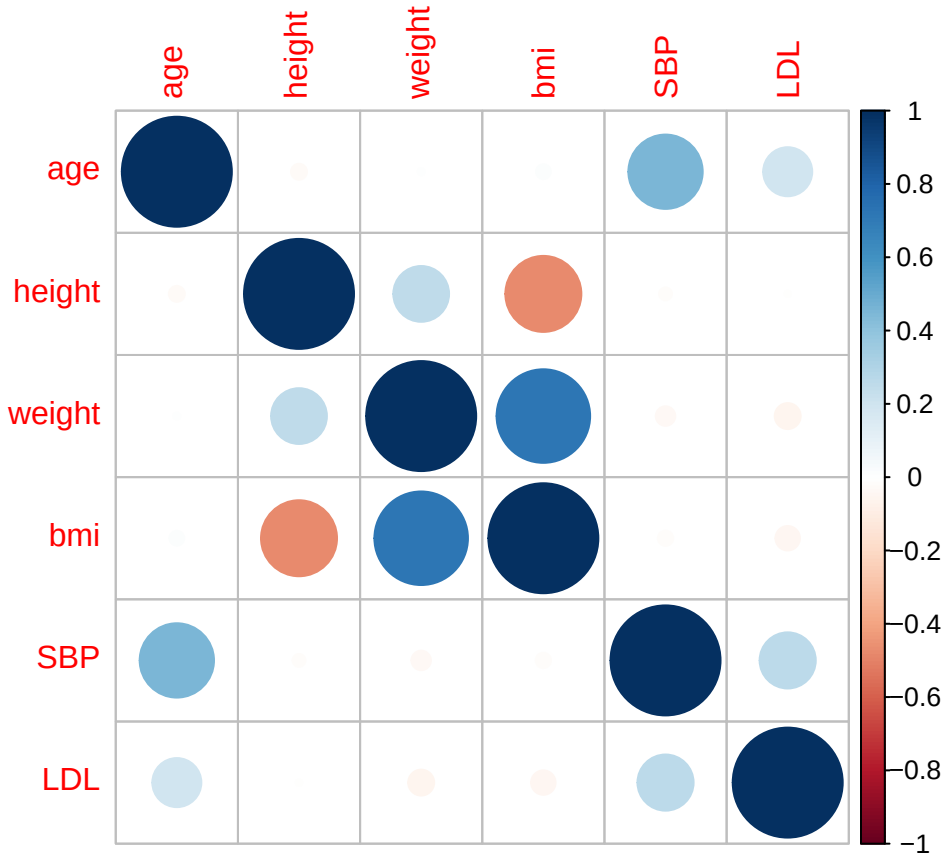
```
# Load recovery.RData environment
load("./recovery.Rdata")

dat %>% na.omit()

# dat1 draw a random sample of 2000 participants Uni:3307
set.seed(3307)

dat1 = dat[sample(1:10000, 2000),]

dat1 =
  dat1[, -1] %>%
  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(
      case_when(study == "A" ~ 1, study == "B" ~ 2, study == "C" ~ 3)
      )
    )

# dat2 draw a random sample of 2000 participants Uni:2493
set.seed(2493)
```

```r
dat2 = dat[sample(1:10000, 2000),]

dat2 =
  dat2[, -1] %>%
  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(
      case_when(study == "A" ~ 1, study == "B" ~ 2, study == "C" ~ 3)
      )
    )

# Merged dataset with unique observation
covid_dat = rbind(dat1, dat2) %>%
  unique()

covid_dat2 = model.matrix(recovery_time ~ ., covid_dat)[, -1]

# Partition dataset into two parts: training data (70%) and test data (30%)
rowTrain = createDataPartition(y = covid_dat$recovery_time, p = 0.7, list = FALSE)

trainData = covid_dat[rowTrain, ]
testData = covid_dat[-rowTrain, ]
```

Data visualization

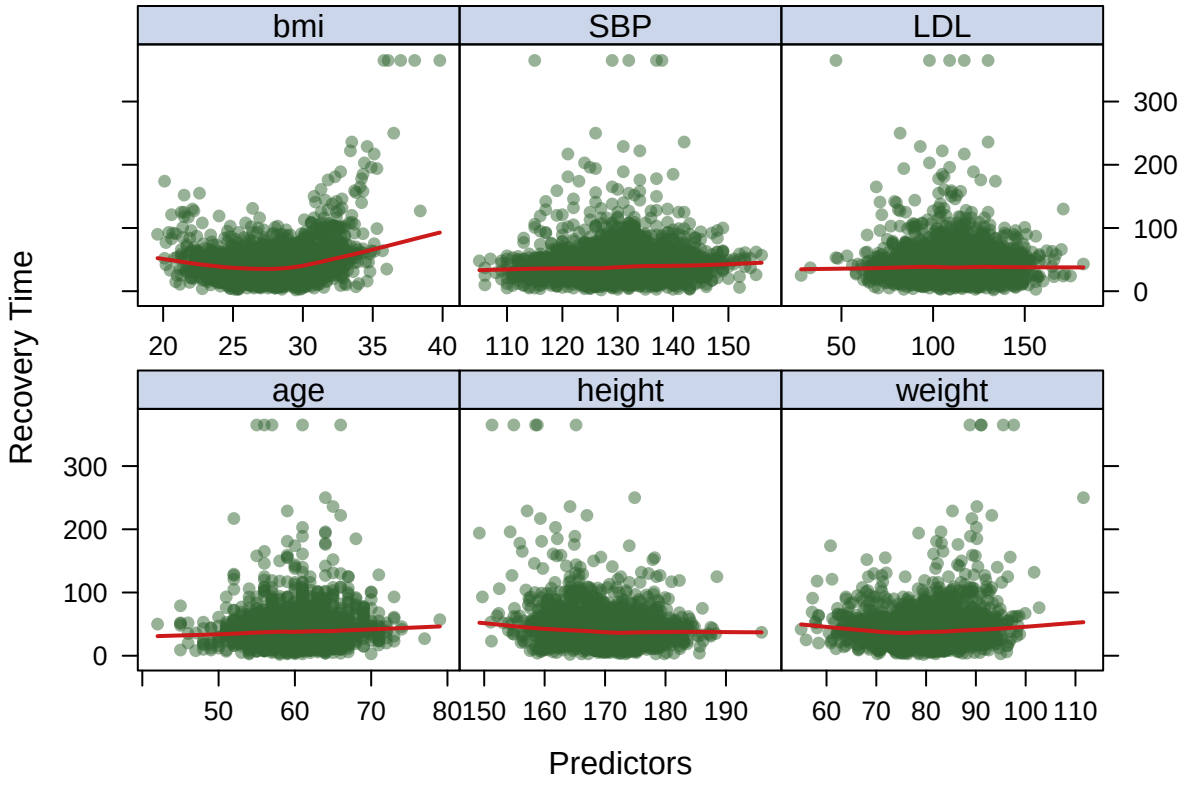
Correlation plot

```r
corr_dat = covid_dat[rowTrain,] %>%
  dplyr::select('age', 'height', 'weight', 'bmi', 'SBP', 'LDL')
corrplot(cor(corr_dat), method = "circle", type = "full")
```

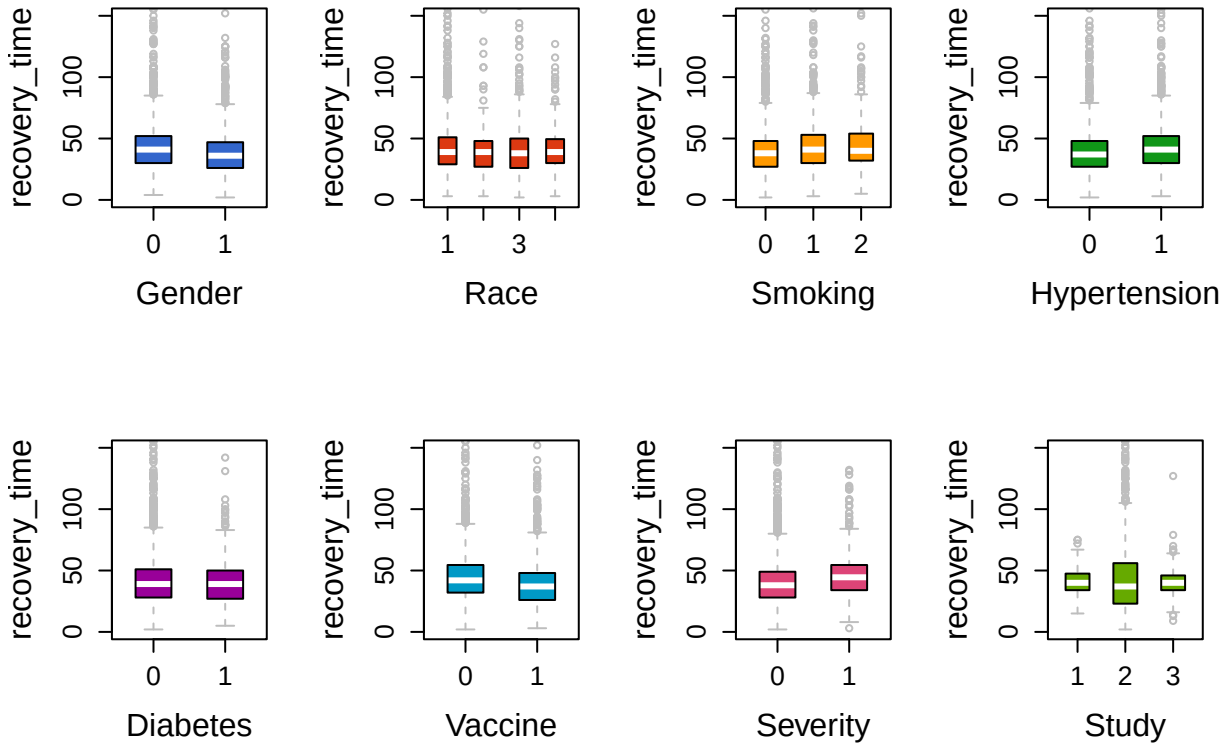


Feature plot

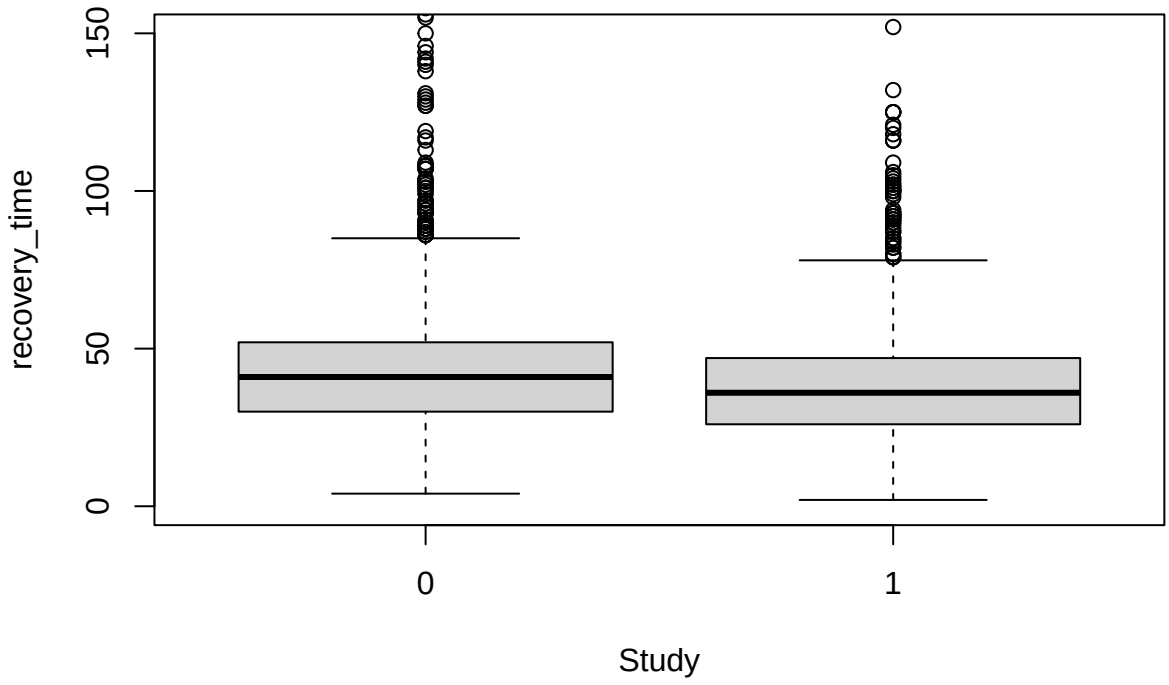
```
vis_trdat = trainData %>%
  dplyr::select('age', 'height', 'weight', 'bmi', 'SBP', 'LDL', 'recovery_time')

theme1 <- trellis.par.get()
theme1$plot.symbol$col <- rgb(.2, .4, .2, .5)
theme1$plot.symbol$pch <- 16
theme1$plot.line$col <- rgb(.8, .1, .1, 1)
theme1$plot.line$lwd <- 2
theme1$strip.background$col <- rgb(.0, .2, .6, .2)
trellis.par.set(theme1)

featurePlot(x = vis_trdat[, 1:6],
            y = vis_trdat[, 7],
            plot = "scatter",
            span = 0.5,
            labels = c("Predictors", "Recovery Time"),
            type = c("p", "smooth"))
```


bmi
SBP
LDL
age
height
weight
Recovery Time
Predictors
0
100
200
300
20
25
30
35
40
110
120
130
140
150
50
100
150
50
60
70
80
150
160
170
180
190
60
70
80
90
100
110

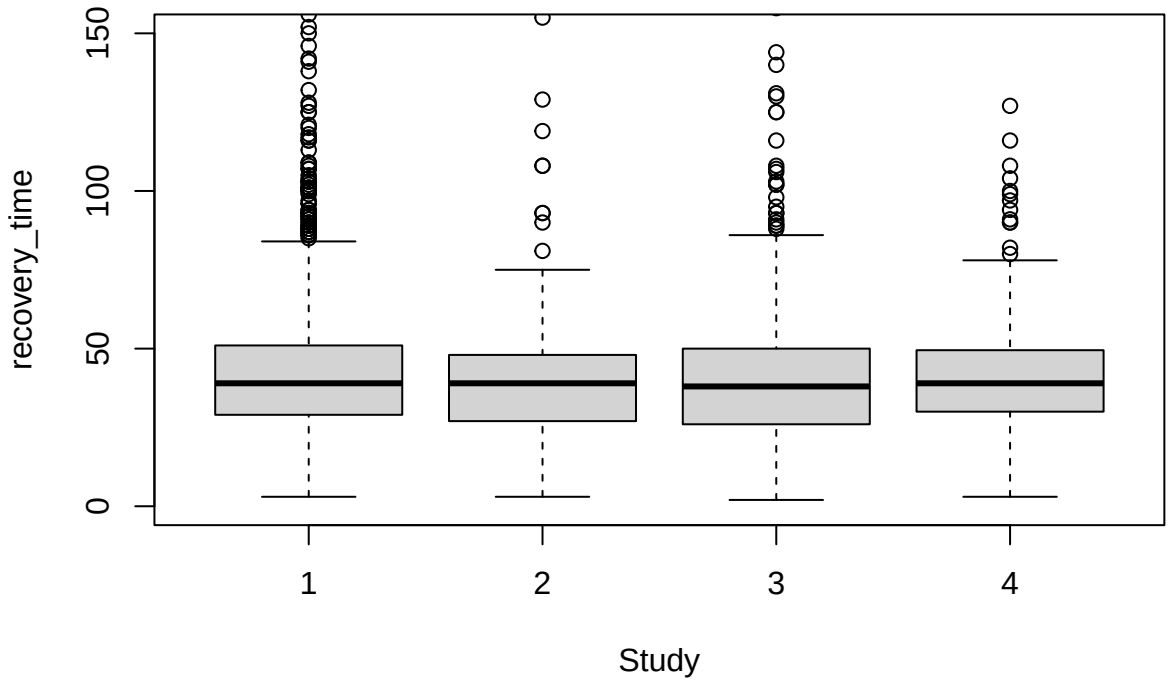
Boxplot



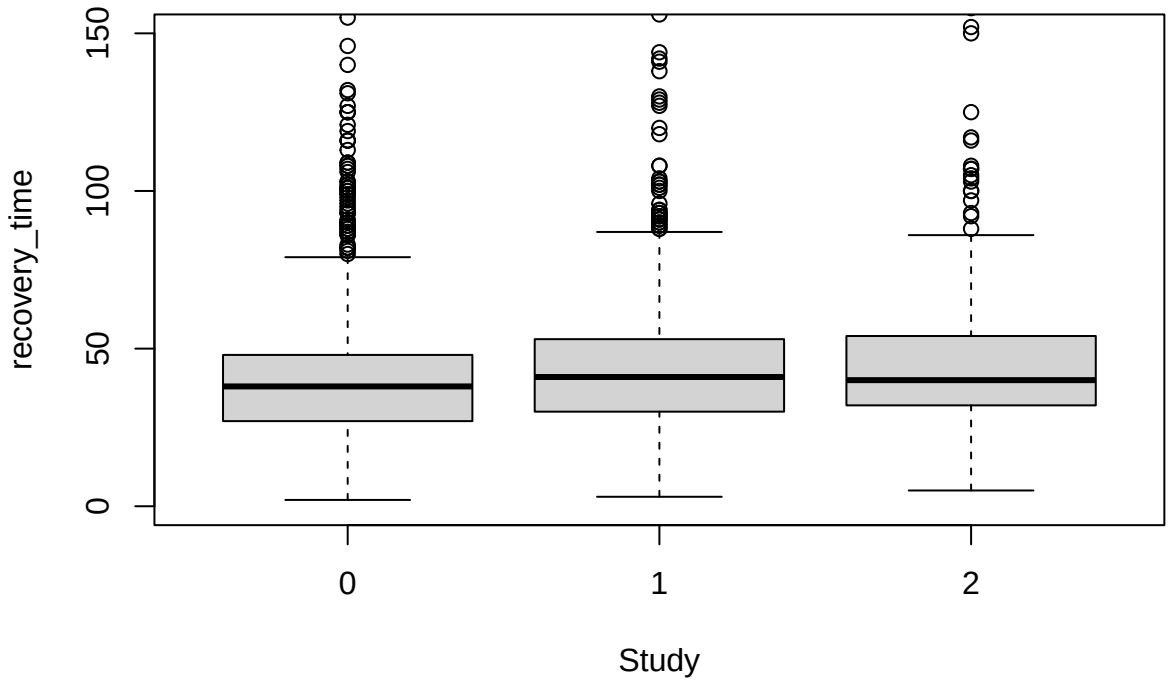

```
bp_gender = boxplot(recovery_time ~ gender, data = trainData, xlab = "Study", ylim = c(0, 150))
```



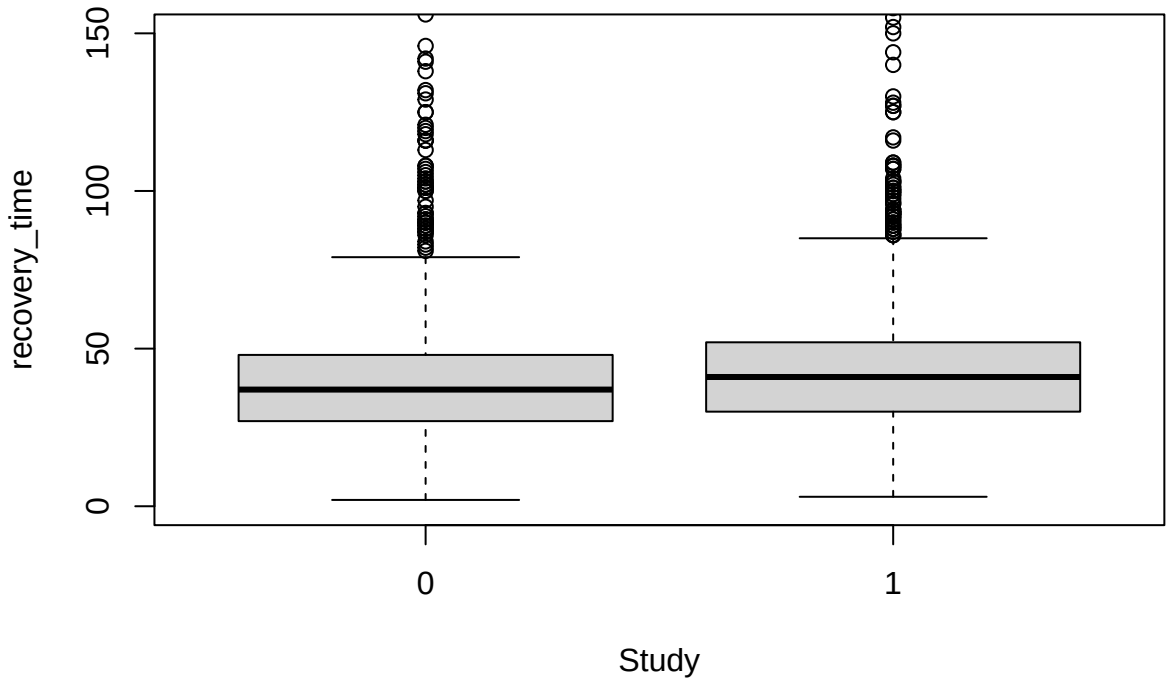

```
bp_race = boxplot(recovery_time ~ race, data = trainData, xlab = "Study", ylim = c(0, 150))
```



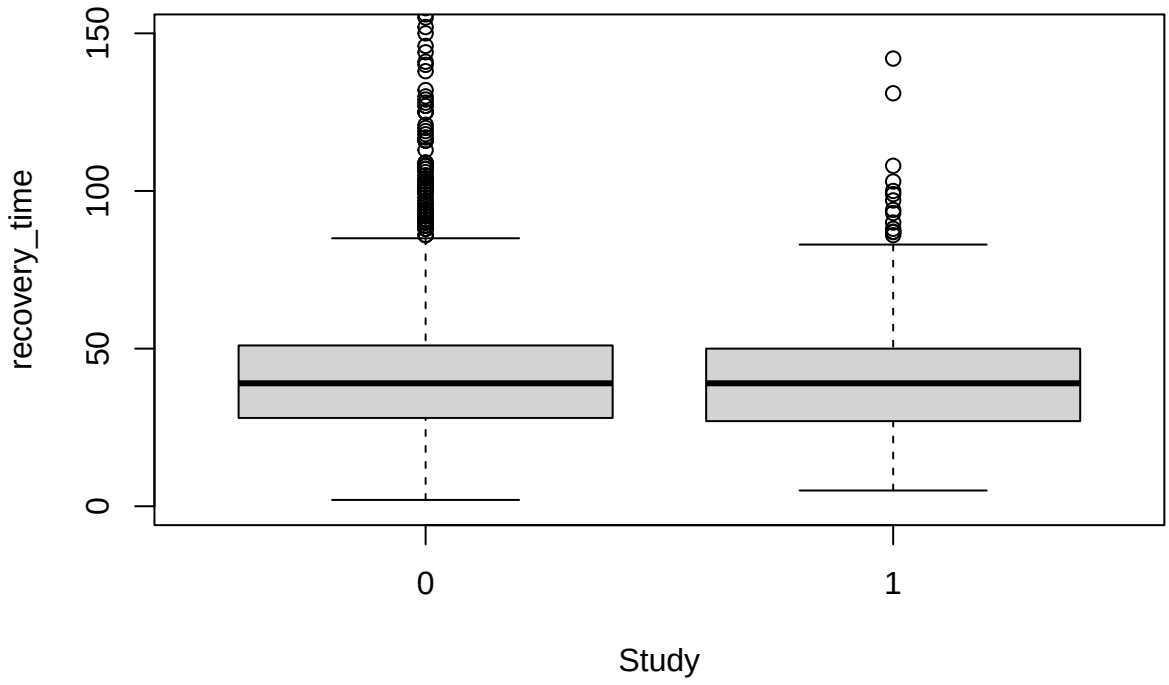

```
bp_smoking = boxplot(recovery_time ~ smoking, data = trainData, xlab = "Study", ylim = c(0, 150))
```



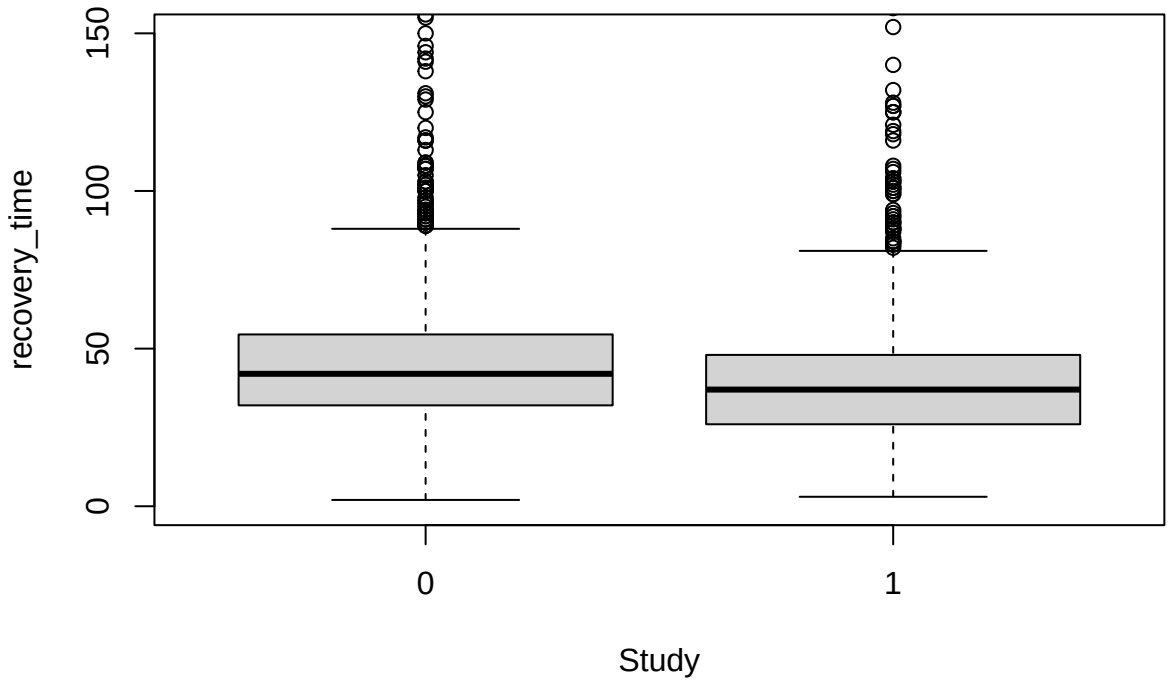

```
bp_hypertension = boxplot(recovery_time ~ hypertension, data = trainData, xlab = "Study", ylim = c(0, 15
```



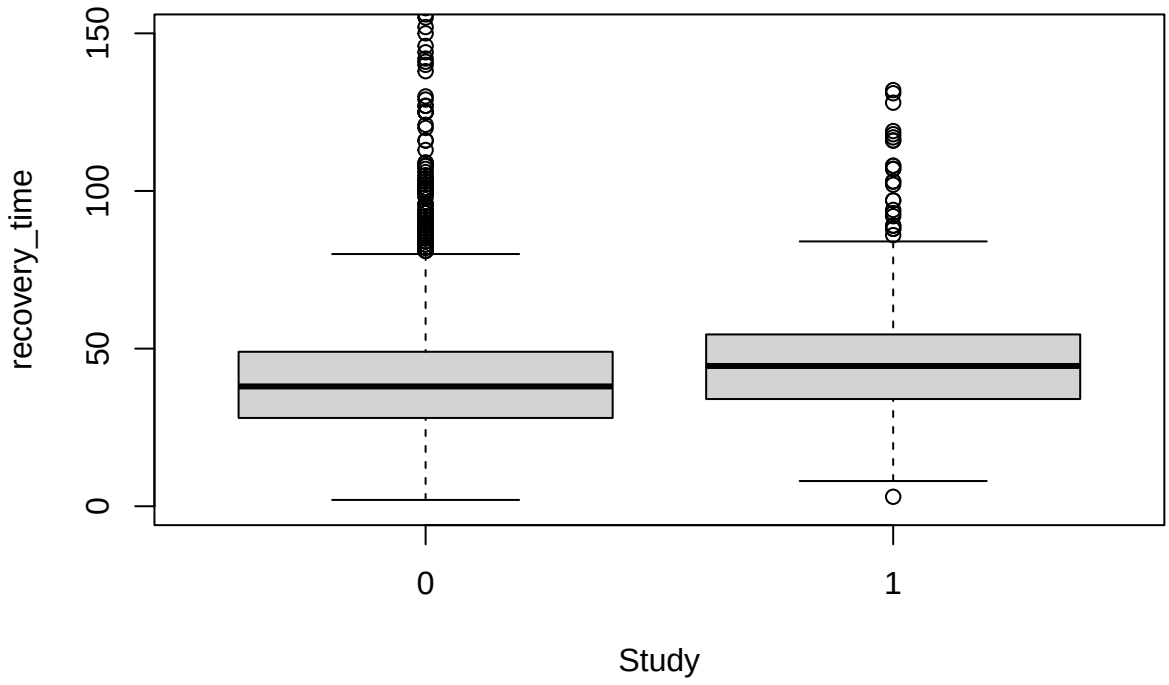

```
bp_diabetes = boxplot(recovery_time ~ diabetes, data = trainData, xlab = "Study", ylim = c(0, 150))
```



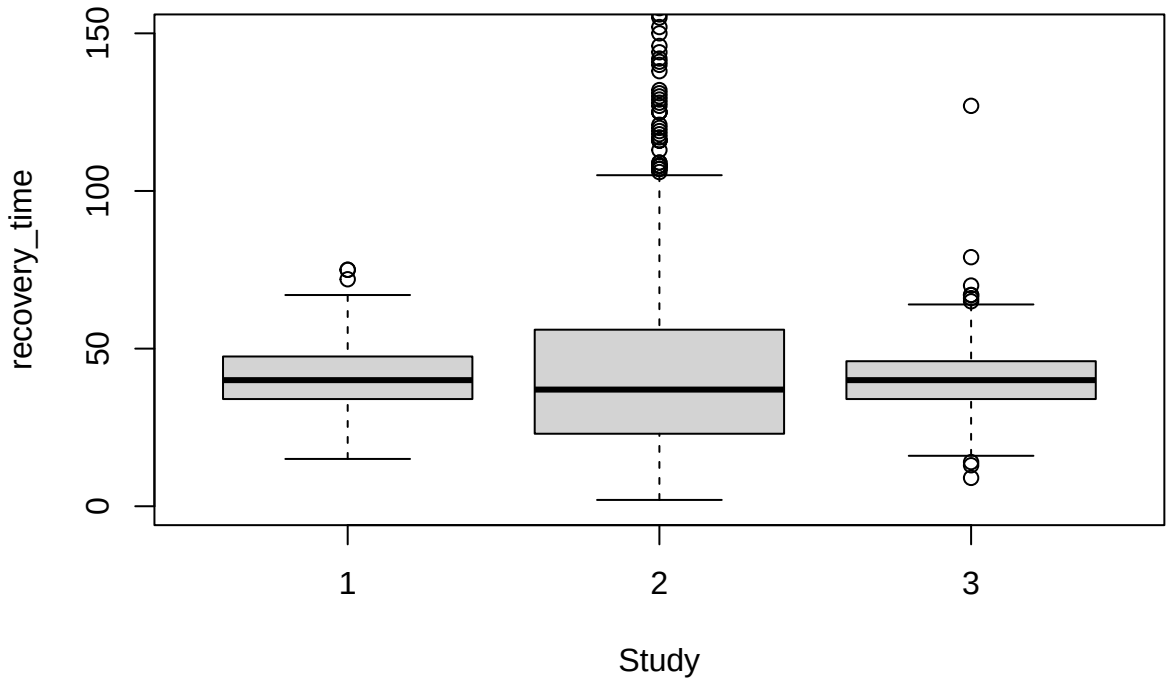

```
bp_vaccine = boxplot(recovery_time ~ vaccine, data = trainData, xlab = "Study", ylim = c(0, 150))
```




```
bp_severity = boxplot(recovery_time ~ severity, data = trainData, xlab = "Study", ylim = c(0, 150))
```




```
bp_study = boxplot(recovery_time ~ study, data = trainData, xlab = "Study", ylim = c(0, 150))
```


recovery_time
0
50
100
150
1
2
3
Study