

P8106 Final Project: Predicting COVID-19 Recovery Time and Identifying Significant Risk Factors

Runze Cui (rc3521), Yuchen Hua (yh3555), Hongpu Min (hm2946)

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Background

[Check the report]

Data:

[Description check the report]

```
# For primary analysis:
# Dataset Loading:
load("data/recovery.Rdata")

set.seed(3521) # Runze Cui's uni(2183):
# Create a first random sample of 2000 participants:
dat1 <- dat[sample(1:10000, 2000),]

set.seed(3555) # Yuchen Hua's uni(3555)
# Create a second random sample of 2000 participants:
dat2 <- dat[sample(1:10000, 2000),]

# Merged the two datasets and remove repeated observations:
dat <- unique(rbind(dat1, dat2))

# Get rid of the id variable from the merged dataset and do the data cleaning:
dat <- dat %>%
  select(-id) %>%
  mutate(gender = as.factor(gender)) %>%
  mutate(race = as.factor(race)) %>%
  mutate(smoking = as.factor(smoking)) %>%
  mutate(hypertension = as.factor(hypertension)) %>%
  mutate(diabetes = as.factor(diabetes)) %>%
  mutate(vaccine = as.factor(vaccine)) %>%
  mutate(severity = as.factor(severity)) %>%
  mutate(study = as.factor(study)) %>%
  na.omit() %>%
  relocate(recovery_time)

head(dat)
```

	recovery_time	age	gender	race	smoking	height	weight	bmi	hypertension
## 8158	52	61	0	1	1	169.9	87.6	30.4	0
## 3387	24	60	1	1	2	173.4	70.6	23.5	0
## 1709	36	60	1	1	1	178.2	79.9	25.1	0
## 4051	23	70	1	4	0	167.4	77.7	27.7	1
## 954	24	63	1	4	0	175.4	88.7	28.8	1
## 531	36	65	0	1	0	160.4	74.4	28.9	1
	diabetes	SBP	LDL	vaccine	severity	study			
## 8158	0	118	103	0	0	C			
## 3387	0	129	101	1	0	B			
## 1709	0	130	107	1	0	A			
## 4051	0	145	128	1	0	B			
## 954	0	131	100	0	0	A			
## 531	0	137	153	1	0	A			

```

# Separate the data as training and test data:
set.seed(3521)
# Specify rows of training data:
trRows <- createDataPartition(dat$recovery_time, p = 0.7, list = FALSE)

# Training data:
training <- dat[trRows, ]
## Covariates' matrix:
x <- model.matrix(recovery_time ~ ., dat)[trRows, -1]
## Response's vector:
y <- dat$recovery_time[trRows]

# Test data:
test <- dat[-trRows, ]
## Covariates' matrix:
x2 <- model.matrix(recovery_time ~ ., dat)[-trRows, -1]
## Response's vector:
y2 <- dat$recovery_time[-trRows]

# For secondary analysis:
dat2 <- dat %>%
  mutate(recovery_time = ifelse(recovery_time >= 30, 1, 0)) %>%
  mutate(recovery_time = as.factor(recovery_time))

# Training data:
training_sec <- dat2[trRows, ]
## Covariates' matrix:
x_sec <- model.matrix(recovery_time ~ ., dat2)[trRows, -1]
## Response's vector:
y_sec <- dat2$recovery_time[trRows]

# Test data:
test_sec <- dat2[-trRows, ]
## Covariates' matrix:
x2_sec <- model.matrix(recovery_time ~ ., dat2)[-trRows, -1]
## Response's vector:
y2_sec <- dat2$recovery_time[-trRows]

```

Exploratory Analysis and Data Visualization

[Description check the report]

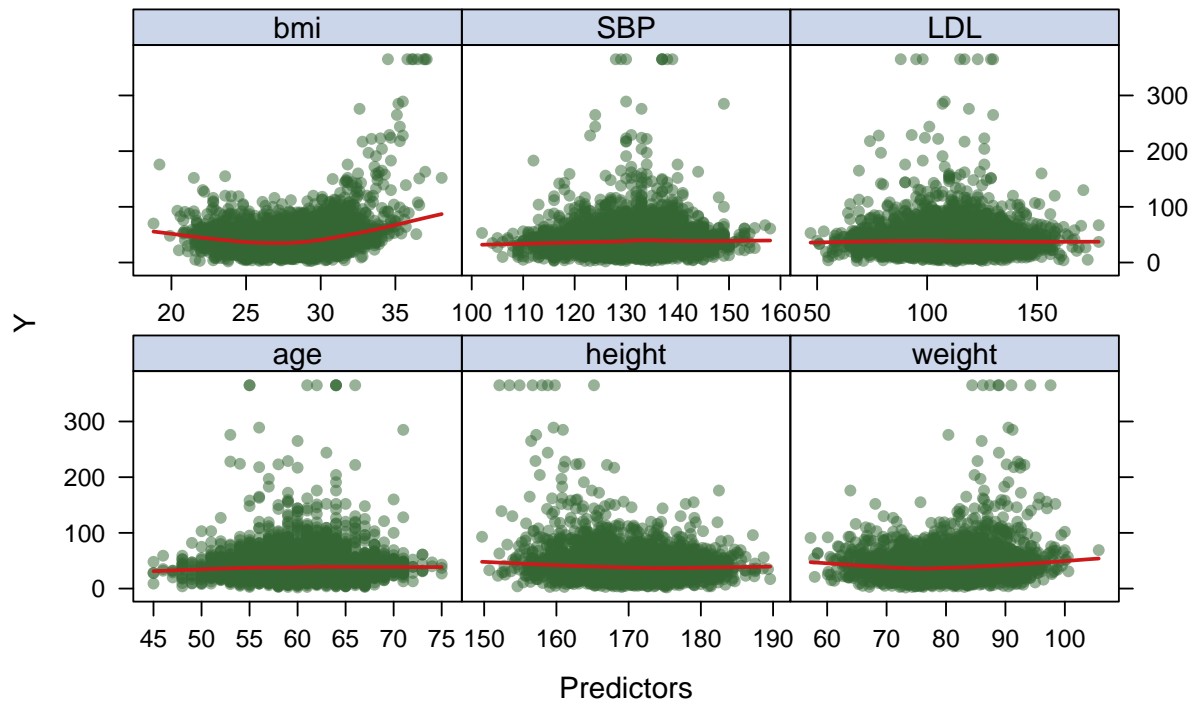
```

# For primary analysis:
## For continuous variables:
theme = trellis.par.get()
theme$plot.symbol$col = rgb(.2, .4, .2, .5)
theme$plot.symbol$pch = 16
theme$plot.line$col = rgb(.8, .1, .1, 1)
theme$plot.line$lwd = 2
theme$strip.background$col = rgb(.0, .2, .6, .2)
trellis.par.set(theme)

```

```
featurePlot(x = dat %>% dplyr::select(age, height, weight, bmi, SBP, LDL),
            y = dat$recovery_time,
            plot = "scatter",
            span = .5,
            labels = c("Predictors", "Y"),
            main = "Figure 1.1. Lattice Plots for Continuous Variables in Primary Analysis",
            type = c("p", "smooth"))
```

Figure 1.1. Lattice Plots for Continuous Variables in Primary Analysis



```
## For categorical variables:
gender_plot = dat %>%
  ggplot(aes(x = gender, y = recovery_time, fill = gender)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Female', 'Male')) +
  ylab("Recovery") +
  theme(legend.position = "none")

race_plot = dat %>%
  ggplot(aes(x = race, y = recovery_time, fill = race)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('White', 'Asian', 'Black', 'Hispanic')) +
  ylab("Recovery") +
  theme(legend.position = "none")

smoking_plot = dat %>%
  ggplot(aes(x = smoking, y = recovery_time, fill = smoking)) +
  geom_violin(color = "black", alpha = .5) +
```

```

scale_x_discrete(labels = c('Never smoked', 'Former smoker', 'Current smoker')) +
ylab("Recovery") +
theme(legend.position = "none")

hyper_plot = dat %>%
  ggplot(aes(x = hypertension, y = recovery_time, fill = hypertension)) +
  geom_violin(color = "black", alpha = .5) +
  ylab("Recovery") +
  scale_x_discrete(labels = c('No', 'Yes')) +
  theme(legend.position = "none")

diabetes_plot = dat %>%
  ggplot(aes(x = diabetes, y = recovery_time, fill = diabetes)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('No', 'Yes')) +
  ylab("Recovery") +
  theme(legend.position = "none")

vac_plot = dat %>%
  ggplot(aes(x = vaccine, y = recovery_time, fill = vaccine)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not vaccinated', 'Vaccinated')) +
  ylab("Recovery") +
  theme(legend.position = "none")

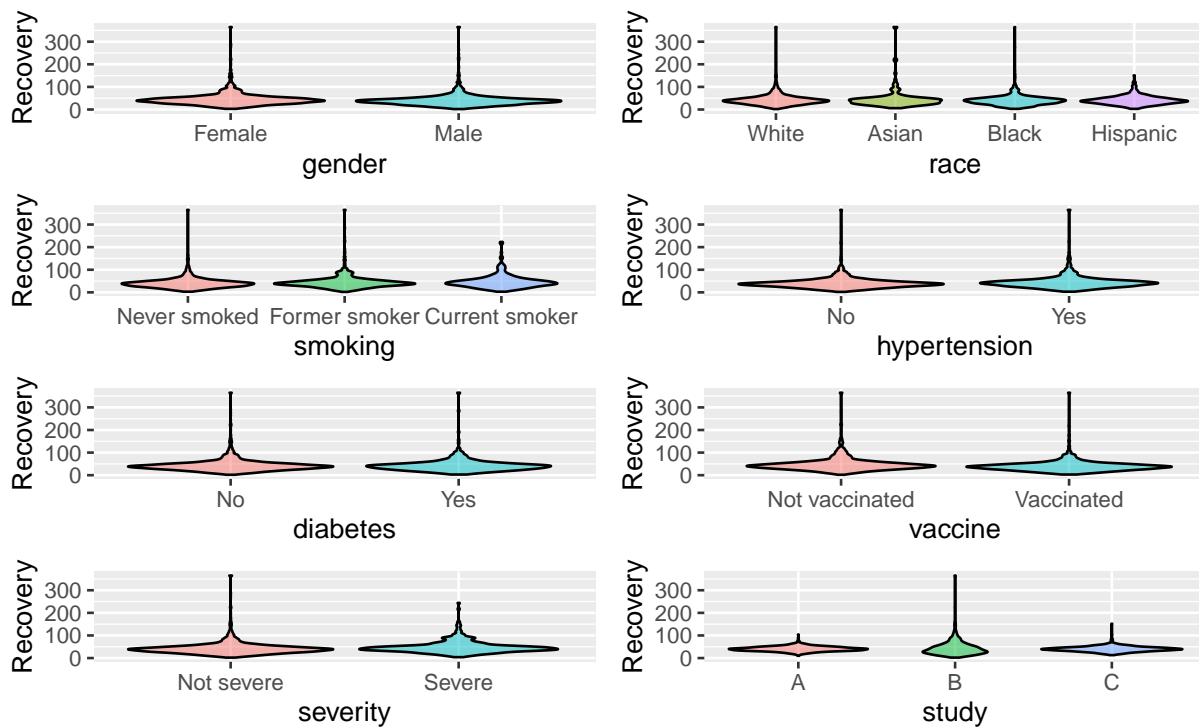
severity_plot = dat %>%
  ggplot(aes(x = severity, y = recovery_time, fill = severity)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not severe', 'Severe')) +
  ylab("Recovery") +
  theme(legend.position = "none")

study_plot = dat %>%
  ggplot(aes(x = study, y = recovery_time, fill = study)) +
  geom_violin(color = "black", alpha = .5) +
  ylab("Recovery") +
  theme(legend.position = "none")

(gender_plot + race_plot + smoking_plot + hyper_plot) / (diabetes_plot + vac_plot + severity_plot + stu
  plot_layout(guides = "collect") +
  plot_annotation(title = "Figure 1.2. Violin Plots for Categorical Variables in Primary Analysis")

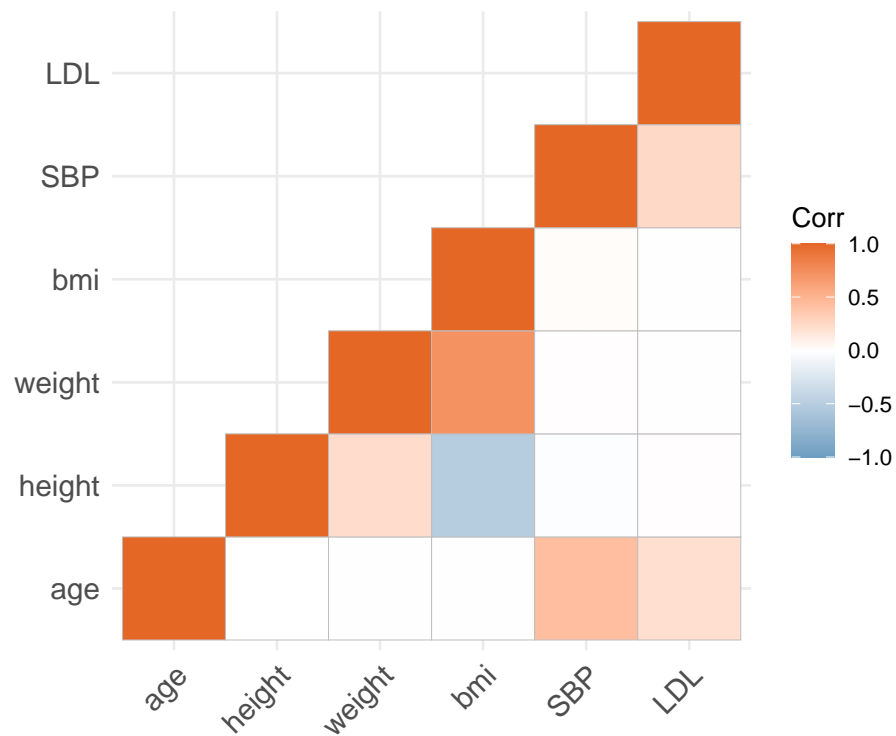
```

Figure 1.2. Violin Plots for Categorical Variables in Primary Analysis



```
## Correlation matrix for continuous variables ONLY:
model.matrix( ~ 0+., data = dat %>% dplyr::select(age, height, weight, bmi, SBP, LDL)) %>%
  cor(use = "pairwise.complete.obs") %>%
  ggcorrplot::ggcorrplot(show.diag = T,
                        type = "lower",
                        lab = F,
                        colors = c("#6D9EC1", "white", "#E46726")) +
  ggtitle("Figure 1.3. Correlation matrix for continuous datasat")
```

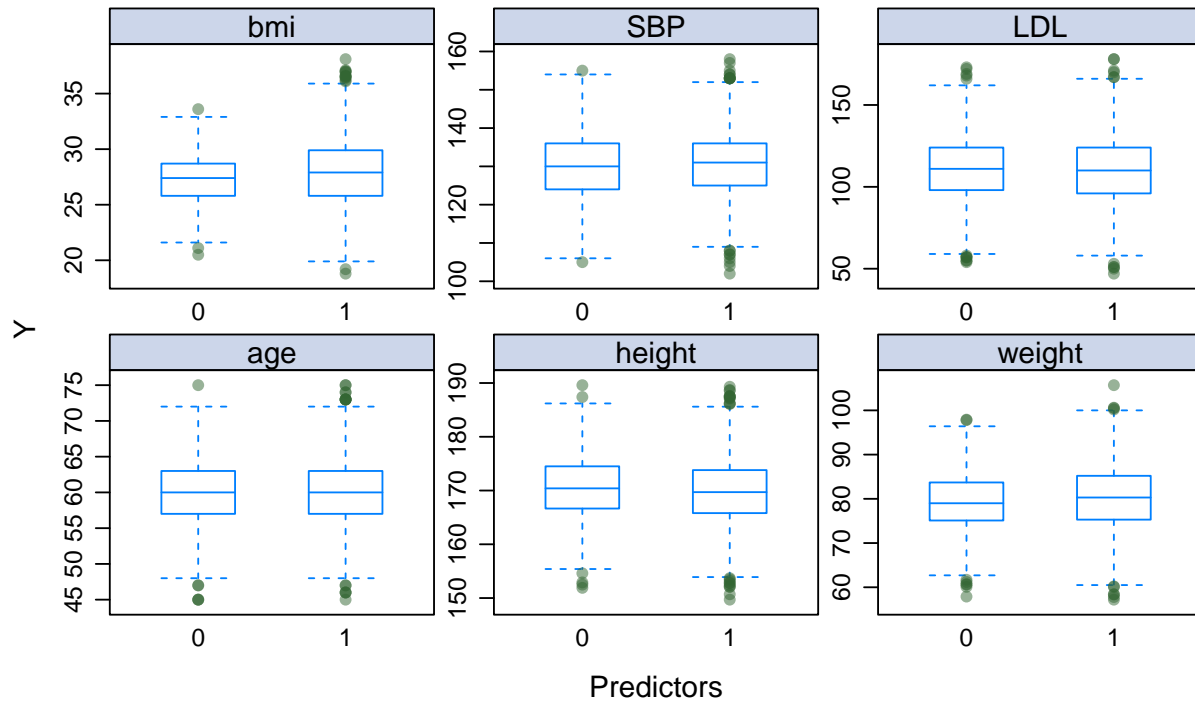
Figure 1.3. Correlation matrix for continuous dataset



```
# For secondary analysis:
## For continuous variables:
theme = trellis.par.get()
theme$plot.symbol$col = rgb(.2, .4, .2, .5)
theme$plot.symbol$pch = 16
theme$plot.line$col = rgb(.8, .1, .1, 1)
theme$plot.line$lwd = 2
theme$strip.background$col = rgb(.0, .2, .6, .2)
trellis.par.set(theme)

featurePlot(x = dat2 %>% dplyr::select(age, height, weight, bmi, SBP, LDL),
            y = dat2$recovery_time,
            plot = "box", pch = "|",
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            labels = c("Predictors", "Y"),
            main = "Figure 1.4. Lattice Plots for Continuous Variables in Secondary Analysis",
            auto.key = list(columns = 2))
```

Figure 1.4. Lattice Plots for Continuous Variables in Secondary Analysis



```
## For categorical variables:
gender_plot_sec = dat2 %>%
  ggplot(aes(x = gender, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Female', 'Male')) +
  ylab("Recovery") +
  theme(legend.position = "none")

race_plot_sec = dat2 %>%
  ggplot(aes(x = race, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('White', 'Asian', 'Black', 'Hispanic')) +
  ylab("Recovery") +
  theme(legend.position = "none")

smoking_plot_sec = dat2 %>%
  ggplot(aes(x = smoking, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Never smoked', 'Former smoker', 'Current smoker')) +
  ylab("Recovery") +
  theme(legend.position = "none")

hyper_plot_sec = dat2 %>%
  ggplot(aes(x = hypertension, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  ylab("Recovery") +
  scale_x_discrete(labels = c('No', 'Yes')) +
```



```

  theme(legend.position = "none")

diabetes_plot_sec = dat2 %>%
  ggplot(aes(x = diabetes, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('No', 'Yes')) +
  ylab("Recovery") +
  theme(legend.position = "none")

vac_plot_sec = dat2 %>%
  ggplot(aes(x = vaccine, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not vaccinated', 'Vaccinated')) +
  ylab("Recovery") +
  theme(legend.position = "none")

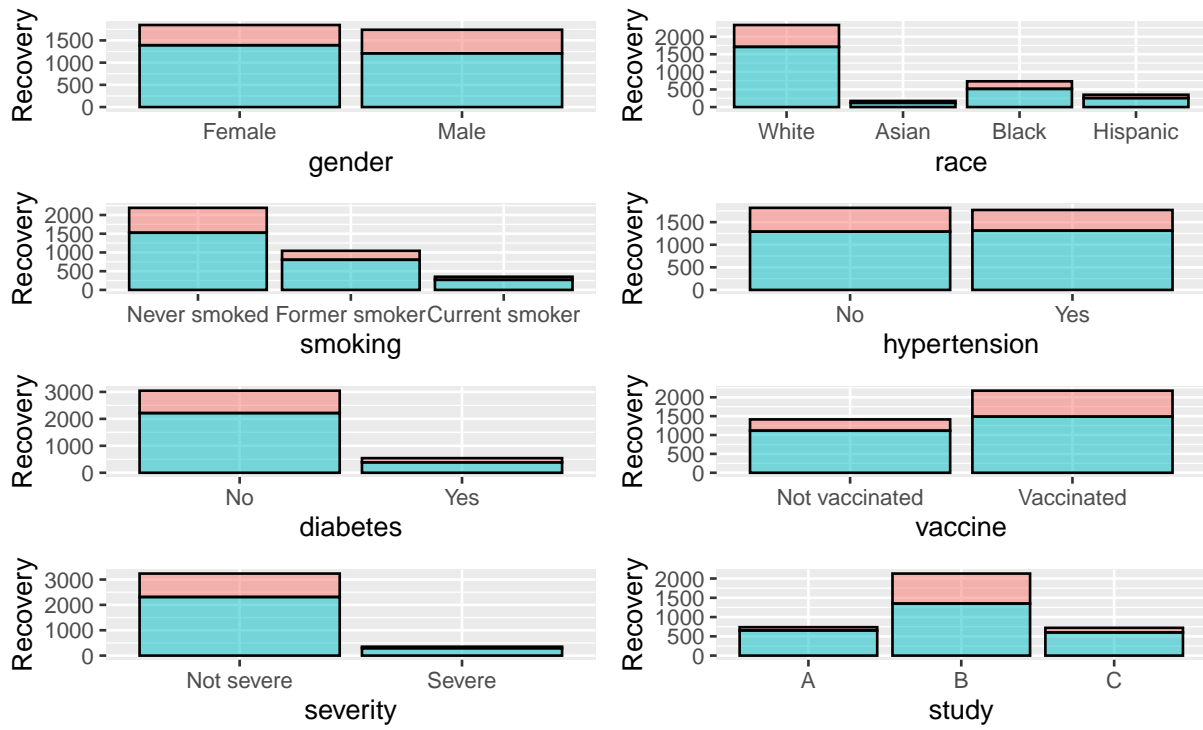
severity_plot_sec = dat2 %>%
  ggplot(aes(x = severity, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not severe', 'Severe')) +
  ylab("Recovery") +
  theme(legend.position = "none")

study_plot_sec = dat2 %>%
  ggplot(aes(x = study, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  ylab("Recovery") +
  theme(legend.position = "none")

(gender_plot_sec + race_plot_sec + smoking_plot_sec + hyper_plot_sec) / (diabetes_plot_sec + vac_plot_sec)
plot_layout(guides = "collect") +
plot_annotation(title = "Figure 1.5. Bar Plots for Categorical Variables in Secondary Analysis")

```

Figure 1.5. Bar Plots for Categorical Variables in Secondary Analysis



Note: red is 0 and blue is 1.

1. Primary Analysis

Recovery time as continuous variable.