HEART FAILURE PREDICTION

CODES

1.Patient count by diabaties status and BP

```
data$Diabetes <- factor(data$Diabetes)

histogram <- ggplot(data = data, aes(x = Diabetes, fill = BP)) +

  geom_bar(stat = "count", position = "dodge") +

  labs(title = "Patient Count By Diabetes Status and BP", x = "Diabetes Status", y = "Number of People") +

  scale_fill_manual(values = c("#000080", "#0000FF", "#4169E1", "#1E90FF", "#87CEEB", "#ADD8E6", "#B0E0E6", "#AFEEEE", "#4682B4", "#6495ED", "#89CFF0", "#0F52BA", "#ADD8E6", "#00CED1", "#000080", "#0000FF", "#008080", "#00FFFF")) + # change fill colors

  theme_minimal()

print(histogram)
```

2. Patient count by Depression status and BP

```
data$Diabetes <- factor(data$Diabetes)

histogram <- ggplot(data = data, aes(x = Depression, fill = BP)) +

  geom_bar(stat = "count", position = "dodge") +

  labs(title = "Patient Count By Depression Status and BP", x = "Depression", y = "Number of People") +

 scale_fill_manual(values = c("#000080", "#0000FF", "#4169E1", "#1E90FF", "#87CEEB", "#ADD8E6", "#B0E0E6", "#AFEEEE", "#4682B4", "#6495ED", "#89CFF0", "#0F52BA", "#ADD8E6", "#00CED1", "#000080", "#0000FF", "#008080", "#00FFFF")) + # change fill colors
```

HEART FAILURE PREDICTION

```
theme_minimal()

print(histogram)
```

3. Patient count by Smoking status and BP

```
data$Diabetes <- factor(data$Diabetes)

histogram <- ggplot(data = data, aes(x = Smoking, fill = BP)) +
```

```
  geom_bar(stat = "count", position = "dodge") +
  labs(title = "Patient Count By Smoking Status and BP", x = "Smoking", y = "Number of People")
+
scale_fill_manual(values = c("#000080", "#0000FF", "#4169E1", "#1E90FF", "#87CEEB",
"#ADD8E6", "#AFEEEE", "#B0E0E6", "#4682B4", "#6495ED", "#89CFF0", "#0F52BA", "#ADD8E6",
"#00CED1", "#000080", "#0000FF", "#008080", "#00FFFF")) + # change fill colors
  theme_minimal()
print(histogram)


4.Patient count by WBC,BP and RBC
library(plotly)
data$Diabetes <- factor(data$Diabetes)
scatterplot_3d <- plot_ly(data = data,
                          x = ~WBC, y = ~BP, z = ~RBC,
                          type = "scatter3d", mode = "markers",
                          marker = list(size = 3, color = "blue")) %>%
  layout(title = "Patient Count By WBC, BP and RBC",
         scene = list(xaxis = list(title = "WBC"),
                      yaxis = list(title = "BP"),
                      zaxis = list(title = "RBC")),
         margin = list(l = 0, r = 0, b = 0, t = 40))
scatterplot_3d
5.Patient count by Age and BP
data$Diabetes <- factor(data$Diabetes)
scatterplot <- ggplot(data = data, aes(x = Age, y = BP)) +
  geom_point(position = "jitter") +
  labs(title = "Patient Count By Age and BP", x = "Age", y = "BP") +
  theme_minimal()
```

```
print(scatterplot)
```

6.confusion Matrix

```
library(ggplot2)

library(gtable)

conf_mat <- matrix(c(55, 2, 2, 15), nrow = 2, byrow = TRUE, dimnames = list(c("Positive", "Negative"), c("Positive", "Negative")))

conf_df <- as.data.frame.table(conf_mat)

plot_conf_mat <- ggplot(data = conf_df, aes(x = Var1, y = Var2, fill = Freq)) +

  geom_tile() +

  scale_fill_gradient(low = "#FFFFFF", high = "#FF0000") +

  labs(title = "Confusion Matrix", x = "", y = "") +

  theme_void()

plot_grob <- ggplotGrob(plot_conf_mat)

plot_grob <- gtable_add_cols(plot_grob, unit(1, "cm"))

plot_grob <- gtable_add_rows(plot_grob, unit(1, "cm"), 0)

plot_grob <- gtable_add_grob(plot_grob, list(rectGrob(gp = gpar(fill = NA)), textGrob("Actual", rot = 270)), t = 1, l = 2)

plot_grob <- gtable_add_grob(plot_grob, list(rectGrob(gp = gpar(fill = NA)), textGrob("Predicted")), t = 2, l = 1)

grid.draw(plot_grob)
```