Statistics 135 – Lab Project

April 27, 2015

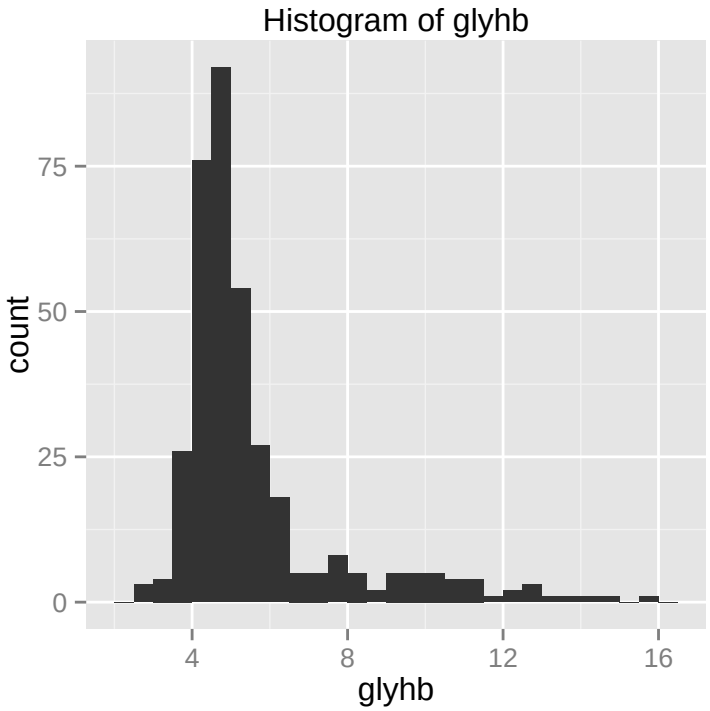
1 Background

```
library("ggplot2")
library("grid")
library("gridExtra")

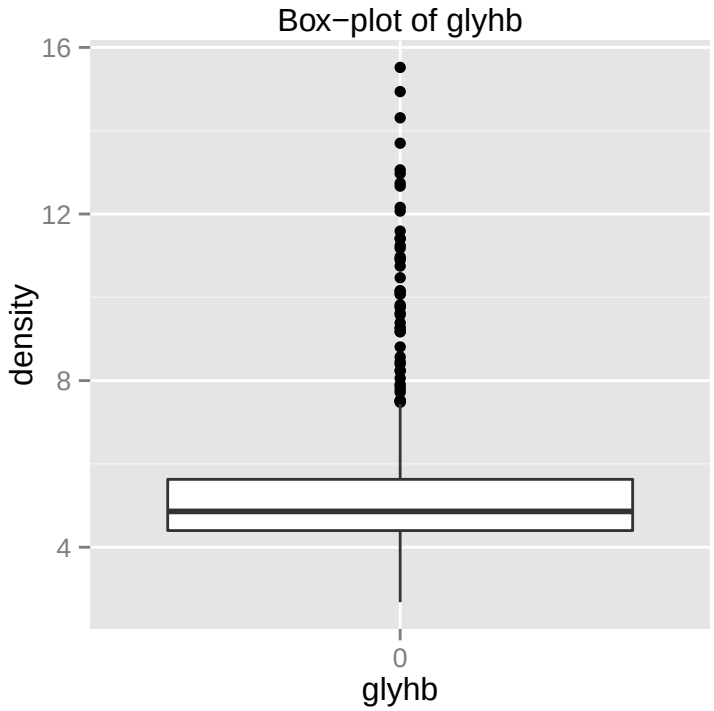
data.df <- na.omit(read.csv("diabetes.csv"))
```

2 Accessing Data, Visualization and Summarization

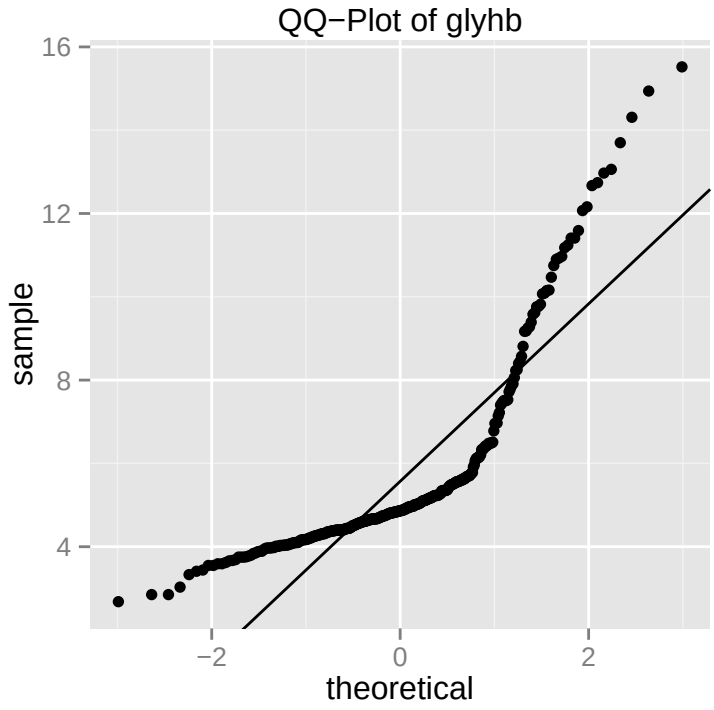
1. ```
   ggplot(data.df) +
     geom_histogram(aes(x=glyhb), binwidth=0.5) +
     labs(title="Histogram of glyhb") +
     theme(plot.title=element_text(size=rel(1)))
   ```




```
ggplot(data.df) +
  geom_boxplot(aes(x=factor(0), y=glyhb)) +
  labs(title="Box-plot of glyhb", x="glyhb", y="density") +
  theme(plot.title=element_text(size=rel(1)))
```
```

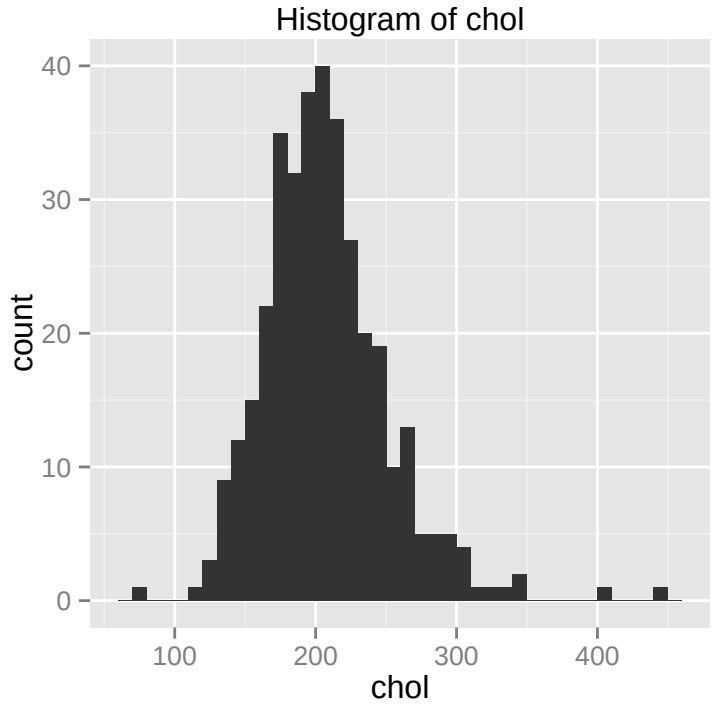



```
ggplot(data.df) +
  stat_qq(aes(sample=glyhb)) +
  geom_abline(aes(intercept=mean(glyhb), slope=sd(glyhb))) +
  labs(title="QQ-Plot of glyhb") +
  theme(plot.title=element_text(size=rel(1)))
```

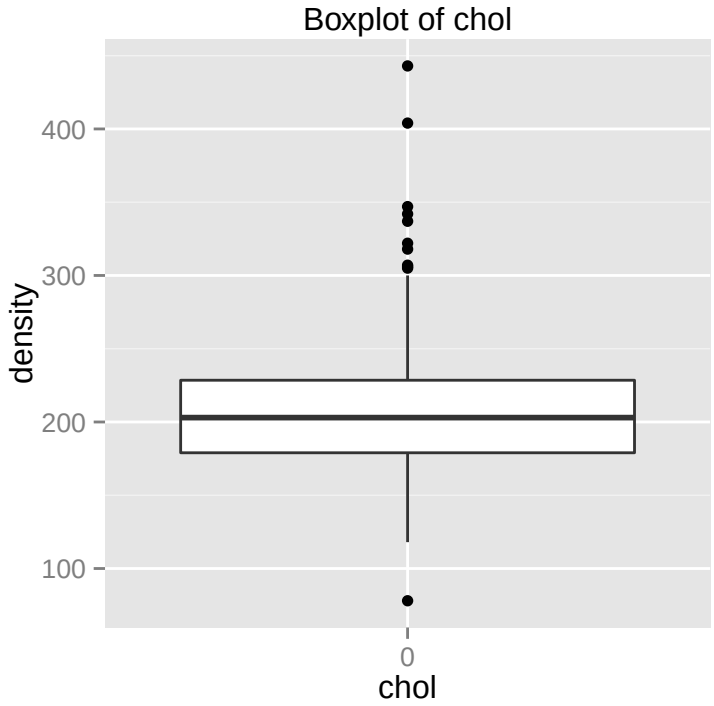


2.
```
ggplot(data.df) +
  geom_histogram(aes(x=chol), binwidth=10) +
  labs(title="Histogram of chol") +
```

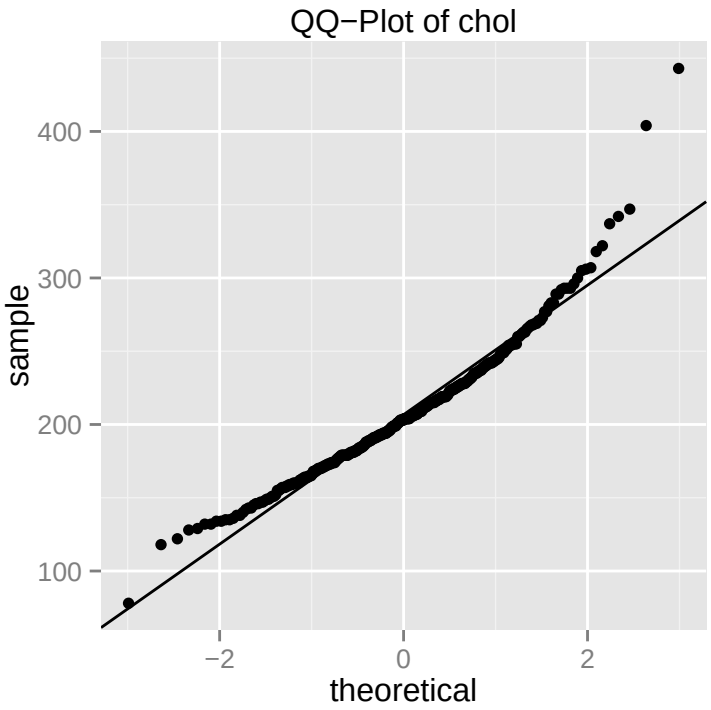
```
  theme(plot.title=element_text(size=rel(1)))
```



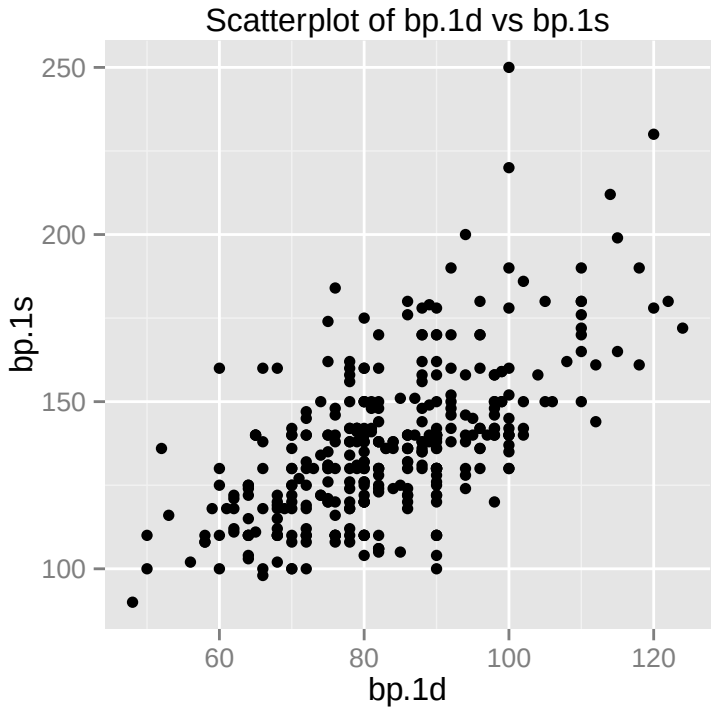

```
ggplot(data.df) +
  geom_boxplot(aes(x=factor(0), y=chol)) +
  labels(title="Boxplot of chol", x="chol", y="density") +
  theme(plot.title=element_text(size=rel(1)))
```



```
ggplot(data.df) +
  stat_qq(aes(sample=chol)) +
  geom_abline(aes(intercept=mean(chol), slope=sd(chol))) +
  labs(title="QQ-Plot of chol") +
  theme(plot.title=element_text(size=rel(1)))
```



3.
```
ggplot(data.df) +
  geom_point(aes(x=bp.1d, y=bp.1s)) +
  labs(title="Scatterplot of bp.1d vs bp.1s") +
  theme(plot.title=element_text(size=rel(1)))
```

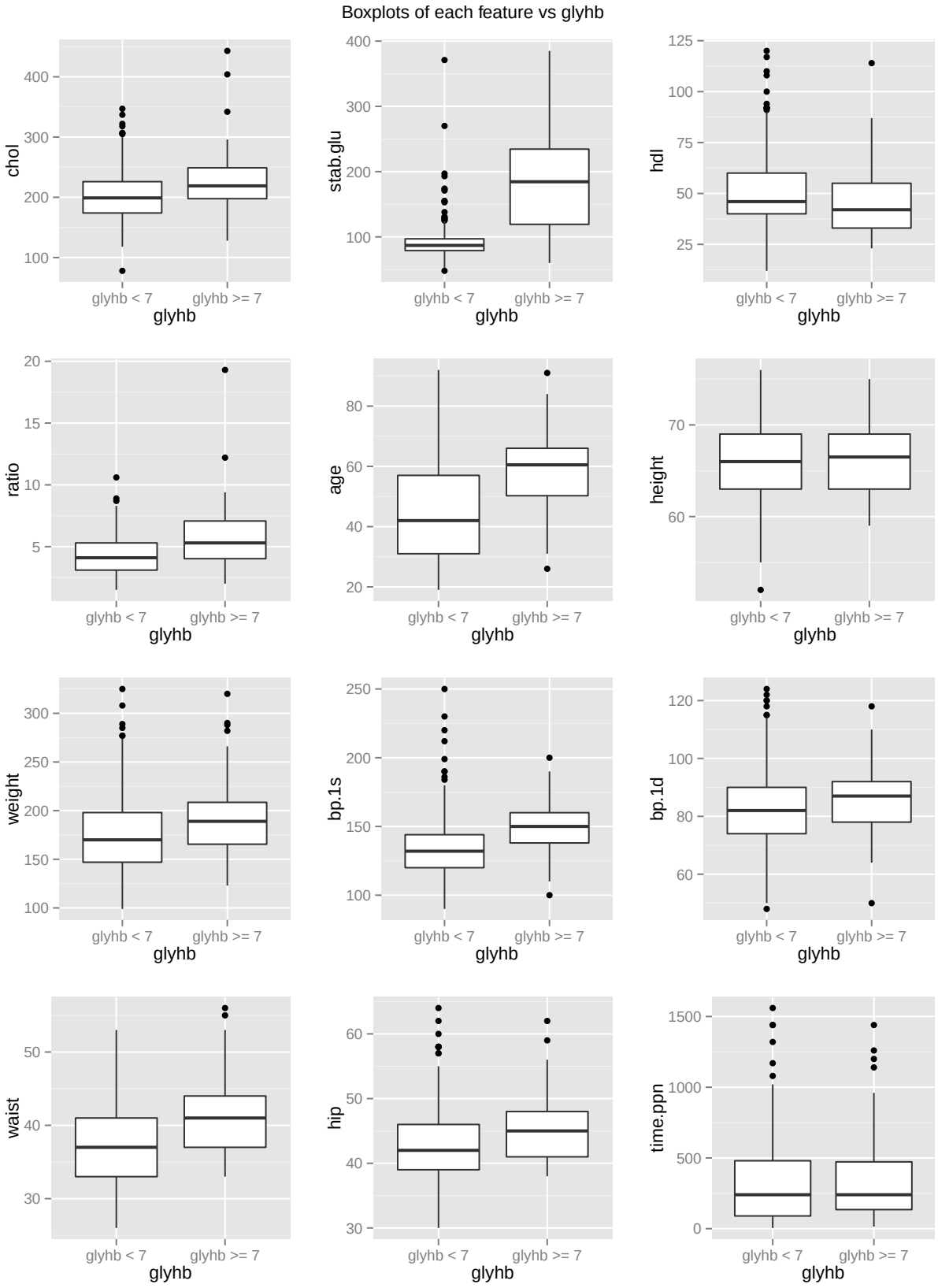



```
ggplot(data.df) +
  geom_point(aes(x=height, y=age)) +
  labs(title="Scatterplot of age vs height") +
  theme(plot.title=element_text(size=rel(1)))
```

4.
```
glyhb.df <- data.frame(data.df, glyhb.cond=NA)
glyhb.df[glyhb.df$glyhb>=7, ]$glyhb.cond <- "glyhb >= 7"
glyhb.df[glyhb.df$glyhb<7, ]$glyhb.cond <- "glyhb < 7"
```

```
features <- c("chol", "stab.glu", "hdl", "ratio", "age", "height", "weight",
              "bp.1s", "bp.1d", "waist", "hip", "time.ppn")
feature.boxplots = list()
for (i in 1:length(features)) {
  feature <- features[i]
  feature.boxplot <- ggplot(data.frame(glyhb.cond=glyhb.df$glyhb.cond,
                                       feature=glyhb.df[, feature])) +
    geom_boxplot(aes(x=glyhb.cond, y=feature)) +
    labs(x="glyhb", y=feature)
  feature.boxplots[[i]] <- feature.boxplot
}

do.call(grid.arrange, c(feature.boxplots, ncol=3,
                        main="Boxplots of each feature vs glyhb"))
```



5.

6.

3 Parametric Inferece

1.

2.

3.

4 Testing

1.
2.
3.
4.
5.
6.

5 Regression

1.
2.
3.
4.
5.
6.
7.