

# Statistics 135 – Lab Project

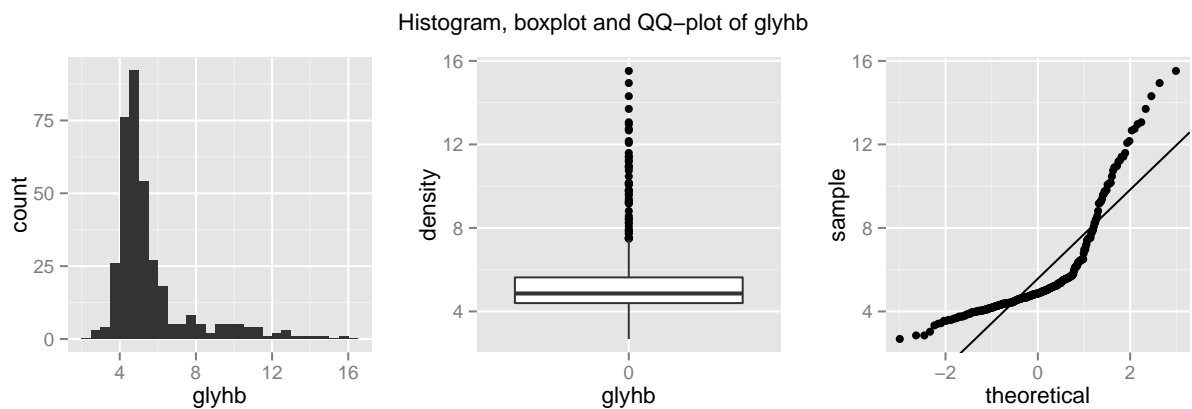
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May 2, 2015

## 1 Background

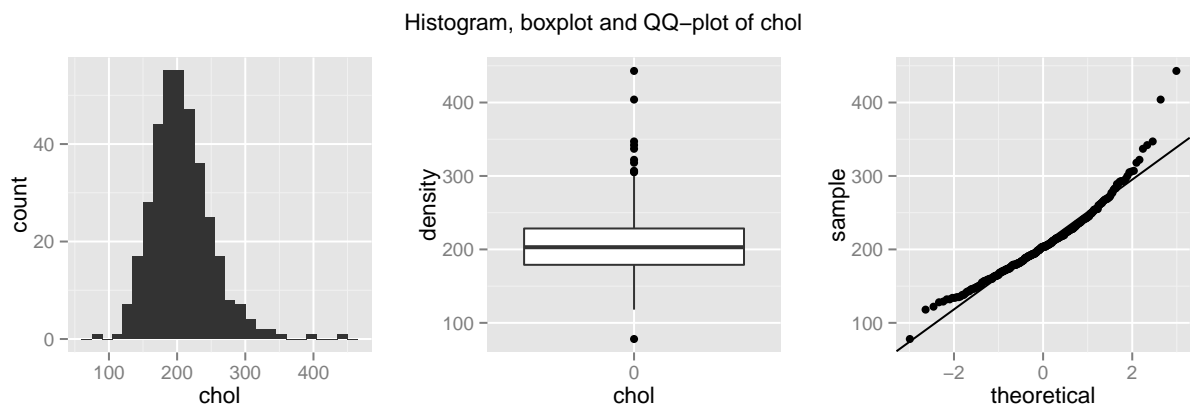
## 2 Accessing Data, Visualization and Summarization

1.



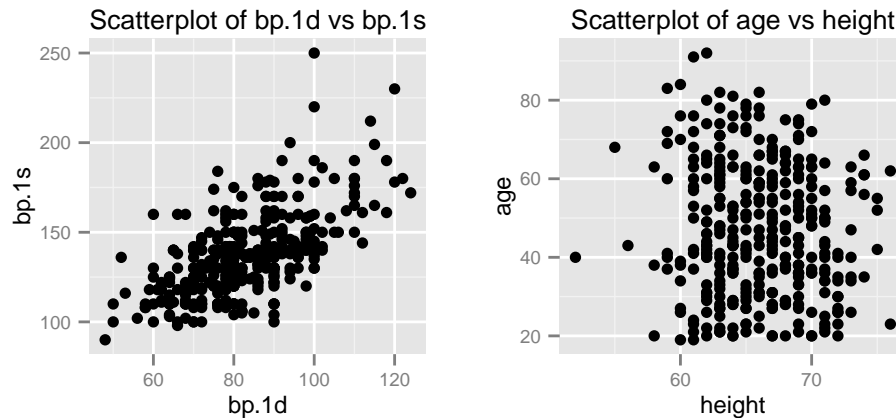
The mean, median and mode of `glyhb` are all approximately 5. The distribution of `glyhb` is left-skewed.

2.



The mean, median and mode of `chol` are all approximately 200. The distribution of `chol` is better approximated with a Gaussian distribution.

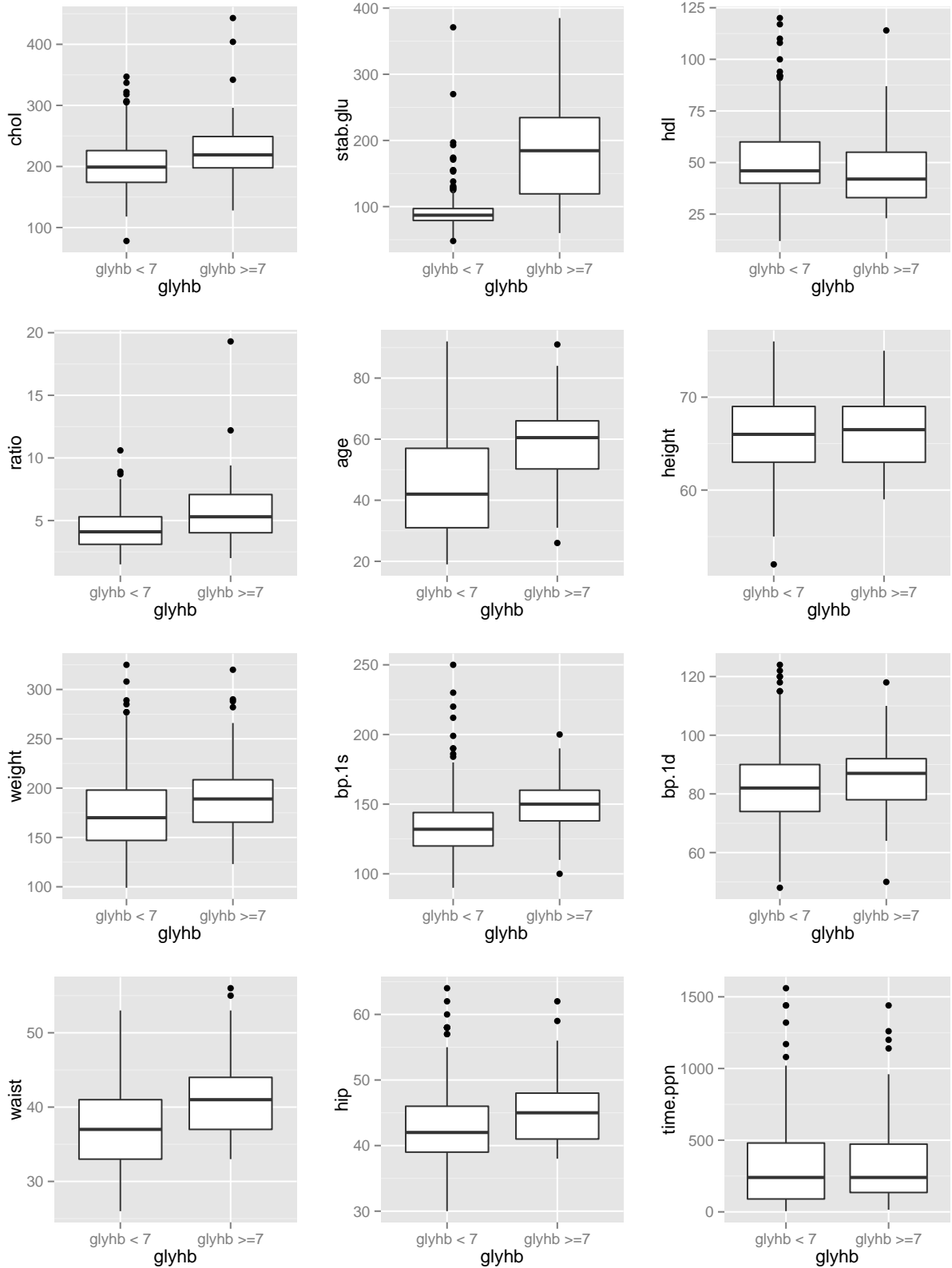
3.



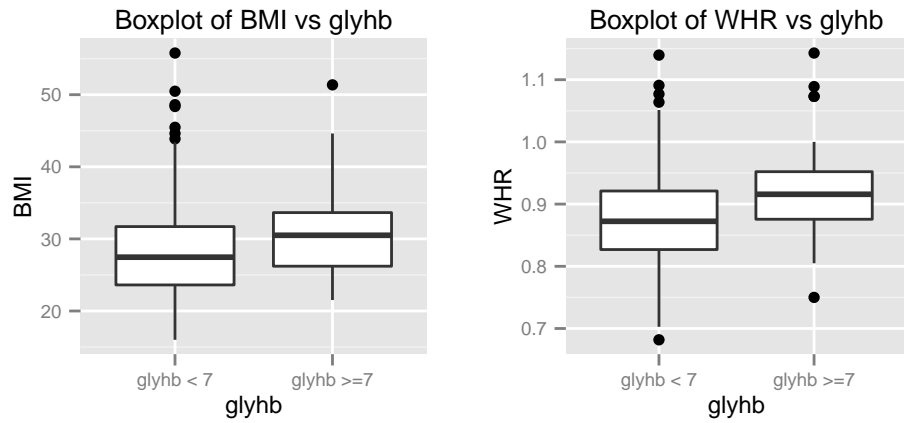
The scatterplot of `bp.1s` and `bp.1d` is near-linear, so they are approximately dependent. The scatterplot of `age` and `weight` is random, so they are approximately independent.

- 4.
- `chol`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `stab.glu`: The two distributions have substantial difference, so it SHOULD BE a relevant feature.
  - `hdl`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `ratio`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `age`: The two distributions have substantial difference, so it SHOULD BE a relevant feature.
  - `height`: The two distributions have little difference, so it MAY NOT BE a relevant feature.
  - `weight`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `bp.1s`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `bp.1d`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `waist`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `hip`: The two distributions have small difference, so it MAY BE a relevant feature.
  - `time.ppn`: The two distributions have small difference, so it MAY NOT BE a relevant feature.

Boxplots of each feature vs glyhb



5.



6. In light of these first experiments, `hdl`, `stab.glu`, `age`, `weight`, `bp.1s`, `bp.1d`, `waist` and `hip` seem related to the presence of type II diabetes; `chol`, `ratio`, `height` and `time.ppn` seem unrelated to the presence of type II diabetes.

### 3 Parametric Inference

1.

$$X \sim \text{Gamma}(\alpha, \beta) = \frac{\beta^\alpha}{\Gamma(\alpha)} x^{\alpha-1} e^{-\beta x}$$

$$E(X) = \frac{\alpha}{\beta}$$

$$E(X^2) = \text{Var}(X) + [E(X)]^2$$

$$= \frac{\alpha}{\beta^2} + \left(\frac{\alpha}{\beta}\right)^2$$

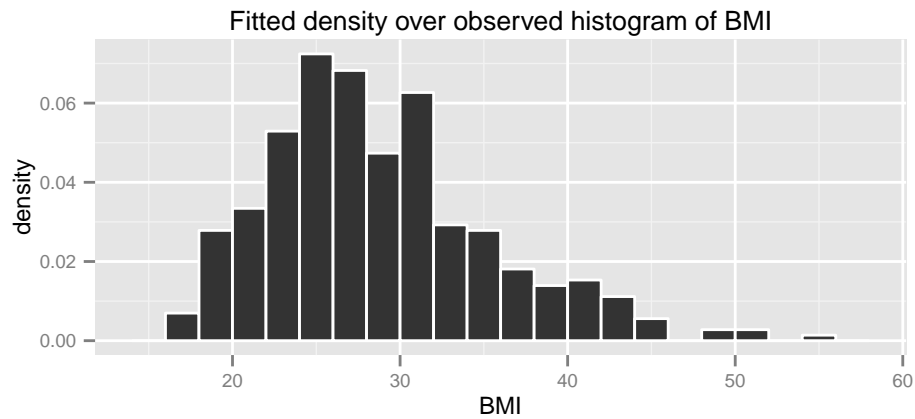
$$= \frac{\alpha(\alpha+1)}{\beta^2}$$

$$\begin{cases} E(X) = \frac{\alpha}{\beta} \\ E(X^2) = \frac{\alpha(\alpha+1)}{\beta^2} \end{cases} \Rightarrow \begin{cases} \alpha = \frac{[E(X)]^2}{\text{Var}(x)} \\ \beta = \frac{E(X)}{\text{Var}(x)} \end{cases} \Rightarrow \begin{cases} \hat{\alpha}_{MOM} = \frac{\bar{X}_n}{\frac{1}{n} \sum_{i=1}^n (X_i - \bar{X}_n)^2} \\ \hat{\beta}_{MOM} = \frac{\bar{X}_n^2}{\frac{1}{n} \sum_{i=1}^n (X_i - \bar{X}_n)^2} \end{cases}$$

```
#####
CI.BMI

##          alpha      beta
## 2.5%    15.87666 0.5460733
## 97.5%   21.62832 0.7591677

#####
```



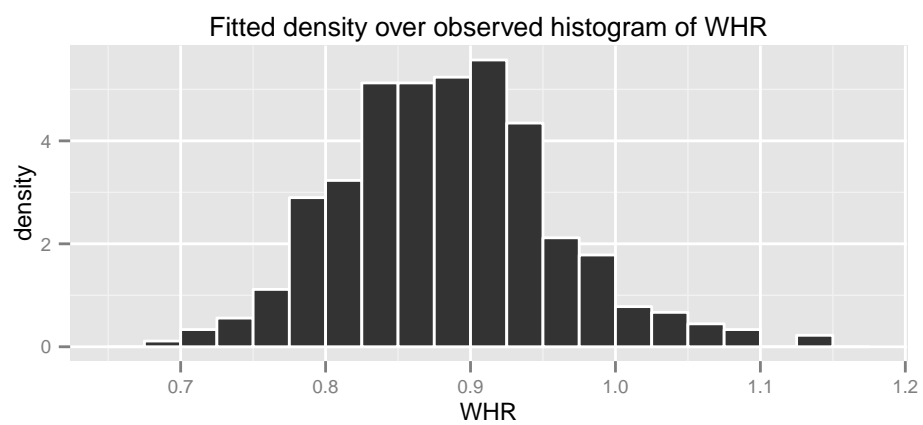
2.

$$\hat{\mu}_{MLE} = \bar{X}_n$$

$$\hat{\sigma}_{MLE}^2 = \frac{1}{n} \sum_{i=1}^n (X_i - \bar{X}_n)^2$$

```
#####
CI.WHR

##          mu      sigma
## 2.5%  0.8747003 0.06788022
## 97.5% 0.8901891 0.08026878
#####
```



```

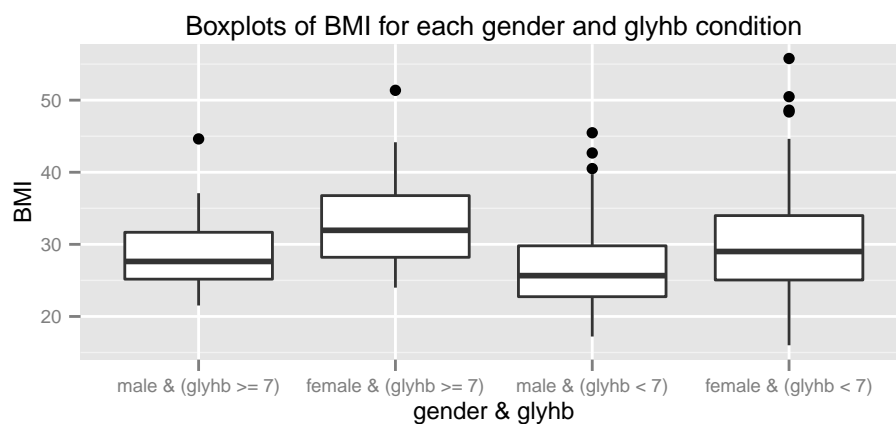
3. #####

CIs.BMI

## $`male & (glyhb >= 7)`
##           mu      sigma
## 2.5%  26.89463  3.533570
## 97.5% 30.97481  7.164682
##
## $`female & (glyhb >= 7)`
##           mu      sigma
## 2.5%  30.90826  4.608429
## 97.5% 35.63231  8.207146
##
## $`male & (glyhb < 7)`
##           mu      sigma
## 2.5%  25.57434  4.711554
## 97.5% 27.47041  6.358453
##
## $`female & (glyhb < 7)`
##           mu      sigma
## 2.5%  28.84236  6.220170
## 97.5% 30.84639  7.862444

#####

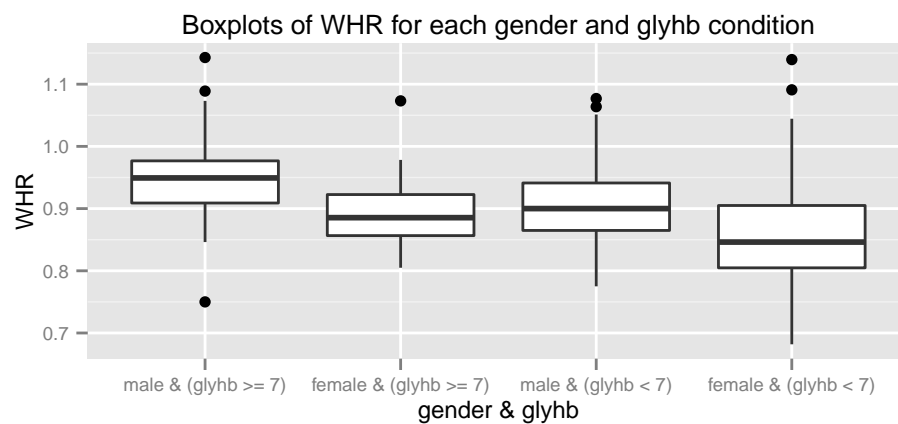
```



- On average, females have higher BMI than males.
- On average, people with type II diabetes (`glyhb >= 7`) have higher BMI than people without type II diabetes (`glyhb < 7`).
- People with type II diabetes (`glyhb >= 7`) have larger confidence intervals of both mean and standard deviation than people without type II diabetes (`glyhb < 7`), regardless of gender.

```
#####
CIs.WHR

## $`male & (glyhb >= 7)`
##           mu           sigma
## 2.5%  0.9202216 0.04735021
## 97.5% 0.9791687 0.10652492
##
## $`female & (glyhb >= 7)`
##           mu           sigma
## 2.5%  0.8754801 0.04013498
## 97.5% 0.9139384 0.07537186
##
## $`male & (glyhb < 7)`
##           mu           sigma
## 2.5%  0.8938359 0.05568191
## 97.5% 0.9172246 0.07075628
##
## $`female & (glyhb < 7)`
##           mu           sigma
## 2.5%  0.8446725 0.06108226
## 97.5% 0.8644300 0.07829550
#####
```



- On average, males have higher WHR than females.
- On average, people with type II diabetes (`glyhb >= 7`) have higher WHR than people without type II diabetes (`glyhb < 7`).
- People with type II diabetes (`glyhb >= 7`) have larger confidence intervals of both mean and standard deviation than people without type II diabetes (`glyhb < 7`), regardless of gender.



## 4 Testing

```
1. #####
gender.glyhb.cond.table

##          glyhb >= 7 glyhb < 7
## male                24      125
## female              30      180

#####
fisher.test(gender.glyhb.cond.table)

##
## Fisher's Exact Test for Count Data
##
## data:  gender.glyhb.cond.table
## p-value = 0.6552
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.6126316 2.1465820
## sample estimates:
## odds ratio
##    1.151538

#####
```

Since the  $p$ -value is 0.655, which is greater than 0.05, we fail to reject the null hypothesis that males and females are equally exposed to type II diabetes, with 5% significance level.

2. We choose to the non-parametric Kruskal-Wallis test, because it does not rely on the assumed normal distribution and less affected by outliers.

```
#####  
kruskal.test(data.df$hdl, as.factor(data.df$glyhb.cond))  
  
##  
## Kruskal-Wallis rank sum test  
##  
## data: data.df$hdl and as.factor(data.df$glyhb.cond)  
## Kruskal-Wallis chi-squared = 7.9732, df = 1, p-value = 0.004748  
  
#####
```

Since the  $p$ -value is 0.00475, which is smaller than 0.05, we reject the null hypothesis that `hdl` has equal means for those with type II diabetes and those without, with 5% significance level.

```
#####  
kruskal.test(data.df$bp.1s, as.factor(data.df$glyhb.cond))  
  
##  
## Kruskal-Wallis rank sum test  
##  
## data: data.df$bp.1s and as.factor(data.df$glyhb.cond)  
## Kruskal-Wallis chi-squared = 22.563, df = 1, p-value = 2.034e-06  
  
#####
```

Since the  $p$ -value is 2.034e-06, which is smaller than 0.05, we reject the null hypothesis that `bp.1s` has equal means for those with type II diabetes and those without, with 5% significance level.

```
#####  
kruskal.test(data.df$bp.1d, as.factor(data.df$glyhb.cond))  
  
##  
## Kruskal-Wallis rank sum test  
##  
## data: data.df$bp.1d and as.factor(data.df$glyhb.cond)  
## Kruskal-Wallis chi-squared = 1.9007, df = 1, p-value = 0.168  
  
#####
```

Since the  $p$ -value is 0.168, which is greater than 0.05, we fail to reject the null hypothesis that `bp.1d` has equal means for those with type II diabetes and those without, with 5% significance level.

```
#####  
kruskal.test(data.df$BMI, as.factor(data.df$glyhb.cond))  
  
##  
## Kruskal-Wallis rank sum test  
##  
## data: data.df$BMI and as.factor(data.df$glyhb.cond)  
## Kruskal-Wallis chi-squared = 9.5655, df = 1, p-value = 0.001983  
  
#####
```

```
#####
```

Since the  $p$ -value is 0.00198, which is smaller than 0.05, we reject the null hypothesis that BMI has equal means for those with type II diabetes and those without, with 5% significance level.

```
#####
```

```
kruskal.test(data.df$WHR, as.factor(data.df$glyhb.cond))
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

```
##
```

```
## data: data.df$WHR and as.factor(data.df$glyhb.cond)
```

```
## Kruskal-Wallis chi-squared = 15.146, df = 1, p-value = 9.95e-05
```

```
#####
```

Since the  $p$ -value is 9.95e-05, which is smaller than 0.05, we reject the null hypothesis that WHR has equal means for those with type II diabetes and those without, with 5% significance level.

```
3. #####
```

```
pi.male.BMI
```

```
## [1] 0.6326667
```

```
CI.pi.male.BMI
```

```
##      2.5%      97.5%
```

```
## 0.5222833 0.7420167
```

```
#####
```

```
pi.male.WHR
```

```
## [1] 0.6853333
```

```
CI.pi.male.WHR
```

```
##      2.5%      97.5%
```

```
## 0.5716667 0.7950000
```

```
#####
```

4. According to the result from part 3.2, we know that WHR has a normal distribution. We assume all patients come from the same population, so the standard deviation is constant.

$$H_0 : N(\mu_0, \sigma^2)$$

$$H_1 : N(\mu_1, \sigma^2)$$

```
#####
mean.male.glyhb.geq7.WHR

## [1] 0.9489365

mean.male.glyhb.l7.WHR

## [1] 0.9058419

sd.male.WHR

## [1] 0.06821165

#####
```

$$\mu_0 = 0.906, \mu_1 = 0.949, \sigma = 0.0682$$

$$\begin{aligned} \text{lik}(x) &= \frac{f_0(x)}{f_1(x)} \\ &= \frac{\frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu_0)^2}{2}}}{\frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu_1)^2}{2}}} \\ &= e^{-2(\mu_1 - \mu_0)x + (\mu_1^2 - \mu_0^2)} \end{aligned}$$

Let  $T := X$ .

$$\begin{aligned} \alpha &= P(T > t \mid H_0) \\ &= P\left(\frac{T - \mu_0}{\sigma} > \frac{t - \mu_0}{\sigma}\right) \\ &= 1 - \Phi\left(\frac{t - \mu_0}{\sigma}\right) \\ &\implies \\ t &= \Phi^{-1}(\alpha)\sigma + \mu_0 \end{aligned}$$

$$\begin{aligned} \beta &= P(T < t \mid H_1) \\ &= P\left(\frac{T - \mu_1}{\sigma} < \frac{t - \mu_1}{\sigma}\right) \\ &= \Phi\left(\frac{t - \mu_1}{\sigma}\right) \\ &= \Phi\left(\frac{\Phi^{-1}(\alpha)\sigma + \mu_0 - \mu_1}{\sigma}\right) \end{aligned}$$

```
#####
t

## [1] 1.01804

power

## [1] 0.1555122

#####
```

$$\alpha \leq 5\% \implies 1 - \beta \leq 0.156$$

We construct a test for type II diabetes for male patient that we reject the null hypothesis if his  $\text{WHR} \geq 1.018$ . The significance of the test is  $\leq 5\%$  and the power of the test is  $\leq 0.156$ .

```

5. #####
gender.BMI.categories

##           male female
## Underweight      5      3
## Healthy          59     43
## Overweight       46     66
## Level 1 Obese    26     52
## Level 2 Obese     9     22
## Level 3 Obese     4     24

#####
chisq.test(gender.BMI.categories)

##
## Pearson's Chi-squared test
##
## data:  gender.BMI.categories
## X-squared = 25.352, df = 5, p-value = 0.0001191

#####

```

Since the  $p$ -value is 0.000119, which is smaller than 0.05, we reject the null hypothesis that male and female population sample has homogeneous distribution of BMI categories, with 5% significance level.

```

#####
gender.WHR.categories

##           male female
## Low          46      4
## Moderate      66     33
## High          20     76
## Very High     17     95

#####
chisq.test(gender.WHR.categories)

##
## Pearson's Chi-squared test
##
## data:  gender.WHR.categories
## X-squared = 126.99, df = 3, p-value < 2.2e-16

#####

```

Since the  $p$ -value is  $2.2e-16$ , which is smaller than 0.05, we reject the null hypothesis that male and female population sample has homogeneous distribution of WHR categories, with 5% significance level.

```

6. #####
summary(aov(glyhb ~ BMI.std * WHR.std, data.df))

##              Df Sum Sq Mean Sq F value Pr(>F)
## BMI.std        5   46.9    9.378   2.104 0.0646 .
## WHR.std        3   16.7    5.583   1.253 0.2907
## BMI.std:WHR.std 14   70.8    5.060   1.135 0.3255
## Residuals     334 1488.7    4.457
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 2 observations deleted due to missingness

#####

```

The interaction effect between BMI and WHR is not significant. BMI is more sensitive to glyhb. Overall, the result is consistent with part 3.3.

## 5 Regression

1. According to the result from part 2.2, we consider `stab.glu`, `age` and BMI the most relevant features for predicting type II diabetes.

```
#####  
err.rate  
  
## [1] 0.0724234  
  
#####
```

2. 

```
#####  
false.pos.rate  
  
## [1] 0.01949861  
  
false.neg.rate  
  
## [1] 0.05292479  
  
#####
```

The False Negatives Rate is 5.29%, which already meets the specifications. The False Positives Rate is 1.95%.



```

3. #####
coefficients(lm(scale(glyhb) ~ scale(stab.glu) +
                scale(age) + scale(BMI), data.df))

##      (Intercept) scale(stab.glu)      scale(age)      scale(BMI)
## -8.995094e-17    6.616784e-01    1.591426e-01    5.695115e-02

#####

```

stab.glu has the largest influence.

```

#####
summary(lm(glyhb ~ hdl + bp.1s + bp.1d, data.df))

##
## Call:
## lm(formula = glyhb ~ hdl + bp.1s + bp.1d, data = data.df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.0818 -1.1474 -0.5394  0.2485  9.3733
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.214778   0.787987   5.349 1.59e-07 ***
## hdl          -0.017816   0.006292  -2.832  0.0049 **
## bp.1s         0.027860   0.006016   4.631 5.11e-06 ***
## bp.1d        -0.018907   0.010102  -1.872  0.0621 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.049 on 355 degrees of freedom
## Multiple R-squared:  0.08292, Adjusted R-squared:  0.07518
## F-statistic: 10.7 on 3 and 355 DF, p-value: 9.485e-07

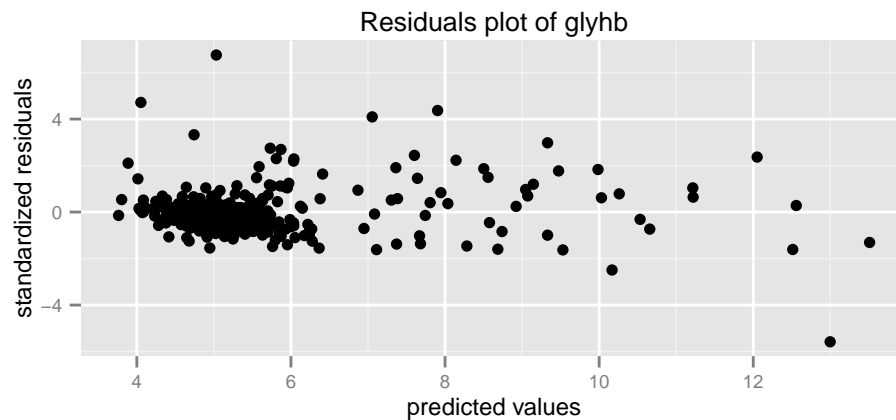
#####

```

Since the  $p$ -value is  $9.485e-07$ , we reject the null hypothesis that hdl, bp.1s and bp.1d do not have any predictive value, with 5% significance level.

4. According to the result from part 4.6, BMI and WHR do not interact. However, if they do interact, we would choose the feature with larger influence (BMI in this case), because the interaction effect will reduce the influence.

5.



```
6. #####  
err.rate  
  
## [1] 0.07520891  
  
#####
```

The linear regression from part 5.2 has a better performance.

```
7. #####  
lm.test.err.rate  
  
## [1] 0.0625  
  
glm.test.err.rate  
  
## [1] 0.0625  
  
#####
```

We obtain better performance than in the training set for both predictors.

## A Appendix

### A.1 Background

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

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

### A.2 Accessing Data, Visualization and Summarization

```
1. glyhb.histogram <- ggplot(data.df) +
  geom_histogram(aes(x=glyhb), binwidth=0.5)

glyhb.boxplot <- ggplot(data.df) +
  geom_boxplot(aes(x=factor(0), y=glyhb)) +
  labs(x="glyhb", y="density")

glyhb.qqplot <- ggplot(data.df) +
  stat_qq(aes(sample=glyhb)) +
  geom_abline(aes(intercept=mean(glyhb), slope=sd(glyhb)))

grid.arrange(glyhb.histogram, glyhb.boxplot, glyhb.qqplot, ncol=3,
  main="Histogram, boxplot and QQ-plot of glyhb")
```

```
2. chol.histogram <- ggplot(data.df) +
  geom_histogram(aes(x=chol), binwidth=15)

chol.boxplot <- ggplot(data.df) +
  geom_boxplot(aes(x=factor(0), y=chol)) +
  labs(x="chol", y="density")

chol.qqplot <- ggplot(data.df) +
  stat_qq(aes(sample=chol)) +
  geom_abline(aes(intercept=mean(chol), slope=sd(chol)))

grid.arrange(chol.histogram, chol.boxplot, chol.qqplot, ncol=3,
  main="Histogram, boxplot and QQ-plot of chol")
```

```
3. bp.1d.bp.1s.scatterplot <- ggplot(data.df) +
  geom_point(aes(x=bp.1d, y=bp.1s)) +
  labs(title="Scatterplot of bp.1d vs bp.1s") +
  theme(text=element_text(size=8.5))

height.age.scatterplot <- ggplot(data.df) +
  geom_point(aes(x=height, y=age)) +
  labs(title="Scatterplot of age vs height") +
  theme(text=element_text(size=8.5))
```

```
grid.arrange(bp.1d.bp.1s.scatterplot, height.age.scatterplot, ncol=2)
```

```
4. data.df <- transform(data.df,
                        glyhb.cond=ifelse(glyhb>=7, "glyhb >=7", "glyhb < 7"))

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

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

```
5. data.df <- transform(data.df, BMI=703*weight/height^2)
   data.df <- transform(data.df, WHR=waist/hip)

features <- c("BMI", "WHR")
feature.boxplots = list()
for (feature in features) {
  feature.boxplot <-
    ggplot(data.frame(glyhb.cond=data.df$glyhb.cond,
                     feature=data.df[[feature]])) +
    geom_boxplot(aes(x=glyhb.cond, y=feature)) +
    labs(title=paste(c("Boxplot of", feature, "vs glyhb"), collapse=" "),
         x="glyhb", y=feature) +
    theme(text=element_text(size=8.5))
  feature.boxplots[[feature]] <- feature.boxplot
}

do.call(grid.arrange, c(feature.boxplots, ncol=2))
```

### A.3 Parametric Inference

```
1. gamma.boot <- function(x) {
  alpha.mom <- mean(x)^2/var(x)
  beta.mom <- mean(x)/var(x)

  bootstrap <- sapply(1:1000, function(i) {
    samples <- sample(x, length(x), replace=TRUE)
    alpha.sample <- mean(samples)^2/var(samples)
    beta.sample <- mean(samples)/var(samples)
    return(c(alpha.sample, beta.sample))
  })
}
```

```

})

CIs <- sapply(1:2, function(i) {
  CI <- quantile(bootstrap[i, ], probs=c(0.025, 0.975))
  return(CI)
})
colnames(CIs) <- c("alpha", "beta")

return(CIs)
}

CI.BMI <- gamma.boot(data.df$BMI)

ggplot(data.df) +
  geom_histogram(aes(x=BMI, y=..density..), binwidth=2, col="white") +
  stat_function(fun=function(x)
    dgamma(x, shape=alpha.mom, rate=beta.mom), col="white") +
  labs(title="Fitted density over observed histogram of BMI") +
  theme(text=element_text(size=8.5))

```

```

2. normal.boot <- function(x) {
  mu.mle <- mean(x)
  sigma.mle <- sd(x)

  bootstrap <- sapply(1:1000, function(i) {
    samples <- sample(x, length(x), replace=TRUE)
    mu.sample <- mean(samples)
    sigma.sample <- sd(samples)
    return(c(mu.sample, sigma.sample))
  })

  CIs <- sapply(1:2, function(i) {
    CI <- quantile(bootstrap[i, ], probs=c(0.025, 0.975))
    return(CI)
  })
  colnames(CIs) <- c("mu", "sigma")

  return(CIs)
}

CI.WHR <- normal.boot(data.df$WHR)

ggplot(data.df) +
  geom_histogram(aes(x=WHR, y=..density..), binwidth=0.025, col="white") +
  stat_function(fun=function(x)
    dnorm(x, mean=mu.mle, sd=sigma.mle), col="white") +
  labs(title="Fitted density over observed histogram of WHR") +
  theme(text=element_text(size=8.5))

```

```

3. data.df <- transform(data.df,
  gender.glyhb.cond=ifelse(gender=="male",

```

```

      ifelse(glyhb>=7, "male & (glyhb >= 7)", "male & (glyhb < 7)"),
      ifelse(glyhb>=7, "female & (glyhb >= 7)", "female & (glyhb < 7)"))))

conditions <- c("male & (glyhb >= 7)", "female & (glyhb >= 7)",
               "male & (glyhb < 7)", "female & (glyhb < 7)")

gamma.boot2 <- function(x) {
  alpha.mom <- mean(x)^2/var(x)
  beta.mom <- mean(x)/var(x)

  bootstrap <- sapply(1:1000, function(i) {
    samples <- sample(x, length(x), replace=TRUE)
    mu.sample <- mean(samples)
    sigma.sample <- sd(samples)
    return(c(mu.sample, sigma.sample))
  })

  CIs <- sapply(1:2, function(i) {
    CI <- quantile(bootstrap[i, ], probs=c(0.025, 0.975))
    return(CI)
  })
  colnames(CIs) <- c("mu", "sigma")

  return(CIs)
}

CIs.BMI <- lapply(conditions, function(x) {
  gender.glyhb.df <- subset(data.df, gender.glyhb.cond==x)
  CIs.BMI <- gamma.boot2(gender.glyhb.df$BMI)
  return(CIs.BMI)
})
names(CIs.BMI) <- conditions

ggplot(data.df) +
  geom_boxplot(aes(x=factor(gender.glyhb.cond, levels=conditions), y=BMI)) +
  labs(title="Boxplots of BMI for each gender and glyhb condition",
       x="gender & glyhb") +
  theme(text=element_text(size=8.5))

CIs.WHR <- lapply(conditions, function(x) {
  gender.glyhb.df <- subset(data.df, gender.glyhb.cond==x)
  CIs.WHR <- normal.boot(gender.glyhb.df$WHR)
  return(CIs.WHR)
})
names(CIs.WHR) <- conditions

ggplot(data.df) +
  geom_boxplot(aes(x=factor(gender.glyhb.cond, levels=conditions), y=WHR)) +
  labs(title="Boxplots of WHR for each gender and glyhb condition",
       x="gender & glyhb") +
  theme(text=element_text(size=8.5))

```

## A.4 Testing

- ```
gender.glyhb.cond.table <- matrix(sapply(conditions, function(x)
  nrow(subset(data.df, gender.glyhb.cond==x))), nrow=2)
colnames(gender.glyhb.cond.table) <- c("glyhb >= 7", "glyhb < 7")
rownames(gender.glyhb.cond.table) <- c("male", "female")
```
- ```
pi.est <- function(x, y) {
  w <- 0
  for (i in 1:length(x)) {
    for (j in 1:length(y)) {
      w <- w + (x[i] > y[j])
    }
  }
  return(w/(length(x)*length(y)))
}
```

```
male.glyhb.geq7.BMI <-
  subset(data.df, gender.glyhb.cond=="male & (glyhb >= 7)")$BMI
male.glyhb.l7.BMI <-
  subset(data.df, gender.glyhb.cond=="male & (glyhb < 7)")$BMI
male.glyhb.geq7.WHR <-
  subset(data.df, gender.glyhb.cond=="male & (glyhb >= 7)")$WHR
male.glyhb.l7.WHR <-
  subset(data.df, gender.glyhb.cond=="male & (glyhb < 7)")$WHR

pi.male.BMI <- pi.est(
  male.glyhb.geq7.BMI,
  male.glyhb.l7.BMI)
pi.male.WHR <- pi.est(
  male.glyhb.geq7.WHR,
  male.glyhb.l7.WHR)

pi.male.BMI.samples <- sapply(1:1000, function(x)
  pi.est(sample(male.glyhb.geq7.BMI, length(male.glyhb.geq7.BMI), replace=TRUE),
    sample(male.glyhb.l7.BMI, length(male.glyhb.l7.BMI), replace=TRUE)))
CI.pi.male.BMI <- quantile(pi.male.BMI.samples, probs=c(0.025, 0.975))

pi.male.WHR.samples <- sapply(1:1000, function(x)
  pi.est(sample(male.glyhb.geq7.WHR, length(male.glyhb.geq7.WHR), replace=TRUE),
    sample(male.glyhb.l7.WHR, length(male.glyhb.l7.WHR), replace=TRUE)))
CI.pi.male.WHR <- quantile(pi.male.WHR.samples, probs=c(0.025, 0.975))
```
- ```
mean.male.glyhb.geq7.WHR <- mean(male.glyhb.geq7.WHR)
mean.male.glyhb.l7.WHR <- mean(male.glyhb.l7.WHR)
sd.male.WHR <- sd(subset(data.df, gender=="male")$WHR)

mu.0 <- mean.male.glyhb.l7.WHR
mu.1 <- mean.male.glyhb.geq7.WHR
sigma <- sd.male.WHR
alpha <- 0.05
```

```
t <- qnorm(1-alpha)*sigma + mu.0
beta <- pnorm((qnorm(1-alpha)*sigma + mu.0 - mu.1)/sigma)
power <- 1 - beta
```

```
5. BMI.labels <- c("Underweight", "Healthy", "Overweight",
                  "Level 1 Obese", "Level 2 Obese", "Level 3 Obese")
data.df$BMI.std <- cut(data.df$BMI, breaks=c(0, 18.5, 25, 30, 35, 40, Inf),
                      labels=BMI.labels, right=F)

gender.BMI.categories <- cbind(table(subset(data.df, gender=="male")$BMI.std),
                               table(subset(data.df, gender=="female")$BMI.std))
colnames(gender.BMI.categories) <- c("male", "female")

WHR.labels <- c("Low", "Moderate", "High", "Very High")
data.df$WHR.std <- factor(NA)
levels(data.df$WHR.std) <- WHR.labels

gender.age.cond <-
  data.df$gender=="male" & data.df$age >= 20 & data.df$age <= 29
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.83, 0.88, 0.94, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="male" & data.df$age >= 30 & data.df$age <= 39
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.84, 0.91, 0.96, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="male" & data.df$age >= 40 & data.df$age <= 49
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.88, 0.95, 1, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="male" & data.df$age >= 50 & data.df$age <= 59
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.90, 0.96, 1.02, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="male" & data.df$age >= 60
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.91, 0.98, 1.03, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="female" & data.df$age >= 20 & data.df$age <= 29
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.71, 0.77, 0.82, Inf), labels=WHR.labels)
```



```

gender.age.cond <-
  data.df$gender=="female" & data.df$age >= 30 & data.df$age <= 39
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.72, 0.78, 0.84, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="female" & data.df$age >= 40 & data.df$age <= 49
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.73, 0.79, 0.87, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="female" & data.df$age >= 50 & data.df$age <= 59
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.74, 0.81, 0.88, Inf), labels=WHR.labels)

gender.age.cond <-
  data.df$gender=="female" & data.df$age >= 60
data.df[gender.age.cond, ]$WHR.std <-
  cut(data.df[gender.age.cond, ]$WHR,
       breaks=c(0, 0.76, 0.83, 0.9, Inf), labels=WHR.labels)

gender.WHR.categories <- cbind(table(subset(data.df, gender=="male")$WHR.std),
                                table(subset(data.df, gender=="female")$WHR.std))
colnames(gender.WHR.categories) <- c("male", "female")

```

## A.5 Regression

- ```

1. glyhb.lm <- lm(glyhb ~ stab.glu + age + BMI, data.df)
glyhb.lm.fit <- predict(glyhb.lm, data.df)

threshold <- function(y, lambda) {
  return(ifelse(y > lambda, 1, 0))
}

lm.err.rate <- function(p, q, lambda) {
  rate <- mean(sapply(p, function(y) threshold(y, lambda)) !=
               sapply(q, function(y) threshold(y, lambda)))
  return(rate)
}

err.rate <- lm.err.rate(data.df$glyhb, glyhb.lm.fit, lambda=7)

```
- ```

2. lm.false.pos.rate <- function(p, q, lambda) {
  rate <- mean(sapply(p, function(x) threshold(x, lambda)) <
               sapply(q, function(x) threshold(x, lambda)))
  return(rate)
}

```

```

lm.false.neg.rate <- function(p, q, lambda) {
  rate <- mean(sapply(p, function(x) threshold(x, lambda)) >
               sapply(q, function(x) threshold(x, lambda)))
  return(rate)
}

false.pos.rate <- lm.false.pos.rate(data.df$glyhb, glyhb.lm.fit, lambda=7)
false.neg.rate <- lm.false.neg.rate(data.df$glyhb, glyhb.lm.fit, lambda=7)

```

5. 

```

glyhb.lm <- lm(glyhb ~ stab.glu + BMI + WHR, data.df)
glyhb.lm.fit <- predict(glyhb.lm, data.df)

ggplot(data.df) +
  geom_point(aes(x=glyhb.lm.fit, y=scale(glyhb-glyhb.lm.fit))) +
  labs(title="Residuals plot of glyhb", x="predicted values", y="standardized residuals")
  theme(text=element_text(size=8.5))

```
6. 

```

glyhb.glm <- glm(as.numeric(glyhb.cond)-1 ~ scale(stab.glu) +
                scale(age) + scale(BMI), data.df, family=binomial)
glyhb.glm.fit <- predict(glyhb.glm, data.df, type="response")

glm.err.rate <- function(p, q, lambda) {
  rate <- mean(xor(as.numeric(p)-1, q >= lambda))
  return(rate)
}

err.rate <- glm.err.rate(data.df$glyhb.cond, glyhb.glm.fit, lambda=0.5)

```
7. 

```

test.df <- transform(test.df,
                     glyhb.cond=ifelse(glyhb>=7, "glyhb >=7", "glyhb < 7"))
test.df <- transform(test.df, BMI=703*weight/height^2)
test.df <- transform(test.df, WHR=waist/hip)

glyhb.test.lm.fit <- predict(glyhb.lm, test.df)
glyhb.test.glm.fit <- predict(glyhb.glm, test.df, type="response")

lm.test.err.rate <- lm.err.rate(test.df$glyhb, glyhb.test.lm.fit, lambda=7)
glm.test.err.rate <- glm.err.rate(test.df$glyhb.cond, glyhb.test.glm.fit, lambda=0.5)

```