Statistics 135 – Lab Project

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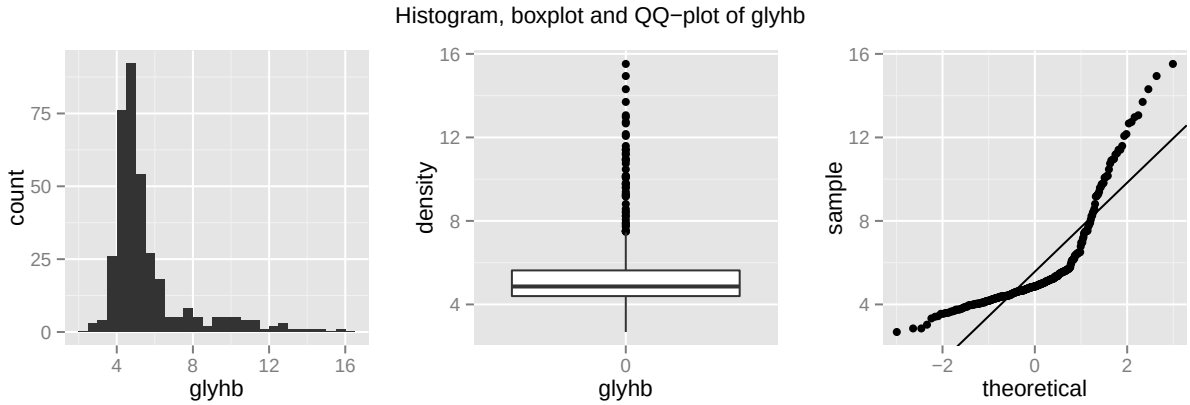
1 Background

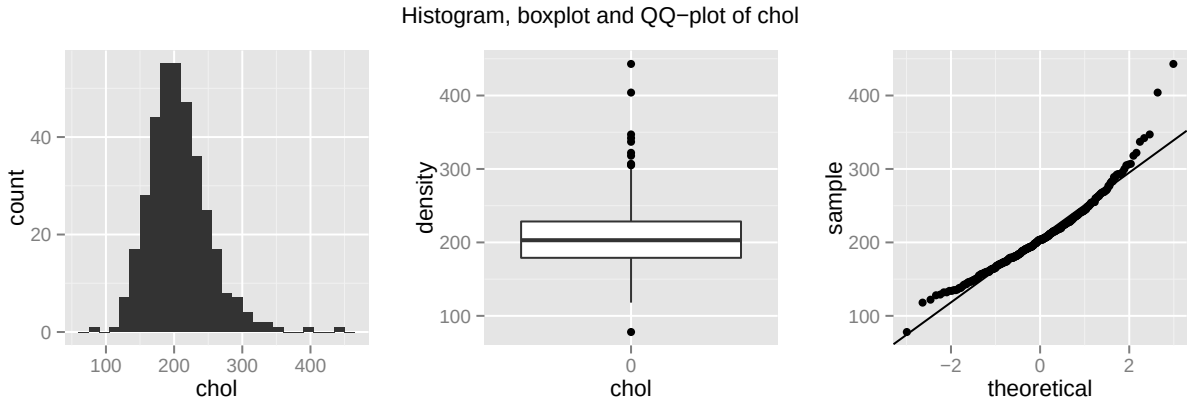
2 Accessing Data, Visualization and Summarization

1.



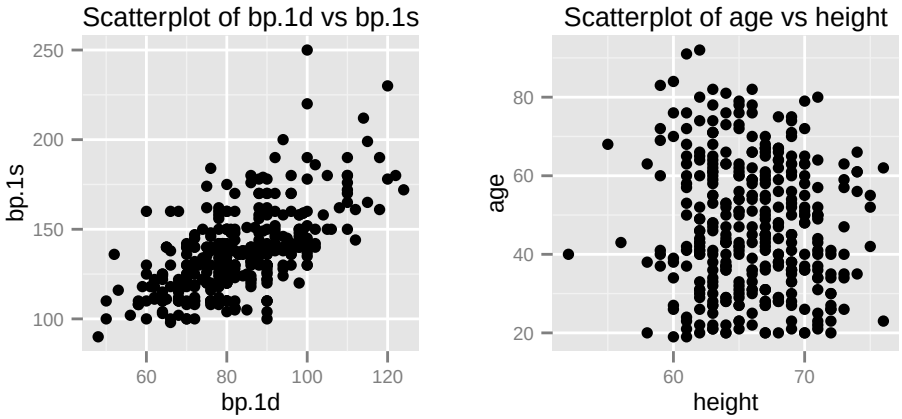
The mean, median and mode of `glyhb` are all approximately 5. The distribution of `glyhb` is left-skewed.

2.



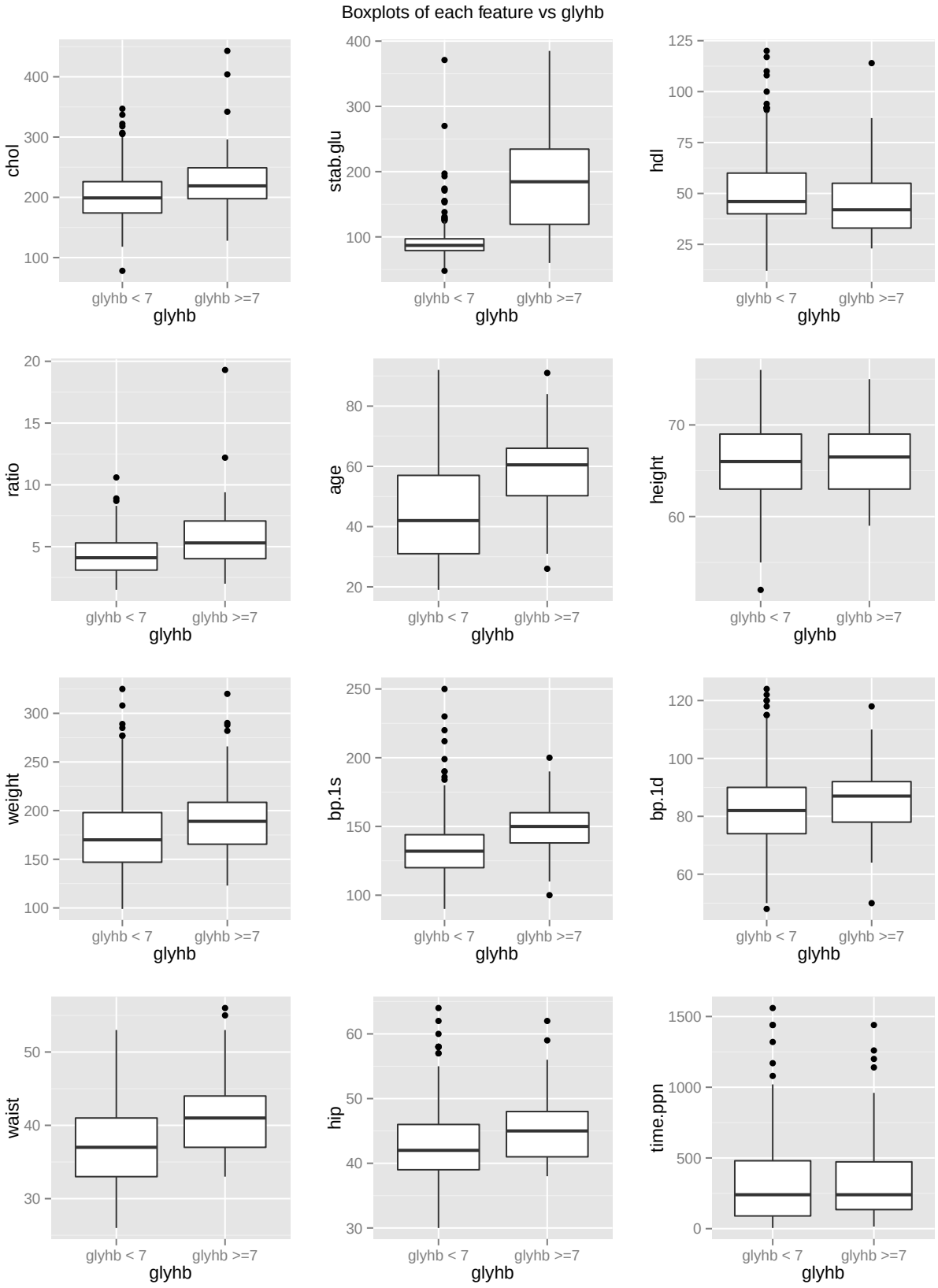
The mean, median and mode of `chol` are all approximately 200. The distribution of `chol` is better approximated with a Gaussian distribution.

3.

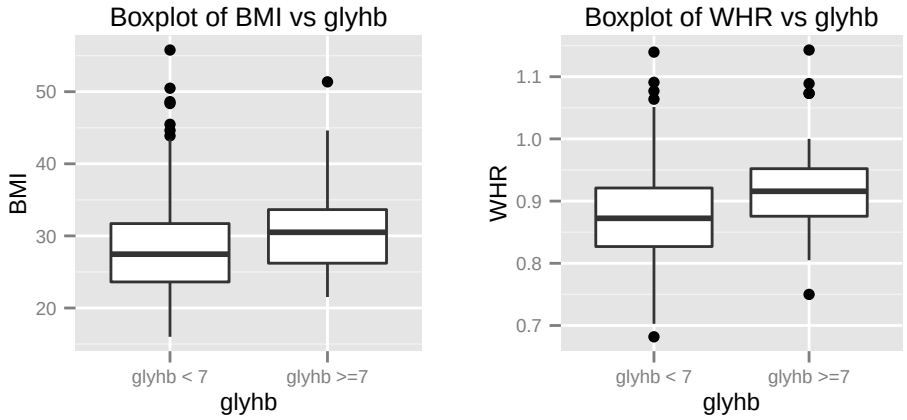


The scatterplot of `bp.1s` and `bp.1d` is near-linear, so they are approximately dependent. The scatterplot of `age` and `weight` is random, so they are approximately independent.

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
chol
stab.glu
hdl
ratio
age
height
weight
bp.1s
bp.1d
waist
hip
time.ppn
glyhb < 7
glyhb >=7
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.

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

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

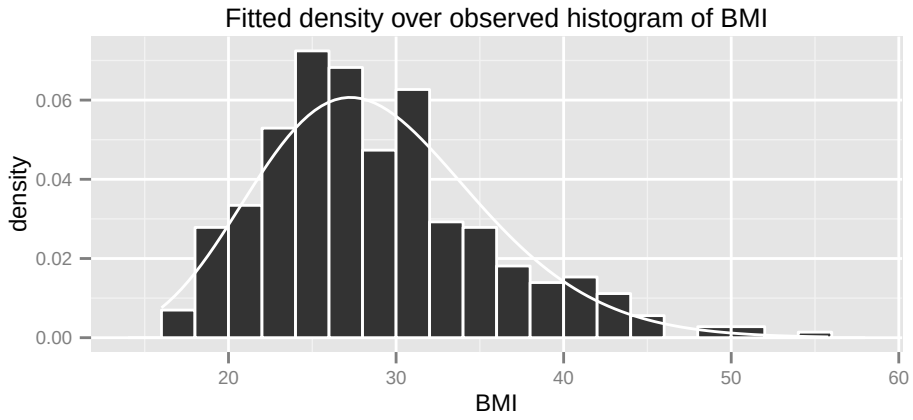
$$\begin{aligned} E(X^2) &= Var(X) + [E(X)]^2 \\ &= \frac{\alpha}{\beta^2} + \left(\frac{\alpha}{\beta}\right)^2 \\ &= \frac{\alpha(\alpha+1)}{\beta^2} \end{aligned}$$

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

```
################################################################################
CI.BMI

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

################################################################################
```



2.

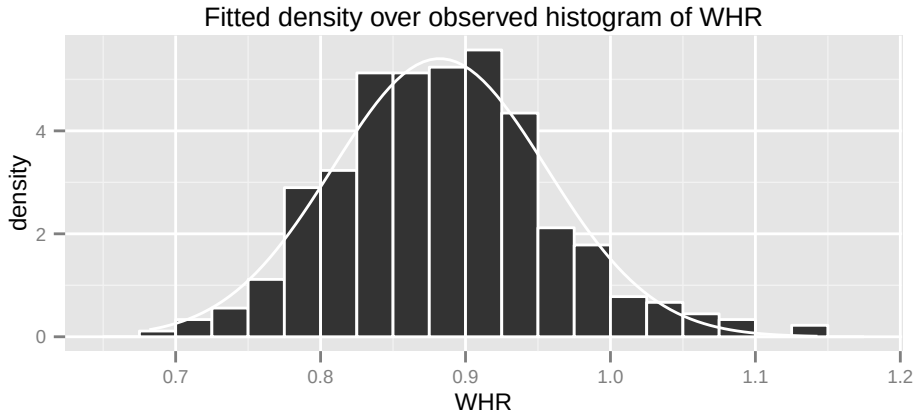
$$\hat{\mu}_{MLE} = \overline{X}_n$$

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

```
################################################################################
CI.WHR

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

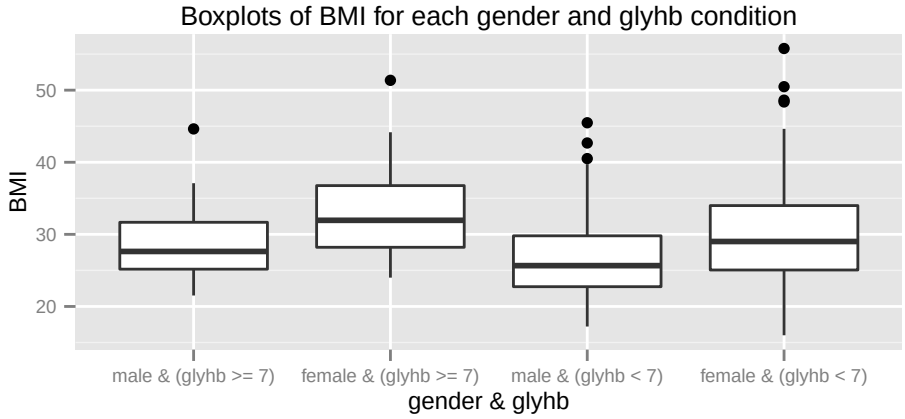
################################################################################
```



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

##############################################################################
```

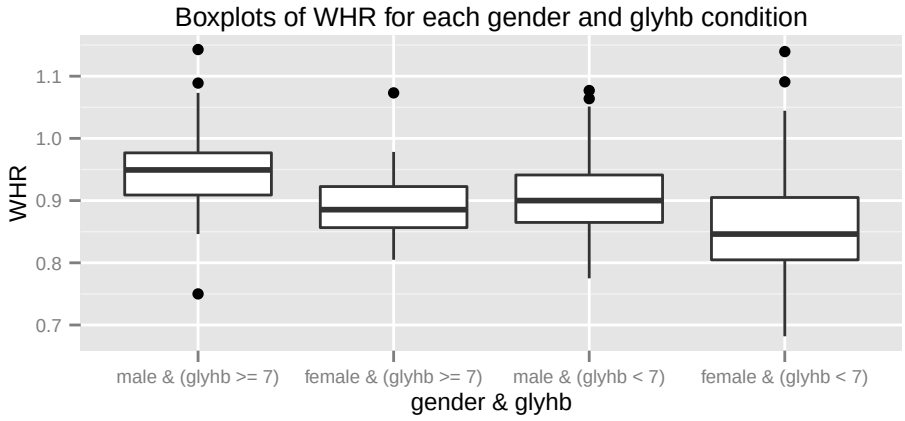


- On average, females have higher BMI than males.
- On average, people with type II diabetes (`glyhb >= 7`) have higher BMI than people without type II diabetes (`glyhb < 7`).
- People with type II diabetes (`glyhb >= 7`) have larger confidence intervals of both mean and standard deviation than people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

################################################################################
```

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

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

Let $T := X$.

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

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

```
################################################################################
t
```

```
## [1] 1.01804
```

```
################################################################################
power
```

```
## [1] 0.1555122
```

```
################################################################################
```

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

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

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     97

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

##
##  Pearson's Chi-squared test
##
## data:  gender.WHR.categories
## X-squared = 128.43, 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   47.7   9.546   2.153 0.0589 .
## WHR.std            3   16.8   5.586   1.260 0.2881
## BMI.std:WHR.std   14   71.2   5.089   1.148 0.3149
## Residuals        336 1489.7   4.434
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##############################################################################
```

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] 0.07520891

################################################################################
```

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 2.23%.
   ```

3.
```
################################################################################
glyhb.lm.coeff

##     (Intercept) scale(stab.glu)      scale(age)      scale(BMI)
##      5.56952646      1.38760997      0.27045152      0.08710214
##      scale(WHR)      scale(hdl)    scale(bp.1s)    scale(bp.1d)
##      0.09519384     -0.06892709      0.10521658     -0.02439215

################################################################################
```

Since `stab.glu` has the largest coefficient, it has the largest influence on the model.

```
################################################################################
summary(glyhb.lm)

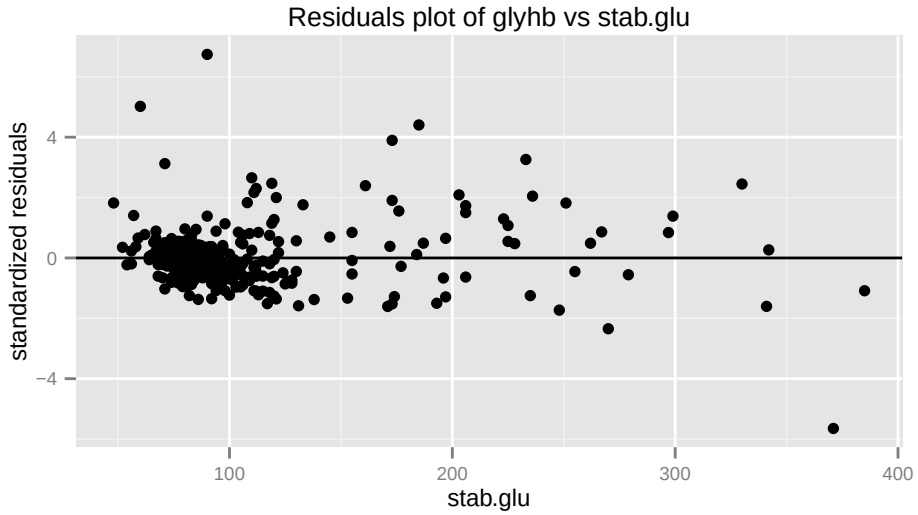
##
## Call:
## lm(formula = glyhb ~ scale(stab.glu) + scale(age) + scale(BMI) +
##     scale(WHR) + scale(hdl) + scale(bp.1s) + scale(bp.1d), data = data.df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.1074 -0.7058 -0.2113  0.4817  9.6762
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.56953    0.07650  72.805  < 2e-16 ***
## scale(stab.glu)  1.38761    0.08259  16.800  < 2e-16 ***
## scale(age)       0.27045    0.09608   2.815  0.00515 **
## scale(BMI)       0.08710    0.08103   1.075  0.28316
## scale(WHR)       0.09519    0.08220   1.158  0.24761
## scale(hdl)      -0.06893    0.08100  -0.851  0.39539
## scale(bp.1s)     0.10522    0.11473   0.917  0.35972
## scale(bp.1d)    -0.02439    0.10333  -0.236  0.81352
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.449 on 351 degrees of freedom
## Multiple R-squared:  0.5463,Adjusted R-squared:  0.5373
## F-statistic: 60.39 on 7 and 351 DF,  p-value: < 2.2e-16

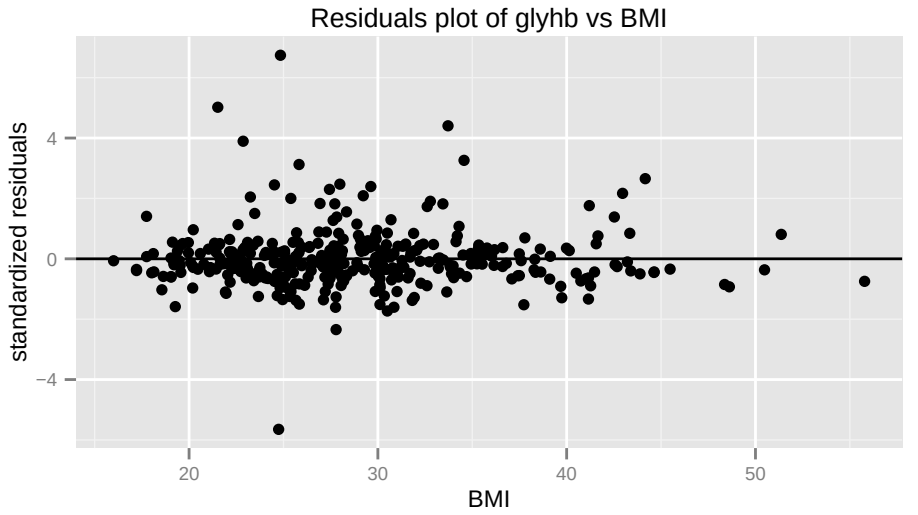
################################################################################
```

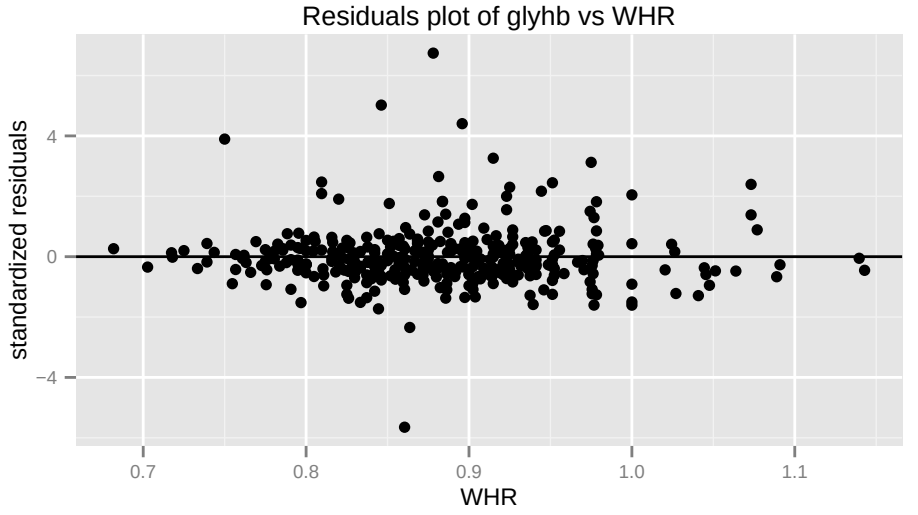
Since the p-values for `hdl`, `bp.1s` and `bp.1d` are 0.395, 0.36 and 0.814 respectively, we fail to reject the null hypothesis that `hdl`, `bp.1s` and `bp.1d` do not have any predictive value, with 5% significance level.

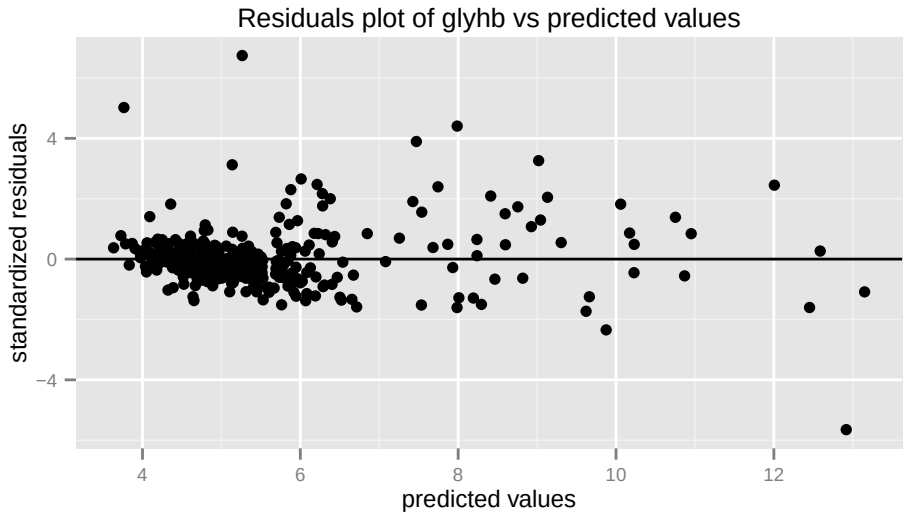
4. According to the result from part 4.6, `BMI` and `WHR` do not interact. However, if they do interact, we would choose the feature with larger influence (`BMI` in this case), because the interaction effect will reduce the influence.

5.


Residuals plot of glyhb vs stab.glu
standardized residuals
4
0
−4
100
200
300
400
stab.glu


Residuals plot of glyhb vs BMI
standardized residuals
4
0
−4
20
30
40
50
BMI


Residuals plot of glyhb vs WHR
standardized residuals
4
0
−4
0.7
0.8
0.9
1.0
1.1
WHR



6.
```
##############################################################################
err.rate

## [1] 0.08077994

##############################################################################
```

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)

alpha.mom <- with(data.df, mean(BMI)^2/var(BMI))
beta.mom <- with(data.df, mean(BMI)/var(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)

mu.mle <- with(data.df, mean(WHR))
sigma.mle <- with(data.df, sd(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

1.
```
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")
```

3.
```
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))
```

4.
```
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 <= 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 <= 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 ~ scale(stab.glu) + scale(age) + scale(BMI) +
                    scale(WHR) + scale(hdl) + scale(bp.1s) + scale(bp.1d), 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)
```

3.
```
glyhb.lm.coeff <- coefficients(glyhb.lm)
```

5.
```
ggplot(data.df) +
  geom_point(aes(x=stab.glu, y=scale(glyhb-glyhb.lm.fit))) +
  geom_abline(aes(intercept=0, slope=0)) +
  labs(title="Residuals plot of glyhb vs stab.glu",
       y="standardized residuals") +
  theme(text=element_text(size=8.5))

ggplot(data.df) +
  geom_point(aes(x=BMI, y=scale(glyhb-glyhb.lm.fit))) +
  geom_abline(aes(intercept=0, slope=0)) +
  labs(title="Residuals plot of glyhb vs BMI",
       y="standardized residuals") +
  theme(text=element_text(size=8.5))

ggplot(data.df) +
  geom_point(aes(x=WHR, y=scale(glyhb-glyhb.lm.fit))) +
  geom_abline(aes(intercept=0, slope=0)) +
  labs(title="Residuals plot of glyhb vs WHR",
       y="standardized residuals") +
  theme(text=element_text(size=8.5))

ggplot(data.df) +
  geom_point(aes(x=glyhb.lm.fit, y=scale(glyhb-glyhb.lm.fit))) +
  geom_abline(aes(intercept=0, slope=0)) +
  labs(title="Residuals plot of glyhb vs predicted values",
       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) + scale(WHR) + scale(hdl) + scale(bp.1s) +
                   scale(bp.1d), data.df, family=binomial)
glyhb.glm.fit <- predict(glyhb.glm, data.df, type="response")
```

```r
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. ```r
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)
```
```