Statistics 135 – Lab Project

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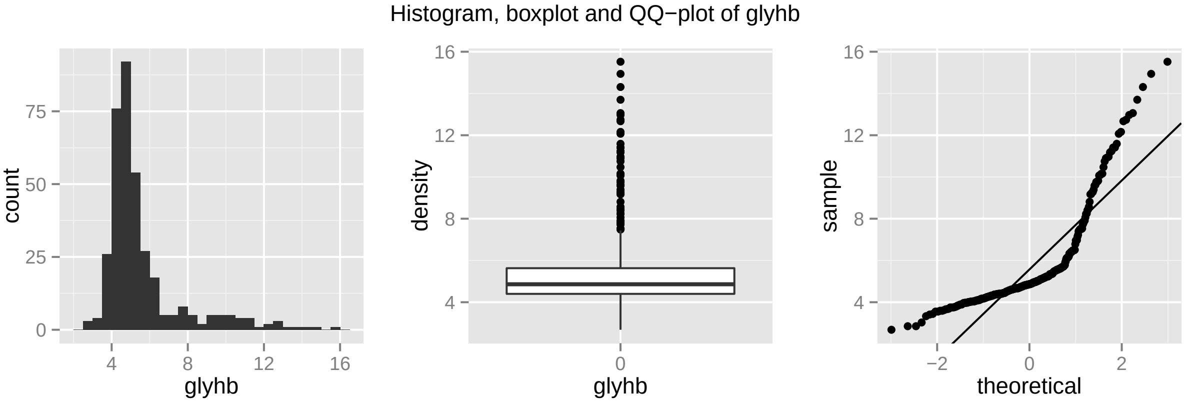
1 Background

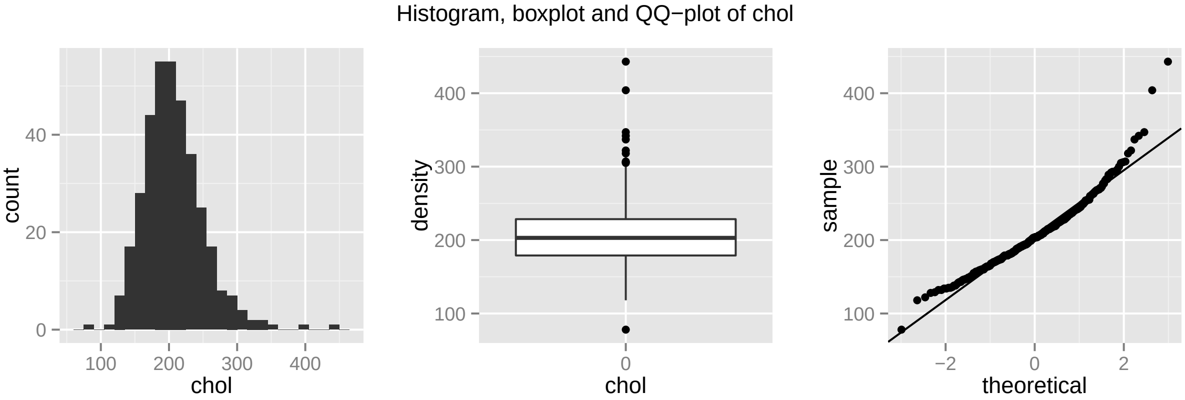
2 Accessing Data, Visualization and Summarization

1.



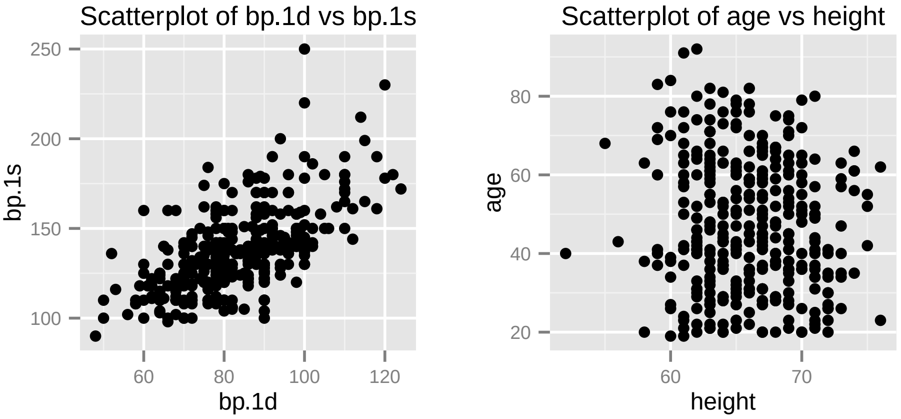
The mean, median and mode of `glyhb` are all approximately 5. The distribution of `glyhb` is left-skewed.

2.



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

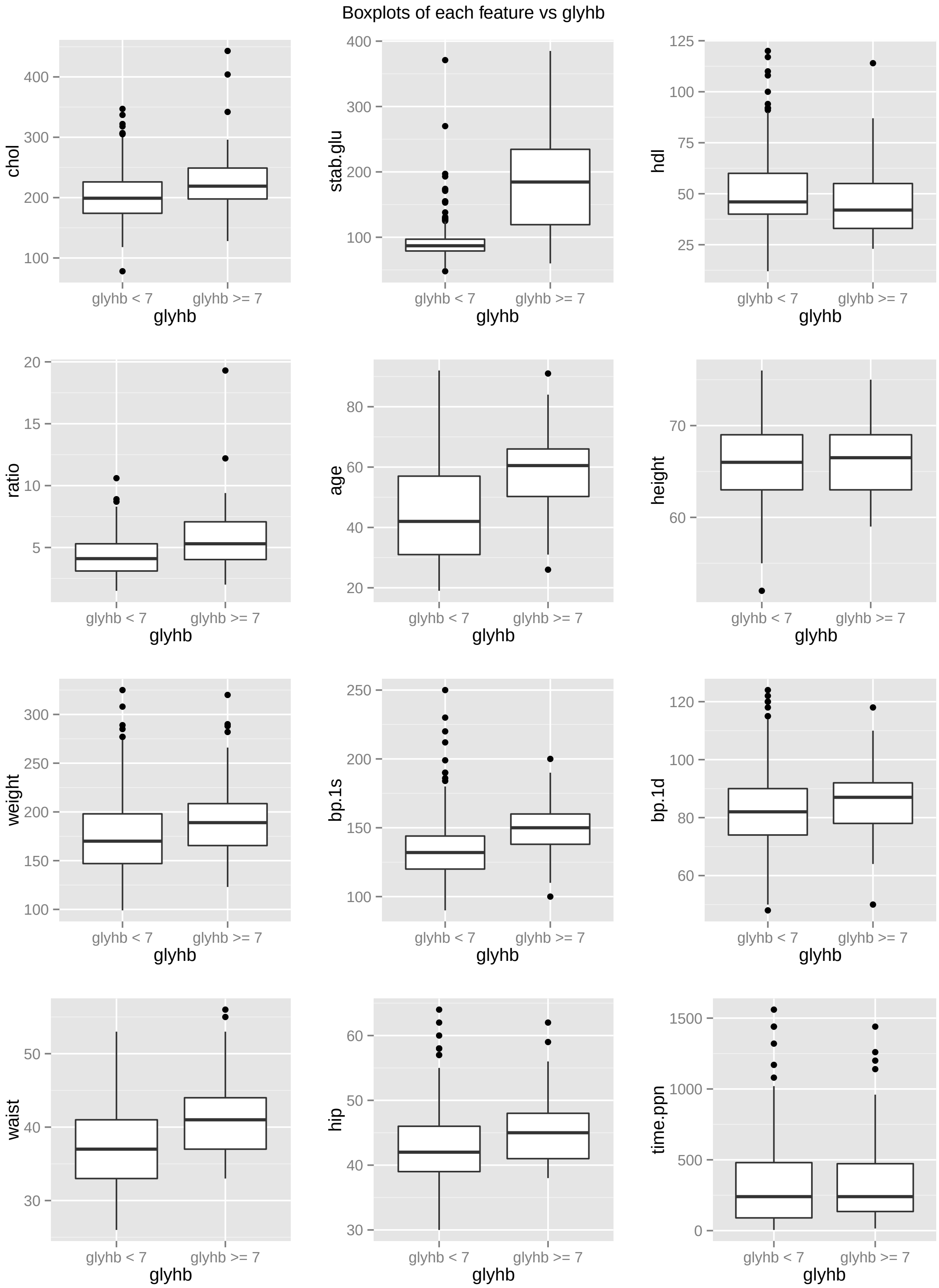
3.



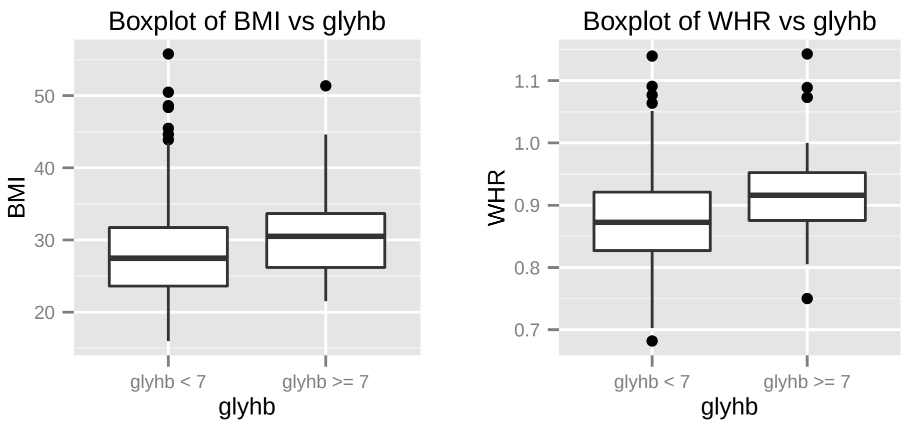
The scatterplot of `bp.1s` and `bp.1d` is near-linear, so they are approximately dependent. The scatterplot of `age` and `weight` is random, so they are approximately independent.

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 may 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 may 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
100
200
300
400
stab.glu
100
200
300
400
hdl
25
50
75
100
125
ratio
5
10
15
20
age
20
40
60
80
height
60
70
weight
100
150
200
250
300
bp.1s
100
150
200
250
bp.1d
60
80
100
120
waist
30
40
50
hip
30
40
50
60
time.ppn
0
500
1000
1500
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.

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

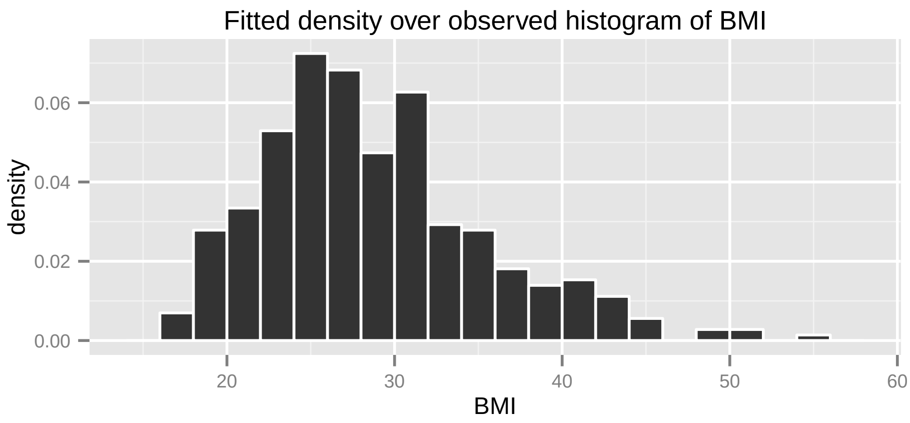
$$E(X) = \frac{\alpha}{\beta}$$

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

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

```
gamma.bootstrap <- 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.bootstrap(data.df$BMI)

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

##            alpha      beta
## 2.5%  15.77434 0.5420062
## 97.5% 21.52204 0.7547185

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

```
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))
```



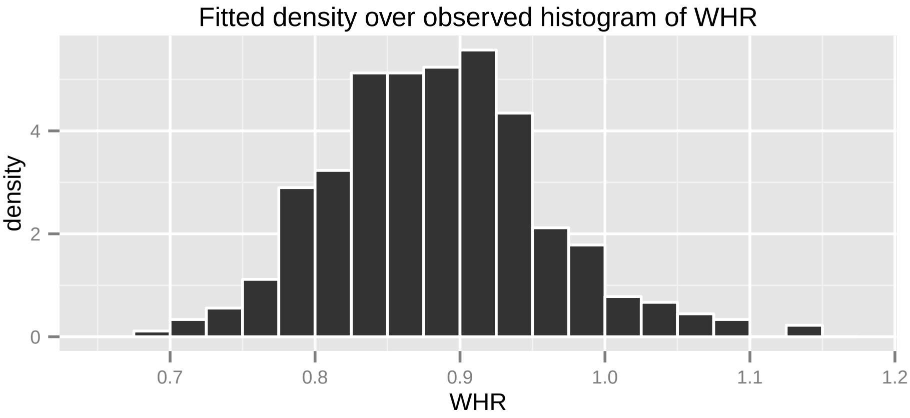
2.

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

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

```
normal.bootstrap <- 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.bootstrap(data.df$WHR)

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

##             mu      sigma
## 2.5%  0.8742232 0.06755450
## 97.5% 0.8898956 0.08004401

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

```
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))
```

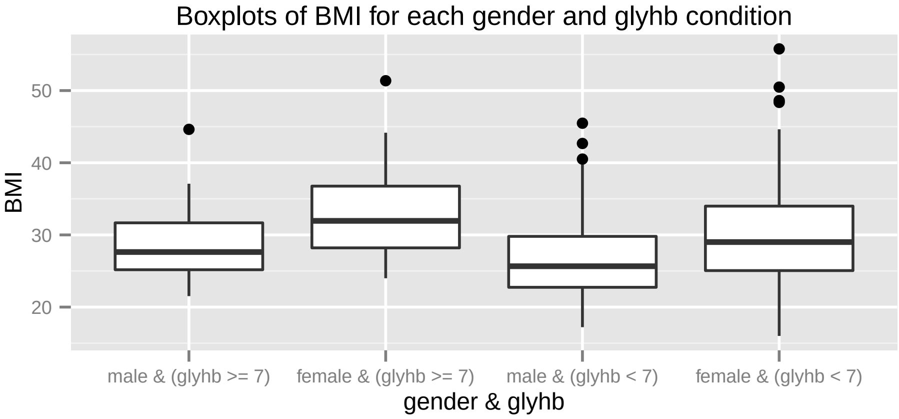


3.
```
data.df$gender.glyhb.cond <- NA
data.df[data.df$gender=="male" & data.df$glyhb>=7, ]$gender.glyhb.cond <-
  "male & (glyhb >= 7)"
data.df[data.df$gender=="female" & data.df$glyhb>=7, ]$gender.glyhb.cond <-
  "female & (glyhb >= 7)"
data.df[data.df$gender=="male" & data.df$glyhb<7, ]$gender.glyhb.cond <-
  "male & (glyhb < 7)"
data.df[data.df$gender=="female" & data.df$glyhb<7, ]$gender.glyhb.cond <-
```

```
  "female & (glyhb < 7)"

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

gamma.bootstrap2 <- 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.bootstrap2(gender.glyhb.df$BMI)
  return(CIs.BMI)
})
names(CIs.BMI) <- conditions

################################################################################
CIs.BMI

## $`male & (glyhb >= 7)`
##             mu    sigma
## 2.5%  26.95963 3.418566
## 97.5% 30.80594 7.070036
##
## $`female & (glyhb >= 7)`
##             mu    sigma
## 2.5%  30.90487 4.660985
## 97.5% 35.69416 8.293779
##
## $`male & (glyhb < 7)`
##             mu   sigma
## 2.5%  25.48804 4.72097
## 97.5% 27.38754 6.40592
##
## $`female & (glyhb < 7)`
##             mu    sigma
## 2.5%  28.76716 6.216621
## 97.5% 30.76864 7.802709
```

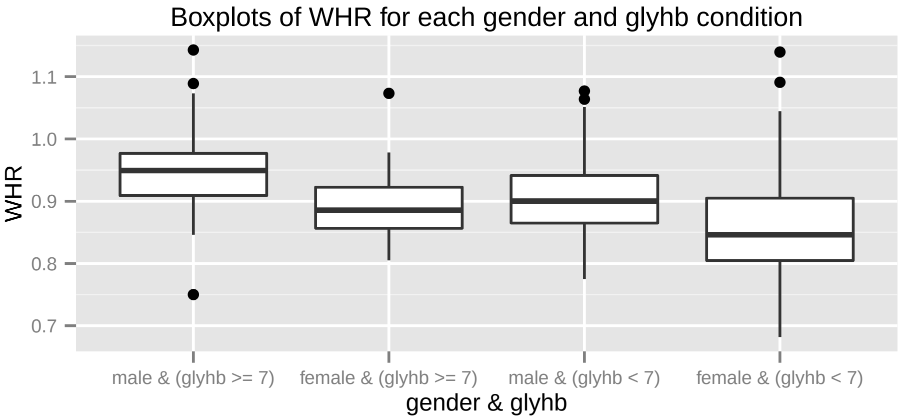
```
################################################################################
```

```
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.bootstrap(gender.glyhb.df$WHR)
  return(CIs.WHR)
})
names(CIs.WHR) <- conditions

################################################################################
CIs.WHR

## $`male & (glyhb >= 7)`
##              mu      sigma
## 2.5%  0.9170921 0.04852926
## 97.5% 0.9807403 0.10435834
##
## $`female & (glyhb >= 7)`
##              mu      sigma
## 2.5%  0.8745839 0.04175829
## 97.5% 0.9151449 0.07790498
##
## $`male & (glyhb < 7)`
##              mu      sigma
## 2.5%  0.8945964 0.05586194
## 97.5% 0.9163876 0.07088215
##
## $`female & (glyhb < 7)`
##              mu      sigma
## 2.5%  0.8445274 0.06136025
## 97.5% 0.8646460 0.07883802

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

```
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))
```



4 Testing

1.

2.

3.

4.

5.

6.

5 Regression

1.

2.

3.

4.

5.

6.

7.