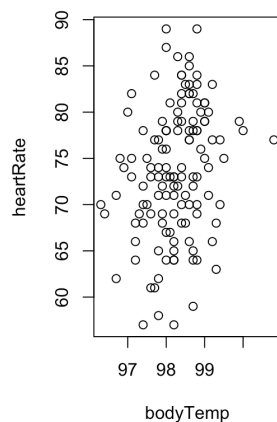Mini Project 5
Kaden Chan

Section 1:

1. a) null Hypothesis: $u_M - u_L = 0$: -0.289 | $Se(M - L) = \sqrt{s_r^2/n_1 + s_i^2/n_2} = .127$
    $T = u_M - u_L / SE = -.289/.127 = -2.285$ | Cutoff = $Z_{0.975} = 1.96$
    |T| > Cutoff, which means reject the null hypothesis so the data contains evidence that males and females differ in body temperature.

    b) null Hypothesis: $u_M - u_F = 0$: -0.785 | $Se(M - F) = \sqrt{s_r^2/n_1 + s_i^2/n_2} = 1.24$
    $T = u_M - u_F / SE = -.785 / 1.24 = -.632$ | cutoff = 1.96
    |T| < Cutoff, which means fail to reject, the data does not contain evidence that males and females differ in heart rate

    c) There is no linear relationship between body temperature and heart rate, correlation calculated to be .25

```r
# Mini Project 5
# Name: Kaden Chan
# Section 1. Answers to the specific questions asked
# Section 2: R code. Your code must be annotated.
# No points may be given if a brief look at the code
# does not tell us what it is doing.

# 1
data <- read.csv("bodytemp-heartrate.csv")

# 1a seperate male and female body_temperature
maleBodyTemp <- data[data$gender == 1, ]$body_temperature
femaleBodyTemp <- data[data$gender == 2, ]$body_temperature

# print mean
cat(mean(maleBodyTemp) - mean(femaleBodyTemp))
meanMale <- mean(maleBodyTemp)
meanFemale <- mean(femaleBodyTemp)

s2Male <- 0 # Calc Standard Error (SE) squared for male
for (p in maleBodyTemp) {
 s2Male <- s2Male + (p - meanMale) * (p - meanMale)
}
s2Male <- s2Male / (length(maleBodyTemp) - 1)

s2Female <- 0 # Calc Standard Error (SE) squared for female
for (p in femaleBodyTemp) {
 s2Female <- s2Female + (p - meanFemale) * (p - meanFemale)
}
s2Female <- s2Female / (length(femaleBodyTemp) - 1)

# calc SE of 2 variables
diffSE <- sqrt(
 s2Male / length(maleBodyTemp) + s2Female / length(femaleBodyTemp)
)

cat("mean diff SE:", diffSE)
# calc T
T <- (mean(maleBodyTemp) - mean(femaleBodyTemp)) / diffSE
cat(T)
```

```r
# calc cutoff
cutoff <- qnorm(1 - 0.05 / 2)
cat(cutoff)
if (abs(T) < cutoff) {
 cat("fail to reject")
} else {
 cat("reject")
}


# 1 b
maleHeartRate <- data[data$gender == 1, ]$heart_rate
femaleHeartRate <- data[data$gender == 2, ]$heart_rate


# print mean
cat(mean(maleHeartRate) - mean(femaleHeartRate))
meanMale <- mean(maleHeartRate)
meanFemale <- mean(femaleHeartRate)


s2Male <- 0 # Calc Standard Error (SE) squared for male
for (p in maleHeartRate) {
 s2Male <- s2Male + (p - meanMale) * (p - meanMale)
}
s2Male <- s2Male / (length(maleHeartRate) - 1)


s2Female <- 0 # Calc Standard Error (SE) squared for female
for (p in femaleHeartRate) {
 s2Female <- s2Female + (p - meanFemale) * (p - meanFemale)
}
s2Female <- s2Female / (length(femaleHeartRate) - 1)


# calc SE of 2 variables
diffSE <- sqrt(
 s2Male / length(maleHeartRate) + s2Female / length(femaleHeartRate)
)
cat(diffSE)
#calc T
T <- (mean(maleHeartRate) - mean(femaleHeartRate)) / diffSE
cat(T)


# calc cutoff
cutoff <- qnorm(1 - 0.05 / 2)
cat(cutoff)
```

```r
if (abs(T) < cutoff) {
 cat("fail to reject")
} else {
 cat("reject")
}

# 1c
bodyTemp <- data[]$body_temperature
heartRate <- data[]$heart_rate

# plot points for bodyTemp and heartRate
plot(bodyTemp, heartRate)
corr <- cor(bodyTemp, heartRate)
cat(corr)
```