STA135 homework6

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5.10

```
growth <- read.table("/Users/Elliot/Github/UCDavis/STA135/resource/STA135_data/T1-4.dat")
growth_length <- growth[, 5:8]
names(growth_length) <- paste0("Length", 2:5)</pre>
```

(a)

Simultaneous confidence intervals:

```
calculate_simultaneous_interval <- function(sample_data, test_mean,</pre>
    alpha, p, flag = T, print_flag = T) {
    names_sample_data <- names(sample_data)</pre>
    sample_data <- as.matrix(sample_data)</pre>
    n <- dim(as.matrix(sample_data))[1]</pre>
    sample_mean <- apply(sample_data, 2, mean)</pre>
    deviation <- sample_mean - test_mean</pre>
    covariance_matrix <- cov(sample_data)</pre>
    F star \leftarrow sqrt((n-1) * p/(n-p) * qf(1-alpha, p, n-p))
    sd_deviation <- sqrt(diag(covariance_matrix)/n)</pre>
    part2 <- F_star * sd_deviation</pre>
    result <- matrix(c(deviation - part2, upper = deviation + part2),</pre>
        n <- dim(as.matrix(sample_data))[2])</pre>
    rownames(result) <- names_sample_data</pre>
    colnames(result) <- c("lower", "upper")</pre>
    if (print_flag)
        print(result)
    if (flag)
        return(F_star)
    return(result)
}
invisible(calculate_simultaneous_interval(growth_length, 0, 0.05,
    4))
```

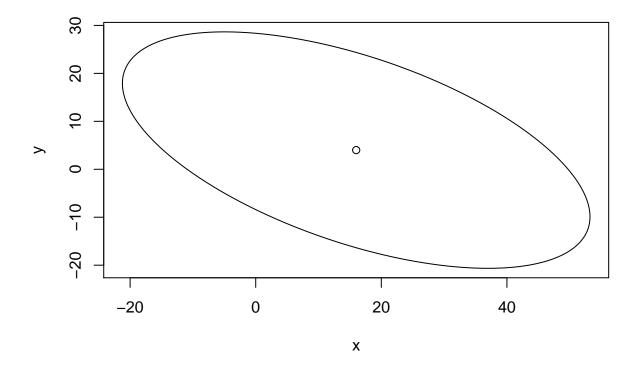
```
## lower upper
## Length2 130.6851 155.8863
## Length3 127.0216 191.5498
## Length4 160.3082 185.9776
## Length5 155.3749 198.9108
```

(b)

simultaneous intervals for changes in length

```
growth_length_change <- as.data.frame(sapply(1:3, function(i) growth_length[,</pre>
    i + 1] - growth_length[, i]))
names(growth_length_change) <- paste0("Length", 3:5, "-Length", 2:4)</pre>
invisible(calculate_simultaneous_interval(growth_length_change, 0,
    0.05, 4))
##
                         lower
                                  upper
## Length3-Length2 -21.22649 53.22649
## Length4-Length3 -22.73077 50.44505
## Length5-Length4 -20.65385 28.65385
(c)
The simultaneous interval is:
growth_length_compare <- as.data.frame(cbind(growth_length[, 2] -</pre>
    growth_length[, 1], growth_length[, 4] - growth_length[, 3]))
names(growth_length_compare) <- paste0("Length", c(3, 5), "-Length",</pre>
    c(2, 4)
invisible(calculate_simultaneous_interval(growth_length_compare, 0,
    0.05, 4))
##
                         lower
                                  upper
## Length3-Length2 -21.22649 53.22649
## Length5-Length4 -20.65385 28.65385
The ellipse:
plot_ellipse <- function(sample_data, F_star, test_point) {</pre>
    n <- dim(sample_data)[1]</pre>
    sample_data_var <- cov(sample_data)</pre>
    sample_data_eigenvalue <- eigen(sample_data_var)$values</pre>
    main_vector <- eigen(sample_data_var)$vectors[, 1]</pre>
    lambda1 <- sqrt(sample_data_eigenvalue)[1]</pre>
    lambda2 <- sqrt(sample data eigenvalue)[2]</pre>
    alpha <- atan(main_vector[2]/main_vector[1])</pre>
    theta \leftarrow seq(0, 2 * pi, length = (1000))
    F_star <- F_star/sqrt(n)</pre>
    a <- lambda1 * F star
    b <- lambda2 * F_star
    x_bar <- unname(apply(sample_data, 2, mean))</pre>
    x \leftarrow x_{bar}[1] + a * cos(theta) * cos(alpha) - b * sin(theta) *
        sin(alpha)
    y \leftarrow x_bar[2] + a * cos(theta) * sin(alpha) + b * sin(theta) *
        cos(alpha)
    plot(x, y, type = "l")
    points(x_bar[1], x_bar[2], type = "p")
    points(test_point[1], test_point[2], type = "p", col = "red")
}
plot_ellipse(growth_length_compare, calculate_simultaneous_interval(growth_length_compare,
    0, 0.05, 4), c(-110, -110))
```

```
## lower upper
## Length3-Length2 -21.22649 53.22649
## Length5-Length4 -20.65385 28.65385
```

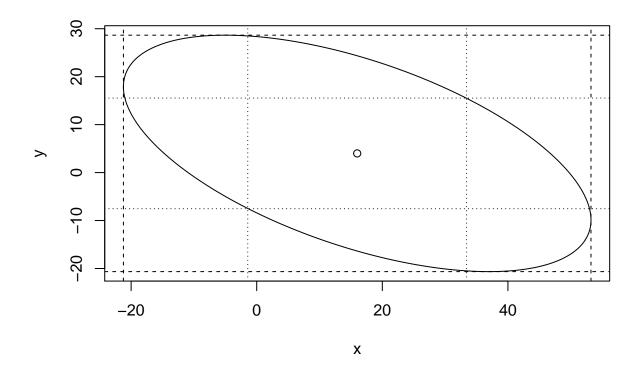


I will revisit the plot in part (e).

(d)

```
calculate_Bonferroni_interval <- function(sample_data, test_mean,</pre>
    alpha, pair, print_flag = T) {
    names_sample_data <- names(sample_data)</pre>
    sample_data <- as.matrix(sample_data)</pre>
    n <- dim(as.matrix(sample_data))[1]</pre>
    sample_mean <- apply(sample_data, 2, mean)</pre>
    deviation <- sample_mean - test_mean</pre>
    covariance_matrix <- cov(sample_data)</pre>
    B \leftarrow qt(1 - alpha/(2 * pair), n - 1)
    sd_deviation <- sqrt(diag(covariance_matrix)/n)</pre>
    part2 <- B * sd_deviation</pre>
    result <- matrix(c(deviation - part2, upper = deviation + part2),</pre>
         n <- dim(as.matrix(sample_data))[2])</pre>
    rownames(result) <- names_sample_data</pre>
    colnames(result) <- c("lower", "upper")</pre>
    if (print_flag)
```

```
print(result)
    return(result)
}
invisible(calculate_Bonferroni_interval(growth_length, 0, 0.05, 7))
##
              lower
                       upper
## Length2 137.3884 149.1831
## Length3 144.1854 174.3860
## Length4 167.1359 179.1498
## Length5 166.9550 187.3307
invisible(calculate_Bonferroni_interval(growth_length_change, 0, 0.05,
    7))
##
                       lower
                                 upper
## Length3-Length2 -1.422784 33.42278
## Length4-Length3 -3.266772 30.98106
## Length5-Length4 -7.538521 15.53852
(e)
The bonferroni interval:
invisible(calculate_Bonferroni_interval(growth_length_compare, 0,
                       lower
                                 upper
## Length3-Length2 -1.422784 33.42278
## Length5-Length4 -7.538521 15.53852
plot_ellipse(growth_length_compare, calculate_simultaneous_interval(growth_length_compare,
    0, 0.05, 4, print_flag = F), c(-110, -110))
s_interval <- as.vector(t(calculate_simultaneous_interval(growth_length_compare,</pre>
    0, 0.05, 4, FALSE, print_flag = F)))
b_interval <- as.vector(t(invisible(calculate_Bonferroni_interval(growth_length_compare,</pre>
    0, 0.05, 7, print_flag = F))))
for (i in 1:2) {
    abline(v = s_interval[i], lty = 2)
    abline(v = b_interval[i], lty = 3)
}
for (i in 3:4) {
    abline(h = s_interval[i], lty = 2)
    abline(h = b_interval[i], lty = 3)
}
```



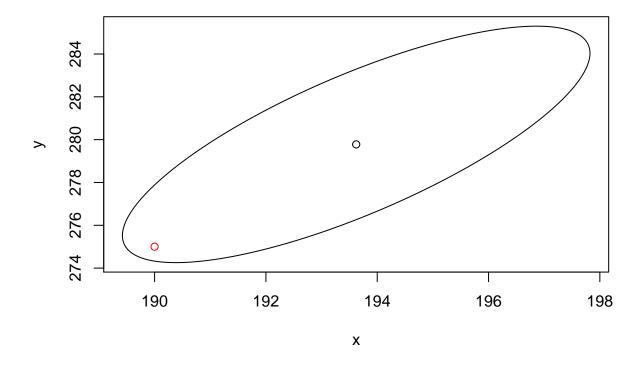
The bigger square with line type lty = 2 is the simultaneous interval, while the inner square with line type lty = 3 is the bonferroni interval. Clearly the bonferroni interval is much small.

5.20

```
kites <- read.table("/Users/Elliot/Github/UCDavis/STA135/resource/STA135_data/T5-12.dat")
names(kites) <- c("tail length", "wing length")</pre>
```

(a)

```
## lower upper
## tail length 189.4217 197.8227
## wing length 274.2564 285.2992
```



Here is the ellipse. The point is in the ellipse, so it is plausible.

(b)

Simultaneous interval:

```
print(calculate_simultaneous_interval(kites, 0, 0.05, 2))
```

```
## lower upper
## tail length 189.4217 197.8227
## wing length 274.2564 285.2992
## [1] 2.564853
```

Bonferroni interval:

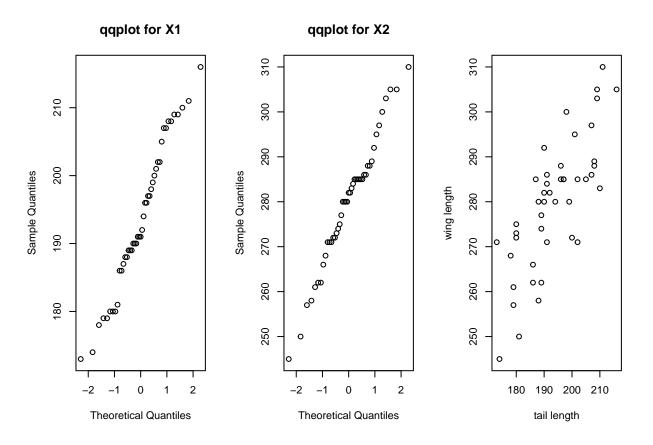
print(calculate_Bonferroni_interval(kites, 0, 0.05, 2))

```
## tail length 189.8216 197.4229
## wing length 274.7819 284.7736
## lower upper
## tail length 189.8216 197.4229
## wing length 274.7819 284.7736
```

The simultaneous interval is a little large than the bonferroni interval. The simultaneous confidence interval will touch the simultaneous confidence region from outside.

(c)

```
par(mfrow = c(1, 3))
qqnorm(kites$`tail length`, main = "qqplot for X1")
qqnorm(kites$`wing length`, main = "qqplot for X2")
with(kites, plot(`tail length`, `wing length`))
```



From the plot we know X_1 and X_2 are not normal. We could transform X_1 .