(7.10.1) 

\[ z_0 = z_{(1-0.05)} = 1.645; \quad z_1 = z_{(1-0.1)} = 1.282 \]

\[ n = \left( \frac{(1.645 + 1.282)(32)}{516 - 620} \right)^2 = 547.56 \approx 548 \]

\[ C = 516 + 1.645 \frac{32}{\sqrt{548}} = 518.25; \quad C = 520 - 1.28 \frac{32}{\sqrt{548}} = 518.25 \]

Select a sample of size 548 and compute \( \bar{x} \). If \( \bar{x} \geq 518.25 \), reject \( H_0 \). If \( \bar{x} < 518.25 \), do not reject \( H_0 \).

(7.10.2) 

\[ z_0 = z_{(1-0.01)} = 2.326; \quad z_1 = z_{(1-0.05)} = 1.645 \]

\[ n = \left( \frac{(2.326 + 1.645)(0.02)}{4.500 - 4.520} \right)^2 = 15.8 \approx 16 \]

\[ C = 4.500 + 2.326 \frac{0.02}{\sqrt{16}} = 4.512; \quad C = 4.520 - 1.645 \frac{0.02}{\sqrt{16}} = 4.512 \]

Select a sample of size 16 and compute \( \bar{x} \). If \( \bar{x} \geq 4.512 \), reject \( H_0 \). If \( \bar{x} < 4.512 \), do not reject \( H_0 \).
Ex 8.2.1

```r
> hw821 <- read.csv("C:/Users/dlabate/Desktop/Teaching/ma4310/EXR_C08_S02_01.csv")
> str(hw821)
'data.frame': 329 obs. of 2 variables:
$ weight: num -0.003 0.05 0.272 0.552 1.116 ...
$ group : int 1 1 1 1 1 1 1 1 1 1 ...

Note that the group variable is not recognized as a factor. Hence we need to reassign it.

> hw821$group <- factor(hw821$group, levels = c(1,2,3,4),labels = c("a30", "a60","a90","a120"))
> str(hw821)
'data.frame': 329 obs. of 2 variables:
$ weight: num -0.003 0.05 0.272 0.552 1.116 ...
$ group : Factor w/ 4 levels "a30","a60","a90",...: 1 1 1 1 1 1 1 1 1 1 ...

> boxplot(weight ~ group, data = hw821, xlab = "Treatment group", ylab = "Weight",
+ frame = FALSE, col = c("#00AFBB",="#E7B800",="#FC4E07","#0000FF"))
```

```
> res.aov <- aov(weight ~ group, data = hw821)
> summary(res.aov)
```
### ANOVA Table

<table>
<thead>
<tr>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>group</td>
<td>3</td>
<td>20.0</td>
<td>6.669</td>
<td>6.242</td>
</tr>
<tr>
<td>Residuals</td>
<td>325</td>
<td>347.2</td>
<td>1.068</td>
<td></td>
</tr>
</tbody>
</table>

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 . ‘.’ 0.1 ‘ ’ 1

> `qf(0.95, df1=3, df2=325)`

[1] 2.632394

**Conclusion:** Since $F = 6.242 > 2.737492$ or since $p < 0.001$, we reject $H_0$. Weight differed significantly among the four training types. Next we run the Tuckey HSD test to determine which pairs of groups are statistically different.

> `TukeyHSD(res.aov)`

Tukey multiple comparisons of means
95% family-wise confidence level

Fit: `aov(formula = weight ~ group, data = hw821)`

<table>
<thead>
<tr>
<th>group</th>
<th>diff</th>
<th>lwr</th>
<th>upr</th>
<th>p adj</th>
</tr>
</thead>
<tbody>
<tr>
<td>a60-a30</td>
<td>-0.447587615</td>
<td>-1.0125162</td>
<td>0.1173410</td>
<td>0.1734399</td>
</tr>
<tr>
<td>a90-a30</td>
<td>0.191059839</td>
<td>-0.1830744</td>
<td>0.5651941</td>
<td>0.5516339</td>
</tr>
<tr>
<td>a120-a30</td>
<td>-0.443557312</td>
<td>-1.0084859</td>
<td>0.1213713</td>
<td>0.1799776</td>
</tr>
<tr>
<td>a90-a60</td>
<td>0.638647454</td>
<td>0.1360387</td>
<td>1.1412562</td>
<td>0.0062693</td>
</tr>
<tr>
<td>a120-a60</td>
<td>0.004030303</td>
<td>-0.6530720</td>
<td>0.6611326</td>
<td>0.9999986</td>
</tr>
<tr>
<td>a120-a90</td>
<td>-0.634617151</td>
<td>-1.1372259</td>
<td>-0.1320084</td>
<td>0.0067138</td>
</tr>
</tbody>
</table>

**Conclusion:** Only the differences a90-a60 and a120-a90 are significant.
Ex 8.2.2

```r
> hw822 <- read.csv("C:/Users/dlabate/Desktop/Teaching/ma4310/EXR_C08_S02_02.csv")
> str(hw822)
'data.frame': 96 obs. of 2 variables:
$ weight: num 11.09 24.41 10.03 -3.16 6.83 ... 
$ group : int 1 1 1 1 1 1 1 1 1 1 ...

Note that the group variable is not recognized as a factor. Hence we need to reassign it.

> hw822$group <- factor(hw822$group, levels = c(1,2,3,4,5),labels = c("RA", "LU","PM", "OA", "O"))
> str(hw822)
'data.frame': 96 obs. of 2 variables:
$ weight: num 11.09 24.41 10.03 -3.16 6.83 ... 
$ group : Factor w/ 5 levels "RA","LU","PM", ..: 1 1 1 1 1 1 1 1 1 1 ...
> boxplot(weight ~ group, data = hw822, xlab = "Diagnosis group", ylab = "Bone density", frame = FALSE, col = c("#00AFBB", "#E7B800", "#FC4E07","#0000FF", "#00FF00"))
```

```r
> res.aov <- aov(weight ~ group, data = hw822)
> summary(res.aov)
```
Df  Sum Sq  Mean Sq  F value  Pr(>F)
group        4    355   88.86   2.277  0.067 .
Residuals    91   3551   39.02
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

**Conclusion:** Since \( p > 0.05 \), we accept \( H_0 \). Bone density did not differ significantly among the five diagnosis groups. Clearly, no Tukey HSD test is needed in this case.
A study investigated the dietary intake of calcium among a cross section of 113 healthy women ages 20–88. The researchers formed four age groupings as follows: Group A, 20.0–45.9 years; group B, 46.0–55.9 years; group C, 56.0–65.9 years; and group D, over 66 years. Calcium from food intake was measured in mg/day.

1. Generate side-by-side boxplots of the data
2. Apply the analysis of variance hypothesis testing to see if you can conclude that there is a difference among population means. Justify your conclusion.
3. Use the Tukey’s HSD procedure to test for significant differences among individual pairs of means, if appropriate. Justify your conclusion.
4. Apply the Shapiro-Wilk test to check that the normality assumption of the data is satisfied.

```r
> dataq3 <- read.csv("C:/Users/dlabate/Desktop/Teaching/ma4310/dataq3.csv")
> str(dataq3)
'data.frame': 113 obs. of 2 variables:
$ calcium: int 1820 2588 2670 1022 1555 222 1197 1249 1520 489 ...
$ Group  : chr "A" "A" "A" "A" ...
> dataq3$Group <- factor(dataq3$Group, levels = c("A","B","C","D"),labels = c("A","B","C","D"))
> str(dataq3)
'data.frame': 113 obs. of 2 variables:
$ calcium: int 1820 2588 2670 1022 1555 222 1197 1249 1520 489 ...
$ Group : Factor w/ 4 levels "A","B","C","D": 1 1 1 1 1 1 1 1 1 1 ...
```

1. Generate side-by-side boxplots of the data

```r
> boxplot(calcium ~ Group, data = dataq3, xlab = "Age group", ylab = "calcium intake", frame = FALSE, col = c("#00AFBB", "#E7B800",="#FC4E07","#0000FF"))
```
2. **Apply the analysis of variance hypothesis testing**

```r
> res.aov <- aov(calcium ~ Group, data = dataq3)
> summary(res.aov)

Df  | Sum Sq | Mean Sq | F value  | Pr(>F)  |
--- | ------ | ------- | -------- | ------- |
Group | 3     | 5931208 | 1977069  | 9.359   | 1.48e-05 *** |
Residuals | 109 | 23026500 | 211252   |

---

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Conclusion: since p-value < 0.05, we reject H0 and conclude that there is a statistically significant difference among the means.

3. **Use the Tukey’s HSD procedure**

```r
> TukeyHSD(res.aov)

Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = calcium ~ Group, data = dataq3)

$Group
  diff  lwr  upr  p adj
B-A  -455.72078  -865.7066  -45.73492 0.0230454
C-A  -574.53605  -913.5892  -235.48294 0.0001356
D-A  -596.63447  -905.3867  -287.88228 0.0000109
C-B   -118.81527  -509.0844  271.45386 0.8568796
D-B  -140.91369  -505.1676  223.34020 0.7443051
D-C    -22.09842  -304.1436  259.94679 0.9969598
```

Conclusion: based on the values of p adj, only the differences between the groups A-B, A-C and A-D are statistically significant.

4. **Apply the Shapiro-Wilk test**

```r
> aov_residuals <- residuals(object = res.aov)
> shapiro.test(x = aov_residuals)

Shapiro-Wilk normality test

data:  aov_residuals
W = 0.97799, p-value = 0.05908
```

Conclusion: since the p-value > 0.05, we can accept H0 that data are approximately normal. In this case, the normality assumption is barely met.