1.

c) H0: Habitat types do not differ in mean cone size ($\mu_1 = \mu_2 = \mu_3$).
Ha: Habitat types differ in mean cone size (at least one $\mu_i$ is different from at least one other $\mu_j$)

By hand,

<table>
<thead>
<tr>
<th></th>
<th>Island absent</th>
<th>Island present</th>
<th>Mainland present</th>
</tr>
</thead>
<tbody>
<tr>
<td>data</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9.6</td>
<td>6.8</td>
<td>6.7</td>
<td></td>
</tr>
<tr>
<td>9.4</td>
<td>6.6</td>
<td>6.4</td>
<td></td>
</tr>
<tr>
<td>8.9</td>
<td>6.0</td>
<td>6.2</td>
<td></td>
</tr>
<tr>
<td>8.8</td>
<td>5.7</td>
<td>5.7</td>
<td></td>
</tr>
<tr>
<td>8.5</td>
<td>5.3</td>
<td>5.6</td>
<td></td>
</tr>
<tr>
<td>8.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sum</td>
<td>53.4</td>
<td>30.4</td>
<td>30.6</td>
</tr>
<tr>
<td>Mean</td>
<td>8.9</td>
<td>6.08</td>
<td>6.12</td>
</tr>
<tr>
<td>SD</td>
<td>0.53</td>
<td>0.62</td>
<td>0.47</td>
</tr>
<tr>
<td>n</td>
<td>6</td>
<td>5</td>
<td>5</td>
</tr>
</tbody>
</table>

$$y_{..} = \frac{1}{16} \sum_{i=1}^{3} y_{..} = \frac{53.4 + 30.4 + 30.6}{16} = 7.15$$

$$SSTrt = \sum_{i=1}^{3} n_i \cdot (\bar{y}_i - \bar{y}_{..})^2 = 6 \cdot (8.9 - 7.15)^2 + 5 \cdot (6.08 - 7.15)^2 + 5 \cdot (6.12 - 7.15)^2 = 29.404$$

$$SS \ Error = \sum_{i=1}^{3} (n_i - 1) s_i^2 = 5 \cdot 0.53^2 + 4 \cdot 0.62^2 + 4 \cdot 0.47^2 = 3.816$$

$$MS \ Trt = \frac{SSTrt}{2} = 14.7020$$

$$MS \ Error = \frac{SS \ Error}{13} = 0.2935$$

$$F = \frac{MS \ Trt}{MS \ Error} = 50.085$$
### ANOVA Table

<table>
<thead>
<tr>
<th></th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatment</td>
<td>2</td>
<td>29.404</td>
<td>14.702</td>
<td>50.085</td>
</tr>
<tr>
<td>Error</td>
<td>13</td>
<td>3.816</td>
<td>0.2935</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>15</td>
<td>33.32</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

$F \sim F$ distribution with $df_1 = 2$ and $df_2 = 13$

$p$-value = $P(F > 50.085)$

\[
= 1 - pf(50.0852,13), \quad \text{using R}
\]

\[
= 7.787145e-07
\]

#### Using R,

Result:

<table>
<thead>
<tr>
<th>Response: conemass</th>
<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>habitat</td>
<td>2</td>
<td>29.404</td>
<td>14.702</td>
<td>50.085</td>
<td>7.787e-07 ***</td>
</tr>
<tr>
<td>Residuals</td>
<td>13</td>
<td>3.816</td>
<td>0.2935</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

---

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

#### Code:

```r
dat=read.csv("15q22LodgepolePineCones.csv")
fit=aov(conemass~habitat,data=dat)
anova(fit)
```

Conclusion:

Since the $p$-value is super small, we reject $H_0$ with overwhelming evidence. It means that mean cone size differs between habitat types.

(d)

These 3 assumptions should be satisfied.

i. Independence of observations between and within samples. Complete Randomized Design

ii. In each treatment, observations come from a normal distribution or the sample size is large.

iii. Equal variances. The population standard deviations of the observations are equal among all treatments.
1) normality assumption

QQplot for residuals:

Since it looks like a straight line, the normality assumption is satisfied.

2) Equal variance

The smallest standard deviation is 0.47 and the largest one is 0.62. If these two standard deviations are very close, then we can say that the equal variance assumption is satisfied.

\[
\frac{0.62}{0.47} = 1.319149 < 2
\]

Thus, the equal variance assumption is likely satisfied.

(e)

Using R,

Result:

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

Fit: aov(formula = conemass ~ habitat, data = dat)

$habitat

<table>
<thead>
<tr>
<th>diff</th>
<th>lwr</th>
<th>upr</th>
<th>p adj</th>
</tr>
</thead>
<tbody>
<tr>
<td>island.present-island.absent</td>
<td>-2.82</td>
<td>-3.6862516</td>
<td>-1.9537484</td>
</tr>
<tr>
<td>mainland.present-island.absent</td>
<td>-2.78</td>
<td>-3.6462516</td>
<td>-1.9137484</td>
</tr>
<tr>
<td>mainland.present-island.present</td>
<td>0.04</td>
<td>-0.8647703</td>
<td>0.9447703</td>
</tr>
</tbody>
</table>
Code:

fit=aov(conemass~habitat,data=dat)
TukeyHSD(fit)

By hand,

Let the mean cone size be $\mu_1$ in the "island absent" environment, $\mu_2$ in the "island present" environment, and $\mu_3$ in the "mainland present" environment.

$s_p = \sqrt{0.2935} = 0.542$

<table>
<thead>
<tr>
<th></th>
<th>$\bar{y}_i - \bar{y}_j$</th>
<th>SE</th>
<th>$T_{ij}$</th>
<th>Critical value</th>
<th>Significantly different?</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 vs 2</td>
<td>2.82</td>
<td>0.33</td>
<td>8.6</td>
<td>2.64</td>
<td>Yes</td>
</tr>
<tr>
<td>1 vs 3</td>
<td>2.78</td>
<td>0.33</td>
<td>8.47</td>
<td>2.64</td>
<td>Yes</td>
</tr>
<tr>
<td>2 vs 3</td>
<td>-0.04</td>
<td>0.343</td>
<td>-0.117</td>
<td>2.64</td>
<td>No</td>
</tr>
</tbody>
</table>

$\bar{y}_1 - \bar{y}_2 = 8.9 - 6.04 = 2.82$

$\bar{y}_1 - \bar{y}_3 = 8.9 - 6.12 = 2.78$

$\bar{y}_2 - \bar{y}_3 = 6.04 - 6.12 = -0.04$

$SE_{\bar{y}_i - \bar{y}_j} = s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}} = 0.542 \sqrt{\frac{1}{6} + \frac{1}{5}} = 0.33$

$SE_{\bar{y}_i - \bar{y}_j} = s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_3}} = 0.542 \sqrt{\frac{1}{6} + \frac{1}{5}} = 0.33$

$SE_{\bar{y}_i - \bar{y}_j} = s_p \sqrt{\frac{1}{n_2} + \frac{1}{n_3}} = 0.542 \sqrt{\frac{1}{5} + \frac{1}{5}} = 0.343$

$T_{12} = \frac{\bar{y}_1 - \bar{y}_2}{SE_{\bar{y}_1 - \bar{y}_2}} = \frac{2.82}{0.33} = 8.6$

$T_{13} = \frac{\bar{y}_1 - \bar{y}_3}{SE_{\bar{y}_1 - \bar{y}_3}} = \frac{2.78}{0.33} = 8.47$

$T_{23} = \frac{\bar{y}_2 - \bar{y}_3}{SE_{\bar{y}_2 - \bar{y}_3}} = \frac{-0.04}{0.343} = -0.117$

Conclusion:

The differences in mean cone size between ‘island present’ and ‘island absent’ and between ‘mainland present’ and ‘island absent’ are significant.
### Table 2

<table>
<thead>
<tr>
<th>Source</th>
<th>d.f.</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatment</td>
<td>(1)</td>
<td>5.4336</td>
<td>(4)</td>
<td>(6)</td>
<td>(7)</td>
</tr>
<tr>
<td>Error</td>
<td>(2)</td>
<td>(3)</td>
<td>(5)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>229</td>
<td>73.9945</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(a)

(1) = # of groups - 1

= 4 - 1 = 3

(2) = df of Total - (1) = 229 - 3 = 226

(3) = SS Total - SS Trt = 73.9945 - 5.4336 = 68.5609

(4) = \( \frac{SS \text{ Trt}}{df \text{ of trt}} = \frac{5.4336}{3} = 1.8112 \)

(5) = \( \frac{SS \text{ Error}}{df \text{ of Error}} = \frac{68.5609}{226} = 0.3034 \)

(6) = \( \frac{MS \text{ Trt}}{MS \text{ Error}} = \frac{1.8112}{0.3034} = 5.97 \)

(7) = 1 - pf(5.97, 3, 226) = 0.00062 (using R)

Now, we carry out the hypothesis test.

H0: Medicine types do not differ in mean of minimal luminal diameter (\( \mu_1 = \mu_2 = \mu_3 = \mu_4 \)).

Ha: Medicine types differ in mean of minimal luminal diameter (at least one mean is different from one other mean).

Test statistics

F ~ F distribution with df₁ = 3 and df₂ = 226

p-value = P(F > 5.97)

= 1 - pf(5.97, 3, 226), using R

= 0.0006

Conclusion:

Since the p-value is extremely small, we reject H0 with very strong evidence. It means that at least one mean of the groups is significantly different from others. So, we can say that this treatment (type of medicine) influences on the "minimal luminal diameter".

(b)

\[ s_p = \sqrt{MS \text{ Error}} = \sqrt{0.3034} = 0.5508 \]
Let $y_1$ be the group of placebo and $y_2$ be the group of probucol + multivitamins.

$$SE_{\bar{y}_1,\bar{y}_2} = s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}} = 0.5508 \cdot \frac{1}{\sqrt{62} + \frac{1}{56}}$$

$$= 0.1015$$

$$\bar{y}_1 - \bar{y}_2 = 1.43 - 1.54 = -0.11$$

$$T_{12} = \frac{\bar{y}_1 - \bar{y}_2}{SE_{\bar{y}_1,\bar{y}_2}} = \frac{-0.11}{0.1015} = -1.084$$

Critical value $\approx 2.66$, (Using d.f. = 50, # of groups = 4)

$2.66 > 1.084$

Conclusion:

Since the critical value is larger than $T_{12}$, the p-value for this pairwise difference is $> .05$ and we cannot reject the null hypothesis $\mu_{\text{placebo}} = \mu_{\text{probucol+multivitamins}}$. Thus, we have no evidence that there is significant difference between means of 'placebo' and 'Probucol+Multivitamins'.

There is NO contradiction with the result of (a). This is because the F-test in ANOVA does not test the same hypothesis as the single test we did with the Tukey-Kramer method. With ANOVA, we showed that at least 2 of the 4 treatments do not have the same mean minimal luminal diameter. The Tukey-Kramer showed that there is no apparent difference between the placebo and the probucol+multivitamins treatments. So the treatments that significantly differ from each other must involve one of the other two treatments: probucol alone, or multivitamins alone. The story is not complete until we finish the Tukey-Kramer method and compare all pairs of treatments.