In The Name of God Statistical Inference HW#3 Amin Asadi 810196410

Problem 1

- a. False, because standard deviation of original sample is influenced by <u>skewness</u> but the standard deviation of the bootstrap distribution is not, because bootstrap distribution is closer to normal.
- b. False, in order to have better representativeness, it is better to use sample size larger than the size of original sample. We often do a resample of 10000 when the size of the original sample may be very small.
- c. False, it is created by resampling(with replacement) from the sample data, not from the population.
- d. True
- e. True
- f. True
- g. True
- h. True
- i. False, if beta is larger ---> alpha is smaller and thus the power will be smaller(because we will reject less often)
 ---> type II error will be larger so we must choose smaller beta.

Checking Conditions:

· Randomness → Independence,

$$\cdot$$
 n = 25 < 30 \rightarrow t-test

a)

Ho.:
$$\mu = 24.3$$
 $SE = \frac{S}{\sqrt{n}} = \frac{1.341}{\sqrt{25}} = \frac{0.26}{5}$

HA: $\mu \neq 24.3$
 $T = \frac{7 - \mu}{SE} = \frac{25.02 - 24.3}{0.26} = 2.71$
 $S = 1.34$
 P -value = $2 \times Pt(2.71, df = 25.1, lower tail)

 $= False$
 $\Rightarrow P$ value $\approx 0.0121 < 0.05$ $\longrightarrow reject Ho$$

b)

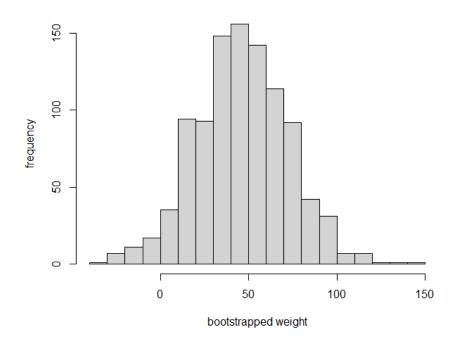
interval:
$$92 \pm SE \times t_{24,0.975}^{*} = 25.02 \pm 0.26 \times 1.95$$

 $\rightarrow interval = (24.47413, 25.58187)$

a.

```
1 #a
 2 \quad \text{num\_reps} = 1000
 3 data = read.csv('Chick.csv')
 4 s1 <- data[data$feed == 'casein', 'weight']
5 s2 <- data[data$feed == 'meatmeal', 'weight']
 6
 7
    n1 <- length(s1)
 8
   n2 <- length(s2)
 9
10 boot_dist = c()
    boot_stats = c()
11
12 - for(i in (1:num_reps)) {
      smp1 = sample(s1, n1, rep=T)
13
      smp2 = sample(s2, n2, rep=T)
14
15
      diff_of_means = mean(smp1)-mean(smp2)
16
      smp\_SE = sqrt(var(smp1)/n1 + var(smp2)/n2)
      boot_dist = c(boot_dist, diff_of_means)
17
18
      boot_stats = c(boot_stats, diff_of_means / smp_SE)
19 - }
20
21 hist(boot_dist, breaks = 20)
```

distribution of bootstrap weights



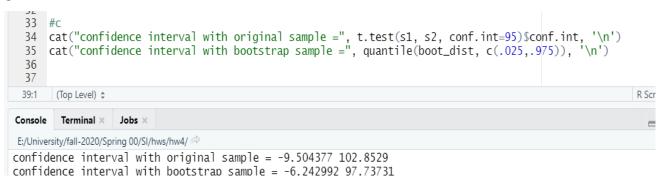
Result: We can see from the distribution that it is close to normal and is roughly symmetric.

b.

```
23
      #calculating the pvalue with original sample
p.value.original = t.test(s1, s2)$p.value
  26 cat("p-value with original sample =", p.value.original, '\n')
  27
  28 #calculating the pvalue with bootstrap samples
      orig.statistic <- t.test(s1, s2)$statistic
      p.value.bootstrap = mean(boot_stats - mean(boot_stats) > orig.statistic)
      cat("p-value with bootstrap samples =", p.value.bootstrap, '\n')
  31
  32
 22:1
       (Top Level) $
        Terminal ×
                   Jobs ×
Console
E:/University/fall-2020/Spring 00/SI/hws/hw4/ A
> source('E:/University/fall-2020/Spring 00/SI/hws/hw4/3.R')
p-value with original sample = 0.09866222
p-value with bootstrap samples = 0.064
```

Result: As we can see here, the p-values are close. P-value with bootstrap samples is a bit less than the p-value of the original.

C.



Result: We can see here that the confidence interval with the bootstrap samples is smaller than the confidence interval with the original sample. This means that the result of the bootstrapping is more accurate.

Checking Conditions:

· Randomness → Independence,

$$\cdot$$
 n1, n2 < 30 \rightarrow t-test

$$n_1 = 10$$
 $n_2 = 13$ $n_{1,2}(30 \rightarrow t:test)$
 $df = n_1 + n_2 - 2 = 21$
 $H_0: M_1 - M_2 = 0$
 $H_A: M_1 - M_2 \neq 0$
 $x_1 - x_2 = 7.34$
 $x_2 = 6.84$
 $x_1 = 5.31$
 $SE = \sqrt{\frac{x_1^2 - x_2}{n_1 + n_2 - 2}} \frac{1}{(n_1 + n_2)}$
 $x_1 = \frac{7.34}{2.62} = 2.8$
 $x_2 = 6.84$
 $x_3 = 5.31$
 $x_4 = \frac{7.34}{2.62} = 2.8$
 $x_4 = \frac{7.34}{2.62} = 2.8$

If we didn't use pooled version of SE:

df = min(13-1, 10-1) = 9
SE = 2.53
T = 2.9

$$T_{9, 0.025} = 2.26$$

T < $T_{9, 0.025} \Rightarrow \text{reject H}_0$

Ho:
$$P_{es} > 0.3$$

Ha: $P_{es} > 0.3$

The larger of the sample size and actual mean the larger the power

Checking Conditions:

· Randomness → Independence,

$$\cdot$$
 n > 30 \rightarrow z-test

a.

Ho:
$$h = 7.5$$
 | $Z = \frac{7.2.7.5}{\frac{5}{5}} = \frac{-0.28}{\frac{1.6}{55}} = -1.29$
HA: $h < 7.5$ | $Z = \frac{7.2.7.5}{\frac{5}{55}} = \frac{-0.28}{\frac{1.6}{55}} = -1.29$
 $2 = 7.22$ | produce = 0.09 \rightarrow produce > 0.05
 $2 = 7.22$ | produce = 0.09 \rightarrow produce > 0.05
 $2 = 7.22$ | produce = 0.09 \rightarrow produce > 0.05

b.

$$p(type \text{ Il error}) = p(\text{rot reject } H_{\bullet} \mid J_{A} = 7.4)$$

$$= p(x) J_{\bullet} - Z_{\bullet,0}^{\bullet} \frac{\sigma}{\sqrt{n}})$$

$$= p(z) J_{\bullet} - 1.64 \times \frac{1.6}{\sqrt{55}} - J_{A}$$

$$= p(z) \frac{7.5 - 7.4}{1.6} - 1.64) = 0.8803$$

a.

 $H_0: \mu_1 = \mu_2 = \mu_3 \implies$ The average score is the same across all three groups

 H_{A} : The average score differ between at least one pair of groups

b.

SST =
$$\sum_{i=1}^{18} (J - \overline{J}) = 972311.1$$

SSG = $\sum_{i=1}^{18} n_i (\overline{J}_i - \overline{J}) = 152477.8 \rightarrow MSG = \frac{SSG}{2} = 76238.9$
SSE = SST - SSG = 819833.3 $\rightarrow MSE = \frac{SSE}{15} = 54655.55$
F = $\frac{MSG}{MSE} = 1.394898$
 $\rightarrow Pr(F) \approx 0.278$

		Df	Sum Sq	Mean Sq	F value	Pr(>F)
Group	Class	3-1 = 2	152477.8	76238.9	1.394898	0.2782289
Error	Residuals	17-2 = 15	819833.3	54655.55		
	Total	18-1 = 17	972311.1			

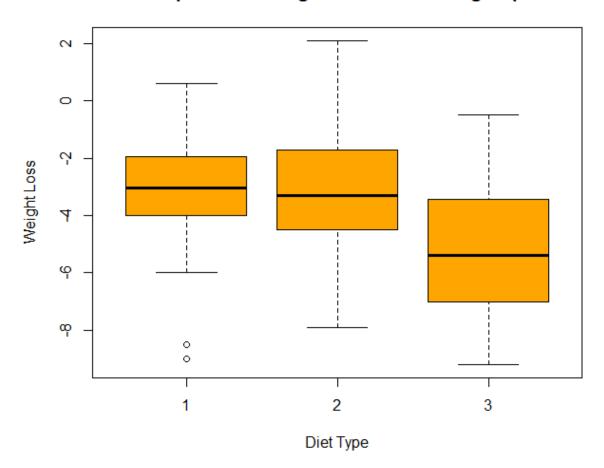
Because p-value is large(greater that 0.05) we fail to reject H₀

Problem 8

a.

Result:

Boxplot of the weight loss across the groups



Result: As we can see in the box plot, the means of groups 1 and 2 are very close to each other and they are different from the mean of group3

8. b,c

Result: As we can see, the F-value is equal to 0.00323 which is smaller than 0.05 so the null hypothesis is rejected. So as we expected, it indicates that there is some difference between some two groups.

d.

```
17
      TukeyHSD(anova.result)
  18
  19
 17:1
      (Top Level) $
Console
       Terminal ×
                  Jobs ×
E:/University/fall-2020/Spring 00/SI/hws/hw4/ A
> TukeyHSD(anova.result)
  Tukey multiple comparisons of means
    95% family-wise confidence level
Fit: aov(formula = weight_loss ~ as.factor(Diet), data = data)
$`as.factor(Diet)`
                      lwr
2-1 0.2740741 -1.332467 1.8806155 0.9124737
3-1 -1.8481481 -3.454690 -0.2416067 0.0201413
3-2 -2.1222222 -3.680796 -0.5636481 0.0047819
```

Result:

- Hypothesis for each two groups a and b is:
 - H₀: The means of group a and b are equal
 - H_A: There is a difference between means of group a and b
- Level of significance for all tests is alpha = 0.05
 - As we can see, the p-value of the comparison between groups 1-2 is large ---> H₀: Not rejected
 - As we can see, the p-value of the comparison between groups 1-3 is less than 0.05 ---> H₀: rejected
 - As we can see, the p-value of the comparison between groups 2-3 is less than 0.05 ---> H₀: rejected

The results is in confirmation with the box plots---> we do have evidence for a significant difference between groups 1-3 and 2-3.

 As we can see in the pairwise comparison results, the estimated differences between means of groups 1-2, 3-1, 3-2 is written in column "diff"

(We have been taught in the Statistical Inference class that alpha for pairwise comparison should be 0.05 divided by 3 but here it is 0.05)