Question 1

H0 : Variance = 0.01
H1: Variance > 0.01
It is a normal distribution, we will divide assumed standard deviation of $0.2/2 = 0.1$. Hence, variance is 0.01.

Since the computed statistics of 92.16 is greater than chi square value of 23.68, the null hypothesis is rejected.

Output 1: Q1 R Code Output

```
> data_q1 <- read.csv("Q1.csv")
> given_sd = 0.1
> given_variance = given_sd * given_sd
> given_variance
[1] 0.01
> sample_var <- var(data_q1$ ..gain_loss)
> SS <- sample_var*14
> X_2 = SS/given_variance
> X_2
[1] 92.16933
> df = 14
> chi_sq = qchisq(0.95,df)
> chi_sq
[1] 23.68479
```

Question 2

$H0$: Delta = 0
$H1$: Mean New > Mean Standard

P value of 0.98 > 0.05, we do not reject the NULL hypothesis. Hence, there is not enough evidence to claim that the new method is better than the standard method.

Output 2: Q2 R Code Output

```
> teaching <- read.csv("teachers.csv")
> t.test(teaching$New,teaching$Standard,paired = F,
+        alternative = "greater")

        Welch Two Sample t-test

data:   teaching$New and teaching$Standard
```

```
t = −2.3066, df = 28.839, p−value = 0.9858
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 −5.047475        Inf
sample estimates:
mean of x mean of y
 18.54375  21.45000
```

Question 3
a)
H0 : Delta = 0
H1: Mean New $\neq MeanStandard$

Pvalue < 0.05, we do reject the NULL hypothesis. There is enough evidence that the new technology is better than the standard technology.

Output 3: Q3(a) R Code Output

```
> p1 = 74/150
> p2 = 73/91
> x1 = 74
> x2 = 73
> n1 = 150
> n2 = 91
> alpha = 0.05
> p_hat = (x1+x2)/(n1+n2)
> z_val = (p1−p2)/sqrt(p_hat*(1−p_hat)*(1/n1+1/n2))
> z_val
[1] −4.765629
> pnorm(z_val)
[1] 9.413283e−07
```

b)
H0 : Delta = 0
H1: Mean Age New $\neq MeanStandard$

pvalue < 0.05, we reject the NULL hypothesis, hence the ages in the groups are not same.

Output 4: Q3(a) R Code Output

```
> s1_age_mean = 5.73
> s1_size = 150
```

```
> s2_age_mean = 9.02
> s2_size = 91
> SE <- sqrt((6.15^2/s1_size)+(6.10^2/s2_size))
> t <- (5.73-9.02)/SE
> t
[1] -4.046489
> df = s1_size + s2_size - 2
> pt(t,df)
[1] 3.511523e-05
```

c)
We got the better results using new technology probably because the children in the new technology group were older than the ones in the standard technology.

Question 4

H0: ud = 0
H1: ud < 0
This is a paired test.

Critical Value for degree of freedom = 7 and alpha = 0.01 = -3.0
t stat value of -2.3407 > -3.00 , we cannot reject the NULL hypothesis.
Also, p value of 0.0259 > 0.01, we do not reject the NULL hypothesis.

There is not enough evidence to conclude that the treatment increased the mean number of surviving fish.

Output 5: Q4 R Code Output

```
> Untreated <- c(5,1,1.8,1,3.6,5,2.6,1)
> treated <- c(5,5,1.2,4.8,5,5,4.4,2)
> alpha = 0.01
> critical_t_val = -3.00
> t.test(Untreated,treated,paired = TRUE,conf.level = 0.99,
alternative = "less")


        Paired t-test

data:  Untreated and treated
t = -2.3407, df = 7, p-value = 0.0259
alternative hypothesis: true difference in means is less than 0
99 percent confidence interval:
      -Inf 0.4001223
```

```
sample estimates:
mean of the differences
                -1.425
```

Question 5

Assuming normal distribution

H0 : Mean = 0.10
H1: Mean < 0.10

pvalue of 0.99 > 0.05, hence we do not reject the NULL hypothesis. There is not enough evidence to conclude that less than 10% of the customers drink another brand.

Output 6: Q5 R Code Output

```
> p = 0.10
> p_hat = 18/100
> n = 100
> SD <- sqrt(p*(1-p)/n)
> SD
[1] 0.03
> z_score = (p_hat - p)/SD
> z_score
[1] 2.666667
> ans_a = pnorm(z_score)
> ans_a
[1] 0.9961696
```