1a)
Command:

```
# Create vector for sodium data
sodium <- c(510, 520, 515, 516, 517, 519, 522, 510)
t.test(sodium, conf.level = 0.96)
```

Output:

```
One Sample t-test

data:  sodium
t = 332.57, df = 7, p-value = 5.868e-16
alternative hypothesis: true mean is not equal to 0
96 percent confidence interval:
 512.2192 520.0308
sample estimates:
mean of x
  516.125
```

1b) As 515 lies within the 96% Confidence Interval Range, yes, it is a reasonable estimate for μ.

1c) We want to test for $H_0 : \mu = 520 \quad \text{vs.} \quad H_1 : \mu < 520$
Command:

```
t.test(sodium, mu = 520, alternative = "less")
```

Output:

```
        One Sample t-test

data:  sodium
t = -2.4969, df = 7, p-value = 0.02059
alternative hypothesis: true mean is less than 520
95 percent confidence interval:
     -Inf 519.0653
sample estimates:
mean of x
  516.125
```

1d) From the test in part (c), R's output shows: $t = -2.4969$
1e) From the test in part (c), R's output shows: $p - value = 0.02059$
1f) As our $p - value$ is $0.02059 \geq 0.01$, we FAIL to reject the null hypothesis H_0

2a) Command we will use `binom.test(...)` with `conf.level = 0.995`:

```
binom.test(x = 27, n = 673, conf.level = 0.995)
```

Output:

```
        Exact binomial test

data:  27 and 673
number of successes = 27, number of trials = 673, p-value < 2.2e-16
alternative hypothesis: true probability of success is not equal to 0.5
99.5 percent confidence interval:
 0.02200314 0.06618312
sample estimates:
probability of success
            0.04011887
```

2b) Now testing $H_0 : p = 0.03 \quad \text{vs.} \quad H_1 : p > 0.03$:
Command:

```
binom.test(x = 27, n = 673, p = 0.03, alternative = "greater")
```

Output:

```
        Exact binomial test

data:  27 and 673
number of successes = 27, number of trials = 673, p-value = 0.08139
alternative hypothesis: true probability of success is greater than 0.03
95 percent confidence interval:
 0.02846628 1.00000000
sample estimates:
probability of success
            0.04011887
```

2c) From the test in part (b), R's output shows: $p - value = 0.08139$

2d) Since the $p - value = 0.08139$ is greater than 0.05, i.e. $0.08139 > 0.05$ we fail to reject H_0. Consequently, we have only *weak or no evidence* against the null hypothesis (i.e., that the true proportion is 0.03 at the 5% significance level.