ST551: HOMEWORK 3

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Question 1

Part A

```r
# Initialize values
X <- 9
n <- 15
p <- 0.4
# Perform the two-sided binomial test
result <- binom.test(X, n, p, alternative = "two.sided")
p_val1 <- result$p.val
print(paste0("p-value of two-sided binomial test = ",p_val1))
```

[1] "p-value of two-sided binomial test = 0.122161408933888"

```r
# Perform the cumulative probability test
prob <- dbinom(0:n, size = n, prob = p)
cum_prob <- sum(prob[0:X])
p_val2 <- 1 - cum_prob
print(paste0("The cumulative probability when X <= 9 results in a p-value = ",
             p_val2))
```

[1] "The cumulative probability when X <= 9 results in a p-value = 0.095047408156672"

Part B

Yes, we fail to reject the null hypothesis @ p = 0.4

```r
alpha <- 0.05
if (p_val1 < alpha) {
  print(paste("p_val =", p_val1,
              "We reject the null  = 0.4"))
} else {
  print(paste("p_val =", p_val1,
              "We fail to reject the null  = 0.4"))
}
```

```
[1] "p_val = 0.122161408933888 We fail to reject the null  = 0.4"
```

```r
if (p_val2 < alpha) {
  print(paste("p_val =", p_val2,
              "We reject the null = 0.4"))
} else {
  print(paste("p_val =", p_val2,
              "We fail to reject the null = 0.4"))
}
```

```
[1] "p_val = 0.095047408156672 We fail to reject the null = 0.4"
```

Part C

```r
# Initialize values
X <- 9
n <- 15
# Calculate the confidence interval
result <- binom.test(X, n, conf.level = 0.95)
conf_interval <- result$conf.int[1:2]
print(paste0("Confidence Interval (95%): [",
             round(conf_interval[1], 3), " <-> ",
             round(conf_interval[2], 3), "]"))
```

```
[1] "Confidence Interval (95%): [0.323 <-> 0.837]"
```

Part D

```r
# Change the null hypothesis to 0.33
p <- 0.33
result2 <- binom.test(X, n, p, alternative = "two.sided")
p_val <- result2$p.val
print(paste0("p-value of two-sided binomial test = ",p_val))
```

```
[1] "p-value of two-sided binomial test = 0.0495120138811161"
```

```r
alpha <- 0.05
if (p_val < alpha) {
  print(paste("p_val =", p_val,
              "Reject the null = 0.33"))
} else {
  print(paste("p_val =", p_val,
              "We fail to reject the null = 0.33"))
}
```

```
[1] "p_val = 0.0495120138811161 Reject the null = 0.33"
```

Part E

The p-value of 0.04951 and the 95% confidence interval

$$0.323, 0.837$$

both indicate significant evidence against the null hypothesis that the proportion is 0.33, aligning with the decision to reject the null hypothesis.

Part F

The explanation is given through the comments below!

```r
# We have 9 successes out of 15 trials.
X <- 9
n <- 15
conf <- 0.95

# Calculate the observed proportion
p <- X / n
# Standard error
SE <- sqrt(p * (1 - p) / n)
# Critical value (z)
z <- qnorm(1 - (1 - conf) / 2)
# Margin of error
ME <- z * SE

# Wilson score confidence interval
lower_bound <- p - ME
upper_bound <- p + ME

# Print the confidence interval
print(paste0("Confidence Interval (", 100 * conf, "%): [",
             round(lower_bound, 3), " <-> ", round(upper_bound, 3), "]"))
```

```
[1] "Confidence Interval (95%): [0.352 <-> 0.848]"
```

Question 2

The usual z-test (the score test) for a binomial proportion to test $H0 : p = p_0$ uses test statistic:

$$z(p_0) = \frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}}$$

where $\hat{p} = X/n$ is the nle proportion. For a two-sided level α test, the null hypothesis is rejected when $|z(p_0)| > z_{1-\alpha/2}$. Invert this test to obtain a confidence interval for p : solve for p_0 that would not be rejected at level α.

Compare the center and length of the resulting interval to the more commonly used Wald interval:

$$\hat{p} \pm z_{1-\alpha/2}\sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

Solving for p_0

So, we want to find values of p_0 such that:

$$\left| \frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}} \right| \leq z_{1-\alpha/2}$$

Square both sides

$$\left(\frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}} \right)^2 \leq \left(z_{1-\alpha/2} \right)^2$$

Simplify

$$\frac{(\hat{p} - p_0)^2}{\frac{p_0(1-p_0)}{n}} \leq \left(z_{1-\alpha/2} \right)^2$$

Now we cross-multiply

$$n(\hat{p} - p_0)^2 \leq p_0(1-p_0) \left(z_{1-\alpha/2} \right)^2$$

Next, move p_0 to the left side:

$$p_0(1-p_0) \left(z_{1-\alpha/2} \right)^2 - n(\hat{p} - p_0)^2 \geq 0$$

This is a quadratic inequality in terms of p_0. We can solve it for p_0 using the quadratic formula. The solutions will be the values of p_0 for which the null hypothesis is not rejected at level α. The resulting interval is our confidence interval for p. Beware! Solving this would take forever, but hopefully this explains enough on how to determine the values of p_0
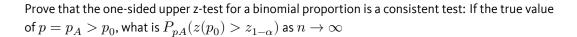
Comparison with Wald Interval

The Wald interval for a proportion is given by:

$$\widehat{p} \pm z_{1-\alpha/2}\sqrt{\frac{\widehat{p}(1-\widehat{p})}{n}}$$

The Wald interval assumes a normal distribution for the nle proportion and centers on it, while the z-test interval, based on the actual binomial distribution, centers on a parameter solution and tends to be wider, better accounting for the binomial nature than the Wald interval, which assumes normality but might not be as reliable for small nle sizes.

Question 3

Prove that the one-sided upper z-test for a binomial proportion is a consistent test: If the true value of $p = p_A > p_0$, what is $P_{pA}(z(p_0) > z_{1-\alpha})$ as $n \to \infty$

Proof of Consistency for the One-Sided Upper Z-Test

Let's explore the idea of consistency in the one-sided upper z-test when we have a really big nle size, denoted as "n." We can use the Central Limit Theorem to help us understand what happens to the nle proportion $\hat{p}$." As "n" gets larger and larger, $\hat{p}$ starts behaving a lot like a normal distribution with an average of "p" and a variance that becomes super tiny, making $\hat{p}$ essentially the same as "p". This makes the test statistic "z" simpler and can be expressed as:

$$z = \frac{p - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}}$$

Moreover, with the nle size growing significantly, the denominator $\sqrt{\frac{p_0(1-p_0)}{n}}$ becomes remarkably small, driving the test statistic z towards infinity. As a result, z approaches infinity as n keeps increasing.

Now, the critical value $z_{1-\alpha}$ remains constant and doesn't change with varying nle sizes. However, as n tends towards infinity, the test statistic z continues to rise and eventually surpasses the fixed critical value $z_{1-\alpha}$ with a certainty of 1.

Thus, when we deal with a substantially large nle size, the probability of rejecting the null hypothesis $P_{p_A}(z(p_0) > z_{1-\alpha})$ reaches a value of 1. This strong convergence showcases the reliability and consistency of the one-sided upper z-test in assessing a binomial proportion, particularly when the true proportion $p = p_A > p_0$.

Question 4

Theoretical approach

1. To find the true probability p of a sample from a Normal(1, 1) distribution being greater than the hypothesized median $m_0 = 0$, we need to use the CDF.

   We can calculate the CDF of the Normal(1, 1) distribution:

   $$p = P(X > 0) = 1 - P(X \leq 0) = 1 - \phi\left(\frac{0-1}{1}\right) = 1 - \phi(-1)$$

   where $\phi(z)$ represents the CDF of a standard normal distribution.

2. We know that in the sign test, if p equals the hypothesized value (in our case, $H_0 = 0.5$), it implies the observed proportion $\hat{p}$ being significantly different from what's expected under the null hypothesis.

   The critical values of $\hat{p}$ can be derived by solving for z:

   $$z < -\phi^{-1}\left(\frac{\alpha}{2}\right)$$
   $$z > \phi^{-1}\left(\frac{\alpha}{2}\right)$$

3. Given everything from above, the probability represents the power of the sign test. It can be expressed as the probability that $\hat{p}$ lies within the range that leads to rejection, given the true value of p.

Therefore, this process gives us a tool for detecting differences from the hypothesized median.

Simulation Approach

```r
set.seed(124)

# Parameters
pop_med <- 1
pop_sd <- 1
n <- 30
n_sim <- 10000
alpha <- 0.05
null_rejection_count <- 0

# Simulation loop
for (i in 1:n_sim) {
  # Generate a random sample from Normal(1, 1)
  samp <- rnorm(n, mean = pop_med, sd = pop_sd)

  # Compute the sample median
  samp_med <- median(samp)

  # Perform a z-test to test whether the population median is 0
  z_stat <- (samp_med - 0) / (pop_sd / sqrt(n))

  # Calculate the p-value for the z-test
  p_val <- 2 * (1 - pnorm(abs(z_stat)))

  # Check if the null hypothesis is rejected (p-value < alpha)
  if (p_val < alpha) {
    null_rejection_count <- null_rejection_count + 1
  }
}

# Calculate the proportion of simulations that reject the null hypothesis
prop_rejected <- null_rejection_count / n_sim
print(paste("Proportion of null rejections: m = 0:", prop_rejected))
```

```
[1] "Proportion of null rejections: m = 0: 0.9985"
```