

(note: Latex for some reason throws a fit when I use the minus sign, so I switched all minus signs with the words 'minus sign')

Part 1: Compare to known click rate

- (a) Derive expressions for $E[\bar{X}]$ and $\text{var}[\bar{X}]$ under the null hypothesis in terms of p_a . You will need to use the properties of expectations and variances described below. Here, I give you the derivation for $E[\bar{X}]$, you need to do the same for $\text{var}[\bar{X}]$.

$$E(\bar{x}) = p_a \quad V(\bar{x}) = V\left(\frac{1}{n} \sum_{i=1}^n x_i\right) = \frac{1}{n^2} V\left(\sum_{i=1}^n x_i\right) = \frac{1}{n^2} \sum_{i=1}^n V(x_i) = \frac{1}{n^2} \sum_{i=1}^n p_a(1 - p_a) = \frac{p_a(1 - p_a)}{n}$$

- (b) Based on your derivation, compute values for $E[\bar{X}]$ and $\text{var}[\bar{X}]$ based on $p_a = 0.5$ and $n = 50$. Use R or python to do this.

```
expected <- pa
variance <- (pa * (1-pa)) / n

cat("Variance: ", variance, "\n")

## Variance: 0.005

cat("Expected Value: ", expected, "\n")

## Expected Value: 0.5
```

- (c) Using the result above, you can now use the CLT by approximating the distribution of \bar{X} as $N(E[\bar{X}], \sqrt{\text{var}(\bar{X})})$. Based on this approximation, compute $P(\bar{X} > p_B)$. Use the R function `pnorm`, or `norm.cdf` in `scipy.stats` to compute this.

```
pb <- 0.6
N <- pnorm(pb, expected, sqrt(variance))
cat("P(mean(x) > 0.6) =", 1 - N)

## P(mean(x) > 0.6) = 0.0786496
```

- (d) Should you reject the null hypothesis $p_B \leq p_A$? Why?

We can only reject the null hypothesis if $P(\bar{x} > 0.6) < \alpha$. In this case, $\alpha = 0.05 < P(\bar{x} > 0.6)$, so we cannot reject the null hypothesis.

- (e) What if you had observed the same $p_B = 0.6$ but with $n = 100$ samples. Should you reject the null hypothesis in this case? Why?

```
variance_100 <- (pb * (1-pb)) / 100

N <- pnorm(pb, expected, sqrt(variance_100))
cat("P(mean(x) > 0.6) =", 1 - N)

## P(mean(x) > 0.6) = 0.02061342
```

Yes. If $n = 100$, $P(\bar{x} > 0.6) < \alpha$, so we should reject the null hypothesis in this scenario.

- (f) What is the smallest value p_B you would reject the null hypothesis with $n = 100$. Use the `qnorm` function in R or `norm.ppf` in `scipy.stats` for this. Denote this smallest value as q_B .

```
variance_100 <- (pb * (1-pb)) / 100

qb <- qnorm(0.95, pb, sqrt(variance_100))
cat("smallest value =", qb)
```

```
## smallest value = 0.680581
```

- (g) Based on (f), the smallest detectable improvement for $p_A = 0.5$ with $n = 100$ is then q_B (minus sign) p_A . What is the smallest detectable improvement in your experiment (that is, with $n = 50$)?

```
qb <- qnorm(0.95, expected, sqrt(variance))

improvement <- qb - pa
cat('Smallest detectable improvement =', improvement)

## Smallest detectable improvement = 0.1163087
```

Part 2: Compare to known click rate

- (a) What are the values of $E[\bar{X}]$ and $\text{var}(\bar{X})$ under the null hypothesis in this case.

```
expected <- pa
variance <- (pa*(1-pa))/n

cat("E(mean(x)) = ", expected, "\n")

## E(mean(x)) = 0.75
cat("var(mean(X)) = ", variance, "\n")

## var(mean(X)) = 0.00375
```

- (b) Based on the CLT approximation, compute $P(\bar{X} > p_B)$ under the null hypothesis.

```
approx <- 1 - pnorm(pb, expected, sqrt(variance))
cat("P(mean(x) > pb) =", approx)

## P(mean(x) > pb) = 0.9928471
```

- (c) Should you reject the null hypothesis $p_B \leq 0.75$? Why?

No. 0.9928471 is significantly greater than 0.05.

- (d) What if you had observed the same $p_B = 0.6$ but with $n = 100$ samples. Should you reject the null hypothesis in this case? Why?

```
n <- 100

variance <- (pa*(1-pa))/n

approx <- 1 - pnorm(pb, expected, sqrt(variance))
cat("P(mean(x) > pb) =", approx)

## P(mean(x) > pb) = 0.999734
```

No. The odds actually go up.

- (e) What is the smallest value p_B you should reject the null hypothesis with $n = 100$. Denote this smallest value as q_B .

```
variance_100 <- (pa * (1-pa)) / 100

qb <- qnorm(.95, expected, sqrt(variance_100))
cat("smallest value =", qb)
```

```
## smallest value = 0.8212243
```

- (f) Based on (e), the smallest detectable improvement for $p_A = 0.75$ with $n = 100$ is then q_B (minus sign) p_A . What is the smallest detectable improvement in your experiment ($n = 50$)?

```
n <- 50

variance <- (pa * (1-pa)) / n

qb <- qnorm(0.95, expected, sqrt(variance))

improvement <- qb - pa
cat('Smallest detectable improvement = ', improvement)

## Smallest detectable improvement = 0.1007263
```

Part 3

Consider your answers for parts (1g) and (2f). Is the smallest detectable improvement in Question (1g) larger or smaller than in Question (2f)? Explain why this makes sense mathematically.

The smallest detectable improvement is larger in 1g than in 2f. This makes sense because we've decreased the variance in part 2 by raising the threshold (p_A). We can't improve as much when there's less variance.

Part 4: Comparing to estimated click rate p_A .

- (a) Derive expressions for $E[Y]$ and $\text{var}(Y)$ under the null hypothesis in terms of $p_A = p_B = p$. You will need to use the properties of expectations and variances described below. Here, I give you the derivation for $E[Y]$, you need to do the same for $\text{var}(Y)$.

$$E[Y] = 0$$

$$\text{var}[Y] = \text{var}[\overline{X_B} - \overline{X_A}] = \text{var}[\overline{X_B}] + \text{var}[\overline{-X_A}] = \frac{p_B(1-p_B)}{n} + \frac{p_A(1-p_A)}{n} = \frac{p_B(1-p_B) + p_A(1-p_A)}{n}$$

- (b) Based on your derivation, compute values for $E[\overline{X}]$ and $\text{var}[\overline{X}]$ based on $p_A = 0.5$ and $n = 50$. Use R or python to do this.

```
n <- 100
na <- 55
sa <- 35
nb <- 45
sb <- 35

estimate_mean <- ((sa + sb) / (nb + na))

cat('mean =', estimate_mean)

## mean = 0.7
```

- (c) Now that you have an estimate of p , compute a value for $\text{var}(Y)$.

```
variance <- ((estimate_mean*(1-estimate_mean)) +
             estimate_mean*(1-estimate_mean)) / n

cat('variance =', variance)
```

```
## variance = 0.0042
```

(d) What is your estimate y of p_B (minus sign) p_A based on the data your recorded for this experiment?

```
pb <- sb / nb
```

```
pa <- sa / na
```

```
p <- pb - pa
```

```
cat('y_hat =', p)
```

```
## y_hat = 0.1414141
```

(e) Using the CLT approximation, what is $P(Y > y)$

```
probability = 1 - pnorm(p, 0, sqrt(variance))
```

```
cat("Our fantastic probability is", probability)
```

```
## Our fantastic probability is 0.01455227
```

(f) Can you reject the null hypothesis of no improvement in this case? Why? Remember, we are using $\alpha = 0.05$.

Yes. Our fantastic probability is less than 0.05, so we should reject the null hypothesis.