Homework 5

Kai Aragaki

Problem 1

A

Power can be calculated as such:

$$Power = Pr\Big(Z > C - \frac{\Delta}{\sqrt{\frac{\sigma_A^2}{n} + \frac{\sigma_B^2}{m}}}\Big) + Pr\Big(Z < -C - \frac{\Delta}{\sqrt{\frac{\sigma_A^2}{n} + \frac{\sigma_B^2}{m}}}\Big)$$

So if we assume $\Delta = 1$ and both $\sigma = \Delta$, $n = m$ and set $Power = 0.8$ then

$$0.8 = Pr\Big(Z > C - \frac{\Delta}{\sqrt{\frac{2\Delta^2}{n}}}\Big) + Pr\Big(Z < -C - \frac{\Delta}{\sqrt{\frac{2\Delta^2}{n}}}\Big)$$

$$0.8 = Pr\Big(Z > C - \frac{1}{\sqrt{\frac{2}{n}}}\Big) + Pr\Big(Z < -C - \frac{1}{\sqrt{\frac{2}{n}}}\Big)$$

$$0.8 = Pr\Big(Z > C - \sqrt{\frac{n}{2}}\Big) + Pr\Big(Z < -C - \sqrt{\frac{n}{2}}\Big)$$

Though not given, it's reasonable to assume that our desired $\alpha = 0.05$, so our critical values C become

$$0.8 = Pr\Big(Z > 1.96 - \sqrt{\frac{n}{2}}\Big) + Pr\Big(Z < -1.96 - \sqrt{\frac{n}{2}}\Big)$$

We then set a threshold value that, when we draw from a normal distribution, we expect to get a value more extreme than it 80% of the time on average. To select such value, we assume that the probability of selecting a value less extreme than these 'thresholds' contributes very minimally to the over 80% power, so much so that we can approximate thusly:

$$0.8 \approx Pr\Big(Z > 1.96 - \sqrt{\frac{n}{2}}\Big)$$

Finding this value is then simple:

```r
z <- qnorm(0.2)
```

The resultant Z is roughly -0.84. This is the value that when we sample from a $Normal(0, 1)$ distribution, we would expect to get values greater than it on average 80% of the time.

Calculating n, then:

$$Z > 1.96 - \sqrt{\frac{n}{2}}$$

$$2(-Z + 1.96)^2 < n$$

so,

```
n_min <- 2 * (-z + 1.96)^2
```

The minimum whole value of n is 16. That is the number of ELISAs we would need per group to obtain a power of 80%.

B

If we only ran 10 ELISAs per group, then

$$Power \approx Pr(Z > 1.96 - sqrt10/2)$$

So our threshold value is

```
z_min <- 1.96 - sqrt(10/2)
```

Giving a probability of

```
p <- pnorm(z_min, lower.tail = FALSE)
```

Approximately 61%

C

Our critical value then shifts to account for a single tailed hypothesis:

```
cv <- qnorm(0.05, lower.tail = FALSE)
```

So our threshold is now:

```
z_min <- cv - sqrt(10/2)
```

Giving a probability of

```
p <- pnorm(z_min, lower.tail = FALSE)
```

Approximately 72%