R2S1Chpt

R2-6

```
N0<-4500
t<-400
N<-4000

# For part 1 where k is constant and the values of alpha are different
k<-800
alpha<-c(0.05, 0.02, 0.01)
ralpha<-qhyper(1-alpha, t, N0-t, k)

# Type II errors in the first part
(power<- (1-phyper(ralpha, t, N-t, k)))
```

```
## [1] 0.3193981 0.1950868 0.1318660
```

```
# For part 2 where the value of alpha is constant and the values of k are changing
k<-c(600, 800, 1000)
alpha<-0.05
ralpha<-qhyper(1-alpha, t, N0-t, k)

# Type II errors for the second part
(power<-(1-phyper(ralpha, t, N-t, k)))
```

```
## [1] 0.2508363 0.3193981 0.3776734
```

R2-8

```
z<-(250-336*0.7)/sqrt(336*0.7*0.3)
((1-pnorm(abs(z), 0, 1) + pnorm(-abs(z), 0, 1)))
```

```
## [1] 0.07808539
```

Now this means each of the tails have an area of 3.9%. Since both of them exceed 2.5% at the tails, we fail to reject the hypothesis

S1-8

To reject the hypothesis, the p-value needs to be less than the percentage that we are given. To calculate the p-value:

```
pbinom(20, 36, 0.7)
```

```
## [1] 0.04703824
```

Since the p value is less than 0.05, we can reject the hypothesis at the 5% level, but since it is greater than 0.01, we fail to reject it at the 1% level.