# Lab 1

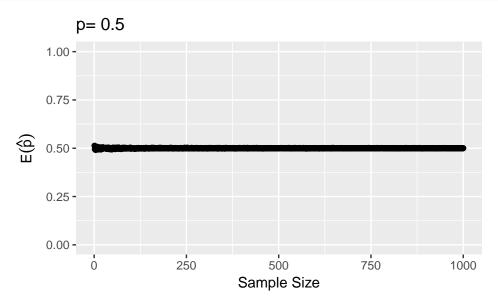
Harry Bendekgey (and Peter Brody-Moore) Math 153: Bayesian Statistics

January 25, 2018

# Problem 1

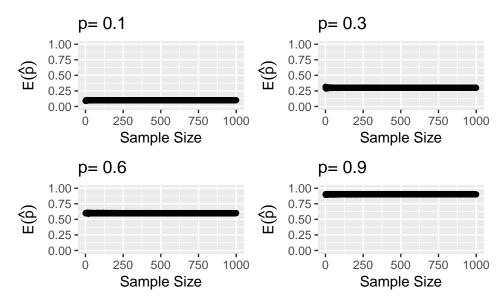
## Analyzing $E(\hat{p})$

We begin by imagining a simple binomial experiment. We want to visualize  $E(\hat{p})$  at various sample sizes. We set p = 0.5 and for every sample size between 1 and 1000 estimate  $E(\hat{p})$ :



We can see that  $E(\hat{p})$  is constant, and that even at the smallest sample sizes, it takes the value 0.5. We claim that  $E(\hat{p}) = p$ . This reflects the property we learned in class:  $E(\hat{\theta}_{MLE}) \to \theta$ .

To confirm our findings, we will run a similar experiment using other values for p:



This confirms our conjecture that  $E(\hat{p}) = p$  is constant. We can also prove this relationship mathematically:

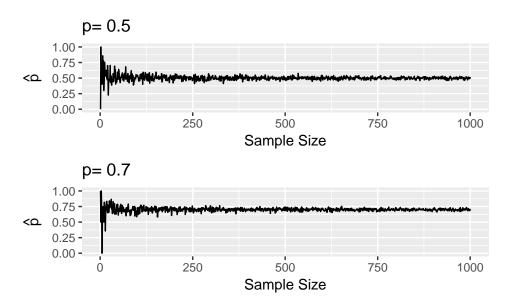
$$E(\hat{p}) = E\left(\frac{1}{n}\sum_{i=1}^{n} X_i\right) = \frac{1}{n}\sum_{i=1}^{n} E(X_i) = \frac{1}{n}\sum_{i=1}^{n} p = \frac{1}{n}(np) = p$$

#### Analyzing $\hat{p}$

We want to show that  $\hat{p}$  converges to p as n gets larger. We graph a single  $\hat{p}$  value for each sample size between 1 and 1000:

```
graph_phats <- function(p) {
    p_hats <- c()
    for (i in 1:length(sample_sizes)) {
        p_hats[i] <- rbinom(1, sample_sizes[i], p) / sample_sizes[i]
    }
    df <- data.frame(sample_sizes,p_hats)
    return(ggplot(df, aes(sample_sizes, p_hats)) +
        geom_line() +
        scale_y_continuous(limits = c(0,1)) +
        labs(x = "Sample Size", y = expression(hat(p)), title = paste("p=",p)))
}

ggarrange(graph_phats(0.5),graph_phats(0.7),ncol=1, nrow=2)</pre>
```



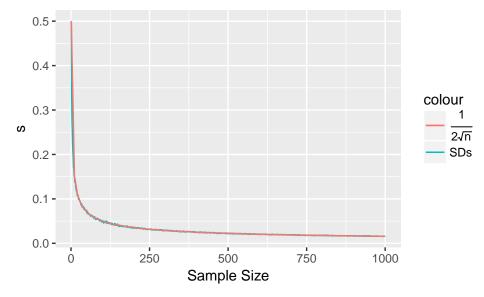
These results match our expectation: as the sample size gets larger,  $\hat{p}$  converges to p.

# Problem 2

#### Analyzing $s_{\hat{p}}$

Using the Central Limit Theorem, we approximate that  $\hat{p} \sim N(p, \sqrt{\frac{p(1-p)}{n}}^2)$ . In the case of p = 0.5 we expect the standard deviation to be  $\sqrt{\frac{0.5^2}{n}} = \frac{1}{2\sqrt{n}}$ . We can confirm that this is true by sampling many  $\hat{p}$  values at different sample sizes and see that it behaves like the equation  $f(x) = \frac{1}{2\sqrt{n}}$ 

```
sds <- c()
for (i in 1:length(sample_sizes)) {
   sds[i] <- sd(rbinom(1000, sample_sizes[i], 0.5) / sample_sizes[i])
}
df <- data.frame(sample_sizes,sds)
fun.1 <- function(x) 1/(2 * sqrt(x))
ggplot(df) +
   geom_line(aes(sample_sizes, sds, color="red")) +
   stat_function(fun = fun.1, aes(color="blue")) +
   scale_color_discrete(labels = c(expression(frac(1,2 * sqrt(n))), "SDs")) +
   labs(x = "Sample Size", y = "s")</pre>
```



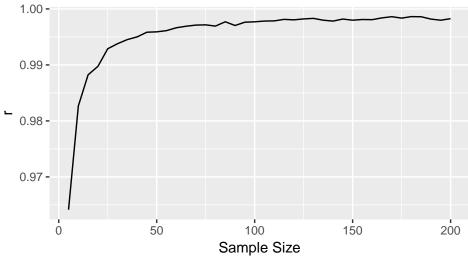
Here we can see that they are almost identical, supporting our claim.

# Analyzing the distribution of $\hat{p}$

We're also interested in if the  $\hat{p}$  values are distributed normally. We do this by constructing normal probability plots. This is done by ordering the data and comparing  $\hat{p}_i$  to  $E(\hat{p}_i)$  where  $\hat{p}_i$  is the  $i^{th}$  smallest  $\hat{p}$  from the distribution. If the data is normally distributed, we expect a linear normal probability plot. To test this hypothesis, we create a normal probability plot for each sample size of interest and calculate their correlation.

```
n <- seq(5,200,5)
cor_npp <- c()
for (i in 1:length(n)) {
   p_hats <- rbinom(1000, n[i], 0.5) / n[i]
   npp <- qqnorm(p_hats)
   cor_npp[i] <- cor(npp$x, npp$y)
}</pre>
```





Here we can see that the distribution of  $\hat{p}$ -values assymptotically approaches normality as the sample size gets bigger.

# Problem 3

## Comparing Bayesian Point Estimators to Maximum Likelihood Estimators

```
bayesian <- function(X){</pre>
  phat <- (sum(X)+10)/(length(X)+20)
  return(phat)
frequentist <- function(X){</pre>
  phat <- sum(X)/length(X)</pre>
  return(phat)
genX <- function(n,p){</pre>
  X <- rbinom(n=n,size=1,prob=p)</pre>
  return(X)
genBPE <- function(n,p){</pre>
  X \leftarrow genX(n,p)
  bpe <- bayesian(X)</pre>
  return(bpe)
genMLE <- function(n,p){</pre>
  X \leftarrow genX(n,p)
  mle <- frequentist(X)</pre>
  return(mle)
bpeMSE <- function(n,p){</pre>
  phats <- replicate(10000,genBPE(n,p)) # generates 10000 phats</pre>
  mse <- mean((phats-p)^2)</pre>
```

```
return(mse)
mleVar <- function(n,p){</pre>
  variance <- var(replicate(10000,genMLE(n,p))) # qenerates 10000 phats</pre>
  return(variance)
num <-c(10,100)
prob <-c(.25,.5,.75)
compare <- NULL # initialize dataframe</pre>
for (p in prob) { # loop through all n's and p's.
  for (n in num){
    mle_var <- mleVar(n,p)</pre>
    bpe_var <- bpeMSE(n,p)</pre>
    compare = rbind(compare, data.frame(n, p, mle_var, bpe_var))
compare
##
            p mle_var bpe_var
## 1 10 0.25 0.01867 0.02994
## 2 100 0.25 0.00184 0.00304
## 3 10 0.50 0.02541 0.00274
## 4 100 0.50 0.00248 0.00170
## 5 10 0.75 0.01851 0.03006
## 6 100 0.75 0.00184 0.00301
```

To compare the Bayesian Point Estimate to the Maximum Likelihood Estimator, we use the mean squared error of 10,000 randomnly generated  $\hat{p}$ 's for the BPE and the variance of 10,000 randomnly generated  $\hat{p}$ 's for the MLE. We compared these two estimators across different combinations of n and p. When looking at the data in the above table, it is clear that the BPE performs much better than the MLE when p=.5. This is likely because the BPE adds 10 to the numerator and 20 to the denominator, pushing our estimator towards .5. Similarly, the MLE performs better for p=.25 and p=.75 because the BPE is pushing away from these values. So, the BPE is preferable if the true value of p is close to .5, and the MLE is preferable otherwise for this given scenario.