# Lab 3: Intro to Decision Theory

*Rebecca C. Steorts and Xingyu Yan*

## Task 1

```r
# set seed
set.seed(123)

# data
sum_x = 1
n = 30
# prior parameters
a = 0.05; b = 1
# posterior parameters
an = a + sum_x
bn = b + n - sum_x
th = seq(0,1,length.out = 100)
like = dbeta(th, sum_x+1,n-sum_x+1)
prior = dbeta(th,a,b)
post = dbeta(th,sum_x+a,n-sum_x+b)
```

We now consider the loss function.

```r
# compute the loss given theta and c
loss_function = function(theta, c){
  if (c < theta){
    return(10*abs(theta - c))
  } else{
    return(l = abs(theta - c))
  }
}
```

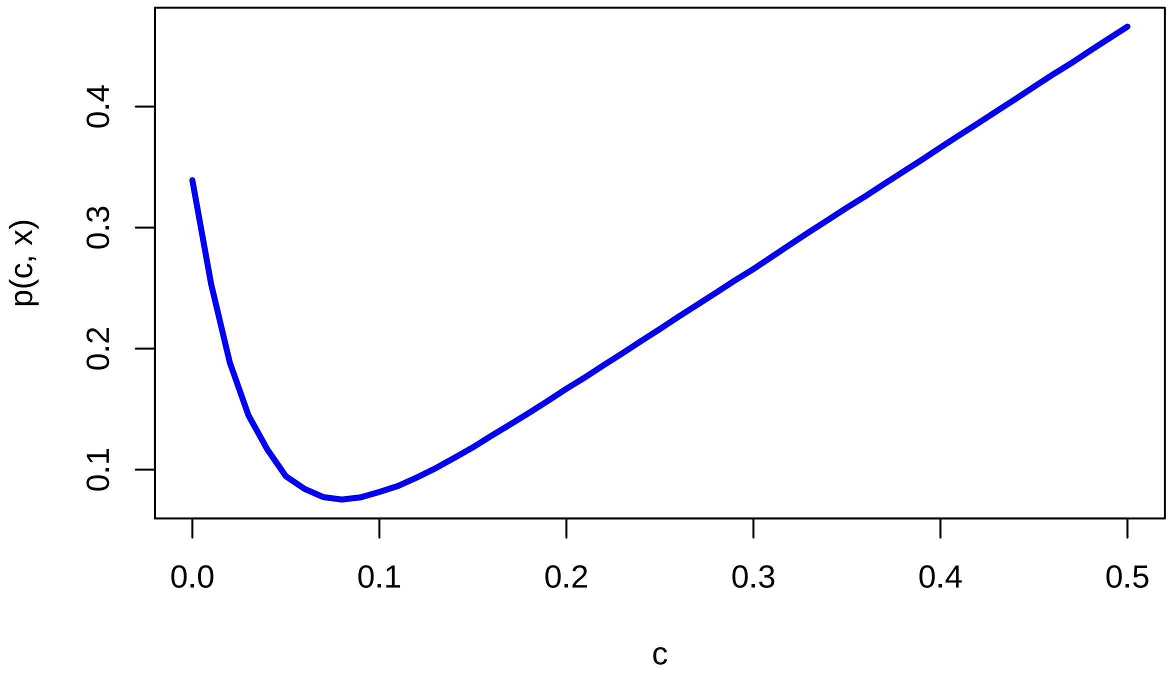
We now write a function **posterior__risk** which is a function of c, parameters a__prior and b__prior for the prior distribution of $\theta$, the summation of $x_i$ sum__x, the number of observations n, and also the number of random draws s.

```r
# compute the posterior risk given c
# s is the number of random draws
posterior_risk = function(c, a_prior, b_prior, sum_x, n, s = 30000){
  # randow draws from beta distribution
  a_post = a_prior + sum_x
  b_post = b_prior + n - sum_x
  theta = rbeta(s, a_post, b_post)
  loss <- apply(as.matrix(theta),1,loss_function,c)
  # average values from the loss function
  risk = mean(loss)
}
# a sequence of c in [0, 0.5]
c = seq(0, 0.5, by = 0.01)
post_risk <- apply(as.matrix(c),1,posterior_risk, a, b, sum_x, n)
head(post_risk)
```

```
## [1] 0.33917940 0.25367603 0.18868962 0.14489894 0.11693106 0.09453471
```

We then look at the Posterior expected loss (posterior risk) for disease prevelance versus c.

```
# plot posterior risk against c
plot(c, post_risk, type = 'l', col='blue',
    lwd = 3, ylab ='p(c, x)' )
```



```
# minimum of posterior risk occurs at c = 0.08
(c[which.min(post_risk)])
```

```
## [1] 0.08
```

## Task 2

We now consider task 2. We set $a = 0.05, 1, 0.05$ and $b = 1, 2, 10$. If we have different prior, the posterior risk is minimized at different c values. The optimal c depends on not only the data, but also the prior setting.

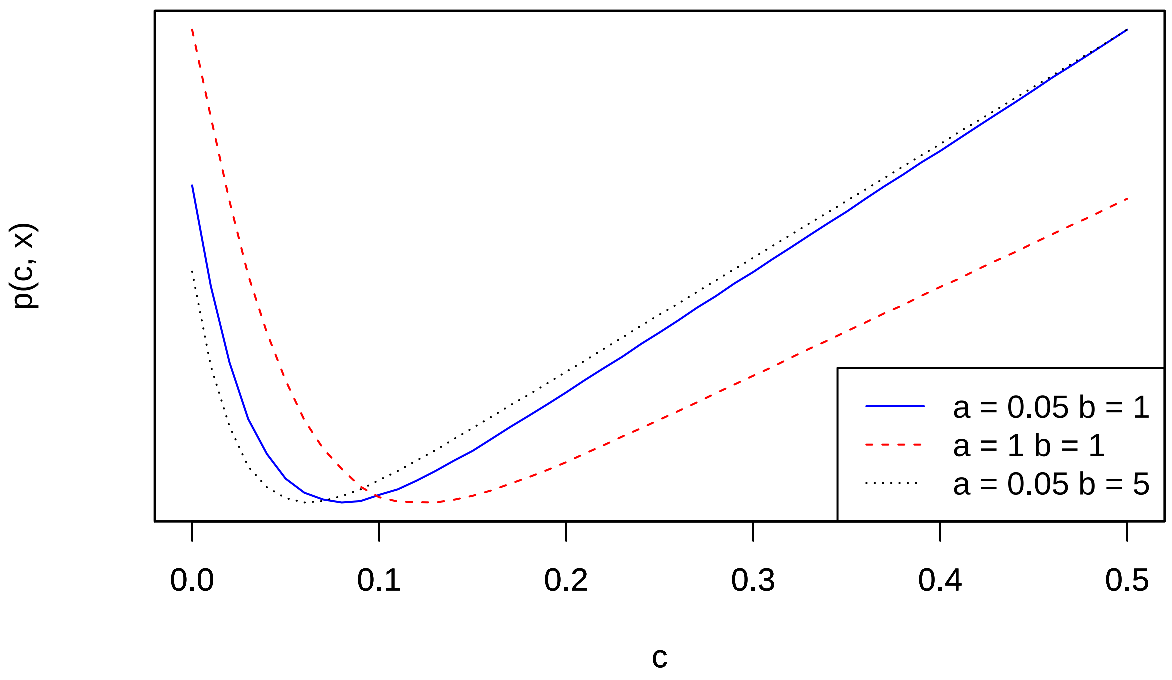
```
# set prior
as = c(0.05, 1, 0.05); bs = c(1, 1, 10)
post_risk = matrix(NA, 3, length(c))

# for each pair of a and b, compute the posterior risks
for (i in 1:3){
  a_prior = as[i]
  b_prior = bs[i]

  post_risk[i,] = apply(as.matrix(c), 1, posterior_risk, a_prior, b_prior, sum_x, n)
}

plot(c, post_risk[1,], type = 'l', col='blue', lty = 1, yaxt = "n", ylab = "p(c, x)")
par(new = T)
plot(c, post_risk[2,], type = 'l', col='red', lty = 2, yaxt = "n", ylab = "")
```

```r
par(new = T)
plot(c, post_risk[3,], type = 'l', lty = 3, yaxt = "n", ylab = "")
legend("bottomright", lty = c(1,2,3), col = c("blue", "red", "black"),
       legend = c("a = 0.05 b = 1", "a = 1 b = 1", "a = 0.05 b = 5"))
```



Note there is a more automated solution but this is the most simple one and is completely correct.

## Task 3

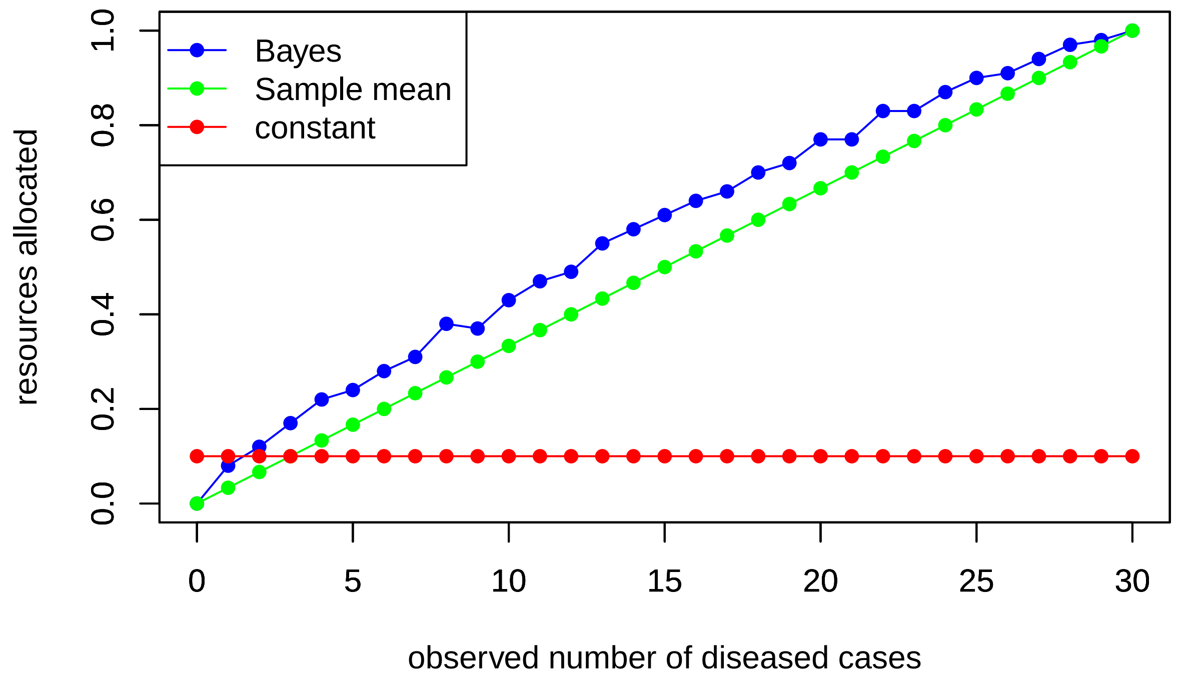
The Bayes procedure always picks c to be a little bigger than $\bar{x}$.

```r
sum_xs = seq(0, 30)
min_c = matrix(NA, 3, length(sum_xs))

# find_optimal_C finds the optimal c under Bayes procedure
# function of sum of x, parameters for prior, number of observations, and number of random draws
find_optimal_C = function(sum_x, a_prior, b_prior, n, s = 500){
  c = seq(0, 1, by = 0.01)
  post_risk =  apply(as.matrix(c), 1, posterior_risk, a_prior, b_prior, sum_x, n, s)
  c[which.min(post_risk)]
}

min_c[1,] = apply(as.matrix(sum_xs), 1, find_optimal_C, a, b, n)
# find optimal c under sample mean
min_c[2,] = (sum_xs)/n
# constant c
min_c[3,] = 0.1

# plot
plot(sum_xs, min_c[1,], col='blue',type = 'o',pch = 16,
     ylab = "resources allocated", xlab = 'observed number of diseased cases',
     ylim = c(0,1))
par(new = T)
plot(sum_xs, min_c[2,], type = 'o', col='green',
     pch = 16, ylab = "", xlab = '', ylim = c(0,1))
par(new = T)
plot(sum_xs, min_c[3,], type = 'o',col = 'red',
     pch = 16, ylab = "", xlab = '', ylim = c(0,1))
legend("topleft", lty = c(1,1,1), pch = c(16,16,16),
       col = c("blue", "green", "red"),
       legend = c("Bayes", "Sample mean", "constant"))
```



## Task 4

For all $\theta$, the Bayes procedure has the lower frequentist risk than the sample mean.

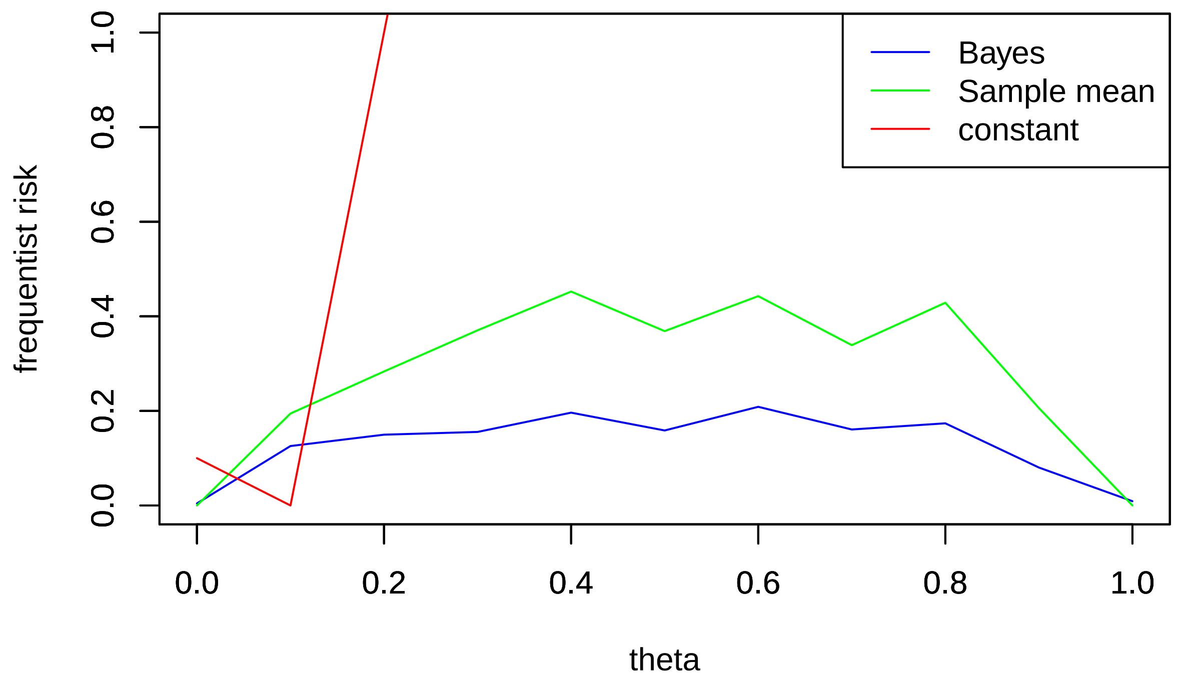
```r
thetas = seq(0, 1, by=0.1)

# frequentist risk for the 3 estimators given a theta
frequentist_risk = function(theta){
  sum_xs = rbinom(100, 30, theta)
  Bayes_optimal = apply(as.matrix(sum_xs), 1, find_optimal_C, a, b, n, s = 100)
  mean_c = sum_xs / 30

  loss1 = apply(as.matrix(Bayes_optimal), 1, loss_function, theta = theta)
  loss2 = apply(as.matrix(mean_c), 1, loss_function, theta = theta )
  risk1 = mean(loss1)
  risk2 = mean(loss2)
  risk3 = loss_function(theta, 0.1)
  return(c(risk1, risk2, risk3))
}
```

```r
# given a sequance a theta, compute frequentist risk for each theta
R = apply(as.matrix(thetas), 1, frequentist_risk)

# plot
plot(thetas, R[1,], col='blue', type = "l",
     ylab = "frequentist risk", xlab = 'theta',ylim = c(0,1))
par(new = T)
plot(thetas, R[2,], type = 'l', col='green',
     ylab = "", xlab = '', ylim = c(0,1))
par(new = T)
plot(thetas, R[3,], type = 'l',col = 'red',
     ylab = "", xlab = '', ylim = c(0,1))
legend("topright", lty = c(1,1,1), col = c("blue", "green", "red"),
       legend = c("Bayes", "Sample mean", "constant"))
```


frequentist risk
theta
Bayes
Sample mean
constant