

STAT340 Project 1

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Question 1.

We have first defined the the matrix with M=8 rows and N=15 columns.
Here at first we are defining three functions, Let is look at the following codes.

```
M <- 8
N <- 15
set.seed(22309988)
A <- matrix(sample(1:(N*M), N*M, replace = FALSE), M, N)

BB= matrix(NA,M,N)

plot_figure <- function() {
  BB <- A
  for(j in 1:N)
    BB[1:M, j] = A[M:1, j]
  image(x = seq(from = 0.5, to = N + 0.5), y = seq(from = 0.5, to = M +
    0.5), z = t(BB), col = gray.colors(n = M * N,
    start = 0, end = 1), xlab = "", ylab = "", axes = FALSE, asp = 1)
  return(BB)
}

plot_numbers <- function(cex = 1) {
  for (i in 1:M) {
    for (j in 1:N) {
      text(j, i, as.character(BB[i,j]),
        col = "brown", cex = cex)
    }
  }
}

plot_path <- function(path, lwd = 2, col = "blue4") {
  xc = c(1:N)
  yc = M - path + 1
  lines(xc, yc, lwd = lwd, col = col)
}

BB = plot_figure()
plot_numbers()
```

105	33	2	63	90	30	111	64	19	113	22	6	116	120	56
109	97	57	10	35	71	86	62	54	55	32	81	49	70	27
92	7	37	98	50	66	102	84	75	112	13	1	39	26	17
46	115	36	87	118	79	53	47	52	5	65	14	69	21	67
18	38	45	85	107	95	16	44	59	101	25	119	58	93	40
80	103	68	82	8	24	110	41	117	73	104	60	89	23	74
28	61	4	15	43	108	51	114	88	3	77	106	94	29	99
91	78	100	72	11	34	42	12	83	48	9	31	20	96	76

The above matrix named A is a $M \times N$ matrix

Now let us write the algorithm for finding the smoothing path using Dynamic programming approach.

```
H <- matrix(NA, M, N)
D <- 1
H[, 1] <- A[, 1]

for(j in 2:N) {
  for(i in 1:M) {
    i.low <- max(1, i-D)
    i.high <- min(M, i+D)
    ii <- i.low - 1 + which.max(H[i.low:i.high, j-1] + A[i, j])
    H[i, j] <- H[ii, j-1] + A[i, j]
  }
}

xs <- numeric(N)
xs[N] <- which.max(H[, N])
for(j in (N-1):1) {
  i.low <- max(1, xs[j+1]-D)
  i.high <- min(M, xs[j+1]+D)
  ii <- i.low - 1 + which.max(H[i.low:i.high, j])
  xs[j] <- ii
}
```

Here the list xs is our most likely path.

Now let us plot the best possible path in the grayscale image generated above with the help of `plot_path()` function that I created.
below is the whole code in a single window.

```
BB= matrix(NA,M,N)
set.seed(22309988)
plot_figure <- function() {
  BB <- A
  for(j in 1:N)
    BB[1:M, j] = A[M:1, j]
  image(x = seq(from = 0.5, to = N + 0.5), y = seq(from = 0.5, to = M +
    0.5), z = t(BB), col = gray.colors(n = M * N,
    start = 0, end = 1), xlab = "", ylab = "", axes = FALSE, asp = 1)
  return(BB)
}
plot_numbers <- function(cex = 1) {
  for (i in 1:M) {
    for (j in 1:N) {
      text(j, i, as.character(BB[i,j]),
        col = "brown", cex = cex)
    }
  }
}

plot_path <- function(path, lwd = 2, col = "blue4") {
  xc = c(1:N)
  yc = M - path + 1
  lines(xc, yc, lwd = lwd, col = col)
}

M <- 8
N <- 15
A <- matrix(sample(1:(N*M), N*M, replace = FALSE), M, N)
H <- matrix(NA, M, N)
D <- 1
H[, 1] <- A[, 1]

BB = plot_figure()
plot_numbers()
for(j in 2:N) {
  for(i in 1:M) {
    i.low <- max(1, i-D)
    i.high <- min(M, i+D)
    ii <- i.low - 1 + which.max(H[i.low:i.high, j-1] + A[i, j])
    H[i, j] <- H[ii, j-1] + A[i, j]
  }
}

xs <- numeric(N)
xs[N] <- which.max(H[, N])
for(j in (N-1):1) {
  i.low <- max(1, xs[j+1]-D)
  i.high <- min(M, xs[j+1]+D)
```

```

ii <- i.low - 1 + which.max(H[i.low:i.high, j])
xs[j] <- ii
}
plot_path(path = xs)

```

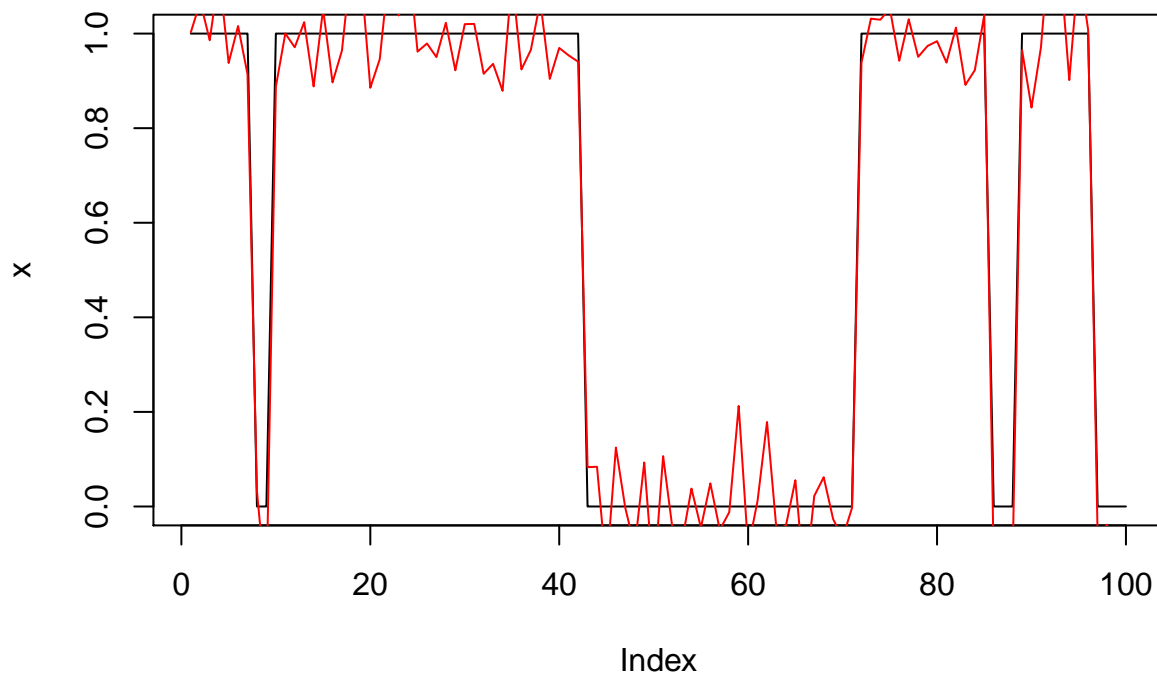


Question 2.

In this problem I am first assigning some initial values to the parameters p, q, σ^2 and for the specified p will simulate a dataset X and consequently Y 's for our validation purposes. Here I have taken $T = 100$ and $p = 0.90, \sigma^2 = 0.1$ for simulation. Code is given below.

```
p <- 0.90
T = 100
sigma_2 <- 0.1
set.seed(234)
x = rep(NA, T)
y = rep(NA, T)

x[1] = 1
for (i in 2:T){
  if (runif(1) < p){
    x[i] = x[i-1]
  }else{
    x[i] = 1-x[i-1]
  }
}
y = rnorm(T, x, sigma_2)
plot(x, type = "l")
lines(y, col = "red")
```



We will use this generated value of Y for our calculations.

Filtering

We will be using the following formula for filtering

$$\pi(X_t|Y_1, Y_2, \dots, Y_t) \propto \pi(X_t|Y_1, Y_2, \dots, Y_{t-1})\pi(Y_t|X_t) \text{ for all } t = 1, 2, \dots, T$$

where the normalizing constant is $Z_t = \pi(Y_t|Y_1, Y_2, \dots, Y_{t-1}) = \sum_{X_t} \pi(X_t|Y_1, Y_2, \dots, Y_t)$

Here the first term in the expression is the prediction for time point t .

Prediction

Formula for Prediction :

$$\pi(X_t|Y_1, Y_2, \dots, Y_{t-1}) = \sum_{X_{t-1}} \pi(X_t|X_{t-1})\pi(X_{t-1}|Y_1, Y_2, \dots, Y_{t-1})$$

The second term is basically the filtering at stage $t - 1$.

Code for filtering and prediction

Code for the above calculation.

```
# we have defined state 1 when x[t] = 1 and state 2 otherwise

filtering_state_1 = rep(NA,T)
filtering_state_2 = rep(NA,T)
prediction_state_1 = rep(NA,T)
prediction_state_2 = rep(NA,T)
Z = rep(NA,T)

prop_filtering_function <- function(prediction,dist_func){
  return(prediction*dist_func)
}

prediction_function <- function(p,filtering1,filtering2,state){
  if (state == 1){
    return(p*filtering1 + (1-p)*filtering2)
  }else{
    return((1-p)*filtering1 + p*filtering2)
  }
}

filtering_and_prediction <- function(p){
  for (t in 1:T){
    if (t == 1){
      prediction_state_1[t] = 0.5
      prediction_state_2[t] = 0.5
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         dist_func_normal(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
```

```

                                dist_func_normal(y[t],0))
norm_constant = prop_filtering_state_1 + prop_filtering_state_2
filtering_state_1[t] = prop_filtering_state_1/norm_constant
filtering_state_2[t] = prop_filtering_state_2/norm_constant
Z[t] = norm_constant
}else{
prediction_state_1[t] = prediction_function(p,filtering_state_1[t-1],
                                           filtering_state_2[t-1],1)
prediction_state_2[t] = prediction_function(p,filtering_state_1[t-1],
                                           filtering_state_2[t-1],0)
prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                  dist_func_normal(y[t],1))
prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                  dist_func_normal(y[t],0))

norm_constant = prop_filtering_state_1 + prop_filtering_state_2
filtering_state_1[t] = prop_filtering_state_1/norm_constant
filtering_state_2[t] = prop_filtering_state_2/norm_constant
Z[t] = norm_constant
}
}
return(matrix(c(filtering_state_1,filtering_state_2,prediction_state_1,
                prediction_state_2,Z),nrow = 5, byrow = TRUE))
}

```

Smoothing

Given Y_1, Y_2, \dots, Y_T the smoothing at time point $t = s$ where $s = 1, 2, \dots, T$ is

$$\pi(X_s|Y_{1:T}) = \sum_{X_{s+1}} \frac{\pi(X_{s+1}|X_s)\pi(X_s|Y_{1:s})\pi(X_{s+1}|Y_{1:T})}{\pi(X_{s+1}|Y_{1:s})}$$

Which is basically a function of filtering at time point s , smoothing at time point $s + 1$ and prediction at time point $s + 1$.

Smoothing code.

```

# we have defined state 1 when x[t] = 1 and state 2 otherwise

smoothing_state_1 = rep(NA,T)
smoothing_state_2 = rep(NA,T)

smoothing_function <- function(p,filtering,smoothing1,prediction1,smoothing2,
                               prediction2,state){
  if (state == 1){
    return((p*filtering*smoothing1/prediction1) +
           ((1-p)*filtering*smoothing2/prediction2))
  }else{
    return(((1-p)*filtering*smoothing1/prediction1) +
           (p*filtering*smoothing2/prediction2))
  }
}

```



```

}

smoothing <- function(p){
  for (t in T:1){
    if (t == T){
      smoothing_state_1[t] = filtering_state_1[t]
      smoothing_state_2[t] = filtering_state_2[t]
    }else{
      smoothing_state_1[t] = smoothing_function(p,filtering_state_1[t],
                                                smoothing_state_1[t+1],
                                                prediction_state_1[t+1],
                                                smoothing_state_2[t+1],
                                                prediction_state_2[t+1],1)

      smoothing_state_2[t] = smoothing_function(p,filtering_state_2[t],
                                                smoothing_state_1[t+1],
                                                prediction_state_1[t+1],
                                                smoothing_state_2[t+1],
                                                prediction_state_2[t+1],0)

    }
  }
  return(return(matrix(c(smoothing_state_1,smoothing_state_2),nrow = 2, byrow = TRUE)))
}

```

Calculation when Y follows normal conditioned on X

Now for the first case when,

$$\pi(Y_t|X_t) \sim N(X_t, \sigma^2)$$

Code:

```

dist_func_normal <- function(y,x){
  return(dnorm(y,x,sqrt(sigma_2)))
}

maximizer <- function(a,b){
  if (a > b){
    return(1)
  }else{
    return(0)
  }
}

# Calculation of filtering and prediction for p = 0.9 as stated earlier
k = filtering_and_prediction(p)
filtering_state_1 = k[1,]
filtering_state_2 = k[2,]
prediction_state_1 = k[3,]
prediction_state_2 = k[4,]

l = smoothing(p)
smoothing_state_1 = l[1,]
smoothing_state_2 = l[2,]

```

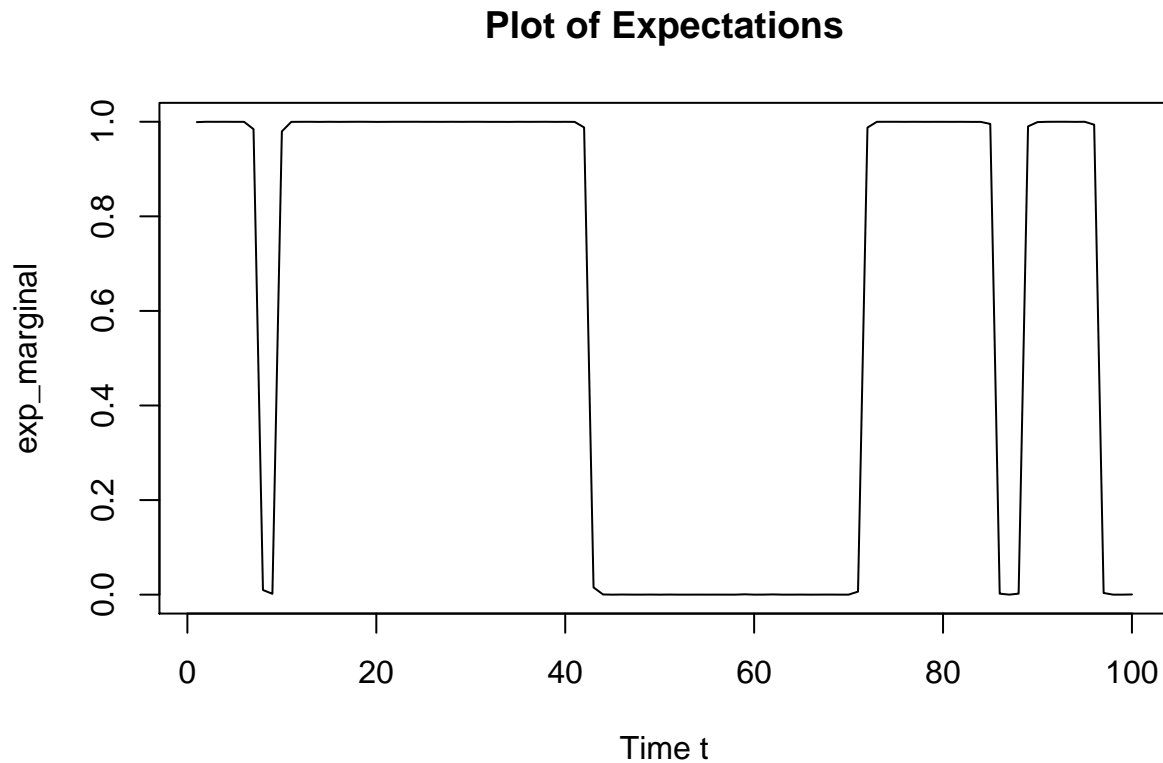
1. For pre-defined values of θ we then can find the marginal mean and standard deviation, which is given by

$$E(X_t|Y_{1:T}) = P(X_t = 1|Y_{1:T}) = \text{Probability of smoothing at time point } t$$

$$V(X_t|Y_{1:T}) = P(X_t = 1|Y_{1:T})(1 - P(X_t = 1|Y_{1:T}))$$

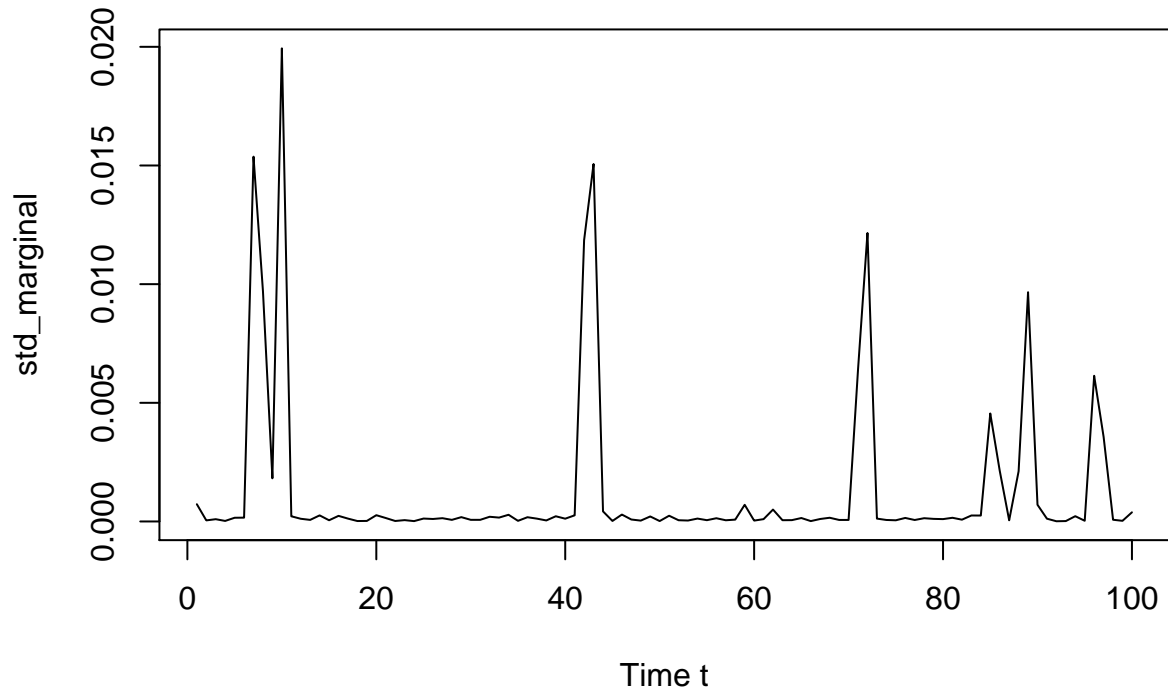
Code : Here we are plotting the expectation and standard deviation over the time points.

```
exp_marginal = smoothing_state_1
std_marginal = smoothing_state_1*smoothing_state_2
plot(exp_marginal,type = "l",xlab = "Time t")
title(main = "Plot of Expectations" )
```



```
plot(std_marginal,type="l",xlab = "Time t")
title(main = "Plot of standard deviations")
```

Plot of standard deviations



Now to find the modal configuration of X , we will have to do sampling over $\pi(X_{1:T}|Y_{1:T})$ and find the mode from there.

Let us look at the following code:

```
maximizer <- function(a,b){
  if (a > b){
    return(1)
  }else{
    return(0)
  }
}
mod_x = rep(NA,T)
Modal_config <- function(p){
  mod_x[T] = maximizer(filtering_state_1[T],filtering_state_2[T])

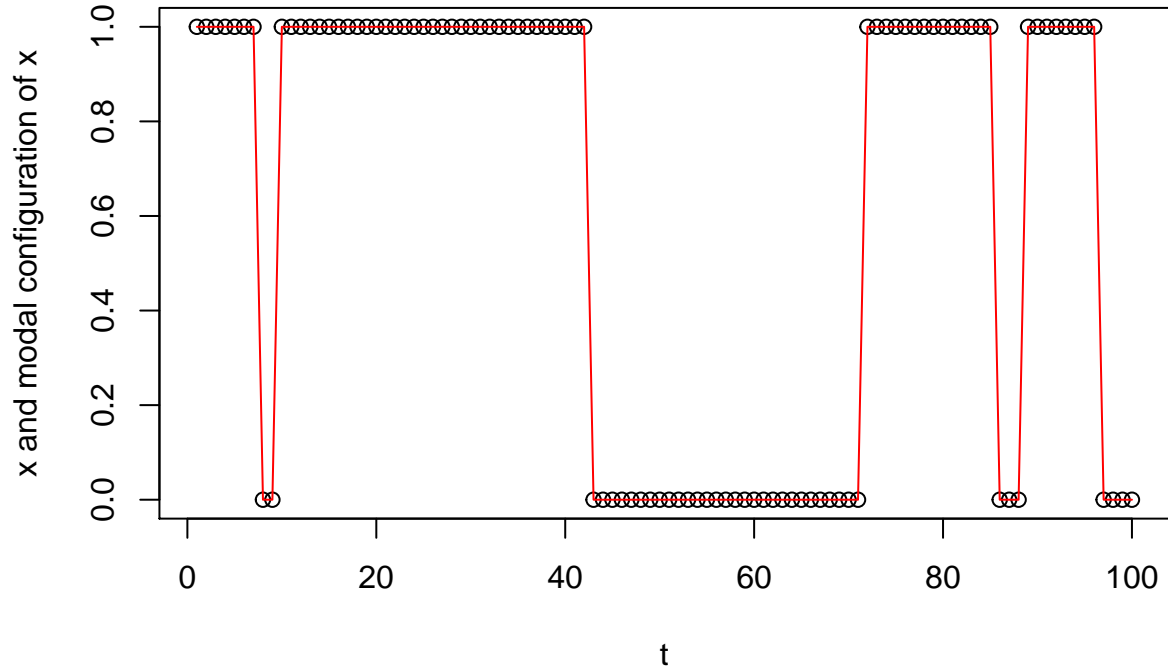
  for (t in (T-1):1){
    if (mod_x[t+1] == 1){
      sampling_state_1 = p*filtering_state_1[t]
      sampling_state_2 = (1-p)*filtering_state_2[t]
    }else{
      sampling_state_1 = (1-p)*filtering_state_1[t]
      sampling_state_2 = p*filtering_state_2[t]
    }
    mod_x[t] = maximizer(sampling_state_1,sampling_state_2)
  }
}
```

```

}
return(mod_x)
}
mod_x = Modal_config(p)

# plotting X and modal configuration of X
plot(x, xlab = "t", ylab = "x and modal configuration of x")
lines(mod_x, col = "red")

```



Hence from the above plot it is quite evident that the xodal configuration of X matches with X very well.

2. Here we have to find posterior mode and distribution of p .

Let us first assume that the prior distribution of p is Uniform(0,1) i.e; $p \sim U(0, 1)$

Now we have to find

$$\begin{aligned}
 p^* &= \operatorname{argmax} \pi(p|Y_{1:T}) \\
 &= \operatorname{argmax} \pi(p)\pi(Y_{1:T}|p)
 \end{aligned}$$

$$\text{Here } \pi(Y_{1:T}|p) \text{ is proportional to } \prod_{i=1}^T Z_i$$

$$\text{and } \pi(p) \sim U(0, 1)$$

$$\text{Hence } p^* = \operatorname{argmax} \prod_{i=1}^T Z_i$$

So, if we plot this function with respect to p we will find the section where p maximizes.

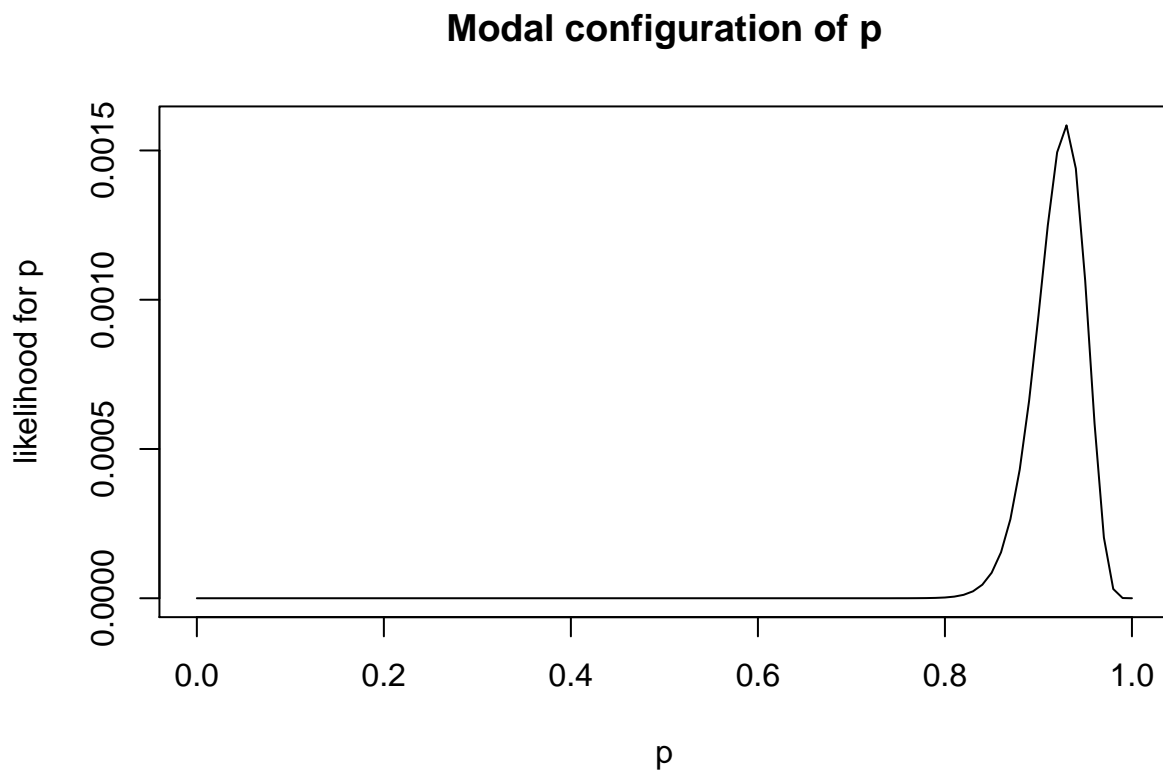
Also by normalizing the product of Z_i 's we can find the posterior distribution of p .

In the following code we have plotted the for both the cases.

code:

```
# modal value of p

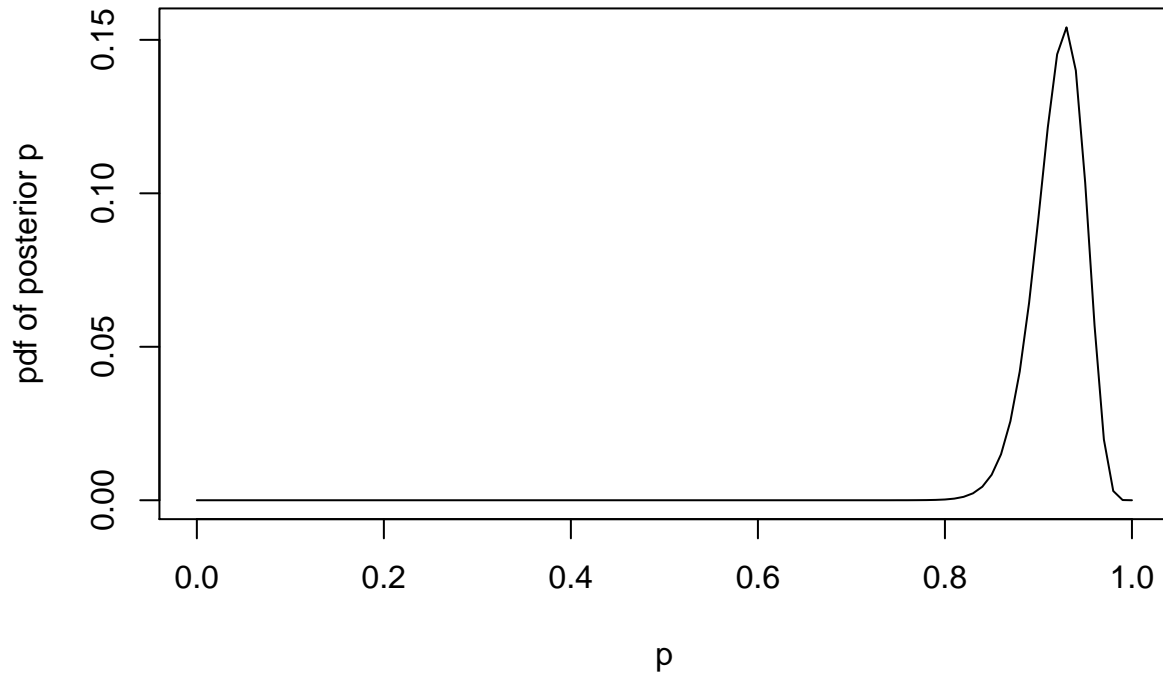
sequence = seq(from = 0, to = 1 , by = 0.01)
likelihood = rep(NA,length(sequence))
for (i in 1:length(sequence)){
  k = filtering_and_prediction(sequence[i])
  Z = k[5,]
  likelihood[i] = prod(Z)
}
plot(sequence,likelihood, type = "l", xlab = "p", ylab = "likelihood for p")
title(main = "Modal configuration of p")
```



```
# posterior distribution of P
normalizing_p = sum(likelihood)

posterior_p = likelihood/normalizing_p
plot(sequence,posterior_p, type = "l", xlab = "p", ylab = "pdf of posterior p" )
title(main = "posterior distribution of p")
```

posterior distribution of p



So we see the modal value of p matches with our initially defined value of p .

3. Here we have to do the same as 1. but after taking the uncertainty of p into consideration. Let us look at the following.

Here $E(X_t|Y_{1:T}, p) = \text{smoothing state 1 probability conditioned on } p$.

$$E(X_t|Y_{1:T}, p) \approx \sum_p E(X_t|Y_{1:T}, p_i) \pi(p_i|Y_{1:T})$$

Writing this in code we get.

```
# marginal expectation conditioned on p
exp_marginal = rep(NA, T)
for (t in 1:T){
  exp_part = rep(NA, length(sequence))
  for (i in 1:length(sequence)){
    k = filtering_and_prediction(sequence[i])
    filtering_state_1 = k[1,]
    filtering_state_2 = k[2,]
    prediction_state_1 = k[3,]
    prediction_state_2 = k[4,]
    Z = k[5,]
    l = smoothing(sequence[i])
    smoothing_state_1 = l[1,]
    exp_part[i] = smoothing_state_1[t]*(prod(Z)/normalizing_p)
  }
}
```

```

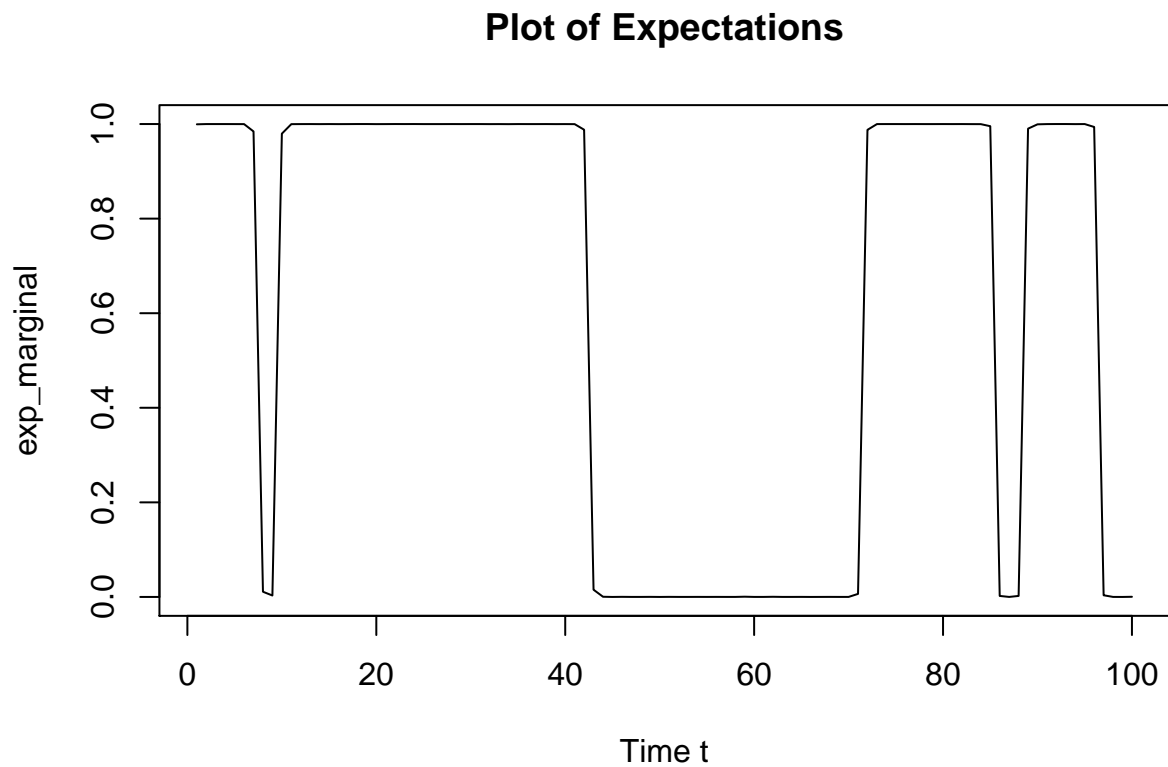
    exp_marginal[t] = sum(exp_part)
}

exp_marginal_2 = exp_marginal

var_marginal = exp_marginal_2 - exp_marginal^2
std_marginal = sqrt(var_marginal)

plot(exp_marginal,type = "l",xlab = "Time t")
title(main = "Plot of Expectations" )

```

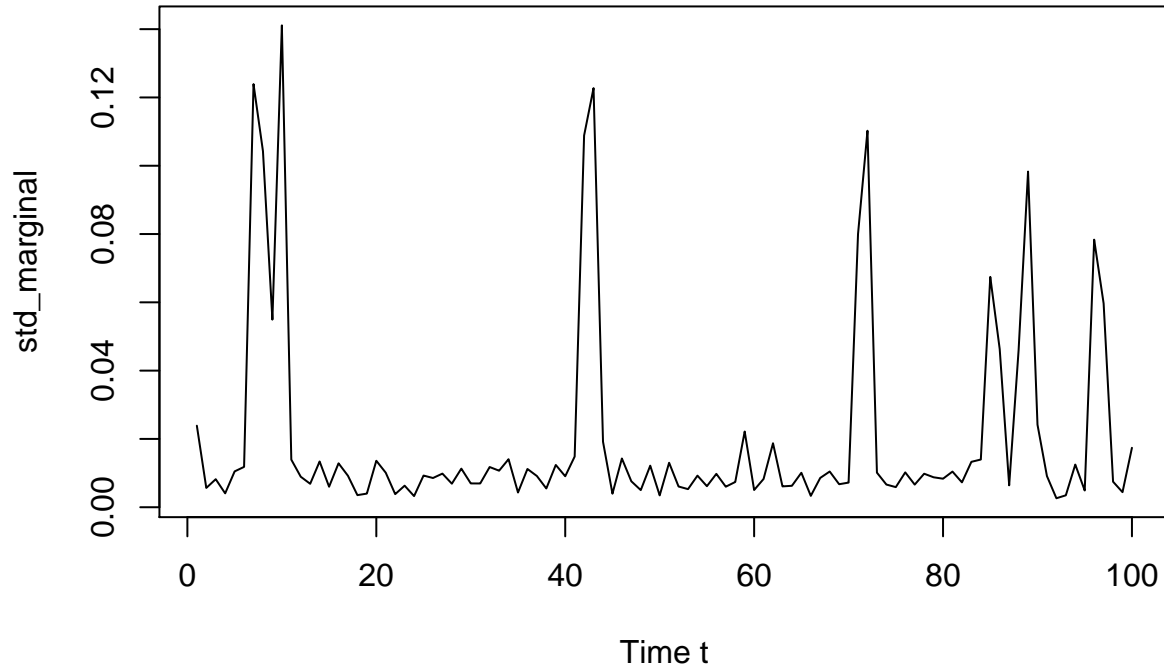


```

plot(std_marginal,type="l",xlab = "Time t")
title(main = "Plot of standard deviations")

```

Plot of standard deviations



Here $\exp_marginal$ is the marginal expectation and $\var_{marginal}$ is the variance of the marginal both conditioned on p .

4. Here we have to find the modal configuration of (x,p) jointly.
Let us write the problem in the following way.

$$\begin{aligned} \text{Here } (p^*, X^*) &= \operatorname{argmax} \pi(p, X_{1:T} | Y_{1:T}) \\ &\propto \operatorname{argmax} \pi(X_{1:T} | Y_{1:T}, p) \pi(p | Y_{1:T}) \end{aligned}$$

So here we will first maximize X as a function of p then put that value above and maximize over p .

code:

```
# Mod (p,x)

# Modal configuration of X conditioned on p
mod_x = rep(NA,T)
mod_x_dist = rep(NA,T)
filtering_state_1= rep(NA,T)
filtering_state_2= rep(NA,T)
Modal_config <- function(p,filtering_state_1,filtering_state_2){
  mod_x_dist[T] = max(filtering_state_1[T],filtering_state_2[T])
  mod_x[T] = maximizer(filtering_state_1[T],filtering_state_2[T])
  for (t in (T-1):1){
    if (mod_x[t+1] == 1){
      sampling_state_1 = p*filtering_state_1[t]
```

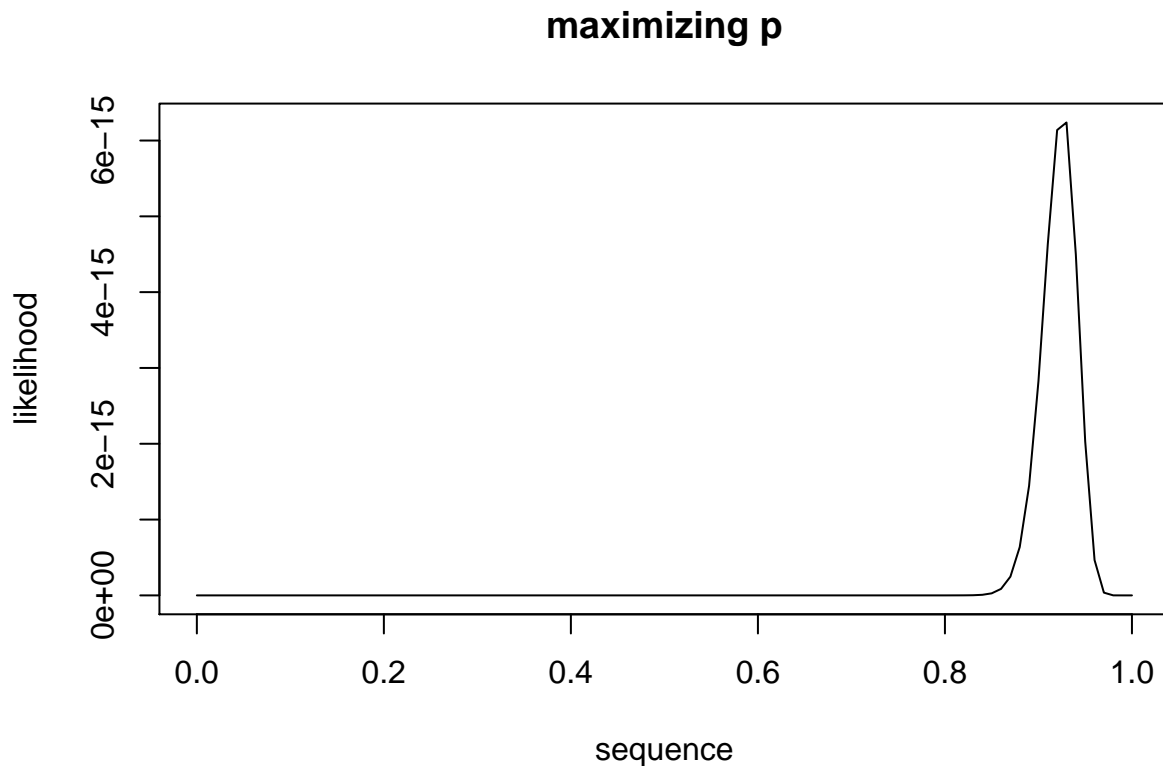


```

        sampling_state_2 = (1-p)*filtering_state_2[t]
    }else{
        sampling_state_1 = (1-p)*filtering_state_1[t]
        sampling_state_2 = p*filtering_state_2[t]
    }
    mod_x_dist[t] = max(sampling_state_1,sampling_state_2)
    mod_x[t] = maximizer(sampling_state_1,sampling_state_2)
}
return(prod(mod_x_dist))
}
sequence = seq(from = 0, to = 1 , by = 0.01)
likelihood = rep(NA,length(sequence))
for (i in 1:length(sequence)){
    k = filtering_and_prediction(sequence[i])
    filtering_state_1 = k[1,]
    filtering_state_2 = k[2,]
    Z = k[5,]
    mod_x_dist = Modal_config(sequence[i],filtering_state_1,filtering_state_2)
    likelihood[i] = prod(Z) * mod_x_dist
}

plot(sequence,likelihood,type="l")
title(main = "maximizing p")

```



Hence, From the plot it is evident that the mode for p is nearing 0.9 and putting this value in the modal configuration we will get the modal configuration of X . Code:

```

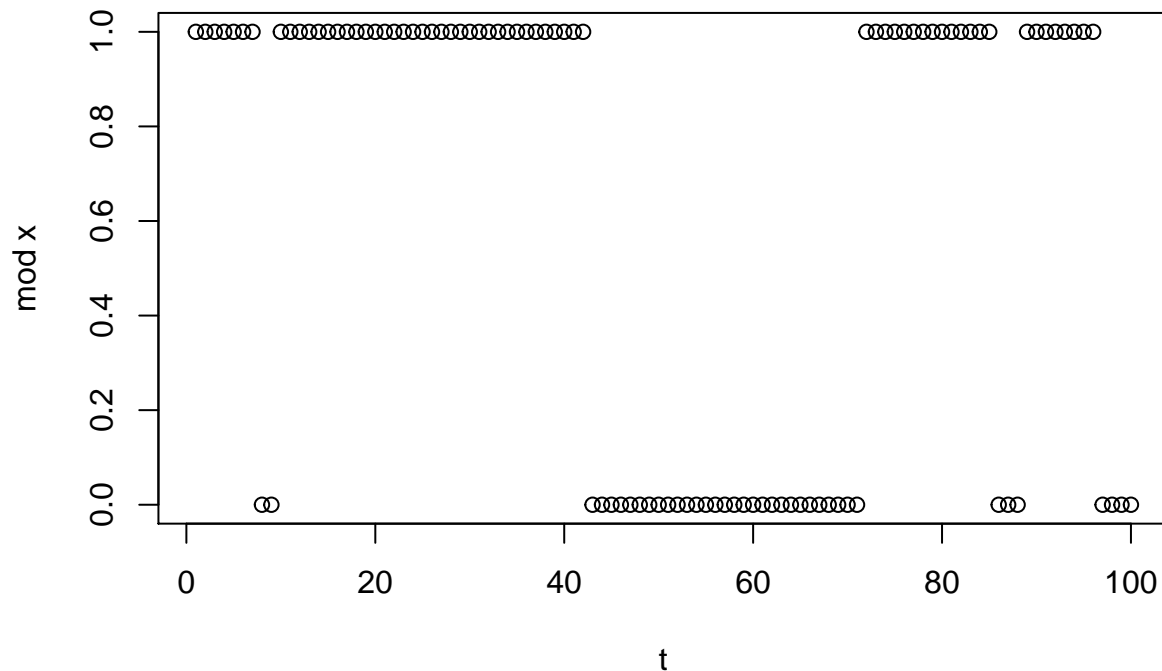
p = 0.9
mod_x = rep(NA,T)
k = filtering_and_prediction(p)
filtering_state_1 = k[1,]
filtering_state_2 = k[2,]
Modal_config <- function(p){
  mod_x[T] = maximizer(filtering_state_1[T],filtering_state_2[T])

  for (t in (T-1):1){
    if (mod_x[t+1] == 1){
      sampling_state_1 = p*filtering_state_1[t]
      sampling_state_2 = (1-p)*filtering_state_2[t]
    }else{
      sampling_state_1 = (1-p)*filtering_state_1[t]
      sampling_state_2 = p*filtering_state_2[t]
    }
    mod_x[t] = maximizer(sampling_state_1,sampling_state_2)
  }
  return(mod_x)
}
mod_x = Modal_config(p)

# plotting X and modal configuration of X
plot(mod_x, xlab = "t",ylab = "mod x",main= "modal configuration of x for p=0.9")

```

modal configuration of x for p=0.9



Calculation when Y follows the Discrete distribution.

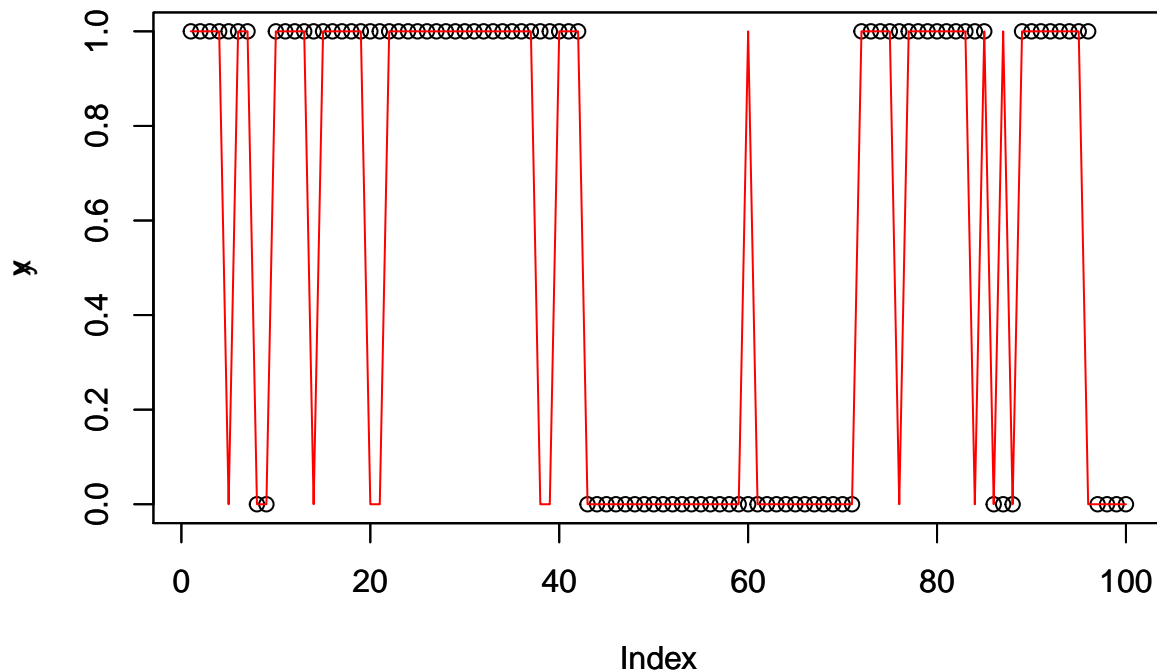
Here the conditional distribution of $y_t|x_t$ is a discrete distribution as follows.

$$y_t|x_t = \begin{cases} x_t & \text{with probability } q \\ 1 - x_t & \text{with probability } 1 - q \end{cases}$$

Let us do the same process as

above under this second distribution also. code:

```
# second distribution of Y
q = 0.9
y = rep(NA,T)
gen_y <- function(q){
  for(i in 1:T){
    if(runif(1) < q){
      y[i] = x[i]
    }else{
      y[i] = 1-x[i]
    }
  }
  return(y)
}
y = gen_y(q)
plot(x)
par(new = T)
plot(y,type="l",col="red")
```



```

dist_func_bernoulli <- function(y,x){
  if ( y == x){
    return(q)
  }else{
    return(1-q)
  }
}

# we have defined state 1 when x[t] = 1 and state 2 otherwise

filtering_state_1 = rep(NA,T)
filtering_state_2 = rep(NA,T)
prediction_state_1 = rep(NA,T)
prediction_state_2 = rep(NA,T)
Z = rep(NA,T)

prop_filtering_function <- function(prediction,dist_func){
  return(prediction*dist_func)
}

prediction_function <- function(p,filtering1,filtering2,state){
  if (state == 1){
    return(p*filtering1 + (1-p)*filtering2)
  }else{
    return((1-p)*filtering1 + p*filtering2)
  }
}

```

```

}

filtering_and_prediction <- function(p){
  for (t in 1:T){
    if (t == 1){
      prediction_state_1[t] = 0.5
      prediction_state_2[t] = 0.5
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         dist_func_bernoulli(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                         dist_func_bernoulli(y[t],0))

      norm_constant = prop_filtering_state_1 + prop_filtering_state_2
      filtering_state_1[t] = prop_filtering_state_1/norm_constant
      filtering_state_2[t] = prop_filtering_state_2/norm_constant
      Z[t] = norm_constant
    }else{
      prediction_state_1[t] = prediction_function(p,filtering_state_1[t-1],
                                                  filtering_state_2[t-1],1)
      prediction_state_2[t] = prediction_function(p,filtering_state_1[t-1],
                                                  filtering_state_2[t-1],0)
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         dist_func_bernoulli(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                         dist_func_bernoulli(y[t],0))

      norm_constant = prop_filtering_state_1 + prop_filtering_state_2
      filtering_state_1[t] = prop_filtering_state_1/norm_constant
      filtering_state_2[t] = prop_filtering_state_2/norm_constant
      Z[t] = norm_constant
    }
  }
  return(matrix(c(filtering_state_1,filtering_state_2,prediction_state_1,
                  prediction_state_2,Z),nrow = 5, byrow = TRUE))
}

# Calculation of filtering and prediction for p = 0.9 as stated earlier
k = filtering_and_prediction(p)
filtering_state_1 = k[1,]
filtering_state_2 = k[2,]
prediction_state_1 = k[3,]
prediction_state_2 = k[4,]

l = smoothing(p)
smoothing_state_1 = l[1,]
smoothing_state_2 = l[2,]

```

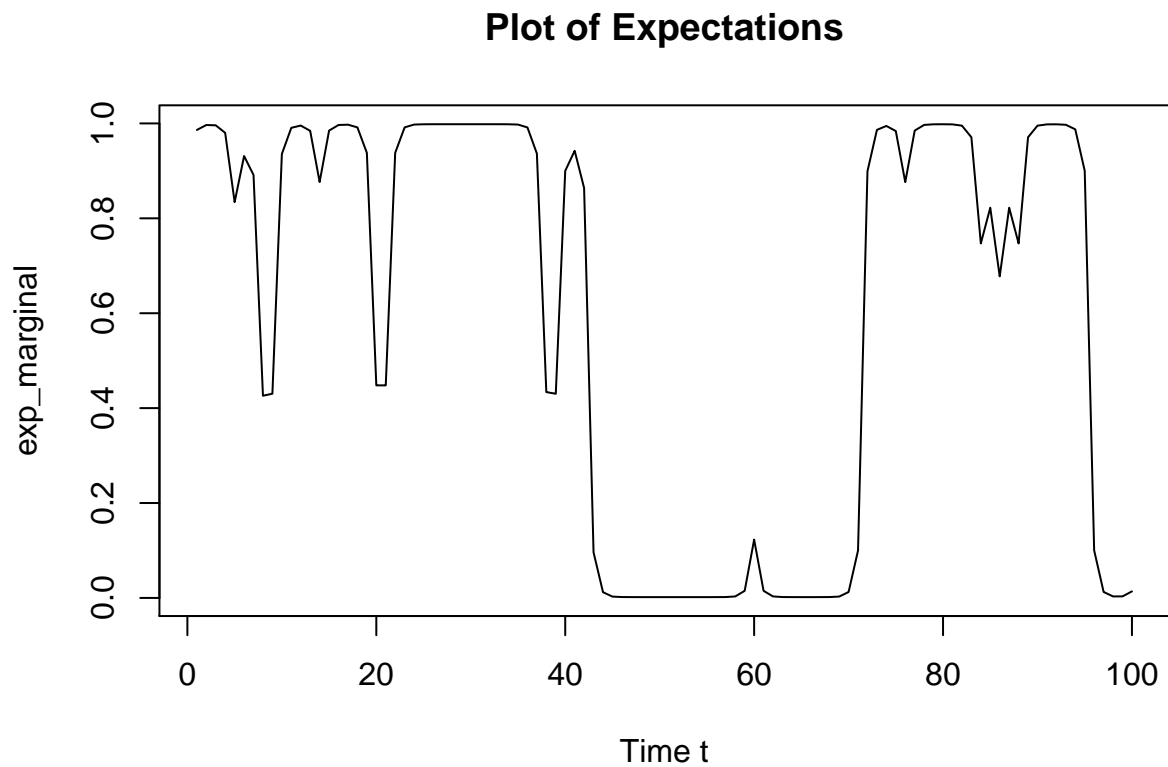
1. For pre-defined values of θ we then can find the marginal mean and standard deviation, which is given by

$$E(X_t|Y_{1:T}) = P(X_t = 1|Y_{1:T}) = \text{Probability of smoothing at time point } t$$

$$V(X_t|Y_{1:T}) = P(X_t = 1|Y_{1:T})(1 - P(X_t = 1|Y_{1:T}))$$

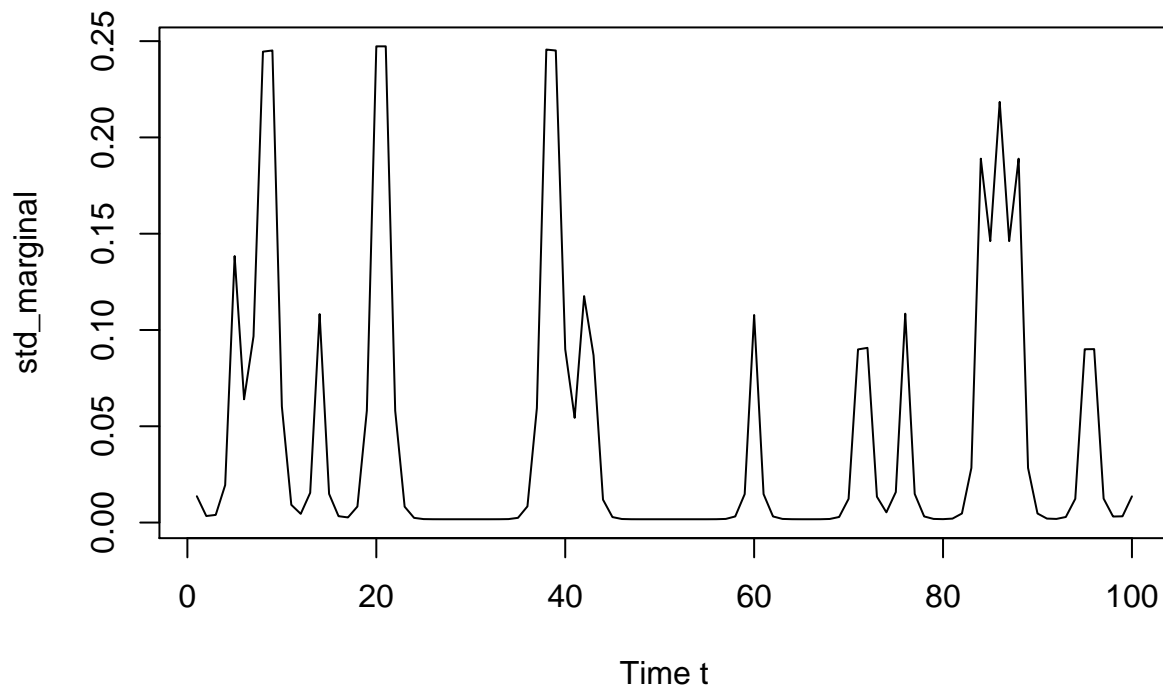
Code : Here we are plotting the expectation and standard deviation over the time points.

```
exp_marginal = smoothing_state_1
std_marginal = smoothing_state_1*smoothing_state_2
plot(exp_marginal,type = "l",xlab = "Time t")
title(main = "Plot of Expectations" )
```



```
plot(std_marginal,type="l",xlab = "Time t")
title(main = "Plot of standard deviations")
```

Plot of standard deviations



Now to find the modal configuration of X , we will have to do sampling over $\pi(X_{1:T}|Y_{1:T})$ and find the mode from there.

Let us look at the following code:

```
maximizer <- function(a,b){
  if (a > b){
    return(1)
  }else{
    return(0)
  }
}
mod_x = rep(NA,T)
Modal_config <- function(p){
  mod_x[T] = maximizer(filtering_state_1[T],filtering_state_2[T])

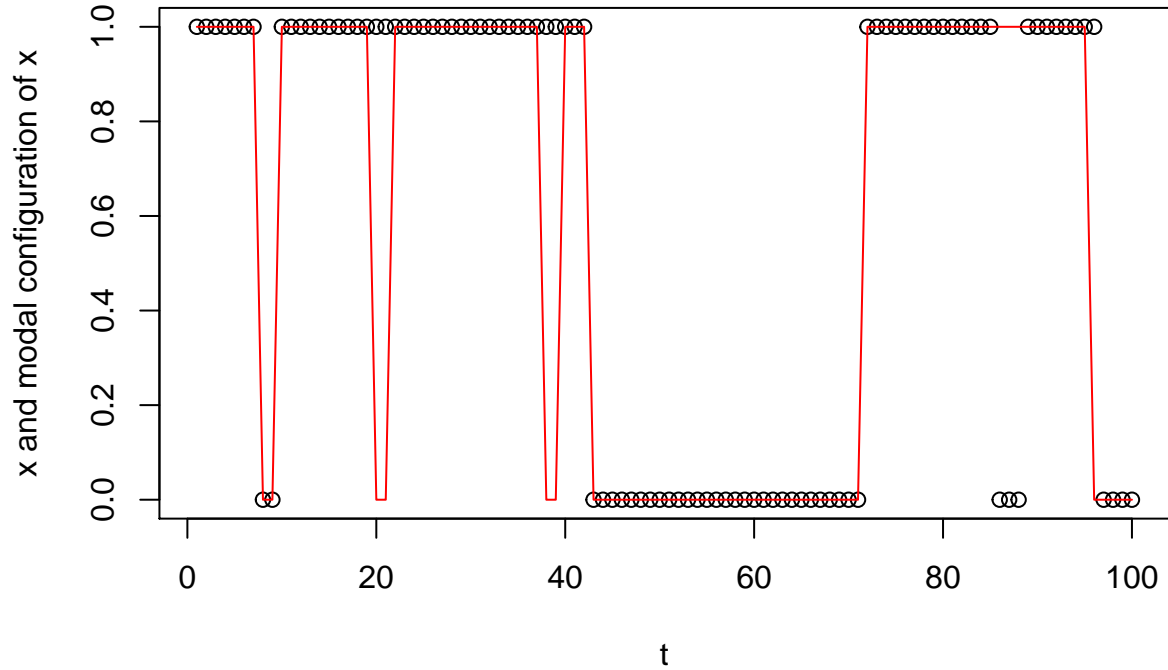
  for (t in (T-1):1){
    if (mod_x[t+1] == 1){
      sampling_state_1 = p*filtering_state_1[t]
      sampling_state_2 = (1-p)*filtering_state_2[t]
    }else{
      sampling_state_1 = (1-p)*filtering_state_1[t]
      sampling_state_2 = p*filtering_state_2[t]
    }
    mod_x[t] = maximizer(sampling_state_1,sampling_state_2)
  }
}
```

```

}
return(mod_x)
}
mod_x = Modal_config(p)

# plotting X and modal configuration of X
plot(x, xlab = "t", ylab = "x and modal configuration of x")
lines(mod_x, col = "red")

```



Hence from the above plot it is quite evident that the modal configuration of X matches with X very well.

2. Here we have to find posterior mode and distribution of p .

Let us first assume that the prior distribution of p is Uniform(0,1) i.e; $p \sim U(0, 1)$

Now we have to find

$$\begin{aligned}
 p^* &= \operatorname{argmax} \pi(p|Y_{1:T}) \\
 &= \operatorname{argmax} \pi(p)\pi(Y_{1:T}|p)
 \end{aligned}$$

$$\text{Here } \pi(Y_{1:T}|p) \text{ is proportional to } \prod_{i=1}^T Z_i$$

$$\text{and } \pi(p) \sim U(0, 1)$$

$$\text{Hence } p^* = \operatorname{argmax} \prod_{i=1}^T Z_i$$

So, if we plot this function with respect to p we will find the section where p maximizes.

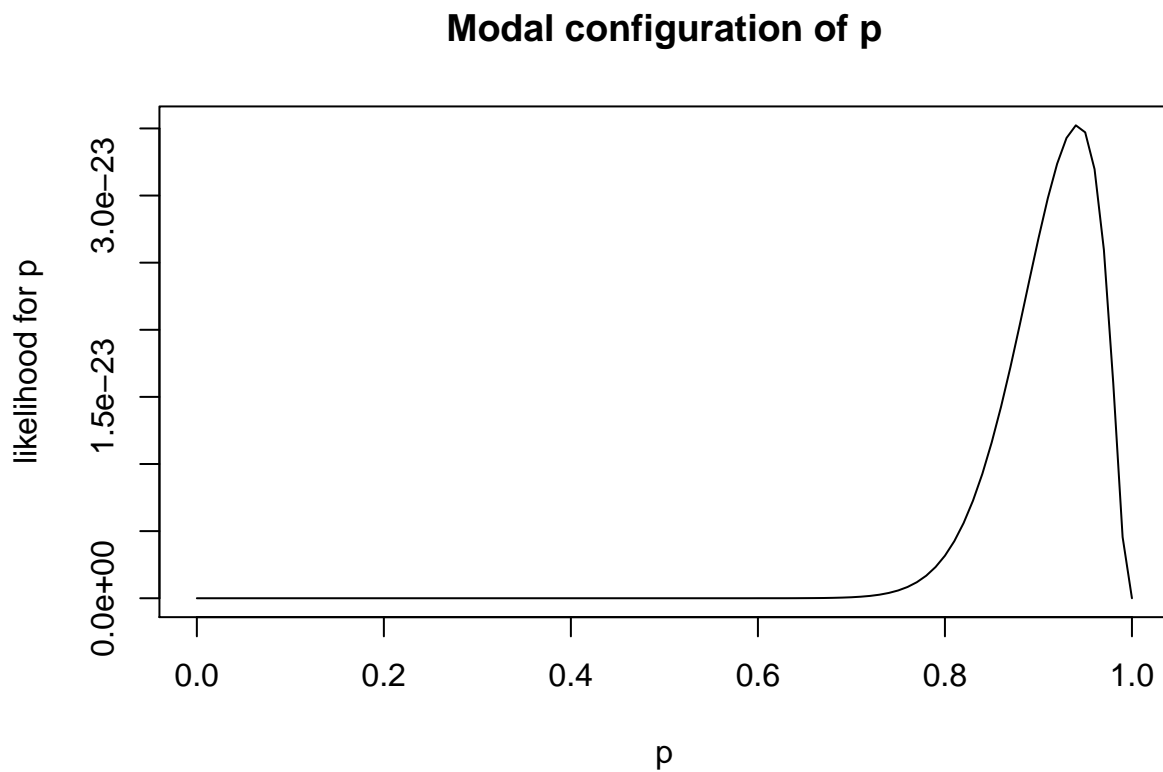
Also by normalizing the product of Z_i 's we can find the posterior distribution of p .

In the following code I have plotted for both the cases.

code:

```
# modal value of p

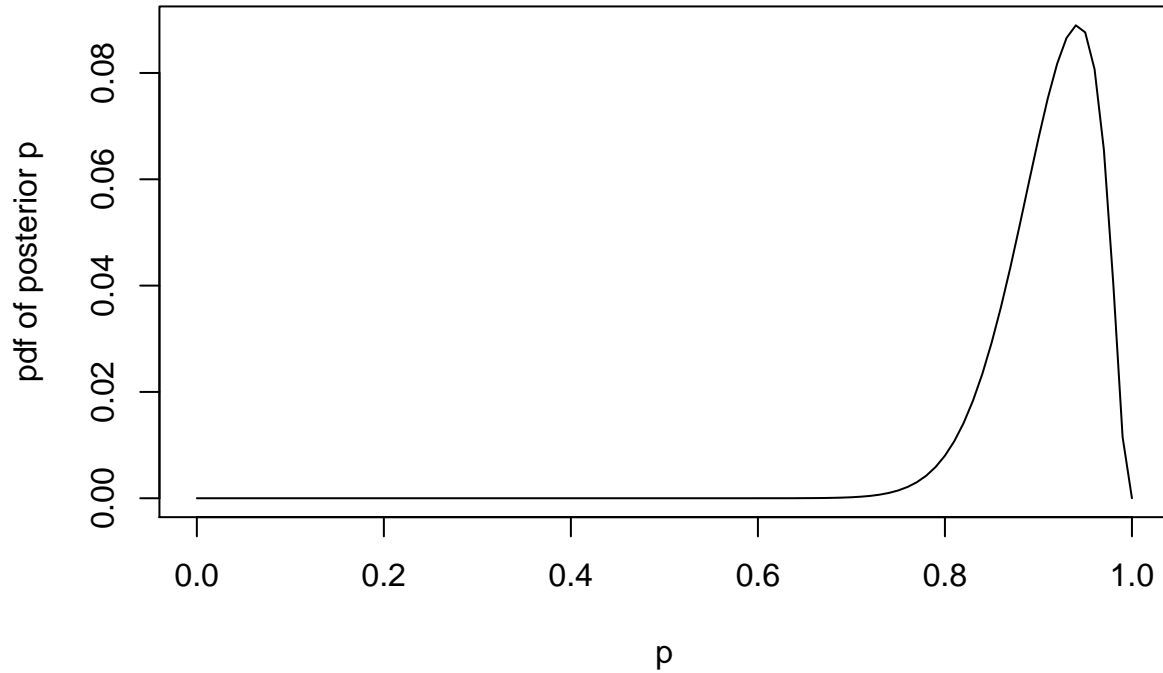
sequence = seq(from = 0, to = 1 , by = 0.01)
likelihood = rep(NA,length(sequence))
for (i in 1:length(sequence)){
  k = filtering_and_prediction(sequence[i])
  Z = k[5,]
  likelihood[i] = prod(Z)
}
plot(sequence,likelihood, type = "l", xlab = "p", ylab = "likelihood for p")
title(main = "Modal configuration of p")
```



```
# posterior distribution of P
normalizing_p = sum(likelihood)

posterior_p = likelihood/normalizing_p
plot(sequence,posterior_p, type = "l", xlab = "p", ylab = "pdf of posterior p" )
title(main = "posterior distribution of p")
```

posterior distribution of p



So we see the modal value of p matches with our initially defined value of p .

3. Here we have to do the same as 1. but after taking the uncertainty of p into consideration. Let us look at the following.

Here $E(X_t|Y_{1:T}, p) = \text{smoothing state 1 probability conditioned on } p$.

$$E(X_t|Y_{1:T}, p) \approx \sum_p E(X_t|Y_{1:T}, p_i) \pi(p_i|Y_{1:T})$$

Writing this in code we get.

```
# marginal expectation conditioned on p
exp_marginal = rep(NA, T)
for (t in 1:T){
  exp_part = rep(NA, length(sequence))
  for (i in 1:length(sequence)){
    k = filtering_and_prediction(sequence[i])
    filtering_state_1 = k[1,]
    filtering_state_2 = k[2,]
    prediction_state_1 = k[3,]
    prediction_state_2 = k[4,]
    Z = k[5,]
    l = smoothing(sequence[i])
    smoothing_state_1 = l[1,]
    exp_part[i] = smoothing_state_1[t]*(prod(Z)/normalizing_p)
  }
}
```

```

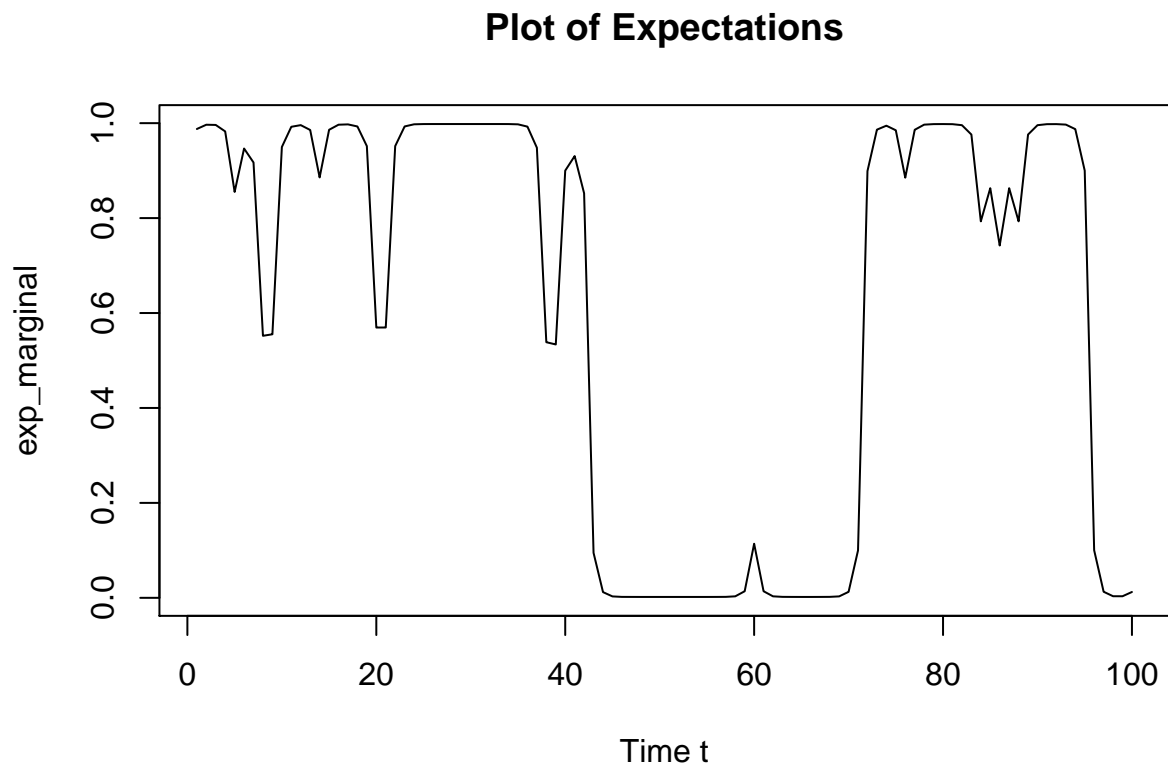
    exp_marginal[t] = sum(exp_part)
}

exp_marginal_2 = exp_marginal

var_marginal = exp_marginal_2 - exp_marginal^2
std_marginal = sqrt(var_marginal)

plot(exp_marginal,type = "l",xlab = "Time t")
title(main = "Plot of Expectations" )

```

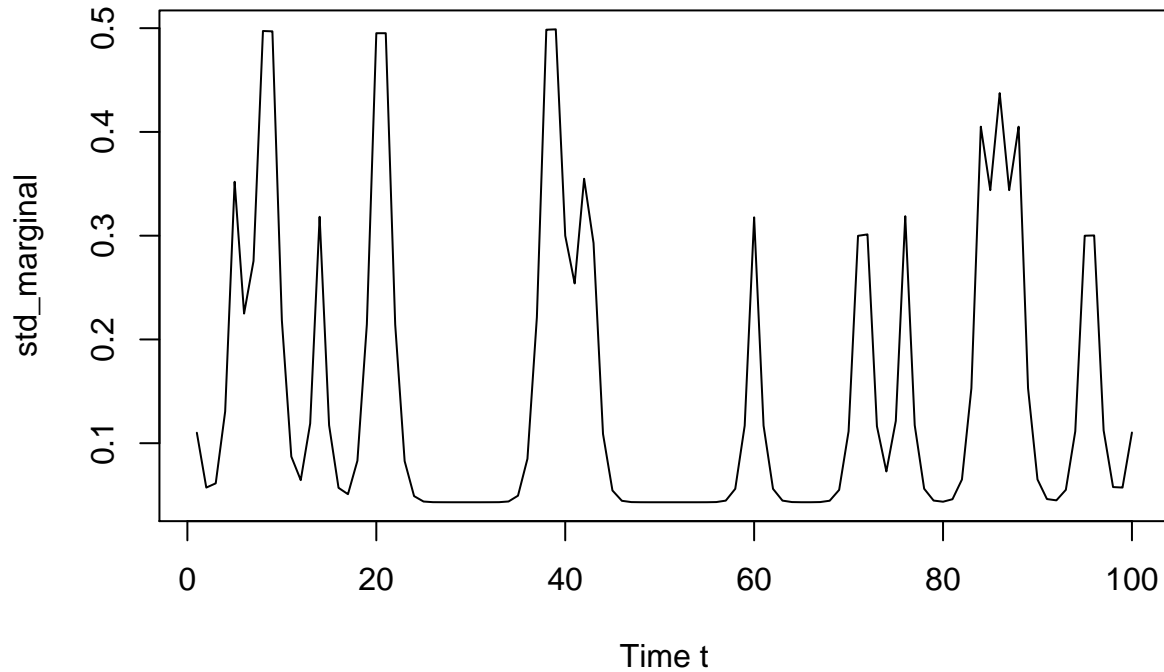


```

plot(std_marginal,type="l",xlab = "Time t")
title(main = "Plot of standard deviations")

```

Plot of standard deviations



Here $\exp_marginal$ is the marginal expectation and $\var_{marginal}$ is the variance of the marginal both conditioned on p .

4. Here we have to find the modal configuration of (x,p) jointly.
Let us write the problem in the following way.

$$\begin{aligned} \text{Here } (p^*, X^*) &= \operatorname{argmax} \pi(p, X_{1:T} | Y_{1:T}) \\ &\propto \operatorname{argmax} \pi(X_{1:T} | Y_{1:T}, p) \pi(p | Y_{1:T}) \end{aligned}$$

So here we will first maximize X as a function of p then put that value above and maximize over p .

code:

```
# Mod (p,x)

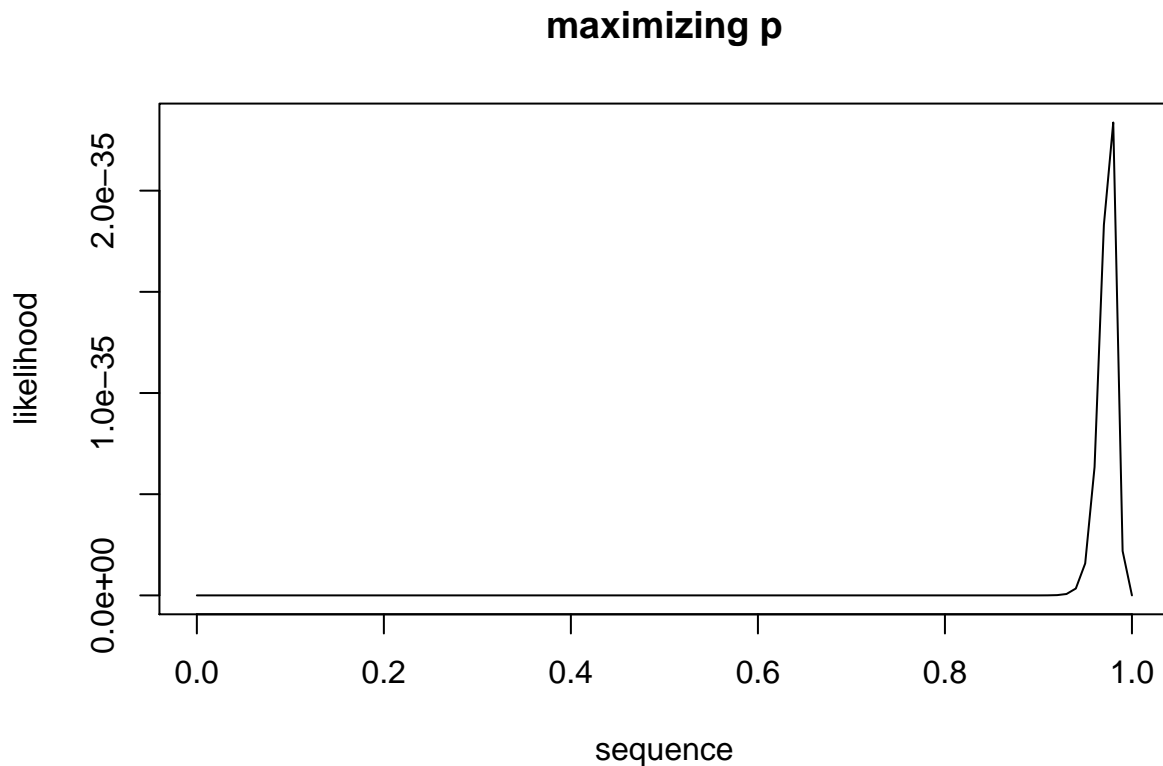
# Modal configuration of X conditioned on p
mod_x = rep(NA,T)
mod_x_dist = rep(NA,T)
filtering_state_1= rep(NA,T)
filtering_state_2= rep(NA,T)
Modal_config <- function(p,filtering_state_1,filtering_state_2){
  mod_x_dist[T] = max(filtering_state_1[T],filtering_state_2[T])
  mod_x[T] = maximizer(filtering_state_1[T],filtering_state_2[T])
  for (t in (T-1):1){
    if (mod_x[t+1] == 1){
      sampling_state_1 = p*filtering_state_1[t]
```

```

        sampling_state_2 = (1-p)*filtering_state_2[t]
    }else{
        sampling_state_1 = (1-p)*filtering_state_1[t]
        sampling_state_2 = p*filtering_state_2[t]
    }
    mod_x_dist[t] = max(sampling_state_1,sampling_state_2)
    mod_x[t] = maximizer(sampling_state_1,sampling_state_2)
}
return(prod(mod_x_dist))
}
sequence = seq(from = 0, to = 1 , by = 0.01)
likelihood = rep(NA,length(sequence))
for (i in 1:length(sequence)){
    k = filtering_and_prediction(sequence[i])
    filtering_state_1 = k[1,]
    filtering_state_2 = k[2,]
    Z = k[5,]
    mod_x_dist = Modal_config(sequence[i],filtering_state_1,filtering_state_2)
    likelihood[i] = prod(Z) * mod_x_dist
}

plot(sequence,likelihood,type="l")
title(main = "maximizing p")

```



Hence, From the plot it is evident that the mode for p is nearing 0.9 and putting this value in the modal configuration we will get the modal configuration of X . Code:

```

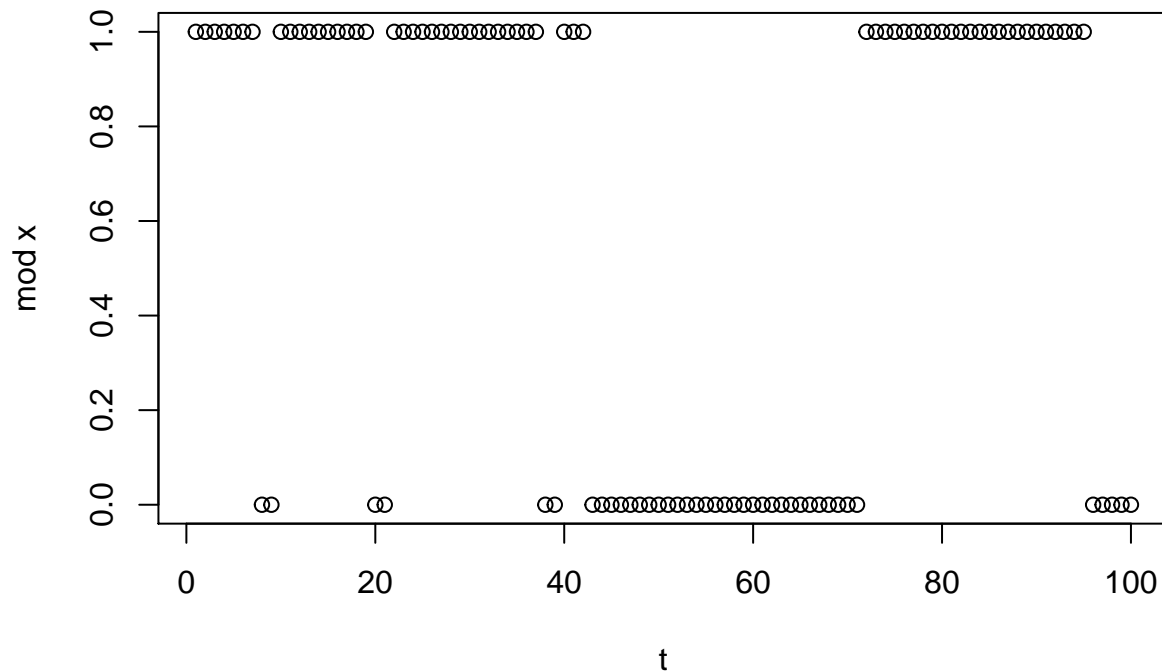
p = 0.9
mod_x = rep(NA,T)
k = filtering_and_prediction(p)
filtering_state_1 = k[1,]
filtering_state_2 = k[2,]
Modal_config <- function(p){
  mod_x[T] = maximizer(filtering_state_1[T],filtering_state_2[T])

  for (t in (T-1):1){
    if (mod_x[t+1] == 1){
      sampling_state_1 = p*filtering_state_1[t]
      sampling_state_2 = (1-p)*filtering_state_2[t]
    }else{
      sampling_state_1 = (1-p)*filtering_state_1[t]
      sampling_state_2 = p*filtering_state_2[t]
    }
    mod_x[t] = maximizer(sampling_state_1,sampling_state_2)
  }
  return(mod_x)
}
mod_x = Modal_config(p)

# plotting X and modal configuration of X
plot(mod_x, xlab = "t",ylab = "mod x",main= "modal configuration of x for p=0.9")

```

modal configuration of x for p=0.9



The above plot shows the modal configuration of X for p=0.9.

Question 3.

I will be using the same code written in problem 2. to solve this problem.

I first have read the **sequence.txt** file then created the discrete probability function for $Y_t|X_t$
Code:

```
y = strsplit(readLines("C:/Users/Monalisha/Desktop/sequence.txt"),"")[[1]]

## Warning in readLines("C:/Users/Monalisha/Desktop/sequence.txt"): incomplete
## final line found on 'C:/Users/Monalisha/Desktop/sequence.txt'

T = length(y)
p = 0.9998

y_cond_distbn <- function(Y,x){
  emission_state_2 = c(0.27,0.2084,0.198,0.3236)
  emission_state_1 = c(0.2462,0.2476,0.2985,0.2077)
  val_y = c("A","C","G","T")
  if(x == 0){
    for(i in 1:4){
      if(Y == val_y[i]){
        return(emission_state_2[i])
      }
    }
  }else{
    for(i in 1:4){
      if(Y == val_y[i]){
        return(emission_state_1[i])
      }
    }
  }
}
```

Here our final aim is to find the most likely state at each time point. In order to do so I have generated the smoothing distribution for the y values and found the mode of this distribution at each time point. In order to authenticate the way I am finding the mode I have done simulation on the same set of emission and transition matrices and found my modal distribution to be fairly correct. code for the modal distribution is given below :

```
filtering_state_1 = rep(NA,T)
filtering_state_2 = rep(NA,T)
prediction_state_1 = rep(NA,T)
prediction_state_2 = rep(NA,T)
Z = rep(NA,T)
prop_filtering_function <- function(prediction,dist_func){
  return(prediction*dist_func)
}
```

```

prediction_function <- function(p,filtering1,filtering2,state){
  if (state == 1){
    return(p*filtering1 + (1-p)*filtering2)
  }else{
    return((1-p)*filtering1 + p*filtering2)
  }
}

maximizer <- function(a,b){
  if (a > b){
    return(1)
  }else{
    return(0)
  }
}

filtering_and_prediction <- function(p){
  for (t in 1:T){
    if (t == 1){
      prediction_state_1[t] = 0.5
      prediction_state_2[t] = 0.5
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         y_cond_distbn(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                         y_cond_distbn(y[t],0))

      norm_constant = prop_filtering_state_1 + prop_filtering_state_2
      filtering_state_1[t] = prop_filtering_state_1/norm_constant
      filtering_state_2[t] = prop_filtering_state_2/norm_constant
      Z[t] = norm_constant
    }else{
      prediction_state_1[t] = prediction_function(p,filtering_state_1[t-1],
                                                  filtering_state_2[t-1],1)
      prediction_state_2[t] = prediction_function(p,filtering_state_1[t-1],
                                                  filtering_state_2[t-1],0)
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         y_cond_distbn(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                         y_cond_distbn(y[t],0))

      norm_constant = prop_filtering_state_1 + prop_filtering_state_2
      filtering_state_1[t] = prop_filtering_state_1/norm_constant
      filtering_state_2[t] = prop_filtering_state_2/norm_constant
      Z[t] = norm_constant
    }
  }
  return(matrix(c(filtering_state_1,filtering_state_2,
                  prediction_state_1,prediction_state_2,Z),nrow = 5, byrow = TRUE))
}

k = filtering_and_prediction(p)
filtering_state_1 = k[1,]
filtering_state_2 = k[2,]
prediction_state_1 = k[3,]
prediction_state_2 = k[4,]

```



```

Z = k[5,]

smoothing_function <- function(p,filtering,smoothing1,prediction1,
                               smoothing2,prediction2,state){
  if (state == 1){
    return((p*filtering*smoothing1/prediction1) +
            ((1-p)*filtering*smoothing2/prediction2))
  }else{
    return(((1-p)*filtering*smoothing1/prediction1) +
            (p*filtering*smoothing2/prediction2))
  }
}

smoothing <- function(p){
  for (t in T:1){
    if (t == T){
      smoothing_state_1[t] = filtering_state_1[t]
      smoothing_state_2[t] = filtering_state_2[t]
    }else{
      smoothing_state_1[t] = smoothing_function(p,filtering_state_1[t],
                                                smoothing_state_1[t+1],
                                                prediction_state_1[t+1],
                                                smoothing_state_2[t+1],
                                                prediction_state_2[t+1],1)
      smoothing_state_2[t] = smoothing_function(p,filtering_state_2[t],
                                                smoothing_state_1[t+1],
                                                prediction_state_1[t+1],
                                                smoothing_state_2[t+1],
                                                prediction_state_2[t+1],0)
    }
  }
  return(return(matrix(c(smoothing_state_1,smoothing_state_2),nrow = 2, byrow = TRUE)))
}

l = smoothing(p)
smoothing_state_1 = l[1,]
smoothing_state_2 = l[2,]

for (i in 1:T){
  mod_x[i] = maximizer(smoothing_state_1[i],smoothing_state_2[i])
}

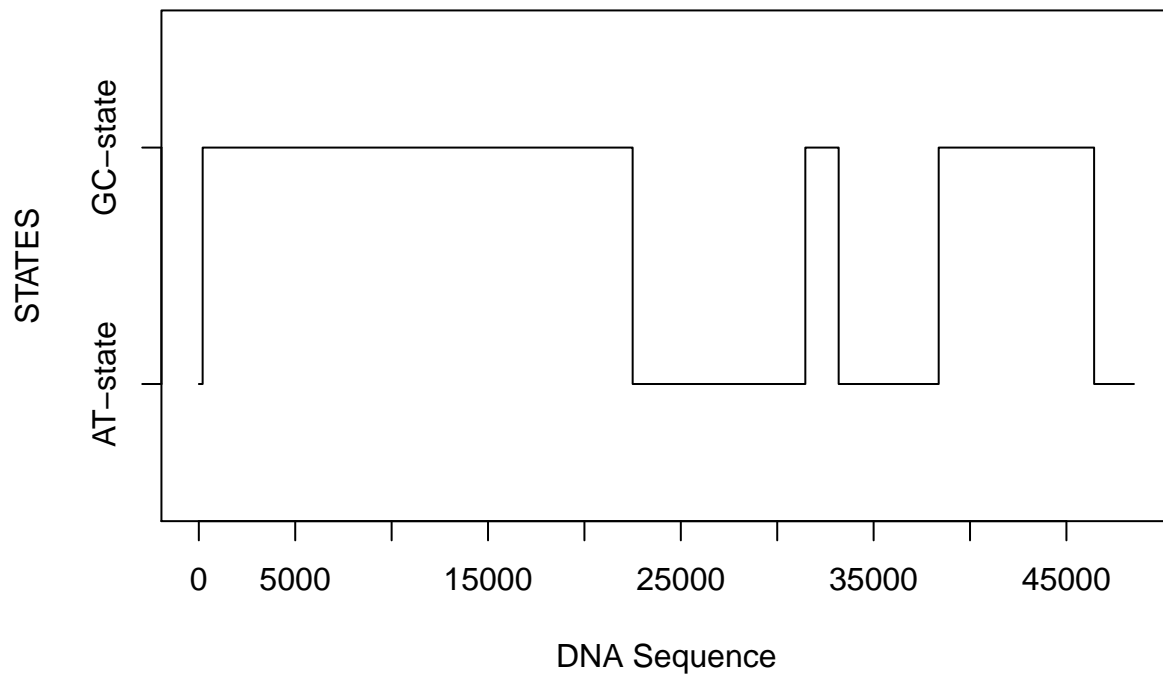
# Plot the sequence

plot(mod_x, main = "Hidden states for the DNA problem",
      xlab = "DNA Sequence", ylab = "STATES", xaxt = "n", yaxt = "n", ylim = c(-0.5,
                                                                                   1.5), type = "l")

axis(side = 1, at = seq(from = 0, to = T, by = 5000))
axis(side = 2, at = c(0, 1), labels = c("AT-state", "GC-state"))

```

Hidden states for the DNA problem



Now we have to find the blocks of each states.

Code:

```
change_index = c(1)
for (i in 2:length(mod_x)){
  if (mod_x[i] != mod_x[i-1]){
    change_index = c(change_index,i)
  }
}

block_DNAsequence = list()
for (i in 1:length(change_index)){
  if (i != length(change_index)){
    block_DNAsequence[[i]] = y[change_index[i]:change_index[i+1]]

  }else{
    block_DNAsequence[[i]] = y[change_index[i]:length(change_index)]
  }
}

state_names = c("AT-state", "GC-state","AT-state", "GC-state",
                "AT-state", "GC-state","AT-state")

for (i in 1:7){
  print(paste0("block number ",i," state name ",state_names[i],
```

```
        " contains ",length(block_DNAsequence[[i]])," elements."))  
}
```

```
## [1] "block number 1 state name AT-state contains 199 elements."  
## [1] "block number 2 state name GC-state contains 22304 elements."  
## [1] "block number 3 state name AT-state contains 8957 elements."  
## [1] "block number 4 state name GC-state contains 1730 elements."  
## [1] "block number 5 state name AT-state contains 5189 elements."  
## [1] "block number 6 state name GC-state contains 8062 elements."  
## [1] "block number 7 state name AT-state contains 46430 elements."
```

```
print(paste0("total number of elements in the sequence is ",  
            length(y)))
```

```
## [1] "total number of elements in the sequence is 48502"
```

Hence the above is the segregation w.r.t the two states.

Question 4.

Here in this problem we first check the simplest case i.e; $L(z, x) = \sum 1_{x_t \neq z_t}$.

The posterior expectation of this expression would be as following

$$E_{x|y}(L(z, x)) = \sum E_{x|y}(1_{x_t \neq z_t}) = \sum (1 - P(x_t = z_t | y_{1:T}))$$

Hence the *argmin* of the above expression will basically be the maximizer of the probability $P(x_t = z_t | y_{1:T})$, which is the smoothing distribution at time t i.e;

$$z^* = \operatorname{argmax} \pi(x_t | y_{1:T})$$

The above is called the Optimal Bayes Estimator(OBE).

Now lets dive into the more complicated case when $L(z, x)$ can be written as

$$L(z, x) = \sum 1_{x_t \neq z_t} + \lambda \sum 1_{[x_t \neq z_t]} 1_{[x_{t+1} \neq z_{t+1}]}$$

Then we can also rewrite the above expression in the following way.

$$L(z, x) = \sum (x_t - z_t)^2 + \lambda \sum (x_t - z_t)^2 (x_{t+1} - z_{t+1})^2$$

Now if we take the posterior expectation over the above expression we will get the following.

$$E_{x|y}L(z, x) = E_{x|y} \sum (x_t - z_t)^2 + \lambda E_{x|y} \sum (x_t - z_t)^2 (x_{t+1} - z_{t+1})^2$$

Now the first term can be written as

$$E_{x|y} \sum (x_t - z_t)^2 = \sum_{t=1}^T E_{x|y} (x_t + z_t - 2 * x_t * z_t) \text{ note that } x_t^2 = x_t \text{ and } z_t^2 = z_t$$

$$\text{Hence } E_{x|y} \sum (x_t - z_t)^2 = \sum_{t=1}^T (Z_t - 2 * Z_t * P(x_t = 1 | y_{1:T})) + \text{Constant}$$

And that of the second term would be

$$\begin{aligned} & \lambda E_{x|y} \sum (x_t - z_t)^2 (x_{t+1} - z_{t+1})^2 \\ &= \lambda \sum_{t=1}^{T-1} z_t z_{t+1} - 2 z_t z_{t+1} \mathbb{E}_{x|y}(x_{t+1}) + z_t \mathbb{E}_{x|y}(x_{t+1}) \\ & \quad - 2 z_t z_{t+1} \mathbb{E}_{x|y}(x_t) + 4 z_t z_{t+1} \mathbb{E}_{x|y}(x_t x_{t+1}) - 2 z_t \mathbb{E}_{x|y}(x_t x_{t+1}) \\ & \quad + z_{t+1} \mathbb{E}_{x|y}(x_t) - 2 z_{t+1} \mathbb{E}_{x|y}(x_t x_{t+1}) + \mathbb{E}_{x|y}(x_t x_{t+1}), \end{aligned}$$

Where $E_{x|y}(x_t) = P(x_t = 1 | y_{1:T})$, $E_{x|y}(x_{t+1}) = P(x_{t+1} = 1 | y_{1:T})$ and $E_{x|y}(x_t x_{t+1}) = P(x_t = 1, x_{t+1} = 1 | y_{1:T})$

It can be easily seen that the expressions for all the above expressions has already been coded in question.2 except for the 3rd expectation Now $E_{x|y}(x_t x_{t+1})$ is basically the inner function which we earlier summing out over x_{t+1} .

Let us now code the above process.

Here for $T=500$, the hidden state has been simulated with transition probability $p = 0.8$ and then based on that a discrete y distribution has been generated same as in question 2. I have created all the stages same as that of question 2 along with that the vector named *joint_smoothing_state_1* has been created which is additionally storing the values of $P(x_t = 1, x_{t+1} = 1 | y_{1:T})$. here q for the discrete distribution of y given x has been taken 0.95. code:

```
# question 4
p <- 0.80
T = 500
set.seed(1234567)
x = rep(NA,T)
y = rep(NA,T)

x[1] = as.numeric(runif(1) > 0.5)
for (i in 2:T){
  if (runif(1) < p){
    x[i] = x[i-1]
  }else{
    x[i] = 1-x[i-1]
  }
}

q = 0.95
y = rep(NA,T)
gen_y <- function(q){
  for(i in 1:T){
    if(runif(1) < q){
      y[i] = x[i]
    }else{
      y[i] = 1-x[i]
    }
  }
  return(y)
}

y = gen_y(q)

dist_func_bernoulli <- function(y,x){
  if ( y == x){
    return(q)
  }else{
    return(1-q)
  }
}

filtering_state_1 = rep(NA,T)
filtering_state_2 = rep(NA,T)
prediction_state_1 = rep(NA,T)
prediction_state_2 = rep(NA,T)
Z = rep(NA,T)

prop_filtering_function <- function(prediction,dist_func){
```

```

    return(prediction*dist_func)
}

prediction_function <- function(p,filtering1,filtering2,state){
  if (state == 1){
    return(p*filtering1 + (1-p)*filtering2)
  }else{
    return((1-p)*filtering1 + p*filtering2)
  }
}

filtering_and_prediction <- function(p){
  for (t in 1:T){
    if (t == 1){
      prediction_state_1[t] = 0.5
      prediction_state_2[t] = 0.5
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         dist_func_bernoulli(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                         dist_func_bernoulli(y[t],0))

      norm_constant = prop_filtering_state_1 + prop_filtering_state_2
      filtering_state_1[t] = prop_filtering_state_1/norm_constant
      filtering_state_2[t] = prop_filtering_state_2/norm_constant
      Z[t] = norm_constant
    }else{
      prediction_state_1[t] = prediction_function(p,filtering_state_1[t-1],
                                                  filtering_state_2[t-1],1)
      prediction_state_2[t] = prediction_function(p,filtering_state_1[t-1],
                                                  filtering_state_2[t-1],0)
      prop_filtering_state_1 = prop_filtering_function(prediction_state_1[t],
                                                         dist_func_bernoulli(y[t],1))
      prop_filtering_state_2 = prop_filtering_function(prediction_state_2[t],
                                                         dist_func_bernoulli(y[t],0))

      norm_constant = prop_filtering_state_1 + prop_filtering_state_2
      filtering_state_1[t] = prop_filtering_state_1/norm_constant
      filtering_state_2[t] = prop_filtering_state_2/norm_constant
      Z[t] = norm_constant
    }
  }
  return(matrix(c(filtering_state_1,filtering_state_2,prediction_state_1,
                  prediction_state_2,Z),nrow = 5, byrow = TRUE))
}

k = filtering_and_prediction(p)
filtering_state_1 = k[1,]
filtering_state_2 = k[2,]
prediction_state_1 = k[3,]
prediction_state_2 = k[4,]

# smoothing
smoothing_state_1 = rep(NA,T)

```

```

smoothing_state_2 = rep(NA,T)
joint_smoothing = rep(NA,T)
smoothing_joint_function <- function(p,filtering,smoothing1,prediction1){
  return(p*filtering*smoothing1/prediction1)
}
smoothing_function <- function(p,filtering,smoothing1,prediction1,smoothing2,prediction2,state){
  if (state == 1){
    return((p*filtering*smoothing1/prediction1) +
           ((1-p)*filtering*smoothing2/prediction2))
  }else{
    return(((1-p)*filtering*smoothing1/prediction1) +
           (p*filtering*smoothing2/prediction2))
  }
}

smoothing <- function(p){
  for (t in T:1){
    if (t == T){
      smoothing_state_1[t] = filtering_state_1[t]
      smoothing_state_2[t] = filtering_state_2[t]

    }else{
      smoothing_state_1[t] = smoothing_function(p,filtering_state_1[t],
                                                smoothing_state_1[t+1],
                                                prediction_state_1[t+1],
                                                smoothing_state_2[t+1],
                                                prediction_state_2[t+1],1)
      smoothing_state_2[t] = smoothing_function(p,filtering_state_2[t],
                                                smoothing_state_1[t+1],
                                                prediction_state_1[t+1],
                                                smoothing_state_2[t+1],
                                                prediction_state_2[t+1],0)
      joint_smoothing[t] = smoothing_joint_function(p,filtering_state_1[t],
                                                    smoothing_state_1[t+1],
                                                    prediction_state_1[t+1])
    }
  }
  return(return(matrix(c(smoothing_state_1,joint_smoothing),nrow = 2, byrow = TRUE)))
}

l = smoothing(p)
smoothing_state_1 = l[1,]
joint_smoothing_state_1 = l[2,]

```

Now in the next phase I have computed the expected loss at each time point and stored the values in the matrix A.

Now to minimize this loss function I have applied the procedure of question 1. but here instead of finding the argmax I have done argmin.

Code:

```

exp_loss_at_t = function(t, z, lambda) {
  # first part

  first_part = z[1] - (2 * z[1] * smoothing_state_1[t]) +
    (lambda*((z[1] * smoothing_state_1[t+1]) - (2 * z[1] * joint_smoothing_state_1[t])))
  # second part
  second_part1 = (z[1] * z[2]) - (2 * z[1] * z[2] * smoothing_state_1[t+1]) -
    (2 * z[1] * z[2] * smoothing_state_1[t]) + (4 * z[1] * z[2] * joint_smoothing_state_1[t]) +
    (z[2] * smoothing_state_1[t]) - (2 * z[2] * joint_smoothing_state_1[t])

  second_part = lambda*second_part1

  return(first_part+second_part)
}

A = matrix(NA, nrow = 2 , ncol = T)
compute_loss_matrix = function(lambda){
  for (t in 1:T){
    if (t!= T) {
      z_0 = exp_loss_at_t(t,c(1,2),lambda) + exp_loss_at_t(t,c(1,1),lambda)
      z_1 = exp_loss_at_t(t,c(2,1),lambda) + exp_loss_at_t(t,c(2,2),lambda)
      A[1,t] = z_0
      A[2,t] = z_1

    }else{
      A[1,t] = 1 - (2 * 1 * smoothing_state_1[t])
      A[2,t] = 2 - (2 * 2 * smoothing_state_1[t])
    }
  }
  return(A)
}

A = compute_loss_matrix(lambda = 1)
M <- 2
N <- T
H <- matrix(NA, M, N)
D <- 1
H[, 1] <- A[, 1]

for(j in 2:N) {
  for(i in 1:M) {
    ii <- which.min(H[, j-1] + A[i, j])
    H[i, j] <- H[ii, j-1] + A[i, j]
  }
}

xs <- numeric(N)
xs[N] <- which.min(H[, N])
for(j in (N-1):1) {
  i.low <- max(1, xs[j+1]-D)
  i.high <- min(M, xs[j+1]+D)
  ii <- i.low - 1 + which.min(H[i.low:i.high, j])
  xs[j] <- ii
}

```



```

}
xs = xs -1

g = (x-xs)^2

print(paste("Misclassification = ",sum(g)))

```

```
## [1] "Misclassification = 22"
```

Hence from above we see that there are 22 misclassifications which is fairly good for $T=500$. Now plotting the predicted vs the actual will give us the following.

```

plot(x, type="l",main = "hidden state in black dots and the prediction in red line",
      lwd = 2,ylab = "actual vs. predicted",xlab = "time")
lines(xs, type="l",col = "red",lwd = 2,
      ylab = NULL,xlab = NULL)

```

hidden state in black dots and the prediction in red line

