Lab2

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Q1.1

```r
Trans <- matrix(0, nrow = 10, ncol = 10)
Emiss <- matrix(0, nrow = 10, ncol = 10)

re_index <- function(i){
  i <- i %% 10
  if (i %% 10 == 0) {
    i = 10
  }
  return(i)
}

for (i in 1:10) {

  Trans[i, i] = 0.5
  Trans[i, re_index(i+1)] = 0.5

  Emiss[i, i] <- 0.2
  Emiss[i, re_index(i+1)] <- 0.2
  Emiss[i, re_index(i-1)] <- 0.2
  Emiss[i, re_index(i+2)] <- 0.2
  Emiss[i, re_index(i-2)] <- 0.2
}


model <- initHMM(States = c(1:10), Symbols = c(1:10),
               transProbs = Trans,
               emissionProbs = Emiss)
model
```

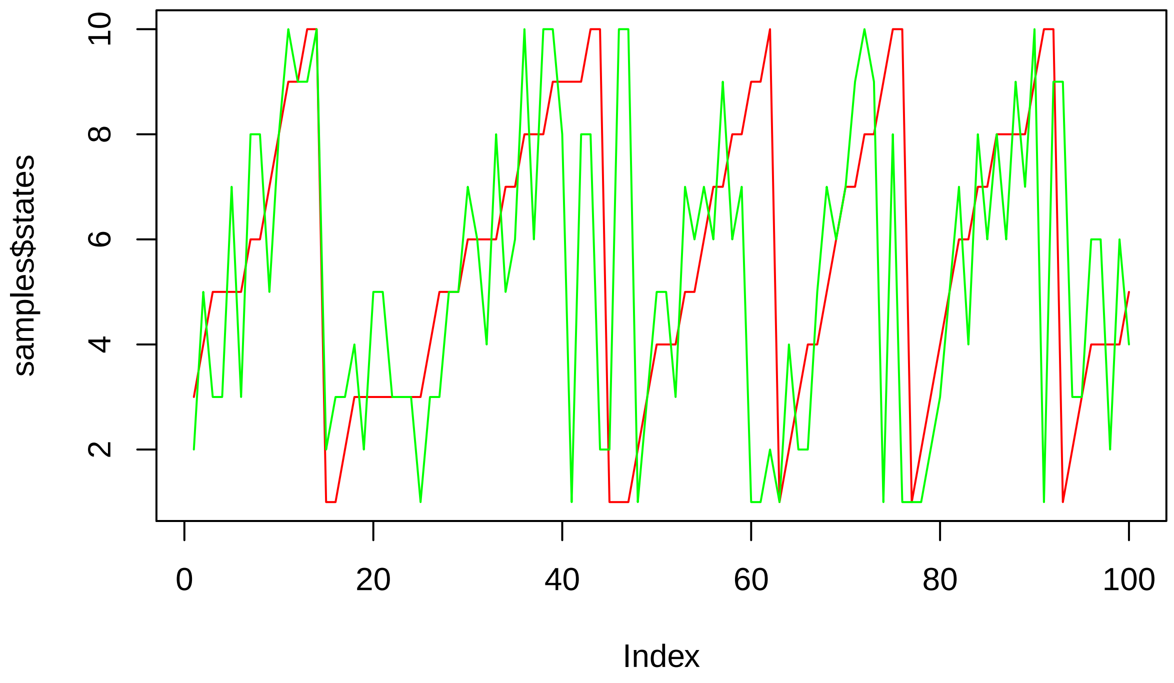
```
## $States
##  [1]  1  2  3  4  5  6  7  8  9 10
##
## $Symbols
##  [1]  1  2  3  4  5  6  7  8  9 10
##
## $startProbs
##    1   2   3   4   5   6   7   8   9  10
## 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
##
## $transProbs
##     to
## from   1   2   3   4   5   6   7   8   9  10
##    1  0.5 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
##    2  0.0 0.5 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0
##    3  0.0 0.0 0.5 0.5 0.0 0.0 0.0 0.0 0.0 0.0
##    4  0.0 0.0 0.0 0.5 0.5 0.0 0.0 0.0 0.0 0.0
##    5  0.0 0.0 0.0 0.0 0.5 0.5 0.0 0.0 0.0 0.0
##    6  0.0 0.0 0.0 0.0 0.0 0.5 0.5 0.0 0.0 0.0
##    7  0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.5 0.0 0.0
##    8  0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.5 0.0
##    9  0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.5
##    10 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5
##
## $emissionProbs
##       symbols
## states   1   2   3   4   5   6   7   8   9  10
##     1  0.2 0.2 0.2 0.0 0.0 0.0 0.0 0.0 0.2 0.2
##     2  0.2 0.2 0.2 0.2 0.0 0.0 0.0 0.0 0.0 0.2
##     3  0.2 0.2 0.2 0.2 0.2 0.0 0.0 0.0 0.0 0.0
##     4  0.0 0.2 0.2 0.2 0.2 0.2 0.0 0.0 0.0 0.0
##     5  0.0 0.0 0.2 0.2 0.2 0.2 0.2 0.0 0.0 0.0
##     6  0.0 0.0 0.0 0.2 0.2 0.2 0.2 0.2 0.0 0.0
##     7  0.0 0.0 0.0 0.0 0.2 0.2 0.2 0.2 0.2 0.0
##     8  0.0 0.0 0.0 0.0 0.0 0.2 0.2 0.2 0.2 0.2
##     9  0.2 0.0 0.0 0.0 0.0 0.0 0.2 0.2 0.2 0.2
##     10 0.2 0.2 0.0 0.0 0.0 0.0 0.0 0.2 0.2 0.2
```

Q1.2

```
set.seed(1234)
samples <- simHMM(model, 100)
samples
```

```
## $states
##   [1]  3  4  5  5  5  5  6  6  7  8  9  9 10 10  1  1  2  3  3  3  3  3  3  3  3
##  [26]  4  5  5  5  6  6  6  6  7  7  8  8  8  9  9  9  9 10 10  1  1  1  2  3  4
##  [51]  4  4  5  5  6  7  7  8  8  9  9 10  1  2  3  4  4  5  6  7  7  8  8  9 10
##  [76] 10  1  2  3  4  5  6  6  7  7  8  8  8  8  9 10 10  1  2  3  4  4  4  4  5
##
## $observation
##   [1]  2  5  3  3  7  3  8  8  5  8 10  9  9 10  2  3  3  4  2  5  5  3  3  3  1
##  [26]  3  3  5  5  7  6  4  8  5  6 10  6 10 10  8  1  8  8  2  2 10 10  1  3  5
##  [51]  5  3  7  6  7  6  9  6  7  1  1  2  1  4  2  2  5  7  6  7  9 10  9  1  8
##  [76]  1  1  1  2  3  5  7  4  8  6  8  6  9  7 10  1  9  9  3  3  6  6  2  6  4
```

```
plot(samples$states, type='l', col='red')
lines(samples$observation, col='green')
```



Q1.3

```
fw <- exp(forward(model, samples$observation))
bw <- exp(backward(model, samples$observation))

filtering <- prop.table(fw, 2)
smoothing <- prop.table(fw*bw, 2)
```

Q1.4

```
filter_postion = apply(filtering, 2, which.max)
smooth_postion = apply(smoothing, 2, which.max)
viterbi_position<- viterbi(model, samples$observation)

acc_filter <- sum(filter_postion == samples$states) / 100
print(paste("Accuracy of filter:",acc_filter) )
```

```
## [1] "Accuracy of filter: 0.63"
```

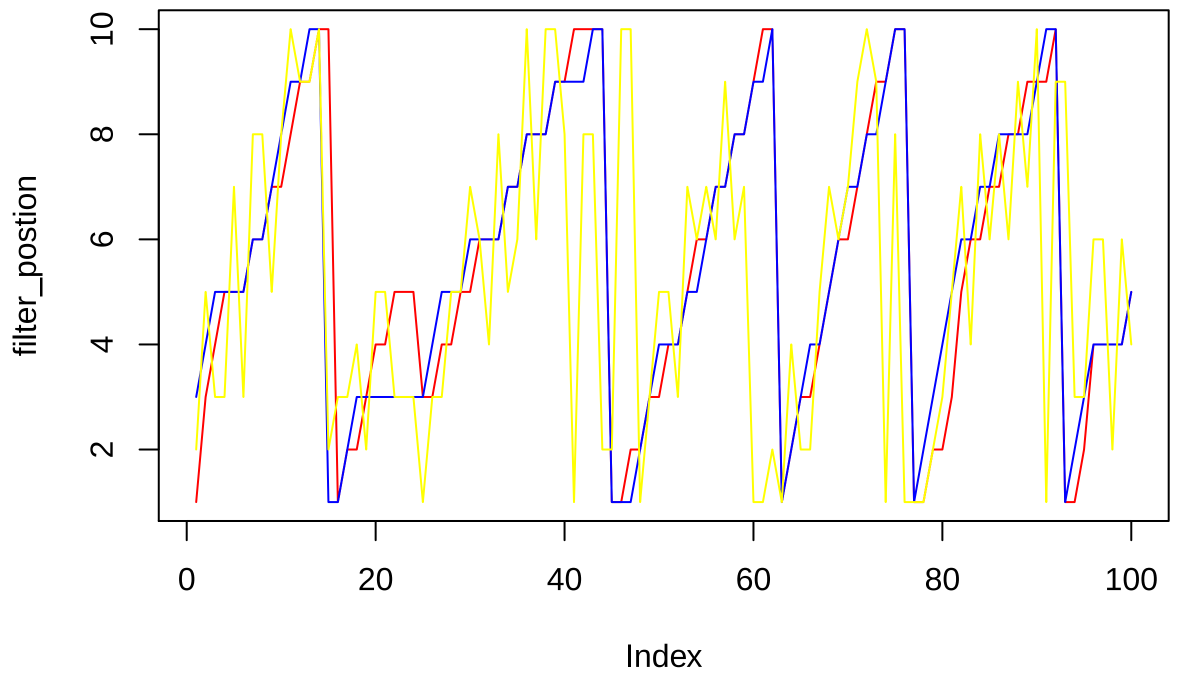
```
acc_smooth <- sum(smooth_postion == samples$states) / 100
print(paste("Accuracy of smooth:",acc_smooth) )
```

```
## [1] "Accuracy of smooth: 0.75"
```

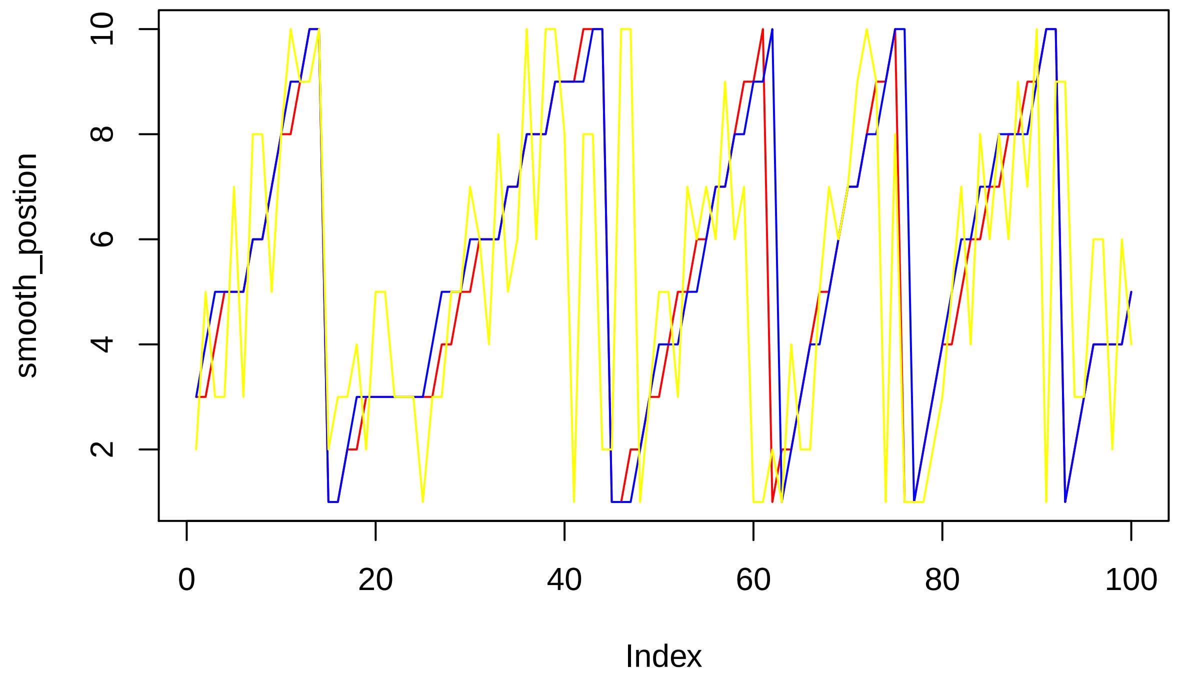
```
acc_viterbi <- sum(viterbi_position == samples$states) / 100
print(paste("Accuracy of viterbi:",acc_viterbi) )
```

```
## [1] "Accuracy of viterbi: 0.49"
```

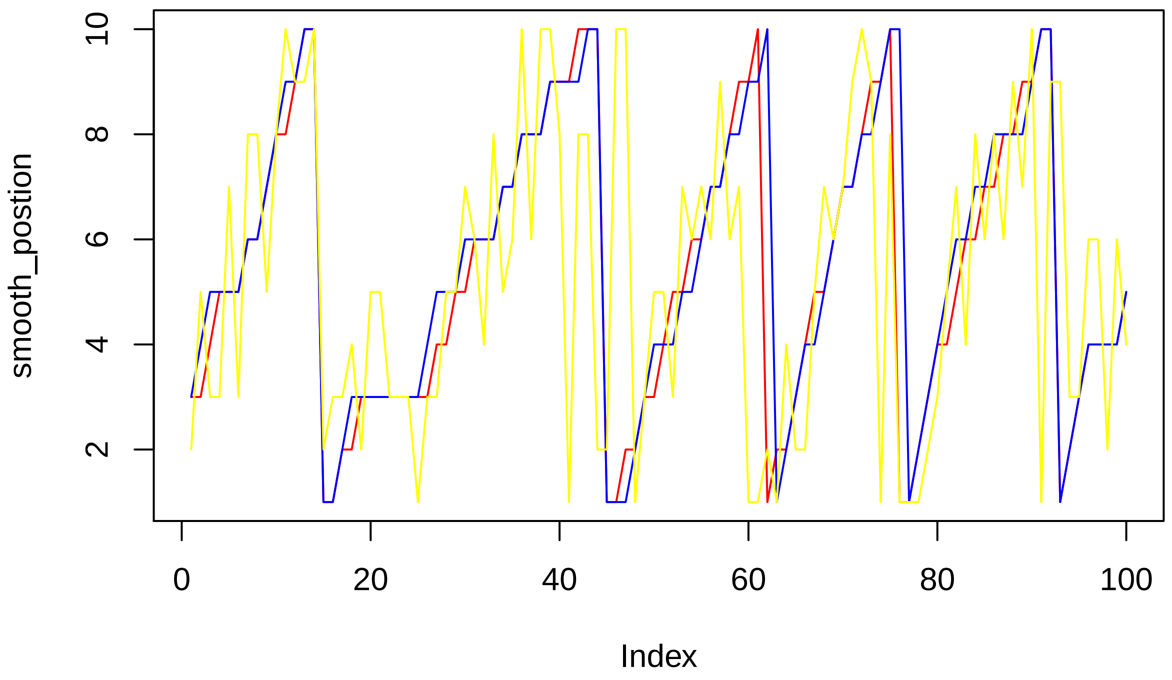
```
plot(filter_postion, type='l', col='red')
lines(samples$states, col='blue')
lines(samples$observation, col='yellow')
```



```r
plot(smooth_postion, type='l', col='red')
lines(samples$states, col='blue')
lines(samples$observation, col='yellow')
```



```r
plot(smooth_postion, type='l', col='red')
lines(samples$states, col='blue')
lines(samples$observation, col='yellow')
```



Q1.5

```r
#set.seed(1234)
repeat_size <- 100
acc_filters <- c()
acc_smooths <- c()
acc_viterbis <- c()

for (i in 1:repeat_size) {

  sample_size <- 100
  samples <- simHMM(model, sample_size)
  fw <- exp(forward(model, samples$observation))
  bw <- exp(backward(model, samples$observation))

  filtering <- prop.table(fw, 2)
  smoothing <- prop.table(fw*bw, 2)

  filter_postion = apply(filtering, 2, which.max)
  smooth_postion = apply(smoothing, 2, which.max)
  viterbi_position<- viterbi(model, samples$observation)

  acc_filter <- sum(filter_postion == samples$states) / sample_size
  acc_smooth <- sum(smooth_postion == samples$states) / sample_size
  acc_viterbi <- sum(viterbi_position == samples$states) / sample_size

  acc_filters <- c(acc_filters, acc_filter)
  acc_smooths <- c(acc_smooths, acc_smooth)
  acc_viterbis <- c(acc_viterbis, acc_viterbi)
}

avg_acc_filter <- mean(acc_filters)
```

```
print(paste("Average accuracy of filtering:",avg_acc_filter) )
```

```
## [1] "Average accuracy of filtering: 0.5411"
```

```
avg_acc_smooth <- mean(acc_smooths)
print(paste("Average accuracy of smoothing:",avg_acc_smooth) )
```

```
## [1] "Average accuracy of smoothing: 0.6819"
```

```
avg_acc_viterbi <- mean(acc_viterbis)
print(paste("Average accuracy of viterbi:",avg_acc_viterbi) )
```

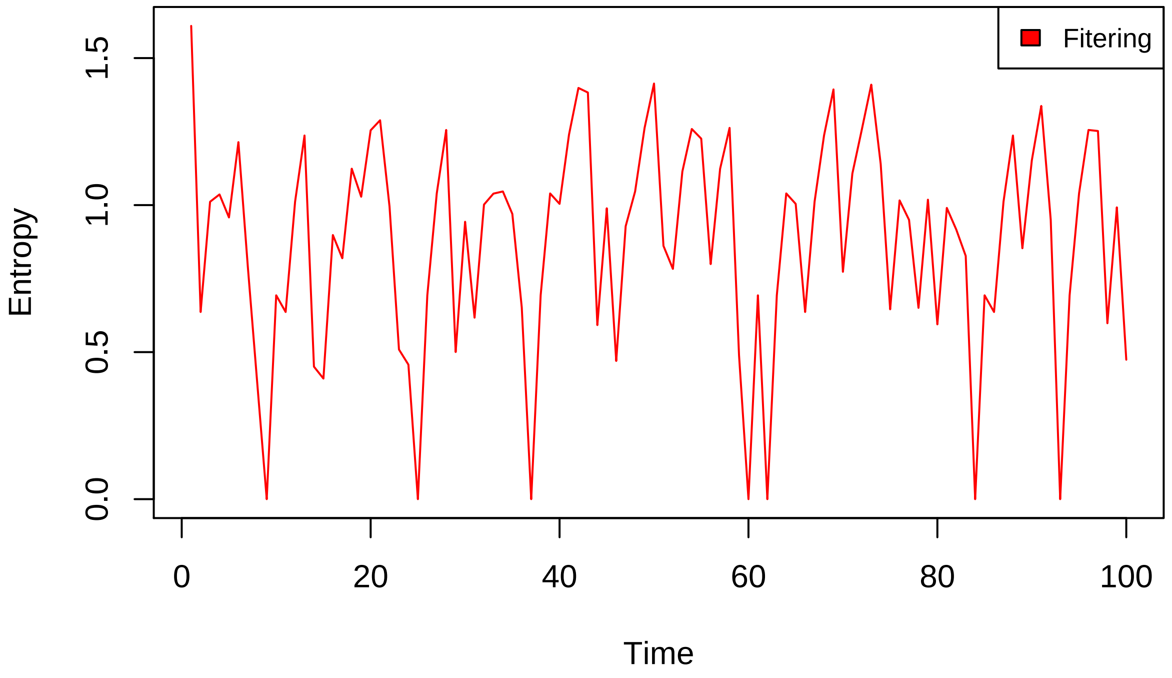
```
## [1] "Average accuracy of viterbi: 0.5124"
```

In general, the smoothed distributions should be more accurate than the filtered distributions. Why ? In general, the smoothed distributions should be more accurate than the most probable paths, too. Why ?

Answer: Smoothed distribution is conditioning on all observations, while filtered distribution is only conditioning on up-to-date observations. Later observations should not effect previous state only if we know the exact physics model and correct observations, but here HMM is probabilistic estimation(we dont have exact physics model as well as correct observations). Therefore HMM is doing probabilistic estimation by Bayes theorem, but we believe state at time t+1, t+2…t+n are dependent on state at time t, therefore the posterior on later observations can be helpful.

Q1.6

```
entropy_filter <- lapply(c(1:100),function(i)entropy.empirical(filtering[,i]))
plot(unlist(entropy_filter), type='l', col='red', xlab = 'Time', ylab = 'Entropy')
legend("topright", legend = c("Fitering"),
         fill = c("red"), cex = 0.8)
```



$$H(x) = -\sum_{n=i}^{N} p_i(x) log p_i(x)$$

According to Information theory, higher entropy indicate higher uncertainty, (i.e. an event happens with probability 1, means no uncertainty, entropy is 0), so the lower entropy the more confidence. As in above plot, we have a very flat trend uncertainty with some disturbance, we didn't see clear increasing or decreasing trend, therefore we can't know better where the robot is in later time (higher confidence).

```r
Z_100= as.matrix(filtering[,100])
t(model$transProbs)%*%Z_100
```

```
##
## to          [,1]
##    1  0.00000000
##    2  0.09090909
##    3  0.50000000
##    4  0.40909091
##    5  0.00000000
##    6  0.00000000
##    7  0.00000000
##    8  0.00000000
##    9  0.00000000
##    10 0.00000000
```

```r
Z_100
```

```
##          [,1]
## 1  0.0000000
## 2  0.1818182
## 3  0.8181818
## 4  0.0000000
## 5  0.0000000
## 6  0.0000000
## 7  0.0000000
## 8  0.0000000
## 9  0.0000000
## 10 0.0000000
```

Appendix

```r
knitr::opts_chunk$set(echo = TRUE)
library(HMM)
library(entropy)
Trans <- matrix(0, nrow = 10, ncol = 10)
Emiss <- matrix(0, nrow = 10, ncol = 10)

re_index <- function(i){
  i <- i %% 10
  if (i %% 10 == 0) {
    i = 10
  }
  return(i)
}
```

```r
for (i in 1:10) {

  Trans[i, i] = 0.5
  Trans[i, re_index(i+1)] = 0.5

  Emiss[i, i] <- 0.2
  Emiss[i, re_index(i+1)] <- 0.2
  Emiss[i, re_index(i-1)] <- 0.2
  Emiss[i, re_index(i+2)] <- 0.2
  Emiss[i, re_index(i-2)] <- 0.2
}


model <- initHMM(States = c(1:10), Symbols = c(1:10),
               transProbs = Trans,
               emissionProbs = Emiss)
model
set.seed(1234)
samples <- simHMM(model, 100)
samples
plot(samples$states, type='l', col='red')
lines(samples$observation, col='green')
fw <- exp(forward(model, samples$observation))
bw <- exp(backward(model, samples$observation))

filtering <- prop.table(fw, 2)
smoothing <- prop.table(fw*bw, 2)
filter_postion = apply(filtering, 2, which.max)
smooth_postion = apply(smoothing, 2, which.max)
viterbi_position<- viterbi(model, samples$observation)

acc_filter <- sum(filter_postion == samples$states) / 100
print(paste("Accuracy of filter:",acc_filter) )
acc_smooth <- sum(smooth_postion == samples$states) / 100
print(paste("Accuracy of smooth:",acc_smooth) )
acc_viterbi <- sum(viterbi_position == samples$states) / 100
print(paste("Accuracy of viterbi:",acc_viterbi) )

plot(filter_postion, type='l', col='red')
lines(samples$states, col='blue')
lines(samples$observation, col='yellow')


plot(smooth_postion, type='l', col='red')
lines(samples$states, col='blue')
lines(samples$observation, col='yellow')

plot(smooth_postion, type='l', col='red')
lines(samples$states, col='blue')
lines(samples$observation, col='yellow')


#set.seed(1234)
```

```r
repeat_size <- 100
acc_filters <- c()
acc_smooths <- c()
acc_viterbis <- c()

for (i in 1:repeat_size) {

  sample_size <- 100
  samples <- simHMM(model, sample_size)
  fw <- exp(forward(model, samples$observation))
  bw <- exp(backward(model, samples$observation))

  filtering <- prop.table(fw, 2)
  smoothing <- prop.table(fw*bw, 2)

  filter_postion = apply(filtering, 2, which.max)
  smooth_postion = apply(smoothing, 2, which.max)
  viterbi_position<- viterbi(model, samples$observation)

  acc_filter <- sum(filter_postion == samples$states) / sample_size
  acc_smooth <- sum(smooth_postion == samples$states) / sample_size
  acc_viterbi <- sum(viterbi_position == samples$states) / sample_size

  acc_filters <- c(acc_filters, acc_filter)
  acc_smooths <- c(acc_smooths, acc_smooth)
  acc_viterbis <- c(acc_viterbis, acc_viterbi)
}

avg_acc_filter <- mean(acc_filters)
print(paste("Average accuracy of filtering:",avg_acc_filter) )
avg_acc_smooth <- mean(acc_smooths)
print(paste("Average accuracy of smoothing:",avg_acc_smooth) )
avg_acc_viterbi <- mean(acc_viterbis)
print(paste("Average accuracy of viterbi:",avg_acc_viterbi) )

entropy_filter <- lapply(c(1:100),function(i)entropy.empirical(filtering[,i]))
plot(unlist(entropy_filter), type='l', col='red', xlab = 'Time', ylab = 'Entropy')
legend("topright", legend = c("Fitering"),
         fill = c("red"), cex = 0.8)
Z_100= as.matrix(filtering[,100])
t(model$transProbs)%*%Z_100
Z_100
```