Lab2

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Contributions

We solved all questions individually and discussed together, we wrote our comment together. Code are mainly from Yifan

Q1.1

```
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
```

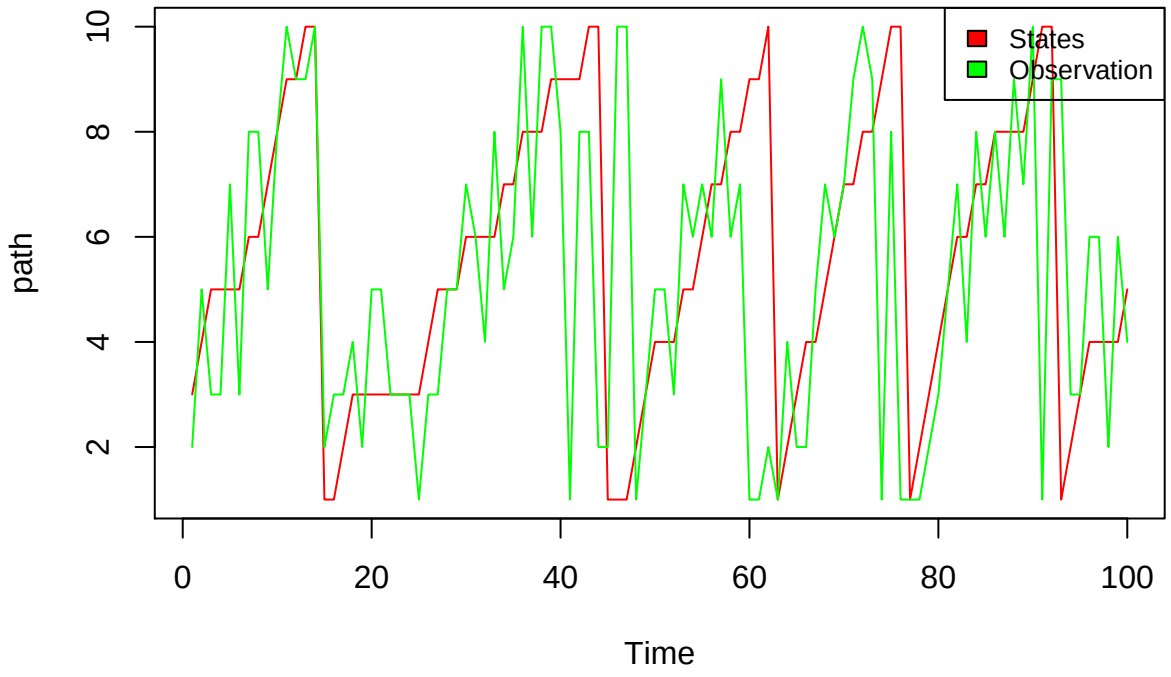
```
##   1   2   3   4   5   6   7   8   9  10
## 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
##
## $transProbs
##     to
## from   1   2   3   4   5   6   7   8   9  10
##   1  0.5 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
##   2  0.0 0.5 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0
##   3  0.0 0.0 0.5 0.5 0.0 0.0 0.0 0.0 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$states, type='l', col='red', xlab = 'Time', ylab = 'path')
lines(samples$observation, col='green')
legend("topright", legend = c("States", "Observation"),
         fill = c("red", "green"), cex = 0.8)
```



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) )
```

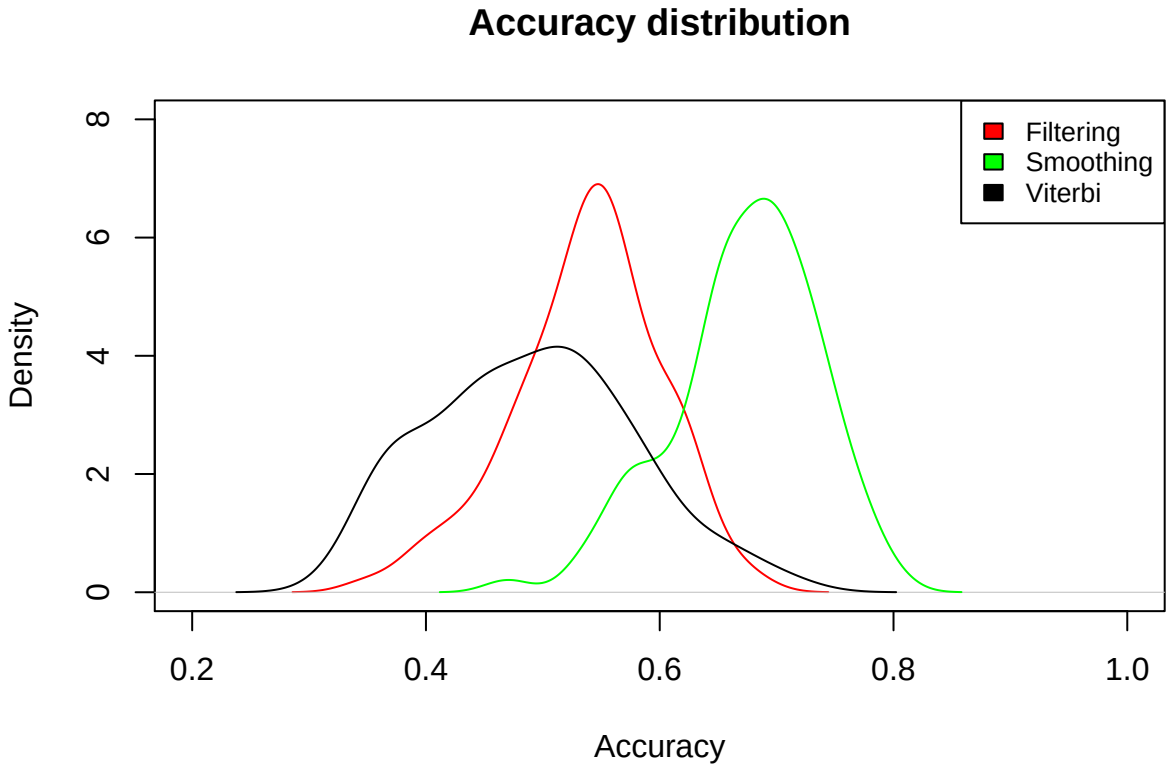
```
## [1] "Accuracy of smooth: 0.75"
```

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

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

Q1.5

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

plot(density(acc_filters),main='Accuracy distribution', xlab = 'Accuracy', xlim=c(0.2,1), ylim=c(0,8),
lines(density(acc_smooths),col='green')
lines(density(acc_viterbis), col='black')
legend("topright", legend = c("Filtering", "Smoothing", "Viterbi"),
         fill = c("red", "green", "black"), cex = 0.8)
```




```
avg_acc_filter <- mean(acc_filters)
print(paste("Average accuracy of filtering:",avg_acc_filter) )
```

```
## [1] "Average accuracy of filtering: 0.5373"
```

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

```
## [1] "Average accuracy of smoothing: 0.6734"
```

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

```
## [1] "Average accuracy of viterbi: 0.4914"
```

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 ?

The filtered distribution is given below:

$$p(z^t|x^{0:t})$$

The smoothing distribution is given below:

$$p(z^t|x^{0:T})$$

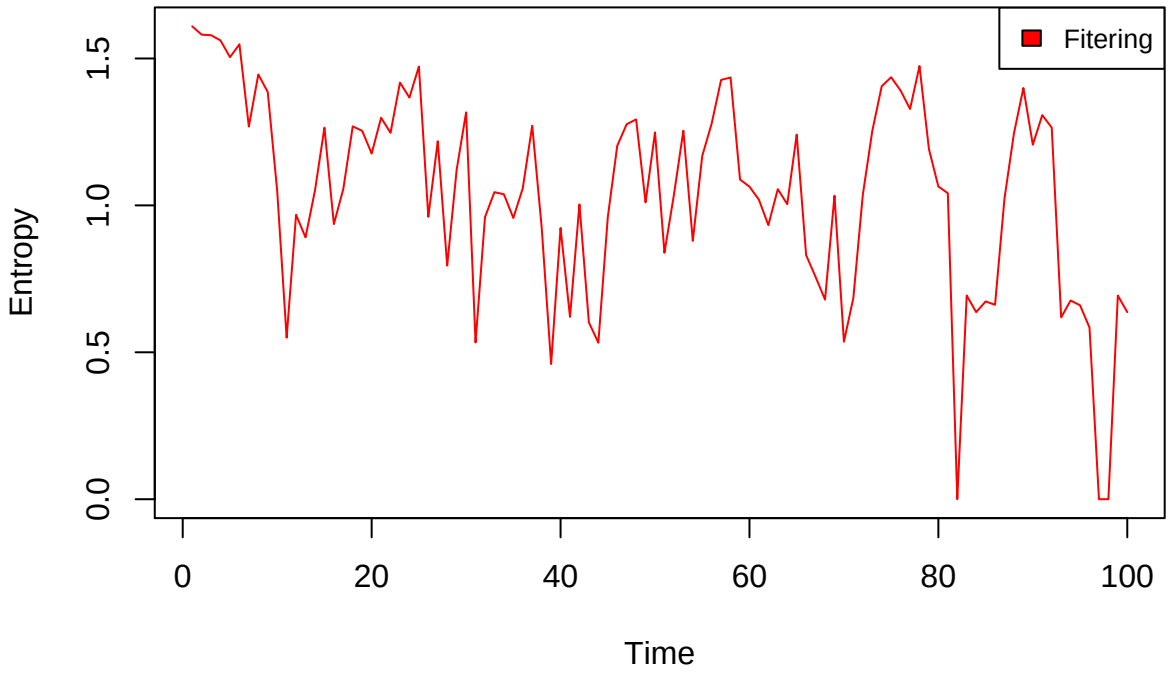
The most probable path:

$$Z_{max}^{0:T} = argmax_{z^{0:T}} P(Z^{0:T}|X^{0:T})$$

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). HMM is doing probabilistic estimation by Bayes theorem, therefore the posterior on more observations can be beneficial to smoothing. For most probable path, this approach try to maximize joint probability of hidden state $P(Z^{0:T}|X^{0:T})$, which can not guarantee the best solution of each hidden state $P(z^t|X^{0:T})$(Smoothing).

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).

Q1.7

$$P(Z_{101}|X_{1:100}) = \sum_{Z_{100}} P(Z_{100}, Z_{101}|X_{1:100}) = \sum_{Z_{100}} P(Z_{100}|X_{1:100}) P(Z_{101}|Z_{100})$$

Notice $P(Z_{100}|X_{1:100})$ is the filtering distribution at time 100, $P(Z_{101}|Z_{100})$ is the transition probability. So, $P(Z_{101}|X_{1:100})$ is the linear combination of transition matrix with filtering distribution $P(Z_{100}|X_{1:100})$, which in the row space of transition matrix.

```
Z_100= as.matrix(filtering[,100])
Z_100
```

```
##          [,1]
## 1  0.3333333
## 2  0.6666667
## 3  0.0000000
## 4  0.0000000
## 5  0.0000000
## 6  0.0000000
## 7  0.0000000
## 8  0.0000000
## 9  0.0000000
## 10 0.0000000
```

```
Z_101 <- t(model$transProbs)%*%Z_100

print(paste("State 101 most likely be", which.max(Z_101)))
```

```
## [1] "State 101 most likely be 2"
```

Appendix

```
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)
}

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$states, type='l', col='red', xlab = 'Time', ylab = 'path')
lines(samples$observation, col='green')
legend("topright", legend = c("States", "Observation"),
         fill = c("red", "green"), cex = 0.8)
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) )

set.seed(123)
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)
}
```

```
plot(density(acc_filters),main='Accuracy distribution', xlab = 'Accuracy', xlim=c(0.2,1), ylim=c(0,8), c
lines(density(acc_smooths),col='green')
lines(density(acc_viterbis), col='black')
legend("topright", legend = c("Filtering", "Smoothing", "Viterbi"),
         fill = c("red", "green", "black"), cex = 0.8)

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])
Z_100
Z_101 <- t(model$transProbs)%*%Z_100

print(paste("State 101 most likely be", which.max(Z_101)))
```