Advanced Machine Learning - Lab 2 - Individual report

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```r
# Load libraries
library(HMM)
```

```
## Warning: package 'HMM' was built under R version 4.0.3
```

```r
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.0.5
```

```r
library(knitr)
library(entropy)
```

```
## Warning: package 'entropy' was built under R version 4.0.5
```

Question 1

We define the transition and emission robability matrices to be used in the second question. We set the transition probability to go from one state to the next to be 0.5 and the emission probabilities to be 0.2 for the 5 points in the interval [i-2 : i+2].

```r
# Parameters
states <- as.character(c(1:10))
symbols <- as.character(c(1:10))
startprob <- rep((1/length(states)), length(states))

# transition matrix
transprob <- diag(x = 0.5, nrow = 10, ncol = 10)
index <- which(transprob == 0.5)
transprob[index[-length(index)] - 1] <- 0.5
transprob[9, 10] <- 0.5
transprob[10, 1] <- 0.5

colnames(transprob) <- as.character(c(1:10))
rownames(transprob) <- as.character(c(1:10))

# Emission Matrix (there's a smarter way of doing this for sure but this works)
emissionprob <- matrix(data = 0, nrow = 10, ncol = 10)
emissionprob[1, c(9, 10, 1, 2, 3)] <- 0.2
emissionprob[2, c(10, 1, 2, 3, 4)] <- 0.2
emissionprob[3, c(1, 2, 3, 4, 5)] <- 0.2
emissionprob[4, c(2, 3, 4, 5, 6)] <- 0.2
emissionprob[5, c(3, 4, 5, 6, 7)] <- 0.2
emissionprob[6, c(4, 5, 6, 7, 8)] <- 0.2
emissionprob[7, c(5, 6, 7, 8, 9)] <- 0.2
emissionprob[8, c(6, 7, 8, 9, 10)] <- 0.2
```

```r
emissionprob[9, c(7, 8, 9, 10, 1)] <- 0.2
emissionprob[10, c(8, 9, 10, 1, 2)] <- 0.2

colnames(emissionprob) <- as.character(c(1:10))
rownames(emissionprob) <- as.character(c(1:10))
```

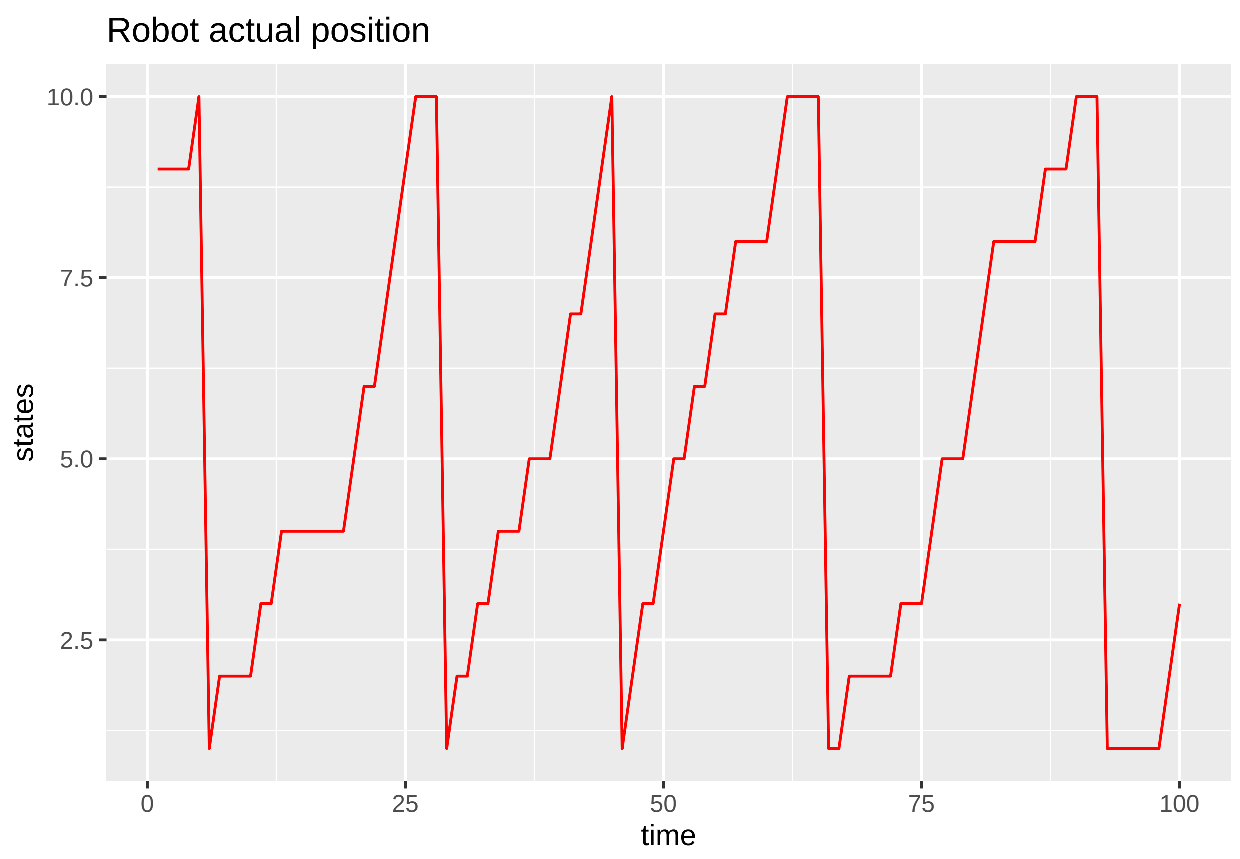
```r
# initialize HMM
HMM <- initHMM(States = states, Symbols = symbols, startProbs = startprob,
               transProbs = transprob, emissionProbs = emissionprob)
```

Question 2

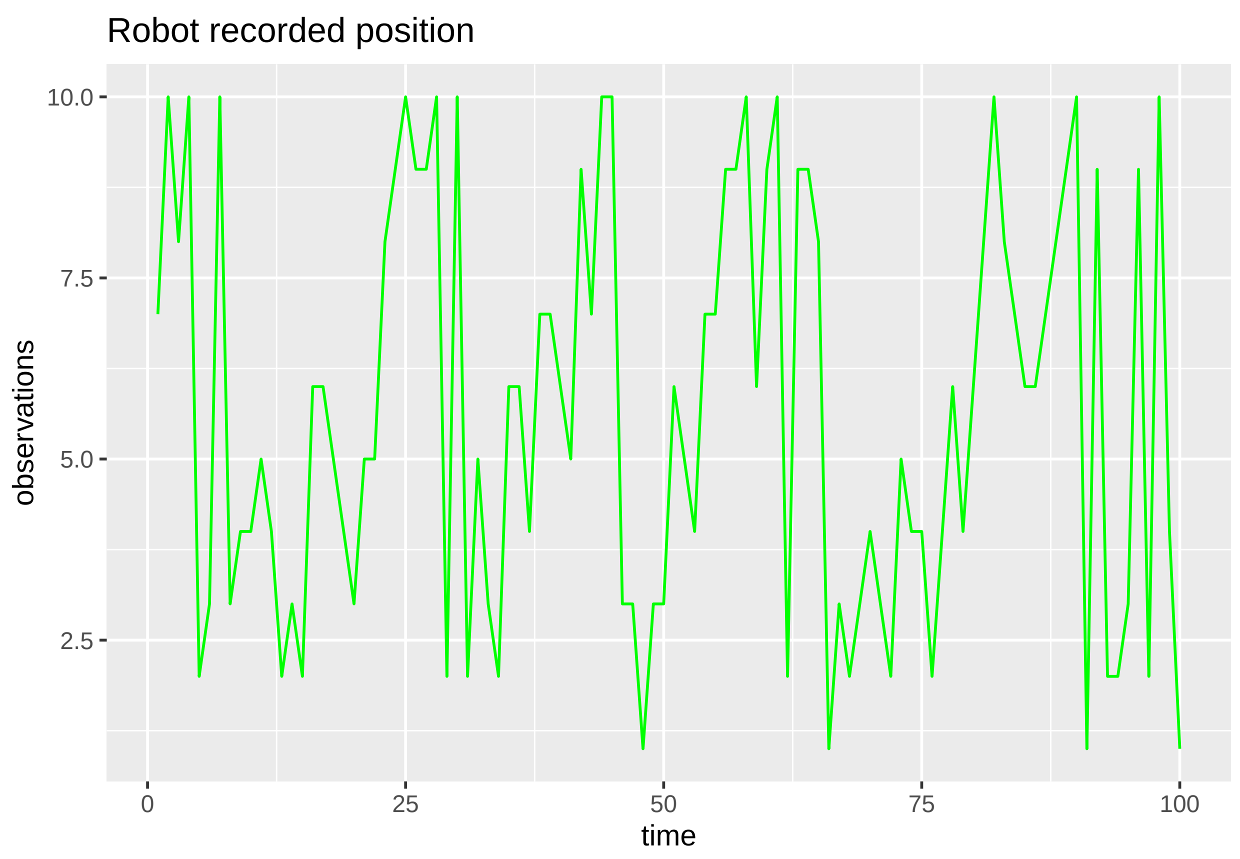
We perform the simulation for 100 time steps and produce the path graphs for the states and the recorded positions.

```r
# We now simulate 100 timesteps
set.seed(12345)
simulation100 <- simHMM(HMM, 100)
```

```r
# plot results
time <- 1:100
states <- as.numeric(simulation100$states)
observations <- as.numeric(simulation100$observation)
df_plot <- data.frame(time, states, observations)

plot_states <- ggplot(df_plot, aes(x = time, y = states))+
  geom_line(col = "red")+
  ggtitle("Robot actual position")

plot_recorded <- ggplot(df_plot, aes(x = time, y = observations))+
  geom_line(col = "green")+
  ggtitle("Robot recorded position")

plot_states
```



```
plot_recorded
```



Question 3

We calculate the filtered, smoothed and viterbi (most probable path) distributions.

```r
# filtered distribution
# alpha
alpha <- exp(forward(hmm = HMM, observation = simulation100$observation))
# beta
beta <- exp(backward(hmm = HMM, observation = simulation100$observation))
# filtered distribution
filter_dist <- prop.table(alpha, margin = 2)
```

```r
# smoothed distribution
smooth_dist <- prop.table(alpha*beta, margin = 2)
```

```r
# most probable path (viterbi algo)
viterbi_path <- viterbi(hmm = HMM, observation = simulation100$observation)
```

Question 4

```r
# accuracy filter
path_filter <- as.character(apply(filter_dist, 2, which.max))
filter_mat <- table(path_filter == simulation100$states)
accuracy_filter <- filter_mat[2]/sum(filter_mat)
```

```r
# accuracy smoothed
path_smooth <- as.character(apply(smooth_dist, 2, which.max))
```

```
smooth_mat <- table(path_smooth == simulation100$states)
accuracy_smooth <- smooth_mat[2]/sum(smooth_mat)
```

```
# accuracy most probable
viterbi_mat <- table(viterbi_path == simulation100$states)
accuracy_viterbi <- viterbi_mat[2]/sum(viterbi_mat)
```

```
cat("The accuracy for the filter distribution is:", accuracy_filter)
```

```
## The accuracy for the filter distribution is: 0.53
```

```
cat("\nThe accuracy for the smoothed distribution is:", accuracy_smooth)
```

```
##
## The accuracy for the smoothed distribution is: 0.74
```

```
cat("\nThe accuracy for the most probable path is:", accuracy_viterbi)
```

```
##
## The accuracy for the most probable path is: 0.56
```

Question 5

```
# prepare data frame for experiment
exp_length <- 30
empt_matrix <- matrix(data = 0, nrow = exp_length, ncol = 3)
df_exp <- as.data.frame(empt_matrix)
colnames(df_exp) <- c("Filtered", "Smoothed", "Viterbi")
```

```
# experiment

for(i in 1:exp_length){
  #simulate data
  simul <- simHMM(HMM, length = 100)
  #get alpha, distribution and accuracy
  alpha <- exp(forward(hmm = HMM, observation = simul$observation))
  filterd <- prop.table(alpha, 2)
  path_filt <- as.character(apply(filterd, 2, which.max))
  filt_table <- table(path_filt == simul$states)
  filt_accuracy <- filt_table[2]/sum(filt_table)
  #get beta and distribution and accuracy
  beta <- exp(backward(hmm = HMM, observation = simul$observation))
  smoothd <- prop.table(alpha*beta, 2)
  path_smooth <- as.character(apply(smoothd, 2, which.max))
  smooth_table <- table(path_smooth == simul$states)
  smooth_accuracy <- smooth_table[2]/sum(smooth_table)
  # viterbi path and accuracy
  vit_path <- viterbi(hmm = HMM, observation = simul$observation)
  vit_table <- table(vit_path == simul$states)
  vit_accuracy <- vit_table[2]/sum(vit_table)
  # record accuracy in data frame
  df_exp[i, ] <- cbind(filt_accuracy, smooth_accuracy, vit_accuracy)
}
```

```
#  print results
kable(df_exp, caption = "Accuracies for the different methods")
```

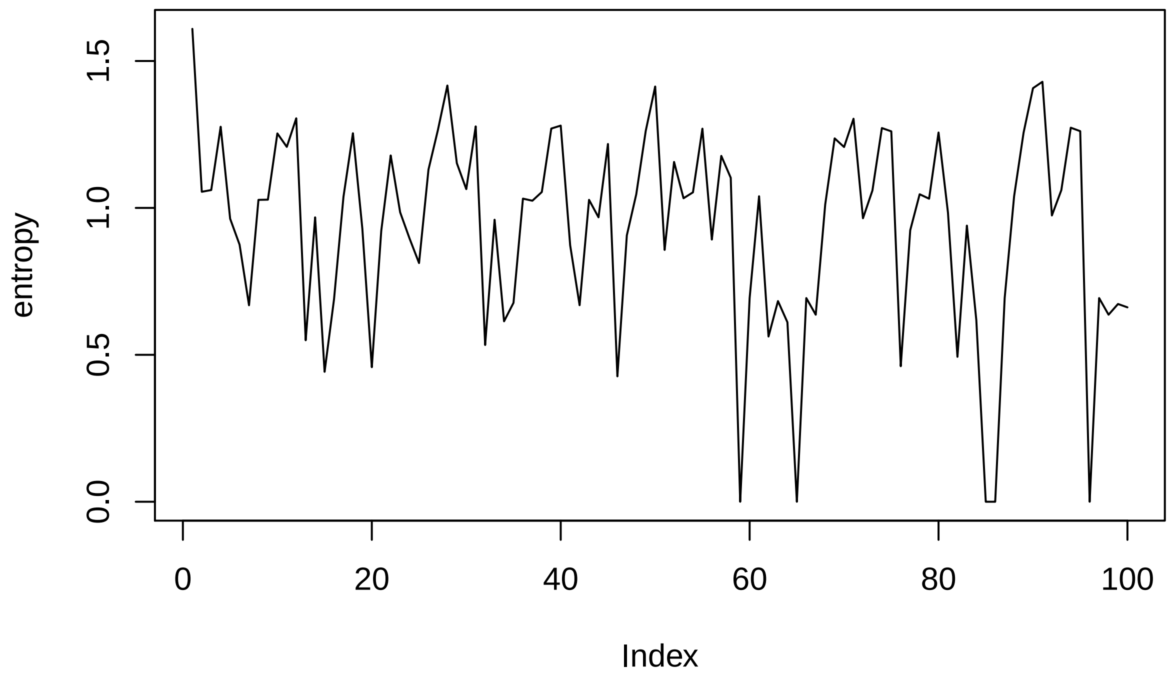
Table 1: Accuracies for the different methods

Filtered	Smoothed	Viterbi
0.46	0.68	0.61
0.49	0.77	0.65
0.49	0.58	0.56
0.60	0.79	0.65
0.54	0.64	0.39
0.54	0.69	0.53
0.52	0.67	0.55
0.52	0.67	0.50
0.45	0.68	0.45
0.52	0.77	0.47
0.39	0.66	0.57
0.48	0.74	0.56
0.40	0.57	0.39
0.50	0.70	0.47
0.47	0.66	0.55
0.62	0.63	0.50
0.61	0.65	0.41
0.45	0.52	0.30
0.51	0.63	0.57
0.57	0.75	0.46
0.51	0.70	0.48
0.51	0.62	0.60
0.58	0.74	0.49
0.56	0.72	0.42
0.55	0.74	0.45
0.54	0.79	0.65
0.57	0.69	0.40
0.44	0.61	0.62
0.55	0.72	0.48
0.53	0.69	0.46

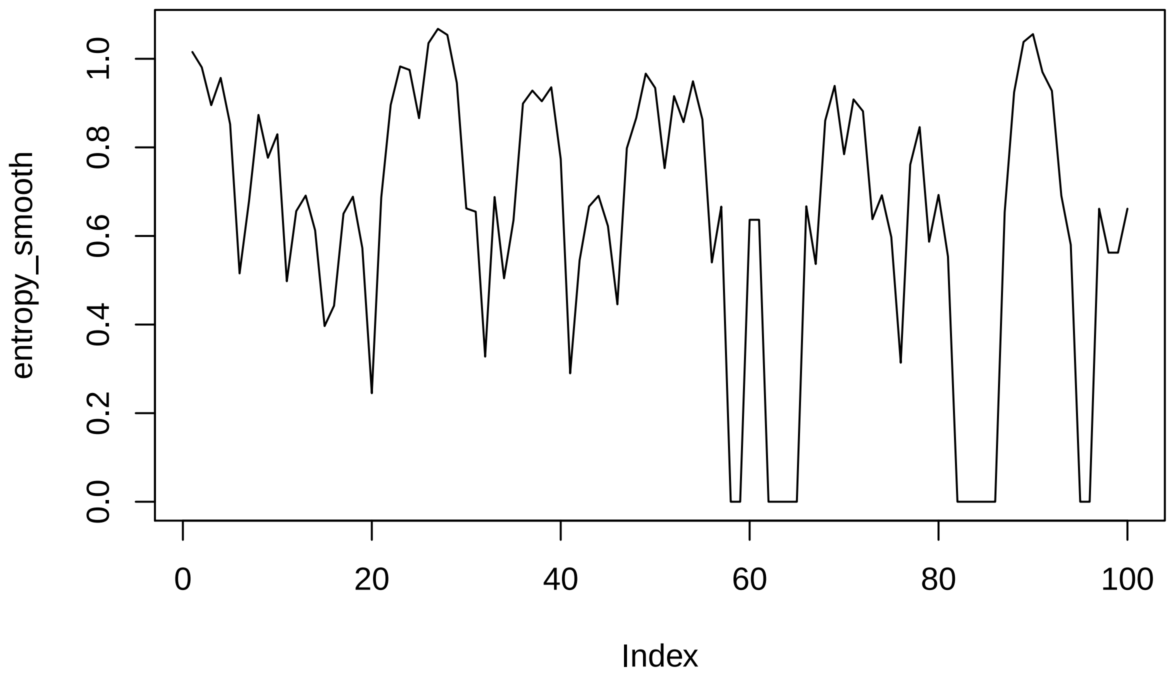
Filtered distribution uses only past data to fit the best model. The Viterbi algorithm has the constrain of making the most probable possible path which affects the accuracy as we are not always taking the most probable position, but the most probable overall path. Here we are interested in the distribution of all Z up to time T. Finally, the smoothing method performs better because it uses all of the data (not necessarily a valid path) in its estimation.

Question 6

```r
# entropy is calculated over each column using entropy.empirical
entropy <- apply(filter_dist, 2, entropy.empirical)
plot(entropy, type = "l")
```



```
entropy_smooth <- apply(smooth_dist, 2, entropy.empirical)
plot(entropy_smooth, type="l")
```



Entropy is not monotonically decreasing with the increase of data so we do not gain more certainty as we add more time steps.

Question 7

we are trying to compute $p(z^{101}|X^{1:100})$

We can add z^{101} in the condition as long as we add $p(Z^{100}|X^{1:100})$ using Bayes theorem. Using the proper independences, we get $\sum p(Z^{101}|Z^{100})p(Z^{100}|X^{100})$

The second factor is the last point of the filtering distribution and the first factor is the transition matrix. We just have to do the matrix multiplication.

```
# We simply have to multiply the last filter_distribution with the transition matrix
dist_101 <- filter_dist[, 100] %*% transprob
dist_101
```

```
##      1      2   3      4 5 6 7 8 9 10
## [1,] 0 0.1875 0.5 0.3125 0 0 0 0 0  0
```

Appendix: All code for this report

```r
knitr::opts_chunk$set(echo = TRUE)
# Load libraries
library(HMM)
library(ggplot2)
library(knitr)
library(entropy)
# Parameters
states <- as.character(c(1:10))
symbols <- as.character(c(1:10))
startprob <- rep((1/length(states)), length(states))

# transition matrix
transprob <- diag(x = 0.5, nrow = 10, ncol = 10)
index <- which(transprob == 0.5)
transprob[index[-length(index)] - 1] <- 0.5
transprob[9, 10] <- 0.5
transprob[10, 1] <- 0.5

colnames(transprob) <- as.character(c(1:10))
rownames(transprob) <- as.character(c(1:10))

# Emission Matrix (there's a smarter way of doing this for sure but this works)
emissionprob <- matrix(data = 0, nrow = 10, ncol = 10)
emissionprob[1, c(9, 10, 1, 2, 3)] <- 0.2
emissionprob[2, c(10, 1, 2, 3, 4)] <- 0.2
emissionprob[3, c(1, 2, 3, 4, 5)] <- 0.2
emissionprob[4, c(2, 3, 4, 5, 6)] <- 0.2
emissionprob[5, c(3, 4, 5, 6, 7)] <- 0.2
emissionprob[6, c(4, 5, 6, 7, 8)] <- 0.2
emissionprob[7, c(5, 6, 7, 8, 9)] <- 0.2
emissionprob[8, c(6, 7, 8, 9, 10)] <- 0.2
emissionprob[9, c(7, 8, 9, 10, 1)] <- 0.2
emissionprob[10, c(8, 9, 10, 1, 2)] <- 0.2

colnames(emissionprob) <- as.character(c(1:10))
rownames(emissionprob) <- as.character(c(1:10))

# initialize HMM
HMM <- initHMM(States = states, Symbols = symbols, startProbs = startprob,
               transProbs = transprob, emissionProbs = emissionprob)

# We now simulate 100 timesteps
set.seed(12345)
simulation100 <- simHMM(HMM, 100)
# plot results
time <- 1:100
states <- as.numeric(simulation100$states)
observations <- as.numeric(simulation100$observation)
df_plot <- data.frame(time, states, observations)

plot_states <- ggplot(df_plot, aes(x = time, y = states))+
  geom_line(col = "red")+
  ggtitle("Robot actual position")

plot_recorded <- ggplot(df_plot, aes(x = time, y = observations))+
  geom_line(col = "green")+
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plot_states
plot_recorded
# filtered distribution
# alpha
alpha <- exp(forward(hmm = HMM, observation = simulation100$observation))
# beta
beta <- exp(backward(hmm = HMM, observation = simulation100$observation))
# filtered distribution
filter_dist <- prop.table(alpha, margin = 2)
# smoothed distribution
smooth_dist <- prop.table(alpha*beta, margin = 2)
# most probable path (viterbi algo)
viterbi_path <- viterbi(hmm = HMM, observation = simulation100$observation)

# accuracy filter
path_filter <- as.character(apply(filter_dist, 2, which.max))
filter_mat <- table(path_filter == simulation100$states)
accuracy_filter <- filter_mat[2]/sum(filter_mat)

# accuracy smoothed
path_smooth <- as.character(apply(smooth_dist, 2, which.max))
smooth_mat <- table(path_smooth == simulation100$states)
accuracy_smooth <- smooth_mat[2]/sum(smooth_mat)
# accuracy most probable
viterbi_mat <- table(viterbi_path == simulation100$states)
accuracy_viterbi <- viterbi_mat[2]/sum(viterbi_mat)
cat("The accuracy for the filter distribution is:", accuracy_filter)
cat("\nThe accuracy for the smoothed distribution is:", accuracy_smooth)
cat("\nThe accuracy for the most probable path is:", accuracy_viterbi)


# prepare data frame for experiment
exp_length <- 30
empt_matrix <- matrix(data = 0, nrow = exp_length, ncol = 3)
df_exp <- as.data.frame(empt_matrix)
colnames(df_exp) <- c("Filtered", "Smoothed", "Viterbi")

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}

#  print results
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# entropy is calculated over each column using entropy.empirical
entropy <- apply(filter_dist, 2, entropy.empirical)
plot(entropy, type = "l")

entropy_smooth <- apply(smooth_dist, 2, entropy.empirical)
plot(entropy_smooth, type="l")
# We simply have to multiply the last filter_distribution with the transition matrix
dist_101 <- filter_dist[, 100] %*% transprob
dist_101
```