

### 01.112 Machine Learning, Fall 2018 Lecture Notes for Week 9

Hidden Markov Models (II)

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# 1 Decoding

Suppose now that we have the HMM parameters (see the example in the previous lecture) and the problem is to predict the underlying tags  $y_1, \ldots, y_n$  corresponding to an observed sequence of words  $x_1, \ldots, x_n$ . In other words, we wish to find:

$$\underset{y_1, \dots, y_n}{\arg \max} p(y_0, y_1, \dots, y_{n+1} | x_1, \dots, x_n; \theta) \tag{1}$$

where we have:

$$p(x_1, \dots, x_n, y_0, y_1, \dots, y_{n+1}; \theta) = \prod_{i=1}^{n+1} a_{y_{i-1}, y_i} \prod_{i=1}^{n} b_{y_i}(x_i)$$
(2)

and  $y_0 = START$  and  $y_{n+1} = STOP$ .

<u>Discussion</u> We have the joint distribution here, but we are interested in a conditional distribution above. What's the connection here?

$$\underset{y_1,\dots,y_n}{\arg\max} p(y_0, y_1, \dots, y_{n+1} | x_1, \dots, x_n; \theta) = \underset{y_1,\dots,y_n}{\arg\max} \frac{p(x_1, \dots, x_n, y_0, y_1, \dots, y_{n+1}; \theta)}{p(x_1, \dots, x_n; \theta)}$$
(3)

Since the term  $p(x_1, ..., x_n)$  is a constant that is independent of ys once the parameters are fixed, we can drop it when taking the  $\arg \max$ :

$$\underset{y_1,\dots,y_n}{\arg\max} \frac{p(x_1,\dots,x_n,y_0,y_1,\dots,y_{n+1};\theta)}{p(x_1,\dots,x_n;\theta)} = \underset{y_1,\dots,y_n}{\arg\max} p(x_1,\dots,x_n,y_0,y_1,\dots,y_{n+1};\theta)$$
(4)

This leads to:

$$\arg\max_{y_1,\dots,y_n} p(y_0,y_1,\dots,y_{n+1}|x_1,\dots,x_n;\theta) = \arg\max_{y_1,\dots,y_n} p(x_1,\dots,x_n,y_0,y_1,\dots,y_{n+1};\theta)$$
(5)

One possible solution for finding the most likely sequence of tags is to do brute force enumeration. Consider the example:  $\{\text{the, dog}\}$ ,  $\mathbf{x}$  = "the the dog". The possible state sequences include:

But there are  $|\mathcal{T}|^n$  possible sequences in total! Solving the tagging problem by enumerating the tag sequences will be prohibitively expensive.

## Viterbi Algorithm

The HMM has a simple dependence structure (recall, tags form a Markov sequence, observations only depend on the underlying tag). We can exploit this structure in a dynamic programming algorithm.

Input:  $\mathbf{x} = x_1, \dots, x_n$  and model parameters  $\theta$ .

Output:  $\arg \max_{y_1,...,y_n} p(x_1,...,x_n,y_0,y_1,...,y_{n+1};\theta)$ .

Now, let's look at a truncated version of the joint probability, focusing on the first k tags for any  $k \in \{1, ..., n\}$  In other words, we define

$$r(y_1, \dots, y_k) = \prod_{i=1}^k a_{y_{i-1}, y_i} \prod_{i=1}^k b_{y_i}(x_i)$$
(6)

where  $k \neq n+1$ . Note that our notation  $r(y_1, \ldots, y_k)$  suppresses any dependence on the observation sequence. This is because we view  $x_1, \ldots, x_n$  as given (fixed). Note that, according to our definition,

$$p(x_1, \dots, x_n, y_0, y_1, \dots, y_{n+1}) = r(y_1, \dots, y_n) \cdot a_{y_n, y_{n+1}} = r(y_1, \dots, y_n) \cdot a_{y_n, \text{STOP}}$$
(7)

Let S(k, v) be the set of tag sequences  $y_1, \ldots, y_k$  such that  $y_k = v$ . In other words, S(k, v) is a set of all sequences of length k whose last tag is v. The dynamic programming algorithm will calculate

$$\pi(k, v) = \max_{(y_1, \dots, y_k) \in S(k, v)} r(y_1, \dots, y_k)$$
(8)

recursively in the forward direction.

In other words,  $\pi(k, v)$  can be thought as solving the maximization problem partially, over all the tags  $y_1, \ldots, y_{k-1}$  with the constraint that we use tag v for  $y_k$ . If we have  $\pi(k, v)$ , then  $\max_v \pi(k, v)$  evaluates  $\max_{y_1, \ldots, y_k} r(y_1, \ldots, y_k)$ . We leave v in the definition of  $\pi(k, v)$  so that we can extend the maximization one step further as we unravel the model in the forward direction. More formally,

• Base case:

$$\pi(0,v) = \begin{cases} 1 & \text{if } v = \text{START (starting state, no observations)} \\ 0 & \text{otherwise} \end{cases}$$
 (9)

• Moving forward recursively: for any  $k \in \{1, ..., n\}$ 

$$\pi(k, v) = \max_{u \in \mathcal{T}} \{ \pi(k - 1, u) \cdot a_{u, v} \cdot b_v(x_k) \}$$
 (10)

In other words, when extending  $\pi(k-1,u), u \in \mathcal{T}$ , to  $\pi(k,v), v \in \mathcal{T}$ , we must transition from  $y_{k-1} = u$  to  $y_k = v$  (part  $a_{u,v}$ ) and generate the corresponding observation  $x_k$  (part  $b_v(x_k)$ ). Then we maximize over the previous tag  $y_{k-1} = u$  so that  $\pi(k,v)$  only depends on the value of  $y_k$ .

 $\bullet$  Finally, we must transition from  $y_n$  to STOP so that

$$\max_{y_1,...,y_n} p(x_1,...,x_n,y_0 = \mathtt{START},y_1,...,y_n,y_{n+1} = \mathtt{STOP}) = \max_{v \in \mathcal{T}} \{\pi(n,v) \cdot a_{v,\mathtt{STOP}}\} (11)$$

The whole calculation can be done in time  $O(n|\mathcal{T}|^2)$ , linear in length, quadratic in the number of tags.

Now, having values  $\pi(k, v)$ , how do we reconstruct the most likely sequence of tags which we denote as  $y_1^*, \ldots, y_n^*$ ? We can do this via *backtracking*. In other words, at the last step,  $\pi(n, v)$  represents maximizations of all  $y_1, \ldots, y_n$  such that  $y_n = v$ . What is the best value for this last tag v, *i.e.*, what is  $y_n^*$ ? It is:

$$y_n^* = \arg\max_{v} \left\{ \pi(n, v) \cdot a_{v, \text{STOP}} \right\}$$
 (12)

Now we can fix  $y_n^*$  and work backwards. What is the best value  $y_{n-1}^*$  such that we end up with tag  $y_n^*$  in position n? It is simply

$$y_{n-1}^* = \arg\max_{u} \{ \pi(n-1, u) \cdot a_{u, y_n^*} \}$$
(13)

and so on.

**<u>Discussion</u>** What is the space complexity of the above algorithm? Is it possible to store the optimal transition information together with the  $\pi(k, v)$ ? If we do so, what is the space complexity? Do we still need to do backtracking in this case?

**Exercise** What if we would like to find the top-k (k > 1) most optimal sequences instead of finding the single most optimal tag sequence?

# **Learning Objectives**

#### You need to know:

- 1. What is decoding for an HMM
- 2. How to perform decoding for an HMM using the Viterbi algorithm
- 3. What is the guarantee of the Viterbi algorithm and how to implement the Viterbi algorithm
- 4. What is the space and time complexity of the Viterbi algorithm