9: Viterbi Algorithm for HMM Decoding Machine Learning and Real-world Data

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Last session: estimating parameters of an HMM

- The dishonest casino, dice edition.
- Two hidden states: L (loaded dice), F (fair dice).
- You don't know which dice is currently in use. You can only observe the numbers that are thrown.
- You estimated transition and emission probabilities (Problem 1 from last time).
- We are now turning to Problem 4.
- We want the HMM to find out when the fair dice was out, and when the loaded dice was out.
- We need to write a decoder.

Decoding: finding the most likely path

■ Definition of decoding: Finding the most likely hidden state sequence X that explains the observation O given the HMM parameters μ .

$$\hat{X} = \underset{X}{\operatorname{argmax}} P(X, O|\mu)$$

$$= \underset{X}{\operatorname{argmax}} P(O|X, \mu) P(X|\mu)$$

$$= \underset{X_1...X_T}{\operatorname{argmax}} \prod_{t=1}^T P(O_t|X_t) P(X_t|X_{t-1})$$

■ Search space of possible state sequences X is $O(N^T)$; too large for brute force search.

Viterbi is a Dynamic Programming Application

(Reminder from Algorithms course) We can use Dynamic Programming if two conditions apply:

- Optimal substructure property
 - An optimal state sequence $X_1 ... X_j ... X_T$ contains inside it the sequence $X_1 ... X_j$, which is also optimal
- Overlapping subsolutions property
 - If both X_t and X_u are on the optimal path, with u > t, then the calculation of the probability for being in state X_t is part of each of the many calculations for being in state X_u .

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The intuition behind Viterbi

- Here's how we can save ourselves a lot of time.
- Because of the Limited Horizon of the HMM, we don't need to keep a complete record of how we arrived at a certain state.
- For the first-order HMM, we only need to record one previous step.
- Just do the calculation of the probability of reaching each state once for each time step.
- Then memoise this probability in a Dynamic Programming table
- This reduces our effort to $O(N^2T)$.
- This is for the first order HMM, which only has a memory of one previous state.

Viterbi: main data structure

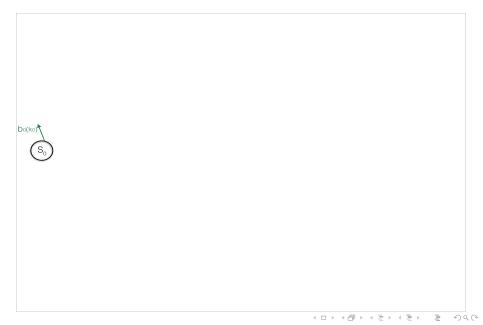
- Memoisation is done using a *trellis*.
- A trellis is equivalent to a Dynamic Programming table.
- The trellis is $(N+2) \times (T+2)$ in size, with states j as rows and time steps t as columns.
- Each cell j, t records the Viterbi probability $\delta_j(t)$, the probability of the most likely path that ends in state s_j at time t:

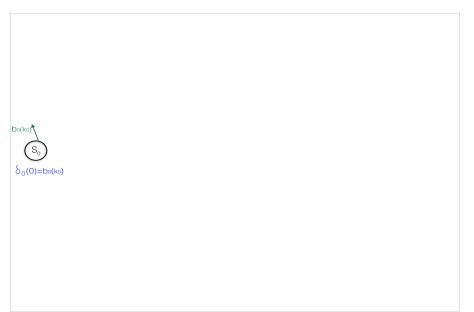
$$\delta_j(t) = \max_{1 \le i \le N} [\delta_i(t-1) a_{ij} b_j(O_t)]$$

- This probability is calculated by maximising over the best ways of going to s_i for each s_i .
- a_{ij} : the transition probability from s_i to s_j
- $b_j(O_t)$: the probability of emitting O_t from destination state s_j

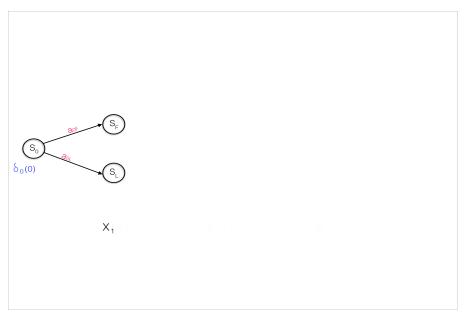
Note: the probability of a state starting the sequence at t=0 is just the probability of it emitting the first symbol.

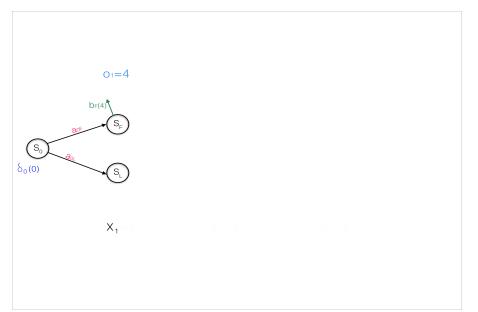


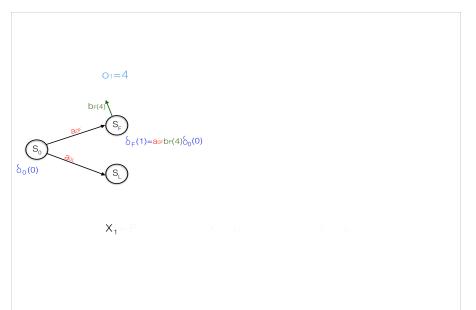




Viterbi algorithm, main step





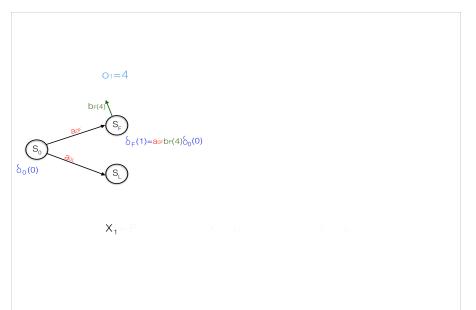


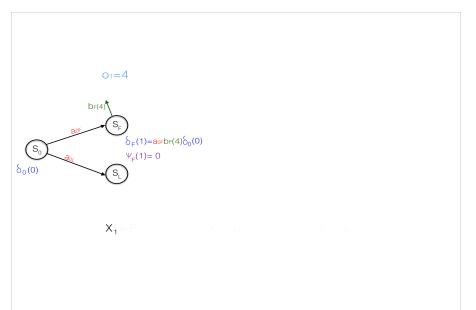
Viterbi algorithm, main step, ψ

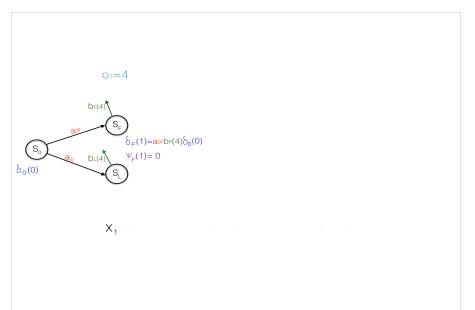
 $\psi_j(t)$ is a helper variable that stores the t-1 state index i on the highest probability path.

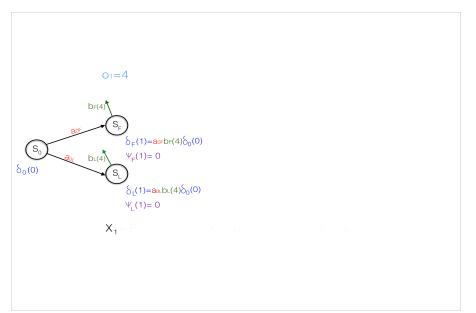
$$\psi_j(t) = \underset{1 < i < N}{\operatorname{argmax}} [\delta_i(t-1) \, a_{ij} \, b_j(O_t)]$$

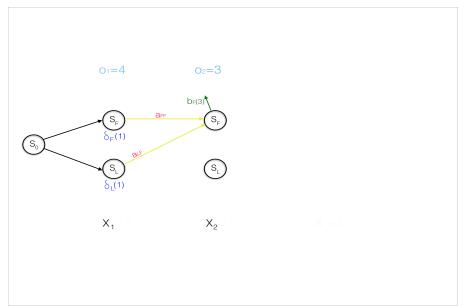
 \blacksquare In the backtracing phase, we will use ψ to find the previous cell/state in the best path.

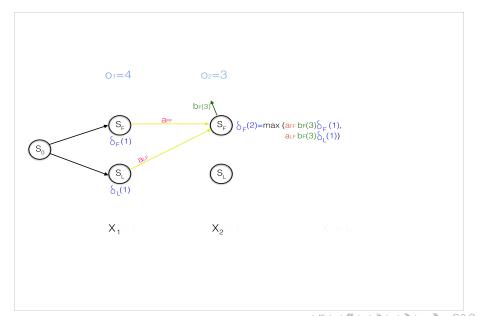


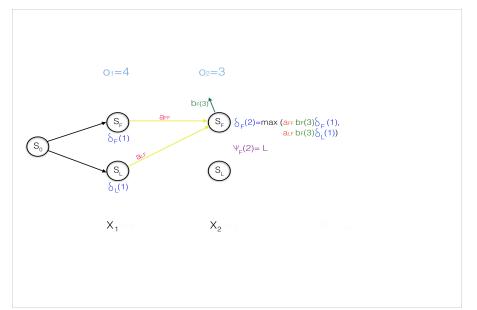


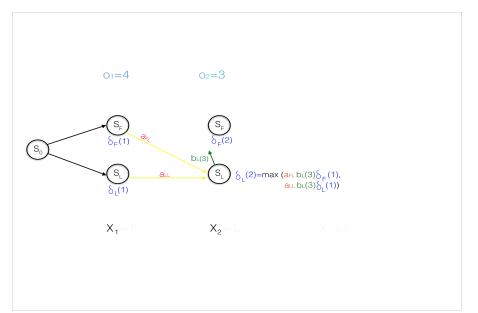


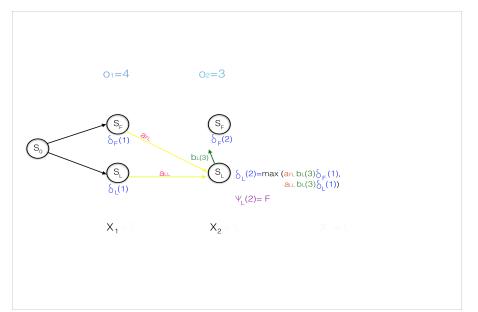


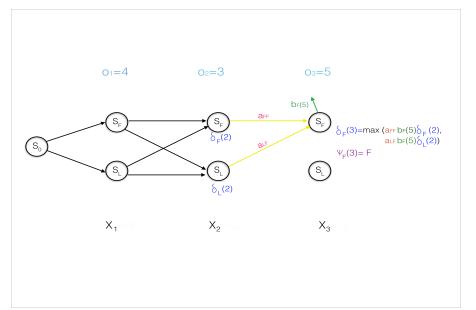


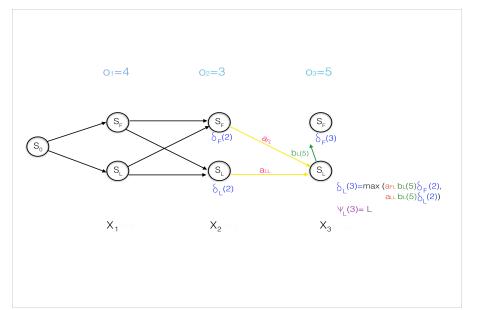




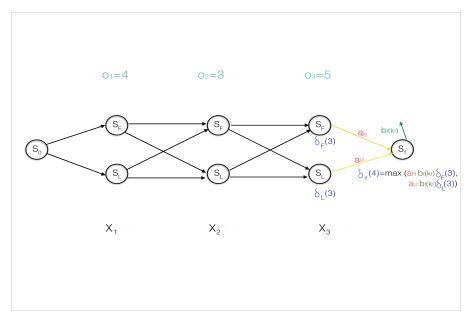




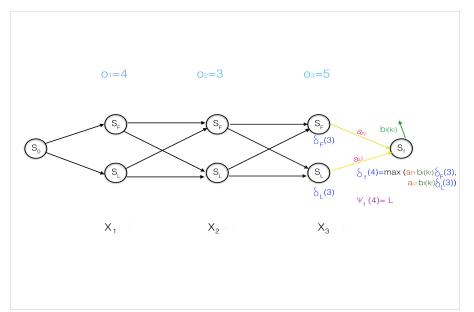


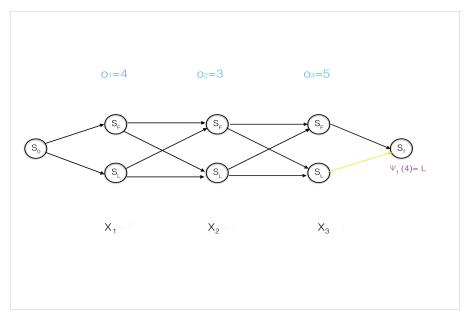


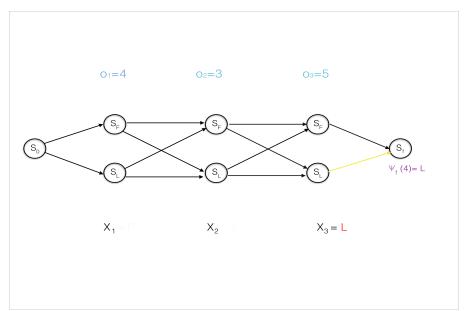
Viterbi algorithm, termination

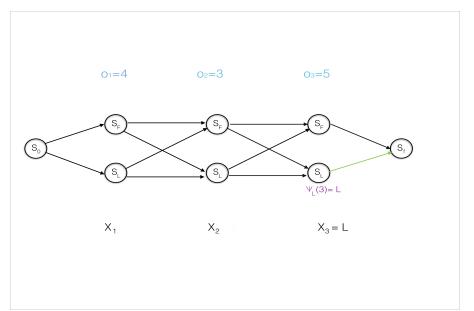


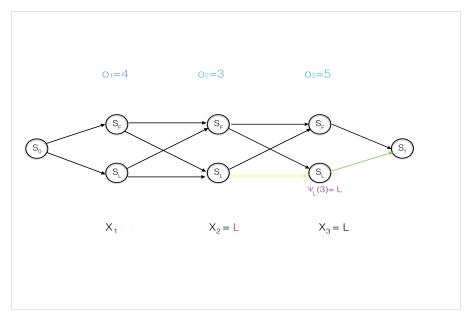
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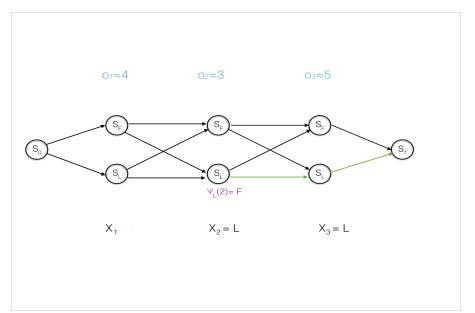


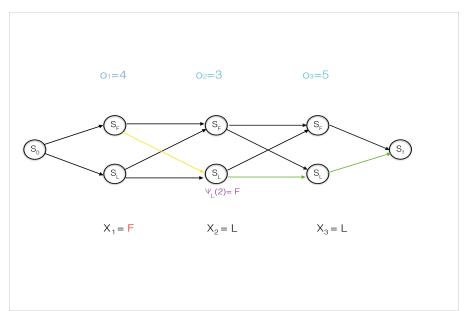


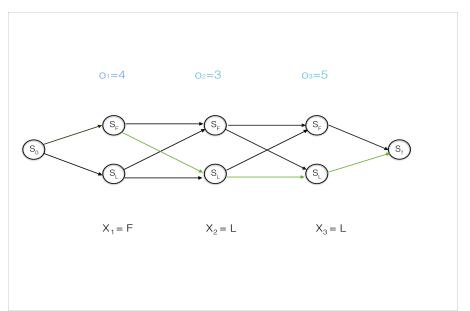


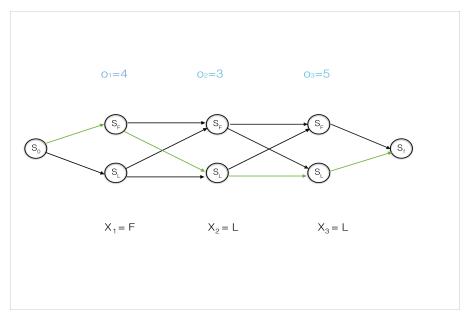












Why is it necessary to keep N states at each time step?

- We have convinced ourselves that it's not necessary to keep more than N ("real") states per time step.
- But could we cut down the table to just a one-dimensional table of *T* time slots by choosing the probability of the best path overall ending in that time slot, in any of the states?
 - This would be the greedy choice
 - But think about what could happen in a later time slot.
 - You could encounter a zero or very low probability concerning all paths going through your chosen state s_j at time t.
 - Now a state s_k that looked suboptimal in comparison to s_j at time t becomes the best candidate.
 - As we don't know the future, this could happen to any state, so we need to keep the probabilities for each state at each time slot.
- But thankfully, no more.

Precision and Recall

- So far, we have measured system success in accuracy or agreement in Kappa.
- But sometimes it's only one type of instances that we find interesting.
- We don't want a summary measure that averages over interesting and non-interesting instances, as accuracy does.
- In those cases, we use precision, recall and F-measure.
- These metrics are imported from the field of information retrieval, where the difference between interesting and non-interesting examples is particularly high.
- Accuracy doesn't work well when the types of instances are unbalanced

Precision and Recall

System says:

Truth is:

	F	L	Total
F	а	b	a+b
L	С	d	c+d
Total	a+c	b+d	a+b+c+d

- Precision of L: $P_L = \frac{d}{b+d}$
- Recall of L: $R_L = \frac{d}{c+d}$
- F-measure of L: $F_L = \frac{2P_LR_L}{P_L + R_L}$
- Accuracy: $A = \frac{a+d}{a+b+c+d}$

Your task today

Task 8:

- Implement the Viterbi algorithm.
- Run it on the dice dataset and measure precision of L (P_L) , recall of L (R_L) and F-measure of L (F_L) .

Literature

- Manning and Schutze (2000). Foundations of Statistical Natural Language Processing, MIT Press. Chapter 9.3.2.
 - We use a state-emission HMM, but this textbook uses an arc-emission HMM. There is therefore a slight difference in the algorithm as to in which step the initial and final $b_j(k_t)$ are multiplied in.
- Jurafsky and Martin, 2nd Edition, chapter 6.4
- Smith, Noah A. (2004). Hidden Markov Models: All the Glorious Gory Details.
- Bockmayr and Reinert (2011). Markov chains and Hidden Markov Models. Discrete Math for Bioinformatics WS 10/11.