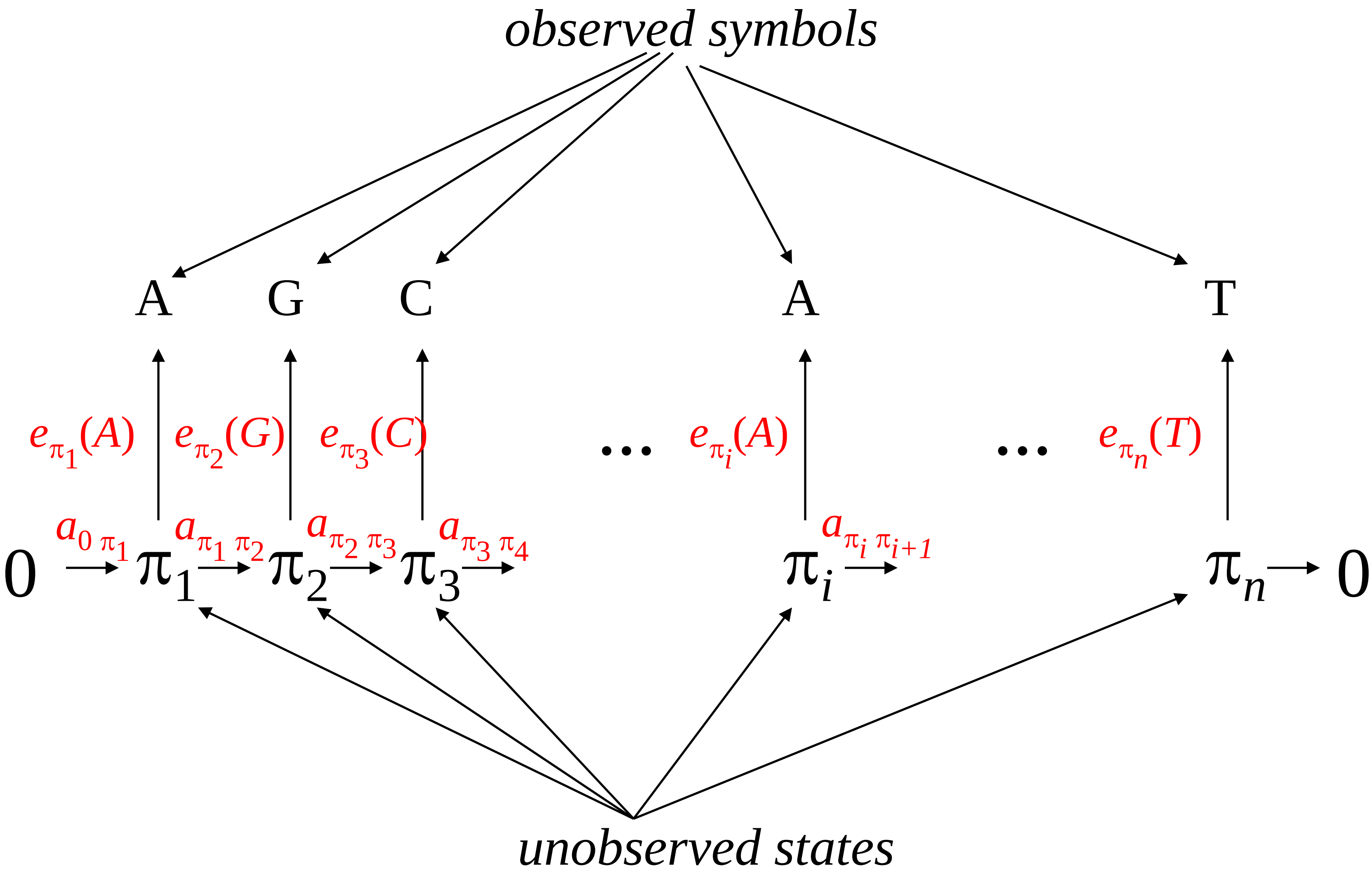
Lecture 14

- HMM probability calculations
  - WDAG
  - Viterbi algorithm

- 2-state HMMs & D-segments

Hidden Markov Model



HMM Probabilities of Sequences

- Prob of sequence of states $\pi_1\pi_2\pi_3 \ldots \pi_n$ is
  $a_{0\pi_1} a_{\pi_1\pi_2} a_{\pi_2\pi_3} a_{\pi_3\pi_4} \ldots a_{\pi_{n\text{-}1}\pi_n}$.
- Prob of seq of observed symbols $b_1b_2b_3 \ldots b_n$,
  conditional on state sequence is
  $e_{\pi_1}(b_1)e_{\pi_2}(b_2)\, e_{\pi_3}(b_3) \ldots e_{\pi_n}(b_n)$
- Joint probability $= a_{0\pi_1} \prod^{n}_{i=1} a_{\pi_i\pi_{i+1}}\, e_{\pi_i}(b_i)$
  (define $a_{\pi_n\pi_{n+1}}$ to be 1)
- (Unconditional) prob of observed sequence
  = sum (of joint probs) over all possible state paths
  - not practical to compute directly, by 'brute force'! We will use dynamic programming.

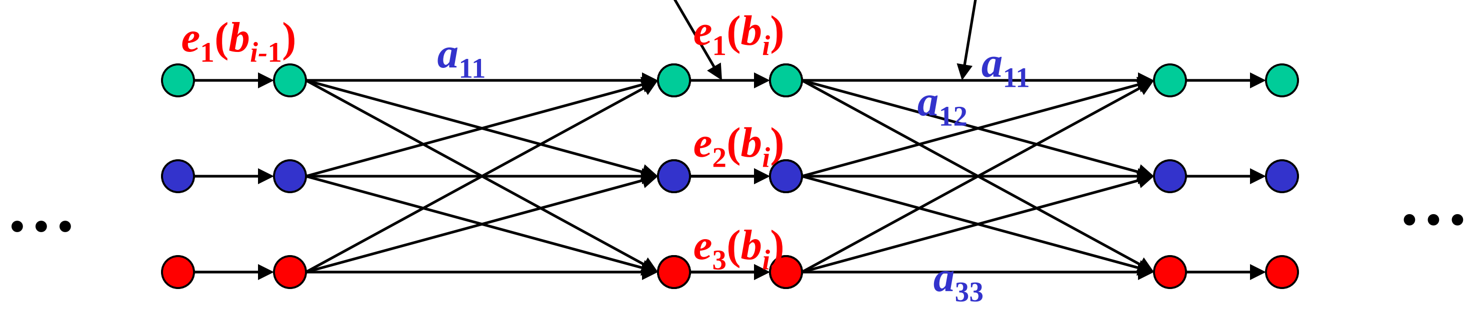
Computing HMM Probabilities

- WDAG structure for sequence HMMs:
  - for i^{th} position in seq ($i = 1, \ldots n$), have 2 nodes for each state:
    - total # nodes = $2ns + 2$, where n = seq length, s = # states
  - Pair of nodes for a given state at i^{th} position is connected by an *emission* edge
    - Weight is the emission prob for i^{th} observed residue
    - Can omit node pair if emission prob = 0
  - Have *transition* edges connecting (right-hand) state nodes at position i with (left-hand) state nodes at position i+1
    - Weights are transition probs
    - Can omit edges with transition prob = 0

WDAG for 3-state HMM, length n sequence

weights are emission probabilities $e_k(b_i)$ for i^{th} residue b_i

weights are transition probabilities a_{kl}

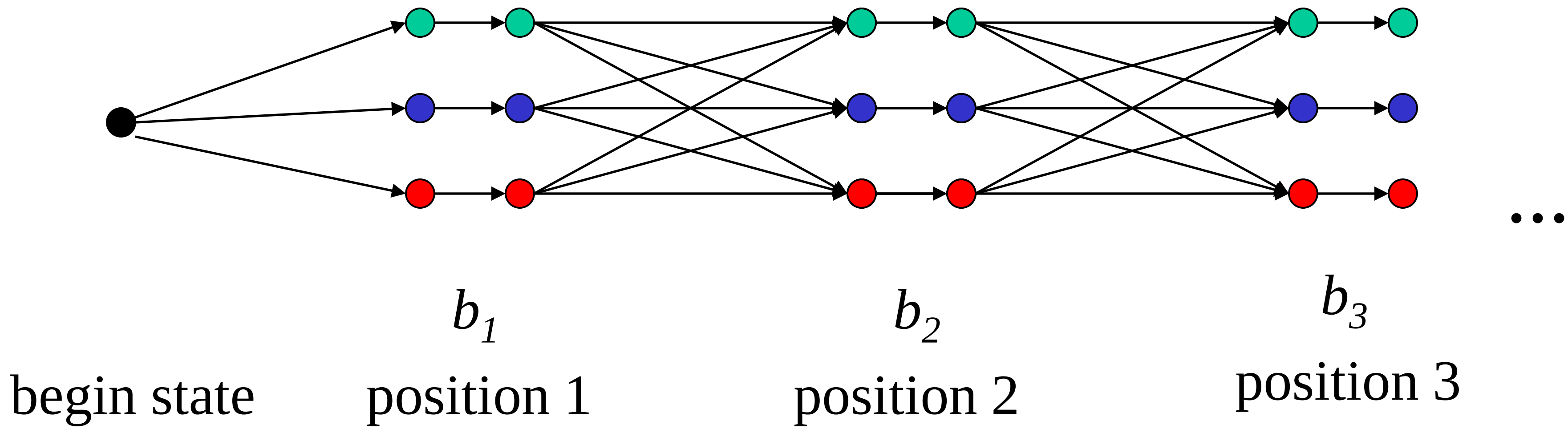


b_{i-1} position i-1

b_i position i

b_{i+1} position i+1

Beginning of Graph

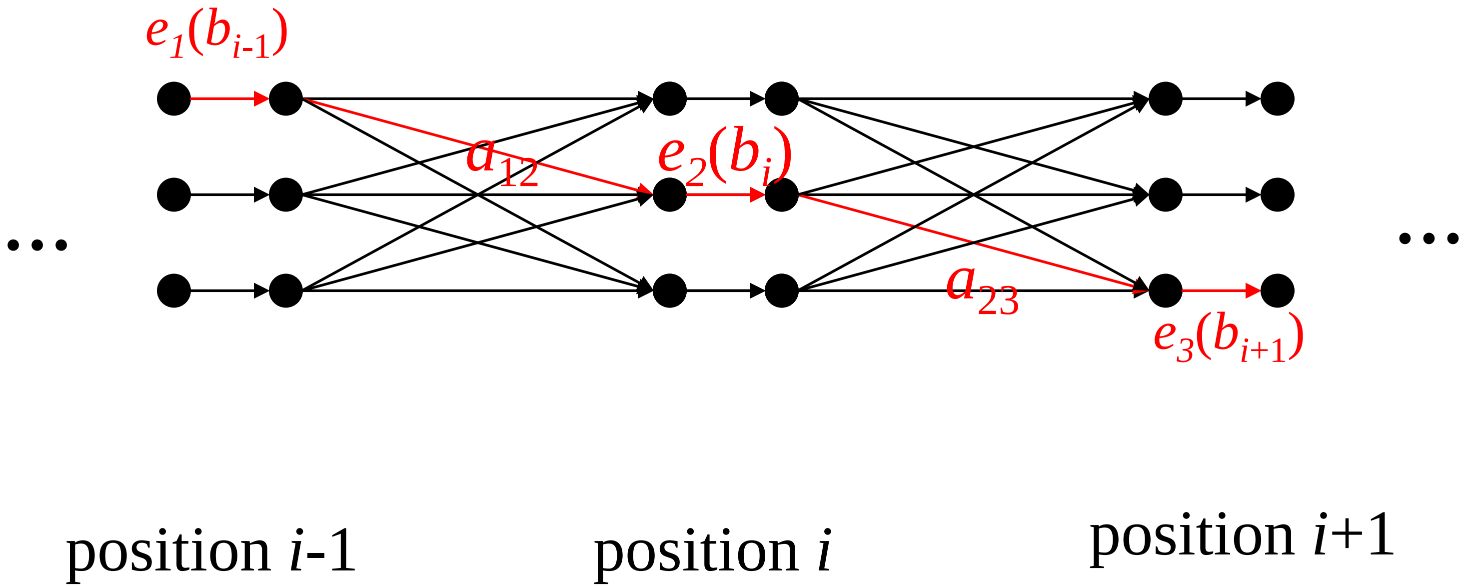


End of graph is similar – but with edges going *to* the end state

- ***Paths*** through graph from begin node to end node correspond to ***sequences of states***
- ***Product weight*** along path
  = ***joint probability*** of state sequence & observed symbol sequence
- ***Highest-weight path*** = ***highest probability state sequence***
- ***Sum*** *of (product) path weights*, ***over all paths***,
  = ***probability of observed sequence***
- ***Sum*** *of (product) path weights* ***over***
  - all paths *going through a particular node*, or
  - all paths *that include a particular edge*,

  divided by prob of observed sequence,
  = ***posterior probability*** of that edge or node

Path Weights



- By general results on WDAGs, can use dynamic programming to find highest weight path:

  = "Viterbi algorithm" to find highest probability path (most probable "parse")

  – in this case can use log probabilities & sum weights

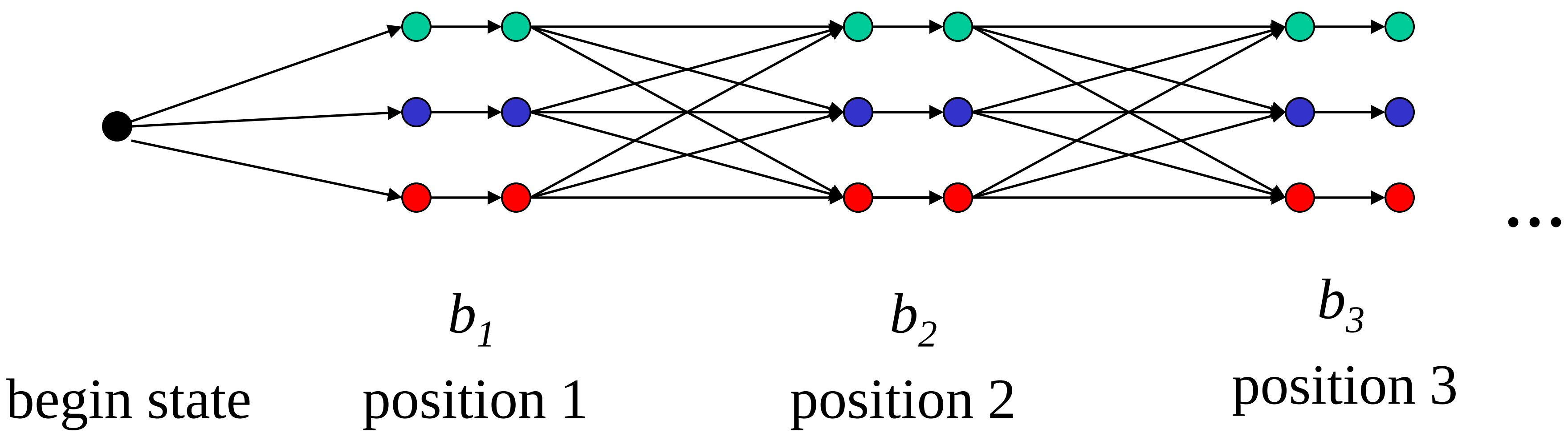
  – (N.B. paths are ***constrained*** to begin at the begin node, and end at the end node!)

The Viterbi path is
the *most probable parse*!

Complexity

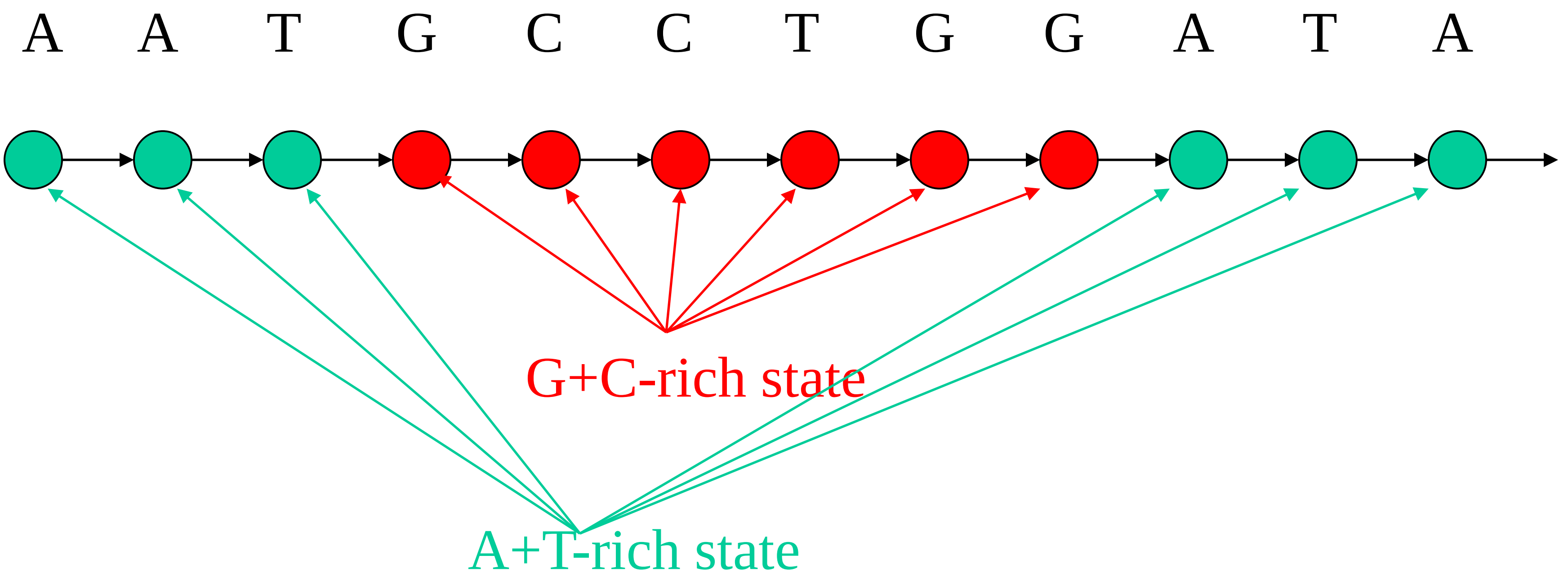
- $= O(|V|+|E|)$, i.e. total # nodes and edges.
- # nodes $= 2ns + 2$
  - where n = sequence length,
  - s = # states.
- # edges $= (n-1)s^2 + ns + 2s$

- So overall complexity is $O(ns^2)$
  - (actually s^2 can be reduced to # ‘allowed’ transitions between states – depends on model topology).

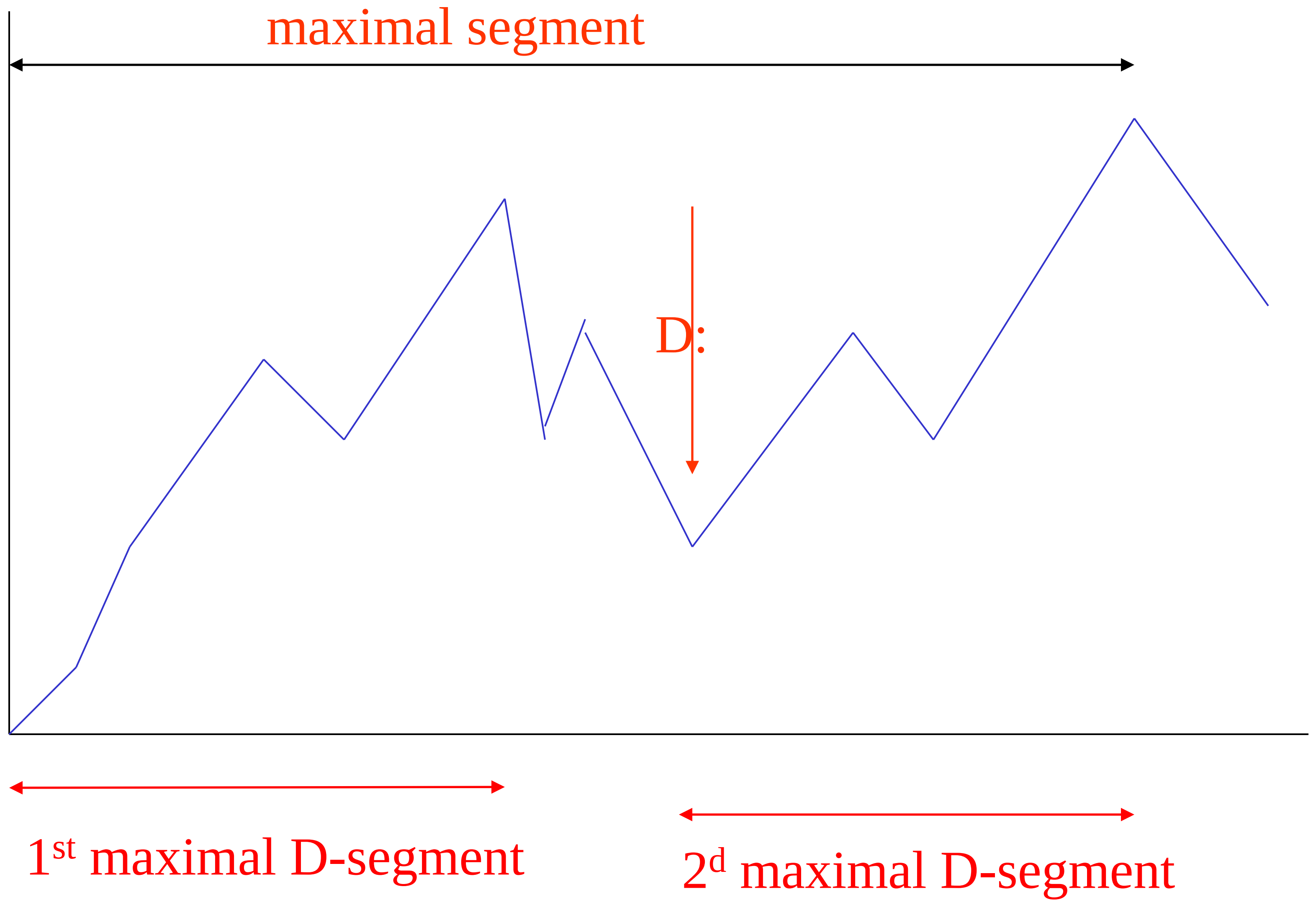

b_1
b_2
b_3
begin state
position 1
position 2
position 3
…

2-state HMMs & D-segments

from lecture 13



from lecture 12



- $O(N)$ algorithm to find all maximal D-segs:

```
cumul = max = 0; start = 1;
for (i = 1; i ≤ N; i++) {
    cumul += s[i];
    if (cumul ≥ max)
        {max = cumul; end = i;}
    if (cumul ≤ 0 or cumul ≤ max + D or i == N) {
        if (max ≥ S)
            {print start, end, max; }
        max = cumul = 0; start = end = i + 1; /* NO BACKTRACKING
            NEEDED! */
    }
}
```

D-segments ≈ 2-state HMMs

- Consider 2-state HMM
  - states 1 & 2, transition probs a_{11}, a_{12}, a_{21}, a_{22}
  - observed symbols $\{r\}$, emission probs $\{e_1(r)\}$, $\{e_2(r)\}$
- Define

  scores $s(r) = \log(e_2(r)\, a_{22}/(e_1(r)\, a_{11}))$

  $S = -D = \log(a_{11}a_{22}/(a_{21}a_{12}))$
- Then if $S > 0$, the maximal D-segments in a sequence $(r_i)_{i=1,n}$ are the state-2 segments in the Viterbi parse
- (can allow for non-.5 initiation probs by starting cumul at non-zero value)

D-segments vs HMMs

- D-segments
  - are very *easy to program*!
  - give Viterbi parse in *just one pass* through the sequence
  - somewhat more flexible (S, D settings)
- HMMs
  - allow more powerful parameter *estimation*
  - can attach *probabilities* to alternative decompositions
  - easily generalize to > 2 *types* of segments– just allow more states