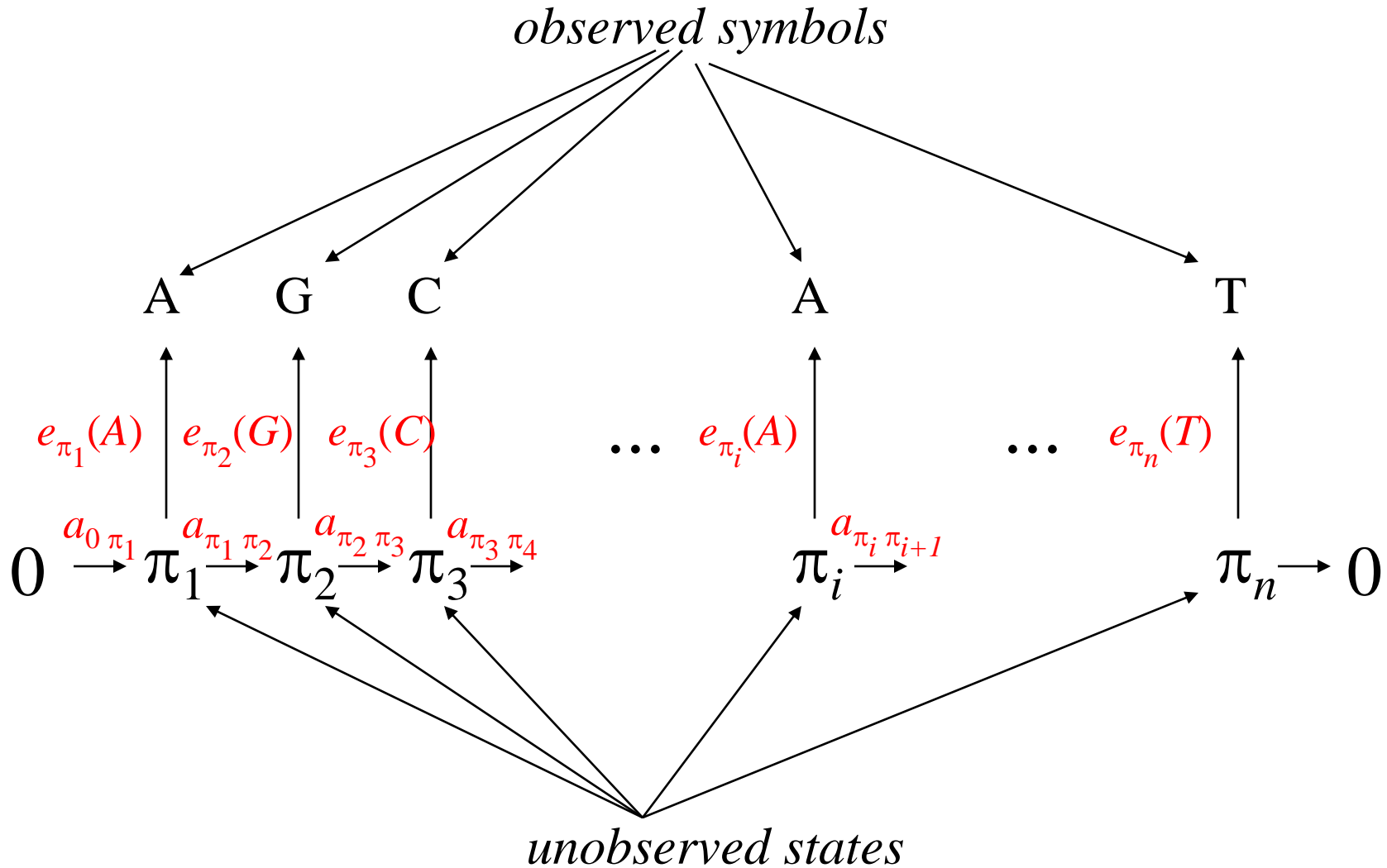


Lecture 13

- HMM probability calculations
 - WDAG
 - Viterbi algorithm
- 2-state HMMs & D-segments

Hidden Markov Model



HMM Probabilities of Sequences

- Prob of **sequence of states** $\pi_1\pi_2\pi_3 \dots \pi_n$ is
 $a_{0\pi_1} a_{\pi_1\pi_2} a_{\pi_2\pi_3} a_{\pi_3\pi_4} \dots a_{\pi_{n-1}\pi_n}$.
- Prob of **seq of observed symbols** $b_1b_2b_3 \dots b_n$,
conditional on state sequence is
 $e_{\pi_1}(b_1)e_{\pi_2}(b_2) e_{\pi_3}(b_3) \dots e_{\pi_n}(b_n)$
- **Joint probability** = $a_{0\pi_1} \prod_{i=1}^n a_{\pi_i\pi_{i+1}} e_{\pi_i}(b_i)$
(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.

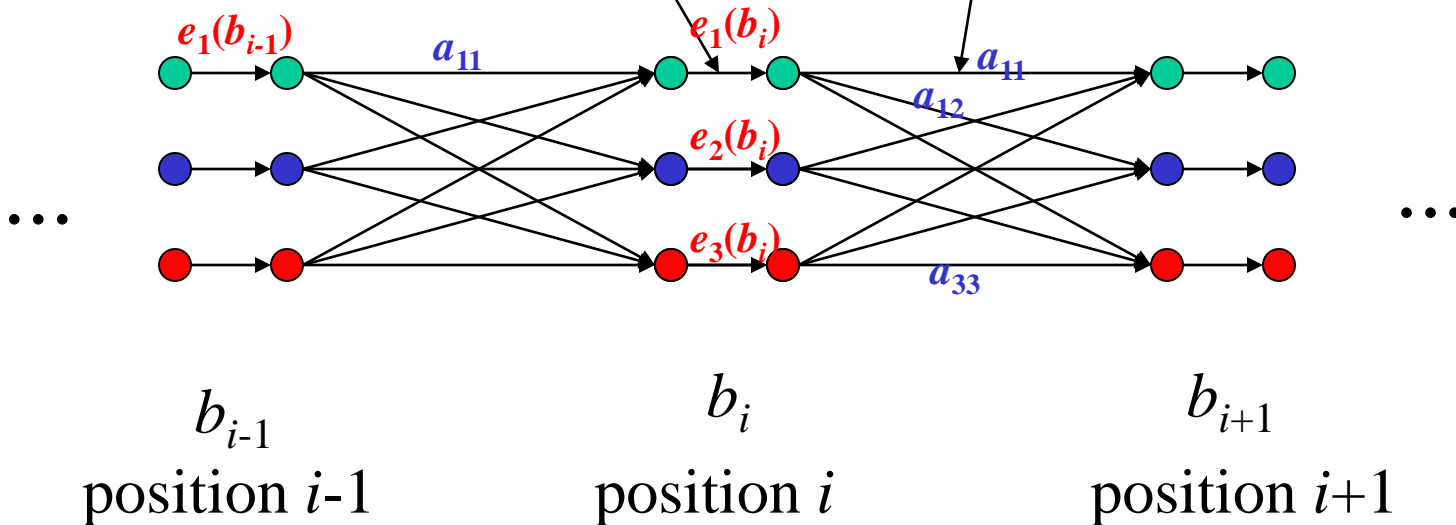
Computing HMM Probabilities

- WDAG structure for sequence HMMs:
 - for i^{th} position in seq ($i = 1, \dots, n$), have 2 nodes for each state:
 - total # nodes = $2ns + 2$, where $n = \text{seq length}$, $s = \# \text{ states}$
 - 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

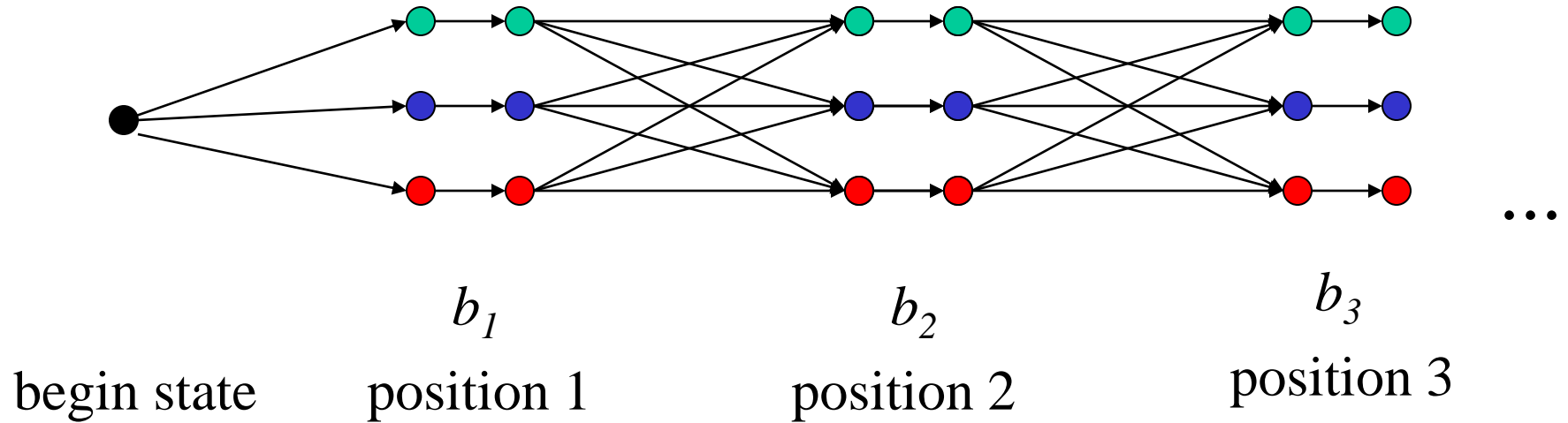
WDAG for 3-state HMM, length n sequence

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

weights are transition
probabilities a_{kl}

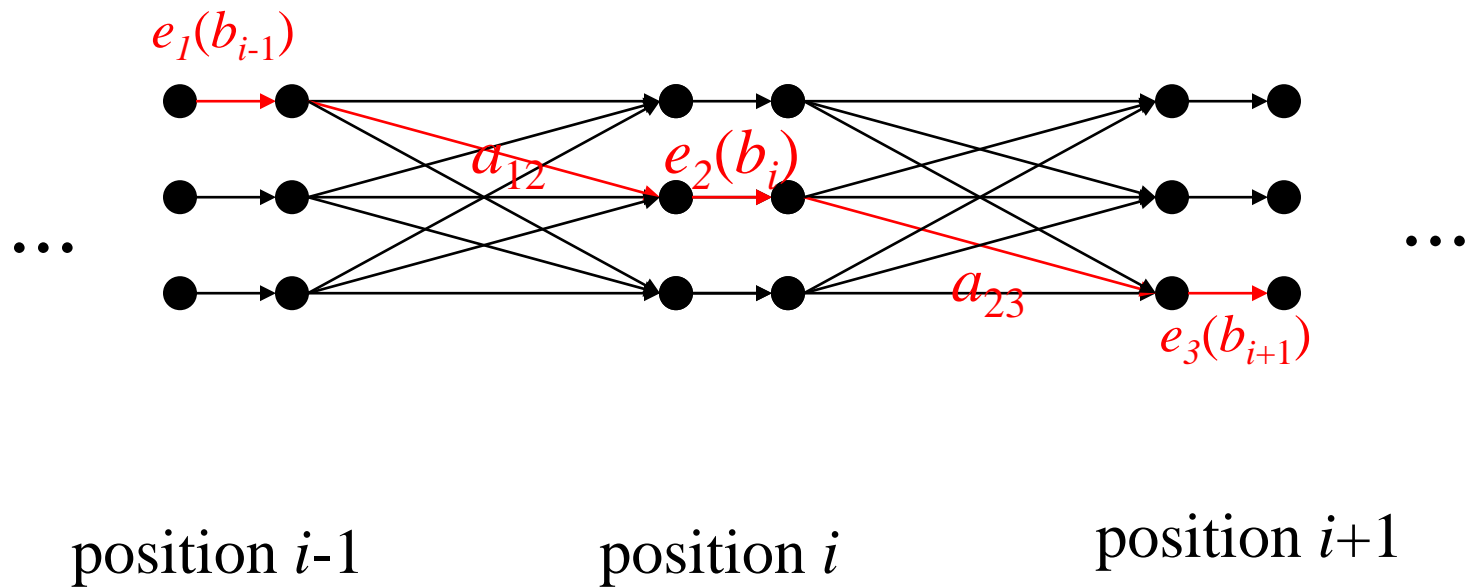


Beginning of Graph



- *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

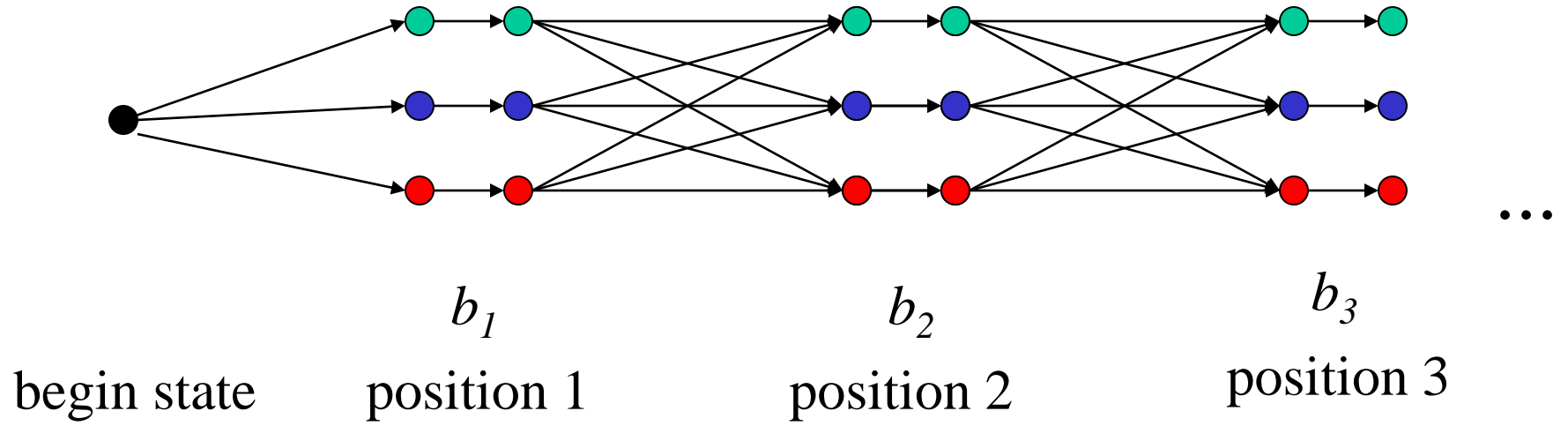


- By general results on WDAGs, can use dynamic programming to find highest weight path:
 - = “**Viterbi algorithm**” to find highest probability path (most probable “parse”)
 - in this case can use log probabilities & sum weights
 - (N.B. paths are constrained to begin at the begin node!)

The Viterbi path is
the *most probable parse!*

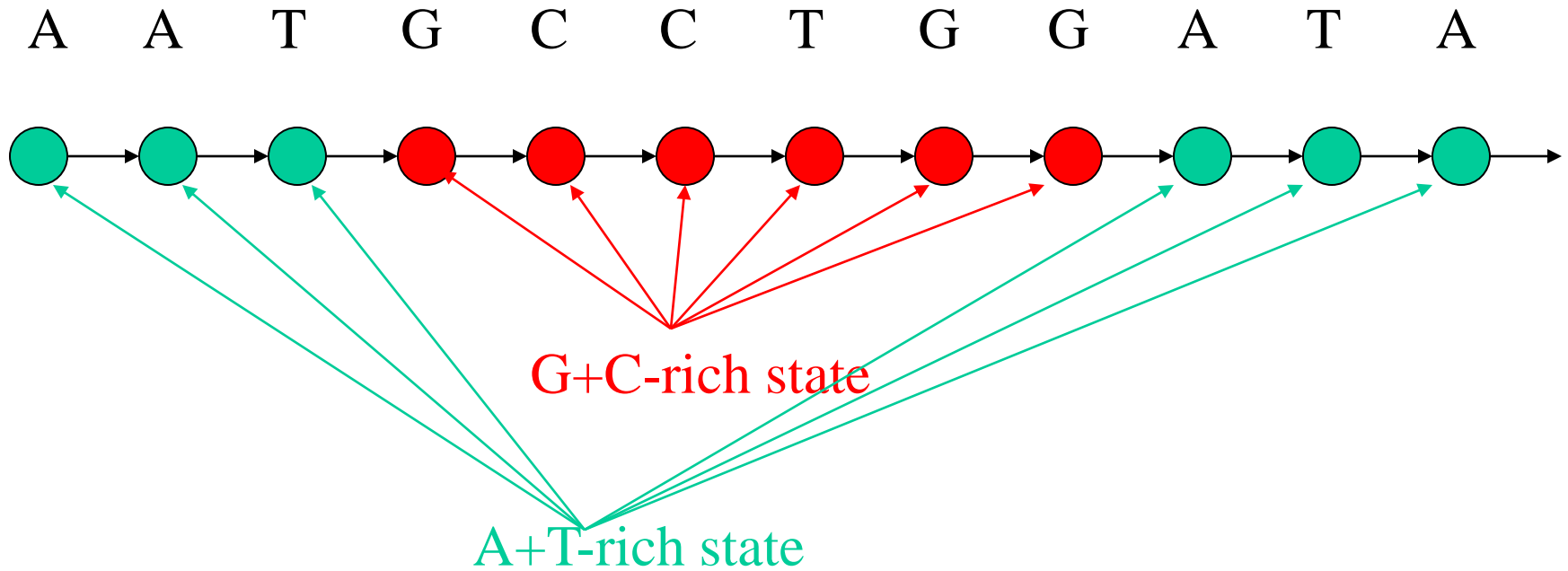
Complexity

- = $O(|V|+|E|)$, 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).

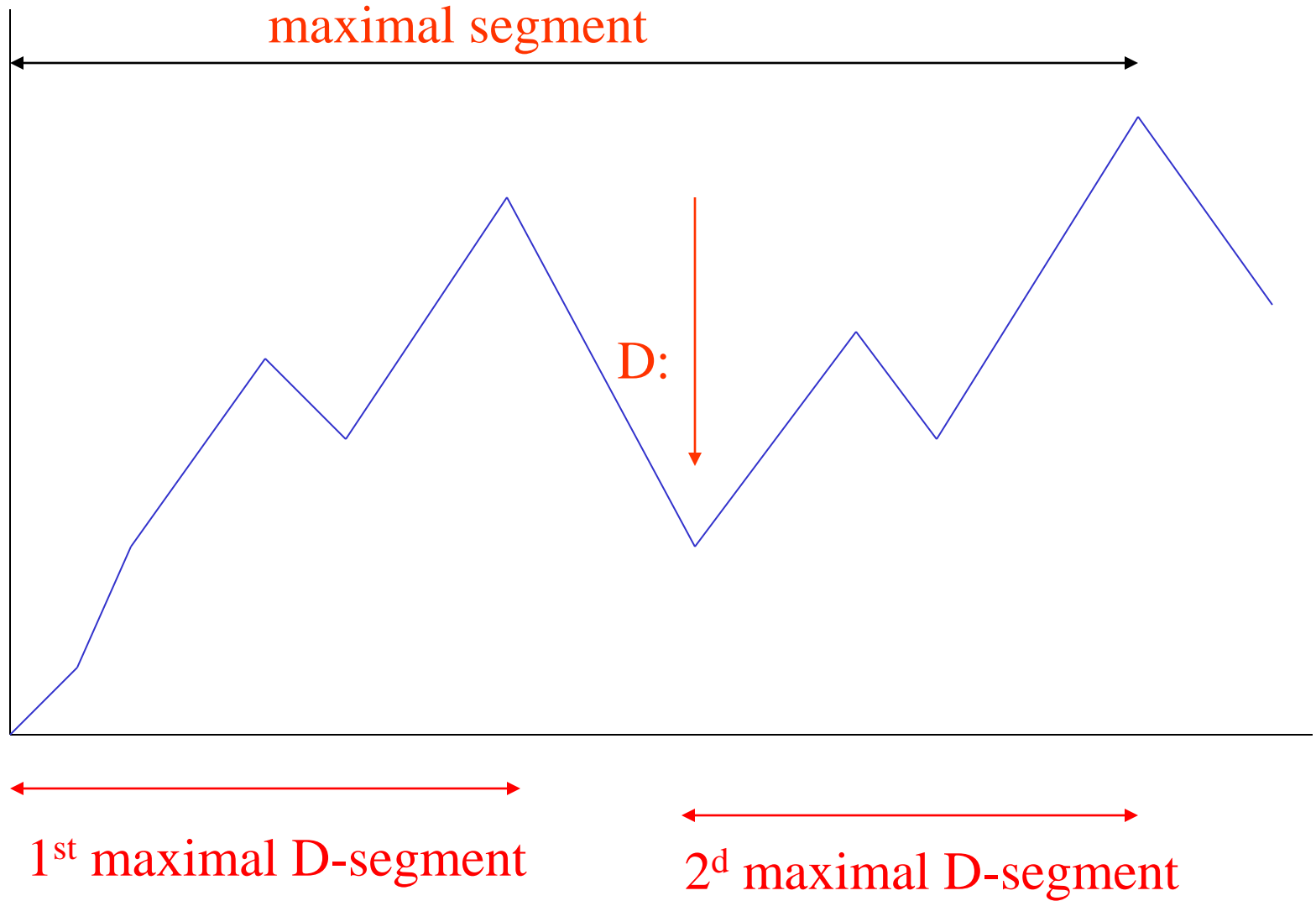


2-state HMMs & D-segments

from lecture 12



from lecture 7



- $O(N)$ 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 \approx 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