

Genome Annotation

The Viterbi algorithm

Outline

- The most probable path task for HMMs
- The Viterbi algorithm

HMM most probable path task

- Given: x
- Do: find a hidden path of states π that maximizes the joint probability of x and π

- Mathematically:

$$\pi^* = \operatorname{argmax}_{\pi} P(x, \pi)$$

- Note that this is equivalent to computing

$$\operatorname{argmax}_{\pi} P(\pi|x)$$

Example

- Consider an candidate CpG island

CGCGC

- Considering our HMM for CpG island model, some possible paths that are consistent with this CpG island are

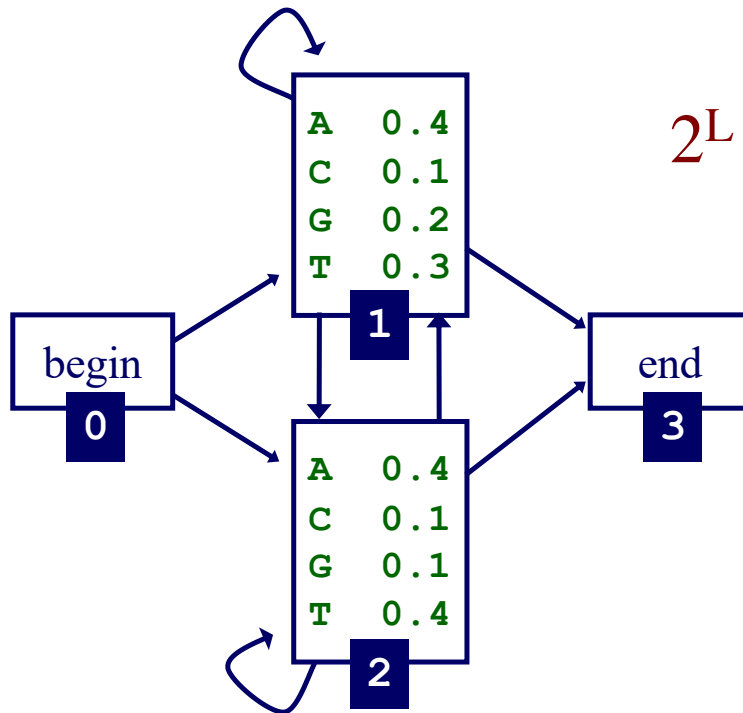
C⁺G⁺C⁺G⁺C⁺

C⁻G⁻C⁻G⁻C⁻

C⁻G⁺C⁻G⁺C⁻

Number of paths

- for a sequence of length L , how many possible paths through this HMM are there?



- the **Viterbi** algorithm enables us to compute the most likely path by efficiently taking a maximum over all possible paths

Finding the Most Probable Path: The Viterbi Algorithm

- Dynamic programming!
- subproblem: define $v_k(i)$ to be the probability of the most probable path accounting for the first i characters of x and ending in state k
$$v_k(i) = \max_{\pi_1, \dots, \pi_i: \pi_i = k} P(x_1, \dots, x_i, \pi_1, \dots, \pi_i)$$
- we want to compute $v_N(L)$, the probability of the most probable path accounting for all of the sequence and ending in the end state
- can define recursively
- can use DP to find $v_N(L)$ efficiently

Derivation of Viterbi recurrence

$$\begin{aligned}v_\ell(i) &= \max_{\pi_1, \dots, \pi_i: \pi_i = \ell} P(x_1, \dots, x_i, \pi_1, \dots, \pi_i) \\&= \max_{\pi_1, \dots, \pi_i: \pi_i = \ell} P(x_1, \dots, x_{i-1}, \pi_1, \dots, \pi_{i-1}) P(\pi_i | \pi_{i-1}) P(x_i | \pi_i) \\&= \max_k \max_{\pi_1, \dots, \pi_i: \pi_{i-1} = k, \pi_i = \ell} P(x_1, \dots, x_{i-1}, \pi_1, \dots, \pi_{i-1}) P(\pi_i | \pi_{i-1}) P(x_i | \pi_i) \\&= \max_k \max_{\pi_1, \dots, \pi_i: \pi_{i-1} = k, \pi_i = \ell} P(x_1, \dots, x_{i-1}, \pi_1, \dots, \pi_{i-1}) a_{kl} e_\ell(x_i) \\&= e_\ell(x_i) \max_k a_{kl} \max_{\pi_1, \dots, \pi_{i-1}: \pi_{i-1} = k} P(x_1, \dots, x_{i-1}, \pi_1, \dots, \pi_{i-1}) \\&= e_\ell(x_i) \max_k a_{kl} \underline{v_k(i-1)}\end{aligned}$$

Finding the Most Probable Path: The Viterbi Algorithm

- initialization:

$$v_0(0) = 1 \quad (0 \text{ is the begin state})$$

$$v_k(0) = 0, \quad \text{for } k \text{ that are not silent states}$$

The Viterbi Algorithm

- recursion for emitting states ($i = 1 \dots L$):

↪
$$v_l(i) = e_l(x_i) \max_k [v_k(i-1) a_{kl}]$$

$$\text{ptr}_l(i) = \arg \max_k [v_k(i-1) a_{kl}]$$

keep track of most probable path

- recursion for silent states:

$$v_l(i) = \max_k [v_k(i) a_{kl}]$$

$$\text{ptr}_l(i) = \arg \max_k [v_k(i) a_{kl}]$$

The Viterbi Algorithm

- termination:

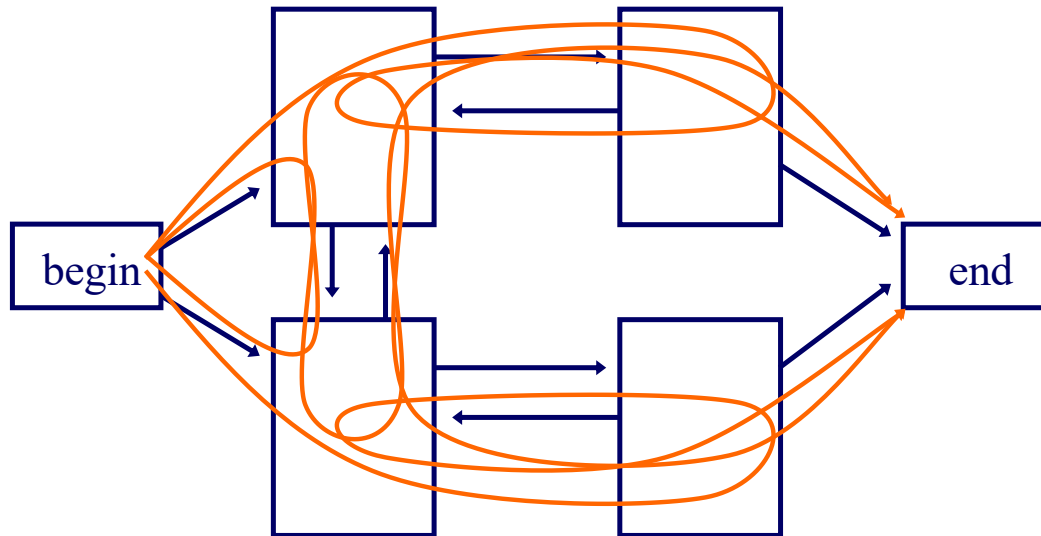
$$\Pr(x, \pi^*) = \max_k (v_k(L) a_{kN})$$

$$\pi_L^* = \arg \max_k (v_k(L) a_{kN})$$

- traceback: follow pointers back starting at π_L^*

Implicitly considering all possible paths

- The Viterbi algorithm effectively considers all possible paths for a sequence
- consider a sequence of length 4...



Numerically stable Viterbi

- Use log probabilities instead

$$\underline{V_k(i) = \log v_k(i)} \quad \underline{\tilde{e}_k(c) = \log e_k(c)} \quad \underline{\tilde{a}_{kl} = \log a_{kl}}$$

- Initialization

$$\underline{V_0(0) = 0} \quad \text{z} \begin{matrix} \log(c_1) \\ \log(c_0) \end{matrix}$$

$V_\ell(0) = -\infty$ for all other (non-silent) states

- Recurrence

$$V_\ell(i) = \tilde{e}_\ell(x_i) + \max_k (V_k(i-1) + \tilde{a}_{k\ell})$$

Using HMM to detect CpG islands

- Recall the 8-state HMM for our CpG island
- Apply the Viterbi algorithm to a DNA sequence on this HMM
- Contiguous assignments of ‘+’ states will correspond to CpG islands

Summary

- Viterbi algorithm efficiently solves the most probable path problem
- Viterbi algorithm is a dynamic programming algorithm
 - subproblem: $v_k(i)$: probability of most probable path for a prefix (i) of the sequence that ends in a given state (k)
- Log-transformed equations are needed for numerical stability when computing on long sequences