1. Show how to compute the forward probabilities for an HMM in log space.

Solution: (similar to the note posted on Piazza) First we take the log of the base case

$$\log f_1(k) = \log \pi_k + \log e_k(x_1).$$

Then in the recursive step, we want to compute

$$\log f_t(k) = \log e_k(x_t) + \log \sum_j f_{t-1}(j)a_{jk}.$$

But we haven't actually been computing the forward probabilities directly, we've been computing them in log space. So what we really have is

$$\log f_t(k) = \log e_k(x_t) + \log \sum_{j} e^{\log f_{t-1}(j)} \cdot e^{\log a_{jk}}.$$

In general, we want to compute an expression of the form

$$\log \sum_{i} e^{d_i}$$
.

The problem arises when all of the d_i are very large negative numbers, which can happen since d_i is the log of a probability, which could be very small. Then when we take the exponential of a very large negative number, the computer returns 0. If this happens for all d_i , we end up trying to take the log of 0, which returns $-\infty$, and this error propagates into our downstream computation. To fix this, we can subtract off the maximum, $D = \max_i \{d_i\}$, from each d_i . This ensures that for at least one d_k , $e^{d_k-D} = e^0 = 1$, so we won't be taking the log of 0. Overall, our computation becomes

$$\log \sum_{i} e^{d_i} = \log \sum_{i} e^{d_i} \cdot e^{D-D} = D + \log \sum_{i} e^{d_i - D}.$$

2. Suppose you are given fixed phylogenetic tree branch lengths t_1, t_2, \dots, t_B and mutation counts $x = x_1, x_2 \dots, x_B$ for each branch. Assuming mutations occur as a Poisson process with mutation rate μ , find the MLE (maximum likelihood estimator) for μ . Recall that if a random variable X is Poisson distributed with parameter λ , then the pmf (probability mass function) for X is $\mathbb{P}_{\lambda}(X = x) = \lambda^x e^{-\lambda}/x!$.

Solution: Let $X = X_1, X_2, \dots, X_B$. Since each branch is independent, we can rewrite the likelihood of our data as

$$L(\mu; x) = \mathbb{P}_{\mu}(X = x) = \prod_{i=1}^{B} \mathbb{P}_{\mu}(X_i = x_i) = \prod_{i=1}^{B} \frac{(\mu t_i)^{x_i} e^{-\mu t_i}}{x_i!}.$$

Then we can take the log to find the log likelihood

$$\ell(\mu; x) = \sum_{i=1}^{B} x_i \log(\mu t_i) - \mu t_i - \log(x_i!).$$

Then take the derivative with respect to μ and set it equal to 0. Finally solve for μ to get

$$\frac{\mathrm{d}\ell(\mu;x)}{\mathrm{d}\mu} = \sum_{i=1}^{B} \frac{x_i}{\mu} - t_i = 0 \quad \Rightarrow \quad \hat{\mu} = \frac{\sum_{i=1}^{B} x_i}{\sum_{i=1}^{B} t_i}.$$

3. The dynamic programming table below shows the fill-in step of Nussinov's RNA folding algorithm on the string S. Fill in the two missing entries, B(3,10) and B(1,12). Then perform back-tracing on both entries to find the optimal secondary structure(s) for S[3...10] and S. Does the number of unique optimal structures equal the number of tracebacks?

Solution:

| \boldsymbol{S} | | A | U | \mathbf{C} | \mathbf{G} | \mathbf{G} | A | U | \mathbf{C} | G | A | A | \mathbf{C} |
|------------------|----|---|---|--------------|--------------|--------------|-------------|----|--------------|------------|------------------|-------------|--------------|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | -11 | 12 |
| A | 1 | 0 | 0 | 0 | 0 | 1 | 2 | /3 | −3 ⁴ | 3 | 3 | 3 | 4 |
| U | 2 | | 0 | 0 | 0 | 1 | 2 <u>K</u> | 2 | 2 | 2 | \3 | 3 | 3 |
| \mathbf{C} | 3 | | | 0 | 0 | 1\$ | -1 <u>-</u> | 1 | 1 | ∠2← | 2 | 2 | 2 |
| \mathbf{G} | 4 | | | | 04 | 0 | 0 | 0 | س ار | 1 | $\overline{1}$ | 1 | 2 |
| \mathbf{G} | 5 | | | | | 0 | 0 | 0- | 1 | 1 | 1 / | 1 | $2 \mid$ |
| \mathbf{A} | 6 | | | | | | 0 | 0 | 0 | 0 | ₁ 14/ | 1 | 1 // |
| U | 7 | | | | | | | 0 | 0 | 0 | 11 | 1 | 1 // |
| \mathbf{C} | 8 | | | | | | | | 0 | 0~ | 0 | 0 | 14 |
| \mathbf{G} | 9 | | | | | | | | | 0 | 0 | 0 | 12 |
| \mathbf{A} | 10 | | | | | | | | | | 0 | 0 ►∕ | 0 |
| \mathbf{A} | 11 | | | | | | | | | | | 0 | 0 |
| \mathbf{C} | 12 | | | | | | | | | | | | 0 |

Let black arrows represent shared paths above. There are 4 traceback paths from B(3,10) (green, cyan, orange, purple), but only 3 unique secondary structures, shown below. There are 2 traceback paths from B(1,12) (red, blue), but both of these paths represent the same RNA secondary structure, shown below.

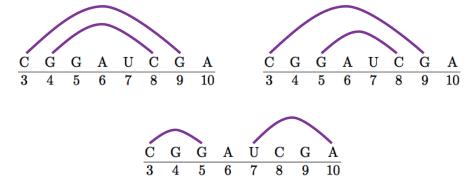


Figure 1: There are three optimal secondary structures for S[3...10].

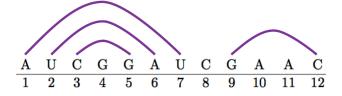


Figure 2: There is one optimal secondary structure for S.

4. Suppose a weighted coin, with probability θ of turning up heads is flipped until the first head occurs. Let X represent the total number of flips prior to getting heads. X is said to be geometrically distributed. Compute the pmf for X, $f(x) = \mathbb{P}(X = x)$. Show that f(x) is a proper probability distribution. Also compute the cmf (cumulative mass function) for X, $F(x) = \mathbb{P}(X \le x)$.

Solution: The probability of getting x tails is $(1-\theta)^x$. Therefore the probability of getting x tails, then getting a head is

$$f(x) = (1 - \theta)^x \theta.$$

To show this is a valid probability distribution, we need to make sure the sum of f(x) over all possible x is 1. Using the formula for an infinite geometric series,

$$\sum_{x=0}^{\infty} f(x) = \theta \sum_{x=0}^{\infty} (1 - \theta)^x = \theta \cdot \frac{1}{1 - (1 - \theta)} = 1.$$

Finally, we can use the formula for a finite geometric series to find F(x),

$$F(x) = \theta \sum_{y=0}^{x} (1 - \theta)^y = \theta \cdot \frac{1 - (1 - \theta)^x}{1 - (1 - \theta)} = 1 - (1 - \theta)^x.$$

- 5. The following are two key properties of expectation.
 - (a) Let X and Y independent discrete random variables. Prove that

$$\mathbb{E}[XY] = \mathbb{E}[X]\mathbb{E}[Y].$$

Does this property imply independence?

Solution: If X and Y are independent, then $\mathbb{P}(X,Y) = \mathbb{P}(X)\mathbb{P}(Y)$. So writing out the expectation of XY, we get

$$\begin{split} \mathbb{E}[XY] &= \sum_{x,y} xy \mathbb{P}(x,y) = \sum_{x} \sum_{y} xy \mathbb{P}(x) \mathbb{P}(y) \\ &= \left(\sum_{x} x \mathbb{P}(x) \right) \cdot \left(\sum_{y} y \mathbb{P}(y) \right) = \mathbb{E}[X] \mathbb{E}[Y]. \end{split}$$

This property does not necessarily imply independence; you can construct random variables that satisfy this equation, but are not independent.

(b) Now let X and Y be arbitrary discrete random variables, and $c,d\in\mathbb{R}$ arbitrary constants. Prove that

$$\mathbb{E}[cX + dY] = c\mathbb{E}[X] + d\mathbb{E}[Y].$$

Does this result require independence of X and Y? Show that if $\mathbb{P}(X \leq Y) = 1$ then $\mathbb{E}[X] \leq \mathbb{E}[Y]$.

Solution: Beginning with the LHS:

$$\begin{split} \mathbb{E}[cX+dY] &= \sum_{x,y} (cx+dy) \mathbb{P}(x,y) \\ &= c \sum_{x,y} x \mathbb{P}(x,y) + d \sum_{x,y} y \mathbb{P}(x,y) \\ &= c \sum_{x} x \sum_{y} \mathbb{P}(x,y) + d \sum_{y} y \sum_{x} \mathbb{P}(x,y) \\ &= c \sum_{x} x \mathbb{P}(x) + d \sum_{y} y \mathbb{P}(y) \\ &= c \mathbb{E}[X] + d \mathbb{E}[Y]. \end{split}$$

No where did we require that X and Y be independent. For the next part of this problem, we can use the result above with c = -1 and d = 1:

$$\mathbb{E}[Y] - \mathbb{E}[X] = \mathbb{E}[Y - X] = \sum_{x,y} (y - x) \mathbb{P}(x,y) \ge 0$$

$$\Rightarrow \quad \mathbb{E}[Y] \ge \mathbb{E}[X].$$