582653 Computational methods of systems biology, Autumn 2009 Homework 3 Group 1: Thursday Nov. 26th 14-16 B119 Group 2: Thursday Nov. 26th 16-18 B119

## General instructions

Problems for each exercise session will be distributed approximately one week before the session. You are expected to be prepared to present your solutions in the exercise session.

## Assignments

1. Given a  $4 \times m$  PWM w and a score threshold R, the p-value is defined as the probability that a given background model produces a sequence with score greater than or equal to R when aligned with w. Let P(i, r) be the probability of getting score r for a PWM containing the first i positions of w. These values can then be evaluated using the following recursion (assuming that entries in w are small integers)

$$P(0,r) = \begin{cases} 1, & \text{if } r = 0\\ 0, & \text{otherwise} \end{cases}$$
$$P(i,r) = \sum_{j \in \Sigma} q_j \cdot P(i-1,r-w[i,j])$$

where  $q_j$  is the probability of residue j in the background model. The p-value for w and R is then equal to  $\sum_{r\geq R} P(m,r)$ . Familiarize yourself with the method. If you are given the p-value  $\pi$ , how do you find the corresponding score threshold? (Hint: Use dynamic programming to evaluate P(m,r) for all r and use the dynamic programming array to find R.) For what values of i and r should P(i,r) be evaluated? Why do we allow only integers in w? What is the asymptotic running time of the method?

- 2. Try MEME at http://meme.sdsc.edu/meme/intro.html. The sequences in http://www.cs.helsinki.fi/u/lmsalmel/cmsb09/exercises/meme-data.fa contain the CREB1 binding site. Synthesize a PWM of length 8 from this data using MEME. Compare your result with the CREB1 profile in the Jaspar database, http://jaspar.cgb.ki.se/ (search for a profile with name CREB1).
- 3. Sketch an algorithm that finds from a given DNA sequence a window of width m such that this window has among all such windows the highest number of binding sites for a given set of PWMs that have score larger than T.
- 4. [Alon, Exercise 2.1]
- 5. [Alon, Exercise 2.2]
- 6. [Alon, Exercise 2.4]