INF281 Exercise 09 solutions

1. BLOSUM

BLOSUM uses several thousand blocks to calculate the probabilities of accepted mutation. Use the following definitions and Block1 & Block2 to solve the problems.

 f_{ab} : Frequencies of an observed pair a and b.

T: Total number of pairs from all blocks.

The number of pairs can be calculated as 1/2wm(m-1).

$$p_a: p_a = f_{aa} + \sum_{e \neq a} f_{ae}/2$$

 $e_{aa}:p_ap_a$

 $e_{ab}: p_a p_b + p_b p_a = 2p_a p_b$

Block1 Block2 CAGC GGA GTAC GTA CAGC

(a) Count the occurrences of all pairs.

	A	G	С	Т
A	2	2	0	2
G	2	2	2	1
С	0	2	4	0
Т	2	1	0	0

(b) Calculate T.

Solution:
$$(1/2 \times 4 \times 3 \times 2) + (1/2 \times 3 \times 2 \times 1) = 12 + 3 = 15$$

(c) Calculate f_{AA} and f_{AG} .

Solution: $f_{AA}: 2/15, \quad f_{AG}: 2/15$

(d) Calculate p_A and p_G .

Solution: $p_A: 8/30, p_G: 9/30$

(e) Calculate e_{AA} and e_{AG} .

Solution: e_{AA} : 64/900, e_{AG} : 144/900

(f) Calculate f_{AA}/e_{AA} and f_{AG}/e_{AG} .

Solution: $f_{AA}/e_{AA}: 1.875, \quad f_{AG}/e_{AG}: 0.833$

2. PPM (Position probability matrix)

PWM (position weight matrix) is a popular method to find sequenced patterns. It can be generated from PPM (position probability matrix) and PFM (position frequency matrix).

Seq1 CAA

Seq2 CAG

Seq3 GAC

Seq4 ATT

(a) Create a PFM from Seq1, Seq2, Seq3, and Seq4.

	1	2	3
A	1	3	1
G	1	0	1
С	2	0	1
Т	0	1	1

(b) Create a PPM from Seq1, Seq2, Seq3, and Seq4.

	1	2	3
A	0.25	0.75	0.25
G	0.25	0	0.25
С	0.5	0	0.25
Т	0	0.25	0.25

3. Sequence profile

A sequence profile is similar to PWM, but it uses a scoring scheme. Use the following definitions to calculate the profile values.

$$Prof_{ra}: \frac{1}{m_r} \sum_{b \in M} R_{ba} F_{rb}$$

 F_{rb} : The number of occurrences of b at position r

 R_{ba} : Pairwise score between b and a

 m_r : The number of residues without gaps at position r

Scoring matrix:

	A	G	С	Т
A	2	1	-3	-2
G	1	3	-2	-1
С	-3	-2	4	1
Т	-2	-1	1	2

Seq1 GT

Seq2 -G

Seq3 CA

(a) Calculate the profile values of position 1.

A1:
$$(1/2) \times ((2 \times 0) + (1 \times 1) + (-3 \times 1) + (-2 \times 0)) = -1$$

G1:
$$(1/2) \times ((1 \times 0) + (3 \times 1) + (-2 \times 1) + (-1 \times 0)) = 1/2$$

C1:
$$(1/2) \times ((-3 \times 0) + (-2 \times 1) + (4 \times 1) + (1 \times 0)) = 1$$

T1:
$$(1/2) \times ((-2 \times 0) + (-1 \times 1) + (1 \times 1) + (2 \times 0)) = 0$$

(b) Calculate the profile values of position 2.

A2:
$$(1/3) \times ((2 \times 1) + (1 \times 1) + (-3 \times 0) + (-2 \times 1)) = 1/3$$

G2:
$$(1/3) \times ((1 \times 1) + (3 \times 1) + (-2 \times 0) + (-1 \times 1)) = 1$$

C2:
$$(1/3) \times ((-3 \times 1) + (-2 \times 1) + (4 \times 0) + (1 \times 1)) = -4/3$$

T2:
$$(1/3) \times ((-2 \times 1) + (-1 \times 1) + (1 \times 0) + (2 \times 1)) = -1/3$$

(c) Make a profile matrix.

	1	2
Α	-1	1/3
G	1/2	1
С	1	-4/3
Т	0	-1/3

4. Profile search

A sequence profile can take gap penalties into account. Calculate the score of the alignment between the DNA profile below and a DNA segment.

A DNA profile of length 4

	Α	G	С	Т	Gap
1	5	-5	-2	-1	10
2	-2	3	4	-7	10
3	1	2	1	-1	5
4	-3	3	-2	7	10

- P1, P2, P3, P4: profile blocks at positions 1 4
- Gap penalty (for segments): 4

(a) Profile search on segment D1

Profile:	P1	P2	Р3	P4
D1:	Α	С	G	Т

Solution: 5 + 4 + 2 + 7 = 18

(b) Profile search on segment D2

Profile:	P1	P2	-	Р3	P4
D2:	Α	С	С	G	Т

Solution: 5+4+(-5)+2+7=13

(c) Profile search on segment D3

Profile:	P1	P2	P3	P4
D3:	A	-	G	Т

Solution: 5 + (-4) + 2 + 7 = 10

(d) Profile search on segment D4

Profile:	P1	P2	-	Р3	P4
D4:	-	Α	С	G	Т

Solution: (-4) + (-2) + (-5) + 2 + 7 = -2