Bio EndSem

Type 3

Sayam Kumar
S20180010157
Page 1

Q-1 Global Alignment

(a) ACGTACG and CTCGAC

Match = 8

Mismatch = -4

Gap = -5

Step 1 Initialization

Add gap scores to previous values

D		C	T	C	G	G	C
	0	-5	-10	-15	-20	-25	-30
A	-5						
C	-10						
G	-15						
T	-20						
A	-25						
C	-30						
G	-35						

Step 2 Forward fill

$$D_{i,j} = \max \begin{cases} D_{i-1,j-1} + \text{match/mismatch} \\ D_{i-1,j} + \text{gap} \\ D_{i,j-1} + \text{gap} \end{cases}$$

Sayam Kumar
S20180010158
Page2

D		C	T	C	G	G	C
	0	-5	-10	-15	-20	-25	-30
A	-5	-4	-9	-14	-19	-24	-29
C	-10	3	-2	-1	-6	-11	-16
G	-15	-2	-1	-6	7	2	-3
T	-20	-7	6	1	2	3	-2
A	-25	-12	1	2	-3	-2	-1
C	-30	-17	-4	9	4	-1	6
G	-35	-22	-9	4	17	12	7

Backtracing

Two answers

(a) $7 \to 12 \to 4 \to 9 \to 1 \to -2 \to 3 \to -5 \to 0$

~~A C G T A C _ G C~~

A C G T A C _ G _
* * * *
_ C _ T _ C G G C

Answer

(b) $7 \to 12 \to 17 \to 9 \to 1 \to 6 \to -2 \to 3 \to -5 \to 0$

A C G T A C G _ _
* * * *
_ C _ T _ C G G C

Answer

Score $= -5 + 8 - 5 + 8 - 5 + 8 + 8 - 5 - 5 = 7$

Sayam Kumar
S20180010159
Page 3

Q2 Local alignment

SPEAKL (PAM)

APPEAL

Gap score = -2
PAM 100

Initialization

		S	P	E	A	K	L
	0	0	0	0	0	0	0
A	0						
P	0						
P	0						
E	0						
A	0						
L	0						

Fill zeroes

forward fill

		S	P	E	A	K	L
	0	0	0	0	0	0	0
A	0	1	1	0	4	2	0
P	0	0	8	6	4	2	0
P	0	0	7	6	7	5	3
E	0	0	5	12	10	8	6
A	0	1	3	10	16	14	12
L	0	0	1	8	14	12	20

backpass

20 → 12 → 14 → 16
→ 12 → 7

Result

S	P	E	A	K	L
A	P	P	E	A	-	L

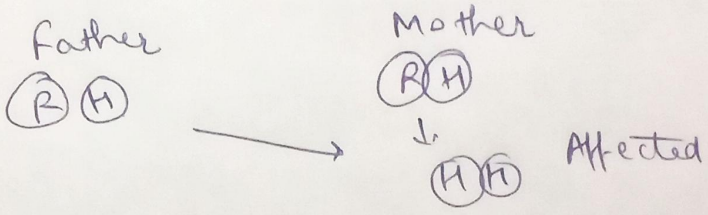
Q-3

Normal Protein val His Leu Thr Pro Glu Glu
Mutated val His Leu Thr Pro Val Glu

Glu → GAG
Val → GUG

This is because of oxygen tension that causes sickle RBC

Example



The proteins should be equally passed.

So, part 3 is answer comparing all pairs.
It has both amino acids in both parent

Father

3' CACATGAACTGAGGACACCTCTTCT

5' GTGCACCTGACTCCTGTGGAGAAGG 3'

Similarly in mother,

pair 3 is the parent for this child.