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Grade	**100.00** out of 100.00

Information

Part 1: In the following set of questions, you are to consider pairwise sequence alignment variations for the strings

TACTGCC

and

GACGAC

with **gap penalty** of **-5** and the following substitution matrix:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

Question 1

Correct

3.00 points out of 3.00

Globe	-	T	A	C	T	G	C	C
-	0	-5	-10	-15	-20	-25	-30	-35
G	-5	d,-2	d,-4	h,-9	h,-14	d,-16	h,-21	h,-26
A	-10	dv,-7	d,2	h,-3	h,-8	dh,-13	dh,-18	dh,-23
C	-15	d,-9	v,-3	d,6	h,1	h,-4	dh,-9	dh,-14
G	-20	v,-14	dv,-8	v,1	d,4	d,5	h,0	h,-5
A	-25	v,-19	d,-10	v,-4	dv,-1	d,5	d,3	
C	-30	dv,-24	v,-15	d,-6	d,-3	v,0		

Consider the **GLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the BLUE entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0
- 1
- 2
- 4
- 6
- 7
- 9 ✓
- 11

Your answer is correct.

The correct answer is:
9

Question 2

Correct

3.00 points out of 3.00

Globe	-	T	A	C	T	G	C	C
-	0	-5	-10	-15	-20	-25	-30	-35
G	-5	d,-2	d,-4	h,-9	h,-14	d,-16	h,-21	h,-26
A	-10	dv,-7	d,2	h,-3	h,-8	dh,-13	dh,-18	dh,-23
C	-15	d,-9	v,-3	d,6	h,1	h,-4	dh,-9	dh,-14
G	-20	v,-14	dv,-8	v,1	d,4	d,5	h,0	h,-5
A	-25	v,-19	d,-10	v,-4	dv,-1	d,5	d,3	
C	-30	dv,-24	v,-15	d,-6	d,-3	v,0		

Consider the **GLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the PINK entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0
- 1
- 2
- 4
- 6
- 7 ✓
- 9
- 11

Your answer is correct.

The correct answer is:
7

Question 3

Correct

3.00 points out of 3.00

Globe	-	T	A	C	T	G	C	C
-	0	-5	-10	-15	-20	-25	-30	-35
G	-5	d,-2	d,-4	h,-9	h,-14	d,-16	h,-21	h,-26
A	-10	dv,-7	d,2	h,-3	h,-8	dh,-13	dh,-18	dh,-23
C	-15	d,-9	v,-3	d,6	h,1	h,-4	dh,-9	dh,-14
G	-20	v,-14	dv,-8	v,1	d,4	d,5	h,0	h,-5
A	-25	v,-19	d,-10	v,-4	dv,-1	d,5	d,3	
C	-30	dv,-24	v,-15	d,-6	d,-3	v,0		

Consider the **GLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the YELLOW entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2 ✓
- -1
- 0
- 1
- 2
- 4
- 6
- 7
- 9
- 11

Your answer is correct.

The correct answer is: -2

Question 4

Correct

9.00 points out of 9.00

Which of the following is the optimal **GLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** ?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- T A C T G C
  G A C G A C
- T A C T G C C
  G A _ C G A C
- T A C G C C
  G A C G A C
- T A C T G C C
  G A C G A C _
- T A C T G C C ✓
  G A C _ G A C
- A C T G C
  A C G A C
- T A C T G C C
  _ G A C G A C

Your answer is correct.

The correct answer is: T A C T G C C
G A C _ G A C

Question 5

Correct

3.00 points out of 3.00

Loc	-	T	A	C	T	G	C	C
-	0	0	0	0	0	0	0	0
G	0	0	d,1	0	0	d,4	0	0
A	0	0	d,4	0	0	d,1	d,2	0
C	0	d,1	0	d,8	h,3	0	d,5	d,6
G	0	0	d,2	v,3	d,6	d,7	h,2	d,3
A	0	0	d,4	0	dv,1	d,7	d,5	
C	0	d,1	0	d,8	h,3	v,2		

Consider the **LOCAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the BLUE entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0
- 1
- 2
- 4
- 6
- 7
- 9
- 11 ✓

Your answer is correct.

The correct answer is:
11

Question 6

Correct

3.00 points out of 3.00

Loc	-	T	A	C	T	G	C	C
-	0	0	0	0	0	0	0	0
G	0	0	d,1	0	0	d,4	0	0
A	0	0	d,4	0	0	d,1	d,2	0
C	0	d,1	0	d,8	h,3	0	d,5	d,6
G	0	0	d,2	v,3	d,6	d,7	h,2	d,3
A	0	0	d,4	0	dv,1	d,7	d,5	
C	0	d,1	0	d,8	h,3	v,2		

Consider the **LOCAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the YELLOW entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0 ✓
- 1
- 2
- 4
- 6
- 7
- 9
- 11

Your answer is correct.

The correct answer is:
0

Question 7

Correct

3.00 points out of 3.00

Loc	-	T	A	C	T	G	C	C
-	0	0	0	0	0	0	0	0
G	0	0	d,1	0	0	d,4	0	0
A	0	0	d,4	0	0	d,1	d,2	0
C	0	d,1	0	d,8	h,3	0	d,5	d,6
G	0	0	d,2	v,3	d,6	d,7	h,2	d,3
A	0	0	d,4	0	dv,1	d,7	d,5	
C	0	d,1	0	d,8	h,3	v,2		

Consider the **LOCAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the PINK entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0
- 1
- 2
- 4
- 6
- 7
- 9 ✓
- 11

Your answer is correct.

The correct answer is:
9

Question 8

Correct

9.00 points out of 9.00

Which of the following is the optimal **LOCAL alignment** of the sequences **TACTGCC** and **GACGAC** ?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- T A C T G C C
  _ G A C G A C

- T A C T G C C
  G A _ C G A C

- T A C T G C C
  G A C G A C _

- T A C T G C C
  G A C _ G A C

- T A C T G C
  G A C G A C

- A C T G C ✓
  A C G A C

- T A C G C C
  G A C G A C

Your answer is correct.

The correct answer is:

A C T G C
A C G A C

Question 9

Correct

3.00 points out of 3.00

SG	-	T	A	C	T	G	C	C
-	0	0	0	0	0	0	0	0
G	0	d,-2	d,1	d,-2	d,-2	d,4	h,-1	d,-2
A	0	d,-2	d,2	d,-1	d,-4	dv,-1	d,2	dh,-3
C	0	d,1	v,-3	d,6	h,1	h,-4	d,3	d,6
G	0	d,-2	d,2	v,1	d,4	d,5	h,0	dv,1
A	0	d,-2	d,2	d,0	dv,-1	d,5	d,3	
C	0	d,1	v,-3	d,6	dh,1	v,0		

Consider the **SEMIGLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the YELLOW entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2 ✓
- -1
- 0
- 1
- 2
- 4
- 6
- 7
- 9
- 11

Your answer is correct.

The correct answer is: -2

Question 10

Correct

3.00 points out of 3.00

SG	-	T	A	C	T	G	C	C
-	0	0	0	0	0	0	0	0
G	0	d,-2	d,1	d,-2	d,-2	d,4	h,-1	d,-2
A	0	d,-2	d,2	d,-1	d,-4	dv,-1	d,2	dh,-3
C	0	d,1	v,-3	d,6	h,1	h,-4	d,3	d,6
G	0	d,-2	d,2	v,1	d,4	d,5	h,0	dv,1
A	0	d,-2	d,2	d,0	dv,-1	d,5	d,3	
C	0	d,1	v,-3	d,6	dh,1	v,0		

Consider the **SEMIGLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the BLUE entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0
- 1
- 2
- 4
- 6
- 7
- 9 ✓
- 11

Your answer is correct.

The correct answer is:
9

Question 11

Correct

3.00 points out of 3.00

SG	-	T	A	C	T	G	C	C
-	0	0	0	0	0	0	0	0
G	0	d,-2	d,1	d,-2	d,-2	d,4	h,-1	d,-2
A	0	d,-2	d,2	d,-1	d,-4	dv,-1	d,2	dh,-3
C	0	d,1	v,-3	d,6	h,1	h,-4	d,3	d,6
G	0	d,-2	d,2	v,1	d,4	d,5	h,0	dv,1
A	0	d,-2	d,2	d,0	dv,-1	d,5	d,3	
C	0	d,1	v,-3	d,6	dh,1	v,0		

Consider the **SEMIGLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** with OPT matrix partially filled above.

Which of the choices is the correct OPT value for the PINK entry?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- -10
- -5
- -4
- -3
- -2
- -1
- 0
- 1
- 2
- 4
- 6
- 7 ✓
- 9
- 11

Your answer is correct.

The correct answer is:
7

Question 12

Correct

9.00 points out of 9.00

Which of the following is the optimal **SEMIGLOBAL alignment** of the sequences **TACTGCC** and **GACGAC** ?

Recall that the gap penalty is -5 and the Substitution scores matrix is this:

Sub	A	G	C	T
A	4	1	-2	-2
G	1	4	-2	-2
C	-2	-2	4	1
T	-2	-2	1	4

- T A C G C C
  G A C G A C
- T A C T G C C
  G A C _ G A C
- A C T G C
  A C G A C
- T A C T G C C
  G A _ C G A C
- T A C T G C C
  _ G A C G A C
- T A C T G C C ✓
  G A C G A C _

Your answer is correct.

The correct answer is:

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

Information

Part II: The next set of questions are **TRUE** or **FALSE** questions. You are to indicate whether the statement in quotations is **TRUE** or **FALSE.**

Question 13

Correct

7.00 points out of 7.00

Indicate whether the following statement is **TRUE** or **FALSE**:

"The time complexity for local pairwise sequence alignment with linear gap penalties is $\Theta(n^2)$ where n is the maximum length of the two input sequences."

Select one:

- True ✓
- False

The correct answer is 'True'.

Question 14

Correct

7.00 points out of 7.00

Indicate whether the following statement is **TRUE** or **FALSE**:

"The PAM-1 mutation probability matrix is symmetric."

Select one:

- True
- False ✓

The correct answer is 'False'.

Question 15

Correct

7.00 points out of 7.00

Indicate whether the following statement is **TRUE** or **FALSE**:

"If M is the PAM-1 mutation probability matrix, then M^n is the PAM-n mutation probability matrix."

Select one:

- True ✓
- False

The correct answer is 'True'.

Question 16

Correct

7.00 points out of 7.00

Indicate whether the following statement is **TRUE** or **FALSE**:

"The time complexity for global pairwise sequence alignment with ***affine*** gap penalties is $\Theta(n^3)$ where n is the maximum length of the two input sequences."

Select one:

- True
- False ✓

The correct answer is 'False'.

Information

Part III: The last questions are **multiple choice** questions. Pick the **unique best answer**.

Question 17

Correct

9.00 points out of 9.00

Consider a global **affine alignment** of the sequences

CAC

and

GACACAGA

with the following parameters:

total gap start score **P = H + G**, **gap extensions score G**, **mismatch** score **S**, and **match** score **M.**

Assume that **M** is positive and greater than S, G, and H.

Furthermore, assume that **G** < 0, and that G $\leq$ **S** < M.

Finally, assume that **H** $\leq$ 0, so that **P** $\leq$ G.

Consider the following two possible alignments of the two sequences:

Alignment 1:
CAC _ _ _ _ _
GACACAGA

Alignment 2:

_ _ CAC _ _ _
GACACAGA

Which of the following claims is TRUE?

a. For any parameter setting respecting the assumptions, Alignment 1 is always the optimal affine alignment.

b. For any parameter setting respecting the assumptions, Alignment 2 is always the optimal affine alignment.

c. None of the other claims are true.

d. When H is zero, Alignment 2 is the optimal affine alignment. But, if we decrease H as the other parameters stay fixed, eventually Alignment 1 becomes the optimal affine alignment (and stays that way). ✓

e. When H is zero, Alignment 1 is the optimal affine alignment. But, if we decrease H as the other parameters stay fixed, eventually Alignment 2 becomes the optimal affine alignment (and stays that way).

Your answer is correct.

The correct answer is: When H is zero, Alignment 2 is the optimal affine alignment. But, if we decrease H as the other parameters stay fixed, eventually Alignment 1 becomes the optimal affine alignment (and stays that way).

Question 18

Correct

9.00 points out of 9.00

Consider a global **affine alignment** of the sequences

AA

and

AAAAAA

with the following parameters:

total gap start score **P = H + G**, **gap extensions score G**, **mismatch** score **S**, and **match** score **M.**

Say that we are given the following setting: P < G < S < 0 < M.

Consider the following possible alignments of the two sequences:

Alignment 1:
A A _ _ _ _
A A A A A A

Alignment 2:

_ A A _ _ _
A A A A A A

Alignment 3:
_ _ A A _ _
A A A A A A

Alignment 4:
_ _ _ A A _
A A A A A A

Alignment 5:
_ _ _ _ A A
A A A A A A

Alignment 6:
A A
A A

Which of the following claims is TRUE?

a. All of the alignments 1 through 5 are the optimal global affine alignments.

b. Alignments 1 and 5 are the only two optimal global affine alignments. ✓

c. Alignment 3 is the only optimal global affine alignment.

d. Alignment 6 is the only optimal global affine alignment.

e. Alignments 2 and 4 are the only optimal global affine alignments.

Your answer is correct.

The correct answer is: Alignments 1 and 5 are the only two optimal global affine alignments.