

Feedback — Week 2 Quiz

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You submitted this quiz on **Thu 6 Aug 2015 4:08 AM PDT**. You got a score of **10.00** out of **10.00**.

Question 1

Consider the following alignment:

```
TCGAC--ATT
CC---GAA-T
```

What is the score of this alignment if the match score is 1, the mismatch penalty is 1, and the indel penalty is 2?

You entered:

Your Answer	Score	Explanation
-10	2.00	
Total	2.00 / 2.00	



Question 2

Consider the following alignment:

```
TACTATTTACAGTAGACACGT
AACAGAC-ATAC-AGATACCT
```

What is the score of the red portion of this alignment as a *local* alignment if the match score is 1,

the mismatch penalty is 3, and the indel penalty is 1?

You entered:

-3

Your Answer		Score	Explanation
-3	✓	2.00	
Total		2.00 / 2.00	

Question 3

Say that the match score is 1, the mismatch penalty is 1, and the indel penalty is 1.

What is the maximum score of a fitting alignment of ACGTCG and GTTGGATTACGAATCGATATCTGTTTG? (Hint: don't make this problem too difficult.)

You entered:

4

Your Answer		Score	Explanation
4	✓	2.00	
Total		2.00 / 2.00	

Question 4

Say that the match score is 1, the mismatch penalty is 0, and the indel penalty is 2.

Score the following overlap alignment.

```
AGTACATCAGAGGAGTT-ACATACTAACG
      AGTTCACAGGCTA-CGTACAGATATTACGACAGGCAGA
```

You entered:

8

Your Answer		Score	Explanation
8	✓	2.00	
Total		2.00 / 2.00	

Question 5

What type of alignment should you use if you are interested in aligning DNA reads forming a contiguous interval of a genome?

Your Answer		Score	Explanation
<input type="radio"/> Global alignment			
<input type="radio"/> Local alignment			
<input type="radio"/> Fitting alignment			
<input checked="" type="radio"/> Overlap alignment	✓	2.00	
Total		2.00 / 2.00	