



Module 3

TOTAL POINTS 10

1. The value in each edit-distance matrix element depends on its neighbors: 1 point
 - ☐ Above, to the left, and to the right
 - ☐ To the left and to the lower-left
 - ☐ To the upper-left, to the left and to the lower-left
 - ☒ Above, to the left, and to the upper-left
2. Say we have filled in the approximate matching matrix and identified the minimum value (say, 2) in the bottom row. Now we would like to know the shape of the corresponding 2-edit alignment, i.e. we would like to know where the insertions, deletions and substitutions are. We use a procedure called: 1 point
 - ☐ Pathing
 - ☒ Traceback
 - ☐ Binary search
 - ☐ Filling
3. Say the edit distance between DNA strings α and β is 407. What is the edit distance between α and βQ (Q concatenated with the base Q)? 1 point
 - ☒ could be any of the other choices
 - ☐ 406
 - ☐ 407
 - ☐ 408
4. Say we are using dynamic programming to find approximate occurrences of P in T . About how many dynamic programming matrix elements do we have to fill in? 1 point
 - ☒ $|P| \cdot |T|$
 - ☐ $|P| + |T|$
 - ☐ $|T|^2$ (squared)
 - ☐ $|P|^2$ (squared)
5. Local alignment is different from global alignment because: 1 point
 - ☒ It finds similarities between substrings rather than between entire strings
 - ☐ It compares three strings instead of two
 - ☐ There is no dynamic programming algorithm for solving it
 - ☐ Insertions and deletions incur no penalty
6. The first law of assembly says that if a prefix of read A is similar to a suffix of read B , then... 1 point
 - ☐ Read B might have a sequencing error at the end
 - ☒ A and B might overlap in the genome
 - ☐ A and B must be from different genomes
 - ☐ A and B should not be joined in the final assembly
7. The second law of assembly says that more coverage leads to... 1 point
 - ☒ more and longer overlaps between reads
 - ☐ more sequencing errors
 - ☐ less accurate results
8. In an overlap graph, the nodes of the graph correspond to 1 point
 - ☐ Genomes

- ☐ Bases
- ☐ Overlaps
- ☒ Reads

9. The overlap graph is a useful structure because:

1 point

- ☒ A reconstruction of the genome corresponds to a path through the graph
- ☐ It makes it faster to compare reads
- ☐ It helps to ignore long overlaps

10. Which of the following is not a reason why an overlap might contain sequence differences (i.e. might not be an exact match):

1 point

- ☐ Polyploidy
- ☐ Sequencing error
- ☒ Insufficient coverage

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