1. The students can be assessed on completion of the assignment itself.

Rubric:
0 – Didn't complete or had no idea what to do.
1 – Completed, and had the general idea, but made some small mistakes which kept them from getting the right numerical answers to the test data.
2 – Got it right.

2. Related question on midterm
 (This question asks them to apply what they've done in a slightly different way, to nucleotides)

Devise optimal match and mismatch parameters for a nucleotide database search where you expect homologous sequences to have 66% identity.

Assume:
      - 25% background frequency of each nucleotide
      - λ = .2
      - all matches are equally likely, and all mismatches are equally likely. ie the matrix looks like
this:

	A	C	G	T
A	m	μ	μ	μ
C	μ	m	μ	μ
G	μ	μ	m	μ
T	μ	μ	μ	m

What are the best parameters (as integers)? Explain the reasoning you used to arrive at this.

Rubric:

2 – got it
1.5 - If made small numerical error (didnt' round, didn't divide by 12 for mismatch etc)
0 – Didn't know how to do it.

3. Attitude and belief (and/or affective) assessments

Creating a scoring matrix helped me achieve a better understanding of the meaning of alignment scores.
      a. stronly agree
      b. agree
      c. undecided
      d. disagree
      e. strongly disagree