**9 Operational Research**

**9.3 Protein Comparison in Bioinformatics**

Question 1:

.

Proof:

To get to , we must consider four possibility:

For getting , we must get the minimum edit distance among the three cases.   
(We only need to consider one of the two starred cases each time as it is depending on whether or not.)  
Case 1 has edit distance   
Case 2 has edit distance   
Case 3 (/4) has edit distance

As replacement takes up 1 edit distance and matching does not take up any edit distance,

Therefore

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Boundary conditions are . This is because it takes deletions to get from to nothing and similarly it takes insertions to get from nothing to .

Question 2: Run the program [editdistanceQ2.m]

The edit distance between ‘shesells’ and ‘seashells’ is 3.

The complexity of the program editdistanceQ2.m is , where m and n are the length of respectively.

This is because for finding the edit distance, we need to calculate the matrix D by using the algorithm suggested in Question 1, .

Assigning boundary conditions: m+n+1 operations  
3 additions, 1 assignment (for ) and 1 comparison for an entry: 5(m-1)x(n-1)

Therefore, the total complexity

Questions 3: Run the program [editdistance\_modQ3.m]

To modify my algorithm so as to produce one possible optimal alignment between two strings, I need to find out the path we get from to . For convenience, I have designed another matrix to store the values in such that . Therefore, my new algorithm aims to find a path from to .

To find the path, we need to work backwards and track how we get to the bottom right of matrix .  
From the values in , we can easily deduce what the operation has been taken to reach .

If

1. We can deduce either replacement or matching has been taking place depending on which takes us from to .

We can deduce that deletion has been taking place which takes us from to .

1. Similarly, if

We can deduce that insertion has been taking place which takes us from to .

It is possible that two or more of the three cases happened at the same time. (Example: ‘ab’ and ‘ba’)   
In fact, no matter which path we take among the three, we should get the same edit distance as each step is only depending on the previous step’s edit distance only but not those before the previous step. As a rule of thumb, my algorithm follows the following priority: replacement/Matching, Deletion and Insertion.

Working backwards to get all the operations in reverse order with this algorithm and present the result in the correct order at the end will gives a possible optimal alignment between two stings.

After running the modified algorithm, the minimum edit distance between protein A and protein B is 84.

First 50 steps of an optimal alignment:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | *With Matching* |  |  |  | *Without Matching* |
| 1 | Match M with M |  |  | 1 | Delete M |
| 2 | Delete G |  |  | 2 | Delete G |
| 3 | Delete L |  |  | 3 | Replace L with M |
| 4 | Replace S with A |  |  | 4 | Delete S |
| 5 | Match D with D |  |  | 5 | Delete D |
| 6 | Delete G |  |  | 6 | Replace G with A |
| 7 | Delete E |  |  | 7 | Replace E with D |
| 8 | Replace W with F |  |  | 8 | Replace W with F |
| 9 | Replace Q with D |  |  | 9 | Replace Q with D |
| 10 | Replace L with A |  |  | 10 | Replace L with A |
| 11 | Match V with V |  |  | 11 | Replace V with V |
| 12 | Match L with L |  |  | 12 | Replace L with L |
| 13 | Replace N with K |  |  | 13 | Replace N with K |
| 14 | Replace V with C |  |  | 14 | Replace V with C |
| 15 | Match W with W |  |  | 15 | Replace W with W |
| 16 | Match G with G |  |  | 16 | Replace G with G |
| 17 | Replace K with P |  |  | 17 | Replace K with P |
| 18 | Match V with V |  |  | 18 | Replace V with V |
| 19 | Match E with E |  |  | 19 | Replace E with E |
| 20 | Replace T with A |  |  | 20 | Replace T with A |
| 21 | Match D with D |  |  | 21 | Replace D with D |
| 22 | Replace L with Y |  |  | 22 | Replace L with Y |
| 23 | Replace A with T |  |  | 23 | Replace A with T |
| 24 | Replace G with T |  |  | 24 | Replace G with T |
| 25 | Replace H with M |  |  | 25 | Replace H with M |
| 26 | Match G with G |  |  | 26 | Replace G with G |
| 27 | Replace Q with G |  |  | 27 | Replace Q with G |
| 28 | Replace E with L |  |  | 28 | Replace E with L |
| 29 | Match V with V |  |  | 29 | Replace V with V |
| 30 | Match L with L |  |  | 30 | Replace L with L |
| 31 | Replace I with T |  |  | 31 | Replace I with T |
| 32 | Replace S with R |  |  | 32 | Delete S |
| 33 | Match L with L |  |  | 33 | Replace L with R |
| 34 | Match F with F |  |  | 34 | Replace F with L |
| 35 | Match K with K |  |  | 35 | Replace K with F |
| 36 | Replace G with E |  |  | 36 | Replace G with K |
| 37 | Match H with H |  |  | 37 | Replace H with E |
| 38 | Match P with P |  |  | 38 | Replace P with H |
| 39 | Match E with E |  |  | 39 | Replace E with P |
| 40 | Match T with T |  |  | 40 | Replace T with E |
| 41 | Replace L with Q |  |  | 41 | Replace L with T |
| 42 | Replace E with K |  |  | 42 | Replace E with Q |
| 43 | Replace K with L |  |  | 43 | Replace K with K |
| 44 | Match F with F |  |  | 44 | Replace F with L |
| 45 | Replace E with P |  |  | 45 | Replace E with F |
| 46 | Match K with K |  |  | 46 | Replace K with P |
| 47 | Match F with F |  |  | 47 | Replace F with K |
| 48 | Replace K with A |  |  | 48 | Replace K with F |
| 49 | Replace H with G |  |  | 49 | Replace H with A |
| 50 | Replace L with I |  |  | 50 | Replace L with G |
| : | : |  |  | : | : |
| : | : |  |  | : | : |
| : | : |  |  | : | : |
| 150 | Match L with L |  |  | 80 | Replace K with K |
| 151 | Match G with G |  |  | 81 | Replace G with A |
| 152 | Match F with F |  |  | 82 | Replace Q with K |
| 153 | Replace Q with S |  |  | 83 | Replace H with G |
| 154 | Match G with G |  |  | 84 | Replace E with S |

Question 4: Run the program [scoreQ4.m]

Noticing we are now maximizing the score for our optimal alignment instead of minimizing the edit distance, the result is likely to be different from the previous question.

Modifying the program [editdistance\_modQ3.m] as we have changed our algorithm slightly to  
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Similar to Question 3, to find the path, we need to work backwards and track how we get to the bottom right of the matrix .

If

1. We can deduce either replacement or matching has been taking place depending on which takes us from to .

We can deduce that deletion has been taking place which takes us from to .

1. Similarly, if

We can deduce that insertion has been taking place which takes us from to .

Similarly, if more than one case appear to be true, we can take any of those operations as the optimum alignment does not depend on the steps before the previous steps.

With the similar approach as Question 3, we present one of the optimal alignments for the maximum score.

After running [scoreQ4.m], the maximum score between protein A and protein B is 287.  
First 50 steps of an optimal alignment:

|  |  |
| --- | --- |
| 1 | Match M with M |
| 2 | Delete G |
| 3 | Delete L |
| 4 | Replace S with A |
| 5 | Match D with D |
| 6 | Delete G |
| 7 | Delete E |
| 8 | Replace W with F |
| 9 | Replace Q with D |
| 10 | Replace L with A |
| 11 | Match V with V |
| 12 | Match L with L |
| 13 | Replace N with K |
| 14 | Replace V with C |
| 15 | Match W with W |
| 16 | Match G with G |
| 17 | Replace K with P |
| 18 | Match V with V |
| 19 | Match E with E |
| 20 | Replace T with A |
| 21 | Match D with D |
| 22 | Replace L with Y |
| 23 | Replace A with T |
| 24 | Replace G with T |
| 25 | Replace H with M |
| 26 | Match G with G |
| 27 | Replace Q with G |
| 28 | Replace E with L |
| 29 | Match V with V |
| 30 | Match L with L |
| 31 | Replace I with T |
| 32 | Replace S with R |
| 33 | Match L with L |
| 34 | Match F with F |
| 35 | Match K with K |
| 36 | Replace G with E |
| 37 | Match H with H |
| 38 | Match P with P |
| 39 | Match E with E |
| 40 | Match T with T |
| 41 | Replace L with Q |
| 42 | Replace E with K |
| 43 | Replace K with L |
| 44 | Match F with F |
| 45 | Replace E with P |
| 46 | Match K with K |
| 47 | Match F with F |
| 48 | Replace K with A |
| 49 | Replace H with G |
| 50 | Replace L with I |
| : | : |
| : | : |
| : | : |
| 147 | Match Y with Y |
| 148 | Match K with K |
| 149 | Match E with E |
| 150 | Match L with L |
| 151 | Match G with G |
| 152 | Match F with F |
| 153 | Replace Q with S |
| 154 | Match G with G |

Question 5:

As we ae taking gaps into account as well, we need to consider a new algorithm. In the modified algorithm, the score and the options we take for each entry in matrix no longer be only depending on the previous step, but also some steps before the previous step.

New algorithm:

For each value in (which is same as each entry in matrix ), we would need to take up to calculations and one comparison operation for ; and similarly calculations and one comparison operation for . Finally, it takes 1 operation to get and 1 comparison operation for getting . As there are values in grid, it has complexity of  
 which is .

If we let takes some fixed value u for all , we can simplified our algorithm into the following:

Matching the gap  
 Matching the gap  
 Replace/Match

In other word, we may consider our algorithm as follow:

Matching the gap  
 Matching the gap  
 Replace/Match

Where

implies an insertion after the optimal alignment changing (inserting at the end);  
 implies a deletion after the optimal alignment changing (deleting at the end);  
 implies a replacement or a matching operation taken for getting .

Therefore, we now have only 1 comparison operation for calculating and and requires 1 addition operation for the algorithm for each entry. In addition, as there are entries in total, the complexity of the new algorithm is .

Boundary conditions are for all

Question 6: Run the program [gapscoreQ5.m]

After running [gapscoreQ5.m], the maximum gap-weighted score between protein C and protein D is 622.  
First 50 steps of an optimal alignment:

|  |  |
| --- | --- |
| 1 | Match M with M |
| 2 | Replace T with S |
| 3 | Replace T with R |
| 4 | Replace C with Q |
| 5 | Match S with S |
| 6 | Insert S |
| 7 | Insert V |
| 8 | Insert S |
| 9 | Insert F |
| 10 | Insert R |
| 11 | Insert S |
| 12 | Insert G |
| 13 | Insert G |
| 14 | Insert S |
| 15 | Match R with R |
| 16 | Replace Q with S |
| 17 | Match F with F |
| 18 | Replace T with S |
| 19 | Replace S with T |
| 20 | Replace S with A |
| 21 | Match S with S |
| 22 | Insert A |
| 23 | Insert I |
| 24 | Insert T |
| 25 | Insert P |
| 26 | Insert S |
| 27 | Insert V |
| 28 | Insert S |
| 29 | Insert R |
| 30 | Insert T |
| 31 | Insert S |
| 32 | Insert F |
| 33 | Insert T |
| 34 | Insert S |
| 35 | Insert V |
| 36 | Insert S |
| 37 | Insert R |
| 38 | Insert S |
| 39 | Insert G |
| 40 | Insert G |
| 41 | Insert G |
| 42 | Insert G |
| 43 | Insert G |
| 44 | Insert G |
| 45 | Insert G |
| 46 | Insert F |
| 47 | Insert G |
| 48 | Insert R |
| 49 | Insert V |
| 50 | Match S with S |
| : | : |
| : | : |
| : | : |
| 631 | Delete K |
| 632 | Delete V |
| 633 | Delete V |
| 634 | Delete S |
| 635 | Delete T |
| 636 | Delete H |
| 637 | Delete E |
| 638 | Delete Q |
| 639 | Delete V |
| 640 | Delete L |
| 641 | Replace R with S |
| 642 | Replace T with F |
| 643 | Match K with K |
| 644 | Replace N with S |

Question 7:

Noticing for any ‘replacing’ operation, we can replace it by a ‘deletion’ and an ‘insertion’ operation. Therefore, the score of replacement of a sequence of length of the same protein in this example will be .

Proof:

Proof:

Instead of introducing the fixed score of inserting/deleting a sequence of length be I let be the score of inserting/deleting a protein. For any protein transformation which involved deletion or insertion of a sequence of length greater than 1, they will have a score . Equality occurs if when inserting/deleting a sequence protein does not give a higher score than simply do replacement operations. However, as , considering all possible protein transformation of length there must be a transformation involving replacement of such that =2u where . Therefore, for , there must exist some , such that .

Hence,

■

Proof:

By induction:  
For n=1,

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
| a | a | 1 |  |
| a | b |  |  |
| b | a |  |  |
| b | b | 1 |  |

Taking all possible sequence pairs and their transformation scores, we get an inequality

(Remark: . )  
Therefore,

If is true, consider

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
| a | a | 1 |  |
| a | b |  |  |
| b | a |  |  |
| b | b | 1 |  |

denoting

Therefore,

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Hence, combining the two lemmas

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Question 8:

Question 9:

Proof:

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Proof:

(1): Consider a substring and we can try to build a new substring in the following manner:  
 Include into as the first element;  
 -if , we stop  
 -if , we continue to add the next element from to .

Existence & (2): From the above algorithm, as the substring , it must stop at some point in the string with the suffix of be the substring .   
(1): In addition, as we start building substring from the first element of , is also the prefix of S.

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By definition, As we proved in , any substring can be extended to the suffix of a prefix of . Therefore, we can rewrite

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Question 10:

With Boundary conditions

Proof:

Notice that we do not take gap into account in this Question, we are having a similar problem as Question 1. This time, we only concern about the positive score because the minimum score for is always 0 as we can always consider take substring of length 0 from and from which gives a score of 0.

To get , we must consider four possibility:

Why only 4 possibility?  
This is because if is the maximum score obtained in , for , one of the possible value will be ), which is described in case 3.   
If ), (where , will not be equal to as .

Similar argument for case (1) and (2).

For case (4), if the score is negative for all case (1) to (3), given that we can take substring of length 0, we can always pick a score of 0 for .

Therefore, we only need to compare these 4 cases.

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Boundary condition:

This is because and and by observation, given , the values of them will be 0.

Question 11: Run the program [scoreQ11.m]

I have created a matrix and run the algorithm suggested in Question 10. The maximum score will be the maximum entry in . Noticing the complexity of [scoreQ11.m] is .

After running the program, 799 for proteins C and D.