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CSC445 - Alon Efrat
4/15/18
Homework 5

1.

	A	B	C	D
A	1	1	1	1
A	1	1	1	1
B	1	2	2	2
B	1	2	2	2
C	1	2	3	3
C	1	2	3	3

There are $2^3 = 8$ different possible alignments here as for A,B,C in "ABCD" there are two possible spots where each of them could be aligned on "AABBCC".

2. **Algorithm:** I would use a modified LCS algorithm. The only modification needed is to replace the step incrementing the total count:

```
// LCS for X[0..m-1], Y[0..n-1]
else if (X[i-1] == Y[j-1])
From: L[i][j] = L[i-1][j-1] + 1;

else if (X[i-1] == Y[j-1])
To : L[i][j] = L[i-1][j-1] + w(X[i-1]) // == w(Y[i-1])
```

Correctness: The maximum length subsequence is always the same as the maximum cost subsequence. To see why this is, note that every letter of any possible subsequence is contained in the maximum subsequence, so because letter weights are all positive, there can be no higher cost subsequence than the maximum length subsequence.
By making the change above we will record the cost of the maximum subsequence instead of the length.
Runtime: Assuming $w(Z)$ runs in constant time, the runtime of our algorithm will be unimpacted. It remains on the order of $O(n^2)$

3. **Algorithm**

```
// X[0..n-1], Y[0..m-1]
def is_subsequence(X,Y,n,m):
    i = 0
    j = 0
    while i < n and j < m:
      if X[i] == Y[j]:
        i += 1
      j += 1
    return i==n
```

Correctness If X is a subsequence of Y then for some integers $a_1, ..., a_n$

$$X[0] = Y[a_1], X[1] = Y[a_2], ..., X[n-1] = Y[a_n]$$

where $0 \le a_1 < a_2 < ... < a_n < m$, meaning that when $j = a_1$, i is set equal to 1, continuing in this way we can see when $j = a_n$, $i = n$ and the loop terminates and the algorithm returns true. Conversely if the algorithm returned true it must have found $a_1, ..., a_n$ that meet the criterion above.
Runtime We can see that j is incremented every loop, and the loop terminates when $j = m$, so there can only be $O(|Y|)$ iterations of the loop, because there are only a constant number of operations

4.

	ϵ	H	E	L	L	O
ϵ	$\underline{0}$	1	2	3	4	5
H	1	$\underline{0}$	1	2	3	4
A	2	$\underline{1}$	1	2	3	4
E	3	2	$\underline{1}$	2	3	4
A	4	3	$\underline{2}$	2	3	4
L	5	4	3	$\underline{2}$	2	3
A	6	5	4	$\underline{3}$	3	3
L	7	6	5	4	$\underline{3}$	4
A	8	7	6	5	$\underline{4}$	4
O	9	8	7	6	5	$\underline{4}$

All downward moves correspond to deleting a character from ”HAEALALAO” (or alternatively inserting a character in ”HELLO”). In this case all diagonal moves represent no change in either string occurring, as none of them increase the edit distance.

$$\text{"HAEALALAO"} \rightarrow \text{"HEALALAO"} \rightarrow \text{"HELALAO"} \rightarrow \text{"HELLAO"} \rightarrow \text{"HELLO"}$$

5. Let $p_0, ..., p_n$ be the points of P, $q_0, ..., q_n$ be the points of Q. At every step there are three possible moves

$$\begin{aligned}(p_i, q_j) &\rightarrow (p_{i+1}, q_{j+1})\\ &\rightarrow (p_i, q_{j+1})\\ &\rightarrow (p_{i+1}, q_j)\end{aligned}$$

We can see that r is the minimum value for which there exists a sequence of moves from (p_0, q_0) to (p_n, q_n) with distances under r at every move. Note that because every move increases i or j by one, and no moves decrease these values, any such sequence must contain under $2n$ moves. So there exists at least one sequence of moves from (p_0, q_0) to (p_n, q_n) with a total cost less than or equal to $(2n)r$. This implies that because $DTW(P, Q)$ finds the lowest sum for any such sequence of moves it will find one with cost less than or equal to $2nr$.

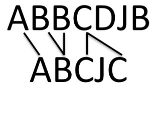
6. **Algorithm** Let $n < m$. The idea here is to use the traditional edit distance algorithm but instead of creating c, a 2-dimensional table with m row and n columns, simply create a one -dimensional array of length n, and repeatedly overwrite it m times. To compute the value of cell i, j in c, we need the value of $i, j-1$, $i-1, j$ and $j-1, i-1$. To compute cell j in our array on the ith iteration, $i, j-1$ is simply the cell before the one we are currently writing. $i-1, j$ is the cell currently in the spot of the cell we are computing and $i-1, j-1$ is the last cell we overrode. We will store this value $(i-1, j-1)$ in memory as we we go.

Correctness The procedure to fill out the first row of our table c with the traditional algorithm is the same as the procedure to fill out our array with our new algorithm. So after one iteration of our algorithm, the array is the same as the first row of c in the traditional algorithm, and as we override values from left to right we clearly have the last value we wrote, the last value we overwrote and the value we are trying to override. As mentioned above, this is the only information we need to calculate the value of any given cell, so by induction, after the final iteration of our algorithm, our array will have the same values as the final row of c. This means that when we report the last index array, it will be the same as the last index of our table.

Runtime Because we have not fundamentally changed the structure of the algorithm, the runtime is the same $O(n^2)$. However, because in this version we only need an array of length n and to remember the last value we overrode, we can conclude that our space complexity is $O(n)$.

7. The algorithm here is similar to Dynamic Time Warping. We still move down the points in P and Q, advancing either one point in P or one point in Q but (this time) never one point in both. If we draw lines in this way, we can be assured that no two will ever cross. We need to know which point to increment at any given time, so the sub-problem we will be looking at is how many lines can be drawn between the first i points in P and the first j points in Q if a line can be drawn between point i and point j. This number is one greater then the maximum number of lines that can be drawn from either the first $i-1$ points of P and the first j points of Q or the first $j-1$ points of Q and the first i points of P. If you can't draw a line between the ith and jth points, it's simply the maximum of the two (either because there labels don't match or they're to far apart). We will store the maximum number of line's ($|L|$) for problem i, j in cell i, j of a table and use it to compute the value of cells $i+1, j$ and $i, j+1$. The correctness of this algorithm follows by induction on the correctness of the sub-problems with the base sub problem being the case where $i = j = 1$ [1].
   Once this is done, the bottom right cell of our table will represent the total maximum number of lines that can be drawn between P and Q. From here we find the actual set S by backtracking through our table c. If a $c[x][y]$ is greater then either of its possible predecessors ($c[x-1][y]$ or $c[x][y-1]$) then there must be a line between $P[x]$ and $Q[y]$ so we add that to our set. After determining if there is such a line, we can backtrack to the maximum of its predecessors and continue in this way until we hit $c[0][0]$. Below is an example of backtracking through c. Bold elements represent lines, underlined elements represent steps in our backtracking that don't draw lines (assuming only points with the same label can be matched).

	A	B	B	C	D	J	B
A	$\underline{\mathbf{1}}$	1	1	1	1	1	1
B	$\underline{1}$	$\underline{\mathbf{2}}$	$\underline{\mathbf{3}}$	3	3	3	4
C	1	2	$\underline{3}$	$\underline{\mathbf{4}}$	4	4	4
J	1	2	3	$\underline{4}$	4	5	5
C	1	2	3	$\underline{\mathbf{5}}$	$\underline{5}$	$\underline{5}$	$\underline{5}$



The runtime of the step where we fill out the grid is on the order of $O(n^2)$, as there are only

[1] e.g. If we have the maximum number of lines between $P[..i]$, $Q[..j-1]$ and the maximum number of lines between $P[..i-1]$, $Q[..j]$ the maximum number of lines between $P[..i]$,$Q[..j]$ will be the greater of these two maximums, plus one if we can connect $P[i]$ and $Q[j]$

a constant number of operations per cell. The backtracking step runs on $O(2n) = O(n)$ because every step we move either up or backwards till we get to the top left corner. So the total runtime of our algorithm is $O(n^2)$.

8. The algorithm I would use here is a modification of the Frechet distance algorithm. The key modification I would make is not to accept a value r and return true if the last two points are under r apart and the result of one of the possible sub-problems is true. Instead return the minimum r for points $P[..i]$ and $Q[..j]$ by returning the maximum of the distance between $P[i], Q[j]$ and k where k is the minimum of the Frechet distances between:

    - $P[..i-1]$ and $Q[..j]$
    - $P[..i]$ and $Q[..j-1]$
    - $P[..i-1]$ and $Q[..j-1]$

    Where these vales are calculated in a similar (recursive) manner. This will give you the minimum Frechet distance as the minimization ensures that you pick sequence of moves that results in the lowest Frechet distance. Put another way the minimum Frechet distance for $p[..i]Q[..j]$ is either the minimum frechet distance between $P[..i]$ and $Q[..j-1]$ or $P[..i-1]$ and $Q[..j]$ or $P[..i-1]$ and $Q[..j-1]$ or the distance between $P[i]$ and $P[j]$ if it's larger then the minimum of the three previous quantities. We can also use the memoization technique mentioned earlier, saving the minimum fringe distance for $P[..i]Q[..j]$ in cell i, j of our table, starting from the top left corner filling in cells from left to right and rows from top to bottom. At the end of the algorithm report the bottom right cell.
    This algorithm runs on the order of $O(n^2)$ as it requires linear time computation of every cell of an n by m matrix.

9. To accomplish this, we will fill out a table $F[1..n][1..n]$ such that each cell is either blue or red. A cell $F[i, j]$ will be blue if the distance between $||p_i - q_j|| \leq L$ or red otherwise. The desired sequence exists if there is a series of either horizontal or vertical steps that get you from the top left to the bottom right without stepping on a red square. To see why this is, consider $F[i][j]$ to represent the points p_i, q_j. From p_i, q_j the only valid moves are to

    (a) p_{i+1}, q_j if $||p_{i+1} - q_j|| \leq L$
    (b) p_{i-1}, q_j if $||p_{i-1} - q_j|| \leq L$
    (c) p_i, q_{j-1} if $||p_i - q_{j-1}|| \leq L$
    (d) p_i, q_{j+1} if $||p_i - q_{j+1}|| \leq L$

    We can see p_0, q_0 is our startpoint and p_n, q_n is our endpoint. Finding this path will be done with a breadth first search from $F[0][0]$ to $F[n][n]$ marking every node we expanded as expanded and storing fringe nodes in a queue [2]. If the queue is empty before $F[n][n]$ is expanded we know there is no path.
    The runtime of the first step is $O(n^2)$ as it requires doing one computation for every cell in an $n \times n$ table. The second step runs involves a breadth first search so it runs on $O(|V| + |E|)$. Clearly this table has n^2 cells (vertices) and every cell is connected to at most 4 of it's neighbors so the number of edges is at most $4n^2$ meaning our algorithm runs on the order of $O(4n^2) + O(n^2) = O(n^2)$.

[2] Because the unweighted edges are zero, we don't need to use a priority queue like in Dijkstra's algorithm

10. First construct a table $F[1..n][1..n]$ such that

$$F[i][j] = ||p_i - p_j||$$

then run dijkstra's algorithm from $F[0][0]$ to $F[n][n]$, considering every cell connected to (i.e. has edges with) the cells directly above, below, and to the right and left of it. By the argument in the last question we know that these are the only valid moves from any particular position. Consider the cost of an edge to be the value of the cell it points to. We can see that the lowest cost path through the table corresponds to the lowest total sum of these lengths, and dijkstra's gives us the lowest cost path through the table so the solution we find is correct.
The runtime of the first step is still $O(n^2)$ as above. However dijkstra's algorithm runs on the order of $O(|E| + |V| \log |V|)$, remembering that $|E| = 4n^2$, $|V| = n^2$ the runtime of this phase will be $O(4n^2 + n^2 \log n^2) = O(4n^2 + 2n^2 \log n) = O(n^2 \log n)$