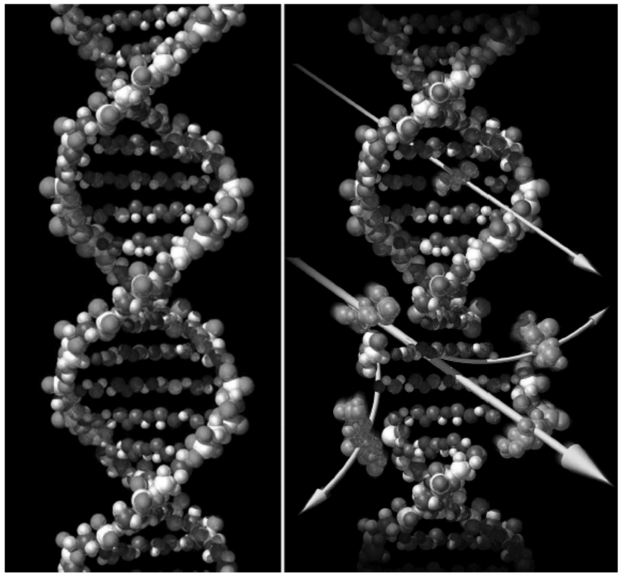
Presentation for use with the textbook, Algorithm Design and Applications, by M. T. Goodrich and R. Tamassia, Wiley, 2015

Dynamic Programming: Longest Common Subsequences

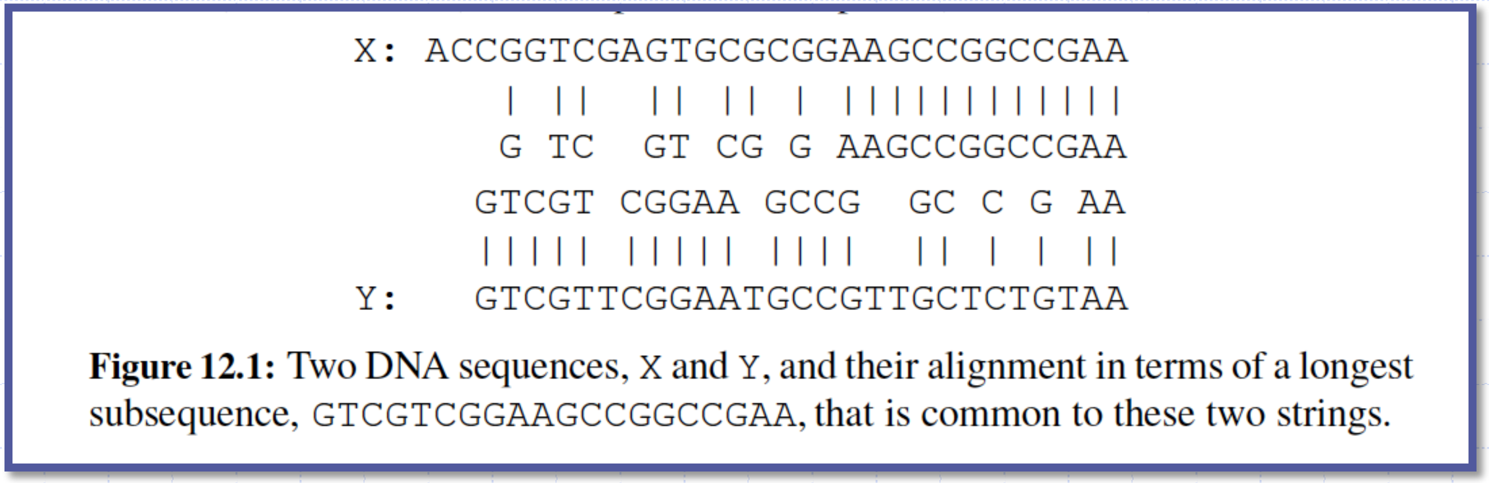

Effects of radiation on DNA's double helix, 2003. U.S. government image. NASA-MSFC.

Application: DNA Sequence Alignment

- DNA sequences can be viewed as strings of **A**, **C**, **G**, and **T** characters, which represent nucleotides.
- Finding the similarities between two DNA sequences is an important computation performed in bioinformatics.
  - For instance, when comparing the DNA of different organisms, such alignments can highlight the locations where those organisms have identical DNA patterns.

Application: DNA Sequence Alignment

- Finding the best alignment between two DNA strings involves minimizing the number of changes to convert one string to the other.

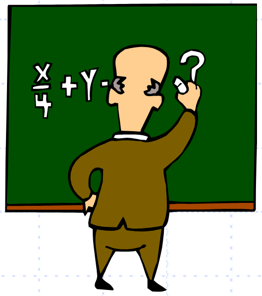


```
X: ACCGGTCGAGTGCGCGGAAGCCGGCCGAA
      | ||  || || | ||||||||||||
      G TC  GT CG G AAGCCGGCCGAA
     GTCGT CGGAA GCCG  GC C G AA
     ||||| ||||| ||||  || | | ||
Y:   GTCGTTCGGAATGCCGTTGCTCTGTAA
```

Figure 12.1: Two DNA sequences, X and Y, and their alignment in terms of a longest subsequence, GTCGTCGGAAGCCGGCCGAA, that is common to these two strings.

- A brute-force search would take exponential time, but we can do much better using **dynamic programming**.

The General Dynamic Programming Technique



- Applies to a problem that at first seems to require a lot of time (possibly exponential), provided we have:
  - **Simple subproblems:** the subproblems can be defined in terms of a few variables, such as j, k, l, m, and so on.
  - **Subproblem optimality:** the global optimum value can be defined in terms of optimal subproblems
  - **Subproblem overlap:** the subproblems are not independent, but instead they overlap (hence, should be constructed bottom-up).

Subsequences

- A ***subsequence*** of a character string $x_0x_1x_2\ldots x_{n-1}$ is a string of the form $x_{i_1}x_{i_2}\ldots x_{i_k}$, where $i_j < i_{j+1}$.
- Not the same as substring!
- Example String: ABCDEFGHIJK
  - Subsequence: ACEGJIK
  - Subsequence: DFGHK
  - Not subsequence: DAGH

The Longest Common Subsequence (LCS) Problem

- Given two strings X and Y, the longest common subsequence (LCS) problem is to find a longest subsequence common to both X and Y
- Has applications to DNA similarity testing (alphabet is {A,C,G,T})
- Example: ABCDEFG and XZACKDFWGH have ACDFG as a longest common subsequence

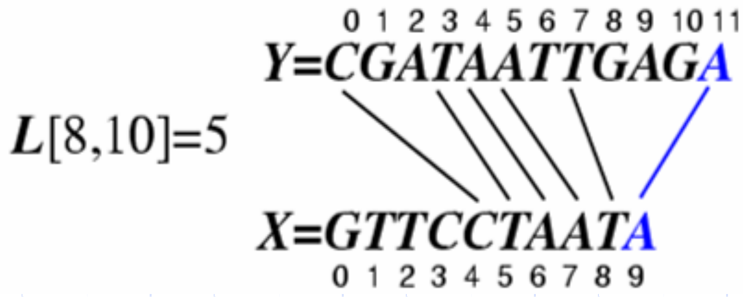
A Poor Approach to the LCS Problem

- A Brute-force solution:
  - Enumerate all subsequences of X
  - Test which ones are also subsequences of Y
  - Pick the longest one.
- Analysis:
  - If X is of length n, then it has 2^n subsequences
  - This is an exponential-time algorithm!

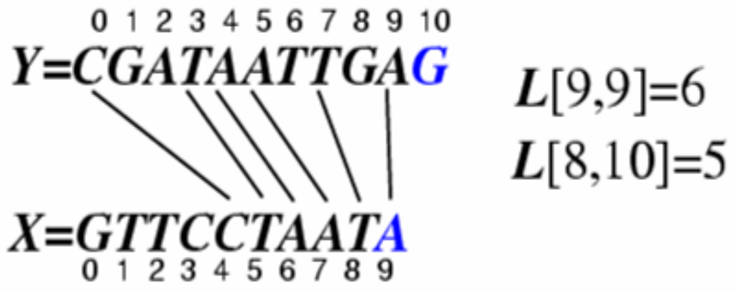
A Dynamic-Programming Approach to the LCS Problem

- Define L[i,j] to be the length of the longest common subsequence of X[0..i] and Y[0..j].
- Allow for -1 as an index, so L[-1,k] = 0 and L[k,-1]=0, to indicate that the null part of X or Y has no match with the other.
- Then we can define L[i,j] in the general case as follows:
  1. If xi=yj, then L[i,j] = L[i-1,j-1] + 1 (we can add this match)
  2. If xi≠yj, then L[i,j] = max{L[i-1,j], L[i,j-1]} (we have no match here)

Case 1:



Case 2:

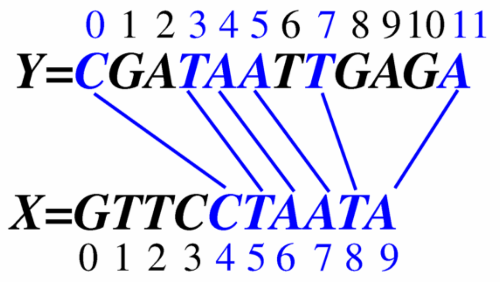


An LCS Algorithm

```
Algorithm LCS(X,Y ):
Input:  Strings X and Y with n and m elements, respectively
Output: For i = 0,…,n-1, j = 0,...,m-1, the length L[i, j] of a longest string
    that is a subsequence of both the string X[0..i] = $x_0x_1x_2…x_i$ and the
    string Y [0.. j] = $y_0y_1y_2…y_j$
for i =1 to n-1 do
    L[i,-1] = 0
for j =0 to m-1 do
    L[-1,j] = 0
for i =0 to n-1 do
    for j =0 to m-1 do
        if $x_i = y_j$ then
            L[i, j] = L[i-1, j-1] + 1
        else
            L[i, j] = max{L[i-1, j] , L[i, j-1]}
return array L
```

Visualizing the LCS Algorithm

L	-1	0	1	2	3	4	5	6	7	8	9	10	11
-1	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	1	1	1	1	1	1	1
1	0	0	1	1	2	2	2	2	2	2	2	2	2
2	0	0	1	1	2	2	2	3	3	3	3	3	3
3	0	1	1	1	2	2	2	3	3	3	3	3	3
4	0	**1**	1	1	2	2	2	3	3	3	3	3	3
5	0	1	1	1	**2**	2	2	3	4	4	4	4	4
6	0	1	1	2	2	**3**	3	3	4	4	5	5	5
7	0	1	1	2	2	3	**4**	4	4	4	5	5	6
8	0	1	1	2	3	3	4	5	**5**	5	5	5	6
9	0	1	1	2	3	4	4	5	5	5	6	6	**6**



Analysis of LCS Algorithm

- We have two nested loops
  - The outer one iterates *n* times
  - The inner one iterates *m* times
  - A constant amount of work is done inside each iteration of the inner loop
  - Thus, the total running time is O(*nm*)
- Answer is contained in L[n,m] (and the subsequence can be recovered from the L table).