# Lezione 14

## Bioinformatica

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Lecture 14: Longest Common Subsequence
- Longest common subsequence (LCS) problem
- BLAST (Basic Local Alignment Search Tool)
- FASTA (FAST Alignement)

# Sommario

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# Dynamic Programming Approach

## LCS : Longest Common Subsequence

Let $X, Y \in Seq$ be the sequences to compare, and $X_i$, $Y_j$ be the subsequences of their first $i$, $j$ characters, respectively.
The integer function

$$LCS : Seq \times Seq \rightarrow Nat$$

gives the integer length of longest common subsequence of any two (sub)sequences, as follows:

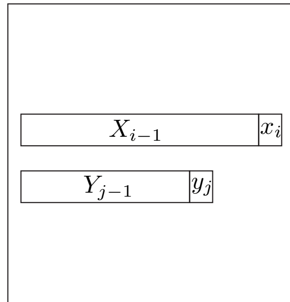
$$LCS(X_i, Y_j) = \begin{cases} 0 & \text{if } i = 0 \text{ or } j = 0 \\ LCS(X_{i-1}, Y_{j-1}) + 1 & \text{if } x_i = y_j \\ \max(LCS(X_i, Y_{j-1}), LCS(X_{i-1}, Y_j)) & \text{if } x_i \neq y_j \end{cases}$$

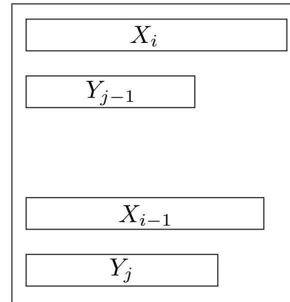
# Longest common subsequence

LCS function defined

$x_i = y_j$

$LCS(X_i, Y_j) = LCS(X_{i-1}, Y_{j-1}) + 1$




$x_i \neq y_j$

$LCS(X_i, Y_j) = \max(LCS(X_i, Y_{j-1}), LCS(X_{i-1}, Y_j))$

# Recursive implementation

just write down in Python the recursive equations above

```
1 def cls(X,Y):
2     i,j = len(X),len(Y)
3     if i == 0 or j == 0: return 0
4     elif X[i-1] == Y[j-1]: return cls(X[:i-1],Y[:j-1])+1
5     else: return max(cls(X[:i],Y[:j-1]),cls(X[:i-1],Y[:j]))
```

```
1 print cls("BASKETBALL","BASEBALL") ≡ 8
```

OK !

```
1 print cls("ABRACADABRA","SUPERCALIFRAGILISTICESPIRALIDOSO")
```

VERY long execution time ... WHY ?

# ... because of recursion nonlinearity

the execution time is exponential with the sequence lengths

a recursion is said linear if the definition right-hand side contains at most one recursive function call

- nonlinear recursion: $\binom{n}{k} = \binom{n-1}{k} + \binom{n-1}{k-1}$ complexity: $O(2^n)$

```
1 def binomial(n,k):
2     if k == 0 or n == k: return 1
3     else: return binomial(n-1,k) + binomial(n-1,k-1)
```

- linear recursion: $\binom{n}{k} = \binom{n-1}{k-1} \times \frac{n}{k}$ complexity: $O(n)$

```
1 def binomial(n,k):
2     if k == 0 or n == k: return 1
3     else: return binomial(n-1,k-1) * n / k
```

# Memoization technique

In computing, “memoization” is an optimization technique used primarily to speed up computer programs by having function calls avoid repeating the calculation of results for previously-processed input

- This technique of saving values that have already been calculated is frequently used
- Memoization is a means of lowering a function’s time cost in exchange for space cost; that is, memoized functions become optimized for speed in exchange for a higher use of computer memory space.
- An efficient LCS procedure requires: saving the solutions to one level of subproblem in a table so that the solutions are available to the next level of subproblems.

## Length of the Longest Common Subsequence

computing the function $LCS : Seq \times Seq \rightarrow Nat$ with memoization

```
def LCS(X, Y):
    m,n = len(X),len(Y)
    # An (m+1) times (n+1) matrix
    C = [[0] * (n+1) for i in range(m+1)]
    for i in range(1, m+1):
        for j in range(1, n+1):
            if X[i-1] == Y[j-1]:
                C[i][j] = C[i-1][j-1] + 1
            else:
                C[i][j] = max(C[i][j-1], C[i-1][j])
    return C
```

## Usage example — LCSfunction

```
>>> X = "AATCC"
>>> Y = "ACACG"
>>> m = len(X)
>>> n = len(Y)
>>> C = LCS(X, Y)
```

```
>>> print C
[[0, 0, 0, 0, 0, 0],
 [0, 1, 1, 1, 1, 1],
 [0, 1, 1, 2, 2, 2],
 [0, 1, 1, 2, 2, 2],
 [0, 1, 2, 2, 3, 3],
 [0, 1, 2, 2, 3, 3]]
```

## Usage example — LCSfunction

```
>>> X = "ATGGCCTGGAC"
>>> Y = "ATCCGGACC"
>>> m = len(X)
>>> n = len(Y)
>>> C = LCS(X, Y)
```

```
>>> print C
[[0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
 [0, 1, 1, 1, 1, 1, 1, 1, 1, 1],
 [0, 1, 2, 2, 2, 2, 2, 2, 2, 2],
 [0, 1, 2, 2, 2, 3, 3, 3, 3, 3],
 [0, 1, 2, 2, 2, 3, 4, 4, 4, 4],
 [0, 1, 2, 3, 3, 3, 4, 4, 5, 5],
 [0, 1, 2, 3, 4, 4, 4, 4, 5, 6],
 [0, 1, 2, 3, 4, 4, 4, 4, 5, 6],
 [0, 1, 2, 3, 4, 5, 5, 5, 5, 6],
 [0, 1, 2, 3, 4, 5, 6, 6, 6, 6],
 [0, 1, 2, 3, 4, 5, 6, 7, 7, 7],
 [0, 1, 2, 3, 4, 5, 6, 7, 8, 8]]
```

## Reading out an LCS

Backtracking on the table from the lower-right corner

```
def backTrack(C, X, Y, i, j):
    if i == 0 or j == 0:
        return ""
    elif X[i-1] == Y[j-1]:
        return backTrack(C, X, Y, i-1, j-1) + X[i-1]
    else:
        if C[i][j-1] > C[i-1][j]:
            return backTrack(C, X, Y, i, j-1)
        else:
            return backTrack(C, X, Y, i-1, j)
```

## Usage example — backTrack function

```
1 >>> X = "AATCC"
2 >>> Y = "ACACG"
3 >>> m = len(X)
4 >>> n = len(Y)
5 >>> C = LCS(X, Y)
```

```
1 >>> print "Some␣LCS:␣'%s'" % backTrack(C, X, Y, m, n)
2 Some LCS: 'AAC'
```

## Usage example — backTrack function

```
1 >>> X = "ATGGCCTGGAC"
2 >>> Y = "ATCCGGACC"
3 >>> m = len(X)
4 >>> n = len(Y)
5 >>> C = LCS(X, Y)
```

```
1 >>> print "Some␣LCS:␣'%s'" % backTrack(C, X, Y, m, n)
2 Some LCS: 'ATCCGGAC'
```

## Reading out all LCSs

```
1  def backTrackAll(C, X, Y, i, j):
2      if i == 0 or j == 0:
3          return set([""])
4      elif X[i-1] == Y[j-1]:
5          return set([Z + X[i-1]
6                 for Z in backTrackAll(C, X, Y, i-1, j-1)
                      ])
7      else:
8          R = set()
9          if C[i][j-1] >= C[i-1][j]:
10             R.update(backTrackAll(C, X, Y, i, j-1))
11         if C[i-1][j] >= C[i][j-1]:
12             R.update(backTrackAll(C, X, Y, i-1, j))
13         return R
```

## Usage example — backTrackAll function

```
1 >>> X = "AATCC"
2 >>> Y = "ACACG"
3 >>> m = len(X)
4 >>> n = len(Y)
5 >>> C = LCS(X, Y)
```

```
1 >>> print "All␣LCSs:␣%s" % backTrackAll(C, X, Y, m, n)
2 All LCSs: set(['ACC', 'AAC'])
```

## Usage example — backTrackAll function

```
1 >>> X = "ATGGCCTGGAC"
2 >>> Y = "ATCCGGACC"
3 >>> m = len(X)
4 >>> n = len(Y)
5 >>> C = LCS(X, Y)
```

```
1 >>> print "All␣LCSs:␣%s" % backTrackAll(C, X, Y, m, n)
2 All LCSs: set(['ATCCGGAC'])
```

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## BLAST program

Comparison of nucleotide or protein sequences

- The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences
- The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches
- BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families
- BLAST makes it easy to examine a large group of potential gene candidates

## BLAST

How to do Batch BLAST jobs

- BLAST makes it easy to examine a large group of potential gene candidates
- Most likely these are isolated as amplified products from a library of some sort
- There is no need to manually cut and paste a 100 sequences in to the BLAST web pages
- Using the BLAST web pages it is possible to input "batches" of sequences into one form and retrieve the results
- There are two methods to do batch BLAST jobs
- The first is through the web interface and the second is using the standalone BLAST binaries and downloaded NCBI databases

TUTORIAL

# BLAST
## Example

- BLAST paper
- QuickStart: Example-Driven Web-Based BLAST Tutorial

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# FASTA
## Example

FASTA stands for FAST-ALL, reflecting the fact that it can be used for a fast protein comparison or a fast nucleotide comparison

- This program achieves a high level of sensitivity for similarity searching at high speed
- This is achieved by performing optimised searches for local alignments using a substitution matrix
- The high speed of this program is achieved by using the observed pattern of word hits to identify potential matches before attempting the more time consuming optimised search
- The trade-off between speed and sensitivity is controlled by the ktup parameter, which specifies the size of the word
- Increasing the ktup decreases the number of background hits
- Not every word hit is investigated but instead initially looks for segment's containing several nearby hits

# FASTA Web services
## Both REST and SOAP web service interfaces are exposed

REST Sample clients are provided for a number of programming languages.

SOAP RPC/encoded SOAP service