# Dynamic Programing#2

# Longest Common Subsequences

#### Subsequences

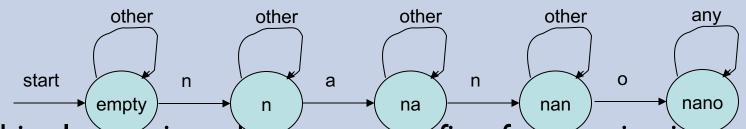
- Suppose we have a sequence X = < x<sub>1</sub>,x<sub>2</sub>,....,x<sub>m</sub>>
   of elements over a finite set S. Then,
  - def: a sequence  $Z = \langle z_1, z_2, \dots, z_k \rangle$  over S is called a subsequence of X if and only if it can be obtained from X by deleting elements
  - i.e. obtained without changing the order of the remaining elements
  - i.e. this means there exist indices  $i_1 < i_2 < ... < i_k$  such that  $z_a = x_{ia}$  for all a in the range 1 < = a < = k.
    - e.g. the following are all subsequences of "president": pred, sdn,
       predent
    - e.g. ABD is a subsequence of ABCDEF.

# Subsequences....

- Alternate definition
  - Given a sequence  $X = \langle x_1, x_2, \ldots, x_m \rangle$  of elements over a finite set S, another sequence  $Z = \langle z_1, z_2, \ldots, z_k \rangle$  is a subsequence of X if there exists a strictly increasing sequence  $\langle z_1, z_2, \ldots, z_k \rangle$  of indices X such that for all  $j = 1, 2, 3, \ldots, k$ , we have  $X_{ij} = z_{j}$ .
    - e.g.  $Z = \langle B, C, D B \rangle$  is a sequence of  $X = \langle A,B,C,B,D,A,B \rangle$  with corresponding index sequence  $\langle 2,3,5,7 \rangle$ .

#### **Determining Subsequences**

- Given the two strings say "nano" and "nematode knowledge", how to find the whether one pattern appears in the other?
- Write an algorithm based on the following



- This always gives the longest prefix of one string in the other...
- But, the issue is what if one pattern does not occur fully in the other....
  - The method in the automata above does not solve the problem, then.

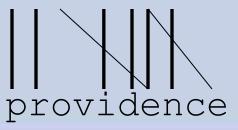
#### Common Subsequence

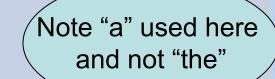
- Suppose that X and Y are two sequences over a set S.
- We say that Z is a common subsequence of X and Y if and only if
  - Z is a subsequence of X and Z is a subsequence of Y
  - e.g. given the subsequences viz.
    - P = cbabca, Q= bcabac and R= abcade
      - The set of CS of P and Q is {Φ, a, aa, ab, aba, abc, ac, b, ba, baa, bab, baba, babc, bac, bb, bba, bbc, bc, bca, c, ca, caa, cab, caba, cabc, cac, cb, cba, cbac, cbc, cc}
      - The set of CS of P and R is: { ₱, a, aa, ab, aba, abc, abca, ac, aca, b, ba, bc, bca, c, ca}
- The longest amongst these is the Longest Common Subsequence

# Longest Common Subsequence (LCS)

- Problem: Given sequences x[1..m] and y[1..n], find a longest common subsequence of both.
- e.g. x=ABCBDAB and y=BDCABA,
  - BCA is a common subsequence and
  - BCBA and BDAB are two LCSs
- e.g. x = president and y = providence
  - pree and den are common subsequence and
  - priden is an LCS.

president





#### LCS: Another view

- Explore the Edit distance between S1 and S2
  - defined as the number of operations required to transform one of them into the other. e.g.

SI: a b c d a c e S2: b a d c a b e

- Length LCSS = 4
- Edit Distance = 3(remove) + 3(add) = 6
- Which are removed? Which are added?

#### **Motivation & Applications**

- Numerous Applications. Most striking ones......
- Biological Applications
  - compare two DNA sequences
    - a strand of DNA consists of string of molecules called bases
    - the possible bases are ADENINE, GUANINE, CYTOSINE, THYMINE (A,G,C,T)
      - thus a DNA sequence is defined over the alphabet (A,G,C,T)
    - e.g. for two different organisms, their DNA sequence may be
      - S<sub>1</sub> = ACCGGTCGAGTGCGCGGAAGCCGGCCGAA and
      - S<sub>2</sub> = GTCGTTCGGAATGCCGTTGCTCTGTAAA

#### **Motivation & Applications....**

- Biological Applications
  - The problem at hand is to determine how similar the two organisms are
    - i.e. compare two strings  $S_1$  and  $S_2$
  - Solution strategies
    - explore whether one is a substring of the other? OR
    - the number of changes required to turn one string into the other
      - should be minimal OR
    - find a third strand  $S_3$  s.t. the bases in  $S_3$  appear in each of  $S_1$  and  $S_2$ 
      - preferably consecutively but at least in the same order....
      - the longer the strand  $S_3$ , more similar the two organisms are
      - This essentially is to determine the longest common subsequence in  $\mathsf{S}_1$  and  $\mathsf{S}_2$

#### **Motivation & Applications....**

- File Comparisons
  - e.g. unix program "diff"
  - works by finding the LCS of the lines of the two files
    - i.e. anyline in the subsequence that would not have changed
- Screen redisplay
  - Used by text editors like "emacs"
    - Especially when used with slow dial-in terminals

- In passing, note that,
  - Longest common substring problem is different from LCS problem, that we attack here.

#### **LCS Solution Alternatives**

- Various alternatives
  - Applying Brute force
  - Writing a recurrence equation & devising a recursive solution
  - Writing a recurrence equation & framing a dynamic programming solution

#### **Brute force solution**

• The basic approach

- The picture can't be displayed.
- For every subsequence of x (of length m), check if it is a subsequence of y (of length n).
- Suppose one has N sequences of lengths  $n_1, n_2, \ldots, n_N$ .
- For a given sequence of length m, how many subsequences can there be ?
  - How do we solve for only two given sequences?
- Analysis:
  - There are 2<sup>m</sup> subsequences of x.
  - Each is to be checked against the subsequence y
    - this check takes O(n) time, since we scan y for first element, and then scan for second element, etc.
  - The worst case running time is  $O(n2^m)$ .

#### **Brute force solution**

- Thus,
  - Naive search
    - remaining sequences or not
    - i.e.  $2^{n1}$   $(n_2 + n_3 + n_4 + \dots n_N)$  .e.  $O(2^{n1} \sum n_i)$

The picture can't be displayed.

• test each of the 2<sup>n1</sup> subsequences of the first sequence against the other sequences to determine whether they are also subsequences of the

e. 
$$O(2^{n_1} \sum_{i>1} n_i)$$

# **Alternative Solution Strategies**

- Can we use divide-and-conquer to solve this problem?
- Can we use Greedy approach to solve this problem?
- We investigate these issues further.....

# Characterizing a LCS

- First question to be answered
  - Does LCs problem exhibit optimal substructure and overlapping subproblems properties?
  - LCS indeed exhibits both these properties.
- Optimal substructure property
  - As compared to finding out LCS of strings of length m and n, it is surely easy to find the same from the two strings (m-I) and (n-I).
- Overlapping subproblems
  - the solution to main subproblem indeed depends on the solution to smaller instances
- We shall formalize these two with the help of a theorem, later.....

# Prefix of a sequence

- Motivation
  - The subproblems become simpler as the sequences become shorter.
  - Shorter sequences are conveniently described using prefixes.
- def:
  - For a given sequence  $X = \langle x_1, x_2, ..., x_m \rangle$ , we define the i<sup>th</sup> prefix of the sequence X by  $X_i$  as
  - e.g. if the given sequence is X = "AABCDA" then,
    - $X_1 = A, X_2 = AA, X_3 = AAB, X_4 = AABC, X_5 = AABCD,...$

- Let  $X = \langle x_1, x_2, ..., x_m \rangle$  and  $Y = \langle y_1, y_2, ..., y_n \rangle$  be two sequences.
- Let  $Z = \langle z_1, z_2, ..., z_k \rangle$  is any LCS of X and Y.
- Then,
  - if  $x_m = y_n$  then certainly  $x_m = y_n = z_k$  and  $Z_{k-1}$  is in LCS( $X_{m-1}$ ,  $Y_{n-1}$ )
- Thus,
  - the problem size is reduced by one to solve it.
  - e.g. apply this approach to the two sequences GUAVA and GREATJAVA
    - The LCS is GAVA
- What is the conclusion ???

- $X_m$  and  $Y_n$  end with  $x_m = y_n$  and
  - LenLCS ....length of the longest common subsequence

$$X_{m}$$
  $x_{1}$   $x_{2}$  ...  $x_{m-1}$   $x_{m}$ 

$$Y_{n}$$
  $y_{1}$   $y_{2}$  ...  $y_{n-1}$   $y_{n}=x_{m}$ 

$$Z_{k}$$
  $z_{1}$   $z_{2}$ ...  $z_{k-1}$   $z_{k}$   $z_{k}$   $z_{m}=x_{m}$ 

- Z<sub>k</sub> is Z<sub>k-1</sub> followed by z<sub>k</sub> = y<sub>n</sub> = x<sub>m</sub> where Z<sub>k-1</sub> is an LCS of X<sub>m-1</sub> and Y<sub>n-1</sub> and
- LenLCS(m, n)=LenLCS(m -1, n -1) + 1

- Again, let  $X = \langle x_1, x_2, ..., x_m \rangle$  and  $Y = \langle y_1, y_2, ..., y_n \rangle$  be two sequences.
- Let  $Z = \langle z_1, z_2, ..., z_k \rangle$  is any LCS of X and Y.
- Then,
  - What is the LCS if  $x_m \neq y_n$  and  $x_m \neq z_k$ ?
    - If  $x_m \neq y_n$  then  $x_m \neq z_k$  implies that Z is in LCS( $X_{m-1}$ , Y)
  - What is the LCS if  $x_m \neq y_n$  and  $x_m \neq z_k$ ?
    - If  $x_m \neq y_n$  then  $y_n \neq z_k$  implies that Z is in LCS(X,  $Y_{n-1}$ )

- $X_{\rm m}$  and  $Y_n$  end with  $x_{\rm m} != y_n$  and
  - LenLCS ....length of the longest common subsequence

$$X_{m}$$
  $X_{1}$   $X_{2}$   $\dots$   $X_{m-1}$   $X_{m}$ 

$$X_{m}$$
  $X_{1}$   $X_{2}$   $\dots$   $X_{m-1}$   $X_{m}$ 

$$\mathbf{Y}_{n}$$
  $\mathbf{y}_{1}$   $\mathbf{y}_{2}$  ...  $\mathbf{y}_{n-1}$   $\mathbf{y}_{n}$ 

$$Y_n$$
  $y_1 y_2 \dots y_{n-1} y_n$ 

$$Z_k$$
  $z_1 z_2 ... z_{k-1} z_k != y_n$ 

$$Z_k$$
  $z_1 z_2 ... z_{k-1} z_k != x_m$ 

- z<sub>k</sub> != y<sub>n</sub> ...hence
- Z<sub>k</sub> is LCS of X<sub>m</sub> and Y<sub>n-1</sub>

- z<sub>k</sub>!= x<sub>m</sub> ...hence
- $Z_k$  is LCS of  $X_{m-1}$  and  $Y_n$
- LenLCS(m, n)= max {LenLCS(m, n-1), LenLCS(m-1, n)}

- An Example
  - Let  $X_n$  = ABCDEFG (n=7),  $Y_m$  = BCDGK (m=5)
  - What could be the last element of the LCS end with?
  - Two cases
    - If the LCS contains the last character as G
      - Then,  $LCS(X_m, Y_n) = LCS(X_n, Y_{m-1})$
    - If the LCS does not end with the (last character) as G
      - Then,  $LCS(X_m, Y_n) = LCS(X_{n-1}, Y_m)$
  - In the example above, if we remove K, then the LCS is easily determined......

#### **Overlapping Subproblems**

- This also exhibits overlapping subproblems property i.e. :
  - If  $x_m = y_n$  then we solve the subproblem to find an element in LCS( $X_{m-1}$ ,  $Y_{n-1}$ ) and append  $x_m$
  - Then, LenLCS(m, n) = LenLCS(m 1, n 1) + 1
  - If  $x_m <> y_n$  then we solve the two subproblems of finding elements in LCS( $X_{m-1}$ ,  $Y_{n-1}$ ) and LCS( $X_{m-1}$ ,  $Y_{n-1}$ ) and choose the longer one.
  - Then,  $LenLCS(m, n) = max \{LenLCS(m, n-1), LenLCS(m-1, n)\}$

#### Theorem: Optimal substructure of an LCS

- Let  $X = \langle x_1, x_2, ..., x_m \rangle$  and  $Y = \langle y_1, y_2, ..., y_n \rangle$  be two sequences and Let  $Z = \langle z_1, z_2, ..., z_k \rangle$  is any LCS of X and Y.
- Then,
  - I. If  $x_m = y_n$  then certainly  $x_m = y_n = z_k$  and  $Z_{k-1}$  is an LCS of  $X_{m-1}$  and  $Y_{n-1}$ )
  - 2. If  $x_m \neq y_n$  then  $x_m \neq z_k$  implies that Z is an LCS of  $X_{m-1}$  and Y
  - 3. If  $x_m \neq y_n$  then  $y_n \neq z_k$  implies that Z is an LCS of X and  $Y_{n-1}$
- Proof:

## **Devising the Recursive Solution**

- Let X and Y be sequences.
- Let c[i,j] = LenLCS[i,j] be the length of an element in  $LCS(X_i, Y_i)$ .

• if i=0 or j=0 c[i,j] =c[i-1,j-1]+1 • if i,j>0 and  $x_i = y_i$ LenLCS[i,j]  $\max(c[i,j-1],c[i-1,j])$  • if i,j>0 and  $x_i <> y_i$ 

# Devising the Recursive solution....

- Let
  - $X_i$  denote the  $i^{th}$  prefix x[1..i] of x[1..m], and
  - $-X_0$  denotes an empty prefix
  - The length of an LCS of  $X_m$  and  $Y_n$  be LenLCS(m, n)
  - Recursive formulation for computing LenLCS(i, j) is based on the facts observed earlier viz.
    - If  $X_i$  and  $Y_j$  end with the same character  $x_i = y_j$ ,
      - the LCS must include the character. If it did not we could get a longer LCS by adding the common character.
    - If  $X_i$  and  $Y_j$  do not end with the same character
      - there are two possibilities:
        - $\triangleright$  either the LCS does not end with  $x_i$ ,
        - $\triangleright$  or it does not end with  $y_i$
    - Let  $Z_k$  denote an LCS of  $X_i$  and  $Y_j$

#### The recurrence equation

Then, the recurrence relation is given by the following:

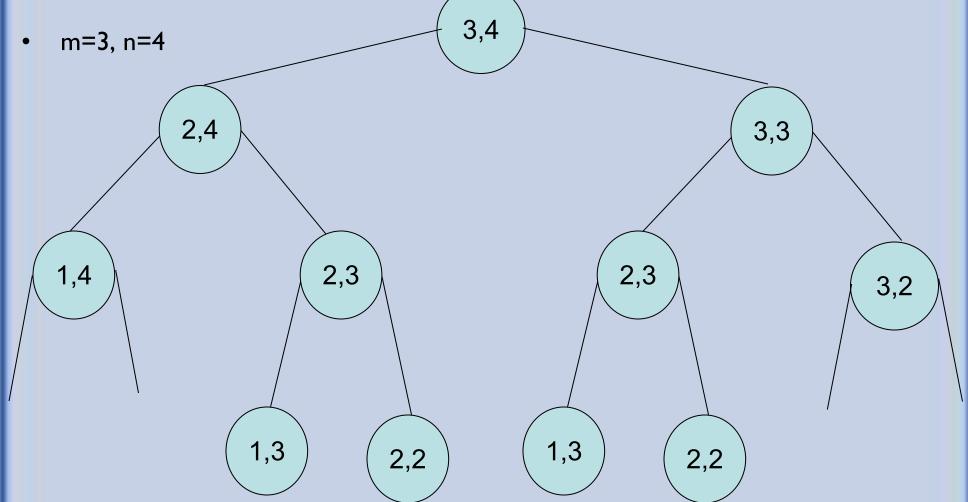
$$lenLCS(i,j) = \begin{cases} 0 & \text{if } i = 0, \text{ or } j = 0 \\ lenLCS(i-1,j-1) + 1 & \text{if } i,j > 0 \text{ and } x_i = y_j \\ \max\{lenLCS(i-1,j), lenLCS(i,j-1)\} & \text{otherwise} \end{cases}$$

#### Recursive algorithm for LCS

```
LCS (x, y, i, j)
1. If x[i] = y[j]
2. then LenLCS[i.j] = LCS(x, y, i-1, j-1)+ 1
3. else LenLCS[i.j]=
    max {LCS(x,y,i-1,j), LCS(x,y,i,j-1)}
```

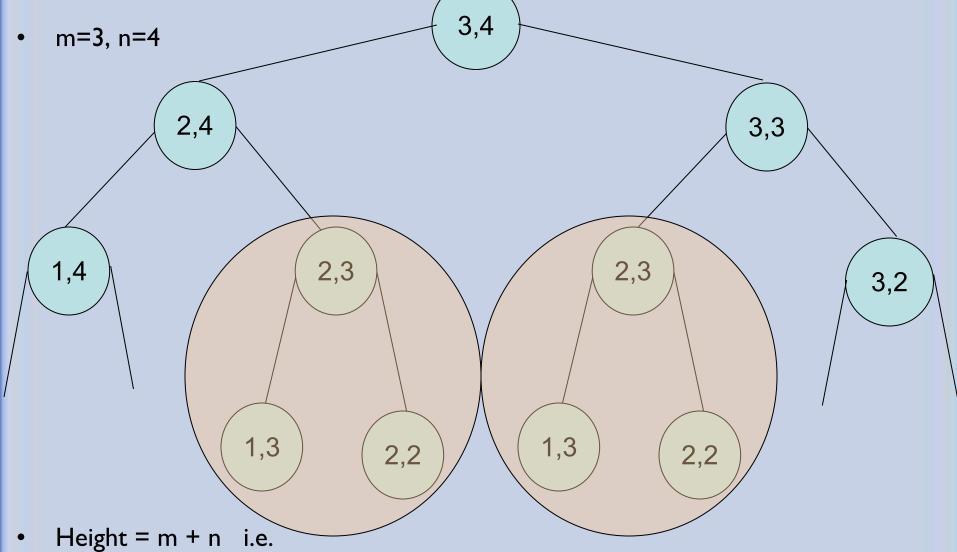
- When does the worst case occur?
  - When the two strings have no matching characters and so the last line always gets executed.
  - Thus, when  $x[i] \neq y[j]$ , in which case the algorithm evaluates two subproblems, each with only one parameter decremented.
  - So, if the bounds are the same (=n, say), the complexity is  $O(2^n)$
  - Does it appear convincing with respect to other such algorithms discussed earlier in D&C?

#### Simulating Recursive algorithm Recursion Tree



- Height = m + n
  - but we're solving subproblems already solved

#### Simulating Recursive algorithm Recursion Tree



- - Work potentially exponential,

#### **Fact**

- On the contrary, if the two sequences have lengths m and n
  - there are exactly (mn) subproblems
    - a pretty small number as compared to being exponential in m OR
       n.

#### Improving the recursive approach: Memoization

- Memoization
  - after computing a solution to a subproblem, store it in a table.
  - In subsequent calls check the table to avoid redoing work.

```
LCS (x, y, i, j)
1. if LenLCS = NIL
2. then if x[i] = y[j]
3. then LenLCS[i.j] = LCS(x, y, i-1, j-1) + 1
4. else LenLCS[i.j] =
    max {LCS(x,y,i-1,j), LCS(x,y,i,j-1)}
```

#### Improving the recursive approach: Memoization

- This is a top down memoization based approach
- Is more efficient
  - each call to the subproblem takes a constant time
  - we call the routine at most twice when we feel in the LenLCS array
  - there are mn entries....
    - hence, total time is O(mn)
- However, we may try for
  - a bottom-up iterative true dynamic programming approach

# **Dynamic Programming Solution**

- To compute length of an element in LCS(X,Y) with |X| = m and |Y| = n, we
  - initialize first row and first column of the array c with 0.
  - calculate LenLCS[I,j] for I <= j <= n,</li>
     LenLCS [2,j] for I <= j <= n</li>
     LenLCS [3,j] for I <= j <= n</li>

Return LenLCS[m,n]

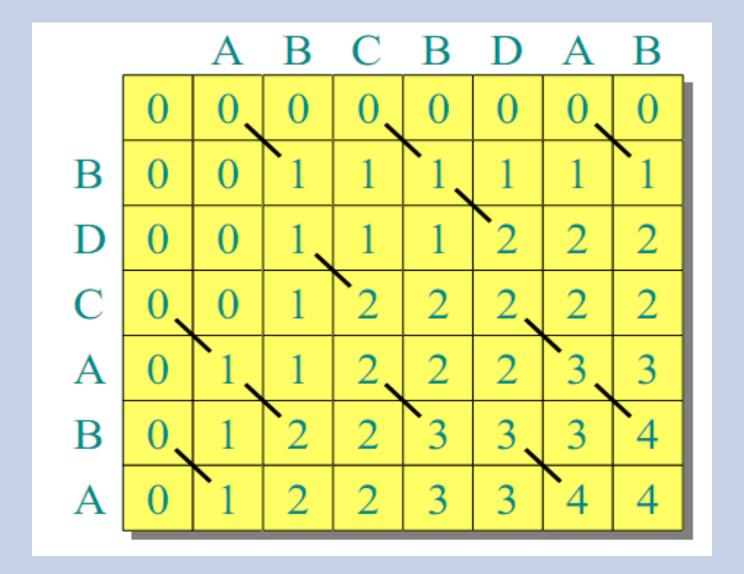
- How can we get an actual longest common subsequence?
  - Store in addition to the array c an array b pointing to the optimal subproblem chosen when computing LenLCS[i,j].

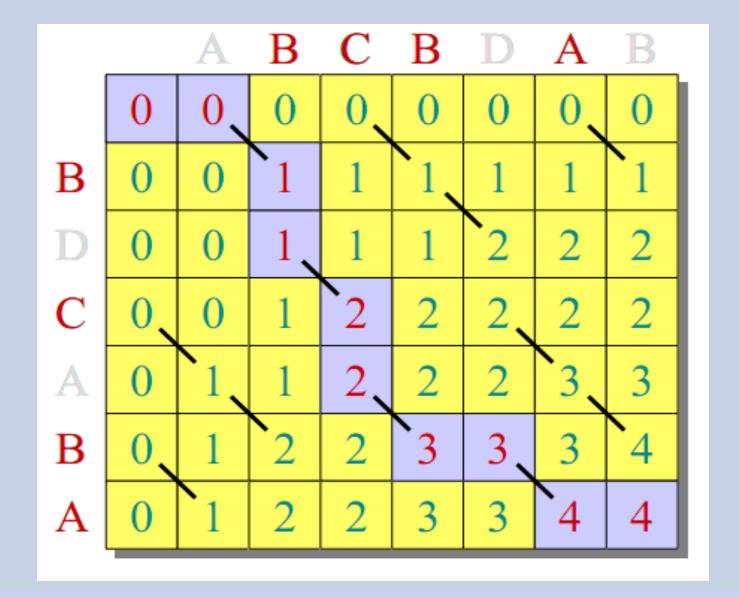
# Algorithm LCS-Length(X,Y)

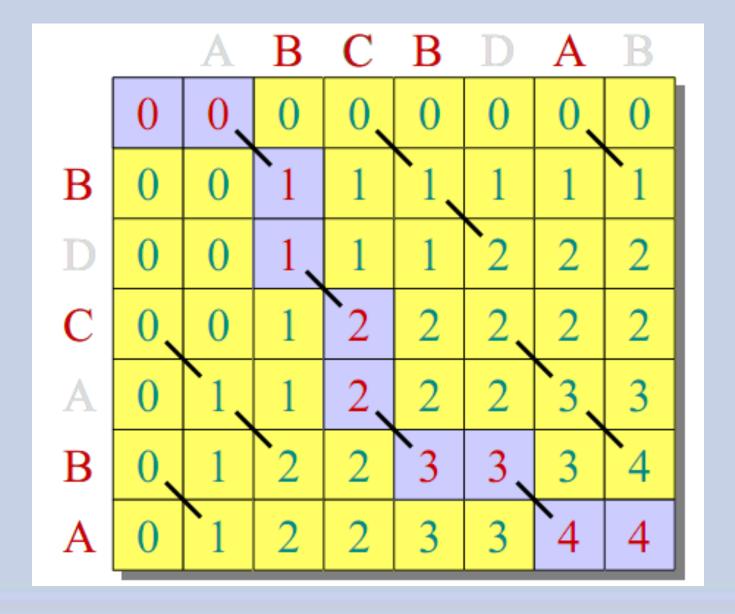
```
RCS =\
1. m = X.Length
2. n = Y.Length
3. let b[1...m, 1...n] and LenLCS[0..m, 0..n] be new tables
4. for i = 1 to m LenLCS[i,0] = 0
5. for j = 1 to m LenLCS[j,0] = 0
6. for i = 1 to m
7. for j = 1 to n
8.
       if x_i == y_i
9.
        LenLCS[i,j] = LenLCS[i-1,j-1] + 1
10.
         b[i,j] = "RSA"
11. elseif LenLCS[i-1,j] >= LenLCS[i,j-1]
12.
          LenLCS[i,j] = LenLCS[i-1,j]
13.
         b[i,j] = "\uparrow"
14. elseif LenLCS[i,j] = LenLCS[i,j-1]
15.
      b[i,j] = " "
16. return LenLCS and b
```

# Algorithm LCS-Length(X,Y)...

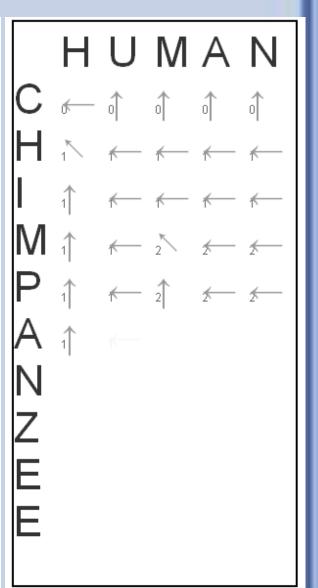
- Whenever, we encounter a reverse slanting arrow
  - we realize that the algorithm has found an element of the LCS
  - however, we encounter the element of the LCS in the reverse order.
  - see the dry run.....
- The complexity of the algorithm is O(m+n).

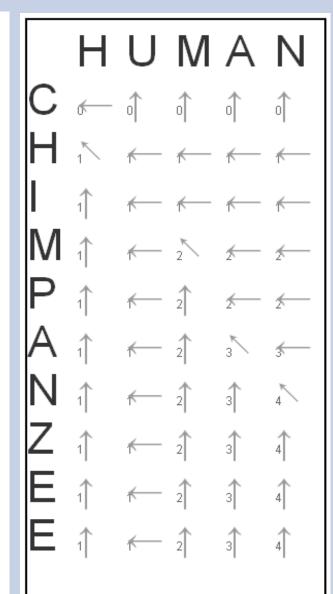


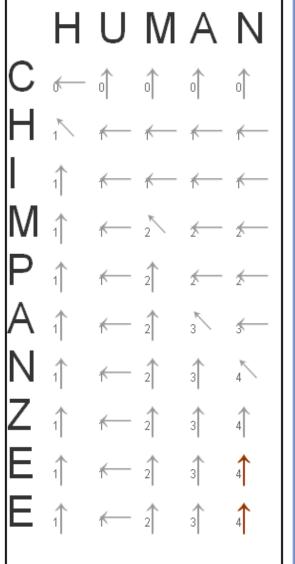


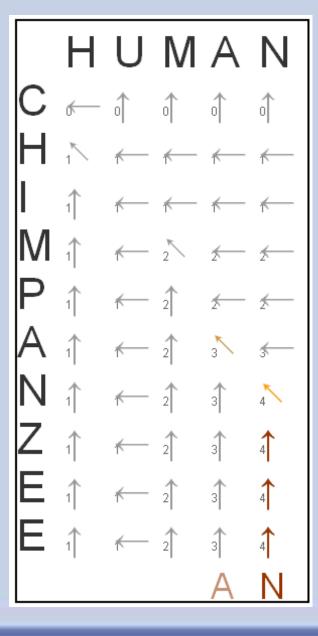


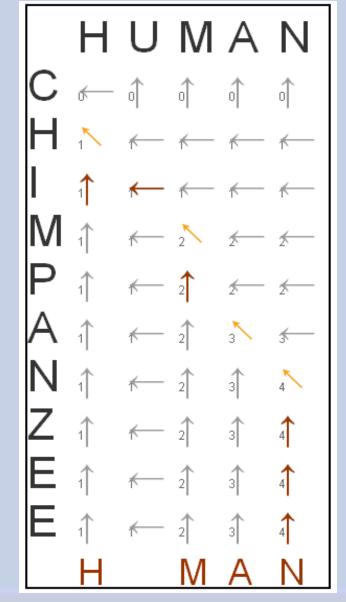
# HUMANI











## Elements of Dynamic Programming : A Review

#### **Elements of Dynamic Programming**

- Three key ingredients (some as in case of greedy)
  - Optimal substructure
  - Overlapping subproblems
  - memoization
- How do we map these three characteristics to any one of the problem that we have solved?

**—** .....

#### **Optimal Substructure**

- When does a problem exhibit optimal substructure?
- When a problem exhibits optimal substructure...
  - either greedy approach or
  - dynamic programming approach may apply
- In dynamic programming
  - one builds the optimal solution to the main problem from optimal solutions to the subproblems
- Thus, the range of subproblems considered must be those included in the optimal solution.

#### Dynamic Programming: Broad paradigm

- Three step process
  - Break the problem into smaller subproblems
  - solve these subproblems optimally
    - the subproblems are further solved following this three step process itself
  - use the discovered optimal solutions to the subproblems in framing the solution to the main problem.

#### How to discover optimal substructure?

- Follow the following steps to unearth a common pattern
  - designing the solution must involve making a choice
    - e.g. .....
  - this picked up choice must lead to one or more subproblems to be solved
  - identify which subproblem to solve and proceed along in the same manner
  - Prove that the solution works using contradiction

#### Optimal Substructure...

- Optimal Substructure varies across problem domains in two ways
  - how many subproblems an optimal solution to the original problem uses
  - how many choices we have in determining which subproblems to use in an optimal solution.
- The running time, therefore, depends on
  - the total number of subproblems and
  - the number of choices to be investigated for each subproblem
- This can best be viewed from subproblem graph
  - as discussed in the Fibonacci problem....

#### Top down OR Bottom up?

 Dynamic programming uses optimal substructure usually in bottom-up fashion.

```
– e.g.....
```

- However, at times we may also devise a top-down solution using dynamic programming
  - e.g.....

#### **Greedy vrs Dynamic**

- Major difference
  - Greedy algorithms make choices quickly...one that is not an informed choice.
  - Dynamic algorithms make the choice of the subproblem to be solved only after evaluating the choices.

#### Dynamic vrs. Divide and Conquer

- In dynamic programming,
  - typically the overlapping of the subproblems is exploited to an advantage whereas
  - in divide & conquer, the overlapping of the subproblems remains independent
- Whenever, the problem can be divided into typically equal sized subproblems,
  - use divide and conquer
  - use dynamic programming otherwise.

## All Pairs Shortest Paths Floyd Warshall's Algorithm

#### All pairs shortest paths

- The problem of finding the shortest path between all pairs of vertices on a graph
  - is akin to making a table of all of the distances between all pairs of cities on a road map.
  - additionally, the route that gives rise to this shortest path also needs to be established.
  - one of many interesting problems that can be solved using graph algorithms.
  - there are a variety of solutions to this problem and
    - the algorithms that can be applied often depend on whether negative weighs are present in the graph.
  - one such algorithm is the Floyd-Warshall All-Pairs-Shortest-Path algorithm.

#### All pairs shortest paths...

- A Variety of solutions to this problem exists
  - which algorithm to apply depend on the whether negative weighs are present in the graph.
- For example,
  - if no negative weights exists then it is possible to run Dijkstra's single-source shortest-path algorithm |V| times which has a run time of  $O(|V|^3)$
  - when negative weights are present the Bellman-Ford algorithm could be run from each vertex.
  - another solution for graphs containing negative weights is known as the 'Slow-All-Pairs-Shortest-Path algorithm has a run time of  $O(|V|^4)$ .

#### Floyd-Warshall's Algorithm

- The Floyd-Warshall All-Pairs-Shortest-Path algorithm
  - uses a dynamic-programming methodology to solve the All-Pairs-Shortest-Path problem.
  - calculates the length of the shortest path between all nodes of a graph in  $O(V^3)$  time.
  - negatively weighed edges may be present, however negatively weighted cycles cause problems with the algorithm.
  - it doesn't actually find the paths, it only finds their lengths.

#### Negative weights and cycles: Difference

- e.g. consider a graph as shown
- There are several paths between A-E

**Path I**: A -> B -> E 20

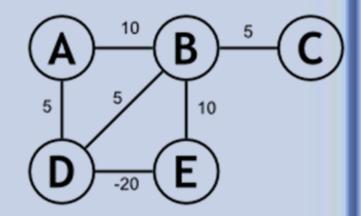
**Path 2**: A -> D -> E 25

**Path 3**: A -> B -> D -> E 35

**Path 4**: A -> D -> B -> E 20



- The cost is 10 20 + 5 = -5.
- i.e. adding this loop to a path once lowers the cost of the path by 5; and adding it twice would lower the cost by 2 \* 5 = 10.
- Thus, negative cycle causes problems.



#### **Broad approach**

- Step I
  - Describe the structure of a shortest path
    - any subpath of a shortest path is a shortest path.
- Step 2
  - Give a recurrence for computing later values from earlier (bottom-up).
- Step 3
  - Give a high-level program (Computing the shortest-paths weights).
- Step 4
  - Constructing a shortest path.

#### Step 1: Structure of a shortest path.

- Algorithm considers the "intermediate" vertices of a shortest path.
- Intermediate Vertices?
- Given a directed graph
  - $G = (V, E), |V| = n, V = \{1,2,...,n\}$
  - The vertices  $v_2$   $v_3$   $v_4$ .... $v_{K-1}$  are known as intermediate vertices of the path  $p = \langle v_1, v_2, v_3, v_4, ..., v_k \rangle$
- the algorithm exploits a relationship between path p and shortest paths from i to j with all intermediate vertices in the set {1,2,...,k-1}.

#### Step 1: Structure of a shortest path.

• Let  $d_{ij}^{(k)}$  be the length of the shortest path from i to j such that all intermediate vertices on the path (if any) are in set  $\{1, 2, \ldots, k\}$ .

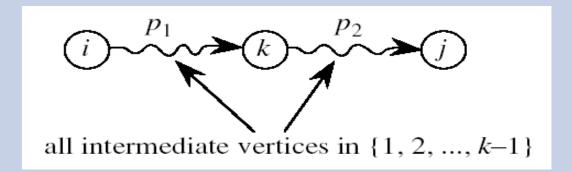
 $d_{ij}^{(0)}$  is set to be  $w_{ij}$ , i.e., no intermediate vertex. Let  $D^{(k)}$  be the  $n \times n$  matrix  $[d_{ij}^{(k)}]$ .

• Claim:  $d_{ij}^{(n)}$  is the distance from i to j. So our aim is to compute  $D^{(n)}$ .

• Subproblems: compute  $D^{(k)}$  for  $k = 0, 1, \dots, n$ .

#### Step 1: Structure of a shortest path....

- Base condition:  $d_{ij}^{(0)} = ?$ 
  - $d_{ij}^{(0)} = w_{ij}$ .
- For k>0:
  - Let  $p=\langle v_i, \ldots, v_j \rangle$  be a shortest path from vertex i to vertex j with all intermediate vertices in  $\{1,2,\ldots,k\}$ .
  - If k is not an intermediate vertex of path p, then all intermediate vertices of path p are in  $\{1,2,...,k-1\}$ .
  - If k is an intermediate vertex, then p is composed of 2 shortest subpaths drawn from  $\{1,2,...,k-1\}$ .



### Step 2: Recursive Formulation for d<sub>ij</sub>(k)

$$d_{ij}^{(k)} = \begin{cases} w_{ij} & \text{if } k = 0 \;, \\ \min\left(d_{ij}^{(k-1)}, d_{ik}^{(k-1)} + d_{kj}^{(k-1)}\right) & \text{if } k \geq 1 \;. \end{cases}$$

d<sub>ij(k)</sub> = weight of a shortest path from vertex i to vertex j for which all intermediate vertices are in the set {1,2,...,k}.

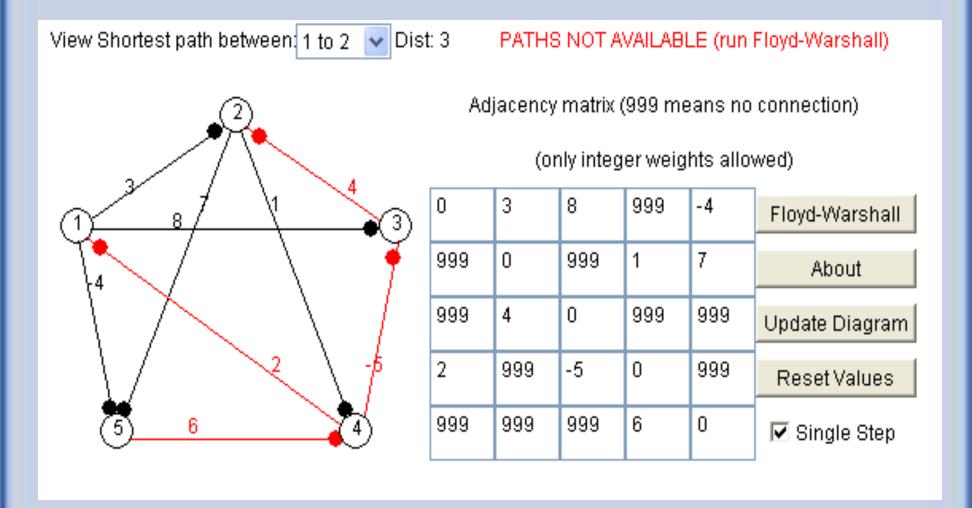
#### Step 3: The Algorithm

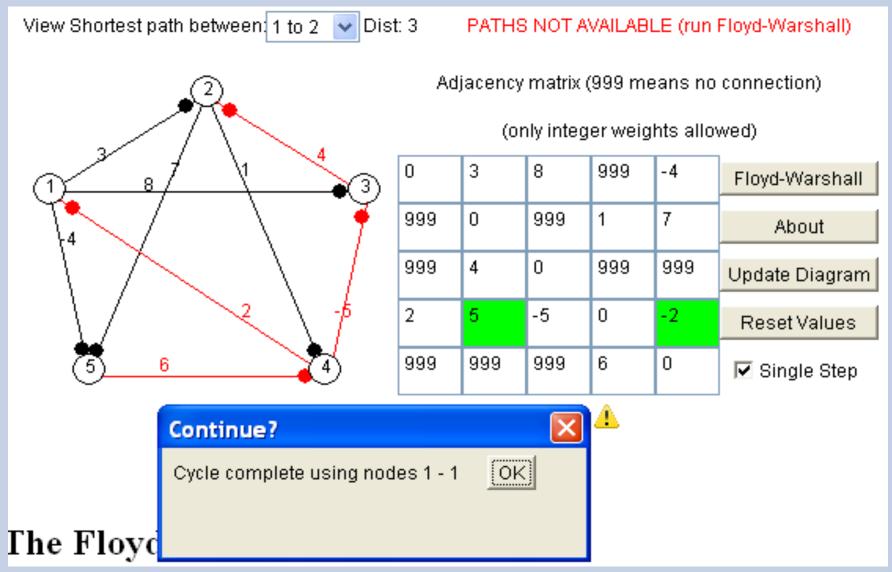
```
FLOYD-WARSHALL (W, n)
D^{(0)} \leftarrow W
for k \leftarrow 1 to n
\mathbf{do} \text{ for } i \leftarrow 1 \text{ to } n
\mathbf{do} \text{ for } j \leftarrow 1 \text{ to } n
\mathbf{do} \text{ do } d_{ij}^{(k)} \leftarrow \min \left( d_{ij}^{(k-1)}, d_{ik}^{(k-1)} + d_{kj}^{(k-1)} \right)
return D^{(n)}
```

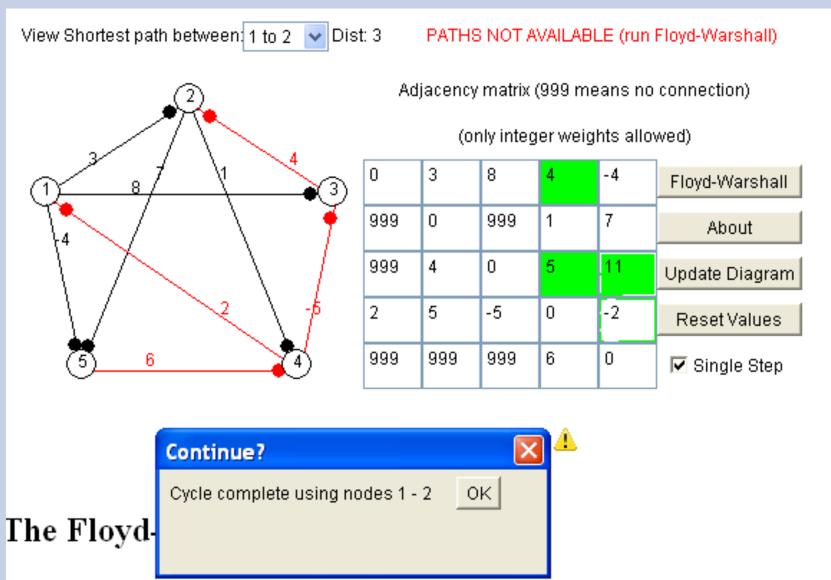
```
    W=(wij), where W<sub>ij</sub> = 0, if i = j
    = the weight of directed edge (i, j), if i != j and (i,j) ∈ E
    = infinite, if i != j and (i, j) !∈ E.
```

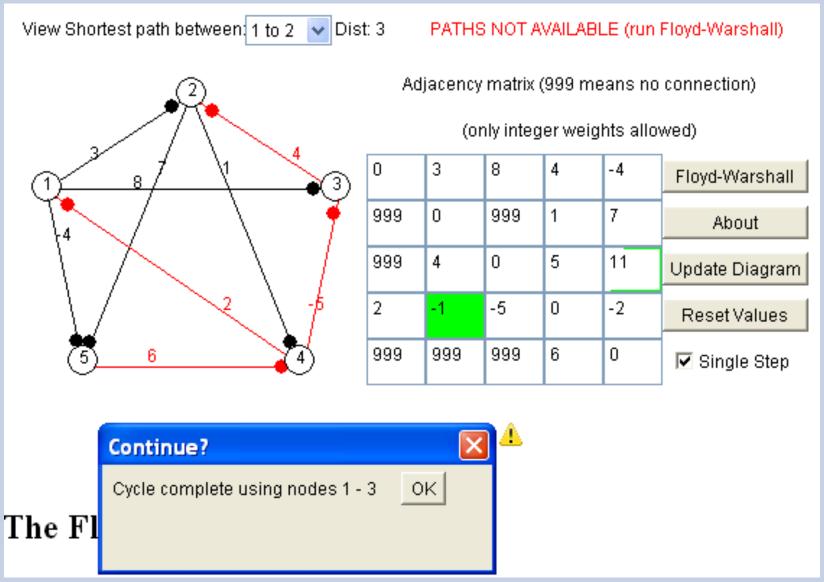
#### Complexity of Floyd-Warshall algorithm.

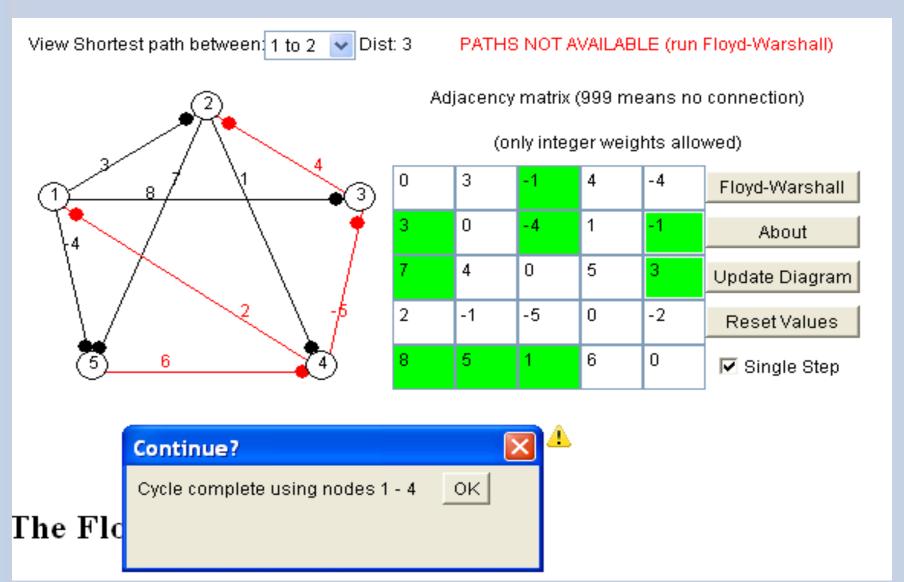
- The running time of the algorithm is determined by the triply nested for loops.
- Because each execution of line-5 takes O(1) time, the algorithms runs in time  $O(n^3)$ .
- Here code is tight, with no elaborate data structures, and so the constant hidden in the Θ-notation is small.
- Thus this algorithm is quit practical for even moderate-sized input graphs.

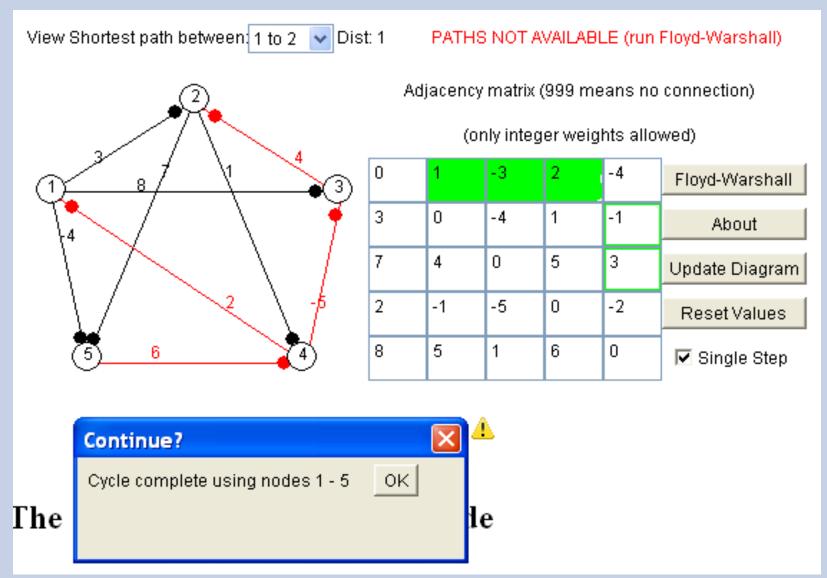




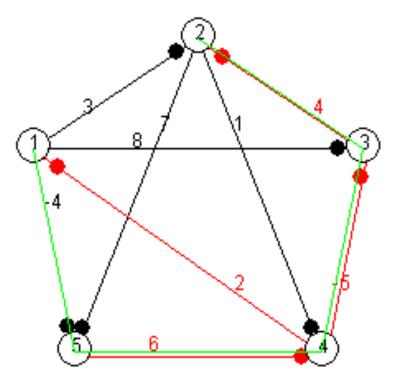








View Shortest path between: 1 to 2 V Dist: 1 PATHS AVAILABLE

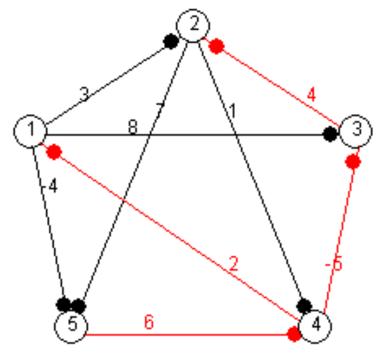


Adjacency matrix (999 means no connection)

(only integer weights allowed)

| 0 | 1  | -3 | 2 | -4 | Floyd-Warshall |
|---|----|----|---|----|----------------|
| 3 | 0  | -4 | 1 | -1 | About          |
| 7 | 4  | 0  | 5 | 3  | Update Diagram |
| 2 | -1 | -5 | 0 | -2 | Reset Values   |
| 8 | 5  | 1  | 6 | 0  | Single Step    |

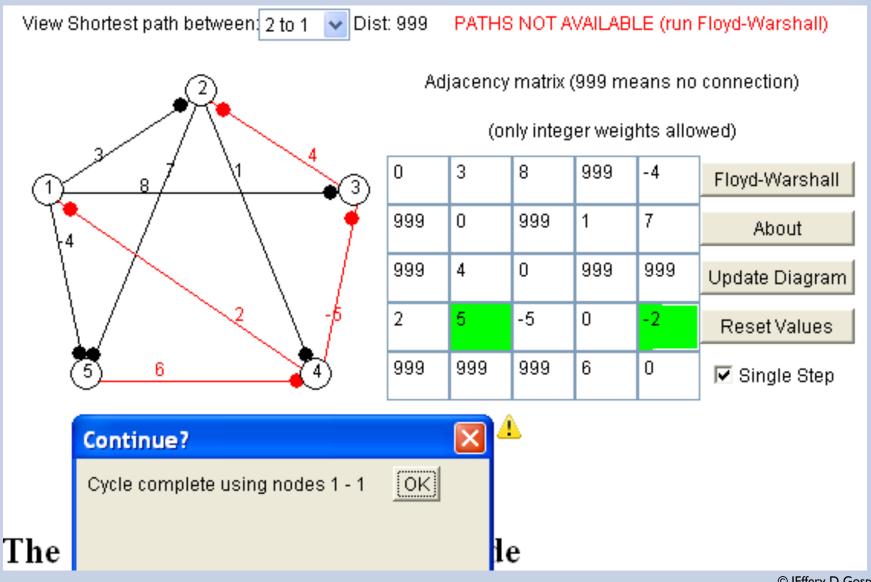
View Shortest path between: 2 to 1 💟 Dist: 999 PATHS NOT AVAILABLE (run Floyd-Warshall)

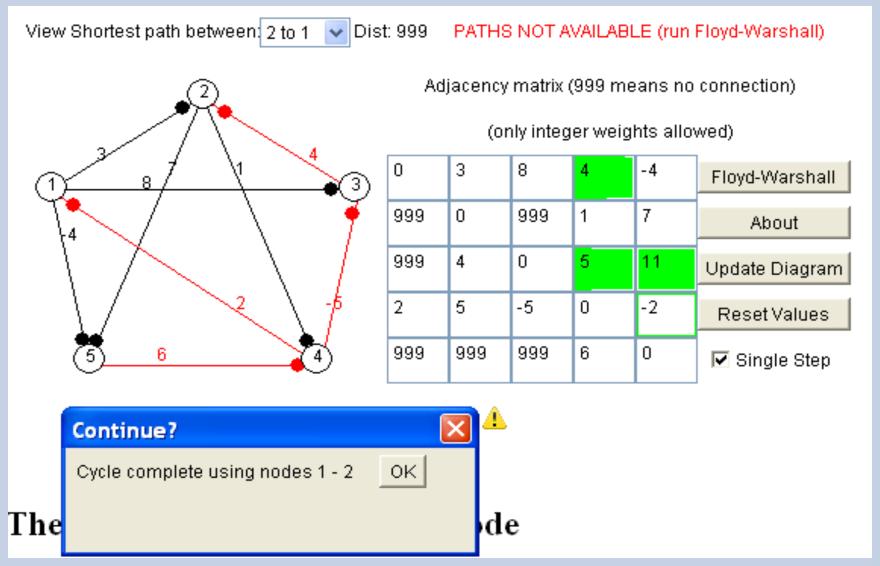


Adjacency matrix (999 means no connection)

(only integer weights allowed)

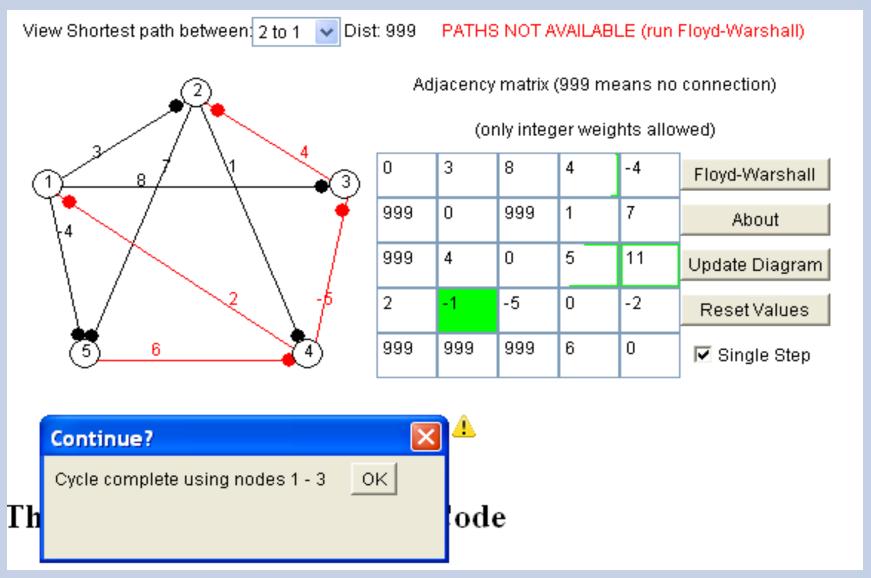
| 0   | 3   | 8   | 999 | -4  | Floyd-Warshall |
|-----|-----|-----|-----|-----|----------------|
| 999 | 0   | 999 | 1   | 7   | About          |
| 999 | 4   | 0   | 999 | 999 | Update Diagram |
| 2   | 999 | -5  | 0   | 999 | Reset Values   |
| 999 | 999 | 999 | 6   | 0   | ☑ Single Step  |

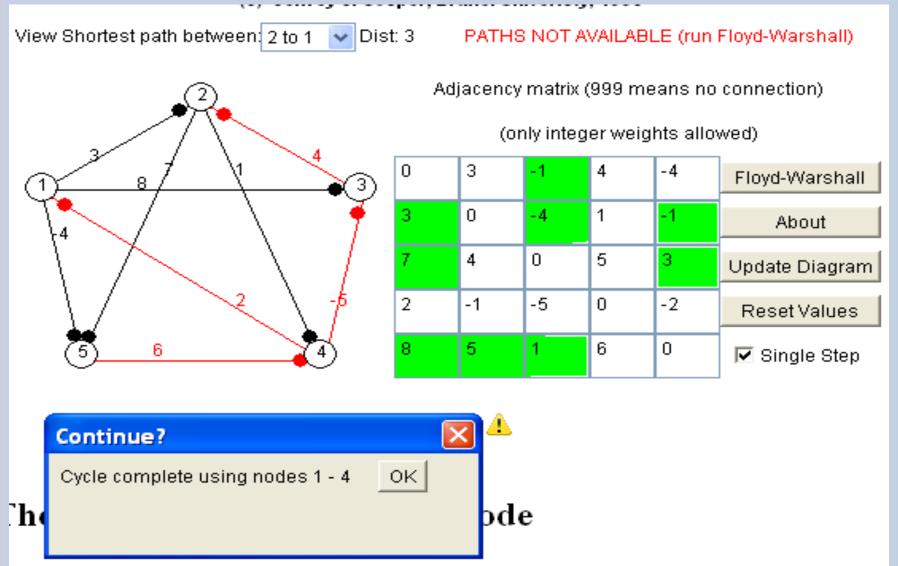


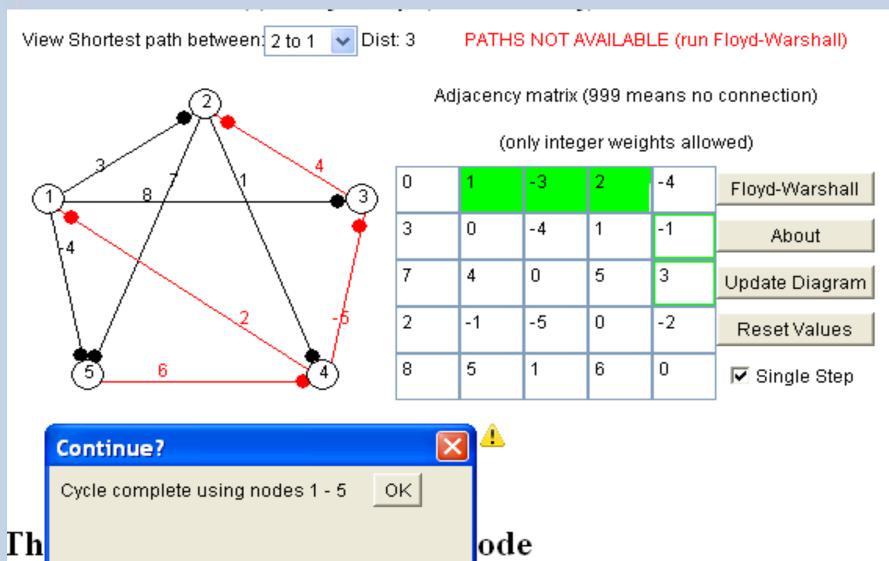


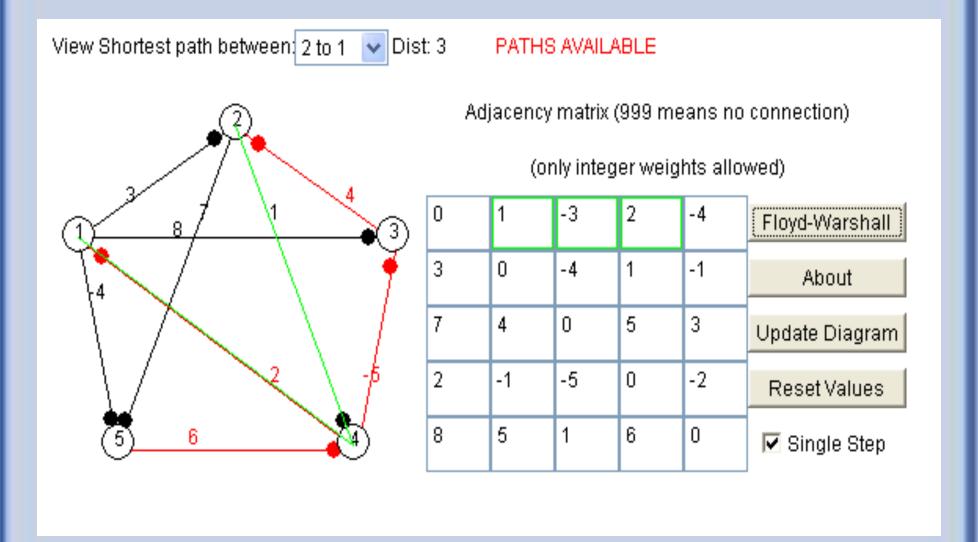
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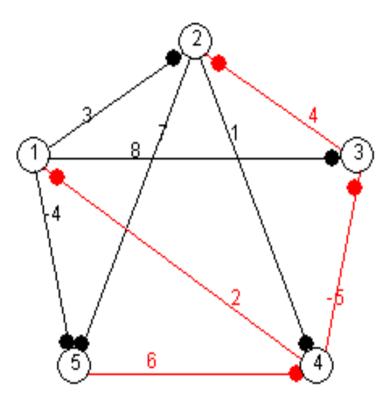








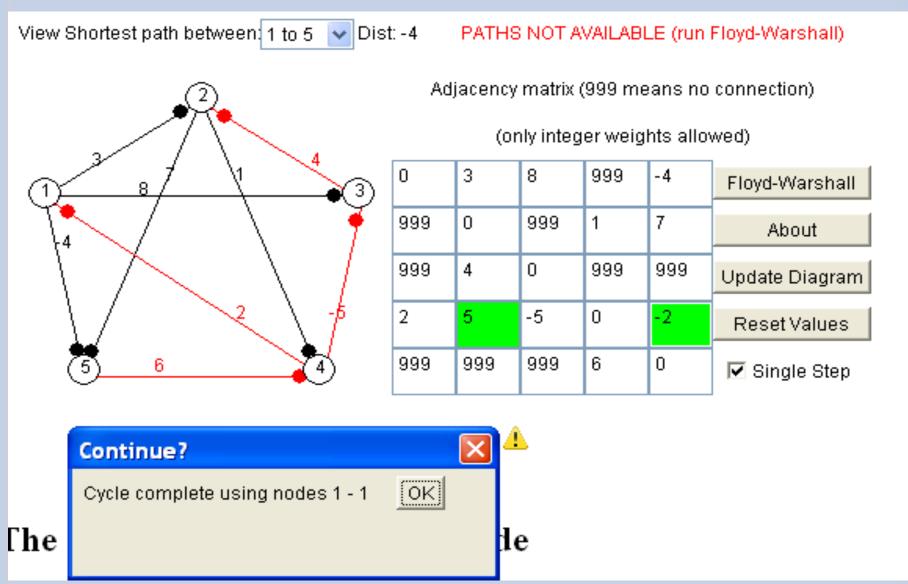
View Shortest path between: 1 to 5 💌 Dist: -4 PATHS NOT AVAILABLE (run Floyd-Warshall)

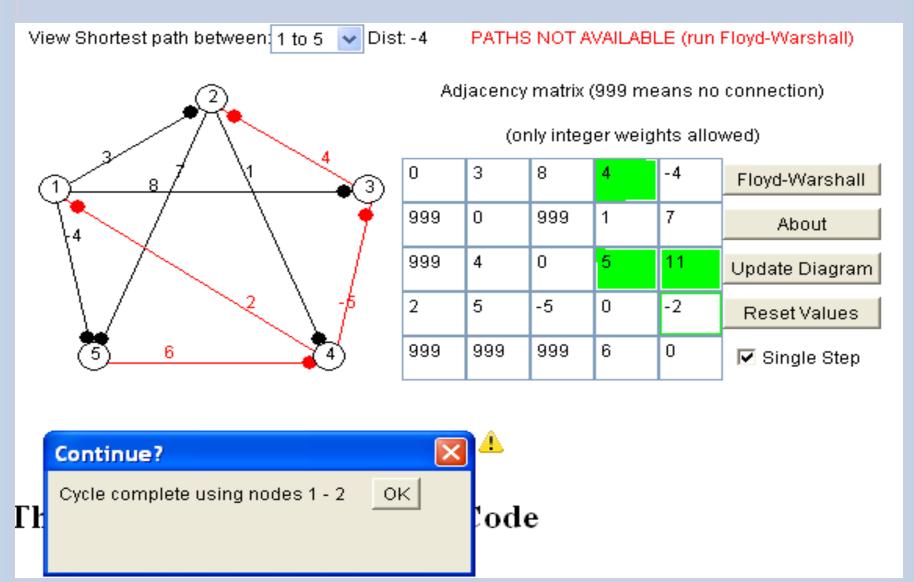


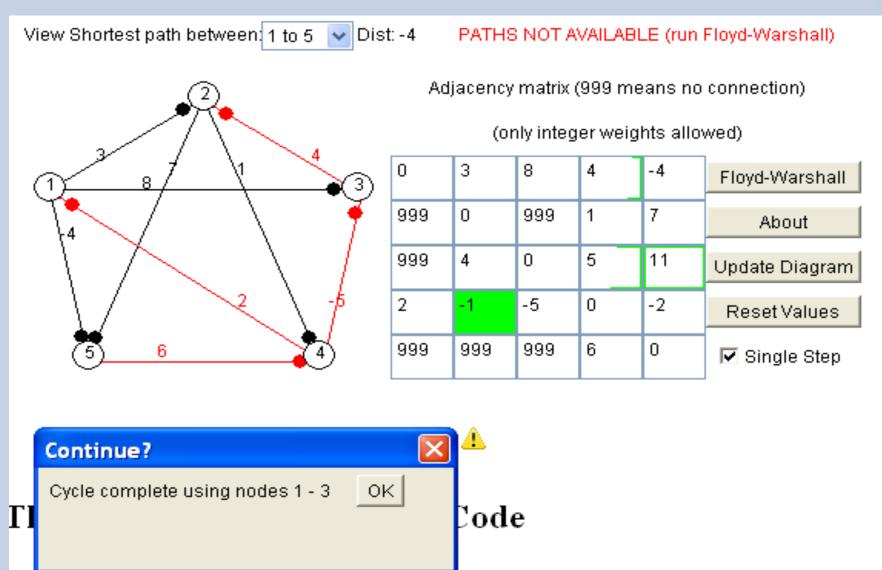
Adjacency matrix (999 means no connection)

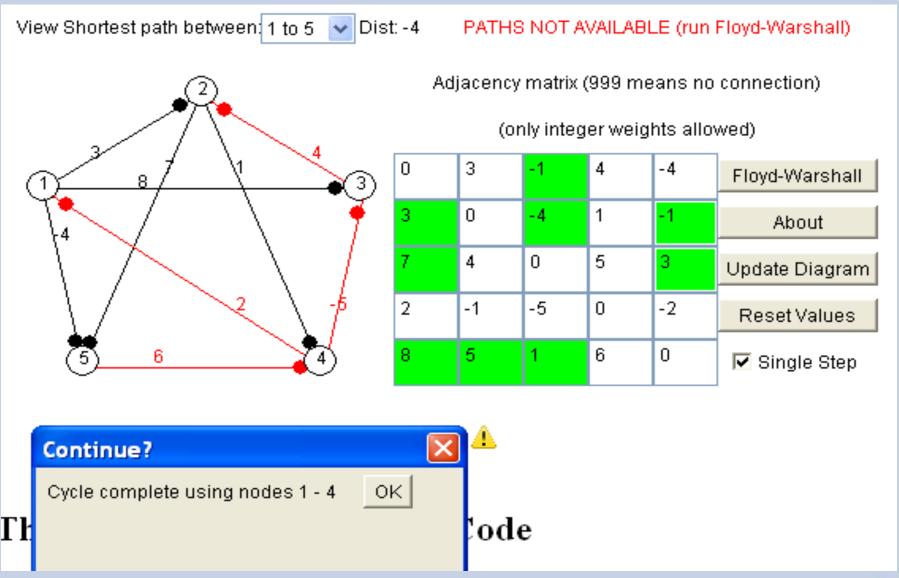
(only integer weights allowed)

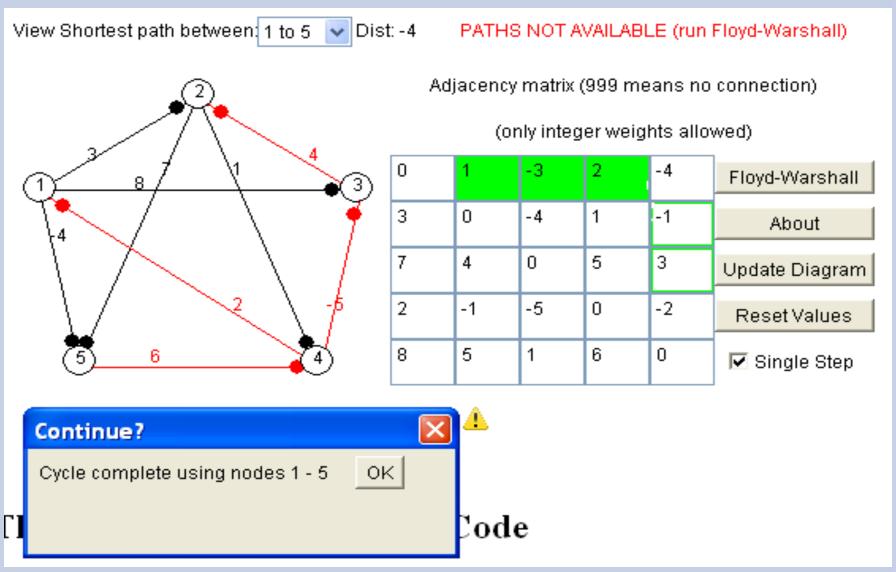
| 0   | 3   | 8   | 999 | -4  | Floyd-Warshall |
|-----|-----|-----|-----|-----|----------------|
| 999 | 0   | 999 | 1   | 7   | About          |
| 999 | 4   | 0   | 999 | 999 | Update Diagram |
| 2   | 999 | -5  | 0   | 999 | Reset Values   |
| 999 | 999 | 999 | 6   | 0   | ✓ Single Step  |



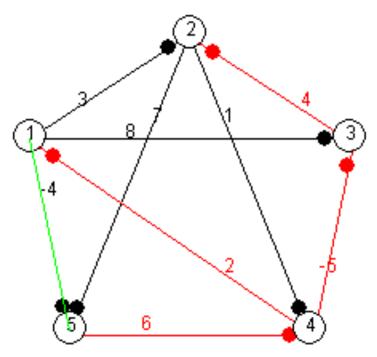








View Shortest path between: 1 to 5 💟 Dist: -4 PATHS AVAILABLE

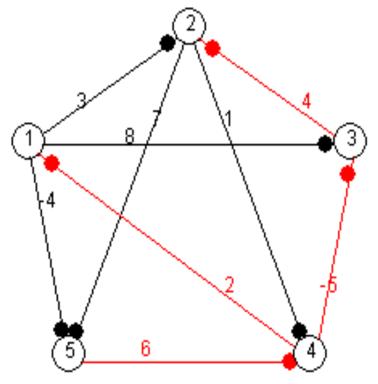


Adjacency matrix (999 means no connection)

(only integer weights allowed)

| 0 | 1  | -3 | 2 | -4 | Floyd-Warshall |
|---|----|----|---|----|----------------|
| 3 | 0  | -4 | 1 | -1 | About          |
| 7 | 4  | 0  | 5 | 3  | Update Diagram |
| 2 | -1 | -5 | 0 | -2 | Reset Values   |
| 8 | 5  | 1  | 6 | 0  | Single Step    |

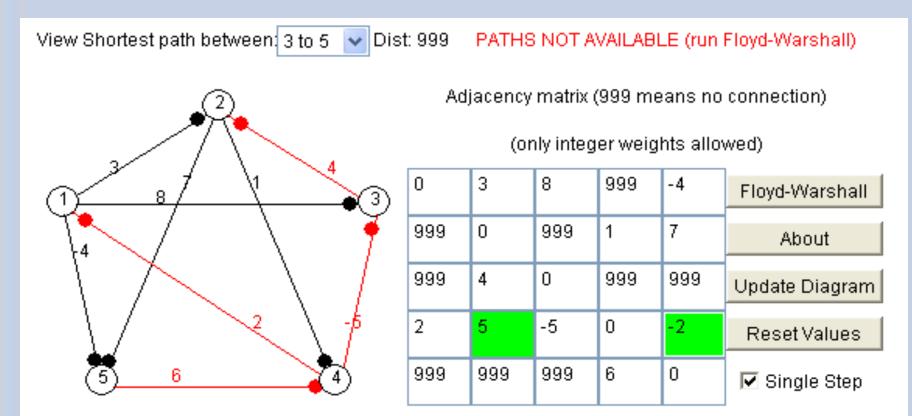
View Shortest path between: 3 to 5 🔻 Dist: 999 PATHS NOT AVAILABLE (run Floyd-Warshall)

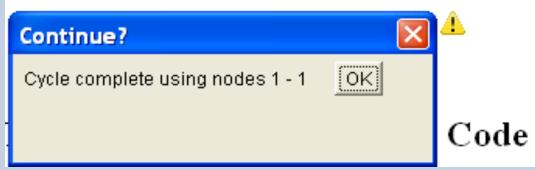


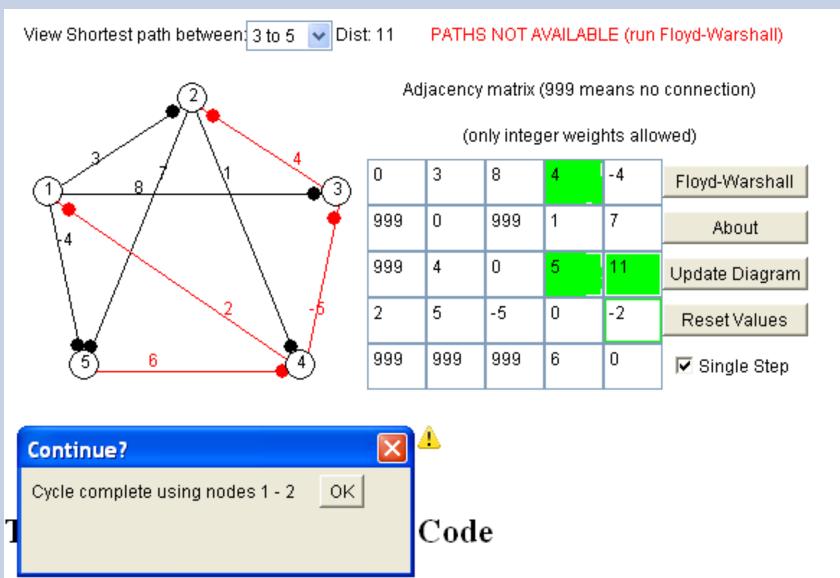
Adjacency matrix (999 means no connection)

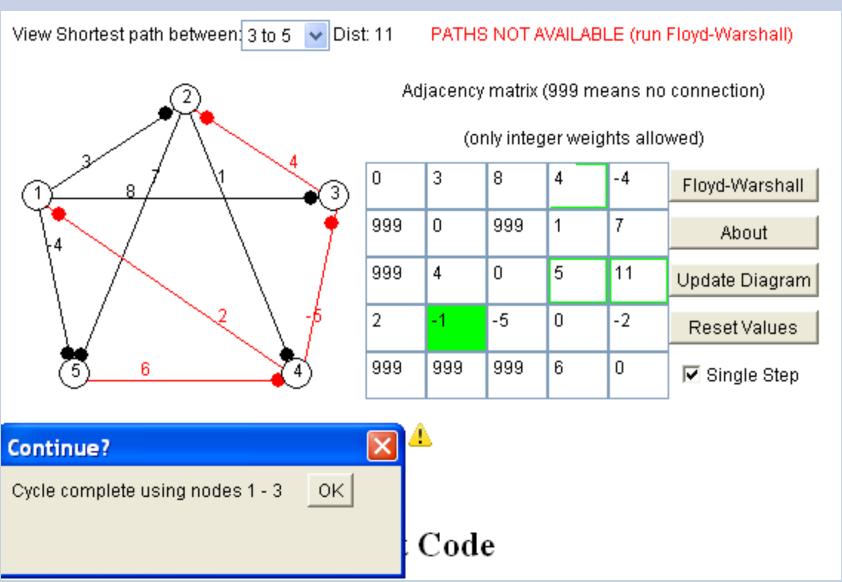
(only integer weights allowed)

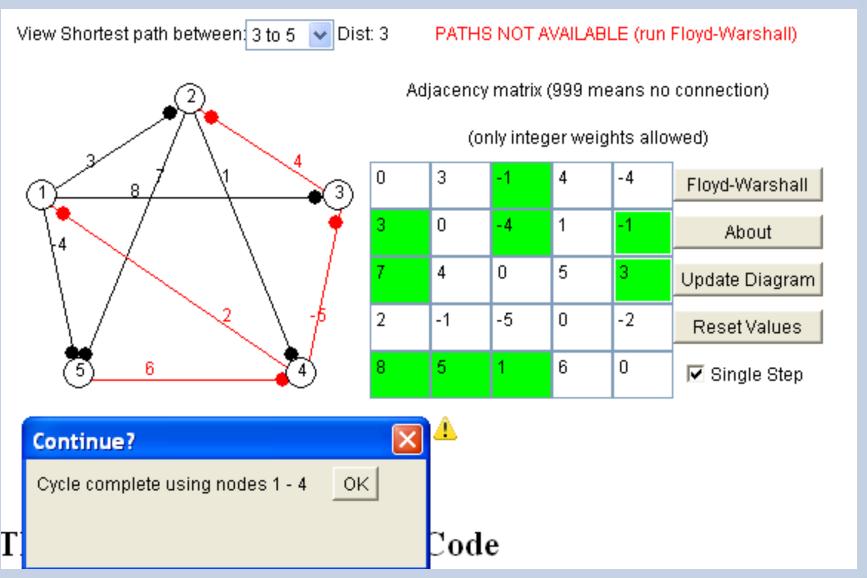
| 0   | 3   | 8   | 999 | -4  | Floyd-Warshall |
|-----|-----|-----|-----|-----|----------------|
| 999 | 0   | 999 | 1   | 7   | About          |
| 999 | 4   | 0   | 999 | 999 | Update Diagram |
| 2   | 999 | -5  | 0   | 999 | Reset Values   |
| 999 | 999 | 999 | 6   | 0   | ☑ Single Step  |

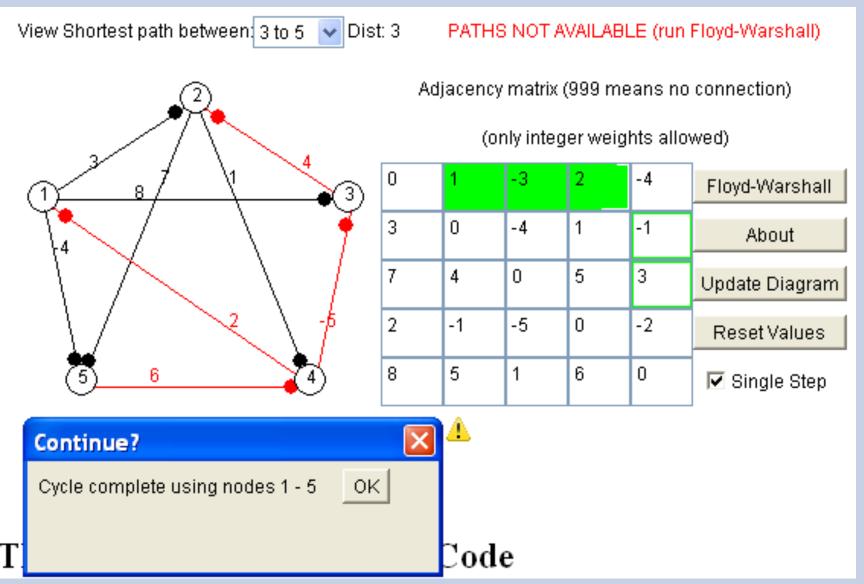












PATHS AVAILABLE

Adjacency matrix (999 means no connection) (only integer weights allowed) -3 0 -4 Floyd-Warshall 3 0 1 -4 -1 5 n 4 Update Diagram 2 -5 0 -2 -1 Reset Values 6 5 0 Single Step

Dist: 3

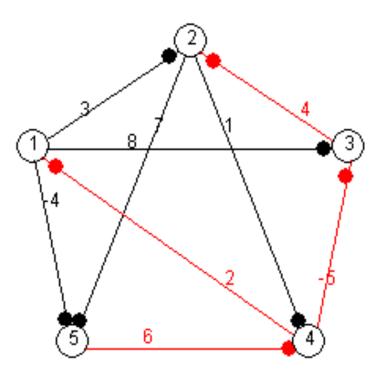
View Shortest path between: 3 to 5

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About

View Shortest path between: 5 to 4 V Dist: 6 PAT

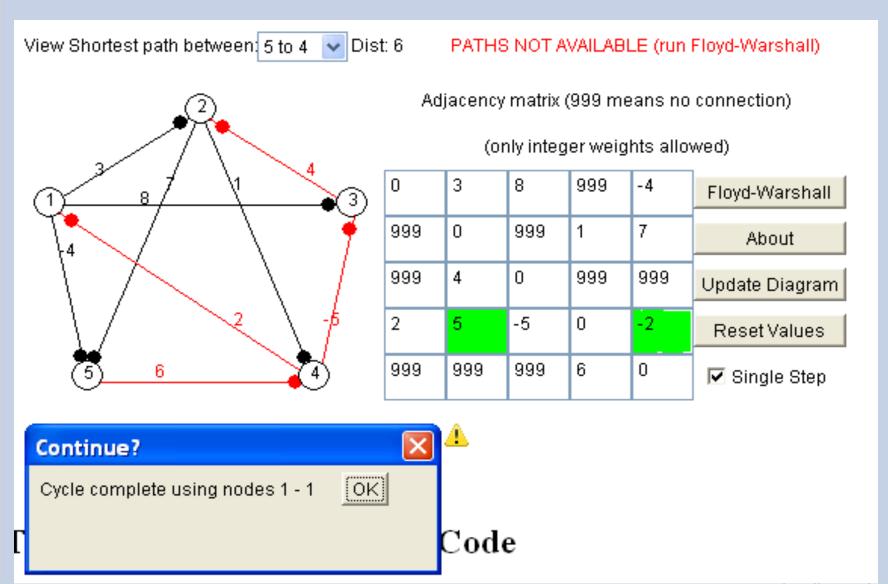
PATHS NOT AVAILABLE (run Floyd-Warshall)

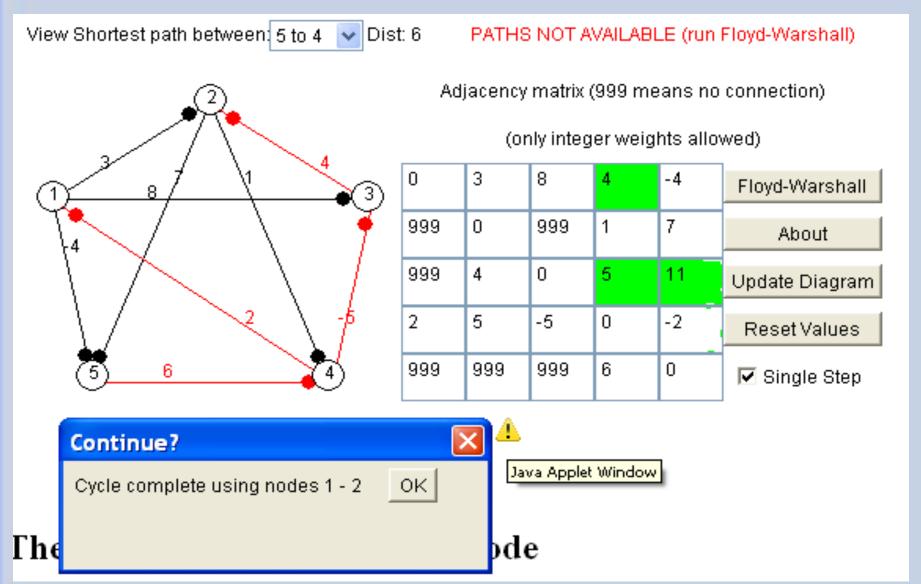


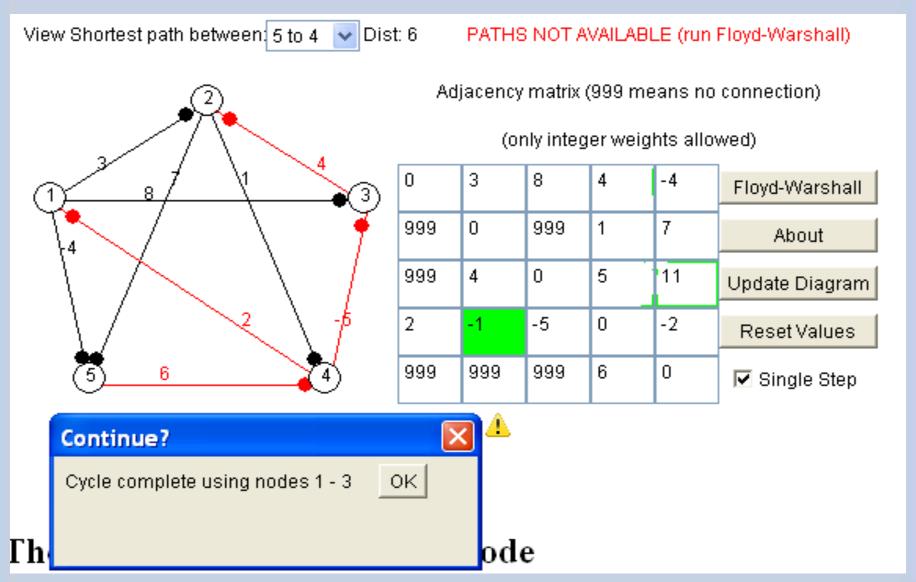
Adjacency matrix (999 means no connection)

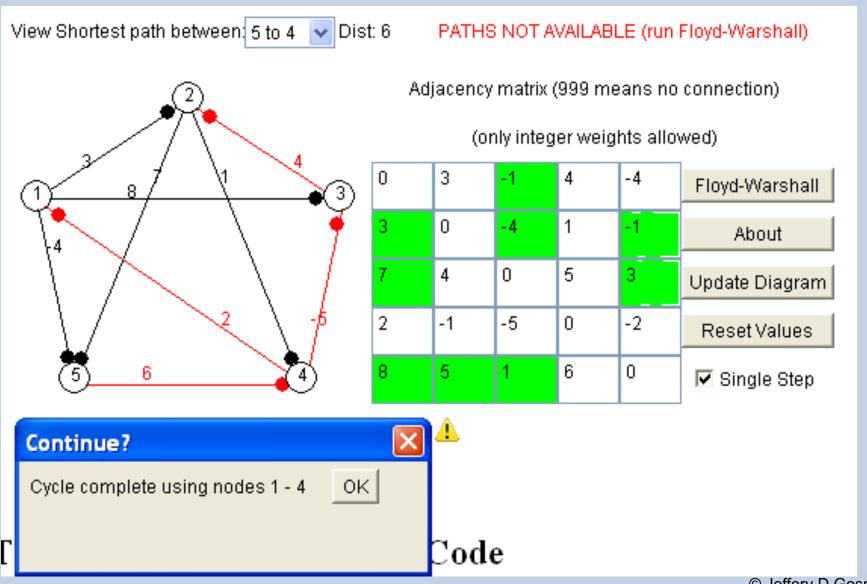
(only integer weights allowed)

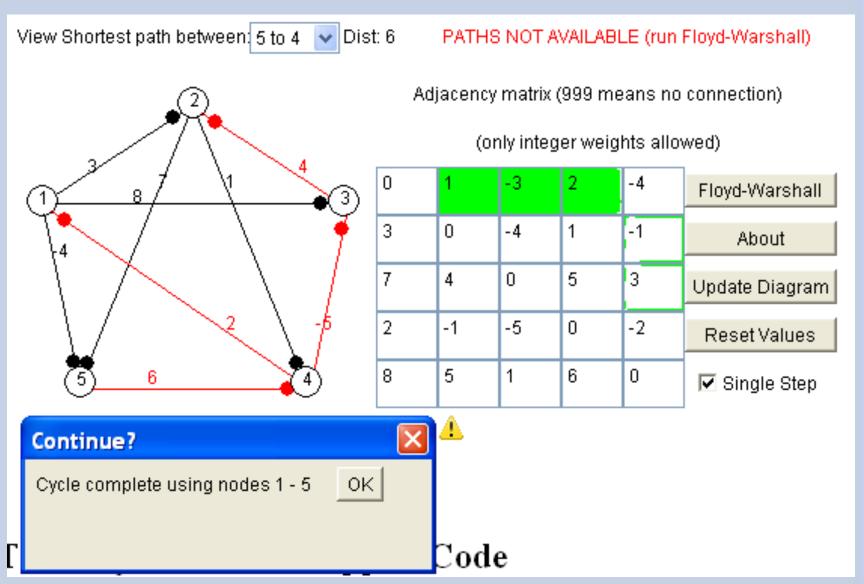
| 0   | 3   | 8   | 999 | -4  | Floyd-Warshall |
|-----|-----|-----|-----|-----|----------------|
| 999 | 0   | 999 | 1   | 7   | About          |
| 999 | 4   | 0   | 999 | 999 | Update Diagram |
| 2   | 999 | -5  | 0   | 999 | Reset Values   |
| 999 | 999 | 999 | 6   | 0   | ✓ Single Step  |











View Shortest path between: 5 to 4 Dist: 6 PATHS AVAILABLE Adjacency matrix (999 means no connection) (only integer weights allowed) -3 0 2 -4 3 0 -4 -1 About 0 5 3 4 Update Diagram -5 0 -1 -2 Reset Values

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Single Step

5

8

6

0

- The solution to a DP problem
  - is typically expressed as a minimum (or maximum) of possible alternate solutions.
  - If r represents the cost of a solution composed of subproblems  $x_1, x_2, ..., x_l$ , then r can be written as

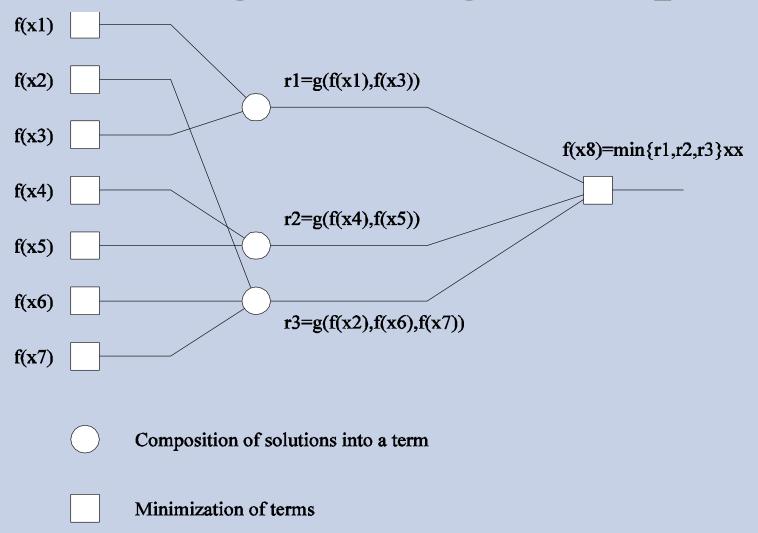
$$r = g(f(x_1), f(x_2), \dots, f(x_l)).$$

Here, g is the composition function.

- If the optimal solution to each problem
  - is determined by composing optimal solutions to the subproblems and
  - selecting the minimum (or maximum),

the formulation is said to be a DP formulation.

## Dynamic Programming: Example



The computation and composition of subproblem solutions to solve problem  $f(x_8)$ .

- The recursive DP equation is also called
  - the functional equation or optimization equation.
  - the equation for the shortest path problem the composition function is f(j) + c(j,x).
    - this contains a single recursive term (f(j)). Such a formulation is called monadic.
  - If the RHS has multiple recursive terms, the DP formulation is called polyadic.

- The dependencies between subproblems can be expressed as a graph.
- If the graph can be levelized/linearized
  - (i.e., solutions to problems at a level depend only on solutions to problems at the previous level),
    - the formulation is called serial, else it is called non-serial.

- Based on these two criteria, we can classify DP formulations into four categories
  - serial-monadic,
  - serial-polyadic,
  - non-serial-monadic,
  - non-serial-polyadic.
- This classification is useful since it identifies concurrency and dependencies that guide parallel formulations.

#### Assignments

- APSP Problem : Floyd Warshall's algorithm
- Optimal Binary Search Trees
- Cutting the Iron Rod problem in CLRS