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CSE 421

RNA Secondary Structure, Sequence Alignment

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Sequence Alignment

Sequence Alignment

Given two strings $x_1, ..., x_m$ and $y_1, ..., y_n$ find an alignment with minimum number of mismatch and gaps.

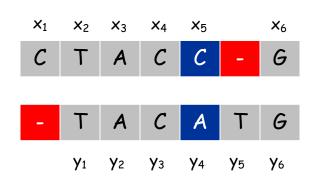
An alignment is a set of ordered pairs $(x_{i_1}, y_{j_1}), (x_{i_2}, y_{j_2}), \dots$ such that $i_1 < i_2 < \dots$ and $j_1 < j_2 < \dots$

Example: CTACCG VS. TACATG.

Sol: We aligned

 x_2-y_1 , x_3-y_2 , x_4-y_3 , x_5-y_4 , x_6-y_6 .

So, the cost is 3.



DP for Sequence Alignment

Let OPT(i,j) be min cost of aligning $x_1, ..., x_i$ and $y_1, ..., y_j$

Case 1: OPT matches x_i, y_j

• Then, pay mis-match cost if $x_i \neq y_j$ + min cost of aligning $x_1, ..., x_{i-1}$ and $y_1, ..., y_{j-1}$ i.e., OPT(i-1, j-1)

Case 2: OPT leaves x_i unmatched

• Then, pay gap cost for $x_i + OPT(i-1,j)$

Case 3: OPT leaves y_i unmatched

• Then, pay gap cost for $y_i + OPT(i, j - 1)$

Bottom-up DP

```
Sequence-Alignment (m, n, x_1x_2...x_m, y_1y_2...y_n) {
   for i = 0 to m
      M[0, i] = i
   for j = 0 to n
      M[j, 0] = j
   for i = 1 to m
      for j = 1 to n
         M[i, j] = min((x_i=y_j? 0:1) + M[i-1, j-1],
                        1 + M[i-1, j],
                        1 + M[i, j-1]
   return M[m, n]
}
```

Analysis: $\Theta(mn)$ time and space. English words or sentences: m, n \leq 10,...,20. Computational biology: m = n = 100,000. 10 billions ops OK, but 40GB array?

Optimizing Memory

If we are not using strong induction in the DP, we just need to use the last (row) of computed values.

```
Sequence-Alignment (m, n, x_1x_2...x_m, y_1y_2...y_n) {
   for i = 0 to m
     M[0, i] = i
   for j = 0 to n
     M[i, 0] = i
   for i = 1 to m
      for j = 1 to n
         M[i, j] = min((x_i=y_j? 0:1) + M[i-1, j-1],
                       1 + M[i-1, j],
                        1 + M[i, j-1])
   return M[m, n]
                                         Just need i - 1, i rows
}
                                            to compute M[i,j]
```

DP with O(m+n) memory

- Keep an Old array containing values of the last row
- Fill out the new values in a New array
- Copy new to old at the end of the loop

```
Sequence-Alignment (m, n, x_1x_2...x_m, y_1y_2...y_n) {
   for i = 0 to m
      O[i] = i
   for i = 1 to m
                                               M[i-1, j-1]
      N[0]=i
       for j = 1 to n
          N[j] = min((x_i=y_j? 0:1) + O[j-1],
                           1 + O[j], \longleftarrow M[i-1, j]
                           1 + N[j-1]) \leftarrow M[i, j-1]
       for j = 1 to n
          O[\dot{j}]=N[\dot{j}]
   return N[n]
}
```

Lesson

Advantage of a bottom-up DP:

It is much easier to optimize the space.

Longest Path in a DAG

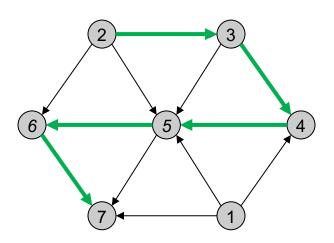
Longest Path in a DAG

Goal: Given a DAG G, find the longest path.

Recall: A directed graph G is a DAG if it has no cycle.

This problem is NP-hard for general directed graphs:

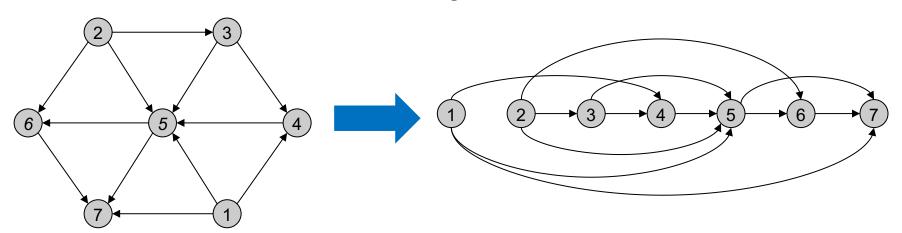
 It has the Hamiltonian Path as a special case



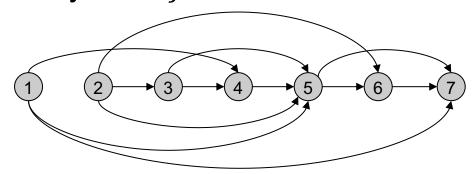
Q: What is the right ordering?

Remember, we have to use that G is a DAG, ideally in defining the ordering

We saw that every DAG has a topological sorting So, let's use that as an ordering.



Suppose we have labelled the vertices such that (i, j) is a directed edge only if i < j.



Let OPT(j) = length of the longest path ending at j Suppose in the longest path ending at j, last edge is (i, j). Then, none of the i + 1, ..., j - 1 are in this path since topological ordering. So,

$$OPT(j) = OPT(i) + 1.$$

Suppose we have labelled the vertices such that (i,j) is a directed edge only if i < j.

Let OPT(j) = length of the longest path ending at j

$$OPT(j) = \begin{cases} 0 & \text{If } j \text{ is a source} \\ 1 + \max_{i:(i,j) \text{ an edge}} OPT(i) & \text{o.w.} \end{cases}$$

```
Let G be a DAG given with a topological sorting: For all edges
(i,j) we have i<j.

Compute-OPT(j) {
    if (in-degree(j)==0)
        return 0
    if (M[j]==empty)
        M[j]=0;
        for all edges (i,j)
            M[j] = max(M[j],1+Compute-OPT(i))
    return M[j]
}
Output max(M[1],...,M[n])</pre>
```

Running Time: O(n + m)Memory: O(n)

Can we output the longest path?

Outputting the Longest Path

```
Let G be a DAG given with a topological sorting: For all edges
(i, i) we have i<i.
Initialize Parent[j]=-1 for all j.
Compute-OPT()){
   if (in-degree(j)==0)
     return 0
   if (M[j]==empty)
     M[j]=0;
                                         Record the entry that
     for all edges (i,j)
                                      we used to compute OPT(j)
       if (M[j] < 1+Compute-OFT(i)</pre>
         M[j]=1+Compute-OPT(i)
         Parent[j]=i
   return M[j]
}
Let M[k] be the maximum of M[1], ..., M[n]
While (Parent[k]!=-1)
   Print k
   k=Parent[k]
```

Longest Increasing Subsequence

Longest Increasing Subsequence

Given a sequence of numbers
Find the longest increasing subsequence

41, 22, 9, 15, 23, 39, 21, 56, 24, 34, 59, 23, 60, 39, 87, 23, 90



41, 22, **9**, **15**, **23**, 39, 21, 56, **24**, **34**, **59**, 23, **60**, 39, **87**, 23, 90

DP for LIS

Let OPT(j) be the longest increasing subsequence ending at j.

Observation: Suppose the OPT(j) is the sequence $x_{i_1}, x_{i_2}, \dots, x_{i_k}, x_j$

Then, $x_{i_1}, x_{i_2}, ..., x_{i_k}$ is the longest increasing subsequence ending at x_{i_k} , i.e., $OPT(j) = 1 + OPT(i_k)$

$$OPT(j) = \begin{cases} 1 & \text{if } x_j > x_i \text{ for all } i < j \\ 1 + \max_{i:x_i < x_j} OPT(i) & \text{o.w.} \end{cases}$$

Remark: This is a special case of Longest path in a DAG: Construct a graph 1,...n where (i,j) is an edge if i < j and $x_i < x_j$.

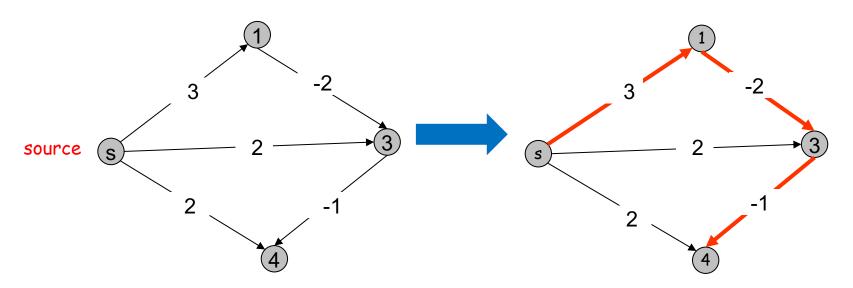
Shortest Paths with Negative Edge Weights

Shortest Paths with Neg Edge Weights

Given a weighted directed graph G = (V, E) and a source vertex s, where the weight of edge (u,v) is $c_{u,v}$

Goal: Find the shortest path from s to all vertices of G.

Recall that Dikjstra's Algorithm fails when weights are negative

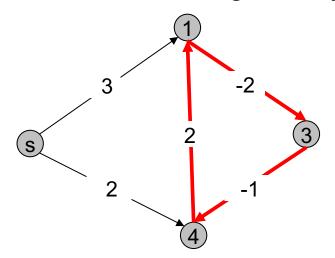


Impossibility on Graphs with Neg Cycles

Observation: No solution exists if G has a negative cycle.

This is because we can minimize the length by going over the cycle again and again.

So, suppose G does not have a negative cycle.



DP for Shortest Path

Def: Let OPT(v, i) be the length of the shortest s - v path with at most i edges.

Let us characterize OPT(v, i).

Case 1: OPT(v, i) path has less than i edges.

• Then, OPT(v,i) = OPT(v,i-1).

Case 2: OPT(v, i) path has exactly i edges.

- Let $s, v_1, v_2, \dots, v_{i-1}, v$ be the OPT(v, i) path with i edges.
- Then, s, v_1, \dots, v_{i-1} must be the shortest $s v_{i-1}$ path with at most i-1 edges. So,

$$OPT(v,i) = OPT(v_{i-1}, i-1) + c_{v_{i-1},v}$$

DP for Shortest Path

Def: Let OPT(v, i) be the length of the shortest s - v path with at most i edges.

$$OPT(v,i) = \begin{cases} 0 & \text{if } v = s \\ \infty & \text{if } v \neq s, i = 0 \\ \min(OPT(v,i-1), \min_{u:(u,v) \text{ an edge}} OPT(u,i-1) + c_{u,v}) \end{cases}$$

So, for every v, OPT(v,?) is the shortest path from s to v.

But how long do we have to run?

Since G has no negative cycle, it has at most n-1 edges. So, OPT(v, n-1) is the answer.

Bellman Ford Algorithm

```
for v=1 to n
    if v ≠ s then
        M[v,0]=∞

M[s,0]=0.

for i=1 to n-1
    for v=1 to n
        M[v,i]=M[v,i-1]
        for every edge (u,v)
            M[v,i]=min(M[v,i], M[u,i-1]+c<sub>u,v</sub>)
```

Running Time: O(nm)

Can we test if G has negative cycles?

Bellman Ford Algorithm

```
for v=1 to n
    if v ≠ s then
        M[v,0]=∞

M[s,0]=0.

for i=1 to n-1
    for v=1 to n
        M[v,i]=M[v,i-1]
        for every edge (u,v)
            M[v,i]=min(M[v,i], M[u,i-1]+c<sub>u,v</sub>)
```

Running Time: O(nm)

Can we test if G has negative cycles?

Yes, run for i=1...2n and see if the M[v,n-1] is different from M[v,2n]

DP Techniques Summary

Recipe:

- Follow the natural induction proof.
- Find out additional assumptions/variables/subproblems that you need to do the induction
- Strengthen the hypothesis and define w.r.t. new subproblems

Dynamic programming techniques.

- Whenever a problem is a special case of an NP-hard problem an ordering is important:
- Adding a new variable: knapsack.
- Dynamic programming over intervals: RNA secondary structure.

Top-down vs. bottom-up:

- Different people have different intuitions
- Bottom-up is useful to optimize the memory