CS/ECE 374 A: Algorithms & Models of Computation, Spring 2020

More DP: Edit Distance and Independent Sets in Trees

Lecture 15 March 10, 2020

Warm-up

Definition

A string is a palindrome if $w = w^R$. Examples: *I*, *RACECAR*, *MALAYALAM*, *DOOFFOOD*

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Problem: Given a string w find the *longest subsequence* of w that is a palindrome.

Example

MAHDYNAMICPROGRAMZLETMESHOWYOUTHEM has MHYMRORMYHM as a palindromic subsequence

Assume w is stored in an array A[1..n]

LPS(i, j): length of longest palindromic subsequence of A[i..j].

Recursive expression/code?

Part I

Edit Distance and Sequence Alignment

Spell Checking Problem

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What does nearness mean?

Question: Given two strings $x_1x_2...x_m$ and $y_1y_2...y_n$ what is a *distance* between them?

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Edit Distance: minimum number of "edits" to transform x into y.

Edit Distance

Definition

Edit distance between words X and Y is the number of letter insertions, letter deletions and letter substitutions required to obtain Y from X.

Example

The edit distance between FOOD and MONEY is at most 4:

 $\underline{F}OOD \rightarrow MO\underline{O}D \rightarrow MON\underline{D} \rightarrow MON\underline{D} \rightarrow MON\underline{E}\underline{D} \rightarrow MON\underline{E}\underline{Y}$

Edit Distance: Alternate View

Alignment

Place words one on top of the other, with gaps in the first word indicating insertions, and gaps in the second word indicating deletions.

F O O D A M O N E Y

Alignment

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34	2	ماح		うしょ
F	0	0		D
\mathbf{M}		Ν	\mathbf{E}	Y
71	72	33	۲	75

Formally, an alignment is a set M of pairs (i, j) $(x_i aligned with y_j)$ such that

• each index appears at most once, and

• there is no crossing: if $(i,j), (i',j') \in M$ and i < i' then j < j'.

In the above example, this is $M = \{(1, 1), (2, 2), (3, 3), (4, 5)\}.$

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Cost of an alignment is:

mismatched columns + # unmatched indices in both strings.

More Examples

X = GOT, Y = GOAT

X = ABCD, Y = EFGH

X = ABCD, Y = EBDH

Edit Distance Problem

Problem

Given two words, find the edit distance between them, i.e., an alignment of smallest cost.

Applications

- Spell-checkers and Dictionaries
- Onix diff
- S DNA sequence alignment ... but, we need a new metric

Similarity Metric

Definition

For two strings X and Y, the cost of alignment M is

- **(**Gap penalty] For each gap in the alignment, we incur a cost δ .
- (a) [Mismatch cost] For each pair p and q that have been matched in M, we incur cost α_{pq} ; typically $\alpha_{pp} = 0$.

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Edit distance is special case when $\delta = \alpha_{pq} = 1$.

An Example

Example

Alternative:

Or a really stupid solution (delete string, insert other string):

What is the edit distance between...

What is the minimum edit distance for the following two strings, if insertion/deletion/change of a single character cost 1 unit?



(A) 1
(B) 2
(C) 3
(D) 4
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Sequence Alignment

- Input Given two words **X** and **Y**, and gap penalty δ and mismatch costs α_{pq}
 - Goal Find alignment of minimum cost

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Question: $X = x_1 \dots x_i \dots x_m$ and $Y = y_1 \dots y_j \dots y_n$. Can I have $(i, n), (m, j) \in M$? NO

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Question: $X = x_1 \dots x_i \dots x_m$ and $Y = y_1 \dots y_j \dots y_n$. Can I have $(i, n), (m, j) \in M$?

Then what are the options for x_m and y_n ?

Edit distance: Alignment view Basic observation

Let
$$X = \gamma x_m$$
 and $Y = \beta y_n$
 γ, β : strings.

Consider last column of the optimal alignment of the two strings:

Observation

Prefixes must have optimal alignment!

$$M': M(m:n)$$
 $M'; s opt for (Y, B)$

Problem Structure

Observation

Let $X = x_1 x_2 \cdots x_m$ and $Y = y_1 y_2 \cdots y_n$. If (x_m, y_n) are not matched then either the x_m remains unmatched or y_n remains unmatched.

$$(y_{i}, x_{i}, y_{i}, y_{j})$$

 $OPT(i, j) = min \begin{cases} OTT(i-1, j-1) + \alpha_{2}a_{i}y_{j} \\ OPT(i-1, j) + 5 \\ OPT(i, j-1) + 5 \\ OPT(i, j-1) + 5 \end{cases}$
 $OPT(0, j) = j S \qquad \forall j$
 $OPT(i, 0) = i S \qquad \forall j$

Problem Structure

Observation

Let $X = x_1 x_2 \cdots x_m$ and $Y = y_1 y_2 \cdots y_n$. If (x_m, y_n) are not matched then either the x_m remains unmatched or y_n remains unmatched.

Case x_m and y_n are matched.
Pay mismatch cost α_{xmyn} plus cost of aligning strings x₁ ··· x_{m-1} and y₁ ··· y_{n-1}
Case x_m is unmatched.
Pay gap penalty plus cost of aligning x₁ ··· x_{m-1} and y₁ ··· y_n
Case y_n is unmatched.
Pay gap penalty plus cost of aligning x₁ ··· x_m and y₁ ··· y_{n-1}

Subproblems and Recurrence

Optimal Costs

Let Opt(i, j) be optimal cost of aligning $x_1 \cdots x_i$ and $y_1 \cdots y_j$. Then

$$Opt(i,j) = \min \begin{cases} \alpha_{x_iy_j} + Opt(i-1,j-1), \\ \delta + Opt(i-1,j), \\ \delta + Opt(i,j-1) \end{cases}$$

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$$Opt\left(\underbrace{x_{i},x_{i}}_{\mathcal{T}},\underbrace{y_{i},y_{j}}_{\mathcal{T}}\right) = \min \begin{cases} \alpha_{x_{i}y_{j}} + Opt(i-1,j-1), \\ \delta + Opt(i-1,j), \\ \delta + Opt(i,j-1) \end{cases}$$

Base Cases: $Opt(i, 0) = \delta \cdot i$ and $Opt(0, j) = \delta \cdot j$

Assume X is stored in array A[1..m] and Y is stored in B[1..n]

EDIST(A[1..m], B[1..n])If (m = 0) return $n\delta$ If (n = 0) return $m\delta$

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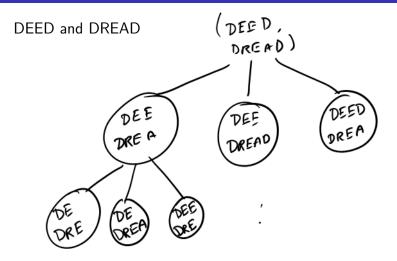
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```

Example



Memoization

Optimal Costs

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Matrix and DAG of Computation

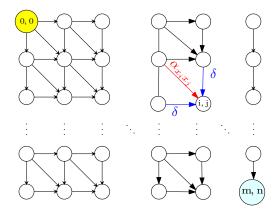


Figure: The iterative algorithm can compute values in row order.

```
 \begin{array}{ll} EDIST(A[1..m], B[1..n]) \\ int & M[0..m][0..n] \\ for \ i = 1 \ to \ m \ do \ M[i,0] = i\delta \\ for \ j = 1 \ to \ n \ do \ M[0,j] = j\delta \end{array}
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EDIST(A[1..m], B[1..n])

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for i = 1 to m do

for j = 1 to n do

M[i, j] = \min \begin{cases} \alpha_{A[i], B[j]} + M[i - 1, j - 1], \\ \delta + M[i - 1, j], \\ \delta + M[i, j - 1] \end{cases}
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Analysis

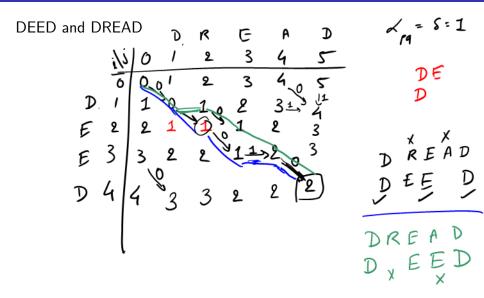
Running time is **O(mn)**.

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Analysis

Running time is O(mn). Space used is O(mn).

Example



Sequence Alignment in Practice

- Typically the DNA sequences that are aligned are about 10⁵ letters long!
- So about 10¹⁰ operations and 10¹⁰ bytes needed
- The killer is the 10GB storage
- Output State St

Optimizing Space

Recall

$$M(i,j) = \min \begin{cases} \alpha_{x_i y_j} + M(i-1,j-1), \\ \delta + M(i-1,j), \\ \delta + M(i,j-1) \end{cases}$$

- Entries in *j*th column only depend on (*j* 1)st column and earlier entries in *j*th column
- Only store the current column and the previous column reusing space; N(i, 0) stores M(i, j 1) and N(i, 1) stores M(i, j)

Computing in column order to save space

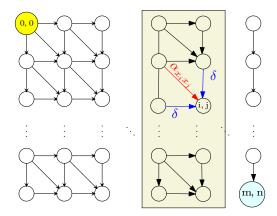


Figure: M(i, j) only depends on previous column values. Keep only two columns and compute in column order.

Space Efficient Algorithm

for all *i* do
$$N[i, 0] = i\delta$$

for $j = 1$ to *n* do
 $N[0, 1] = j\delta$ (* corresponds to $M(0, j)$ *)
for $i = 1$ to *m* do
 $N[i, 1] = \min \begin{cases} \alpha_{x_i y_j} + N[i - 1, 0] \\ \delta + N[i - 1, 1] \\ \delta + N[i, 0] \end{cases}$
for $i = 1$ to *m* do
Copy $N[i, 0] = N[i, 1]$

Analysis

Running time is O(mn) and space used is O(2m) = O(m)

Analyzing Space Efficiency

- From the m × n matrix M we can construct the actual alignment (exercise)
- Matrix N computes cost of optimal alignment but no way to construct the actual alignment
- Space efficient computation of alignment? More complicated algorithm see notes and Kleinberg-Tardos book.

Part II

Longest Common Subsequence Problem

LCS Problem

Definition

LCS between two strings X and Y is the length of longest common subsequence between X and Y.

Example

LCS between ABAZDC and BACBAD is

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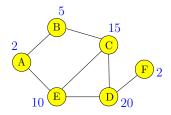
Derive a dynamic programming algorithm for the problem.

Part III

Maximum Weighted Independent Set in Trees

Maximum Weight Independent Set Problem

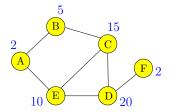
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- Goal Find maximum weight independent set in G



Maximum Weight Independent Set Problem

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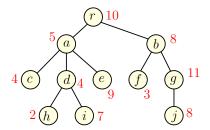


Maximum weight independent set in above graph: $\{B, D\}$

Maximum Weight Independent Set in a Tree

Input Tree T = (V, E) and weights $w(v) \ge 0$ for each $v \in V$

Goal Find maximum weight independent set in T



Maximum weight independent set in above tree: ??

For an arbitrary graph G:

- Number vertices as v_1, v_2, \ldots, v_n
- Solutions Find recursively optimum solutions without v_n (recurse on $G v_n$) and with v_n (recurse on $G v_n N(v_n)$ & include v_n).
- If graph G is arbitrary there was no good ordering that resulted in a small number of subproblems.

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What about a tree?

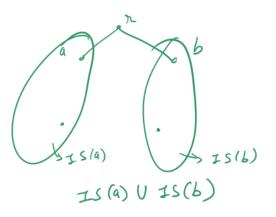
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What about a tree? Natural candidate for v_n is root r of T?

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Case $r \not\in \mathcal{O}$:



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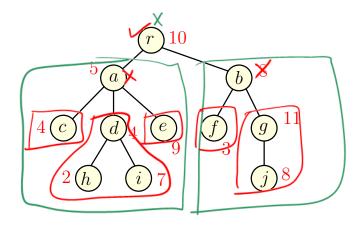
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How many of them? O(n)

Example



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Compute OPT(u) bottom up.

What is an ordering of nodes of a tree T to achieve above?

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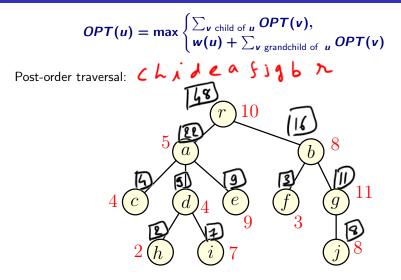
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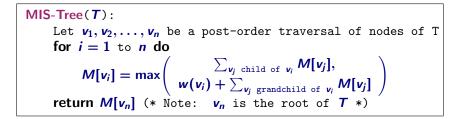
What is an ordering of nodes of a tree *T* to achieve above? Post-order traversal of a tree.

Example

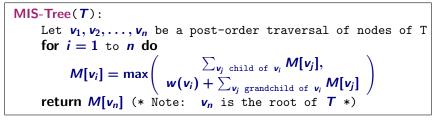


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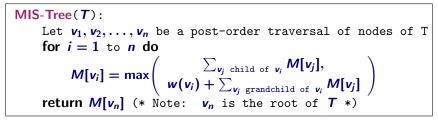


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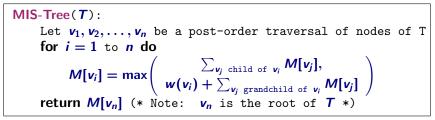
Space:

Declare M[1..n]. M[v] stores the max weighted independent set value for tree T(v).



Space: O(n) to store the value at each node of TRunning time:

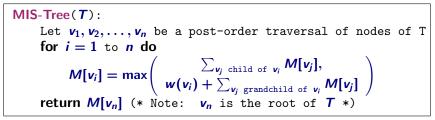
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Naive bound: O(n²) since each M[v_i] evaluation may take O(n) time and there are n evaluations.

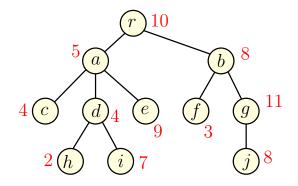
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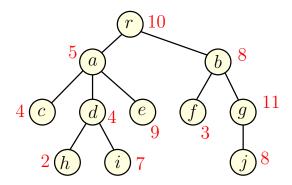
Space: O(n) to store the value at each node of TRunning time:

Naive bound: O(n²) since each M[v_i] evaluation may take O(n) time and there are n evaluations.

Example



Example



Better running time: A value M[d] is accessed only by a (parent) and r (grand parent) $\Rightarrow O(n)$.

Takeaway Points

- Oynamic programming is based on finding a recursive way to solve the problem. Need a recursion that generates a small number of subproblems.
- Given a recursive algorithm there is a natural DAG associated with the subproblems that are generated for given instance; this is the dependency graph. An iterative algorithm simply evaluates the subproblems in some topological sort of this DAG.
- The space required to evaluate the answer can be reduced in some cases by a careful examination of that dependency DAG of the subproblems and keeping only a subset of the DAG at any time.