



Chapter 3 Dynamic Programming

Algorithm Theory WS 2019/20

Fabian Kuhn

Dynamic Programming (DP)



$DP \approx Recursion + Memoization$

Recursion: Express problem *recursively* in terms of (a 'small' number of) *subproblems* (of the same kind)

Memoize: Store solutions for subproblems reuse the stored solutions if the same subproblems has to be solved again

Weighted interval scheduling: subproblems W(1), W(2), W(3), ...

runtime = #subproblems · time per subproblem

String Matching Problems



Edit distance:

- For two given strings A and B, efficiently compute the
 edit distance D(A, B) (# edit operations to transform A into B)
 as well as a minimum sequence of edit operations that
 transform A into B.
- Example: mathematician → multiplication:

Edit Distance



Given: Two strings $A=a_1a_2\dots a_m$ and $B=b_1b_2\dots b_n$

Goal: Determine the minimum number D(A, B) of edit operations required to transform A into B

Edit operations:

- a) Replace a character from string A by a character from B
- **b) Delete** a character from string A
- c) Insert a character from string B into A

```
ma-them--atician
multiplicatio--n
```

Edit Distance – Cost Model



- Cost for **replacing** character a by b: $c(a, b) \ge 0$
- Capture insert, delete by allowing $a = \varepsilon$ or $b = \varepsilon$:
 - Cost for **deleting** character $a: c(a, \varepsilon)$
 - Cost for **inserting** character $b: c(\varepsilon, b)$
- Triangle inequality:

$$c(a,c) \le c(a,b) + c(b,c)$$

→ each character is changed at most once!

• Unit cost model:
$$c(a,b) = \begin{cases} 1, & \text{if } a \neq b \\ 0, & \text{if } a = b \end{cases}$$

Recursive Structure



Optimal "alignment" of strings (unit cost model)

bbcadfagikccm and abbagflrgikacc:

Consists of optimal "alignments" of sub-strings, e.g.:

• Edit distance between $A_{1,m}=a_1\dots a_m$ and $B_{1,n}=b_1\dots b_n$:

$$D(A,B) = \min_{k,\ell} \{ D(A_{1,k}, B_{1,\ell}) + D(A_{k+1,m}, B_{\ell+1,n}) \}$$

Computation of the Edit Distance



Let
$$A_k\coloneqq a_1\dots a_k$$
 , $B_\ell\coloneqq b_1\dots b_\ell$, and
$$D_{k,\ell}\coloneqq D(A_k,B_\ell)$$



B _____

Computation of the Edit Distance



Three ways of ending an "alignment" between A_k and B_ℓ :

1. a_k is replaced by b_ℓ :

$$D_{k,\ell} = D_{k-1,\ell-1} + c(a_k, b_\ell)$$

2. a_k is deleted:

$$D_{k,\ell} = D_{k-1,\ell} + c(a_k, \varepsilon)$$

3. b_{ℓ} is inserted:

$$D_{k,\ell} = D_{k,\ell-1} + c(\varepsilon, b_{\ell})$$

Computing the Edit Distance

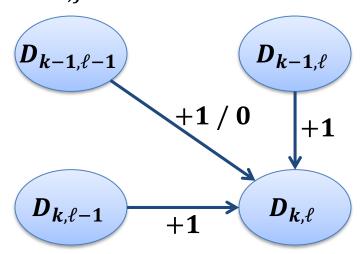


• Recurrence relation (for $k, \ell \geq 1$)

$$D_{k,\ell} = \min \begin{cases} D_{k-1,\ell-1} + c(a_k, b_\ell) \\ D_{k-1,\ell} + c(a_k, \varepsilon) \\ D_{k,\ell-1} + c(\varepsilon, b_\ell) \end{cases} = \min \begin{cases} D_{k-1,\ell-1} + 1 / 0 \\ D_{k-1,\ell} + 1 \\ D_{k,\ell-1} + 1 \end{cases}$$

unit cost model

• Need to compute $D_{i,j}$ for all $0 \le i \le k$, $0 \le j \le \ell$:



Recurrence Relation for the Edit Distance



Base cases:

$$D_{0,0} = D(\varepsilon, \varepsilon) = 0$$

$$D_{0,j} = D(\varepsilon, B_j) = D_{0,j-1} + c(\varepsilon, b_j)$$

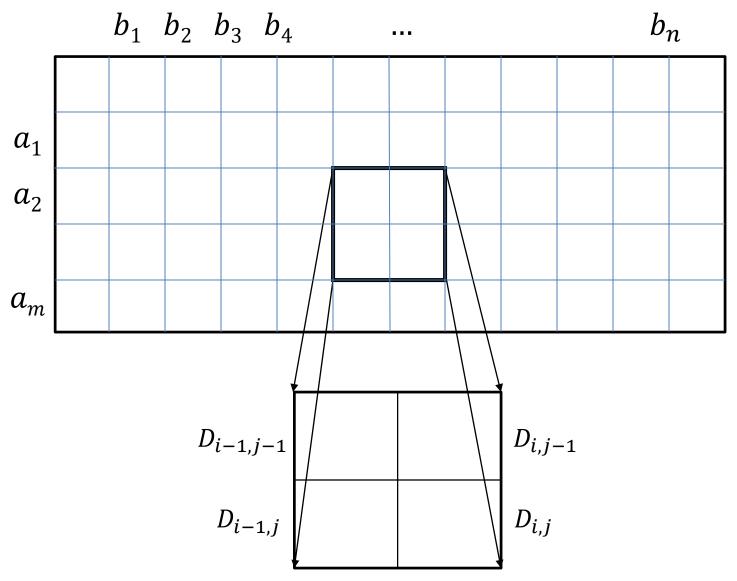
$$D_{i,0} = D(A_i, \varepsilon) = D_{i-1,0} + c(a_i, \varepsilon)$$

Recurrence relation:

$$egin{aligned} egin{aligned} oldsymbol{D_{k-1,\ell-1}} + oldsymbol{c}(oldsymbol{a_k,\ell-1}) + oldsymbol{c}(oldsymbol{a_k,\ell-1}) + oldsymbol{c}(oldsymbol{a_k,\ell-1}) + oldsymbol{c}(oldsymbol{e_k,\ell-1}) \end{aligned}$$

Order of solving the subproblems





Algorithm for Computing the Edit Distance



Algorithm *Edit-Distance*

Input: 2 strings
$$A = a_1 \dots a_m$$
 and $B = b_1 \dots b_n$

Output: matrix
$$D = (D_{ij})$$

$$1 D[0,0] := 0;$$

2 for
$$i := 1$$
 to m do $D[i, 0] := i$;

3 for
$$j := 1$$
 to n do $D[0, j] := j$;

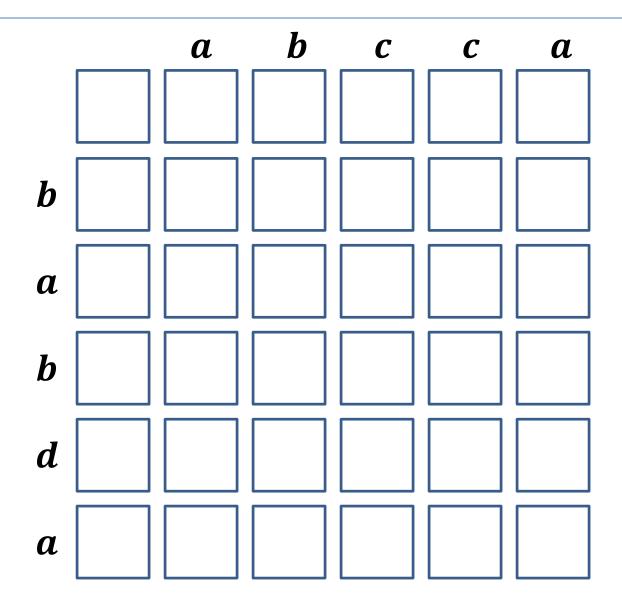
4 for
$$i := 1$$
 to m do

5 for
$$j := 1$$
 to n do

6
$$D[i,j] := \min \begin{cases} D[i-1,j] + 1 \\ D[i,j-1] + 1 \\ D[i-1,j-1] + c(a_i,b_i) \end{cases}$$
;

Example





Edit Operations



		a	<u>b</u>	<u> </u>	<u> </u>	a
	0	1	2	3	4	5
b	1	1	1	2	3	4
a	2	1	2	2	3	3
b	3	2	1	2	3	4
d	4	3	2	2	3	4
a	5	4	3	3	3	3

Computing the Edit Operations

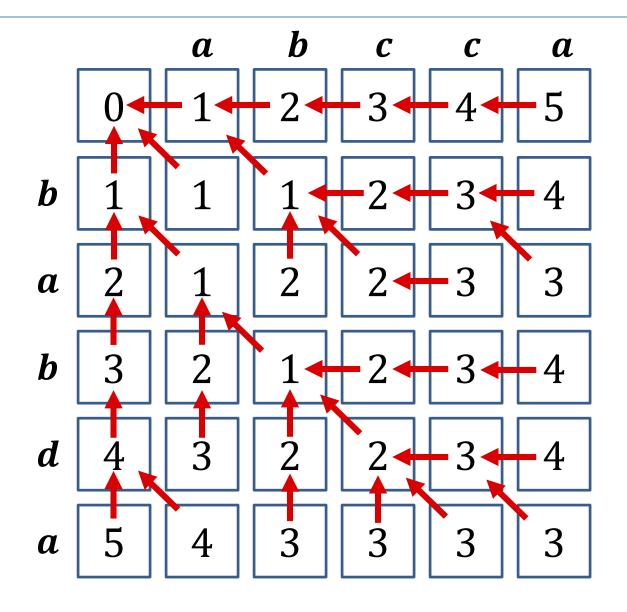


```
Algorithm Edit-Operations(i, j)
Input: matrix D (already computed)
Output: list of edit operations
1 if i = 0 and j = 0 then return empty list
2 if i \neq 0 and D[i,j] = D[i-1,j] + 1 then
     return Edit-Operations(i-1,j) \circ "delete a_i"
4 else if j \neq 0 and D[i,j] = D[i,j-1] + 1 then
     return Edit-Operations(i, j - 1) \circ ,, insert b_i"
5
  else //D[i,j] = D[i-1,j-1] + c(a_i,b_i)
     if a_i = b_i then return Edit-Operations (i-1, j-1)
     else return Edit-Operations(i-1, j-1) \circ "replace a_i by b_i"
8
```

Initial call: *Edit-Operations*(*m*,*n*)

Edit Operations





Edit Distance: Summary



• Edit distance between two strings of length m and n can be computed in O(mn) time.

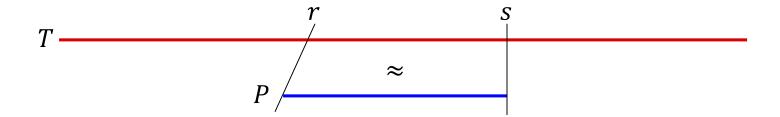
- Obtain the edit operations:
 - for each cell, store which rule(s) apply to fill the cell
 - track path backwards from cell (m, n)
 - can also be used to get all optimal "alignments"
- Unit cost model:
 - interesting special case
 - each edit operation costs 1



Given: strings $T = t_1 t_2 \dots t_n$ (text) and $P = p_1 p_2 \dots p_m$ (pattern).

Goal: Find an interval [r, s], $1 \le r \le s \le n$ such that the sub-string $T_{r,s} \coloneqq t_r \dots t_s$ is the one with highest similarity to the pattern P:

$$\underset{1 \le r \le s \le n}{\operatorname{arg min}} D(T_{r,s}, P)$$





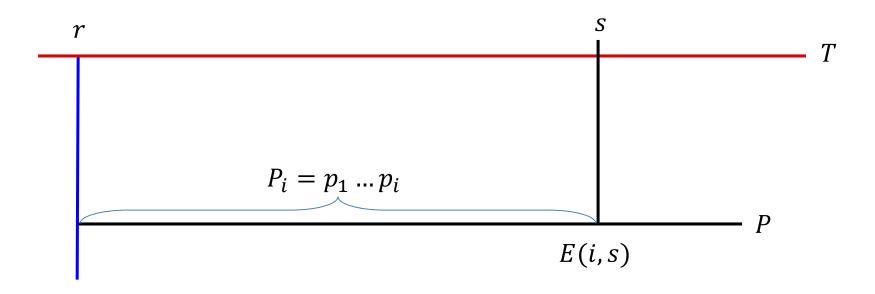
Naive Solution:

for all $1 \le r \le s \le n$ do compute $D(T_{r,s}, P)$ choose the minimum



A related problem:

• For each position s in the text and each position i in the pattern compute the minimum edit distance E(i,s) between $P_i = p_1 \dots p_i$ and any substring $T_{r,s}$ of T that ends at position s.





Three ways of ending optimal alignment between T_b and P_i :

1. t_b is replaced by p_i :

$$E_{b,i} = E_{b-1,i-1} + c(t_b, p_i)$$

2. t_b is deleted:

$$E_{b,i} = E_{b-1,i} + c(t_b, \varepsilon)$$

3. p_i is inserted:

$$E_{b,i} = E_{b,i-1} + c(\varepsilon, p_i)$$



Recurrence relation (unit cost model):

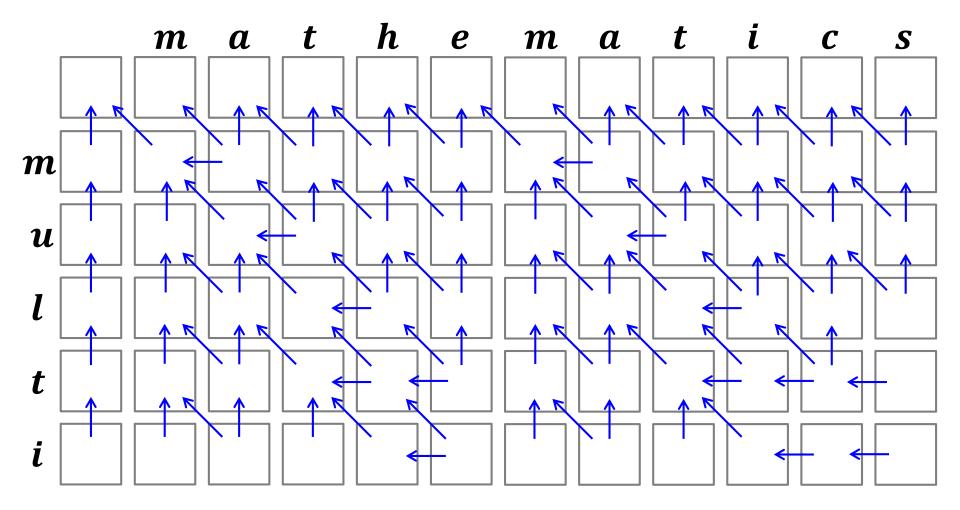
$$E_{b,i} = \min egin{cases} E_{b-1,i-1} + 1 / 0 \ E_{b-1,i} + 1 \ E_{b,i-1} + 1 \end{pmatrix}$$

Base cases:

$$E_{0,0} = 0$$
 $E_{0,i} = i$
 $E_{i,0} = 0$

Example







- Optimal matching consists of optimal sub-matchings
- Optimal matching can be computed in O(mn) time
- Get matching(s):
 - Start from minimum entry/entries in bottom row
 - Follow path(s) to top row
- Algorithm to compute E(b,i) identical to edit distance algorithm, except for the initialization of E(b,0)

Related Problems in Bioinformatics



Sequence Alignment:

Find optimal alignment of two given DNA, RNA, or amino acid sequences.

Global vs. Local Alignment:

- Global alignment: find optimal alignment of 2 sequences
- Local alignment: find optimal alignment of sequence 1
 (patter) with sub-sequence of sequence 2 (text)