
Longest Common Subsequence (LCS)

Chapter 15

p 390

Longest Common Subsequence

- Problem: Let $x_1x_2\dots x_m$ and $y_1y_2\dots y_n$ be two sequences over some alphabet.
 - We assume they are strings of characters
- Find a longest common subsequence (LCS) of $x_1x_2\dots x_m$ and $y_1y_2\dots y_n$

Many other string operations have the same basic structure.

Example

- $x_1x_2x_3x_4x_5x_6x_7x_8 = b a c b f f c b$
- $y_1y_2y_3y_4y_5y_6y_7y_8y_9 = d a b e a b f b c$
- Longest Common Subsequence is:

A subsequence is a set of characters that appear in left- to-right order, *but not necessarily consecutively*.

Dynamic Programming

- LCS can be solved using dynamic programming
 1. Characterize the structure of an optimal solution
 2. Recursively define the value of an optimal solution
 3. Compute the value of an optimal solution bottom-up
 4. Construct an optimal solution from the computed information

- Optimal substructure:

If $z = z_1z_2\dots z_p$ is a LCS of $x_1x_2\dots x_m$ and $y_1y_2\dots y_n$, then

At least one of these must hold

- $x_m = y_n$, and $z_1z_2\dots z_{p-1}$ is an LCS of $x_1x_2\dots x_{m-1}$ and $y_1y_2\dots y_{n-1}$,
- $x_m \neq y_n$, and $z_1z_2\dots z_p$ is an LCS of $x_1x_2\dots x_{m-1}$ and $y_1y_2\dots y_n$,
- $x_m \neq y_n$, and $z_1z_2\dots z_p$ is an LCS of $x_1x_2\dots x_m$ and $y_1y_2\dots y_{n-1}$.

Step 2: Recursive Solution

Let c_{ij} = length of LCS of $x_1x_2\dots x_i$ and $y = y_1y_2\dots y_j$.

$$c[i,j] = \begin{cases} 0 & \text{if } i = 0 \text{ or } j = 0, \\ 1 + c[i-1,j-1] & \text{if } x_i = y_j, \\ \max(c[i-1,j], c[i,j-1]) & \text{if } x_i \neq y_j. \end{cases}$$

$$b[i,j] = \begin{cases} \text{"↖"} & \text{if } x_i = y_j, \\ \text{"↑"} & \text{if } x_i \neq y_j \text{ and } c[i-1,j] \geq c[i,j-1], \\ \text{"←"} & \text{if } x_i \neq y_j \text{ and } c[i-1,j] < c[i,j-1]. \end{cases}$$

We compute the $c[i,j]$ and $b[i,j]$ in order of increasing $i+j$, or alternatively in order of increasing i , and for a fixed i , in order of increasing j .

LCS-LENGTH(X, Y, m, n)

Step 3&4

let $b[1..m, 1..n]$ and $c[0..m, 0..n]$ be new tables

for $i = 1$ **to** m

$c[i, 0] = 0$

for $j = 0$ **to** n

$c[0, j] = 0$

for $i = 1$ **to** m

for $j = 1$ **to** n

if $x_i == y_j$

$c[i, j] = c[i - 1, j - 1] + 1$

$b[i, j] = \text{“}\nearrow\text{”}$

else if $c[i - 1, j] \geq c[i, j - 1]$

$c[i, j] = c[i - 1, j]$

$b[i, j] = \text{“}\uparrow\text{”}$

else $c[i, j] = c[i, j - 1]$

$b[i, j] = \text{“}\leftarrow\text{”}$

return c and b

Example

b,c matrices combined

i \ j	0	1 d	2 a	3 b	4 e	5 a	6 b	7 f	8 b	9 c
0	0	0	0	0	0	0	0	0	0	0
1 b	0									
2 a	0									
3 c	0									
4 b	0									
5 f	0									
6 f	0									
7 c	0									
8 b	0									


```
PRINT-LCS( $b, X, i, j$ )  
  if  $i == 0$  or  $j == 0$   
    return  
  if  $b[i, j] == \text{“}\nearrow\text{”}$   
    PRINT-LCS( $b, X, i - 1, j - 1$ )  
    print  $x_i$   
  elseif  $b[i, j] == \text{“}\uparrow\text{”}$   
    PRINT-LCS( $b, X, i - 1, j$ )  
  else PRINT-LCS( $b, X, i, j - 1$ )
```

String Similarity

- Edit Distance
 - Levenshtein
 - minimize changes

- Sequence Alignment
 - Needleman-Wunsch
 - maximize similarity
 - by giving weights to types of differences

<http://xlinux.nist.gov/dads/HTML/Levenshtein.html>

Edit Distance

- How many insertions, deletions, replacements will transform one string into another?
 - Damerau-Levenshtein includes transpositions as a special case the → teh

$$\text{lev}_{a,b}(i, j) = \begin{cases} \max(i, j) & \text{if } \min(i, j) = 0, \\ \min \begin{cases} \text{lev}_{a,b}(i-1, j) + 1 \\ \text{lev}_{a,b}(i, j-1) + 1 \\ \text{lev}_{a,b}(i-1, j-1) + [a_i \neq b_j] \end{cases} & \text{otherwise.} \end{cases}$$

http://en.wikipedia.org/wiki/Levenshtein_distance

Levenshtein

Edit Distance Matrix

ATCGTT vs AGTTAC

		A	G	T	T	A	C	
	0	1	2	3	4	5	6	j
A	1							
T	2							
C	3							
G	4							
T	5							
T	6							

i

Backtracking

deletion

UP

insertion

LEFT

match/mismatch

DIAG

Sequence Alignment

- Similarity based on gaps and mismatches.
- Alignment
 - matched pairs from both strings
 - no crossings
- Generalized form of Levenshtein
 - additional parameters:
 - gap penalty, δ
 - mismatch cost ($\alpha_{x,y}$; $\alpha_{x,x} = 0$)



Kleinberg, Tardos, Algorithm Design, Pearson Addison Wesley, 2006, p 278

<http://www.aw-bc.com/info/kleinberg/>

Recurrence

- Two strings $x_1 \dots x_m$ and $y_1 \dots y_n$
- In an optimal alignment, M , at least one of the following is true:
 - (x_m, y_n) is in M
 - x_m is not matched
 - y_n is not matched

Recurrence

- So, for i and $j > 0$
- $\text{opt}(i,j) = \min[\alpha_{x_i,y_j} + \text{opt}(i-1,j-1),$
 $\delta + \text{opt}(i-1,j), \quad // x_i \text{ is not matched}$
 $\delta + \text{opt}(i,j-1)] \quad // y_j \text{ is not matched}$
- (x_i, y_j) is in an optimal alignment M for this subproblem iff the minimum achieved is achieved by the first of these three values.

Sequence Alignment Graph

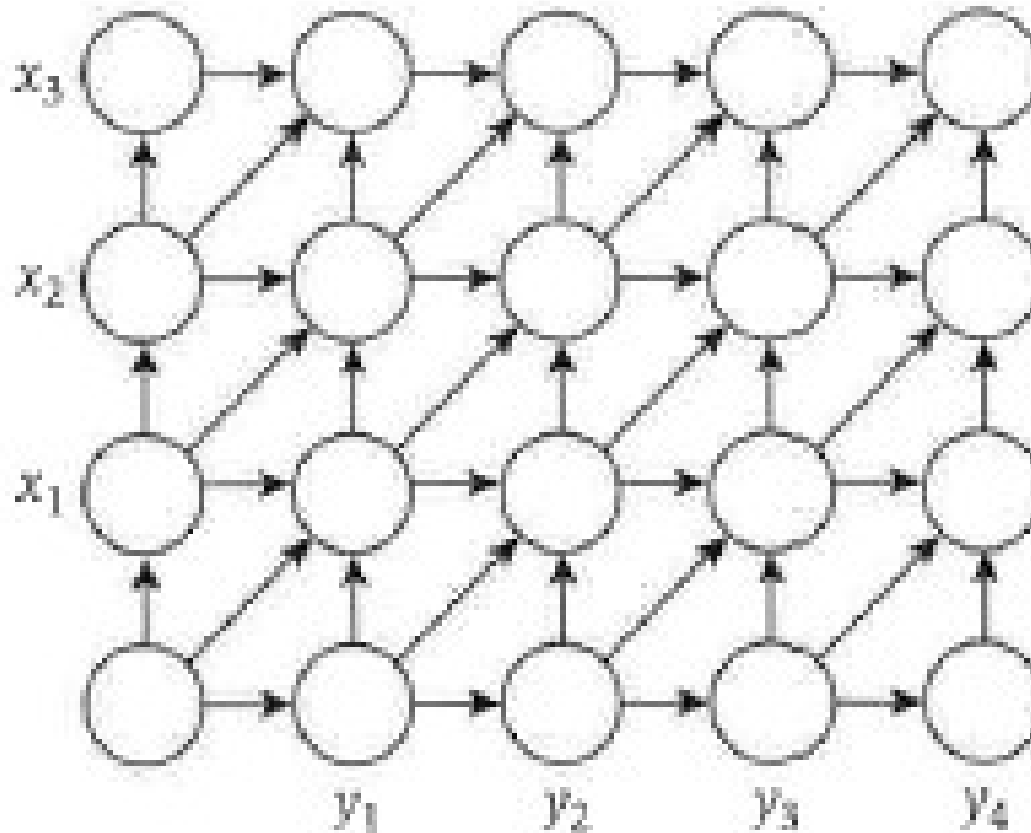


Figure 6.17 A graph-based picture of sequence alignment.

Kleinberg, Tardos, p 283

Recover Alignment

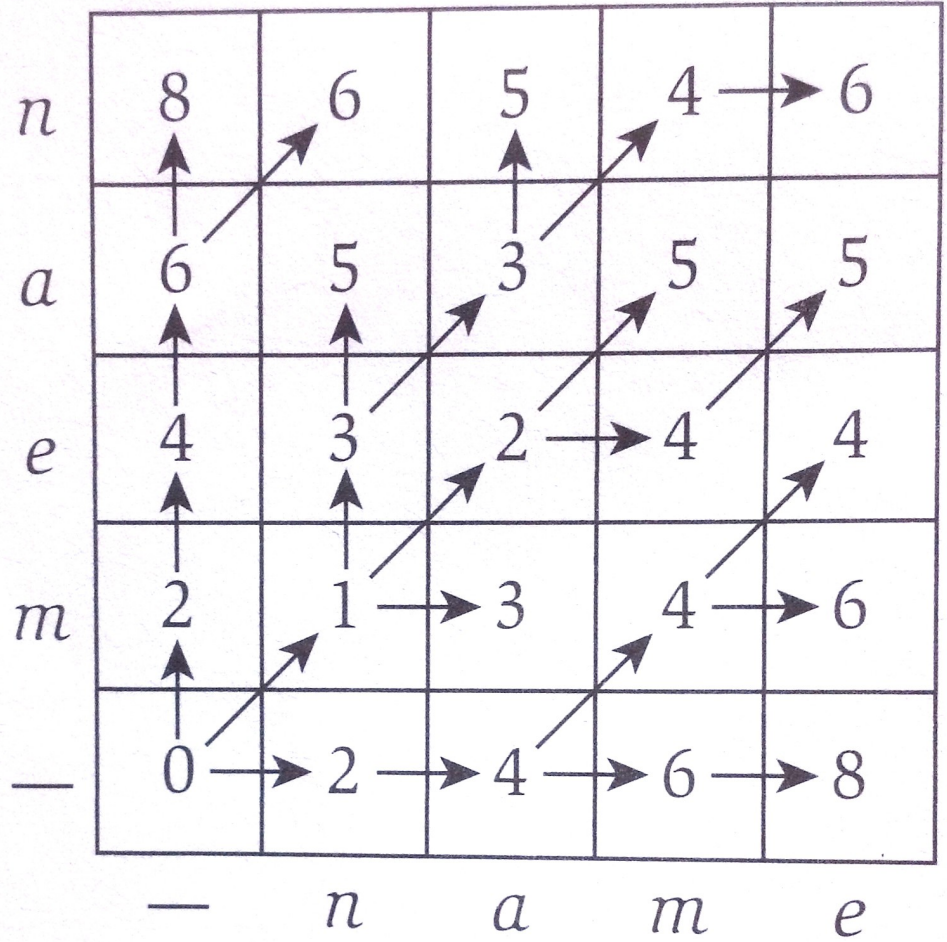


Figure 6.18 The OPT values for the problem of aligning the words *mean* to *name*.

Sequence Alignment (space efficient)

Kleinberg, Tardos, p 285

- Hirschberg - 1975

- value: need the current and previous column

Space-Efficient-Alignment(X, Y)

Array $B[0 \dots m, 0 \dots 1]$

Initialize $B[i, 0] = i\delta$ for each i (just as in column 0 of A)

For $j = 1, \dots, n$

$B[0, 1] = j\delta$ (since this corresponds to entry $A[0, j]$)

For $i = 1, \dots, m$

$$B[i, 1] = \min[\alpha_{x_i y_j} + B[i - 1, 0], \\ \delta + B[i - 1, 1], \delta + B[i, 0]]$$

Endfor

Move column 1 of B to column 0 to make room for next iteration:

Update $B[i, 0] = B[i, 1]$ for each i

— Endfor

Actual Alignment

- How do we recover the actual alignment?
 - We need the entire matrix?

Algorithm

Divide-and-Conquer-Alignment(X, Y)

Let m be the number of symbols in X

Let n be the number of symbols in Y

If $m \leq 2$ or $n \leq 2$ then

 Compute optimal alignment using Alignment(X, Y)

 Call Space-Efficient-Alignment($X, Y[1:n/2]$)

 Call Backward-Space-Efficient-Alignment($X, Y[n/2 + 1:n]$)

 Let q be the index minimizing $f(q, n/2) + g(q, n/2)$

 Add $(q, n/2)$ to global list P

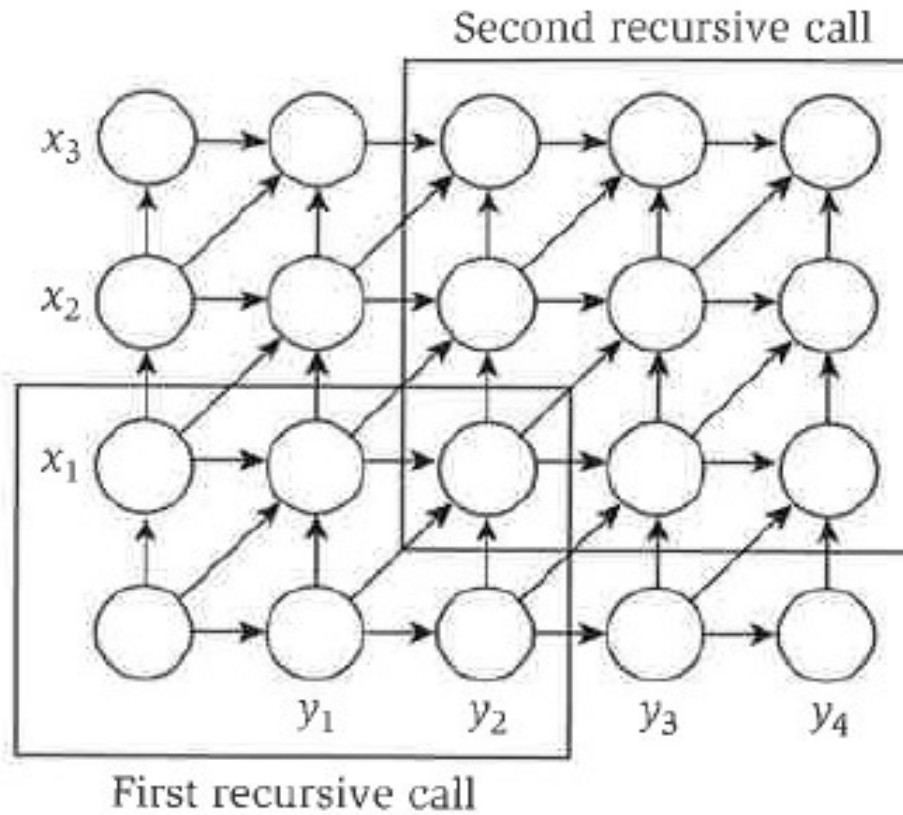
 Divide-and-Conquer-Alignment($X[1:q], Y[1:n/2]$)

 Divide-and-Conquer-Alignment($X[q + 1:n], Y[n/2 + 1:n]$)

Return P

Kleinberg, Tardos, p 288

6.7 Sequence Alignment in Linear Space via Divide and Conquer



Kleinberg, Tardos, p 289

String Matching / Searching

- Naive

Not Dynamic Programming because there are not subproblems.

- **Horspool**¹

- Boyer-Moore¹

But precompute a table to help you solve the problem.

- Rabin Karp²

- **Knuth Morris Pratt**²

¹ Levitin, Introduction to The Design and Analysis of Algorithms, 3rd edition, Pearson Addison Wesley, p 259

² CLRS, p 990 &1002

Naive

```
int naiveSearch(string, pattern)
{
    retVal = -1;
    mismatch = true;

    for( i=0; i < string.length - pattern.length &&
        true == mismatch ; i++)
    {
        mismatch = false;
        for( j =0; j<pattern.length && !mismatch ; j++)
        {
            if( string[i] != pattern[j] )
            {
                mismatch = true;
            }
        }
        if ( !mismatch)
        {
            retVal = i;
        }
    }
    return retVal;
}
```


Horspool

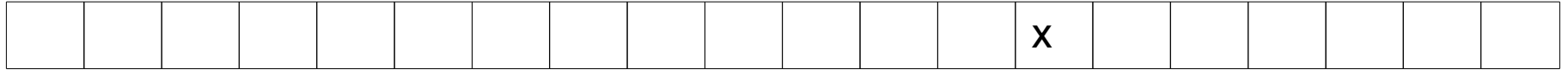
- match the pattern right to left
- on mismatch, shift the pattern smartly
 - by 1+ character
- Preprocess string to determine shifting
 - build a table for shifts for each valid character

Example

need a better string!

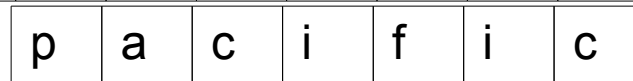
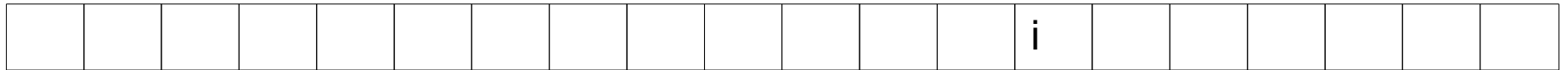
String

← character comparisons

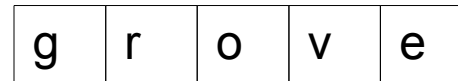
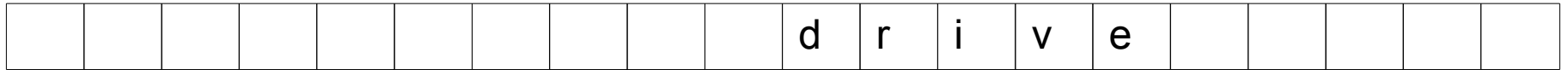


→ pattern movement

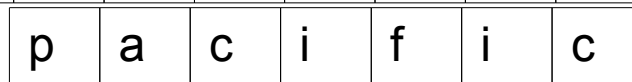
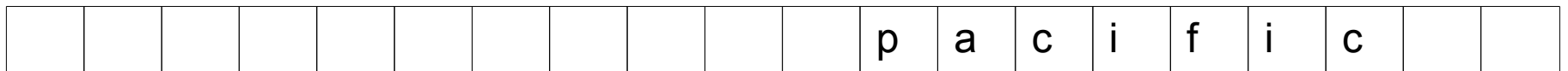
String



String



String



Shifting

- $t(c) =$

the pattern's length, m , if c is not among the first $m-1$ characters of the pattern

the distance from the rightmost c among the first $m-1$ characters of the pattern to its last character, otherwise

p	a	c	i	f	i	c
---	---	---	---	---	---	---

a	b	c	f	i	...	p	...	x	y	z
								7		

```

Horspool(P[0..m-1], T[0..n-1])
  T ← ComputeShifts(P)           ‘ Generate table of shifts
  i ← m - 1                       ‘ Position of pattern’s right end
  while i ≤ n - 1
    k ← 0                          ‘ Number of matched characters
    while k ≤ m - 1 and P[m-1-k] = T[i-k]
      k++
    if k = m
      return “Match at “ + (i - m + 1)
    else
      i ← i + T[i]
  return -1                       ‘ No match found

```

¹ Levitin, Introduction to The Design and Analysis of Algorithms, 3rd edition, Pearson Addison Wesley, p 262