# Week 04: Alignment

 ${\sf FanFly}$ 

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#### **Fdit Distance**

**Edit distance** is a way to quantify the "distance" between two strings.

- The distance is calculated by counting the minimum number of operations needed to transform one string into the other.
- Different definitions of an edit distance use different sets of string operations.

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## Edit Distance (cont.)

Suppose that we want to find the edit distance between weather and whether, and we only allow insertion and deletion of a character in a string.

- We can transform weather into whether by inserting an h and deleting an a, and thus the edit distance between them is 2.
- Note that if we remove the different parts from both strings, we will get their longest common subsequence, i.e., wether.
- Conversely, if we can find their longest common subsequence, we can calculate their edit distance.

## Longest Common Subsequence

Now we introduce the longest common subsequence problem.

#### The Longest Common Subsequence Problem

- Input: Two sequences A and B of lengths n and m, respectively.
- Output: A longest common subsequence of A and B.

We can find a longest common subsequence of two sequences by finding an alignment between them.

Note that there may be more than one longest common subsequences.

```
mea--surement -measur-ement -amus--ement am--u-sement
```

#### Recurrence Relation

Let us look at some examples.

Let  $A = A' \cdot x$  and  $B = B' \cdot y$ , where x and y are the last elements of A and B, respectively.

• If x = y, then we have

$$LCS(A, B) = LCS(A', B') \cdot x.$$

Otherwise, we have

$$LCS(A, B) = LCS(A, B')$$
 or  $LCS(A, B) = LCS(A', B)$ .

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#### Recursive Method

Thus, it can be solved recursively!

```
def lcs(A, B, n, m):
if n == 0 or m == 0:
   return A[:0]
elif A[n - 1] == B[m - 1]:
    return lcs(A, B, n - 1, m - 1) + A[n - 1]
else:
    P = lcs(A, B, n - 1, m)
    Q = lcs(A, B, n, m - 1)
    if len(P) > len(Q):
       return P
    else:
        return 0
```

## Time Complexity of Recursive Method

What is its time complexity? We have

$$T(n, m) = \begin{cases} O(1), & \text{if } n = 0 \text{ or } m = 0 \\ T(n, m - 1) + T(n - 1, m) + O(1), & \text{otherwise.} \end{cases}$$

Thus, we can conclude that

$$T(n,m) = \Theta\left(\frac{(n+m)!}{n! \cdot m!}\right),$$

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which is really inefficient.

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# Dynamic Programming

Why the recursive method is so inefficient?

- It solves the same subproblem over and over again.
- If the algorithm can remember the solutions to the solved subproblems, then it can become more efficient.

	m	a	s	k
i	-	-	-	_
d	_	-	-	-
е	-	-	-	-
a	-	a	a	a
s	-	a	as	as

• This improvement is called **dynamic programming**.

# Dynamic Programming (cont.)

With dynamic programming, we can solve the longest common subsequence problem efficiently.

- Assume that the length of longest common subsequence is  $\ell$ .
- The content of each entry can be computed in  $\Theta(\ell)$  time.
- Thus, we can solve the problem in  $O(nm\ell)$  time.

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### **Improvement**

In fact, the time complexity can be improved to O(nm) if we only memoize the length of the longest common subsequence.

	m	a	s	k
i	0	0	0	0
d	0	0	0	0
е	0	0	0	0
a	0	1	1	1
s	0	1	2	2

### Exercise #1

Let A and B be sequences of lengths n and m, respectively.

If the length of longest common subsequence of A and B is  $\ell$ , what is the edit distance between A and B?

Assume that only insertion and deletion are allowed to perform.

#### Solution

The edit distance between A and B is  $(n - \ell) + (m - \ell) = n + m - 2\ell$ .

### Exercise #2

Let A be a sequence of length n that does not have repeating elements. Hoe many nonempty subsequences does A have?

#### Solution

It has  $2^n - 1$  nonempty subsequences.

## Exercise #3

Let A and B be sequences and let f be a scoring function. Suppose that

$$f(x,y) = \begin{cases} p, & \text{if } x = y \\ q, & \text{otherwise.} \end{cases}$$

For any alignment, we can compute its score according to the scoring function.

# Exercise #3 (cont.)

For example, the alignment below has score 3p + 6q.

Please determine the value of p and q such that the maximum score of alignment of A and B is equal to the length of their longest common subsequence.

#### Solution

This property is satisfied when p=1 and q=0.