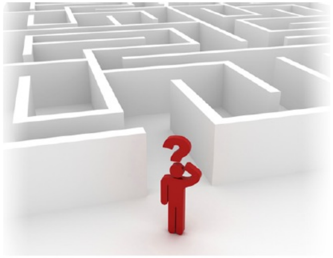


Algorithms: Design and Analysis, Part II

Introduction

Motivating Application: Sequence Alignment

Motivation

Sequence alignment: Fundamental problem in computational genomics.

Input: Two strings over the alphabet $\{A,C,G,T\}$. [Portions of one or more genomes]

Problem: Figure out how similar the two strings are.

Example:

```
A  G  G  G  C  T
A  G  G  C  A
```

Example applications:

- Extrapolate function of genome substrings.
- Similar genomes can reflect proximity in evolutionary tree.

Measuring Similarity

Question: What does similar mean?

Intuition: AGGGCT, AGGCA are similar because they can be "nicely aligned".

Idea: Measure similarity via quality of "best" alignment.

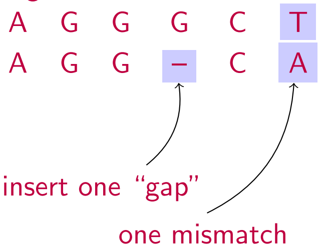
Assumption: Have experimentally determined *penalties* for gaps and the possible matches.

Example:

A G G G C T

A G G C A

Alignment:



Problem Statement

Input: 2 strings over {A,C,G,T}.

- Penalty $pen_{gap} \geq 0$ for each gap.
- Penalty $pen_{AT} \geq 0$ for mismatching A and T.
- etc.

Output: Alignment of the strings that minimizes the total penalty
$\Rightarrow$ Called the Needleman-Wunsch score [1970].

Small NW score $\approx$ Similar Strings

Algorithms are Fundamental

Note: This measure of genome similarity would be useless without an efficient algorithm to find the best alignment.

Brute-force search: Try all possible alignments, remember the best one.

Question: Suppose each string has length 500. Roughly how many possible alignments are there?

A) # of students in this class $\approx 10^4 - 10^5$

B) # of people on earth $\approx 10^9 - 10^{10}$

C) # of atoms in known universe $\approx 10^{80}$

D) More than any of the above $\geq 2^{500} \geq 10^{125}$

Point: Need a fast, clever algorithm.

Solution: Straightforward dynamic programming.