Needleman-Wunsch
n=3

Motivation

- Multiple sequence alignment instead of pairwise
- is an extension of Needleman-Wunsch with n = 2
- Gives optimal alignment, but there can be multiple ones
- Use of dynamic programming

- Input: Three sequences a, b and c
- |a| = m; |b| = n; |c| = o
- Data structure: A three dimensional matrix
- Runtime and space complexity: $O(m*n*o) \sim O(n^3)$

Recursion

$$D_{i,j,k} = \begin{cases} D_{i-1,j-1,k-1} + w(a_i, b_j, c_k) \\ D_{i-1,j-1,k} + w(a_i, b_j, -) \\ D_{i-1,j,k-1} + w(a_i, -, c_k) \\ D_{i,j-1,k-1} + w(-, b_j, c_k) \\ D_{i-1,j,k} + w(a_i, -, -) \\ D_{i,j-1,k} + w(-, b_j, -) \\ D_{i,j,k-1} + w(-, -c_k) \end{cases}$$

Problems

- What is for sequences n > 3?

- Runtime get exponential! —> $O(n^n)$

List of references

- Lecture “Multiples Sequence Alignment - Basics” Bioinformatics I, Prof. Backofen

  URL: http://www.bioinf.uni-freiburg.de//Lehre/Courses/2014_SS/V_Bioinformatik_1/multiple-alignment.pdf, visited: 13/11/2014