Sequence Alignment Algorithms

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Why learn about alignment algorithms?



- All publicly available alignment programs do the same thing
 - Sequence alignment using amino acids substitution matrices and affine gap penalties
- This is fast but not optimal
 - Protein alignment is done much more accurate using sequence profiles and position specific gap penalties (price for gaps depends on the structure)
- Must implement your own alignment algorithm to do this





- What you have been told is not entirely true :-)
 - Alignment algorithms are more complex
- The true sequence alignment algorithm story
 - The slow algorithm (O3)
 - The fast algorithm (O2)

Sequence alignment The old Story

Pairwise alignment: the solution



CBS

Alignment depicted as path in matrix





Alignment depicted as path in matrix





Meaning of point in matrix: all residues up to this point have been aligned (but there are many different possible paths).

Position labeled "x": TC aligned with TC



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Any given point in matrix can only be reached from three possible positions (you cannot "align backwards").

=> Best scoring alignment ending in any given point in the matrix can be found by choosing the highest scoring of the three possibilities.

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score(x,y-1) - gap-penalty

score(x,y) = max

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score(x,y) = max { score(x,y-1) - gap-penalty
score(x,y) = max { score(x-1,y-1) + substitution-score(x,y)

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score(x,y) = max $\begin{cases} score(x,y-1) - gap-penalty \\ score(x-1,y-1) + substitution-score(x,y) \\ score(x-1,y) - gap-penalty \end{cases}$





Any given point in matrix can only be reached from three possible positions (you cannot "align backwards").

=> Best scoring alignment ending in any given point in the matrix can be found by choosing the highest scoring of the three possibilities.

Each new score is found by choosing the maximum of three possibilities. For each square in matrix: keep track of where best score came from.

Fill in scores one row at a time, starting in upper left corner of matrix, ending in lower right corner.

score(x,y) = max $\begin{cases} score(x,y-1) - gap-penalty \\ score(x-1,y-1) + substitution-score(x,y) \\ score(x-1,y) - gap-penalty \end{cases}$



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1 -1

1

Т



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But in reality is a little more complex





Any given point in matrix can only be reached from three possible positions (you cannot "align backwards").

=> Best scoring alignment ending in any given point in the matrix can be found by choosing the highest scoring of the three possibilities.



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Blosum 50 matrix

А -3 -3 R 0 0 -3 3 -3 C -3 Е G н -4 -3 2 5 -3 3 3 0 -3 -3 -3 к Μ 0 -1 2 3 1 0 n Ρ -2 -3 -3 10 -3 S -3 0 т W Y

How does it work? (The slow way O3)

V

L

L

Ρ



TEREO



And now you!

How does it work? Fill out the D matrix



S CBS

0 (for local alignment)

- Check all positions in (green) row and column to check score for gap extension.
- \cdot CPU intensive (O3)

V

20

11

2

0

V

L

L

Ρ

How does it work (The slow way O3)



0 (for local alignment)



to check score for gap extension.

 \cdot CPU intensive (O3)

And now the fast algorithm (O2)



$$D_{m,n} = Max \begin{cases} D_{m+1,n+1} + d(m,n), \text{match} \\ P_{m,n}, \text{insertion in database} \\ Q_{m,n}, \text{insertion in query} \\ 0 \end{cases}$$

Database (m)



Affine gap penalties $w_k = w_1 + u \cdot (k-1)$

Open a gap Extending a gap

And now the fast algorithm (O2)

 $P_{m,n}$

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And now the true algorithm (cont.)



$$D_{m,n} = Max \begin{cases} D_{m+1,n+1} + d(m,n), \text{match} \\ P_{m,n}, \text{insertion in database} \\ Q_{m,n}, \text{insertion in query} \\ 0 \end{cases}$$

Query (n)

$$P_{m,n} = Max \Big[D_{m+1,n} + w_1, P_{m+1,n} + u \Big]$$
$$Q_{m,n} = Max \Big[D_{m,n+1} + w_1, Q_{m,n+1} + u \Big]$$



$$P_{m,n} = Max \Big[D_{m+1,n} + w_1, P_{m+1,n} + u \Big]$$

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$$P_{m,n} = Max[5-5, -1-1] = 0$$

W₁ = -5 U = -1

How does it work (D,Q,P, and E-matrices)



<u>P works horizontally</u>

$$P_{m,n} = Max \Big[D_{m+1,n} + w_1, P_{m+1,n} + u \Big]$$

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$$P_{m,n} = Max[5-5, -1-1] = 0$$

W₁ = -5 U = -1









How does it work. Eij-matrix. (Keeping track on the path)

$$D_{m,n} = Max \begin{cases} D_{m+1,n+1} + d(m,n), \text{match} & \mathbf{1} \\ D_{m+1,n} + w_1, \text{ insertion (opening) in database} & \mathbf{4} \\ P_{m+1,n} + u, \text{ insertion (extenton) in database} & \mathbf{5} \\ D_{m,n+1} + w_1, \text{ insertion (opening) in query} & \mathbf{2} \\ Q_{m,n+1} + u, \text{ insertion (opening) in query} & \mathbf{2} \\ 0 & \mathbf{Database (m)} \\ eij = 1 \text{ match} & eij = 2 \text{ gap-opening database} & eij = 4 \text{ gap-opening query} & \mathbf{0} \\ eij = 5 \text{ gap-extension query} &$$

How does it work (D,Q,P, and E-matrices)

How does it work (D,Q,P, and E-matrices)

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VLILP VL-LP

And the alignment. Gap extensions

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0 G

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15 -5 -1 = 9?

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5 -5 -1 = 9?

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VLIALP VL--LP 15 -5 -1 = 9? *** 5 -5 -1 = 9?

And now you!

eij = 1 match eij = 2 gap-opening database eij = 3 gap-extension database eij = 4 gap-opening query eij = 5 gap-extension query D is highest Q is highest, gap open Q is highest, gap extension P is highest, gap open P is highest, gap extension

Blosum50 scoring matrix

| | A | R | N | D | С | Q | E | G | н | I | L | K | м | F | P | S | т | W | Y | v |
|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| A | 5 | -2 | -1 | -2 | -1 | -1 | -1 | 0 | -2 | -1 | -2 | -1 | -1 | -3 | -1 | 1 | 0 | -3 | -2 | 0 |
| R | -2 | 7 | -1 | -2 | -4 | 1 | 0 | -3 | 0 | -4 | -3 | 3 | -2 | -3 | -3 | -1 | -1 | -3 | -1 | -3 |
| N | -1 | -1 | 7 | 2 | -2 | 0 | 0 | 0 | 1 | -3 | -4 | 0 | -2 | -4 | -2 | 1 | 0 | -4 | -2 | -3 |
| D | -2 | -2 | 2 | 8 | -4 | 0 | 2 | -1 | -1 | -4 | -4 | -1 | -4 | -5 | -1 | 0 | -1 | -5 | -3 | -4 |
| С | -1 | -4 | -2 | -4 | 13 | -3 | -3 | -3 | -3 | -2 | -2 | -3 | -2 | -2 | -4 | -1 | -1 | -5 | -3 | -1 |
| Q | -1 | 1 | 0 | 0 | -3 | 7 | 2 | -2 | 1 | -3 | -2 | 2 | 0 | -4 | -1 | 0 | -1 | -1 | -1 | -3 |
| E | -1 | 0 | 0 | 2 | -3 | 2 | 6 | -3 | 0 | -4 | -3 | 1 | -2 | -3 | -1 | -1 | -1 | -3 | -2 | -3 |
| G | 0 | -3 | 0 | -1 | -3 | -2 | -3 | 8 | -2 | -4 | -4 | -2 | -3 | -4 | -2 | 0 | -2 | -3 | -3 | -4 |
| н | -2 | 0 | 1 | -1 | -3 | 1 | 0 | -2 | 10 | -4 | -3 | 0 | -1 | -1 | -2 | -1 | -2 | -3 | 2 | -4 |
| I | -1 | -4 | -3 | -4 | -2 | -3 | -4 | -4 | -4 | 5 | 2 | -3 | 2 | 0 | -3 | -3 | -1 | -3 | -1 | 4 |
| L | -2 | -3 | -4 | -4 | -2 | -2 | -3 | -4 | -3 | 2 | 5 | -3 | 3 | 1 | -4 | -3 | -1 | -2 | -1 | 1 |
| ĸ | -1 | 3 | 0 | -1 | -3 | 2 | 1 | -2 | 0 | -3 | -3 | 6 | -2 | -4 | -1 | 0 | -1 | -3 | -2 | -3 |
| м | -1 | -2 | -2 | -4 | -2 | 0 | -2 | -3 | -1 | 2 | 3 | -2 | 7 | 0 | -3 | -2 | -1 | -1 | 0 | 1 |
| F | -3 | -3 | -4 | -5 | -2 | -4 | -3 | -4 | -1 | 0 | 1 | -4 | 0 | 8 | -4 | -3 | -2 | 1 | 4 | -1 |
| P | -1 | -3 | -2 | -1 | -4 | -1 | -1 | -2 | -2 | -3 | -4 | -1 | -3 | -4 | 10 | -1 | -1 | -4 | -3 | -3 |
| s | 1 | -1 | 1 | 0 | -1 | 0 | -1 | 0 | -1 | -3 | -3 | 0 | -2 | -3 | -1 | 5 | 2 | -4 | -2 | -2 |
| т | 0 | -1 | 0 | -1 | -1 | -1 | -1 | -2 | -2 | -1 | -1 | -1 | -1 | -2 | -1 | 2 | 5 | -3 | -2 | 0 |
| W | -3 | -3 | -4 | -5 | -5 | -1 | -3 | -3 | -3 | -3 | -2 | -3 | -1 | 1 | -4 | -4 | -3 | 15 | 2 | -3 |
| Y | -2 | -1 | -2 | -3 | -3 | -1 | -2 | -3 | 2 | -1 | -1 | -2 | 0 | 4 | -3 | -2 | -2 | 2 | 8 | -1 |
| v | 0 | -3 | -3 | -4 | -1 | -3 | -3 | -4 | -4 | 4 | 1 | -3 | 1 | -1 | -3 | -2 | 0 | -3 | -1 | 5 |

W₁ = -2 U = -1

m

The alignment

Query sequence alignment Database sequence alignment

Summary

- Alignment is more complicated than what you have been told.
- Simple algorithmic tricks allow for alignment in O2 time
- More heuristics to improve speed
 - Limit gap length
 - Look for high scoring regions

