

Traceback: Initialize Problem

The default scoring scheme.

Default sequences to align.

Match :

Mismatch :

Gap :

Sequence A:

Sequence B:

Note:
Due to the screen resolution of computer monitors, this program automatically rearranges the input so that the longer sequence is always assigned to Sequence A and the shorter sequence is always assigned to Sequence B. This rearrangement of input is only specific to this program and is not necessarily part of the Needleman-Wunch algorithm.

Scores can be altered.

New sequences can also be tried.

Match :

Mismatch :

Gap :

Sequence A:

Sequence B:

Note:
Due to the screen resolution of computer monitors, this program automatically rearranges the input so that the longer sequence is always assigned to Sequence A and the shorter sequence is always assigned to Sequence B. This rearrangement of input is only specific to this program and is not necessarily part of the Needleman-Wunch algorithm.

Hit Submit

Creates Traceback/Alignment Problem

Match :

Mismatch :

Gap :

Sequence A:

Sequence B:

		Sequence A							
		A	G	T	G	T	A	G	
Sequence B	A	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
	G	0 0	0 0	0 0	0 0	0 0	0 0	0 0	
	A	0 0	2 0	-2 0	-2 0	-2 0	-2 0	2 0	-2 0
	G	0 0	0 2	2 2	2 2	2 2	2 2	2 2	2 2
	A	0 0	-2 2	4 2	0 2	4 2	0 2	0 2	4 2
	T	0 0	0 2	2 4	4 4	4 4	4 4	4 4	4 4
	G	0 0	2 2	0 4	2 4	2 4	2 4	6 4	2 4
A	0 0	0 2	2 4	4 4	4 4	4 4	4 6	6 6	
T	0 0	-2 2	0 4	6 4	2 4	6 4	2 6	4 6	
A	0 0	0 2	2 4	4 6	6 6	6 6	6 6	6 6	
A	0 0	2 2	0 4	2 6	4 6	4 6	8 6	4 6	
G	0 0	0 2	2 4	4 6	6 6	6 6	6 8	8 8	
G	0 0	-2 2	4 4	2 6	8 6	4 6	4 8	10 8	
G	0 0	0 2	2 4	4 6	6 8	8 8	8 8	8 10	

Sequence A:

Sequence B:

Traceback: Solve Traceback

		Sequence A						
		A	G	T	G	T	A	G
	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
A	0 0	2 0	-2 0	-2 0	-2 0	-2 0	2 0	-2 0
	0 0	0 2	2 2	2 2	2 2	2 2	2 2	2 2
G	0 0	-2 2	4 2	0 2	4 2	0 2	0 2	4 2
	0 0	0 2	2 4	4 4	4 4	4 4	4 4	4 4
A	0 0	2 2	0 4	2 4	2 4	2 4	6 4	2 4
	0 0	0 2	2 4	4 4	4 4	4 4	4 6	6 6
T	0 0	-2 2	0 4	6 4	2 4	6 4	2 6	4 6
	0 0	0 2	2 4	4 6	6 6	6 6	6 6	6 6
A	0 0	2 2	0 4	2 6	4 6	4 6	8 6	4 6
	0 0	0 2	2 4	4 6	6 6	6 6	6 8	8 8
G	0 0	-2 2	4 4	2 6	8 6	4 6	4 8	10 8
	0 0	0 2	2 4	4 6	6 8	8 8	8 8	8 10

Start bottom right.

		Sequence A						
		A	G	T	G	T	A	G
	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
A	0 0	2 0	-2 0	-2 0	-2 0	-2 0	2 0	-2 0
	0 0	0 2	2 2	2 2	2 2	2 2	2 2	2 2
G	0 0	-2 2	4 2	0 2	4 2	0 2	0 2	4 2
	0 0	0 2	2 4	4 4	4 4	4 4	4 4	4 4
A	0 0	2 2	0 4	2 4	2 4	2 4	6 4	2 4
	0 0	0 2	2 4	4 4	4 4	4 4	4 6	6 6
T	0 0	-2 2	0 4	6 4	2 4	6 4	2 6	4 6
	0 0	0 2	2 4	4 6	6 6	6 6	6 6	6 6
A	0 0	2 2	0 4	2 6	4 6	4 6	8 6	4 6
	0 0	0 2	2 4	4 6	6 6	6 6	6 8	8 8
G	0 0	-2 2	4 4	2 6	8 6	4 6	4 8	10 8
	0 0	0 2	2 4	4 6	6 8	8 8	8 8	8 10

Yellow=Correct Path
Red=Incorrect Path

6 4	2 6	4 6
6 6	6 6	6 6
4 6	8 6	4 6
6 6	6 8	8 8
4 6	4 8	10 8
8 8	8 8	8 10

Path Determined by High Score!

		Sequence A						
		A	G	T	G	T	A	G
	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
A	0 0	2 0	-2 0	-2 0	-2 0	-2 0	2 0	-2 0
	0 0	0 2	2 2	2 2	2 2	2 2	2 2	2 2
G	0 0	-2 2	4 2	0 2	4 2	0 2	0 2	4 2
	0 0	0 2	2 4	4 4	4 4	4 4	4 4	4 4
A	0 0	2 2	0 4	2 4	2 4	2 4	6 4	2 4
	0 0	0 2	2 4	4 4	4 4	4 4	4 6	6 6
T	0 0	-2 2	0 4	6 4	2 4	6 4	2 6	4 6
	0 0	0 2	2 4	4 6	6 6	6 6	6 6	6 6
A	0 0	2 2	0 4	2 6	4 6	4 6	8 6	4 6
	0 0	0 2	2 4	4 6	6 6	6 6	6 8	8 8
G	0 0	-2 2	4 4	2 6	8 6	4 6	4 8	10 8
	0 0	0 2	2 4	4 6	6 8	8 8	8 8	8 10

Finish Traceback to top right corner by touching squares.

Second choice is horizontal gap over vertical.

What do you do when highest values are equal? Which way do you go?

When scores are equal for alternative paths, the algorithm chooses **the DIAGONAL first**.

Second choice is always the HORIZONTAL path.

0 2	4 2	0 2
4 4	4 4	4 4
2 4	2 4	2 4
4 4	4 4	4 4
6 4	2 4	6 4
4 6	6 6	6 6

Tracing back from this cell, there are two equally good choices with highest values in both top corner (diagonal) and bottom left (horizontal). **Diagonal will be chosen first** over either horizontal or vertical. (This is standard practice.)

Traceback: Align Sequences

		Sequence A							
		A	G	T	G	T	A	G	
Sequence B	A	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
	G	0 0	-2 2	4 2	0 2	4 2	0 2	0 2	4 2
	A	0 0	2 2	0 4	2 4	2 4	2 4	6 4	2 4
	T	0 0	-2 2	0 4	6 4	2 4	6 4	2 6	4 6
	A	0 0	2 2	0 4	2 6	4 6	4 6	8 6	4 6
	T	0 0	-2 2	4 4	2 6	8 6	4 6	4 8	10 8
	A	0 0	0 2	2 4	4 6	6 6	6 6	6 8	8 8
	G	0 0	-2 2	4 4	2 6	8 6	4 6	4 8	10 8

Enter Alignment based on traceback.

Sequence A:

Sequence B:

Click button to evaluate

Let's Try Again

		Sequence A					
		A	G	T	G	T	
Sequence B	A	0 0	0 0	0 0	0 0	0 0	0 0
	G	0 0	-2 2	4 2	0 2	4 2	0 2
	A	0 0	2 2	0 4	2 4	2 4	2 4
	T	0 0	-2 2	0 4	6 4	2 4	6 4
	A	0 0	2 2	0 4	2 6	4 6	4 6
	T	0 0	-2 2	4 4	2 6	8 6	4 6
	A	0 0	0 2	2 4	4 6	6 6	6 6
	G	0 0	-2 2	4 4	2 6	8 6	4 6

Answers

kelleybioinfo.org/algorithms/dynamicprogrammin...

A. Correct Sequence: AG-TGTAG
Your Answer: AG-TGTAG

B. Correct Sequence: AGA--TAG
Your Answer: AGA-T-AG

Misaligned answers are in red.

Results: Oops! One error.

Sequence A:

Sequence B:

Results: That's better!

		Sequence A					
		A	G	T	G	T	
Sequence B	A	0 0	0 0	0 0	0 0	0 0	0 0
	G	0 0	-2 2	4 2	0 2	4 2	0 2
	A	0 0	2 2	0 4	2 4	2 4	2 4
	T	0 0	-2 2	0 4	6 4	2 4	6 4
	A	0 0	2 2	0 4	2 6	4 6	4 6
	T	0 0	-2 2	4 4	2 6	8 6	4 6
	A	0 0	0 2	2 4	4 6	6 6	6 6
	G	0 0	-2 2	4 4	2 6	8 6	4 6

Answers

kelleybioinfo.org/algorithms/dynamicprogrammin...

A. Correct Sequence: AG-TGTAG
Your Answer: AG-TGTAG

B. Correct Sequence: AGA--TAG
Your Answer: AGA--TAG

Misaligned answers are in red.

Results: That's better!

Sequence A:

Sequence B:

Score Table: DNA

Click the Calculate Scores to start.

TRACEBACK

Match :

Mismatch :

Gap :

Sequence A:

Sequence B:

Evaluate Reset Concept Mode

Calculate Scores

This will bring you to the Score Table.

SCORE TABLE

Scoring scheme and sequences are randomly generated.

Match :

Mismatch :

Gap :

Sequence A:

Sequence B:

Try Another Traceback

		Sequence A					
		A	T	G	G	G	T
Sequence B	A	0 0	0 0	0 0	0 0	0 0	0 0
	T	0 0	-2 2	4 2	0 2	0 2	0 2
	G	0 0	-2 2	0 4	6 4	6 4	2 4
	G	0 0	-2 2	0 4	6 4	8 6	4 6
	G	0 0	-2 2	0 4	6 6	8 8	8 8
	G	0 0	-2 2	0 4	6 6	8 8	10 8

Generate new problem

Return to traceback

Fill in values based on Match, Mismatch, Gap Values. (See Background information on Needleman-Wunsch.)

Bottom left value is the highest score of all three other values in the cell.

Green=Correct
Red=Incorrect

