



# What is the problem?

We want to compare two DNA sequences and find the best way to align one to the other. This is easy when only a few bases differ:

```

ACGGTAGGGATATACCTACGAGCTCACAT
| | | | | | | | | | | | | | | | | |
ACGGTAGGCATTTACCTACGAGGTCACAT
    
```

Here only three bases are different and the sequences are identical at 26 positions.

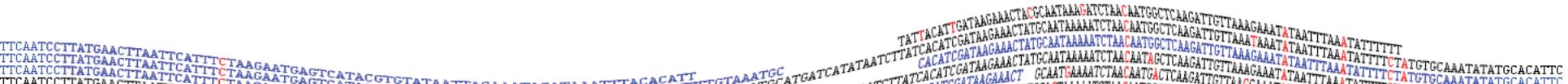


# What is the problem?

We want to compare two DNA sequences and find the best way to align one to the other. When the two sequences differ more the optimal alignment is not easy to find:

```
ACGGTAGGGATATACCTACGAGCTCACAT  
|| || |      |||      |      || |  
ACCGTCGACCCGTACGACTCTGACGTCCT
```

In this comparison 11 bases are identical and 18 are different.



# What is the problem?

We want to compare two DNA sequences and find the best way to align one to the other. When the two sequences differ more the optimal alignment is not easy to find:

```
ACGGTAGGGATATACCTACGAG - CTCACAT - - -  
|| || |   | | |||| | || || |  
ACCGTCG - - - - ACCCGTACGACTCTGACGTCCT
```

Another possibility is to add a gap in each sequence and thereby increase the number of identities to 17.



# What is the problem?

We want to compare two DNA sequences and find the best way to align one to the other. When the two sequences differ more the optimal alignment is not easy to find:

```
ACGGTAGGGATATACC - TAGGAGCTC - - ACAT
|| || |      |  || ||| | |||  || |
ACCGTCG - - - - AC - CCGTACGA - CTCTGACGTCCT
```

Yet another possibility is to add five gaps in both sequences and thereby increase the number of identities to 19.





# How many different alignments exist?

The number of possible alignments has been given in a paper by Angela Torres, Alberto Cabada and Juan J. Nieto: DNA Sequence 2003, 1-4.

Let  $f(n,m)$  be the number of alignments of two sequences of length  $n$  and  $m$ , then we have the following recursive formula:

$$f(n,m) = f(n-1,m) + f(n,m-1) + f(n-1,m-1)$$

since there are three possibilities to elongate an alignment from  $n-1$  and  $m-1$  to length  $n$  and  $m$ .



# What is the number of different possible alignments?

Starting with  $f(0,m) = f(n,0) = f(0,0) = 1$  for all  $n,m > 0$

We obtain:

$$f(1,1) = 3$$

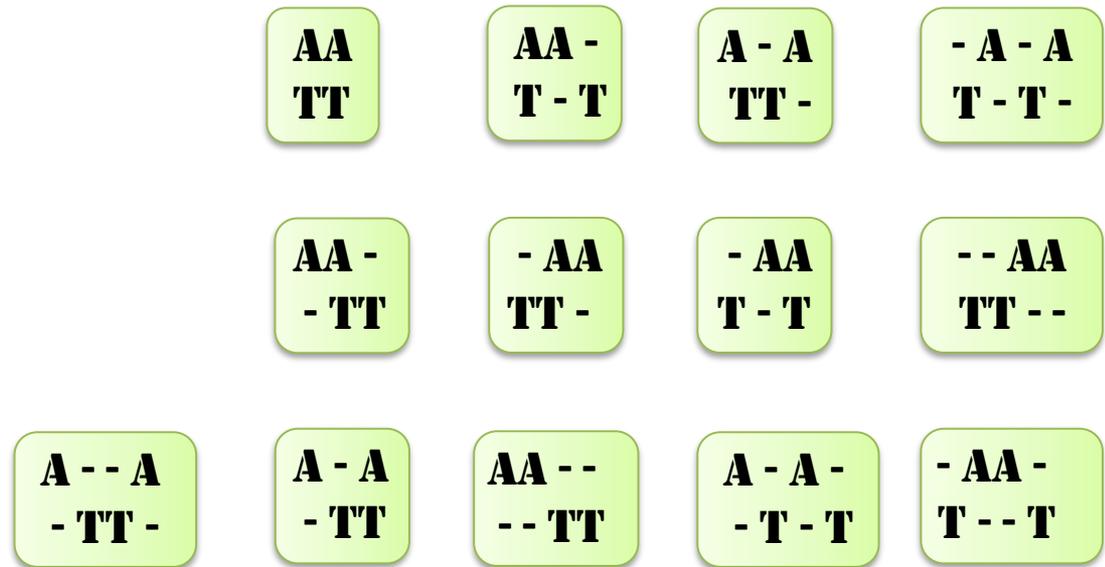
$$f(2,2) = 13$$

$$f(3,3) = 63$$

...

$$f(10,10) = 8097453$$

$$f(100,100) = 2 * 10^{74}$$



All 13 alignments of two sequences of length 2



# How to measure the quality of an alignment?

Two sequences of realistic length can have a multitude of different possible alignments which differ in quality.

We have to find a measure (a metric) for the quality of an alignment.

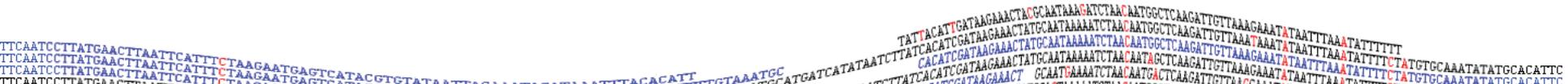
And we have to find method to search through all possible alignments to be able to choose the optimal one.



# How to measure the quality of an alignment?

**ACGGTAGGGATATACC - TACGAGCTC - - ACAT - - -**  
**|| || | | || |||| | || |**  
**ACCGTCG - - - - AC - CCGTACGA - CTCTGACGTCCT**

Count the number of identical/similar bases:  
19



# How to measure the quality of an alignment?

```

ACGGTAGGGATATACC - TACGAGCTC -- ACAT ---
  || || |      |  || |||| | || |  || |
ACCGTCG ---- AC - CCGTACGA - CTCTGACGTCCT
  
```

Count the number of different bases or mismatches: 4

G/C = 1x

A/C = 1x

T/A = 1x

A/G = 1x

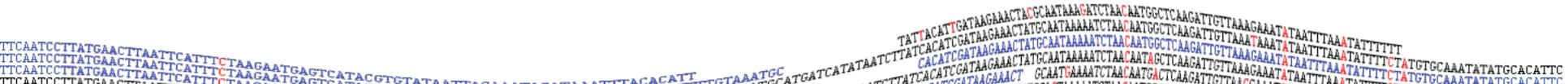


# How to measure the quality of an alignment?

**ACGGTAGGGATATACC - TACGAGCTC - - ACAT - - -**  
**|| || | | || |||| | || |**  
**ACCGTCG - - - - AC - CCGTACGA - CTCTGACGTCCT**

Count the number of gaps:

6

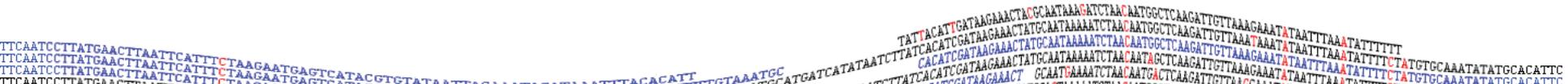


# How to measure the quality of an alignment?

**ACGGTAGGGATATACC - TACGAGCTC - - ACAT - - -**  
**|| || | | || |||| | || |**  
**ACCGTCG - - - - AC - CCGTACGA - CTCTGACGTCCT**

Count the gaps of different sizes:

- 3x 1 base
- 1x 2 bases
- 1x 4 bases
- 1x 3 bases end gap





# Similarity matrix CDNAFULL for DNA with ambiguous bases

Base in sequence 1

Base in sequence 2

	A	T	G	C	S	W	R	Y	K	M	B	V	H	D	N	U
A	5	-4	-4	-4	-4	1	1	-4	-4	1	-4	-1	-1	-1	-2	-4
T	-4	5	-4	-4	-4	1	-4	1	1	-4	-1	-4	-1	-1	-2	5
G	-4	-4	5	-4	1	-4	1	-4	1	-4	-1	-1	-4	-1	-2	-4
C	-4	-4	-4	5	1	-4	-4	1	-4	1	-1	-1	-1	-4	-2	-4
S	-4	-4	1	1	-1	-4	-2	-2	-2	-2	-1	-1	-3	-3	-1	-4
W	1	1	-4	-4	-4	-1	-2	-2	-2	-2	-3	-3	-1	-1	-1	1
R	1	-4	1	-4	-2	-2	-1	-4	-2	-2	-3	-1	-3	-1	-1	-4
Y	-4	1	-4	1	-2	-2	-4	-1	-2	-2	-1	-3	-1	-3	-1	1
K	-4	1	1	-4	-2	-2	-2	-2	-1	-4	-1	-3	-3	-1	-1	1
M	1	-4	-4	1	-2	-2	-2	-2	-4	-1	-3	-1	-1	-3	-1	-4
B	-4	-1	-1	-1	-1	-3	-3	-1	-1	-3	-1	-2	-2	-2	-1	-1
V	-1	-4	-1	-1	-1	-3	-1	-3	-3	-1	-2	-1	-2	-2	-1	-4
H	-1	-1	-4	-1	-3	-1	-3	-1	-3	1	-2	-2	-1	-2	-1	-1
D	-1	-1	-1	-4	-3	-1	-1	-3	-1	-3	-2	-2	-2	1	-1	-1
N	-2	-2	-2	-2	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-2
U	-4	5	-4	-4	-4	1	-4	1	1	-4	-1	-4	-1	-1	-2	5

TTCAATCCTTATGAACTTAATTCAATTCCTAAGAA  
 TTCAATCCTTATGAACTTAATTCAATTCCTAAGAA  
 TTCAATCCTTATGAACTTAATTCAATTCCTAAGAA

AAATATTTTT  
 AAATATTTTTCTATGTGCAATATATGCACATTC  
 AAATATTTTTCTATGTGCAATATATGCACATTC  
 AAATATTTTTCTATGTGCAATATATGCACATTC

# Similarity matrix CDNAFULL for DNA with ambiguous bases

Base in sequence 1

Base in sequence 2

	A	T	G	C	S	W	R	Y	K	M	B	V	H	D	N	U
A	5	-4	-4	-4	-4	1	1	-4	-4	1	-4	-1	-1	-1	-2	-4
T	-4	5	-4	-4	-4	1	-4	1	1	-4	-1	-4	-1	-1	-2	5
G	-4	-4	5	-4	-4	-4	1	-4	1	-4	-1	-1	-4	-1	-2	-4
C	-4	-4	-4	5	1	-4	-4	1	-4	1	-1	-1	-1	-4	-2	-4
S	-4	-4	-4	1	5	-4	-4	1	-4	1	-1	-1	-3	-3	-1	-4
W	1	1	1	1	1	5	1	1	1	1	1	1	1	1	1	1
R	1	1	1	1	1	1	5	1	1	1	1	1	1	1	1	1
Y	-4	1	-4	1	-2	-2	-4	-1	-2	-2	-1	-3	-1	-3	-1	1
K	-4	1	1	-4	-2	-2	-2	-2	-1	-4	-1	-3	-3	-1	-1	1
M	1	-4	-4	1	-2	-2	-2	-2	-4	-1	-3	-1	-1	-3	-1	-4
B	-4	-1	-1	-1	-1	-3	-3	-1	-1	-3	-1	-2	-2	-2	-1	-1
V	-1	-4	-1	-1	-1	-3	-1	-3	-3	-1	-2	-1	-2	-2	-1	-4
H	-1	-1	-4	-1	-3	-1	-3	-1	-3	1	-2	-2	-1	-2	-1	-1
D	-1	-1	-1	-4	-3	-1	-1	-3	-1	-3	-2	-2	-2	1	-1	-1
N	-2	-2	-2	-2	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-2
U	-4	5	-4	-4	-4	1	-4	1	1	-4	-1	-4	-1	-1	-2	5

This matrix was created by

Todd Lowe 12/10/92

Uses ambiguous nucleotide codes, probabilities rounded to nearest integer.

Lowest score = -4, Highest score = 5

TTCAATCCTTATGAACTTAATTCATTCTAAGAA  
TTCAATCCTTATGAACTTAATTCATTCTAAGAA  
TTCAATCCTTATGAACTTAATTCATTCTAAGAA

AAATATTTTT  
AAATATTTTTATGTGCAATATATGCACATTC  
AAATATTTTTATGTGCAATATATGCACATTC



# BLOSUM62 similarity matrix for protein sequence comparisons

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	B	Z	X	*
A	4	-1	-2	-2	0	-1	-1	0	-2	-1	-1	-1	-1	-2	-1	1	0	-3	-2	0	-2	-1	0	-4
R	-1	5	0	-2	-3	1	0	-2	0	-3	-2	2	-1	-3	-2	-1	-1	-3	-2	-3	-1	0	-1	-4
N	-2	0	6	1	-3	0	0	0	1	-3	-3	0	-2	-3	-2	1	0	-4	-2	-3	3	0	-1	-4
D	-2	-2	1	6	-3	0	2	-1	-1	-3	-4	-1	-3	-3	-1	0	-1	-4	-3	-3	4	1	-1	-4
C	0	-3	-3	-3	9	-3	-4	-3	-3	-1	-1	-3	-1	-2	-3	-1	-1	-2	-2	-1	-3	-3	-2	-4
Q	-1	1	0	0	-3	5	0	-3	-3	-1	-1	-3	-1	-2	-3	0	-1	-2	-1	-2	0	3	-1	-4
E	-1	0	0	2	-4	2	5	-2	0	-3	-3	1	-2	-3	-1	0	-1	-3	-2	-2	1	4	-1	-4
G	0	-2	0	-1	-3	-2	6	2	-4	-4	-2	-3	-2	-3	-2	0	-2	-2	-3	-3	-1	-2	-1	-4
H	-2	0	1	-1	-3	0	2	8	3	3	1	2	2	2	2	2	-2	-2	2	-3	0	0	-1	-4
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	4	2	-3	1	0	-3	-2	-1	-3	-1	3	-3	-3	-1	-4
L	-1	-2	-3	-4	-1	-3	-4	-3	-4	2	4	-1	0	0	0	0	-1	-2	1	1	1	1	-1	-4
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5	-1	-3	-1	0	-1	-3	-2	-2	0	1	-1	-4
M	-1	-1	-2	-3	-1	0	3	3	1	2	2	5	0	-2	-1	-1	-1	-1	-1	1	-3	-1	-1	-4
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6	-4	-2	-2	1	3	-1	-3	-3	-1	-4
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	2	-4	7	-1	-1	-4	-3	-2	-2	-1	-2	-4
S	1	-1	1	0	-1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	-4
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5	-2	-2	0	-1	-1	0	-4
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11	2	-3	-4	-3	-2	-4
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	-1	-3	-2	-1	-4
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4	-3	-2	-1	-4
B	-2	-1	3	4	-3	0	1	-1	0	-3	-4	0	-3	-3	-2	0	-1	-4	-3	-3	4	1	-1	-4
Z	-1	0	0	1	-3	3	4	-2	0	-3	-3	1	-1	-3	-1	0	-1	-3	-2	-2	1	4	-1	-4
X	0	-1	-1	-1	-2	-1	-1	-1	-1	-1	-1	-1	-1	-1	-2	0	0	-2	-1	-1	-1	-1	-1	-4
*	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	1

This matrix was created by Henikoff and Henikoff, 1992

Based on local conserved 'Block' regions in protein alignments

Lowest score = -4, Highest score = 11

# Penalties

Gap opening penalty: -5  
Gap length penalty -1  
End gap penalty 0

1 base gap: -5  
2 base gap: -6  
3 base gap: -7  
etc.



# Alignment score

```
ACGGTAGGGATATACC - TACGAGCTC -- ACAT ---  
|| || |   | || |||| | || | || |  
ACCGTCG ---- AC - CCGTACGA - CTCTGACGTCCT
```

Matches: +19  
Mismatches: 0  
Gaps: -25  
Gap-length: -4  
End gap: 0  
Sum: -10



# Alignment score

```
ACGGTAGGGATATACCTACGAGCTCACAT
|| || |      |||      |  | |
ACCGTCGACCCGTACGACTCTGACGTCCT
```

Matches: +11

Mismatches: 0

Gaps: 0

Gap-length: 0

End gap: 0

Sum: +11



# Needleman and Wunsch

Needleman and Wunsch algorithm:

Stepwise search

Example with identity matrix only (no accounting for gaps and mismatches)  
Optimizes number of identities.

# Needleman and Wunsch

Recursive formula for the calculation of the best score of an alignment:

$$F_{ij} = \max_{h < i, k < j} \{ F_{h,j-1} + S(A_i, B_j), F_{i-1,k} + S(A_i, B_j) \}$$

Where:

$A_i$  is the sequence symbol in the first sequence at position  $i$

$B_j$  is the sequence symbol in the second sequence at position  $j$

$S(A_i, B_j)$  is the similarity matrix value comparing symbol  $A_i$  with  $B_j$

$F_{ij}$  is the optimal alignment score comparing subsequence  $A_1$  to  $A_i$  with the subsequence  $B_1$  to  $B_j$ .

# Comparison matrix filled with values from similarity matrix

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	

Gap opening: 0  
 Gap extension: 0  
 End gap: 0











































































































































Start filling the comparison matrix from lower left to upper right by noting in each cell the best possible score of any alignment from lower left to this cell.

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	1	2	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
	<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
	<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
	<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	

























































































Start filling the comparison matrix from lower left to upper right by noting in each cell the best possible score of any alignment from lower left to this cell.

12

<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
<b>A</b>	1	1	2	3	3	5	6	0	1	1	0	0	0
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1 <b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

1

13



































































































Use backtracking to find the actual alignment.

12	<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
	<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
	<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
	<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
	<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
	<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
	<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
	<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
	<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
	<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
	<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Use backtracking to find the actual alignment.

12	<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
	<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
	<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
	<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
	<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
	<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
	<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
	<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
	<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
	<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
	<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Use backtracking to find the actual alignment.

12	<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
	<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
	<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
	<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
	<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
	<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
	<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
	<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
	<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
	<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
	<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Use backtracking to find the actual alignment.

12	<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
	<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
	<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
	<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
	<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
	<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
	<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
	<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
	<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
	<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
	<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>
		1											13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1 <b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>
	1												13



# „Low road“

12	<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
	<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
	<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
	<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
	<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
	<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
	<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
	<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
	<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
	<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
	<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

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13

**GC**  
**||**  
**GC**

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

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13

**GGC**  
**|||**  
**GGC**

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

**A - GGC**

| | | |

**AAGGC**

1

1

13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

**TA - GGC**  
 || |||  
**TAAGGC**

1

1

13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

**AATA - GGC**  
 | | | |  
**A - TAAGGC**

1

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13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

**AAATA - GGC**  
 || || |||  
**AA - TAAGGC**

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13

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

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13

**CAAATA - GGC**  
 ||| || |||  
**CAA - TAAGGC**

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

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13

**GCAAATA - GGC**  
 |||| | | |||  
**GCAA - TAAGGC**

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

1

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13

**CGCAAATA - GGC**  
 | | | | | | | | | |  
**CGCAA - TAAGGC**

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

1

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13

**A - CGCAAATA - GGC**  
 | | | | | | | | | |  
**ACCGCAA - TAAGGC**

This an alignment with exactly 11 matches.

Use backtracking to find the actual alignment.

12

<b>C</b>	0	2	3	3	5	4	5	6	7	8	8	9	11
<b>G</b>	0	1	2	4	4	4	5	6	7	8	9	10	9
<b>G</b>	0	1	2	4	3	4	5	6	7	8	9	9	8
<b>A</b>	1	1	2	3	3	5	6	6	8	8	7	7	7
<b>T</b>	0	1	2	3	3	4	5	7	6	7	7	7	7
<b>A</b>	1	1	2	3	3	5	6	6	7	7	6	6	6
<b>A</b>	1	1	2	3	3	5	6	5	6	6	5	5	5
<b>A</b>	1	1	2	3	3	5	5	4	5	5	4	4	4
<b>C</b>	0	2	3	2	4	3	3	3	3	3	3	3	4
<b>G</b>	0	1	2	3	2	2	2	2	2	2	3	3	2
<b>C</b>	0	2	2	1	2	1	1	1	1	1	1	1	2
<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>

1

1

13

**A - CGCAAAT - AGGC**  
 | | | | | | | | | |  
**ACCGCAA - TAAGGC**

Another path results in another alignment. Also with 11 matches.

# All 14 different alignments with 11 matches:

**A - CGCAAAT - AGGC**  
| | | | | | | | | |  
**ACCGCAA - TAAGGC**

**A - CGCAAAT - AGGC**  
| | | | | | | | | |  
**ACCGCA - ATAAGGC**

**A - CGCAAAT - AGGC**  
| | | | | | | | | |  
**ACCGC - AATAAGGC**

**A - CGCAAATA - GGC**  
| | | | | | | | | |  
**ACCGCAA - TAAGGC**

**A - CGCAAATA - GGC**  
| | | | | | | | | |  
**ACCGCA - ATAAGGC**

**A - CGCAAATA - GGC**  
| | | | | | | | | |  
**ACCGC - AATAAGGC**

**AC - GCAAAT - AGGC**  
| | | | | | | | | |  
**ACCGCAA - TAAGGC**

**AC - GCAAAT - AGGC**  
| | | | | | | | | |  
**ACCGCA - ATAAGGC**

**AC - GCAAAT - AGGC**  
| | | | | | | | | |  
**ACCGC - AATAAGGC**

**AC - GCAAATA - GGC**  
| | | | | | | | | |  
**ACCGCAA - TAAGGC**

**AC - GCAAATA - GGC**  
| | | | | | | | | |  
**ACCGCA - ATAAGGC**

**AC - GCAAATA - GGC**  
| | | | | | | | | |  
**ACCGC - AATAAGGC**

**AC - GCAA - ATAGGC**  
| | | | | | | | | |  
**ACCGCAATA - AGGC**

**A - CGCAA - ATAGGC**  
| | | | | | | | | |  
**ACCGCAATA - AGGC**

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -3  
 Gap extension: -1  
 End gap: 0

# The best alignment has 9 matches

12	<b>C</b>	0	1	1	1	2	2	1	1	2	2	3	7	9
	<b>G</b>	0	0	1	1	2	1	1	2	2	3	7	8	4
	<b>G</b>	0	1	0	2	1	1	2	2	2	6	7	3	3
	<b>A</b>	1	0	1	1	1	2	2	2	6	6	2	3	2
	<b>T</b>	0	1	1	1	1	1	2	5	5	2	3	2	2
	<b>A</b>	1	1	1	1	1	2	4	5	2	3	2	2	1
	<b>A</b>	1	1	0	1	1	3	5	1	2	2	2	1	1
	<b>A</b>	1	0	1	1	2	4	1	1	1	2	1	1	2
	<b>C</b>	0	1	1	2	3	0	1	0	1	1	1	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	1	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -3  
 Gap extension: -1  
 End gap: 0

# Backtracing

12	<b>C</b>	0	1	1	1	2	2	1	1	2	2	3	7	9
	<b>G</b>	0	0	1	1	2	1	1	2	2	3	7	8	4
	<b>G</b>	0	1	0	2	1	1	2	2	2	6	7	3	3
	<b>A</b>	1	0	1	1	1	2	2	2	6	6	2	3	2
	<b>T</b>	0	1	1	1	1	1	2	5	5	2	3	2	2
	<b>A</b>	1	1	1	1	1	2	4	5	2	3	2	2	1
	<b>A</b>	1	1	0	1	1	3	5	1	2	2	2	1	1
	<b>A</b>	1	0	1	1	2	4	1	1	1	2	1	1	2
	<b>C</b>	0	1	1	2	3	0	1	0	1	1	1	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	1	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
	1													13

Gap opening: -3  
 Gap extension: -1  
 End gap: 0

No gaps are introduced because of penalties.

The best alignment with 9 matches:

```
- ACGCAAATAGGC  
  | | | | | | | |  
ACCGCAATAAGGC
```

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>C</b>	0	2	1	0	1	0	0	0	0	0	0	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0	
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0	
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	
	<b>T</b>	0	0	0	0	0	0	1	0	0	0	0	0	
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	
	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
	1												13	

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>T</b>	0	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0
	<b>T</b>	0	0	0	0	0	0	1	0	0	0	0	0
	<b>A</b>	1	1	1	0	1	3	4	5	5 <sup>4.5</sup>	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>
	1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0	
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0	
	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	
	<b>T</b>	0	1	1	1	0	1	3	5	5	5	4.5	3.5	3
	<b>A</b>	1	1	1	0	1	3	4	5	5	4.5	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
	1												13	

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>G</b>	0	0	0	1	0	0	0	0	0	0	1	1	0
	<b>A</b>	1	0	1	1	1	1.5	3	3.5	6	6	5	4.5	3.5
	<b>T</b>	0	1	1	1	0	1	3	5	5	5	4.5	3.5	3
	<b>A</b>	1	1	1	0	1	3	4	5	5	4.5	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	0	1	0	0	0	0	0	1	1	0	
	<b>G</b>	0	1	0	2	1	1	1.5	3	4	6	7	6	4.5
	<b>A</b>	1	0	1	1	1	1.5	3	3.5	6	6	5	4.5	3.5
	<b>T</b>	0	1	1	1	0	1	3	5	5	5	4.5	3.5	3
	<b>A</b>	1	1	1	0	1	3	4	5	5	4.5	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	0	1	0	0	0	0	0	0	1	
	<b>G</b>	0	0	1	1	2	1	1	2	3	5	7	8	6
	<b>G</b>	0	1	0	2	1	1	1.5	3	4	6	7	6	4.5
	<b>A</b>	1	0	1	1	1	1.5	3	3.5	6	6	5	4.5	3.5
	<b>T</b>	0	1	1	1	0	1	3	5	5	5	4.5	3.5	3
	<b>A</b>	1	1	1	0	1	3	4	5	5	4.5	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	1	2	2	1	1	2	4.5	5	7	9
	<b>G</b>	0	0	1	1	2	1	1	2	3	5	7	8	6
	<b>G</b>	0	1	0	2	1	1	1.5	3	4	6	7	6	4.5
	<b>A</b>	1	0	1	1	1	1.5	3	3.5	6	6	5	4.5	3.5
	<b>T</b>	0	1	1	1	0	1	3	5	5	5	4.5	3.5	3
	<b>A</b>	1	1	1	0	1	3	4	5	5	4.5	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

# Calculation of the best alignment using gap penalties

12	<b>C</b>	0	1	1	1	2	2	1	1	2	4.5	5	7	9
	<b>G</b>	0	0	1	1	2	1	1	2	3	5	7	8	6
	<b>G</b>	0	1	0	2	1	1	1.5	3	4	6	7	6	4.5
	<b>A</b>	1	0	1	1	1	1.5	3	3.5	6	6	5	4.5	3.5
	<b>T</b>	0	1	1	1	0	1	3	5	5	5	4.5	3.5	3
	<b>A</b>	1	1	1	0	1	3	4	5	5	4.5	3	2	1
	<b>A</b>	1	1	0	1	2	3	5	3	3	3	2	1	1
	<b>A</b>	1	0	1	2	2	4	3	1.5	2	2	1	1	2
	<b>C</b>	0	1	2	2	3	1	1	0	1	1	0	2	3
	<b>G</b>	0	0	2	2	0	1	0	1	1	0	2	2	0
	<b>C</b>	0	2	1	0	1	0	1	1	0	1	1	0	1
1	<b>A</b>	1	0	0	0	0	1	1	0	1	1	0	0	0
	<b>A</b>	<b>C</b>	<b>C</b>	<b>G</b>	<b>C</b>	<b>A</b>	<b>A</b>	<b>T</b>	<b>A</b>	<b>A</b>	<b>G</b>	<b>G</b>	<b>C</b>	
		1												13

Gap opening: -1  
 Gap extension: -0.5  
 End gap: 0  
 Mismatches: 0

The 3 best alignments with 9 or 10 matches (and score=9):

**- ACGCAAATAGGC**  
| | | | | | | | | |  
**ACCGCAATAAGGC**

**A - CGCAAATAGGC**  
| | | | | | | | | |  
**ACCGCAATAAGGC**

**AC - GCAAATAGGC**  
| | | | | | | | | |  
**ACCGCAATAAGGC**

# Summary

The Needleman-Wunsch algorithm finds an optimal alignment.

This alignment is not always unique.

Choose the right penalty parameters to reflect the biology of your sequences.

# Literature

This algorithm was first published by Saul B. Needleman and Christian D. Wunsch in 1970, for the comparison of two protein sequences:

## **A General Method Applicable to the Search for Similarities in the Amino Acid Sequence of Two Proteins**

SAUL B. NEEDLEMAN AND CHRISTIAN D. WUNSCH

*Department of Biochemistry, Northwestern University, and  
Nuclear Medicine Service, V. A. Research Hospital  
Chicago, Ill. 60611, U.S.A.*

*(Received 21 July 1969)*

J. Mol. Biol., 48 (1970), pp. 443–453

TTCAAATCCTTATGAACTTAATTCATTTCTAAGAATGAGTCATACGCTATATAATTGCAAAATGAAATTTAGACATTCTGTAATGCGATGATCATATAATCTTATCACATCGATAAGAACTATGCAATAAAAATCTAACAAATGGCTCAAGATTGTTAAAGAAATAAATTTAAATATTTTTT  
TATTACATTGATAAGAACTACCAATAAGATCTAACAAATGGCTCAAGATTGTTAAAGAAATAAATTTAAATATTTTTT  
CACATCGATAAGAACTATGCAATAAAAATCTAACAAATGGCTCAAGATTGTTAAAGAAATAAATTTAAATATTTTTT  
TTCAAATCCTTATGAACTTAATTCATTTCTAAGAATGAGTCATACGCTATATAATTGCAAAATGAAATTTAGACATTCTGTAATGCGATGATCATATAATCTTATCACATCGATAAGAACTATGCAATAAAAATCTAACAAATGGCTCAAGATTGTTAAAGAAATAAATTTAAATATTTTTT  
TTCAAATCCTTATGAACTTAATTCATTTCTAAGAATGAGTCATACGCTATATAATTGCAAAATGAAATTTAGACATTCTGTAATGCGATGATCATATAATCTTATCACATCGATAAGAACTATGCAATAAAAATCTAACAAATGGCTCAAGATTGTTAAAGAAATAAATTTAAATATTTTTT

# Links

An extensive explanation of the algorithm can also be found in Wikipedia:

<https://de.wikipedia.org/wiki/Needleman-Wunsch-Algorithmus>

The EMBOSS sequence analysis package **needle** program does Needleman-Wunsch alignments online:

For protein comparisons:

[http://www.ebi.ac.uk/Tools/psa/emboss\\_needle/](http://www.ebi.ac.uk/Tools/psa/emboss_needle/)

For nucleic acid comparisons:

[http://www.ebi.ac.uk/Tools/psa/emboss\\_needle/nucleotide.html](http://www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html)



# Exercises

Compare these two protein sequences using the Needleman and Wunsch algorithm. Change the gap open and gap extension penalties.

```
>NP_001315822.1 alcohol dehydrogenase [Malus domestica]
MSNTAGQVIRCRAAVAWAWEAGKPLVIEEVEVAPPQANEVRIKILFTSLCHTD
VYFWEAKGQNPLFPRIYGH EAGGIVESVGEGVTDLKAGDHVLPVFTGECK
DCAHCKSEESNMCDLLRINTDRGVMLSDGKSRSFSIKGKPIYHFVGTSTFSE
YTVVHVGCLAKINPSAPLTKVCLLSCGISTGLGATLNVAKPKKGSTVAVFG
LGAVGLAAAEGARLSGASRIIGVDLHSDRFEEAKKFGVTEFVNPKAHEKPV
QEVIAELTNRGVDRSIECTGSTEAMISAFECVHDGWGVAVLVGVPHKDAVF
KTHPVNFLNERTLKGTFFGNYKTRTDIPSVVEKYMNKELELEKFI THKVPF
SEINKAFEYMLKGEGLRCCIIRMEE
```

```
>NP_001189342.1| alcohol dehydrogenase [Homo sapiens]
MAASCVLLHTGQKMPLIGLGTWKSEPGQVKA AVKYALSVGYRHIDCAAIYG
NEPEIGEALKEDVGPGKAVPREELFVTSKLNWNTKHHPEDVEPALRKTLDL
QLEYLDLYLMHWPYAFERGDNPF PKNADGTICYDSTHYKETWKALEALVAK
GLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARG
LEVTAYSPLGSSDRAWRPDEPVLLLEEPVVLALAEKYGRSPAQILLRWQVQ
RKVICIPKSITPSRILQNIKVFDFTFSPEEMKQLNALNKNWRYIVPMLTVD
GKRVPRDAGHPLYPFNDPY
```