

Alignment

Sept 16, 2015

ANNOUNCEMENTS

ALIGNMENT – THINK BLAST

Q ANCQE
D ANC**G**E versus ANCQE
 ANC**H**E

BLOSUM MATRIX

	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val
Ala	4																			
Arg	-1	5																		
Asn	-2	0	6																	
Asp	-2	-2	1	6																
Cys	0	-3	-3	-3	9															
Gln	-1	1	0	0	-3	5														
Glu	-1	0	0	2	-4	2	5													
Gly	0	-2	0	-1	-3	-2	-2	6												
His	-2	0	1	-1	-3	0	0	-2	8											
Ile	-1	-3	-3	-3	-1	-3	-3	-4	-3	4										
Leu	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4									
Lys	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5								
Met	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5							
Phe	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6						
Pro	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7					
Ser	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4				
Thr	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5			
Trp	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11		
Tyr	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	
Val	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4

BLOSUM MATRIX

BLOSUM 80	BLOSUM 62	BLOSUM 45
PAM 1	PAM 120	PAM 250
<i>Less divergent</i> ← → <i>More divergent</i>		

Alignment Algorithms

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ALGORITHMS

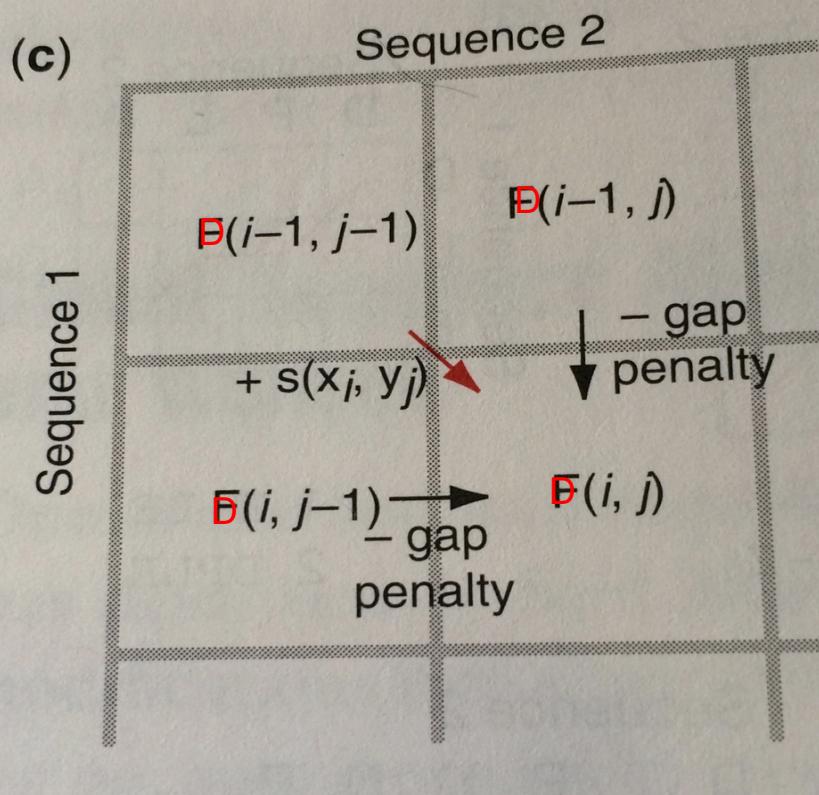
Global Alignment : Needleman – Wunsch

ALGORITHMS

Global Alignment Step 1: set up scoring matrix

ALGORITHMS

Global Alignment
Step 2: score matrix

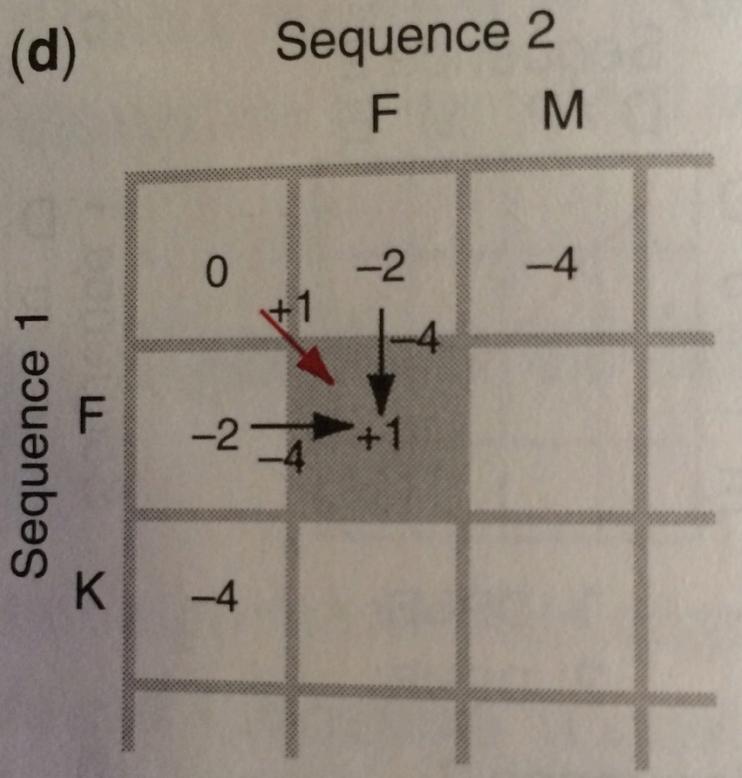


$$D(i, j) = \max \left\{ \begin{array}{l} D(i - 1, j - 1) + s(x_i, y_j) \\ D(i - 1, j) + g \\ D(i, j - 1) + g \end{array} \right.$$

ALGORITHMS

Global Alignment Step 2: score matrix

(d)



ALGORITHMS

Global Alignment
Step 2: score matrix

		Sequence 2								
		F	M	D	T	P	L	N	E	
0	-2	-4	-6	-8	-10	-12	-14	-16		
F	-2	+1	-1	-3	-5	-7	-9	-11	-13	
K	-4	-1	-1	-3	-5	-7	-9	-11	-13	
H	-6	-3	-3	-3	-5	-7	-9	-11	-13	
M	-8	-5	-2	-4	-5	-7	-9	-11	-13	
E	-10	-7	-4	-4	-6	-7	-9	-11	-10	
D	-12	-9	-6	-3	-5	-7	-9	-11	-12	
P	-14	-11	-8	-5	-5	-4	-6	-8	-10	
L	-16	-13	-10	-7	-7	-6	-3	-5	-7	
E	-18	-15	-12	-9	-9	-8	-5	-5	-4	

ALGORITHMS

Global Alignment

Step 2: score matrix

		Sequence 2								
		F	M	D	T	P	L	N	E	
A	0	-2	-4	-6	-8	-10	-12	-14	-16	
	F	-2	+1	-1	-3	-5	-7	-9	-11	-13
K	-4	-1	-1	-3	-5	-7	-9	-11	-13	
H	-6	-3	-3	-3	-5	-7	-9	-11	-13	
M	-8	-5	-2	-4	-5	-7	-9	-11	-13	
E	-10	-7	-4	-4	-6	-7	-9	-11	-10	
D	-12	-9	-6	-3	-5	-7	-9	-11	-12	
P	-14	-11	-8	-5	-5	-4	-6	-8	-10	

$$D(i, j) = \max \left\{ \begin{array}{l} D(i - 1, j - 1) + s(x_i, y_j) \\ D(i - 1, j) + g \\ D(i, j - 1) + g \end{array} \right.$$

-6	-3	-5	7
-8	-5	-5	-4

ALGORITHMS

Global Alignment

Step 3:

ID optimal alignment

ALGORITHMS

Global Alignment
Step 3:
ID optimal alignment

		Sequence 2								
		F	M	D	T	P	L	N	E	
Sequence 1	0	-2	-4	-6	-8	-10	-12	-14	-16	
	F	-2 +1	-1	-3	-5	-7	-9	-11	-13	
	K	-4 -1	-1	-3	-5	-7	-9	-11	-13	
	H	-6 -3	-3	-3	-5	-7	-9	-11	-13	
	M	-8 -5	-2	-4	-5	-7	-9	-11	-13	
	E	-10 -7	-4	-4	-6	-7	-9	-11	-10	
	D	-12 -9	-6	-3 -5	-5	-7	-9	-11	-12	
	P	-14 -11	-8	-5	-5	-4	-6	-8	-10	
	L	-16 -13	-10	-7	-7	-6	-3 -5	-5	-7	
	E	-18 -15	-12	-9	-9	-8	-5	-5	-4	

ALGORITHMS

Global Alignment

Step 3:

ID optimal alignment

		Sequence 2							
		F	M	D	T	P	L	N	E
Sequence 1	0	-2	-4	-6	-8	-10	-12	-14	-16
	F	-2 +1	-1	-3	-5	-7	-9	-11	-13
	K	-4 -1	-1	-3	-5	-7	-9	-11	-13
	H	-6 -3	-3	-3	-5	-7	-9	-11	-13
	M	-8 -5	-2	-4	-5	-7	-9	-11	-13
	E	-10 -7	-4	-4	-6	-7	-9	-11	-10
	D	-12 -9	-6	-3 -5	-5	-7	-9	-11	-12
	P	-14 -11	-8	-5	-5	-4	-6	-8	-10
	L	-16 -13	-10	-7	-7	-6	-3 -5	-5	-7
	E	-18 -15	-12	-9	-9	-8	-5	-5	-4

Advanced Search

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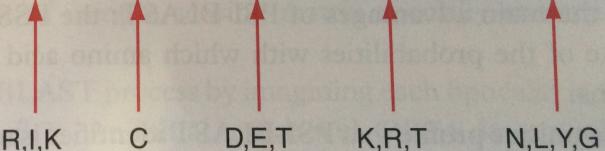
ADVANCED SEARCH

PSI-BLAST

ADVANCED SEARCH

PSI-BLAST

66	FTVDENGQMSATAKGRVRLFNNWDVCADMIGSFTDTEPAFKMKYWGVASFLQKGNDH	125
63	FSVDEKGHMSATAKGRVRLLSNWEVCADMVGTFDTEDPAFKMKYWGVASFLQRGNDDH	122
34	FSVDEKGHMSATAKGRVRLLSNWEVCADMVGTFDTEDPAFKMKYWGVASFLQRGNDDH	93
2	MSATAKGRVRLNNWDVCADMVGTFDTEDPAFKMKYWGVASFLQKGNDH	53
65	FKIEDNGKTTATAKGRVRILDKLELCANMVGTFIETNDPAKYRMKYHGLALILERGLDDH	124
44	FSVDESGKVATATAHGRVII1LNNWEMCANMFGTFEDTPDPAKFKMRYWGAAASYLQTGNDDH	103
44	FSVDGSGKVATATAQGRVII1LNNWEMCANMFGTFEDTPDPAKFKMRYWGAAASYLQSGNDDH	103
63	FTIHEDGAMTATAKGRVII1LNNWEMCANMFGTMATFETTPDPAKFKMRYWGAAASYLQTGNDDH	121
60	FKVEEDGTMTATAIGRVIILNNWEMCANMFGTFEDTEPAFKMKYWGAAASYLQTGYDDH	111
81	FKVQEDGTMTATATGRVII1LNNWEMCANMFGTFEDTEEPARFKMKYWGAAASYLQTGYDDH	141
1	MVGTFDTEDPAFKMKYWGVASFLQKGNDH	32
38	FSVDGSGKMTATAQGRVII1LNNWEMCANMFGTFEDTPDPAKFKMRYWGAAASYLQSGNDDH	97
65	YTVEEDGTMTASSKGRVKLFGFWWVICADMAAQYDPTTPAKMYMTYQGLASYLSSGGDNY	12



ADVANCED SEARCH

PSI-BLAST

