Evolutionary Thinking 2022
TA session
week 1 – Alignment and Distance Matrix

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Outline

1. Learning outcome of today (30 minutes)

Sequence Alignment

Distance Matrix

Examples: Manual align a pair sequence using dynamic progamming

3. Group Working on MEGA exercises (60 minutes)

Learning outcome of today

Sequence Alignment

What are the materials that we need for doing a sequence alignment ? (5 minutes discussion)

Learning outcome of today

Sequence Alignment

What are the materials that we need for doing a sequence alignment ? (5 minutes discussion)

1. Sequences (two or more)

2. Scoring system (From simple to complex)

3. Algorithms (Examples – DP/Needleman and Wunsch)

Learning outcome of today

Scoring system

Match +
Mismatch -
Gap -

Gap open –
Gap continue -

Learning outcome of today

DP/Needleman-Wunsch alignment – pairwise

C	A	T	T	A	T	C	G
C	G	T	T	-	T	C	G

Global maximized alignment score

$\max S_{1->x,1->y} =$

Max

{

$\max S_{1->x-1,1->y} + S_{x,y|x-1,y}$

$\max S_{1->x,1->y-1} + S_{x,y|x,y-1}$

$\max S_{1->x-1,1->y-1} + S_{x,y|x-1,y-1}$

}

Learning outcome of today

Match 5
Mismatch -3
Gap -4
Gap extension -1

Dynamic Programming alignment – pairwise

		C	A	T	T	A	T	C	G
	0	0	0	0	0	0	0	0	0
C	0								
G	0								
T	0								
T	0								
T	0								
C	0								
G	0								

Learning outcome of today

Match 5
Mismatch -3
Gap -4
Gap extension -1

Dynamic Programming alignment – pairwise

Group solving (15 minutes)

		C	A	T	T	A	T	C	G
	0	0	0	0	0	0	0	0	0
C	0								
G	0								
T	0								
T	0								
T	0								
C	0								
G	0								

Learning outcome of today

Match 5
Mismatch -3
Gap -4
Gap extension -1

Dynamic Programming alignment – pairwise

Group solving (15 minutes)

		C	A	T	T	A	T	C	G
	0	0	0	0	0	0	0	0	0
C	0	5	1	0	-1	-2	-3	5	1
G	0	1	2	-2	-3	-4	-5	1	10
T	0	0	-2	7	3	2	1	0	6
T	0	-1	-3	3	12	8	7	6	5
T	0	-2	-4	2	8	9	13	9	8
C	0	5	1	1	7	5	9	18	14
G	0	1	2	0	6	4	8	14	23

Learning outcome of today

Match 5
Mismatch -3
Gap -4
Gap extension -1

Dynamic Programming alignment – pairwise

Finding maximum

		C	A	T	T	A	T	C	G
	0	0	0	0	0	0	0	0	0
C	0	5	1	0	-1	-2	-3	5	1
G	0	1	2	-2	-3	-4	-5	1	10
T	0	0	-2	7	3	2	1	0	6
T	0	-1	-3	3	12	8	7	6	5
T	0	-2	-4	2	8	9	13	9	8
C	0	5	1	1	7	5	9	18	14
G	0	1	2	0	6	4	8	14	23

Learning outcome of today

Match 5
Mismatch -3
Gap -4
Gap extension -1

Dynamic Programming alignment – pairwise

Trace back

		C	A	T	T	A	T	C	G
	0	0	0	0	0	0	0	0	0
C	0	5	1	0	-1	-2	-3	5	1
G	0	1	2	-2	-3	-4	-5	1	10
T	0	0	-2	7	3	2	1	0	6
T	0	-1	-3	3	12	8	7	6	5
T	0	-2	-4	2	8	9	13	9	8
C	0	5	1	1	7	5	9	18	14
G	0	1	2	0	6	4	8	14	23

Learning outcome of today

Match 5
Mismatch -3
Gap -4
Gap extension -1

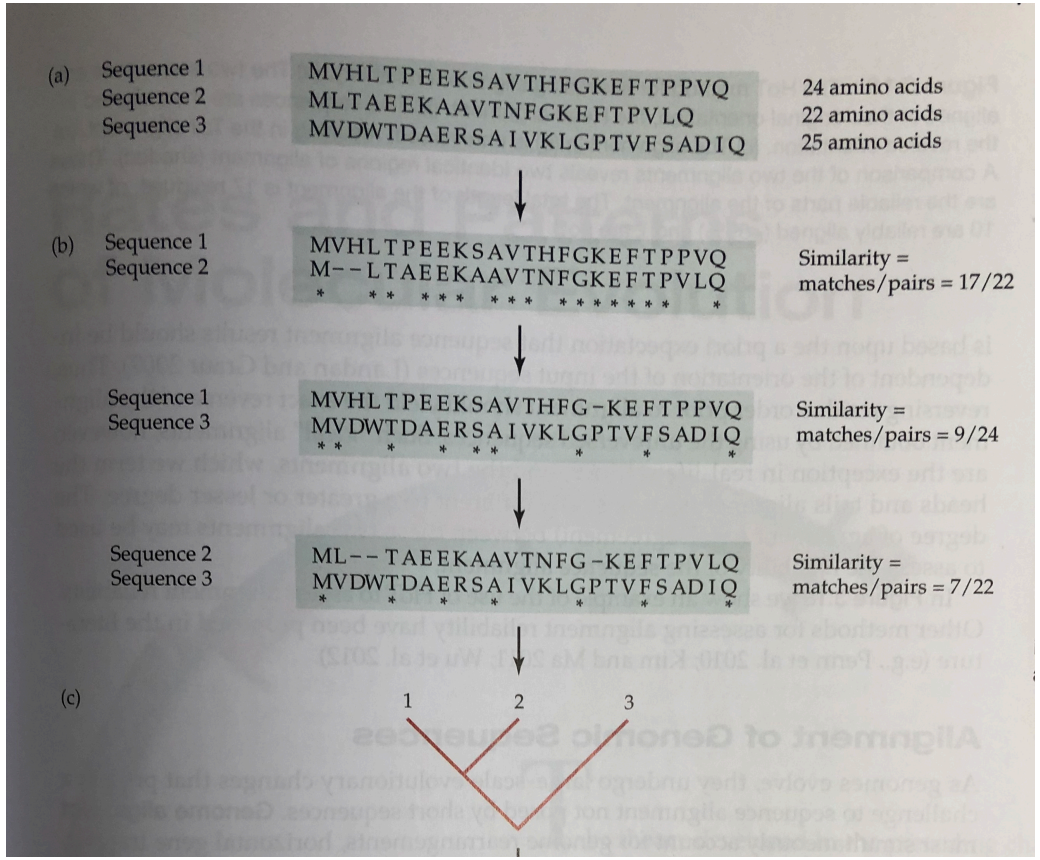
Dynamic Programming alignment – pairwise

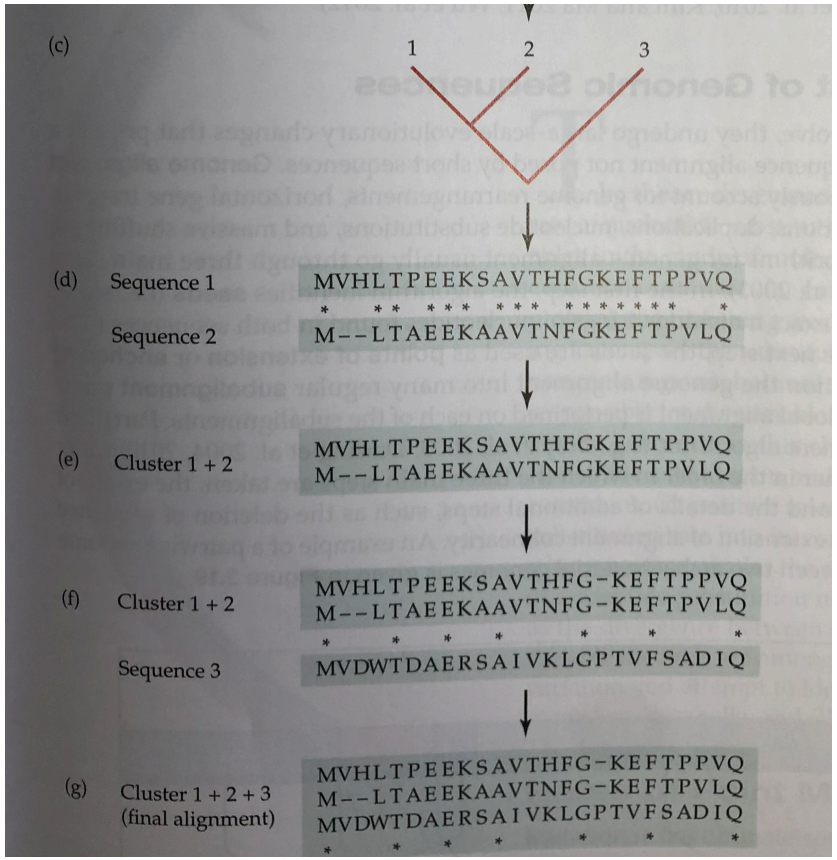
Find alignment

		C	A	T	T	A	T	C	G
	0	0	0	0	0	0	0	0	0
C	0	5	1	0	-1	-2	-3	5	1
G	0	1	2	-2	-3	-4	-5	1	10
T	0	0	-2	7	3	2	1	0	6
T	0	-1	-3	3	12	8	7	6	5
T	0	-2	-4	2	8	9	13	9	8
C	0	5	1	1	7	5	9	18	14
G	0	1	2	0	6	4	8	14	23

Learning outcome of today

Multiple Sequence Alignment – Extension of pair wise alignment (Graur P104-105)





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