

Pair-wise Alignment

Dynamic Programming

- Dynamic Programming allow Optimal Alignment between two sequences
- Allow Insertion and Deletion or Alignment with gaps
- Needleman and Wunsch Algorithm (1970) for global alignment
- Smith & Waterman Algorithm (1981) for local alignment
- Important Steps
 - Create DOTPLOT between two sequences
 - Compute SUM matrix
 - Trace Optimal Path

Steps for Dynamic Programming

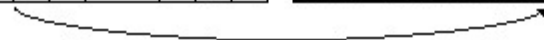
Start Computing the Sum Matrix

```

new_value_cell(R,C) <=
  cell(R,C)                                ( Old value, either 1 or 0 )
  + Max[
    cell (R+1, C+1),                        ( Diagonally Down, no gaps )
    cells(R+1, C+2 to C_max),               ( Down a row, making col. gap )
    cells(R+2 to R_max, C+2)               ( Down a col., making row gap )
  ]
  
```

	A	B	C	N	Y	R	Q	C	L	C	R	P	M
A	1												
Y					1								
C			1					1	1				
Y					1								
N					1								
R						1					1		
C			1					1	1				
K													
C			1					1	1				
R						1					1		
B		1											
P												1	

	A	B	C	N	Y	R	Q	C	L	C	R	P	M
A	1												
Y					1								
C			1					1	1				
Y					1								
N					1								
R						1					1		
C			1					1	1				
K													
C			1					1	1		1		
R						1					2	0	0
B	1	2	1	1	1	1	1	1	1	1	1	0	0
P	0	0	0	0	0	0	0	0	0	0	0	1	0



Steps for Dynamic Programming

Keep Going

	A	B	C	N	Y	R	Q	C	L	C	R	P	M
A	1												
Y					1								
C			1					1	1				
Y					1								
N				1									
R						1					1		
C			1					1	1				
K													
C			1					1	1				
R						1					2	0	0
B	1	2	1	1	1	1	1	1	1	1	1	0	0
P	0	0	0	0	0	0	0	0	0	0	0	1	0

	A	B	C	N	Y	R	Q	C	L	C	R	P	M
A	1												
Y					1								
C			1					1	1				
Y					1								
N				1									
R						5	4	3	3	2	2	0	0
C	3	3	4	3	3	3	3	4	3	3	1	0	0
K	3	3	3	3	3	3	3	3	3	2	1	0	0
C	2	2	3	2	2	2	2	2	3	2	3	1	0
R	2	1	1	1	1	2	1	1	1	1	2	0	0
B	1	2	1	1	1	1	1	1	1	1	1	0	0
P	0	0	0	0	0	0	0	0	0	0	0	1	0



Steps for Dynamic Programming

Alternate Tracebacks

A B C - N Y R Q C L C R - P M
 A Y C Y N - R - C K C R B P

	A	B	C	N	Y	R	Q	C	L	C	R	P	M
A	8	7	6	6	5	4	4	3	3	2	1	0	0
Y	7	7	6	6	6	4	4	3	3	2	1	0	0
C	6	6	7	6	5	4	4	4	3	3	1	0	0
Y	6	6	6	5	6	4	4	3	3	2	1	0	0
N	5	5	5	6	5	4	4	3	3	2	1	0	0
R	4	4	4	4	4	5	4	3	3	2	2	0	0
C	3	3	4	3	3	3	3	4	3	3	1	0	0
K	3	3	3	3	3	3	3	3	3	2	1	0	0
C	2	2	3	2	2	2	2	3	2	3	1	0	0
R	2	1	1	1	1	2	1	1	1	1	2	0	0
B	1	2	1	1	1	1	1	1	1	1	1	0	0
P	0	0	0	0	0	0	0	0	0	0	0	1	0

Important Terms in Pairwise Sequence Alignment

Global Alignment

- Suite for similar sequences
- Nearly equal length
- Overall similarity is detected

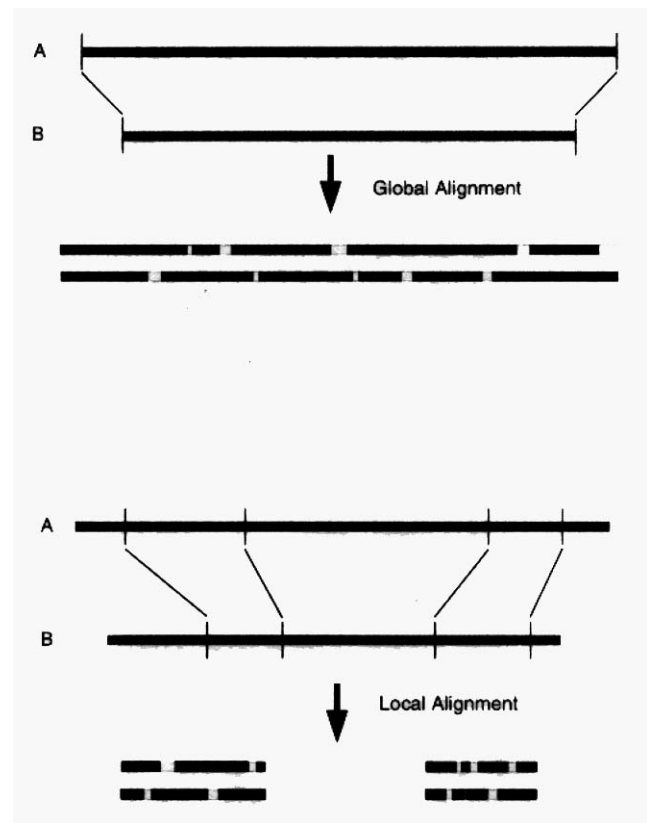
Local Alignment

- Isolate regions in sequences
- Suitable for database searching
- Easy to detect repeats

• Gap Penalty (Opening + Extended)

ALTGTRTG . . . CALGR ...

AL . GTRTGTGPCALGR ...



Global alignment

```
1 AGGATTGGAATGCTCAGAAGCAGCTAAAGCGTGTATGCAGGATTGGAATTAAAGAGGAGGTAGACCG... 67
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 AGGATTGGAATGCTAGGCTTGATTGCCTACCTGTAGCCACATCAGAAGCACTAAAGCGTCAGCGAGACCG 70
```

Two sequences sharing several local regions of local similarity

Algorithm: **GAP**

(Needleman & Wunsch)

Produces an **end-to-end** alignment

