Gaps

Kim ChangGi 2015. 3. 17

#### Definition

- A gap is any maximal, consecutive run of spaces in a single string of a given alignment

• Example

С	Т	Т	Т	Α	А	С	-	-	Α	-	Α	С
С	-	-	-	С	Α	С	С	С	Α	Т	-	С

• 4 Gaps with 7 spaces

• Why not 3 Gaps?

### • Example

С	Т	Т	Т	Α	А	С	-	-	Α	-	Α	С
С	-	-	-	С	Α	С	С	С	Α	Т	-	С

### • 4 Gaps with 7 spaces

- Why not 3 Gaps?
  - Contiguous deletion & insertion are counted as different gap.

Simplest object function (include gaps)

-each gaps contribute 
$$W_g$$
, independent of how long the gap is (so that 's( $x$ , \_) = s(\_,  $x$ ) = 0') 
$$\sum_{i=1}^{l} s(S'_1(i), S'_2(i)) - kW_g$$

### • Example

S	а	b	С	d	-
а	1	-3	-2	0	-1
b		3	-2	-1	-2
С			0	-4	-2
d				3	-1
-					0

S` <sub>1</sub>	С	a	c	-	d	b	d
S <sub>2</sub>	c	-	1	b	d	b	-
score	0	-1	-2	-2	3	3	-1

Score = 0

### • Example

S	а	b	С	d	-
а	1	-3	-2	0	0
b		3	-2	-1	0
С			0	-4	0
d				3	0
-					0

S` <sub>1</sub>	С	a	С	-	d	b	d
$S_2$	c	-	-	b	d	b	-
score	0	0	0	0	3	3	0

Score =  $6 - 3W_g$ 

## Why gaps?

# In many biological application, Insertion or Deletion is important

- Mutation is important, and gaps are justification of mutation.
- Because mutations make insertion or deletion.

### • Example for long insertion or deletion

- unequal crossing over in meiosis
- DNA slippage during replication
- insertion of transposable element into a DNA string
- insertion of DNA by retroviruses
- translocations of DNA between chromosomes

#### • What is cDNA

- -in generate a protein, an RNA molecule is transcribed from the DNA of the gene
- : it calls mRNA
- and hunt for the location of the gene, mRNA is used to create a DNA
- : it calls cDNA

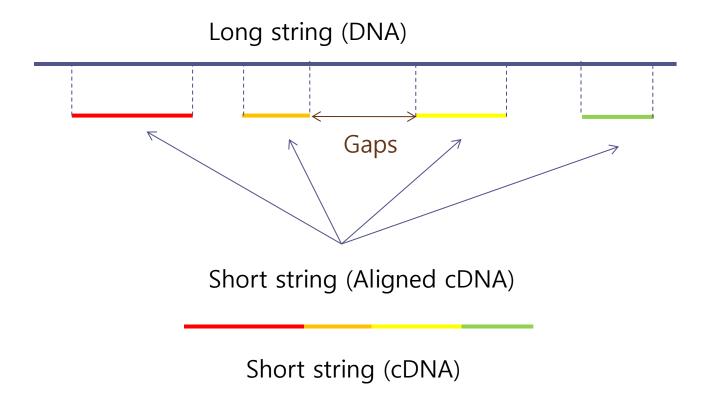
#### Exon

- contribute to the code for the protein
- Short

#### Intron

- intervening sequence (does not include code for protein)
- Long

### • Example



- You don't want to set a large penalty for spaces
  - -if not, it would align all string close together
- Also, want a rather high penalty for mismatches
  - -when cDNA is correctly cut up, there are small percentage of mismatchs
- Of course, positive match value
  - -need explanation?

### • Longest common subsequence problem occur

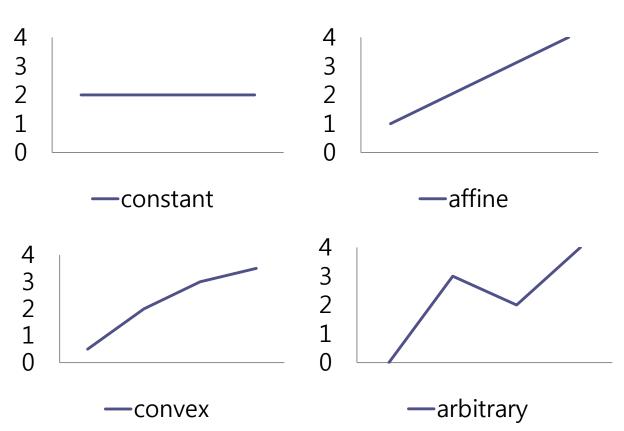
- DNA has only four letter in roughly equal amount
- intron is too longer than exon
- some sequencing error
- under this condition, all of the characters in cDNA exactly match with DNA stirng
- Under this condition cDNA matches all of the character in DNA

Long string (DNA)

- Examine in detail four general types of gap weight
  - constant
  - affine
  - convex
  - arbitrary

### • Examine in detail four general types of gap weight

- constant
- affine
- convex
- arbitrary



### Constant gap

- space is free
- each gap is given a weight of  $W_g$ , independent of the number of spaces in the gap
- $W_m$  for match,  $W_{ms}$  for mismatch

### Constant gap

- Find an alignment A to maximize

$$[W_m(\#matches) - W_{ms}(\#mismatches) - W_g(\#gaps)]$$

### Constant gap

- Find an alignment A to maximize

$$[\mathbf{W}_m(\# \mathrm{matches}) - \, \mathbf{W}_{ms}(\# \mathrm{mismatches}) - \, \mathbf{W}_g(\# \mathrm{gaps})]$$

#### • If

$$-W_m = 3, W_{ms} = 2, W_g = 1$$

S <sub>1</sub>	b	c	a	1	1	f	d	g
S <sub>2</sub>	b	c	b	e	g	d	d	g

### Constant gap

- Find an alignment A to maximaize

$$[W_m(\#matches) - W_{ms}(\#mismatches) - W_g(\#gaps)]$$

#### • If

$$-W_m = 3, W_{ms} = 2, W_g = 1$$

S <sub>1</sub>	b	С	a	-	1	f	d	g
S <sub>2</sub>	b	С	b	e	g	d	d	g

$$W_m(\# matches) - W_{ms}(\# mismatches) - W_g(\# gaps)$$
  
=  $(3*4) - (2*2) - (1*1) = 12 - 4 - 1 = 7$ 

### Constant gap

- Find an alignment A to maximize (adopt the alphabet-dependent weights for matches and mismatches)

$$\sum_{i=1}^{1} s(S'_{1}(i), S'_{2}(i)) - W_{g}(\#gaps)$$
$$\cdot s(x, \_) = s(\_, x) = 0$$

 $\cdot$  S'<sub>1</sub> and S'<sub>2</sub> represent the strings S<sub>1</sub> and S<sub>2</sub> after insertion spaces

- Examine in detail four general types of gap weight
  - constant
  - affine
  - convex
  - arbitrary

### Affine gap weight

- add a weight  $W_s$  for each space in the gap
  - $W_g$  (gap initiation weight): cost of starting a gap
  - $W_s$  (gap extension weight): cost of extending the gap by one space

- a single gap of length q is given by the affine function  $W_g + qW_s$ 

- generalization of the constant gap weight (constant gap weight model is simply the affine model with  $W_s = 0$ .)

### Affine gap weight

- Find an alignment A to maximize

$$[W_m(\#matches) - W_{ms}(\#mismatches) - W_g(\#gaps) - W_s(\#spaces)]$$

#### • If

$$-W_m = 3, W_{ms} = 2, W_g = 1, W_s = 2$$

S <sub>1</sub>	b	С	a	-	-	f	d	g
S <sub>2</sub>	b	c	b	e	g	d	d	g

$$W_m(\# matches) - W_{ms}(\# mismatches) - W_g(\# gaps) - W_s(\# spaces)$$
  
=  $(3*4) - (2*2) - (1*1) - (2*2) = 12 - 4 - 1 - 4 = 3$ 

### Affine gap weight

- Find an alignment A to maximize (adopt the alphabet-dependent weights for matches and mismatches)

$$\sum_{i=1}^{1} s(S'_{1}(i), S'_{2}(i)) - W_{g}(\#gaps) - W_{s}(\#spaces)$$
$$\cdot s(x, \_) = s(\_, x) = 0$$

 $\cdot$  S'<sub>1</sub> and S'<sub>2</sub> represent the strings S<sub>1</sub> and S<sub>2</sub> after insertion spaces

### Affine gap weight

- Find an alignment A to maximize (adopt the alphabet-dependent weights for matches and mismatches)

$$\sum_{i=1}^{l} s(S'_{1}(i), S'_{2}(i)) - W_{g}(\#gaps) - W_{s}(\#spaces)$$

• If  $W_g = 1$ ,  $W_s = 2$ 

S' <sub>1</sub>	c	a	С	-	1	b	d
S' 2	С	a	b	С	d	b	-
score	0						

S	a	b	c	d	•
a	1	-3	-2	0	0
b		3	-1	-4	0
c			0	-3	0
d				3	0
-					0

### Affine gap weight

- Find an alignment A to maximize (adopt the alphabet-dependent weights for matches and dismatches)

$$\sum_{i=1}^{l} s(S'_{1}(i), S'_{2}(i)) - W_{g}(\#gaps) - W_{s}(\#spaces)$$

• If  $W_g = 1$ ,  $W_s = 2$ 

S' <sub>1</sub>	С	a	С	-	-	b	d
S'2	С	a	b	С	d	b	ı
score	0	1	-1	0			

S	a	b	С	d	-
a	1	-3	-2	0	0
b		3	-1	-4	0
С			0	-3	0
d				3	0
-					0

### Affine gap weight

- Find an alignment A to maximize (adopt the alphabet-dependent weights for matches and dismatches)

$$\sum_{i=1}^{l} s(S'_{1}(i), S'_{2}(i)) - W_{g}(\#gaps) - W_{s}(\#spaces)$$

• If  $W_g = 1$ ,  $W_s = 2$ 

S' <sub>1</sub>	С	a	С	-	-	b	d
S'2	С	a	b	С	d	b	-
score	0	1	-1	0	0	3	0

S	a	b	c	d	-
a	1	-3	-2	0	0
b		3	-1	-4	0
c			0	-3	0
d				3	0
-					0

$$(0+1-1+0+3+0)-(1*2)-(2*3)=-5$$

### Affine gap weight

- The affine gap weight model is the most commonly used gap model in the molecular biology literature
- Example : program FASTA
  - FASTA is a DNA and protein sequence alignment software
  - default setting:  $W_g = 10$ ,  $W_s = 2$
- more deeply section 11.8.6 (PPT 54 page)

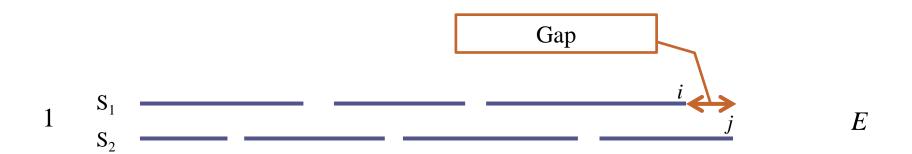
- Examine in detail four general types of gap weight
  - constant
  - affine
  - convex
  - arbitrary

### • Convex gap weight

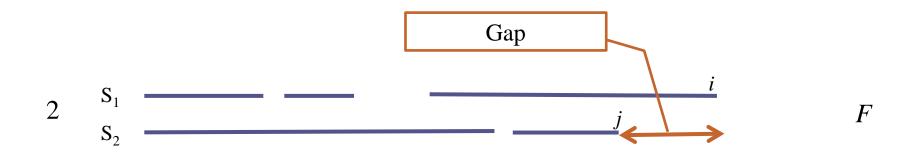
- used in some biological phenomena
- each additional space in a gap contributes less to the gap weight than the preceding space
- -example :  $W_g + \log q$

- Arbitrary gap weight are similar to Section 11.6.1
  - but more detailed than Section 11.6.1
- To alignment string S<sub>1</sub> and S<sub>2</sub>
  - prefixes  $S_1[1 ... i]$  of  $S_1$
  - prefixes  $S_2[1 ... j]$  of  $S_2$

• Any alignment of those two prefixes is one of the following three types.



- Character  $S_1(i)$  is aligned to a character strictly, to the left of character  $S_2(j)$
- The alignment ends with a gap in  $S_1$
- Define E(i, j) as the maximum value of any alignment of type 1;



- Character  $S_1(i)$  is aligned to a character strictly, to the right of character  $S_2(j)$
- The alignment ends with a gap in S<sub>2</sub>
- Define F(i,j) as the maximum value of any alignment of type 2;

- Characters  $S_1(i)$  and  $S_2(j)$  are aligned opposite each other.
- This includes both the case that  $S_1(i) = S_2(j)$  and that  $S_1(i) \neq S_2(j)$
- Define G(i,j) as the maximum value of any alignment of type 3;

#### Definition

- Define E(i, j) as the maximum value of any alignment of type 1;
- Define F(i, j) as the maximum value of any alignment of type 2;
- Define G(i, j) as the maximum value of any alignment of type 3;
- Finally V(i,j) as the maximum value of the three terms E(i,j), F(i,j), G(i,j)

### Recurrences for the case of arbitrary gap weight

- By dividing the types of alignments into three case
  - We can write the following recurrences that establish V(i, j)

$$V(i,j) = \max [E(i,j), F(i,j), G(i,j)]$$

$$G(i,j) = V(i-1,j-1) + s(S_1(i), S_2(j))$$

$$E(i,j) = \max_{0 \le k \le j-1} [V(i,k) - w(j-k)]$$

$$F(i,j) = \max_{0 \le l \le j-1} [V(l,j) - w(i-l)]$$

- To complete the recurrences, we need to specify
  - the base cases
  - and where the optimal alignment value is found
  - If all spaces are included in the objective function
    - base case is:

$$V(i, 0) = -w(i)$$

$$V(0, j) = -w(j)$$

$$E(i, 0) = -w(i)$$

$$F(0, j) = -w(j)$$

G(0, 0) = 0 [but G(i, j) is undefined if only j or i is 0]

- To complete the recurrences, we need to specify
  - the base cases
  - and where the optimal alignment value is found
  - When end space and end gaps are free:

$$V(i,0)=0$$

$$V(0,j)=0$$

### • Example

		С	а	b	С	b	<u>d</u>
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
a	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$w(i) = 10 * \sin i$$

Want to find V(4,3)

$$V(4,3) = \max [E(4,3), F(4,3), G(4,3)]$$

S	a	b	c	d	-
a	1	-3	-2	0	0
b		3	-1	-4	0
С			0	-3	0
d				3	0
-					0

		С	a	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
a	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	<b>4</b> ?		
b	7						
d	9						

$$G(4,3) = V(3,2) + s(S_1(3), S_2(2))$$
  
-7 + 0 = -7

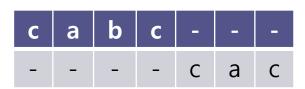
S	a	b	С	d	-
a	1	-3	-2	0	0
b		3	-1	-4	0
c			0	-3	0
d				3	0
-					0

		С	а	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
a	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$E(4,3) = \max_{0 \le k \le 2} [V(4,k) - w(3-k)]$$

		С	a	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
а	-9	-8	1	-7	-,2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$E(4,3) = \max_{0 \le k \le 2} [V(4,k) - w(3-k)]$$
$$V(4,0) - w(3-0) = 7 + 1 = 8$$

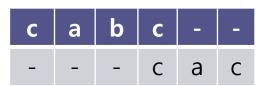


		С	a	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1 I	4	9
a	-9	-8	1	-7	- <u>,2</u>	0	1
С	-1	-9	-7	0	?-		
b	7						
d	9						

$$E(4,3) = \max_{0 \le k \le 2} [V(4,k) - w(3-k)]$$

$$V(4,0) - w(3-0) = 7 - 1 = 6$$

$$V(4,1) - w(3-1) = -1 - 9 = -10$$



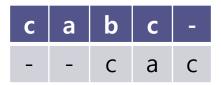
		С	a	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
a	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$E(4,3) = \max_{0 \le k \le 2} [V(4,k) - w(3-k)]$$

$$V(4,0) - w(3-0) = 7 - 1 = 6$$

$$V(4,1) - w(3-1) = -1 - 9 = -10$$

$$V(4,2) - w(3-2) = -2 - 8 = -10$$



		С	а	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
а	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$E(4,3) = \max_{0 \le k \le 2} [V(4,k) - w(3-k)]$$

$$V(4,0) - w(3-0) = 7 - 1 = 6$$

$$V(4,1) - w(3-1) = -1 - 9 = -10$$

$$V(4,2) - w(3-2) = -2 - 8 = -10$$

$$E(4,3) = \max[6, -10, -10] = 6$$

		С	а	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
а	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$F(4,3) = \max_{0 \le l \le 3} [V(l,3) - w(4-l)]$$

		С	a	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
а	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	?		
b	7						
d	9						

$$F(4,3) = \max_{0 \le l \le 3} [V(l,3) - w(4-l)]$$

$$V(0,3) - w(4-0) = -1 + 7 = 6$$

$$V(1,3) - w(4-1) = -9 - 1 = -10$$

$$V(2,3) - w(4-2) = -7 - 9 = -16$$

$$V(3,3) - w(4-3) = 0 - 8 = -8$$

$$F(4,3) = \max[6, -10, -16, -8] = 6$$

		С	а	b	С	b	d
	0	-8	-9	-1	7	9	2
С	-8	0	-8	-9	-1	4	9
a	-9	-8	1	-7	-2	0	1
С	-1	-9	-7	0	6		
b	7						
d	9						

$$V(4,3) = max[-7,6,6] = 6$$

- Theorem 11.8.1
  - Assuming that  $|S_1|=n$  and  $|S_2|=m$ 
    - the recurrences can be evaluated in  $O(nm^2+n^2m)$  time

### • Theorem 11.8.1

- Assuming that  $|S_1|=n$  and  $|S_2|=m$ 
  - the recurrences can be evaluated in  $O(nm^2+n^2m)$  time

### proof

- an (n+1)x(m+1) size table are filled from left to right, up to down
- To fill a cell (i, j)
- To evaluate E(i, j) examines j cells of row i,
  - $m(m+1)/2 = O(m^2)$  to evaluate E for that row  $n = O(nm^2)$
- To evaluate F(i, j) examines i cells of column j,
  - $n(n+1)/2 = O(n^2)$  to evaluate F for that column  $m = O(n^2m)$
- To evaluate G(i, j) examines one other cell  $\Longrightarrow O(nm)$
- Since there are *n* rows and *m* columns give  $O(nm^2+n^2m)$

### Proof

		С	а	b	С	b	d
	0	<b></b>					
С	<b>←</b>	1	2	3	4	5	_6
а		2					
С		3					
b		4					
d		5					

$$m = 6, n = 5$$

# Affine (and constant) gap weight

- Recall that the objective is to find as alignment to maximize  $[\ W_m(\#\ matches)\ -\ W_m(\#\ mismatches)\ -\ W_g(\#\ gaps)\ -\ W_s\ (\#\ spaces)\ ]$
- We will use the same variables in arbitrary gap weight V(i, j), E(i, j), F(i, j), G(i, j)
- In the affine gap weight model w(q+1)  $w(q) = W_s$ 
  - for any gap length q greater than 0

# Recurrences for affine gap weights

The base Case where end gaps are included:

$$V(i, 0) = E(i, 0) = -W_g - iW_s$$
  
 $V(0, j) = F(0, j) = -W_g - jW_s$ 

• If end spaces are free and end gaps are free

$$V(i, 0) = V(0, j) = 0$$

## Recurrences for affine gap weights

### Following recursive case:

- $V(i, j) = \max [E(i, j), F(i, j), G(i, j)]$ 
  - $G(i, j) = V(i-1, j-1) + W_m$  (if S1 = S2)
  - $G(i, j) = V(i-1, j-1) + W_{ms}$  (if  $S1 \neq S2$ )
  - $E(i, j) = \max [E(i, j-1), V(i, j-1) W_g] W_s$ 
    - S<sub>1</sub> end with a gap
  - $F(i, j) = \max [F(i-1, j), V(i-1, j) W_g] W_s$ 
    - S<sub>2</sub> end with a gap

### Example

		С	а	b	С	b	d
	0	-3	-4	-5	-6	-7	-8
С	-3	0	-3	-4	-5	-6	-7
a	-4	-3	1	-2	-3	-4	-5
С	-5	-4	-5	-6	?		
b	-6						
d	-7						

$$W_g = 2$$
,  $W_s = 1$ 

Want to find V(4,3)

$$V(4,3) = \max [E(4,3), F(4,3), G(4,3)]$$

S	a	b	c	d
a	1	-3	-2	0
b		3	-1	-4
С			0	-3
d				3
-				

		С	a	b	С	b	d
	0	-3	-4	-5	-6	-7	-8
С	-3	0	-3	-4	-5	-6	-7
a	-4	-3	1	-2	-3	-4	-5
С	-5	-4	-5	-6	<b>4</b> ?		
b	-6						
d	-7						

$$W_g = 2$$
,  $W_s = 1$ 

$$G(4,3) = V(3,2) + s(S_1(3), S_2(2))$$
  
=  $-2 + 0 = -2$ 

S	a	b	c	d
a	1	-3	-2	0
b		3	-1	-4
С			0	-3
d				3
-				

		С	a	b	С	b	d
	0	-3	-4	-5	-6	-7	-8
С	-3	0	-3	-4	-5	-6	-7
a	-4	-3	1	-2	-3	-4	-5
С	-5	-4	-5	-6	<b>\</b> ?		
b	-6						
d	-7						

$$W_g = 2$$
,  $W_s = 1$ 

$$E(4,3) = \max[E(4,2), V(4,2) - 2] - 1$$
$$= \max[-8, -5] - 1$$
$$= -5 - 1 = -6$$

0	-3	-4	-5	-6	-7	-8
-3	-4	-5	-6	-7	-8	-9
-4	-5	-6	-7	-8	-9	-10
-5	-6	-7	-8	?		
-6						
-7						

		С	a	b	С	b	d
	0	-3	-4	-5	-6	-7	-8
С	-3	0	-3	-4	-5	-6	-7
a	-4	-3	1	-2	-3	-4	-5
С	-5	-4	-5	-6	?		
b	-6						
d	-7						

$$W_g = 2$$
,  $W_s = 1$ 

$$F(4,3) = \max[F(3,3), V(3,3) - 2] - 1$$
$$= \max[-8, -8] - 1$$
$$= -8 - 1 = -9$$

0	-3	-4	-5	-6	-7	-8
-3	-4	-5	-6	-7	-8	-9
-4	-5	-6	-7	-8	-9	-10
-5	-6	-7	-8	?		
-6						
-7						

		С	a	b	С	b	d
	0	-3	-4	-5	-6	-7	-8
С	-3	0	-3	-4	-5	-6	-7
a	-4	-3	1	-2	-3	-4	-5
С	-5	-4	-5	-6	-2		
b	-6						
d	-7						

$$W_g = 2$$
,  $W_s = 1$ 

$$V(4,3) = \max [E(4,3), F(4,3), G(4,3)]$$
$$= \max [-6, -9, -2]$$
$$= -2$$

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• The optimal alignment with affine gap weights can be computed in O(nm) time, the same time as for optimal alignment without a gap term

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### proof

- an (n+1)x(m+1) size table are filled from left to right, up to down
- each of cell calculate E(i, j), F(i, j), G(i, j) for V(i, j)
- E(i, j), F(i, j), G(i, j) are calculated in constant time

### • O(nm) time