Local alignment

Given a string **P** (“pattern”) of length **m** and a string **T** (“text”) of length **n**, find substrings **a** and **b** of **P** and **T** respectively having maximal optimal global alignment score.

Example:

P = xyaxbacsll, **T** = pqraxabcstvq

Event	Example	Penalty
Match	TTG ||| TTG	+15
Mismatch	GTG | | GAG	-30
Gap in text	ATC | | A–C	-30
Gap in pattern	C–G | | CCG	-30

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Example:

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Answer:

a: a x - b a c s

b: a x a b - c s

15 + 15 + (-30) + 15 + (-30) + 15 + 15

Score = 15

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Match	TTG ||| TTG	+15
Mismatch	GTG | | GAG	-30
Gap in text	ATC | | A–C	-30
Gap in pattern	C–G | | CCG	-30

Smith-Waterman

Text

Pattern	-	c	c	c	t	t	c	c	t	t	a	c	g	c	g	a	c	c	c	a
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t	0																			
c	0																			
t	0																			
t	0																			
a	0																			
c	0																			
g	0																			
a	0																			
c	0																			

Event	Penalty
Match	+15
Mismatch	-30
Gap in text	-40
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Smith-Waterman

When filling in a cell...

$$H(i,j) = \max \begin{cases} 0 \\ H(i-1,j-1) + w(a_i, b_j) \\ H(i-1,j) + w(a_i, -) \\ H(i,j-1) + w(-, b_j) \end{cases}$$

Text

Pattern	-	c	c	c	t	t	c	c	t	t	a	c	g	c	g	a	c	c	c	a
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t	0																			
c	0																			
t	0																			
t	0																			
a	0																			
c	0																			
g	0																			
a	0																			
c	0																			

$w(a_i, b_j)$ Match or mismatch

$w(a_i, -)$ Text gap

$w(-, b_j)$ Pattern gap

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Consider diagonal move from upper-left (match or mismatch)

Text

Pattern	-	c	c	c	t	t	c	c	t	t	a	c	g	c	g	a	c	c	c	a
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t	0																			
c	0																			
t	0																			
t	0																			
a	0																			
c	0																			
g	0																			
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Consider diagonal move from upper-left (match or mismatch)

Consider vertical move from above (gap in text)

Text

Pattern	-	c	c	c	t	t	c	c	t	t	a	c	g	c	g	a	c	c	c	a
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t	0																			
c	0																			
t	0																			
t	0																			
a	0																			
c	0																			
g	0																			
a	0																			
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Consider diagonal move from upper-left (match or mismatch)

Consider vertical move from above (gap in text)

Consider horizontal move from left (gap in pattern)

Text

Pattern	-	c	c	c	t	t	c	c	t	t	a	c	g	c	g	a	c	c	c	a
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t	0																			
c	0																			
t	0																			
t	0																			
a	0																			
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Consider diagonal move from upper-left (match or mismatch)

Consider vertical move from above (gap in text)

Consider horizontal move from left (gap in pattern)

Text

Pattern		-	c	c	c	t	t	c	c	t	t	a	c	g	c	g	a	c	c	c	a
	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t		0	0	0	0	15	15	0	0	15	15	0	0	0	0	0	0	0	0	0	0
c		0	15	15	15	0	0	30	15	0	0	0	15	0	15	0	0	15	15	15	0
t		0	0	0	0	30	15	0	0	30	15	0	0	0	0	0	0	0	0	0	0
t		0	0	0	0	15	45	5	0	15	45	5	0	0	0	0	0	0	0	0	0
a		0	0	0	0	0	5	15	0	0	5	60	20	0	0	0	15	0	0	0	15
c		0	15	15	15	0	0	20	30	0	0	20	75	35	15	0	0	30	15	15	0
g		0	0	0	0	0	0	0	0	0	0	0	35	90	50	30	0	0	0	0	0
a		0	0	0	0	0	0	0	0	0	0	15	0	50	60	20	45	5	0	0	15
c		0	15	15	15	0	0	15	15	0	0	0	30	10	65	30	5	60	20	15	0

$w(a_i, b_j)$ Match or mismatch

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Event	Penalty
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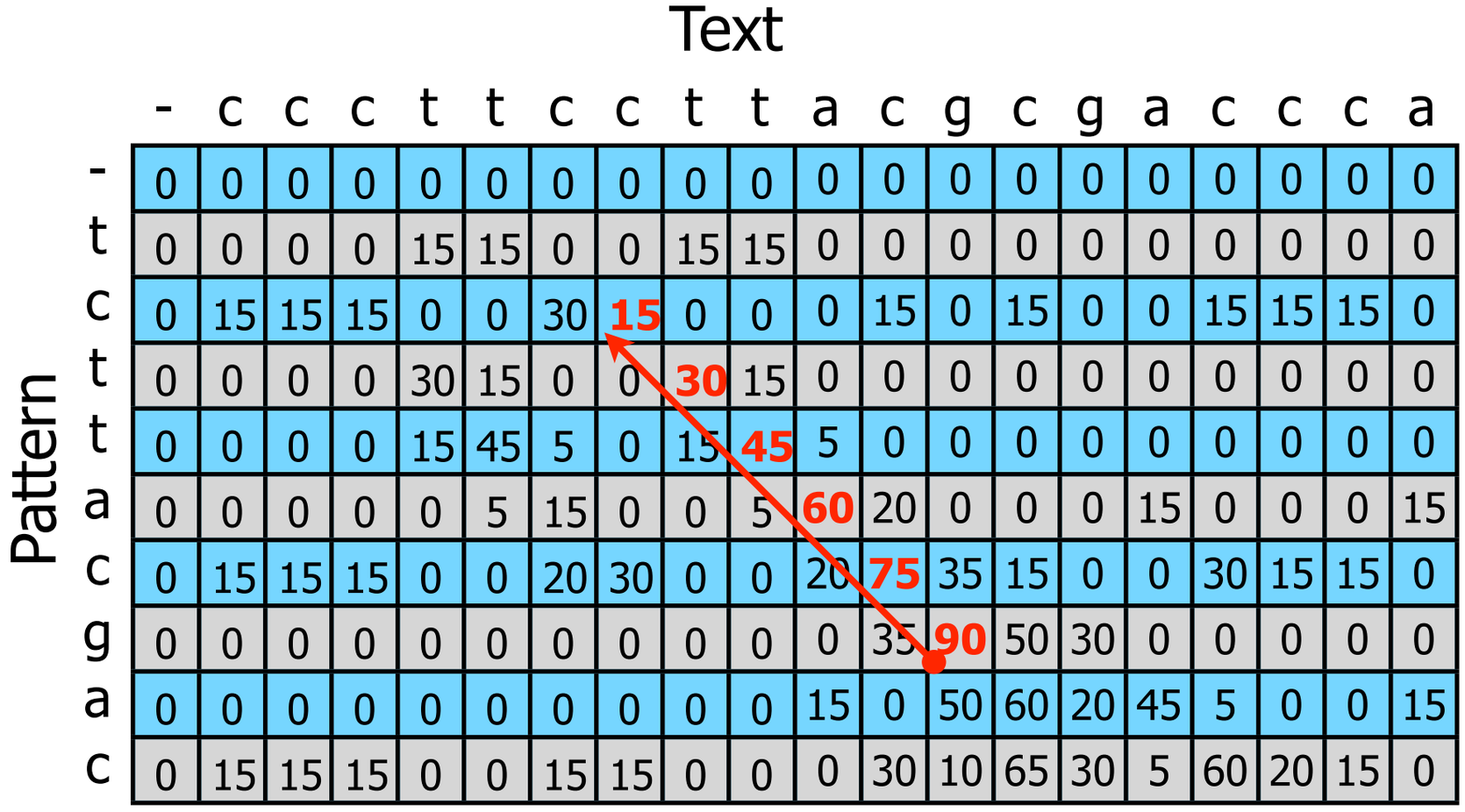
Gap in text	-40
Gap in pattern	-40

Smith-Waterman

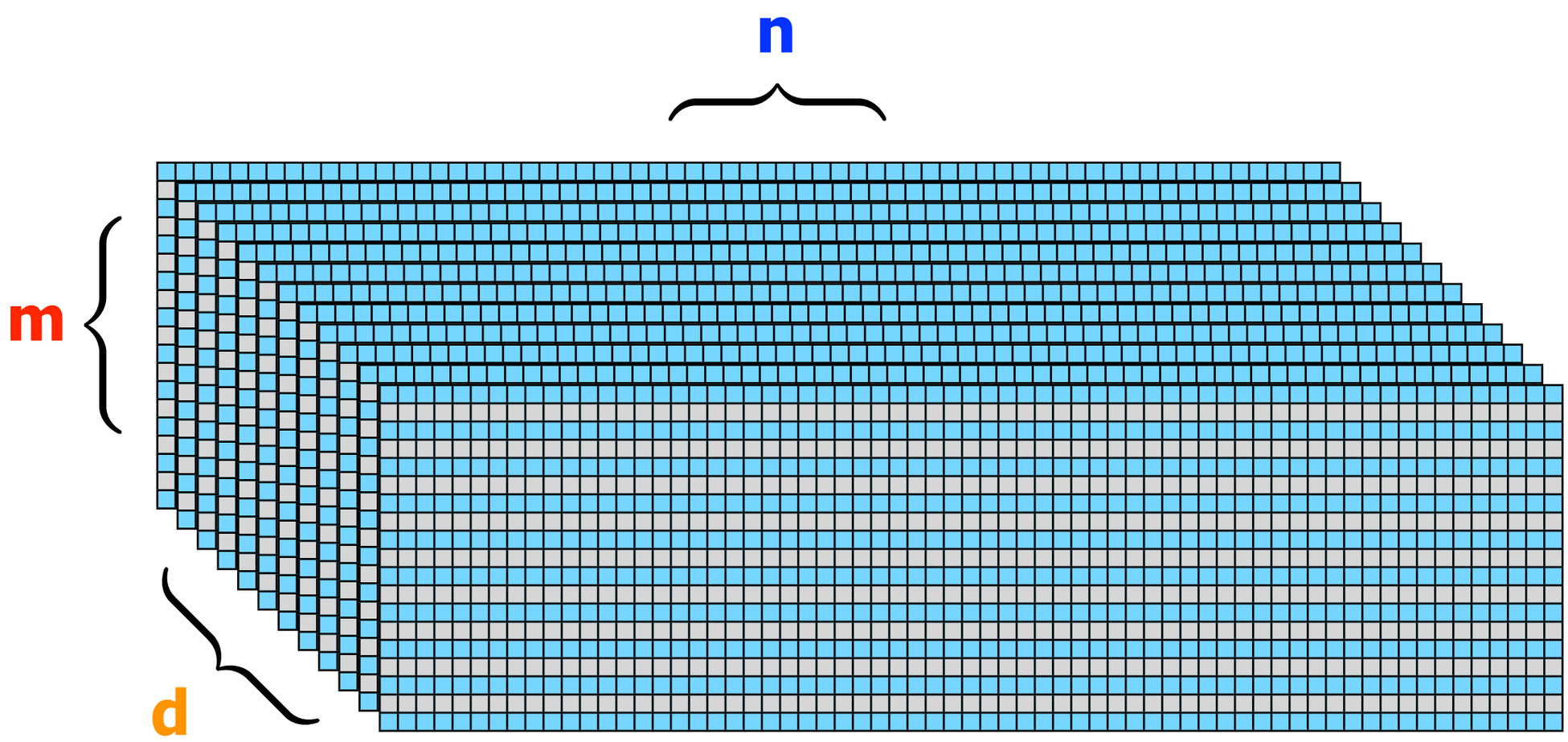
Answer:
```
  c t t a c g
  | | | | | |
  c t t a c g
```

Score: 90



Smith-Waterman

Alignining **d** reads of length **m** to reference of length **n** is O(**dmn**)



Dynamic programming alignment

d = 6 x 10^9 reads
m = 100 nt
} ≈ 1 week-long run of
n = 3 x 10^9 nt ≈ human

Illumina HiSeq 2000

Total of **d** x **m** x **n** = 2 x 10^{21} cell updates

100 processors, each capable of 100 billion cell updates per second, would take >6 years