

Space-Efficient Alignment

CMSC 858S

Space Usage

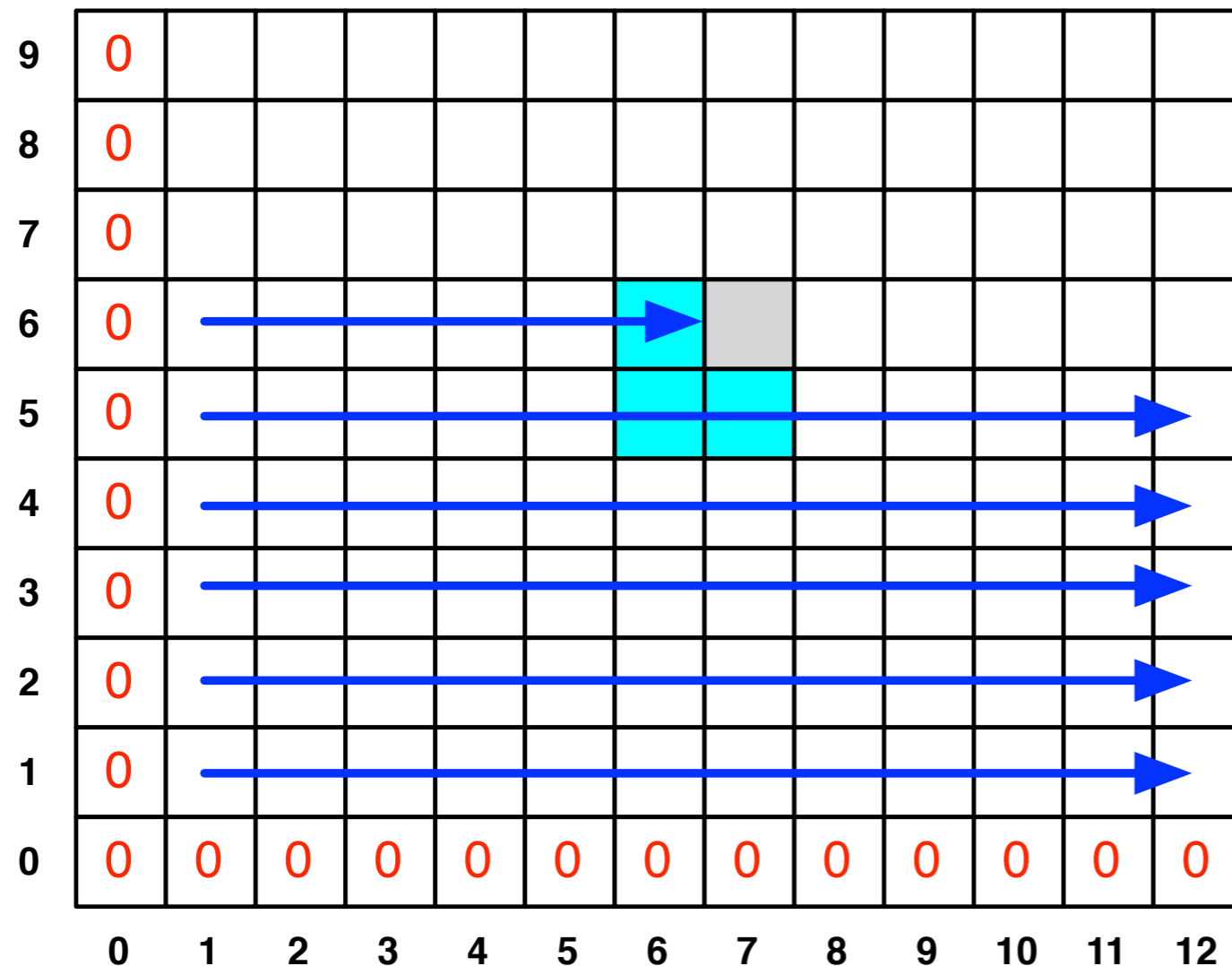
- $O(n^2)$ is pretty low space usage, but for a 10 Gb genome, you'd need a huge amount of memory.
- Can we use less?
 - Hirschberg's algorithm

Linear Space for Alignment **Scores**

- If you are only interested in the **cost** or **score** of an alignment, you need to use only $O(n)$ space.
- How?

Linear Space for Alignment **Scores**

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- How?



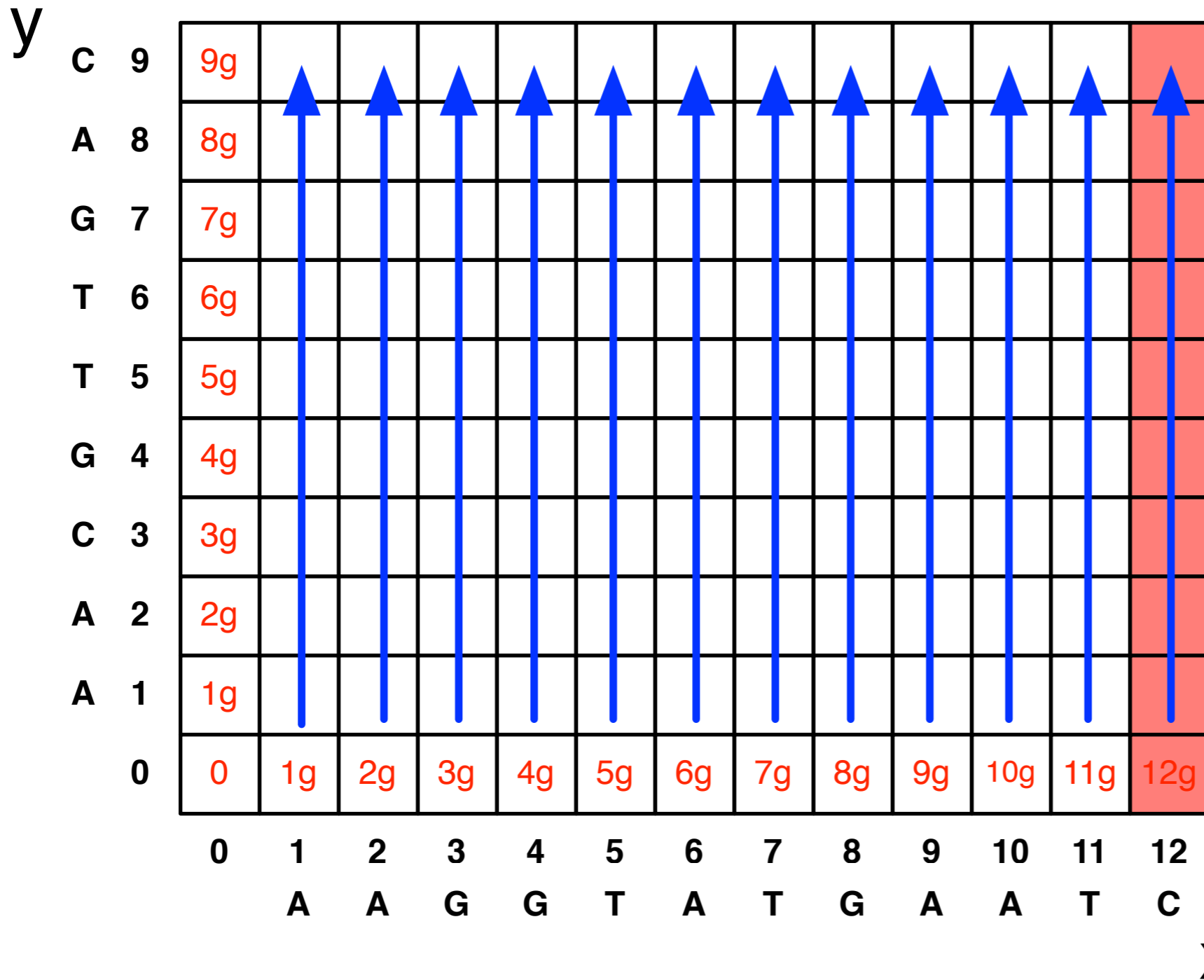
When filling in an entry (gray box) we only look at the current and previous rows.

Only need to keep those two rows in memory.

We can do more...

- Given 2 strings X and Y , we can, in linear space and $O(nm)$ time, compute the **cost** of aligning...
 - every prefix of X with Y
 - X with every prefix of Y
 - a particular prefix of X with every prefix of Y
 - a particular suffix of X with every suffix of Y
- How can we do that?

Fill in the matrix by columns...



What is this column?

Fill in the matrix by columns...

y

C	9	9g												
A	8	8g	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	
G	7	7g												
T	6	6g												
T	5	5g												
G	4	4g												
C	3	3g												
A	2	2g												
A	1	1g												
0	0	0	1g	2g	3g	4g	5g	6g	7g	8g	9g	10g	11g	12g
	0	1	2	3	4	5	6	7	8	9	10	11	12	
		A	A	G	G	T	A	T	G	A	A	T	C	

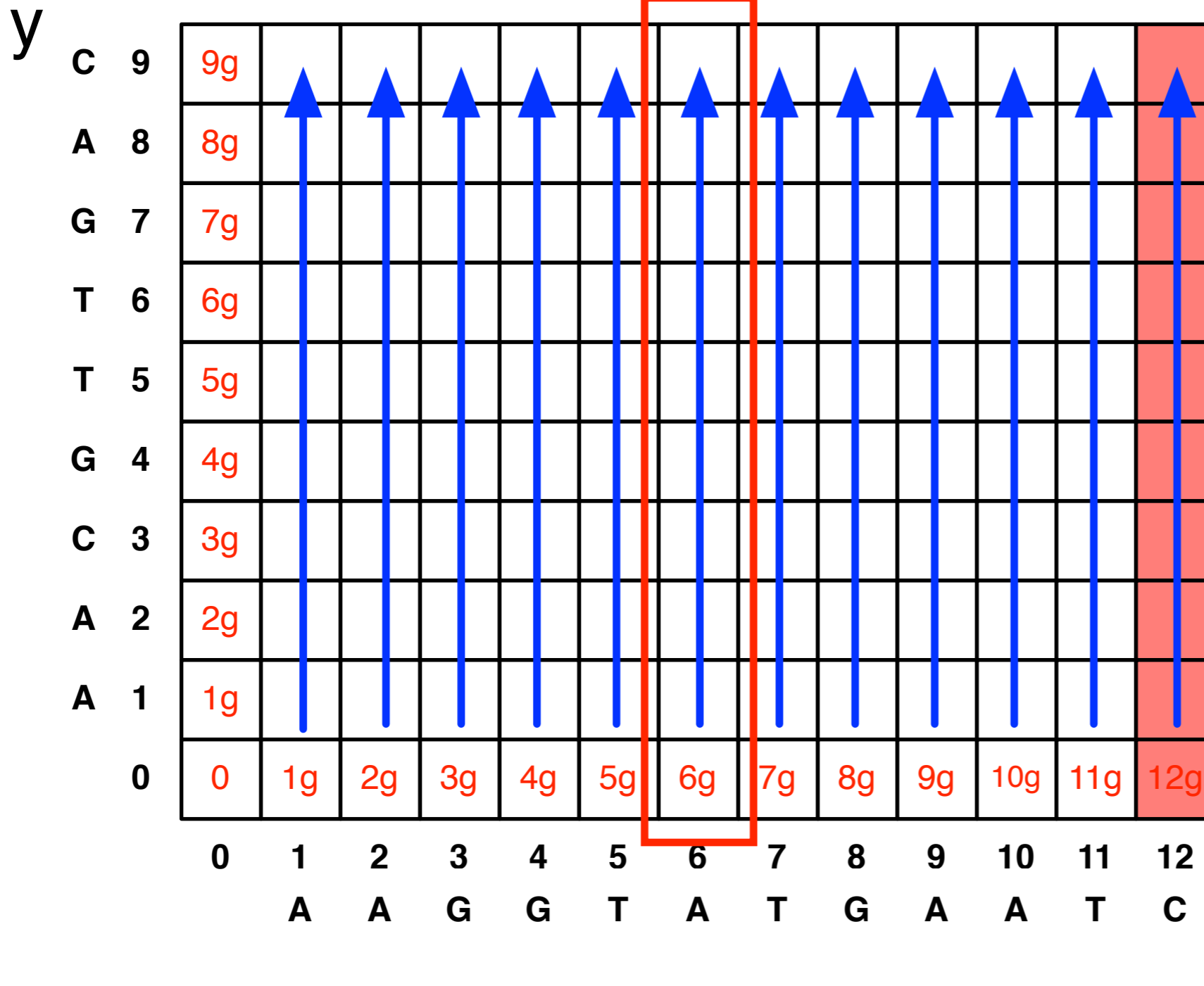
x

What is this column?

Best scores between X and all prefixes of Y

Fill in the matrix by columns...

Best scores between a prefix of X and all prefixes of Y

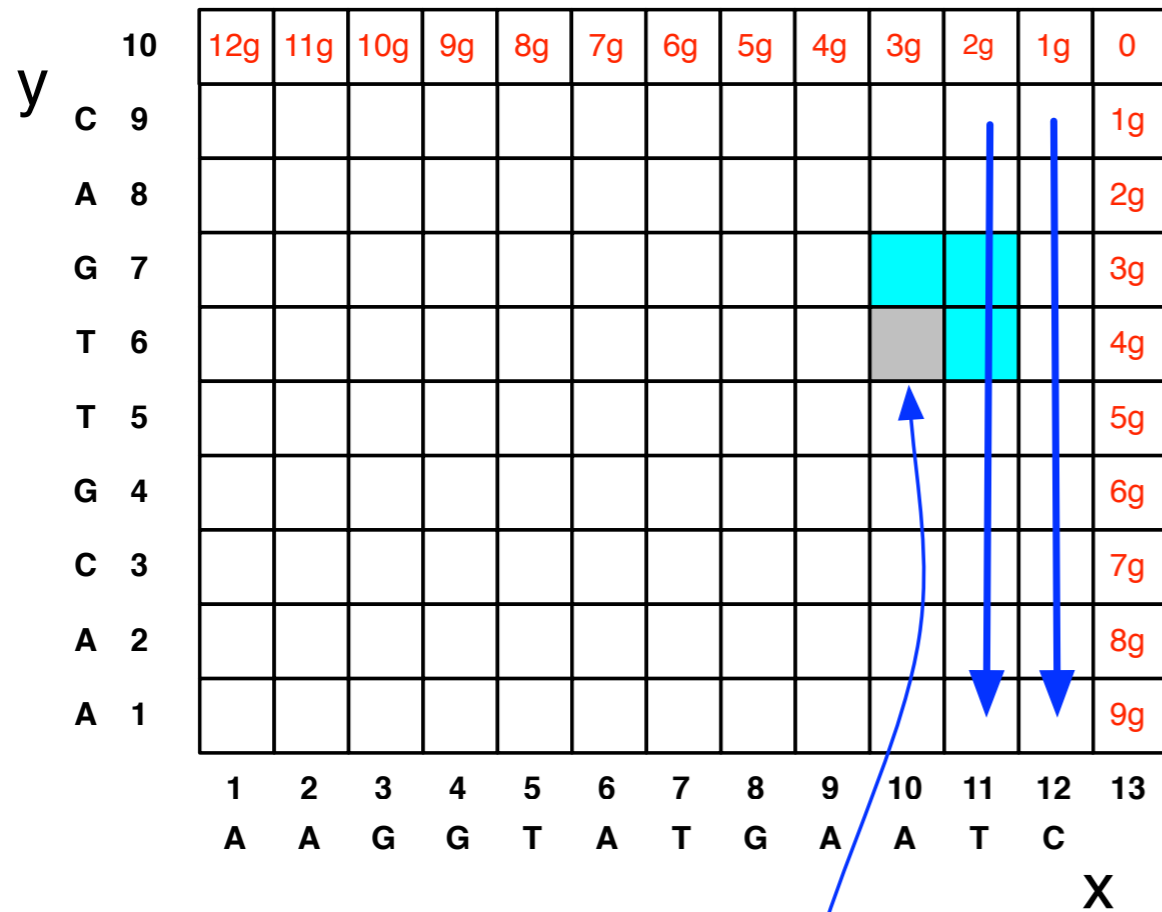


What is this column?

Best scores between X and all prefixes of Y

X

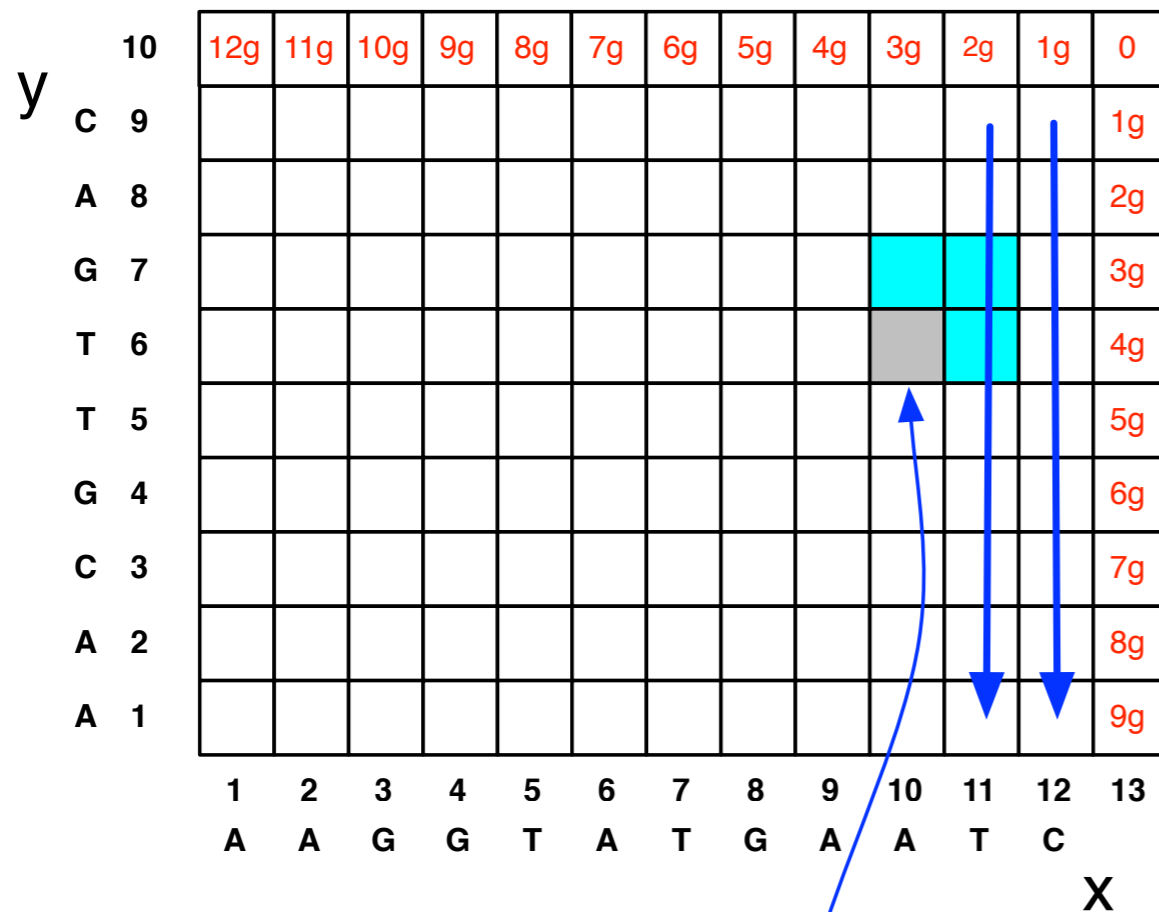
Cost of Alignment Between X and All Suffixes of Y



Best alignment
between suffix x[10..]
and suffix y[6..]

$$B[i, j] = \min \begin{cases} \text{cost}(x_i, y_j) + B[i + 1, j + 1] \\ \text{gap} + B[i, j + 1] \\ \text{gap} + B[i + 1, j] \end{cases}$$

Cost of Alignment Between X and All Suffixes of Y

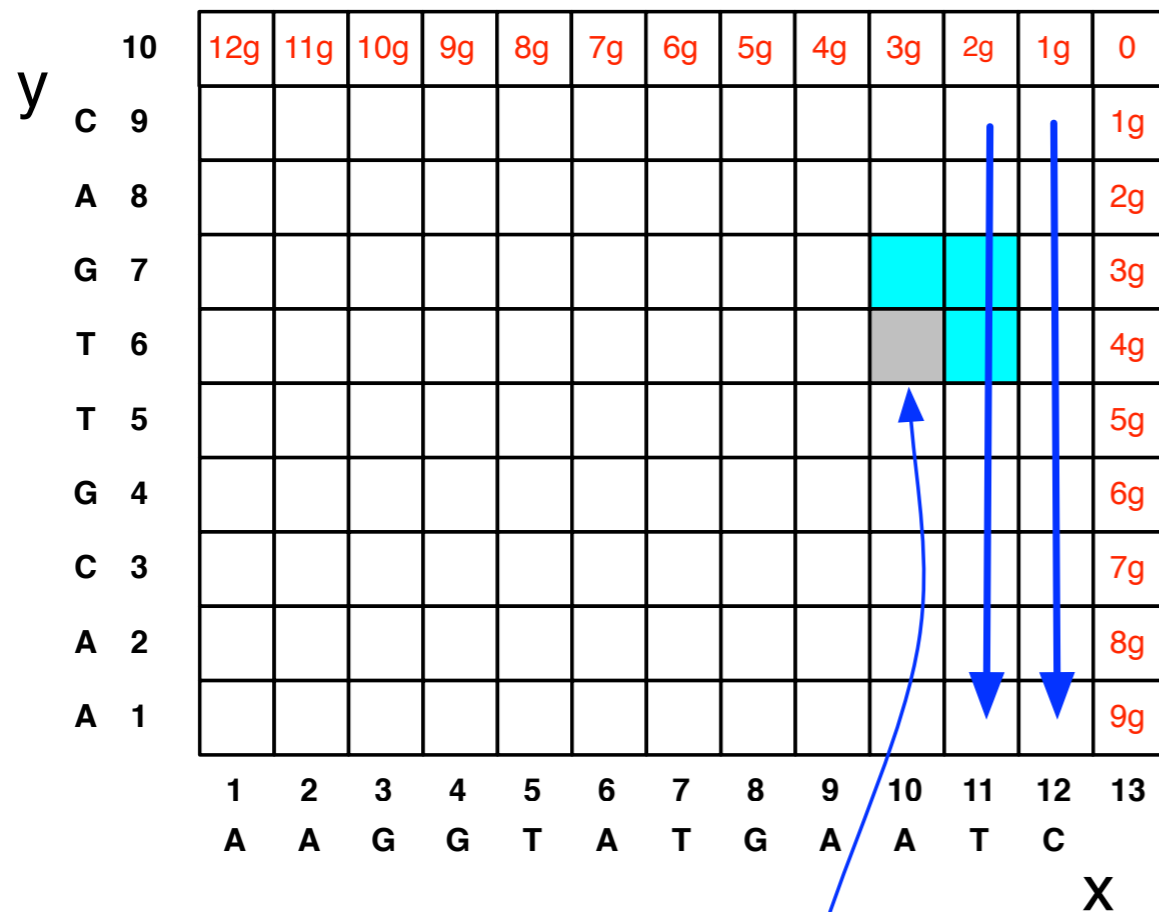


Best alignment
between suffix x[10..]
and suffix y[6..]

Exactly the same reasoning as doing the “forward” dynamic programming.

$$B[i, j] = \min \begin{cases} \text{cost}(x_i, y_j) + B[i + 1, j + 1] \\ \text{gap} + B[i, j + 1] \\ \text{gap} + B[i + 1, j] \end{cases}$$

Cost of Alignment Between X and All Suffixes of Y



Best alignment between suffix x[10..] and suffix y[6..]

“Backward” dynamic programming.

Exactly the same reasoning as doing the “forward” dynamic programming.

$$B[i, j] = \min \begin{cases} \text{cost}(x_i, y_j) + B[i + 1, j + 1] \\ \text{gap} + B[i, j + 1] \\ \text{gap} + B[i + 1, j] \end{cases}$$

Can We Find the Alignment in $O(n)$ Space?

- Surprisingly, yes, we can output the optimal alignment in linear space.
- This will cost us some extra computation but only a constant factor
- for such a dramatic reduction in space, it's often worth it.
- **Idea:** a divide-and-conquer algorithm to compute half alignments.

Divide & Conquer

- General algorithmic design technique:
 - Split large problem into a few subproblems.
 - Recursively solve each subproblem.
 - Merge the resulting answers.
- You probably know such algorithms:
 - Merge sort
 - Quick sort

Notation

- **AlignValue**(x, y) = compute the *cost* of the best alignment between x and y in $O(\min |x|, |y|)$ space.
- Finding the actual alignment is equivalent to finding all the cells that the **optimal backtrace** passes through.
- Call the optimal backtrace the **ArrowPath**.

First Attempt At Space Efficient Alignment

In the optimal alignment, the first $n/2$ characters of x are aligned with the first q characters of y for some q .

```
      12345678
x = ACGTACTG
y = A-GT-CTG
          
      q = 3
```

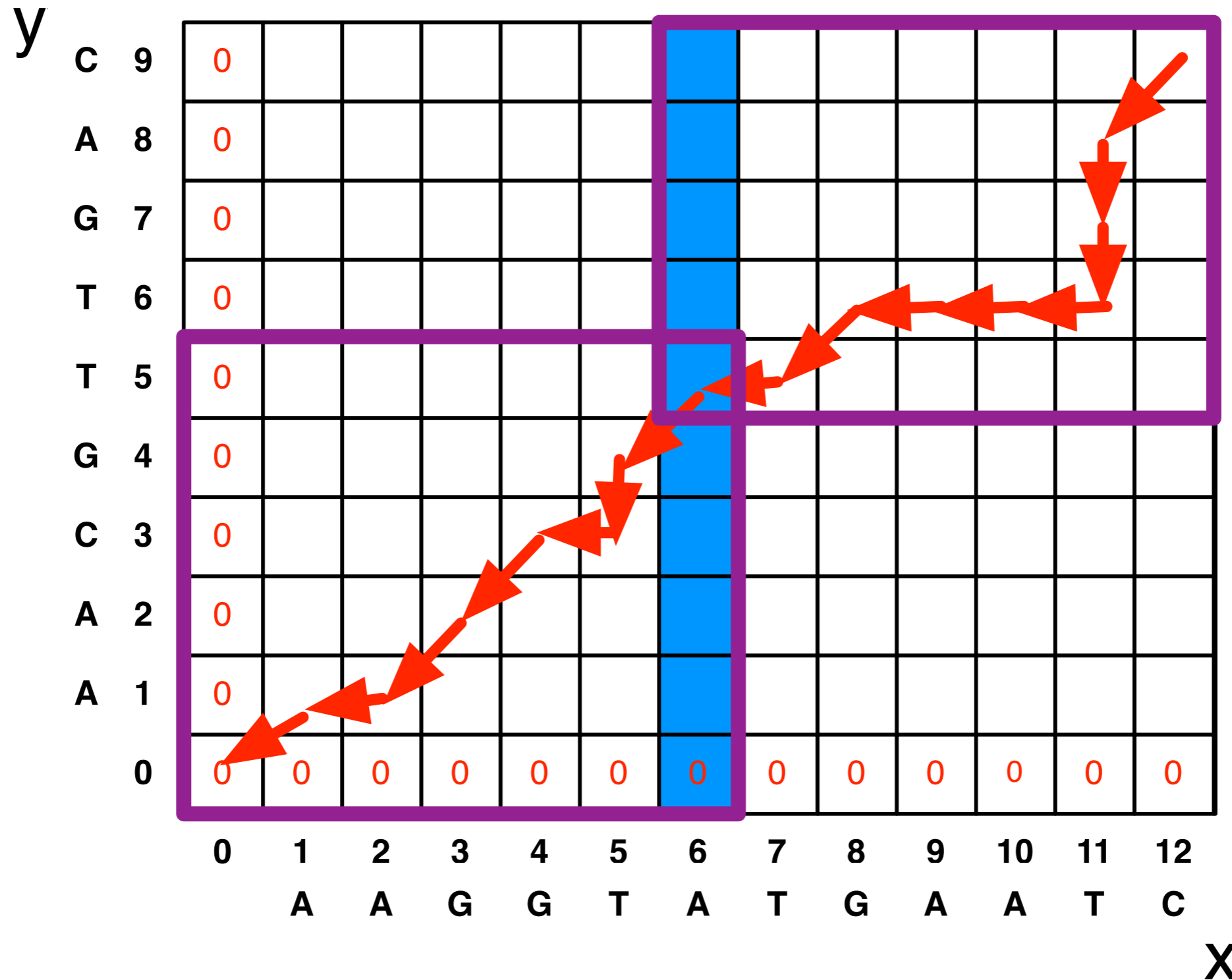
We don't know q , so we have to try *all* possible q .

```
ArrowPath := []
def Align(x, y):
  n := |x|; m := |y|
  if n or m ≤ 2: use standard alignment      O(n) or O(m) space
  for q := 0..m:
    v1 := AlignValue(x[1..n/2], y[1..q])    O(n+m) space
    v2 := AlignValue(x[n/2+1..n], y[q+1..m]) O(n+m) space
    if v1 + v2 < best: bestq = q; best = v1 + v2
```

```
Add (n/2, bestq) to ArrowPath
Align(x[1..n/2], y[1..bestq])
Align(x[n/2+1..n], y[bestq+1..m])
```

find the q that minimizes
the cost of the alignment

The Best Path Uses Some Cell in the Middle Column



Problem

- This works in linear space.
- BUT: not in $O(nm)$ time.
- It's too expensive to solve all those `AlignValue` problems in the **for** loop.
- Define:
 - **AllyPrefixCosts**(x, i, y) = returns an array of the scores of optimal alignments between `x[1..i]` and all prefixes of `Y`.
 - **AllySuffixCosts**(x, i, y) = returns an array of the scores of optimal alignments between `x[i..n]` and all suffixes of `y`.
 - These are implemented as described in previous slides by returning the last row or last column of the DP matrix.

Space Efficient Alignment

12345678
x = ACGTACTG
y = A-GT-CTG
 └───┘
 q = 3

We still try all possible q , but we use the fact that we can compute the cost between a given prefix and *all* suffixes in linear space.

```
ArrowPath := []
```

```
def Align(x, y):  
  n := |x|; m := |y|  
  if n or m ≤ 2: use standard alignment  $O(n)$  or  $O(m)$  space
```

```
YPrefix := AllYPrefixCosts(x, n/2, y)  
YSuffix := AllYSuffixCosts(x, n/2+1, y) }  $O(n+m)$  space
```

```
for q := 0..m:  
  cost = YPrefix[q] + YSuffix[q+1]  
  if cost < best: bestq = q; best = cost
```

find the q that minimizes the cost of the alignment, using the costs of aligning X to prefixes and suffixes of Y

```
Add (n/2, bestq) to ArrowPath  
Align(x[1..n/2], y[1..bestq])  
Align(x[n/2+1..n], y[bestq+1..m])
```

Running Time Recurrence, I

Full recurrence:

$$\begin{aligned} T(n, 2) &\leq cn && \text{Align}(x[n/2+1..n], y[\text{best}q+1..m]) \\ T(2, m) &\leq cm \\ T(n, m) &\leq \underbrace{cmn}_{\text{Align}(x[1..n/2], y[1..\text{best}q])} + T(n/2, q) + \overbrace{T(n/2, m - q)} \end{aligned}$$

Too complicated because we don't know what q is.

Simplify: assume both sequences have length n , and that we get a perfect split in half every time, $q=n/2$:

$$T(n) \leq 2T(n/2) + cn^2$$

Solves as:

$$T(n) = O(n^2)$$

Running Time Recurrence, 2

$$T(n, 2) \leq cn$$

$$T(2, m) \leq cm$$

$$T(n, m) \leq cmn + T(n/2, q) + T(n/2, m - q)$$

Guess: $T(n, m) \leq kmn$, for some k .

Proof, by induction:

Base cases: If $k \geq c$ then $T(n, 2) \leq cn \leq c2n \leq k2n = kmn$

Induction step: Assume $T(m', n') \leq km'n'$ for pairs (m', n') with a product smaller than mn :

$$\begin{aligned} T(m, n) &\leq cmn + T(n/2, q) + T(n/2, m - q) \\ &\leq cmn + kqn/2 + k(m - q)n/2 \quad \leftarrow \text{apply induction hypothesis} \\ &= cmn + kqn/2 + kmn/2 - kqn/2 \\ &= (c + k/2)mn \end{aligned}$$

$$k = 2c \implies T(m, n) \leq 2cmn = kmn$$



Recap

- Can compute the cost of an alignment easily in linear space.
- Can compute the cost of a string with all suffixes of a second string in linear space.
- Divide and conquer algorithm for computing the *actual* alignment (traceback path in the DP matrix) in linear space.
- Still uses $O(nm)$ time!