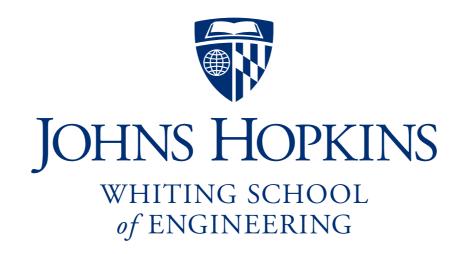
# Dynamic Programming & Edit Distance

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#### Approximate matching for biosequences

Some widely used approximate matching algorithms for DNA (& other strings) came from the biological community, aiming to bring alignments into closer harmony with biological processes that mutate strings

```
Score = 248 bits (129), Expect = 1e-63
Identities = 213/263 (80%), Gaps = 34/263 (12%)
Strand = Plus / Plus
Query: 161 atatcaccacgtcaaaggtgactccaactcca---ccactccattttgttcagataatgc 217
        Sbjct: 481 atatcaccacgtcaaaggtgactccaact-tattgatagtgttttatgttcagataatgc 539
Query: 218 ccgatgatcatgtcatgcagctccaccgattgtgagaacgacagcgacttccgtcccagc 277
        Sbjct: 540 ccgatgactttgtcatgcagctccaccgattttg-g-----ttccgtcccagc 586
Query: 278 c-gtgcc--aggtgctgcctcagattcaggttatgccgctcaattcgctgcgtatatcgc 334
        Sbjct: 587 caatgacgta-gtgctgcctcagattcaggttatgccgctcaattcgctgggtatatcgc 645
Query: 335 ttgctgattacgtgcagctttcccttcaggcggga-----ccagccatccgtc 382
        Query: 383 ctccatatc-accacgtcaaagg 404
        Sbjct: 706 atccatatcaaccacgtcaaagg 728
```

# Hamming / edit distance

For X, Y where |X| = |Y|, hamming distance = minimum # substitutions needed to turn one into the other

For *X*, *Y*, *edit distance* = minimum # edits (substitutions, insertions, deletions) needed to turn one into the other

### Finding distances

Strategy: walk along both strings. For each position, compare the characters in both strings at that position. If not equal, increment hamming distance:

# Finding distances

Finding Hamming distance between strings is pretty easy. What about edit distance?

If |X| = |Y| what can we say about the relationship between **editDistance**(X, Y) and **hammingDistance**(X, Y)?

editDistance $(X, Y) \leq \text{hammingDistance}(X, Y)$ 

If x and y are different lengths, what can we say about **editDistance**(X, Y)?

editDistance
$$(X, Y) \ge ||X| - |Y||$$

*X*: ? ?

Y: ????

Python example: http://bit.ly/CG\_DP\_EditDist

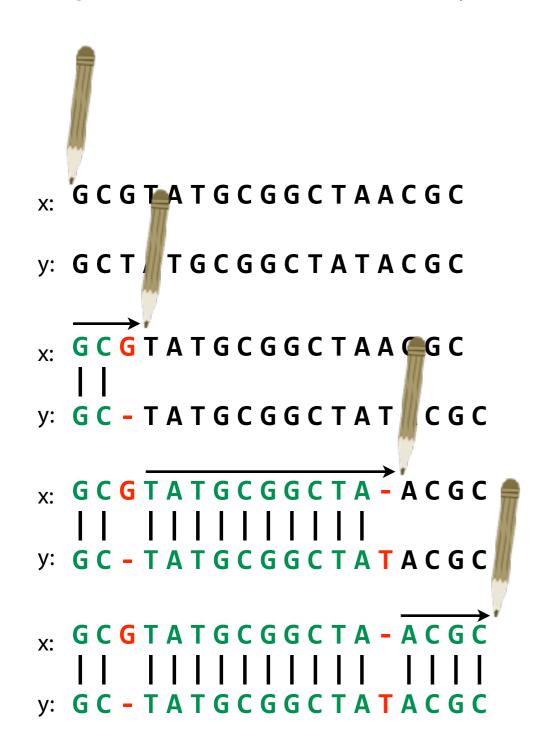
TGGCCGCAAAAACAGC

Y
AATGCCGCGAAAAAAAAAA

**editDistance**(*X*[:-1], *Y*[:-1]) = 147

Knowing distances between substrings of X & Y (or prefixes, suffixes) tells you something about overall distance

Imagine edits are introduced by an optimal editor working left-to-right:

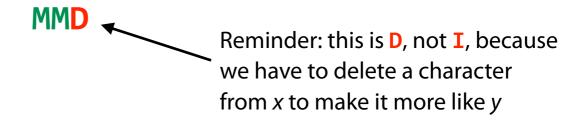


Edit transcript summarizes how editor turns x into y

#### Operations:

M = match, R = replace,

I = insert into x, D = delete from x



MMDMMMMMMMMI

Alignments:

Edit transcripts (w/r/t x):

```
X: GCGTATGCGGCTA-ACGC
y: GC-TATGCGGCTATACGC
```

MMDMMMMMMMMMIMMM

Distance = 2

```
replacement (AKA substitution/mismatch)
X: GCGTATGAGGCTA-ACGC
y: GC-TATGCGGCTATACGC
```

MMDMMMMRMMMMMIMMMM

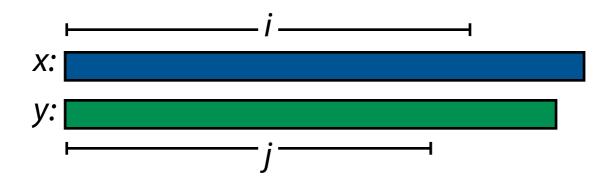
Distance = 3

```
x: the longest----
y: ---longest day
```

DDDDMMMMMMTT

Distance = 8

D[i, j]: edit distance between length-i prefix of x and length-j prefix of y



Optimal edit transcript for D[i, j] is built by extending a shorter one by 1 operation. 3 options:

Append D to transcript for D[i-1, j]

Append I to transcript for D[i, j-1]

Append M or R to transcript for D[i-1, j-1]

D[i, j] and its transcript come from 1 of these 3 choices, whichever has fewest edits D[|x|, |y|] is the overall edit distance

Let 
$$D[0,j]=j,$$
 and let  $D[i,0]=i$  
$$D[i-1,j]+1$$
 Otherwise, let  $D[i,j]=\min \left\{ \begin{array}{l} D[i-1,j]+1 \\ D[i,j-1]+1 \\ D[i-1,j-1]+1 \end{array} \right.$  diagonal (M or R) 
$$D[i-1,j-1]+\delta(x[i-1],y[j-1])$$

 $\delta(a,b)$  is 0 if a=b,1 otherwise

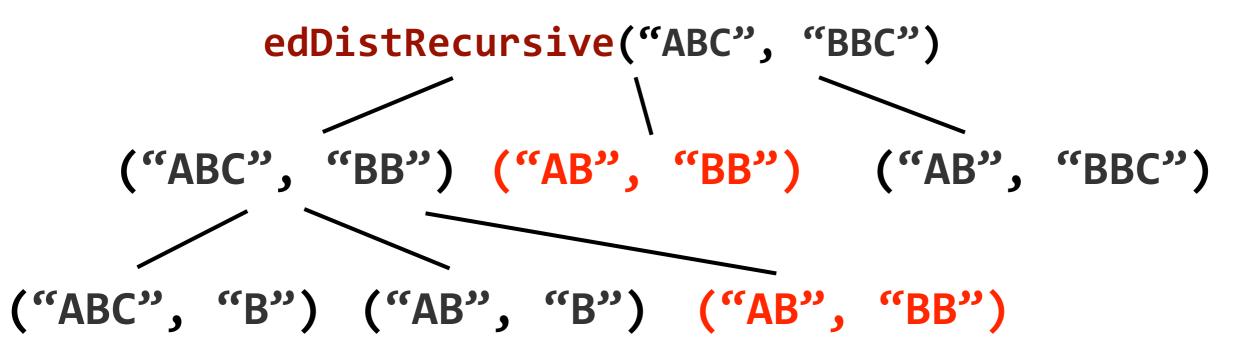
```
Let D[0,j]=j, and let D[i,0]=i  \text{Otherwise, let }D[i,j]=\min \left\{ \begin{array}{l} D[i-1,j]+1\\ D[i,j-1]+1\\ D[i-1,j-1]+\delta(x[i-1],y[j-1]) \end{array} \right.  \delta(a,b) is 0 if a=b, 1 otherwise
```

Direct implementation of recurrence above:

Python example: http://bit.ly/CG\_DP\_EditDist

```
>>> import datetime as d
>>> st = d.datetime.now(); \
... edDistRecursive("Shakespeare", "shake spear"); \
... print (d.datetime.now()-st).total_seconds()
3
31.498284
```

Takes >30 seconds for a small problem



Some subtrees are identical!

```
n = 0
def edDistRecursive(a, b):
    global n
    if len(a) == 0:
        return len(b)
    if len(b) == 0:
        return len(a)
    if a == 'Shake' and b == 'shake':
       n += 1
    delt = 1 if a[-1] != b[-1] else 0
    return min(edDistRecursive(a[:-1], b[:-1]) + delt,
               edDistRecursive(a[:-1], b) + 1,
               edDistRecursive(a, b[:-1]) + 1)
```

```
>>> edDistRecursive("Shakespeare", "shake spear")
3
>>> n
8989
```

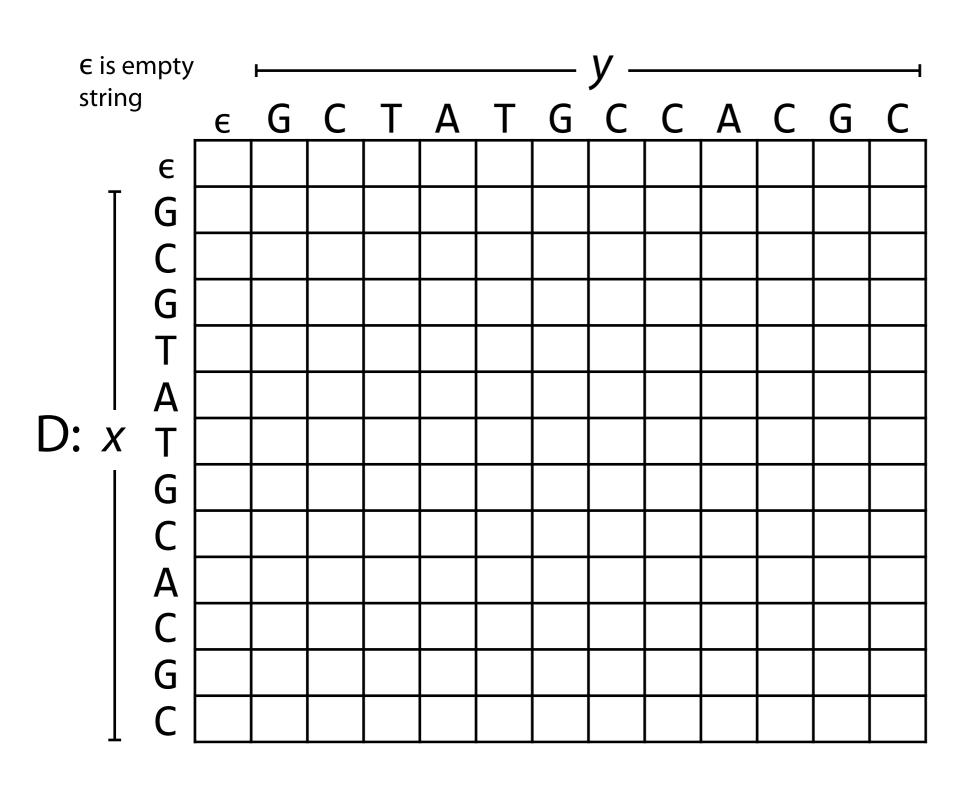
Subproblems (D[i, j]s) are reused many times; no need to recalculate them

```
Reusing
solutions to
subproblems is
memoization:
                     def edDistRecursiveMemo(a, b, memo):
                         if len(a) == 0:
                             return len(b)
                         if len(b) == 0:
                             return len(a)
  Return memo,
                         if (len(a), len(b)) in memo:
  if available
                             return memo[(len(a), len(b))]
                         delt = 1 if a[-1] != b[-1] else 0
                         ans = min(edDistRecursiveMemo(a[:-1], b[:-1], memo) + delt,
                                   edDistRecursiveMemo(a[:-1], b, memo) + 1,
                                   edDistRecursiveMemo(a, b[:-1], memo) + 1)
  Memoize D[i, j] \longrightarrow memo[(len(a), len(b))] = ans
                         return ans
```

```
>>> import datetime as d
>>> st = d.datetime.now(); \
... edDistRecursiveMemo("Shakespeare", "shake spear", {}); \
... print (d.datetime.now()-st).total_seconds()
3
0.000593
```

edDistRecursiveMemo is a top-down dynamic programming approach

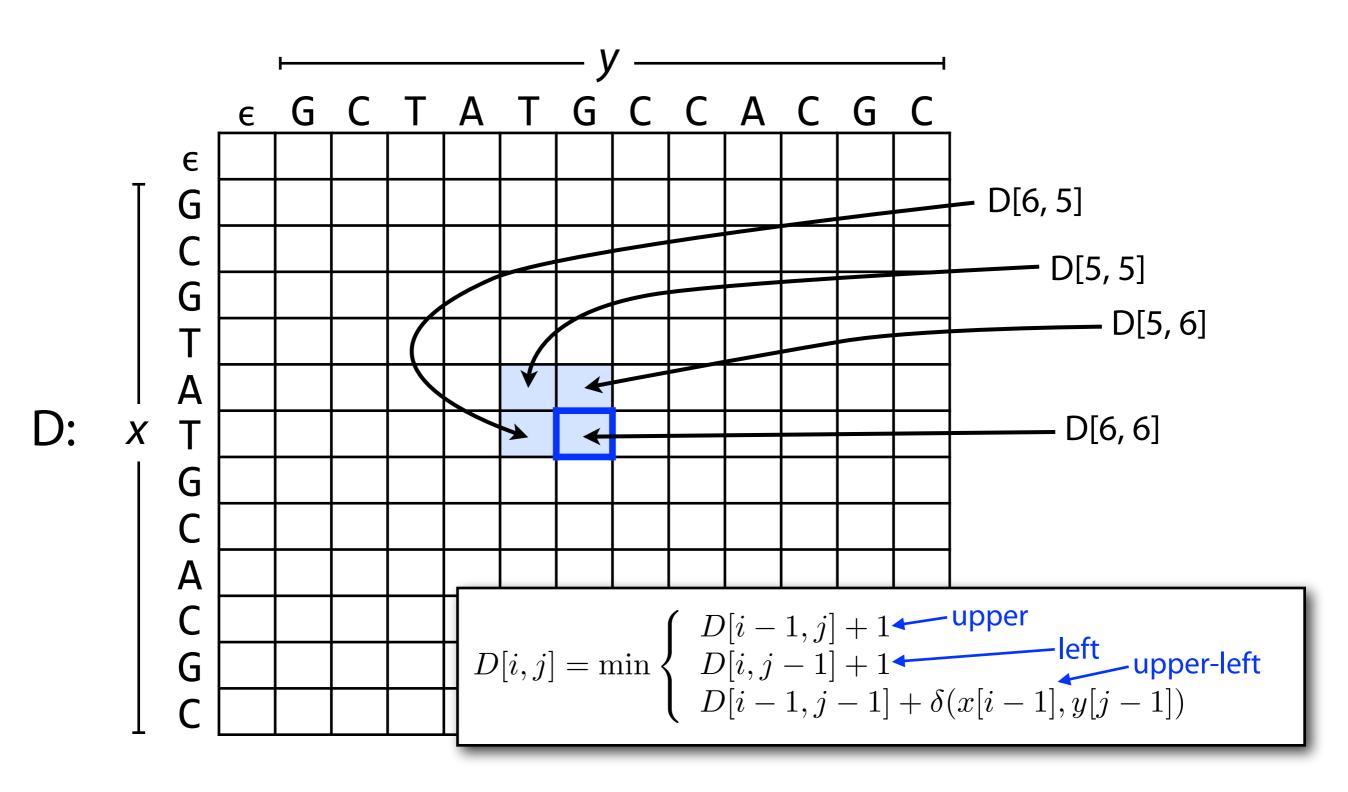
Alternative is *bottom-up*: fill a table (matrix) of D[*i*, *j*]s:



Let 
$$n = |x|, m = |y|$$

D:  $(n+1) \times (m+1)$  matrix

D[i, j] = edit distance b/tlength-i prefix of x and length-j prefix of y



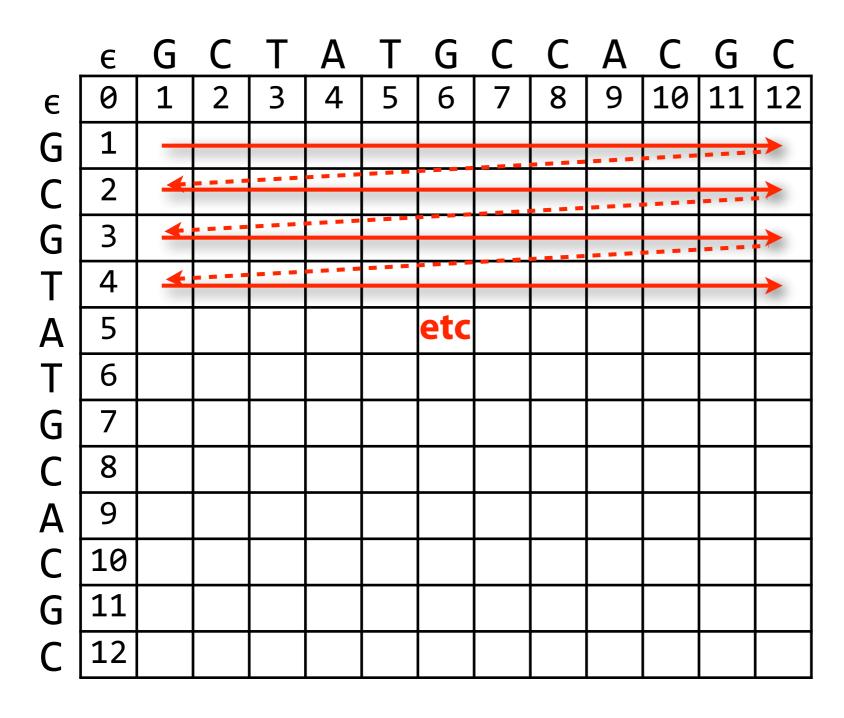
Cell depends upon its upper, left, and upper-left neighbors

```
First few lines
Of edDistDp:

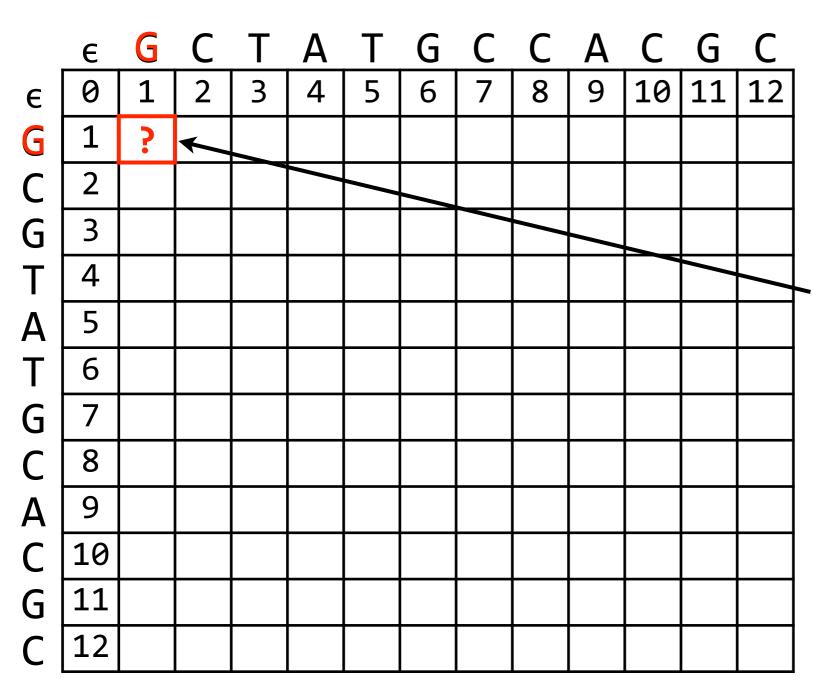
D = numpy.zeros((len(x)+1, len(y)+1), dtype=int)
D[0, 1:] = range(1, len(y)+1)
D[1:, 0] = range(1, len(x)+1)
```

	_€_	G			<u>A</u>		G			<u>A</u>		G	<u> </u>
$\epsilon$	0	1	2	<b>M</b>	4	5	6	7	8	9	10	11	12
G	1												
C	2												
G	3												
Т	4												
А	5												
Т	6												
G	7												
C	8												
Α	9												
C	10												
G	11												
C	12												

Initialize D[0, j] to j, D[i, 0] to i



Fill remaining cells from top row to bottom and from left to right



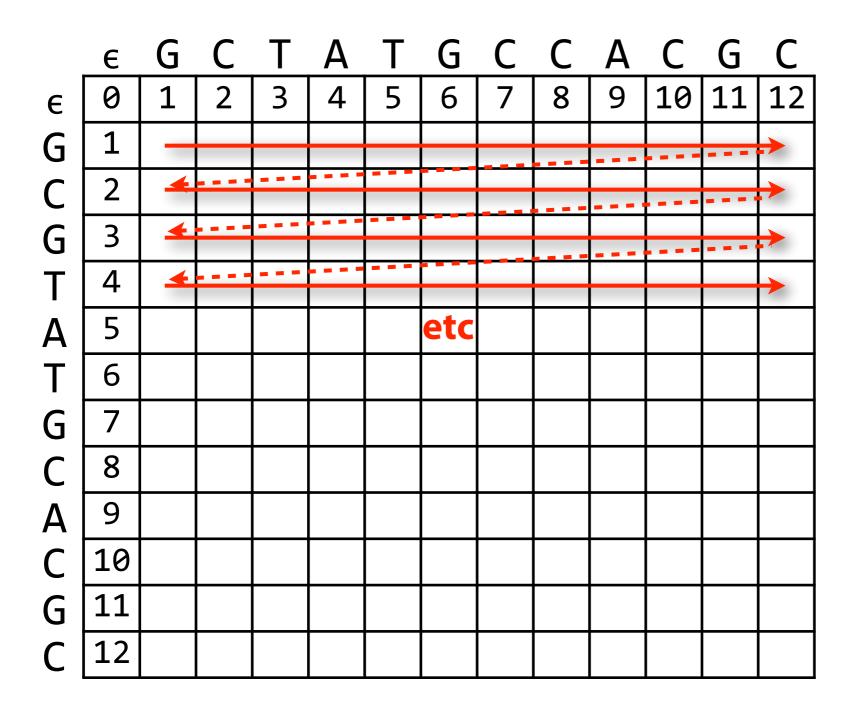
Fill remaining cells from top row to bottom and from left to right

What goes here in i=1,j=1?

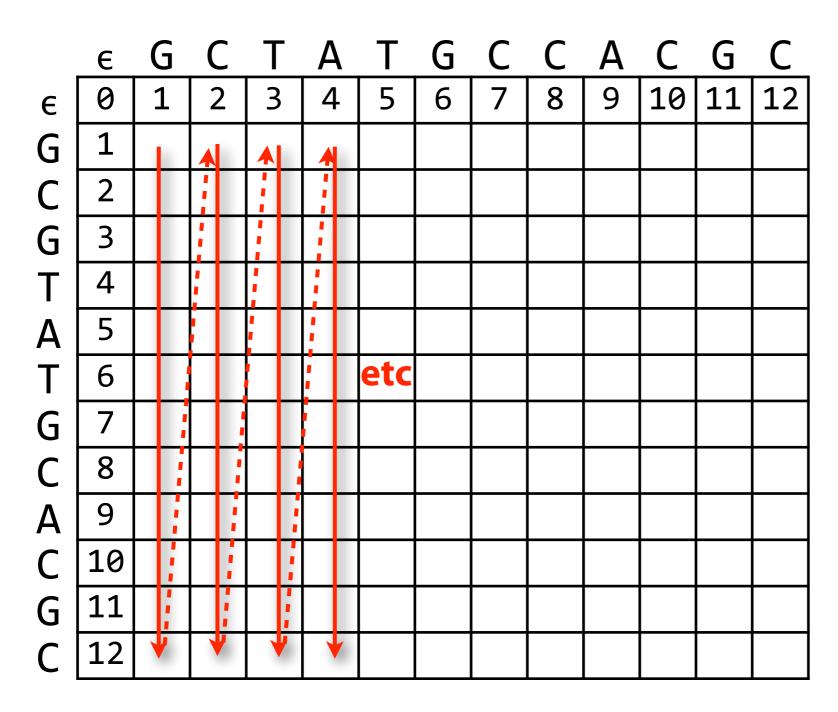
	$\epsilon$	G	C	T	Α	T	G	C	C	Α	C	G	<u>C</u>
$\epsilon$	0	1	2	ന	4	5	6	7	8	9	10	11	12
G	1	0	1	2	3	4	5	6	7	8	9	10	11
C	2	1	0	1	2	3	4	5	6	7	8	9	10
G	3	2	1	1	2	3	3	4	5	6	7	8	9
T	4	3	2	1	2	2	3	4	5	6	7	8	9
Α	5	4	3	2	1	2	3	4	5	5	6	7	8
Τ	6	5	4	3	2	1	2	3	4	5	6	7	8
G	7	6	5	4	3	2	1	2	3	4	5	6	7
C	8	7	6	5	4	3	2	1	2	3	4	5	6
Α	9	8	7	6	5	4	3	2	2	2	3	4	5
C	10	9	8	7	6	5	4	3	2	3	2	<b>M</b>	4
G	11	10	9	8	7	6	5	4	3	3	3	2	3
C	12	11	10	9	8	7	6	5	4	4	3	3	2 <

Fill remaining cells from top row to bottom and from left to right

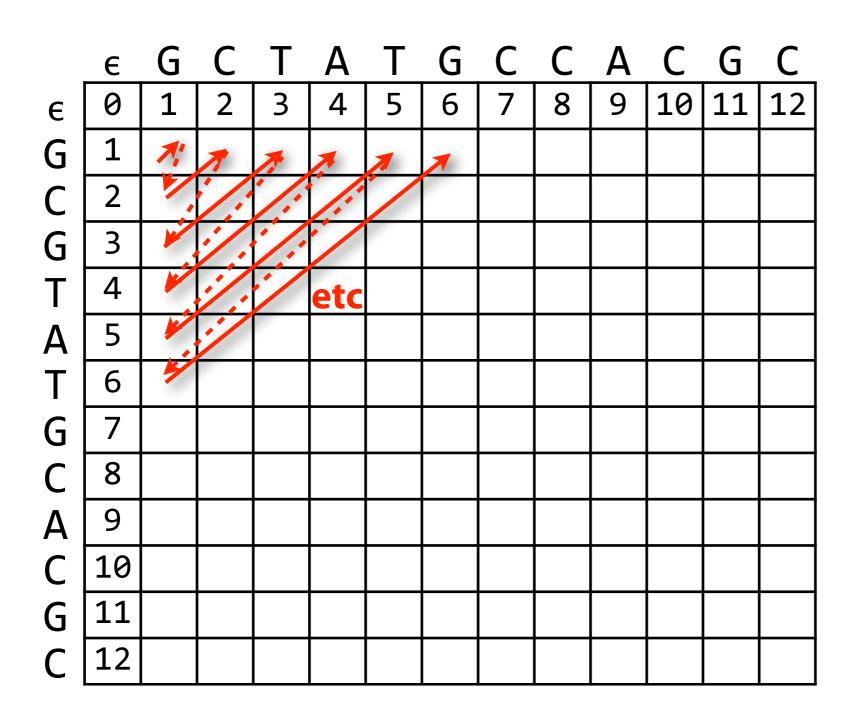
Edit distance for x, y



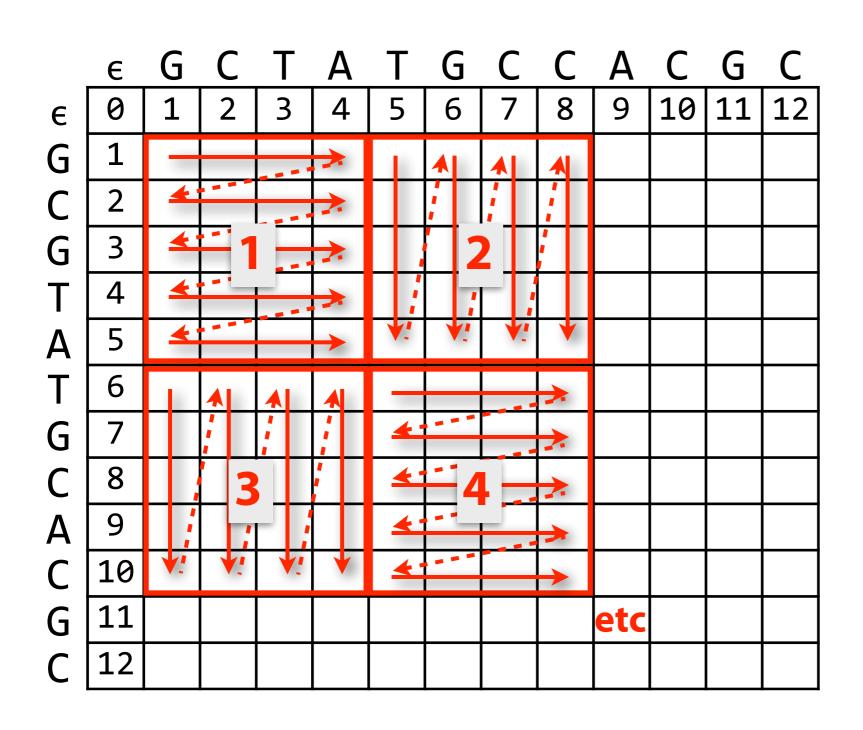
Could we have filled the cells in a different order?



Yes: e.g. invert the loops



Or by anti-diagonal



Or in blocks

	$\epsilon$	G	C	Т	Α	Т	G	C	C	Α	C	G	C
$\epsilon$	0	1	2	3	4	5	6	7	8	9	10	11	12
G	1	0	1	2	3	4	5	6	7	8	9	10	11
C	2	1	0	1	2	3	4	5	6	7	8	9	10
G	3	2	1	1	2	3	3	4	5	6	7	8	9
T	4	3	2	1	2	2	3	4	5	6	7	8	9
Α	5	4	3	2	1	2	3	4	5	5	6	7	8
Τ	6	5	4	3	2	1	2	3	4	5	6	7	8
G	7	6	5	4	3	2	1	2	3	4	5	6	7
C	8	7	6	5	4	3	2	1	2	3	4	5	6
Α	9	8	7	6	5	4	3	2	2	2	3	4	5
C	10	9	8	7	6	5	4	3	2	3	2	3	4
G	11	10	9	8	7	6	5	4	3	3	3	2	3
C	12	11	10	9	8	7	6	5	4	4	3	3	2

← Edit distance for x, y

But where and what are the 2 edits?

Traceback corresponds to an optimal alignment / edit transcript

	€	G	C	T	Α	T	G	C	C	Α	C	G	C	
$\epsilon$	0	1	2	3	4	5	6	7	8	9	10	11	12	
G	1	0	1	2	3	4	5	6	7	8	9	10	11	
C	2	1	0	1	2	3	4	5	6	7	8	9	10	
G	3	2	1	1	2	3	3	4	5	6	7	8	9	
T	4	3	2	1	2	2	3	4	5	6	7	8	9	
Α	5	4	3	2	1	2	3	4	5	5	6	7	8	
Τ	6	5	4	3	2	1	2	3	4	5	6	7	8	
G	7	6	5	4	3	2	1	2	3	4	5	6	7	
C	8	7	6	5	4	3	2	1	2	3	4	5	6	
Α	9	8	7	6	5	4	3	2	2	2	3	4	5	
C	10	9	8	7	6	5	4	3	2	3	2	3	4	
G	11	10	9	8	7	6	5	4	3	3	3	2≺	3	<ul><li>A: From here</li></ul>
C	12	11	10	9	8	7	6	5	4	4	3	3	2	—— Q: How did I get he

Traceback corresponds to an optimal alignment / edit transcript

	$\epsilon$	G	C	T	Α	Т	G	C	C	Α	C	G	C	
$\epsilon$	0	1	2	3	4	5	6	7	8	9	10	11	12	
G	1	0	1	2	<b>M</b>	4	5	6	7	8	9	10	11	
C	2	1	0	1	2	M	4	5	6	7	8	9	10	
G	3	2	1	1	2	M	3	4	5	6	7	8	9	
T	4	3	2	1	2	2	3	4	5	6	7	8	9	
Α	5	4	M	2	1	2	3	4	5	5	6	7	8	
T	6	5	4	M	2	1	2	M	4	5	6	7	8	
G	7	6	5	4	M	2	1	2	3	4	5	6	7	
C	8	7	6	5	4	M	2	1	2	3	4	5	6	
Α	9	8	7	6	5	4	3	2	2	2	3	4	5	
C	10	9	8	7	6	5	4	3	2	M	2<	m	4	<ul><li>A: From here</li></ul>
G	11	10	9	8	7	6	5	4	3	3	3	2	4	——— Q: How did I get here?
C	12	11	10	9	8	7	6	5	4	4	3	3	2	

Traceback corresponds to an optimal alignment / edit transcript

	$\epsilon$	G	C	Т	Α	Т	G	C	C	Α	C	G	C	
$\epsilon$	0	1	2	3	4	5	6	7	8	9	10	11	12	
G	1	0	1	2	3	4	5	6	7	8	9	10	11	
C	2	1	0	1	2	M	4	5	6	7	8	9	10	
G	3	2	1	1	2	M	M	4	5	6	7	8	9	
T	4	3	2	1	2	2	M	4	5	6	7	8	9	
Α	5	4	3	2	1	2	M	4	5	5	6	7	8	
T	6	5	4	M	2	1	2	M	4	5	6	7	8	
G	7	6	5	4	3	2	1	2	3	4	5	6	7	
C	8	7	6	5	4	M	2	1	2	3	4	5	6	
Α	9	8	7	6	5	4	<b>M</b>	2	2	2 <	(3	4	5	A: From here
C	10	9	8	7	6	5	4	3	2	3	2	<b>M</b>	4	—— Q: How did I get here?
G	11	10	9	8	7	6	5	4	3	3	3	1	3	
C	12	11	10	9	8	7	6	5	4	4	3	3	2	

Traceback corresponds to an optimal alignment / edit transcript

	E	G	C	Т	Α	Т	G	C	C	Α	C	G	C	_
$\epsilon$	0	1	2	3	4	5	6	7	8	9	10	11	12	
G	1	0	1	2	3	4	5	6	7	8	9	10	11	
C	2	1	0	1	2	M	4	5	6	7	8	9	10	
G	3	2	1	1	2	M	<b>M</b>	4	5	6	7	8	9	
T	4	3	2	1	2	2	M	4	5	6	7	8	9	
Α	5	4	3	2	1	2	3	4	5	5	6	7	8	
T	6	5	4	3	2	1	2	<b>A</b>	4	5	6	7	8	A: From here
G	7	6	5	4	3	2	1	2	<b>(</b>	4	5	6	7	Q: How did I get here?
C	8	7	6	5	4	3	2	1	12	3	4	5	6	
Α	9	8	7	6	5	4	3	2	2	2	3	4	5	
C	10	9	8	7	6	5	4	3	2	3	2	3	4	
G	11	10	9	8	7	6	5	4	3	3	3	4	3	
C	12	11	10	9	8	7	6	5	4	4	3	3	2	

Traceback corresponds to an optimal alignment / edit transcript

At each step, ask: which neighbor ( $\nabla$ ,  $\leftarrow$  or  $\uparrow\uparrow$ ) gave the minimum?

	$\epsilon$	G	C	T	Α	Τ	G	C	C	Α	C	G	<u>C</u>
$\epsilon$	Ø	1	2	3	4	5	6	7	8	9	10	11	12
G	1	2	1	2	3	4	5	6	7	8	9	10	11
C	2	1		1	2	3	4	5	6	7	8	9	10
G	3	2	1	1	2	3	3	4	5	6	7	8	9
T	4	3	2	X	2	2	3	4	5	6	7	8	9
Α	5	4	3	2	X	2	3	4	5	5	6	7	8
T	6	5	4	3	2	×	2	3	4	5	6	7	8
G	7	6	5	4	3	2	H	4	3	4	5	6	7
C	8	7	6	5	4	3	2	1	S. C.	3	4	5	6
Α	9	8	7	6	5	4	3	2	2	24	3	4	5
C	10	9	8	7	6	5	4	3	2	3	24	3	4
G	11	10	9	8	7	6	5	4	3	3	3	2	3
C	12	11	10	9	8	7	6	5	4	4	3	3	2

Alignment:

Edit transcript:

MMDMMMMIMMMMM

To find the edit distance and the alignment we did: (a) table filling, (b) traceback

	E	G	C	Т	Α	Т	G	C	C	Α	C	G	C
$\epsilon$	0	1	2	3	4	5	6	7	8	9	10	11	12
G	1	2	1	2	3	4	5	6	7	8	9	10	11
C	2	1		1	2	3	4	5	6	7	8	9	10
G	3	2	4	1	2	3	3	4	5	6	7	8	9
T	4	3	2	×	2	2	3	4	5	6	7	8	9
Α	5	4	3	2	×	2	3	4	5	5	6	7	8
Т	6	5	4	3	2	×	2	3	4	5	6	7	8
G	7	6	5	4	3	2	H	9	3	4	5	6	7
C	8	7	6	5	4	3	2	1	2	3	4	5	6
Α	9	8	7	6	5	4	3	2	2	2	3	4	5
C	10	9	8	7	6	5	4	<b>M</b>	2	M	34	3	4
G	11	10	9	8	7	6	5	4	3	3	3	2	3
C	12	11	10	9	8	7	6	5	4	4	3	3	2

If |X| = m and |Y| = n, how much work is table filling?

Filling (m + 1)(n + 1)
cells, each requiring
constant work, so O(mn)

How much work is traceback?

Each step goes  $\nabla$ ,  $\Leftarrow$  or  $\uparrow$ .

Worst case: traceback never moves diagonally, requiring  $m \Uparrow$ 's and  $n \Leftarrow$ 's, so O(m + n)

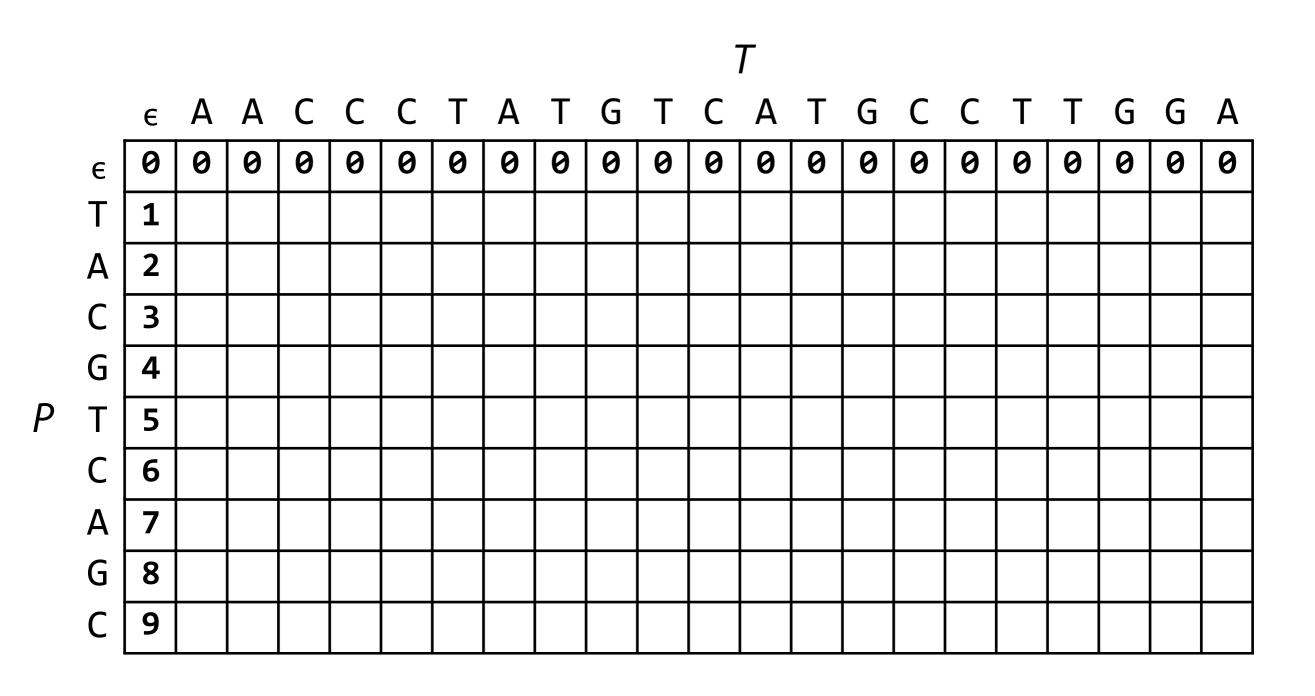
### Edit distance: summary

Matrix-filling dynamic programming algorithm is O(mn) time and space

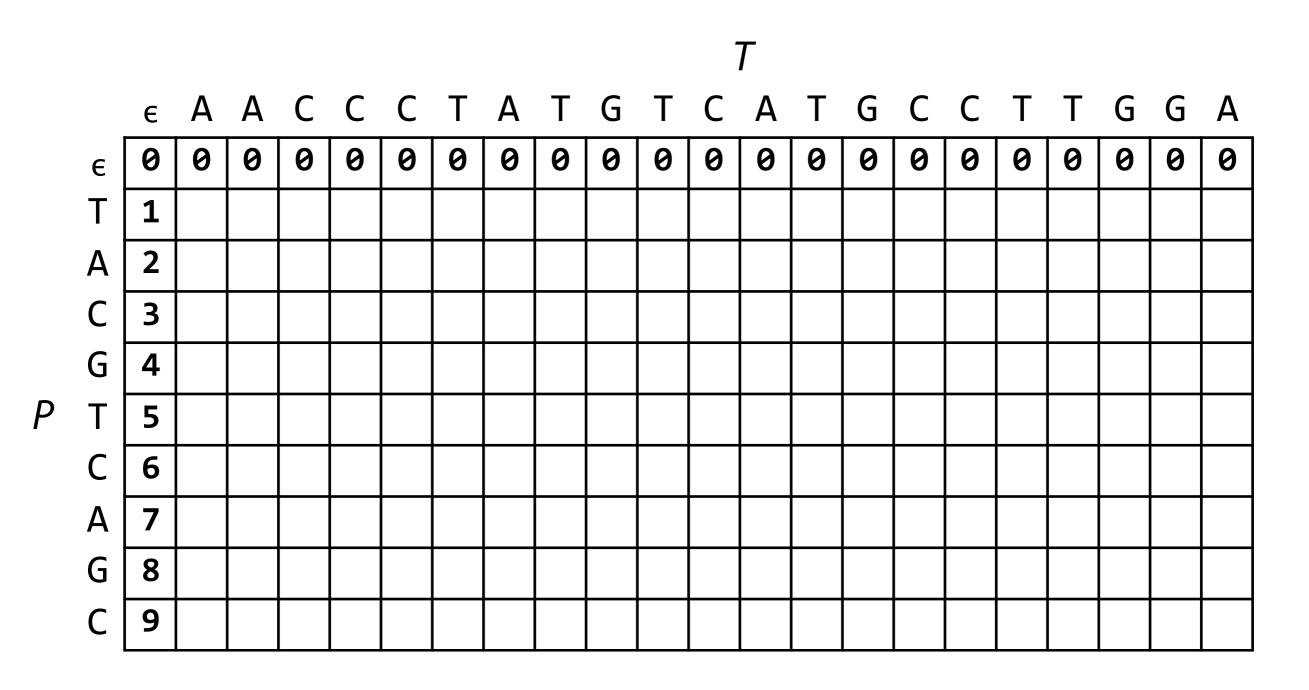
FillIng matrix is O(mn) space and time, yields edit distance

Traceback is O(m + n) time, yields optimal alignment / edit transcript

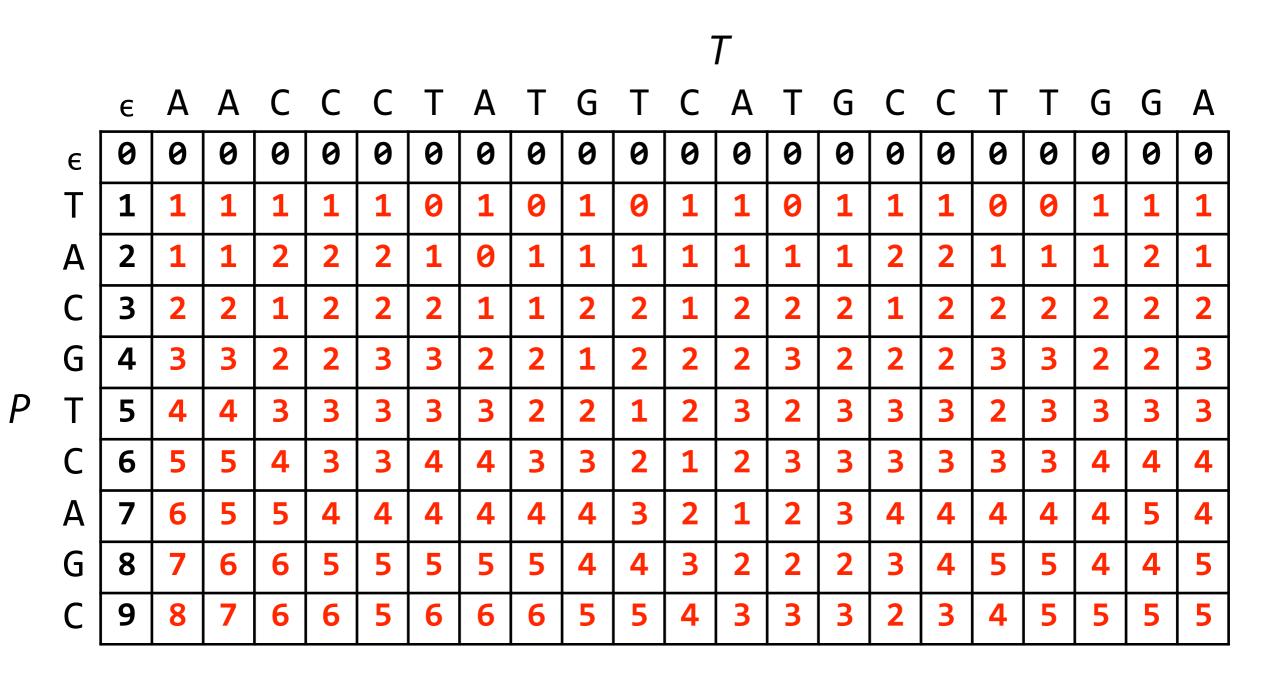
Can we search for the occurrence of *P* in *T* with least edits?



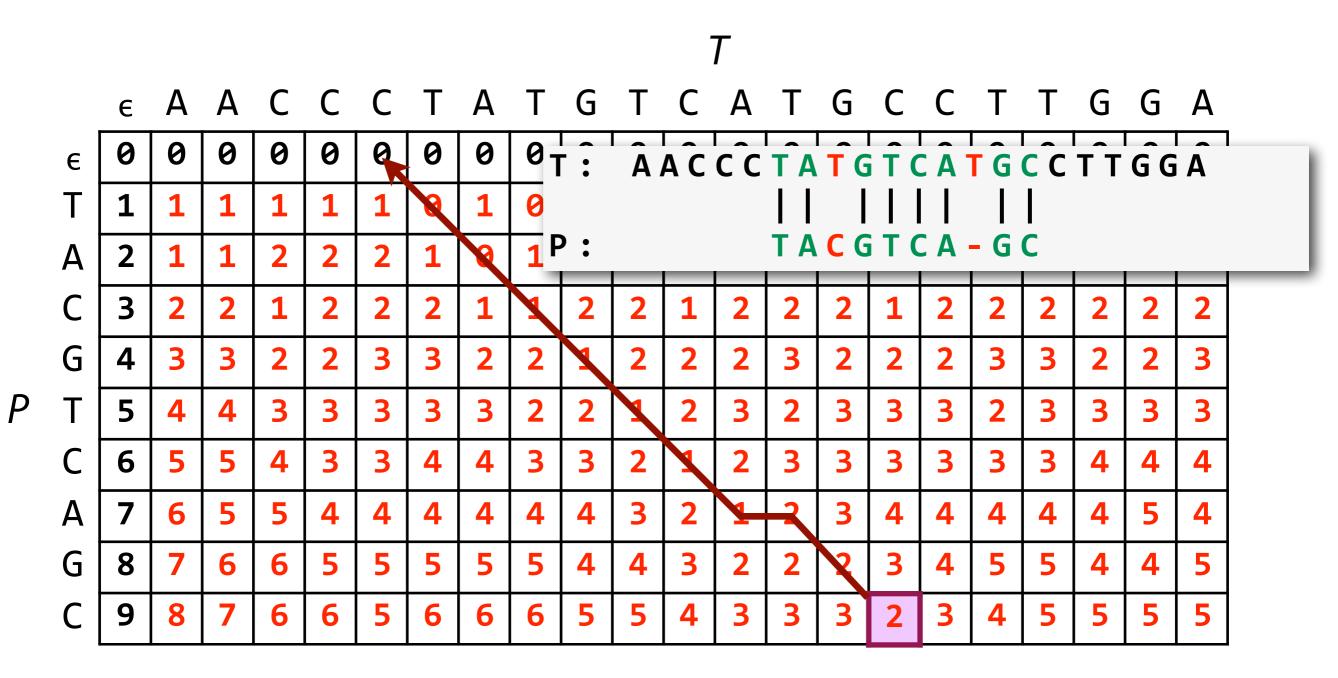
1. Initialize first row with 0's rather than increasing integers, then fill matrix



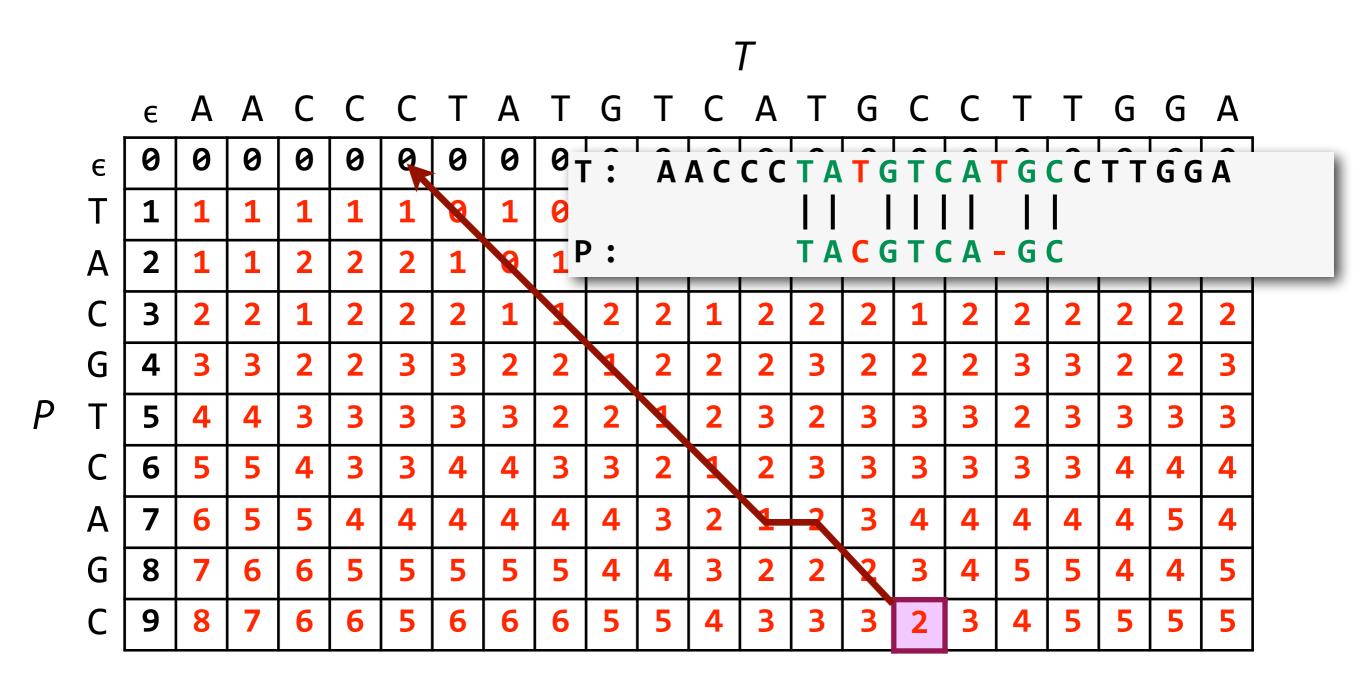
1. Initialize first row with 0's rather than increasing integers, then fill matrix



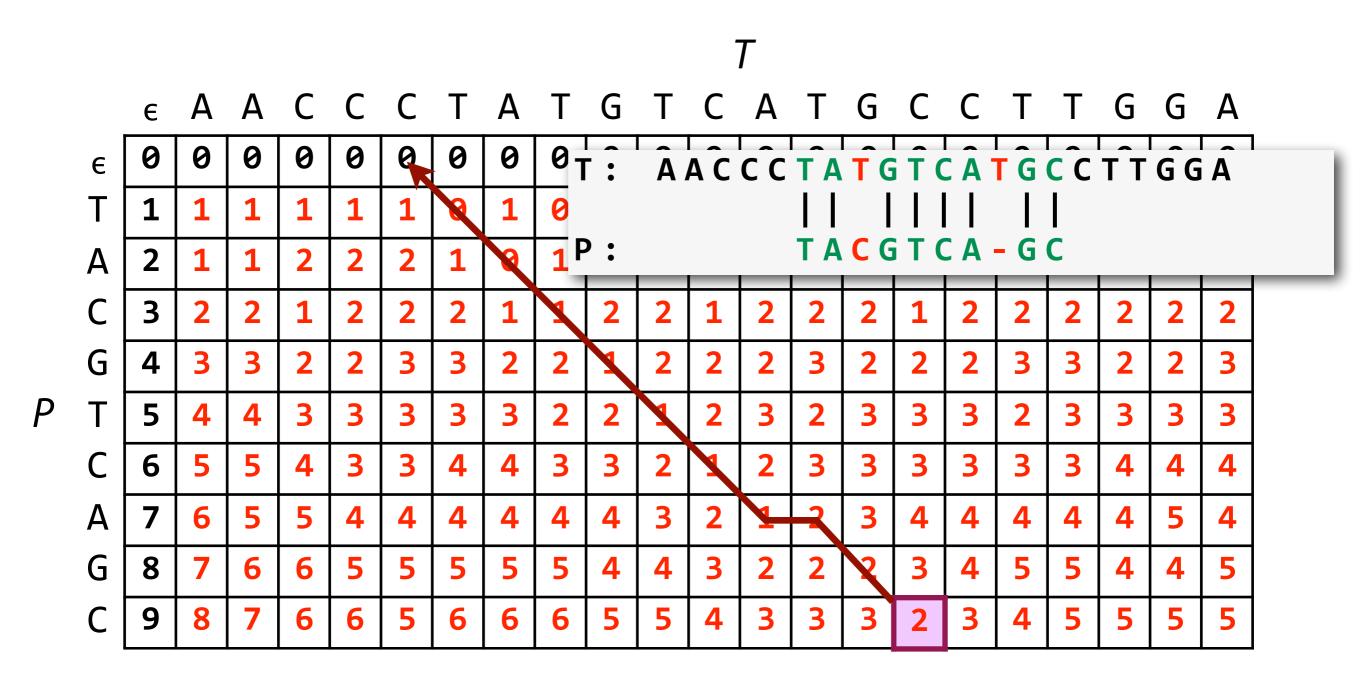
- 1. Initialize first row with 0's rather than increasing integers, then fill matrix
- 2. Pick lowest edit distance in the bottom row, traceback to top row



D[i, j] equals the optimal edit distance between the length-i prefix of P and...



D[i, j] equals the optimal edit distance between the length-i prefix of P and a substring of T ending at position j.



How would you find *all* occurrences of P in T with  $\leq k$  edits?

