Space-efficient alignment



Space is often the limiting factor

O(nm) time is a problem, but as I've said, we **strongly believe** we can't to much better.

Can we do better in terms of space?

It turns out we can — at the same asymptotic time complexity!

Combining dynamic programming with the divide-and-conquer algorithm design technique.

Hirshberg's algorithm

Consider our DP matrix:

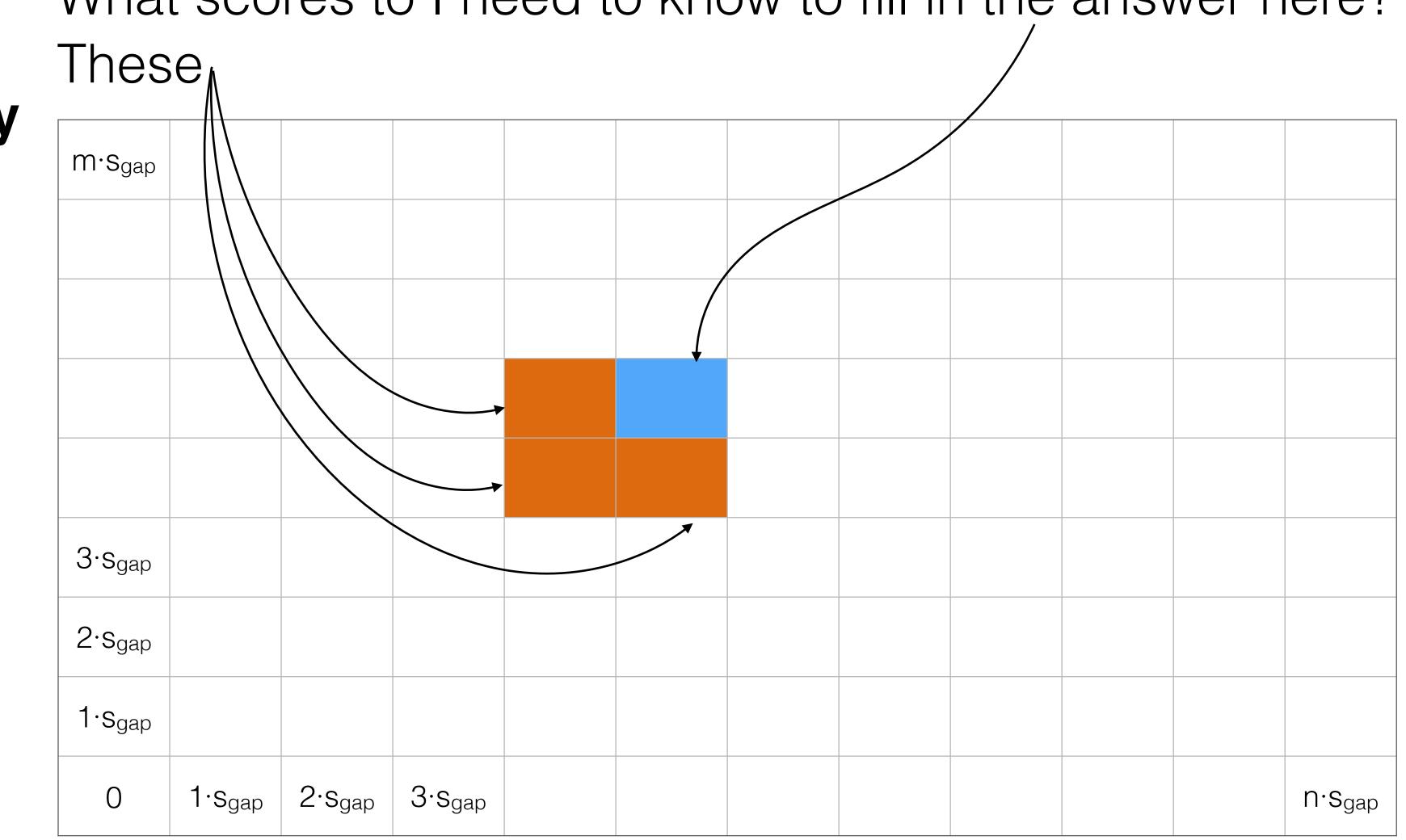
У

m·s _{gap}							
3·s _{gap}							
2·s _{gap}							
1·s _{gap}							
0	1·s _{gap}	2·s _{gap}	3·s _{gap}				n·s _{gap}

What scores to I need to know to fill in the answer here?

3.sgap 2·s_{gap} 1.Sgap 1·sgap 2·sgap 3·sgap n·s_{gap}

What scores to I need to know to fill in the answer here?



If we fill rows left - right, and bottom to top, to fill in row i, we *only* need scores from row i-1.

y

m·s _{gap}							
3·s _{gap}							
2·s _{gap}							
1·s _{gap}							
0	1·s _{gap}	2·s _{gap}	3·s _{gap}				n·s _{gap}

Columns also work; if we go left - right, and bottom to top, to fill in column i, we only need scores from col i-1.

y

m·s _{gap}							
3·s _{gap}							
2·s _{gap}							
1·s _{gap}							
0	1·s _{gap}	2·s _{gap}	3·s _{gap}				n·s _{gap}

If we fill rows left - right, and bottom to top, to fill in row i, we *only* need scores from row i-1.

Thus, we can compute the optimal *score*, keeping at most 2 rows / columns in memory at once.

Each row / column is *linear* in the length of one of the strings, and so we can compute the optimal *score*, in *linear space*.

How can we compute the optimal alignment?

This method won't work for computing the optimal alignment; we need *all* rows to be able to follow the backtracking arrows.

How can we find the optimal *alignment* in linear space?

Hirschberg's algorithm provides a solution.

Consider, again, the meaning of the DP matrix What is contained in the highlighted row?

У

m·s _{gap}							
3·s _{gap}							
2·s _{gap}							
1·S _{gap}							
0	1·s _{gap}	2·s _{gap}	3·s _{gap}				n·s _{gap}

Consider, again, the meaning of the DP matrix score of *every* prefix of **x** against *all* of **y** in this row

m·s_{gap} 3.sgap 2·sgap 1·sgap 2·sgap 3·sgap n·s_{gap}

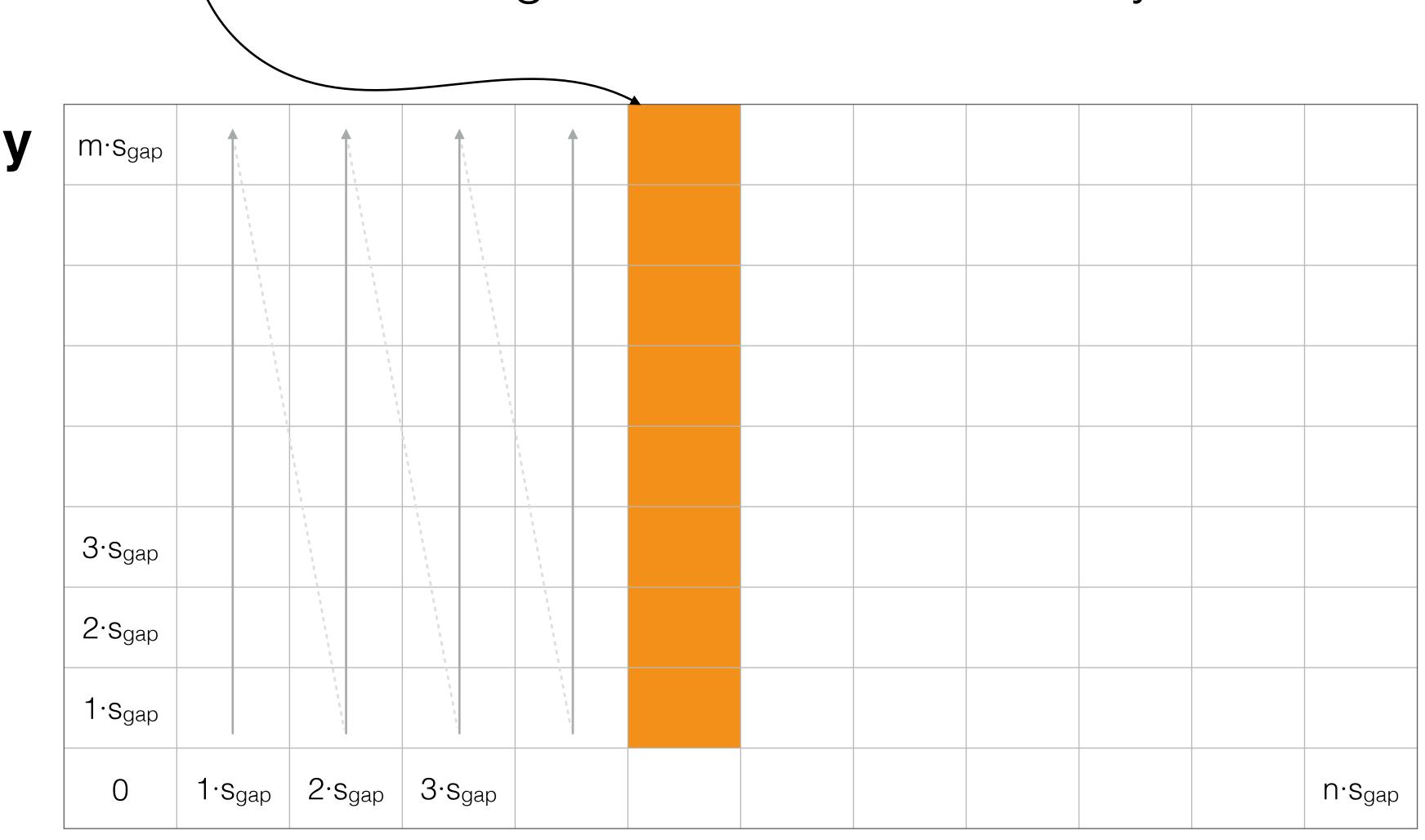
Consider, again, the meaning of the DP matrix What is contained in the highlighted column?

m·s_{gap} 3.sgap 2·sgap 1·sgap 2·sgap 3·sgap n·s_{gap}

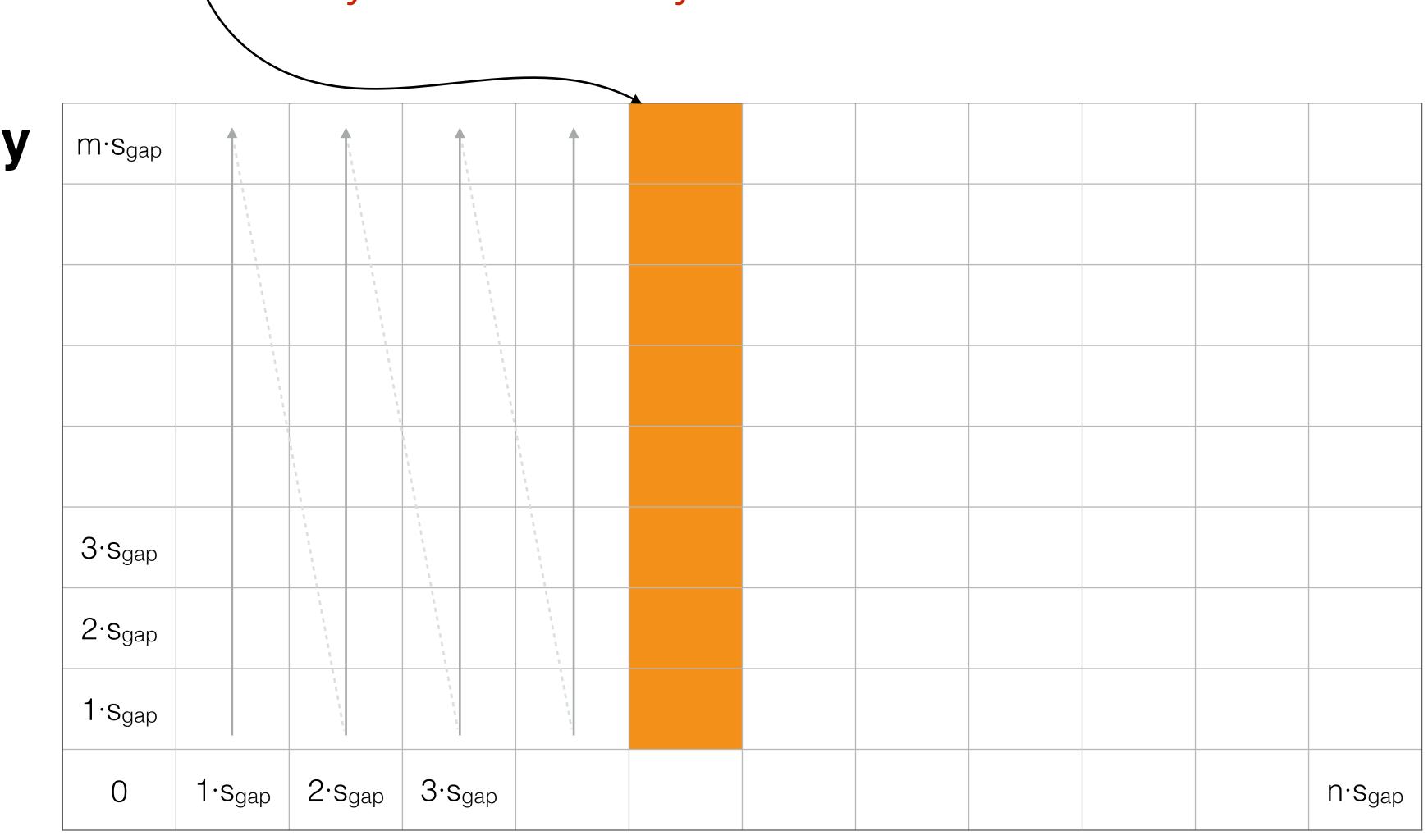
Consider, again, the meaning of the DP matrix score of *every* prefix of **y** against *all* of **x** in this column

m·s_{gap} 3.sgap 2·sgap 1·sgap 2·sgap 3·sgap n·s_{gap}

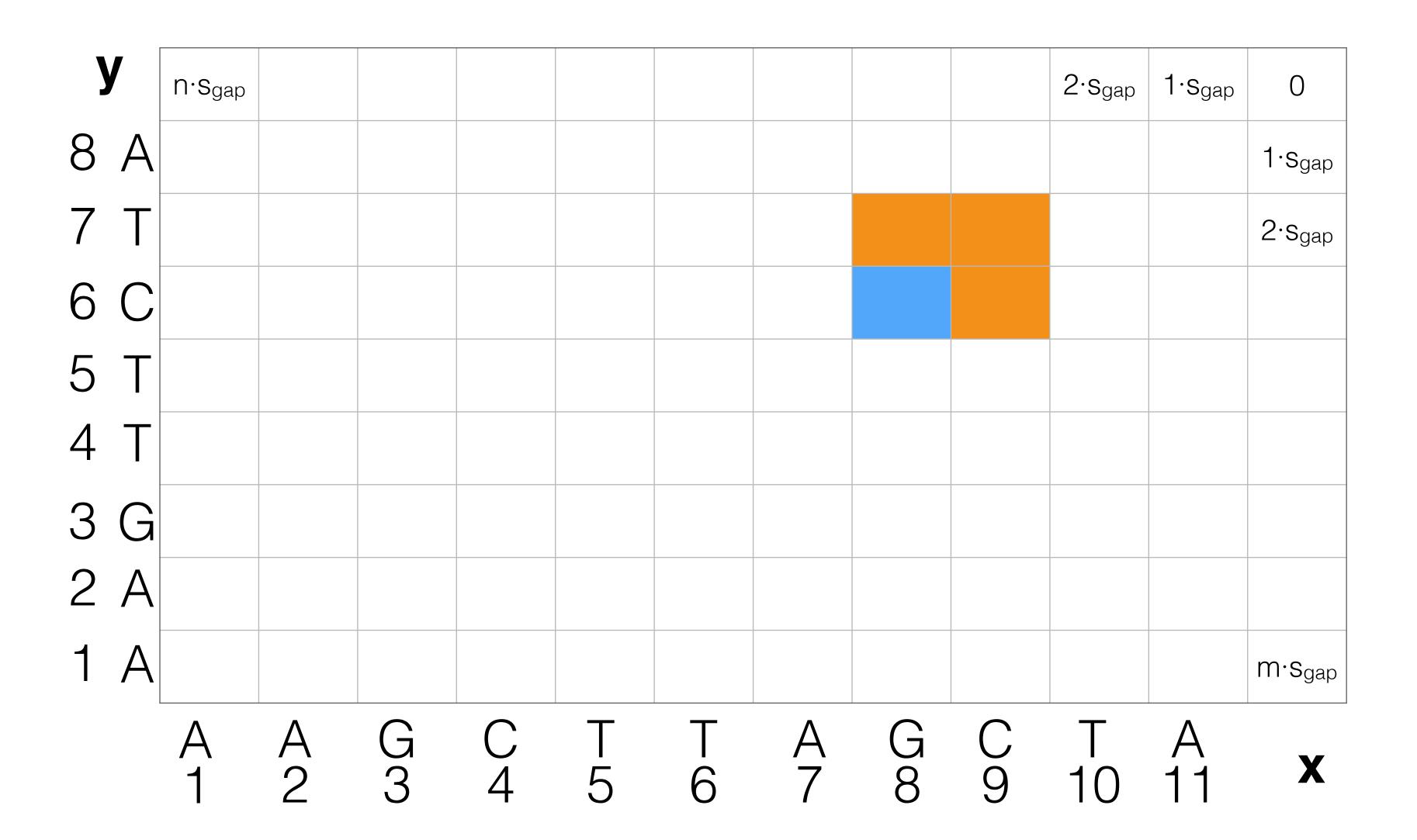
score of *every* prefix of **y** against ith prefix of **x** in the ith column. How do we get these values efficiently?



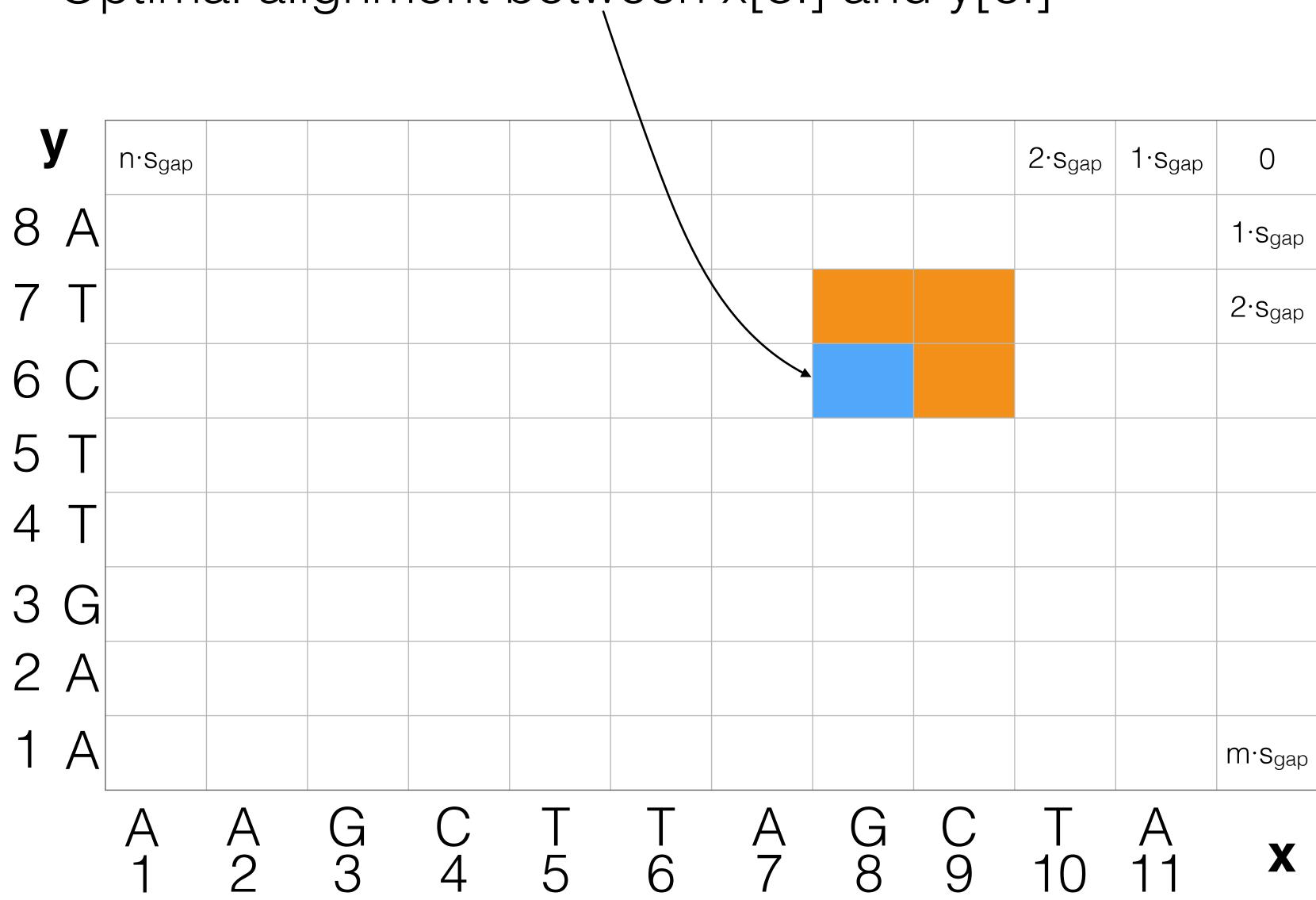
score of *every* prefix of **y** against ith prefix of **x** in the ith column. Easy if we fill in by columns instead of rows.



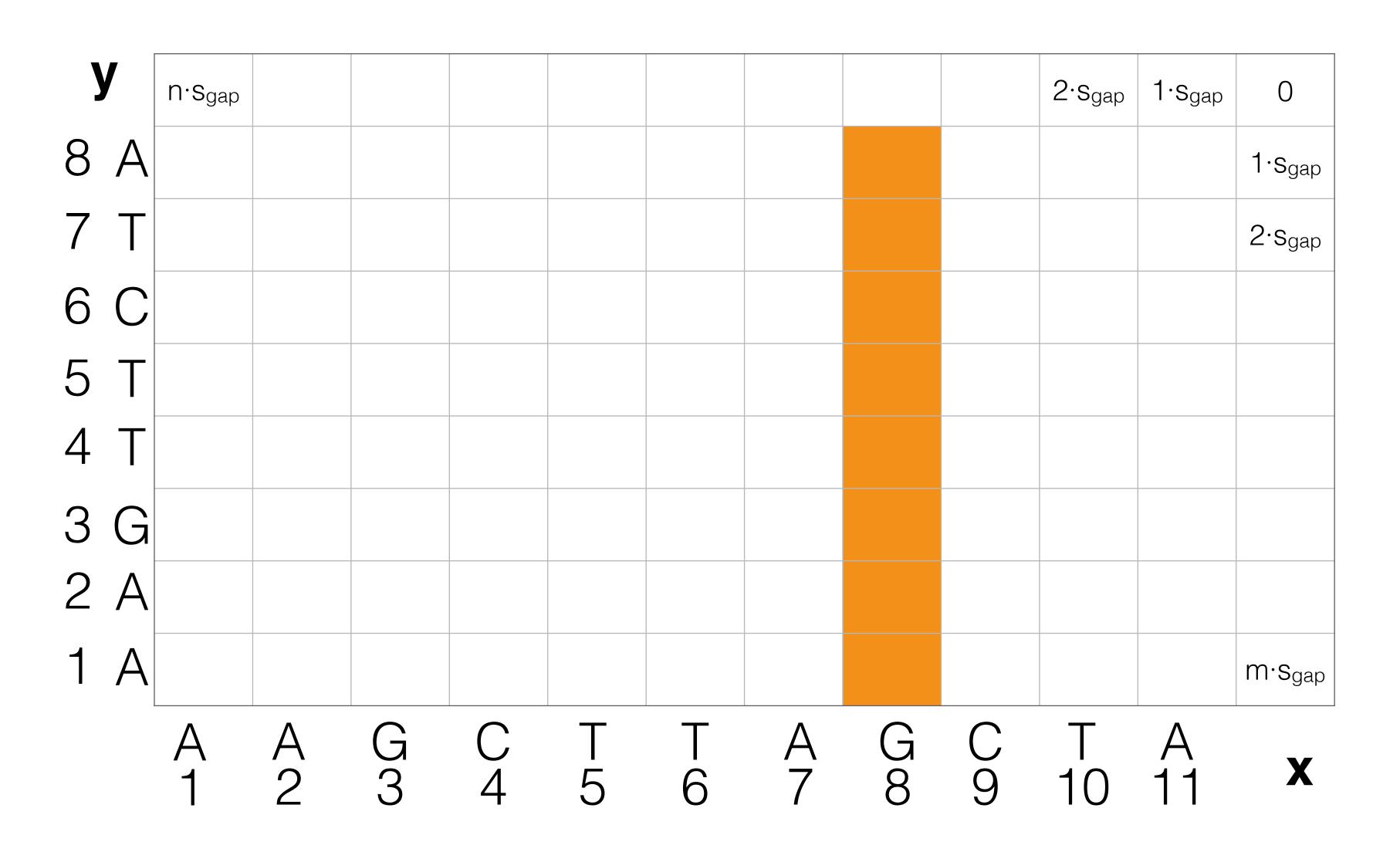
Consider filling in the DP matrix from the *opposite* direction (top right to bottom left)



Optimal alignment between x[8:] and y[6:]



This lets us compute optimal score between a *suffix* of **x** with *all suffixes* of **y**



Prefixes (forward):

$$OPT[i, j] = \max \begin{cases} score(x_i, y_j) + OPT'[i - 1, j - 1] \\ gap + OPT[i, j - 1] \\ gap + OPT[i - 1, j] \end{cases}$$

Suffixes (backward):

OPT'
$$[i, j] = \max \begin{cases} \text{score}(x_{i+1}, y_{j+1}) + \text{OPT'}[i+1, j+1] \\ \text{gap} + \text{OPT'}[i, j+1] \\ \text{gap} + \text{OPT'}[i+1, j] \end{cases}$$

This lets us build up optimal alignments for increasing length suffixes of ${\bf x}$ and ${\bf y}$

Prefixes (forward):

$$\begin{aligned} &\operatorname{OPT}\left[i,j\right] = \max \begin{cases} \operatorname{score}\left(x_{i},y_{j}\right) + \operatorname{OPT'}\left[i-1,j-1\right] \\ &\operatorname{gap} + \operatorname{OPT}\left[i,j-1\right] \\ &\operatorname{gap} + \operatorname{OPT}\left[i-1,j\right] \end{cases} \\ &\operatorname{Suffixes}\left(\operatorname{backward}\right): \\ &\operatorname{OPT'}\left[i,j\right] = \max \begin{cases} \operatorname{score}\left(x_{i+1},y_{j+1}\right) + \operatorname{OPT'}\left[i+1,j+1\right] \\ &\operatorname{gap} + \operatorname{OPT'}\left[i,j+1\right] \\ &\operatorname{gap} + \operatorname{OPT'}\left[i+1,j\right] \end{cases} \end{aligned}$$

This lets us build up optimal alignments for increasing length suffixes of ${\bf x}$ and ${\bf y}$

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Suffixes (backward):

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note: thé slight change in indexing here. It will make writing our solution easier.

How does this help us compute the optimal alignment in linear space?

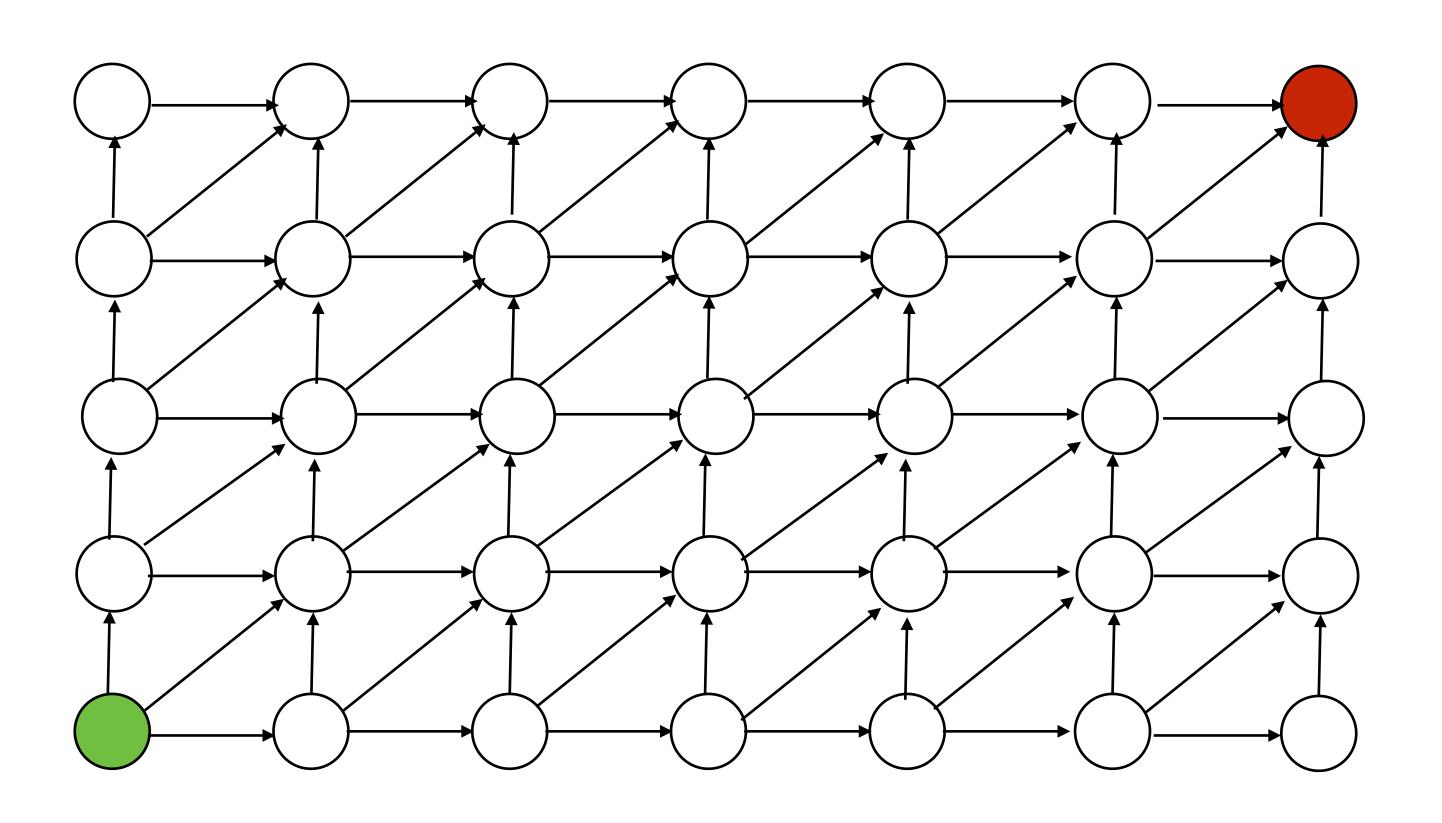
Algorithmic idea: Combine both dynamic programs using divide-and-conquer

Divide-and-conquer splits a problem into smaller subproblems and combines the results (much like DP).

Examples: MergeSort & Karatsuba multiplication

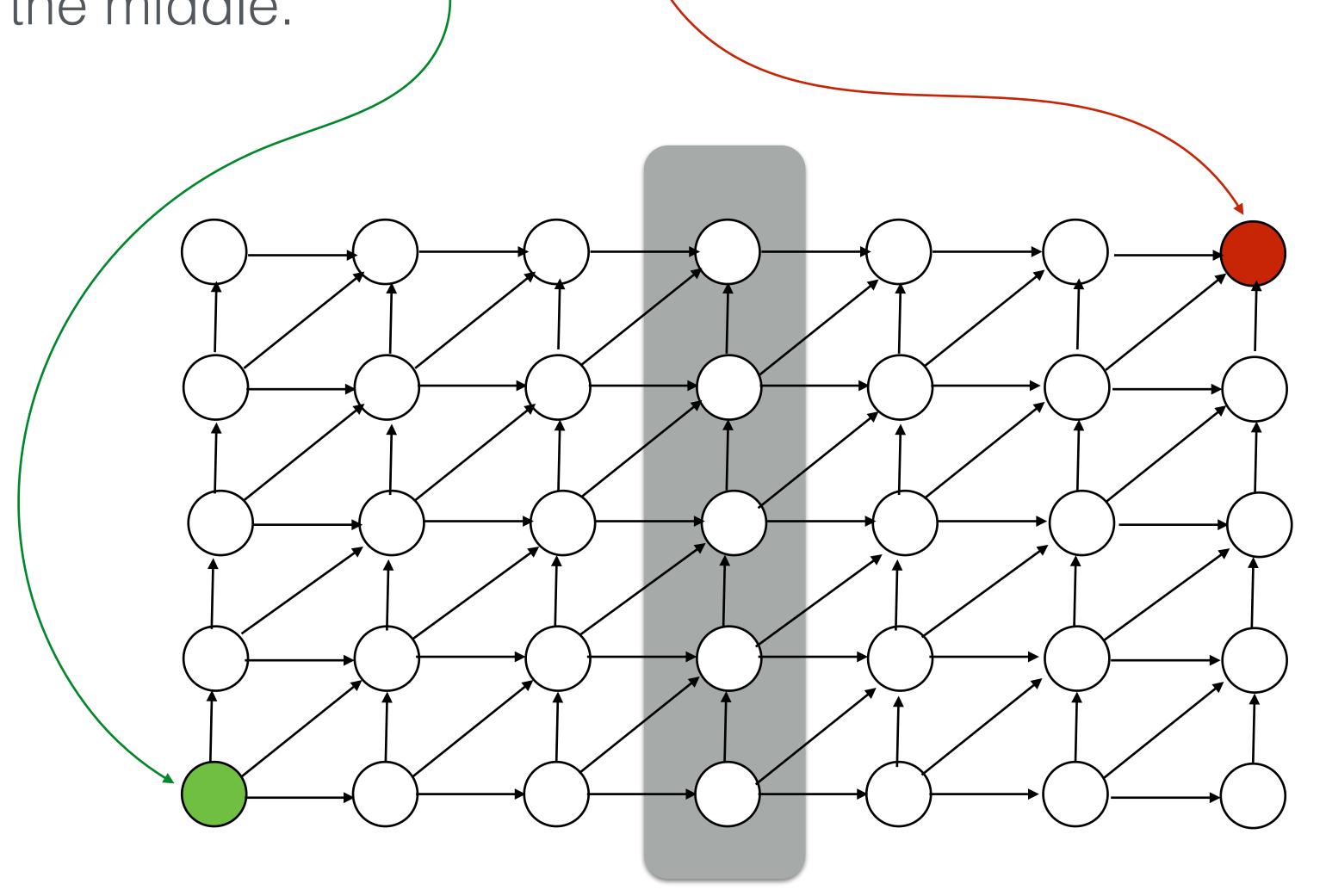
Think about this in "graph" land

What do we know about the structure of the optimal path in our "edit-DAG"?

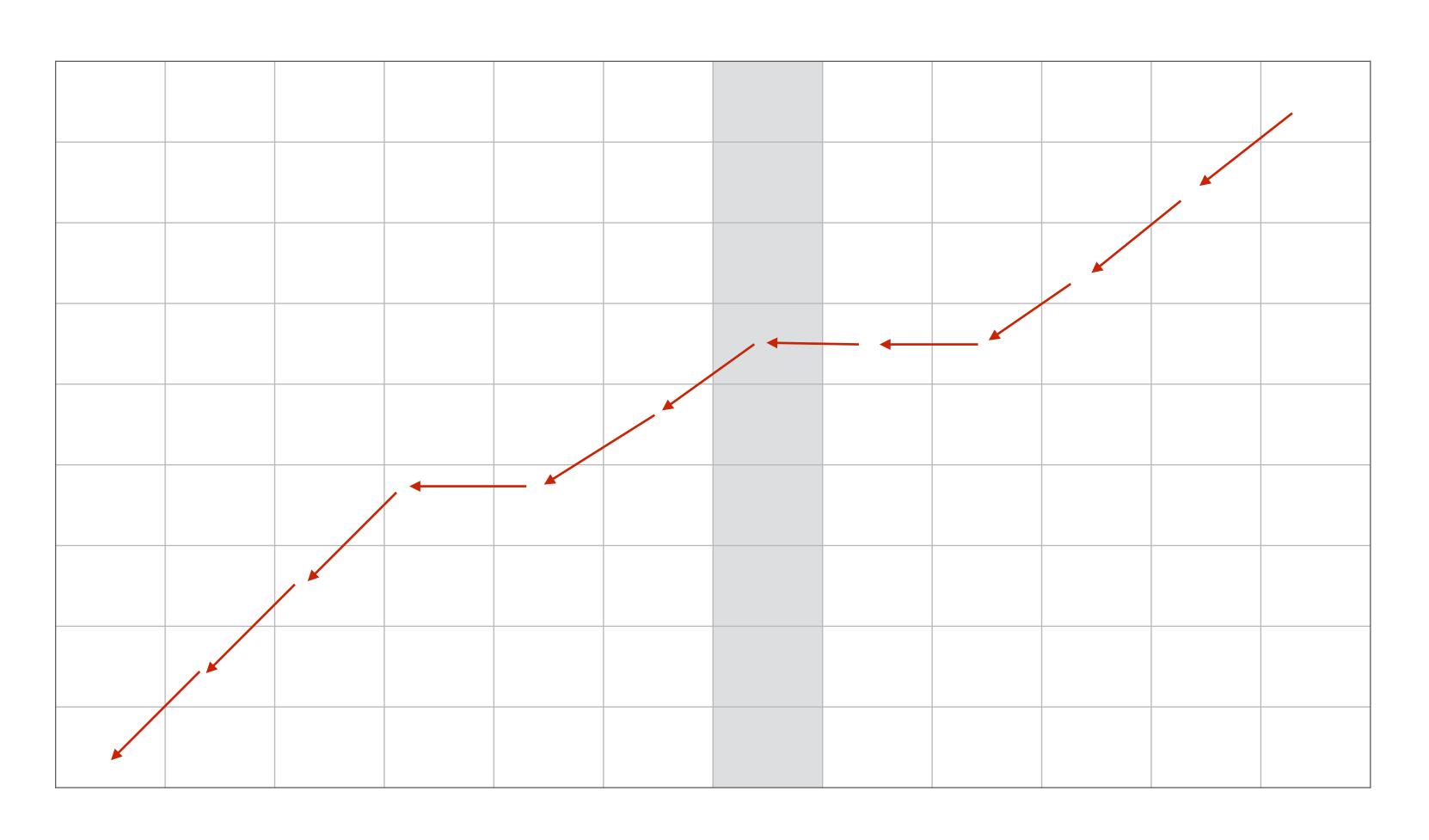


Think about this in "graph" land

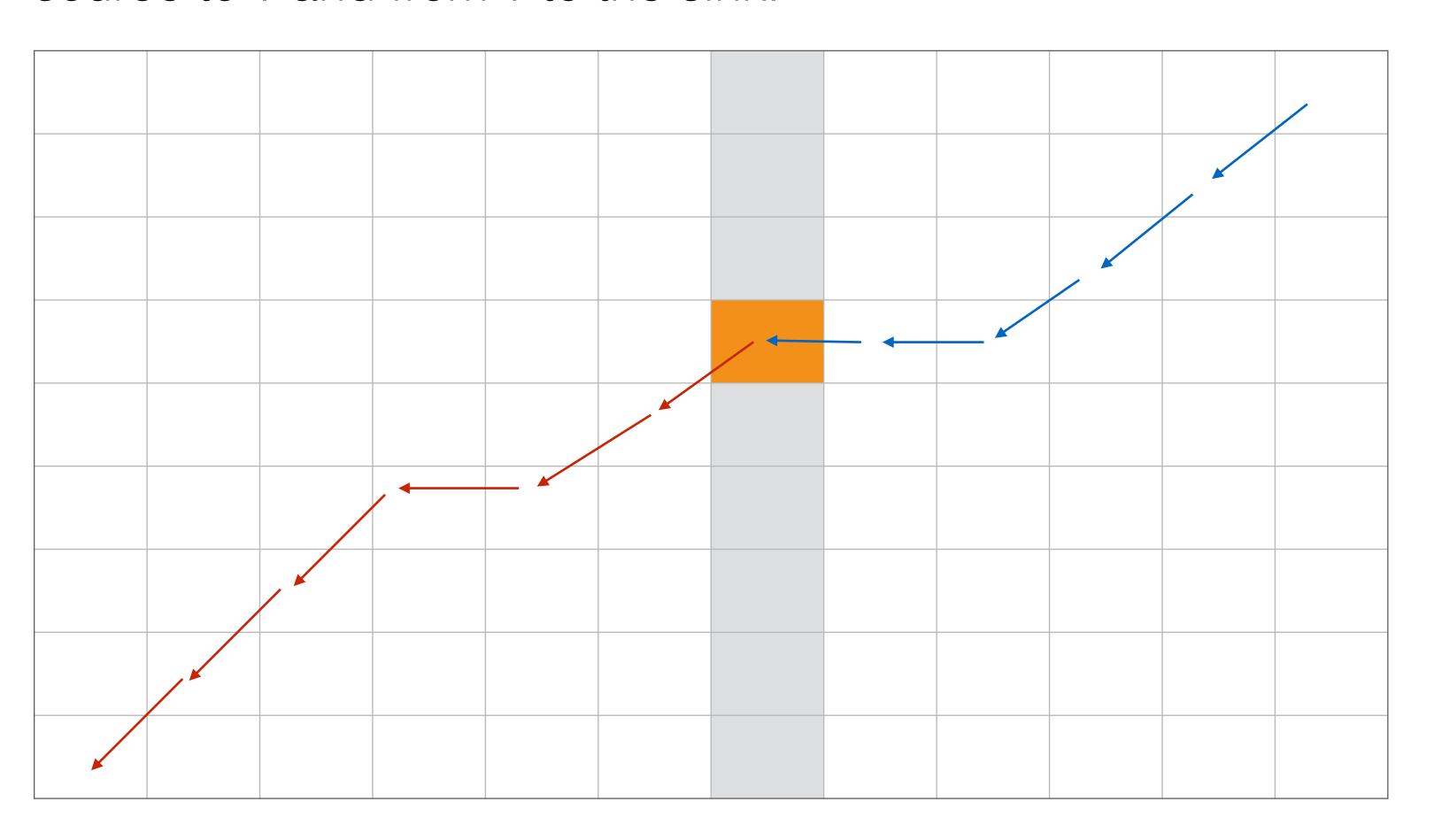
Can't get from here to there without passing through the middle.



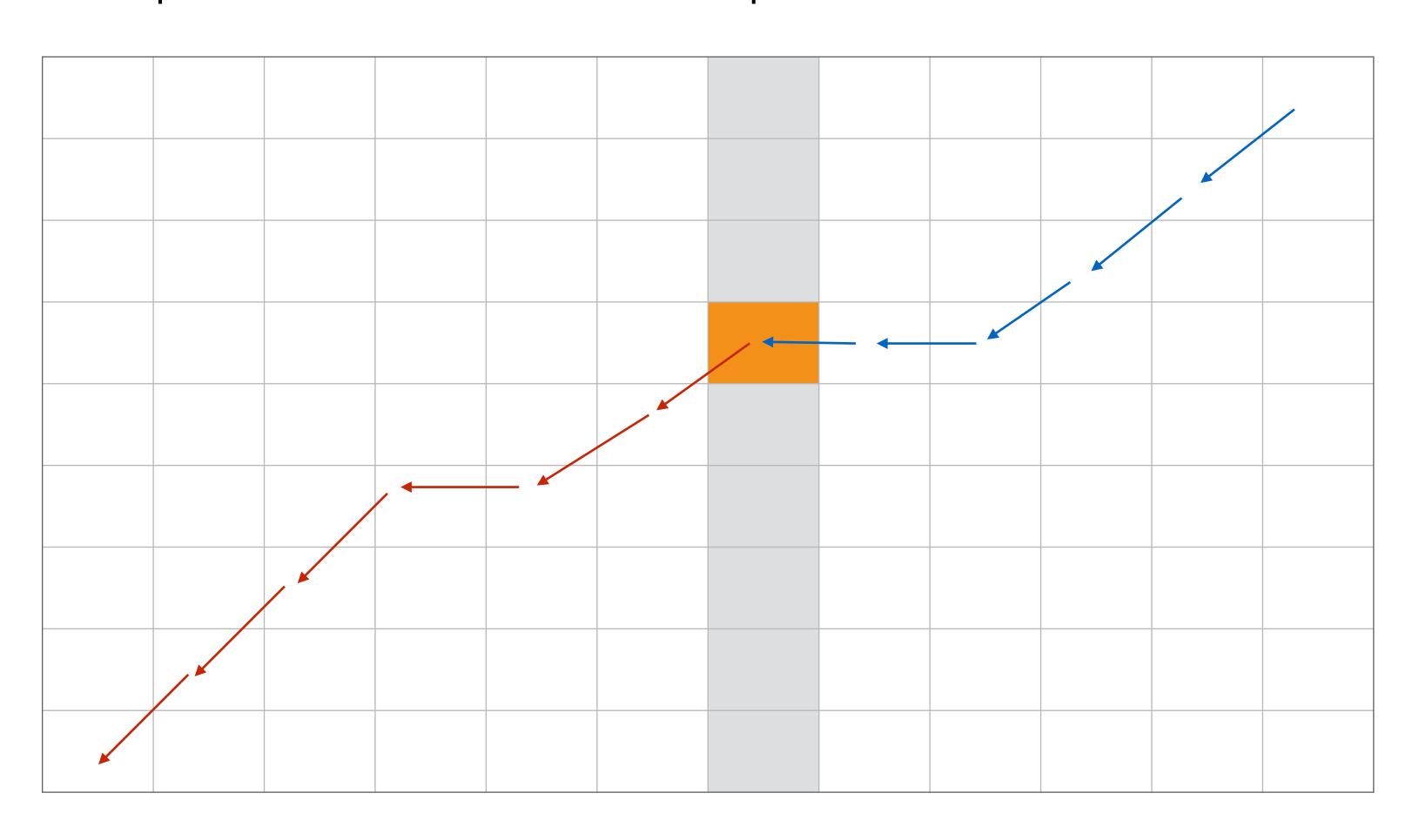
Consider the middle column — we *know* that the optimal aln. must use some cell in this column; which one?



It uses the cell (i,j) such that OPT[i,j] + OPT'[i,j] has the **highest score**. Equivalently, the *best path* uses some vertex *v* in the middle col. and glues together the best paths from the source *to* v and *from* v to the sink.

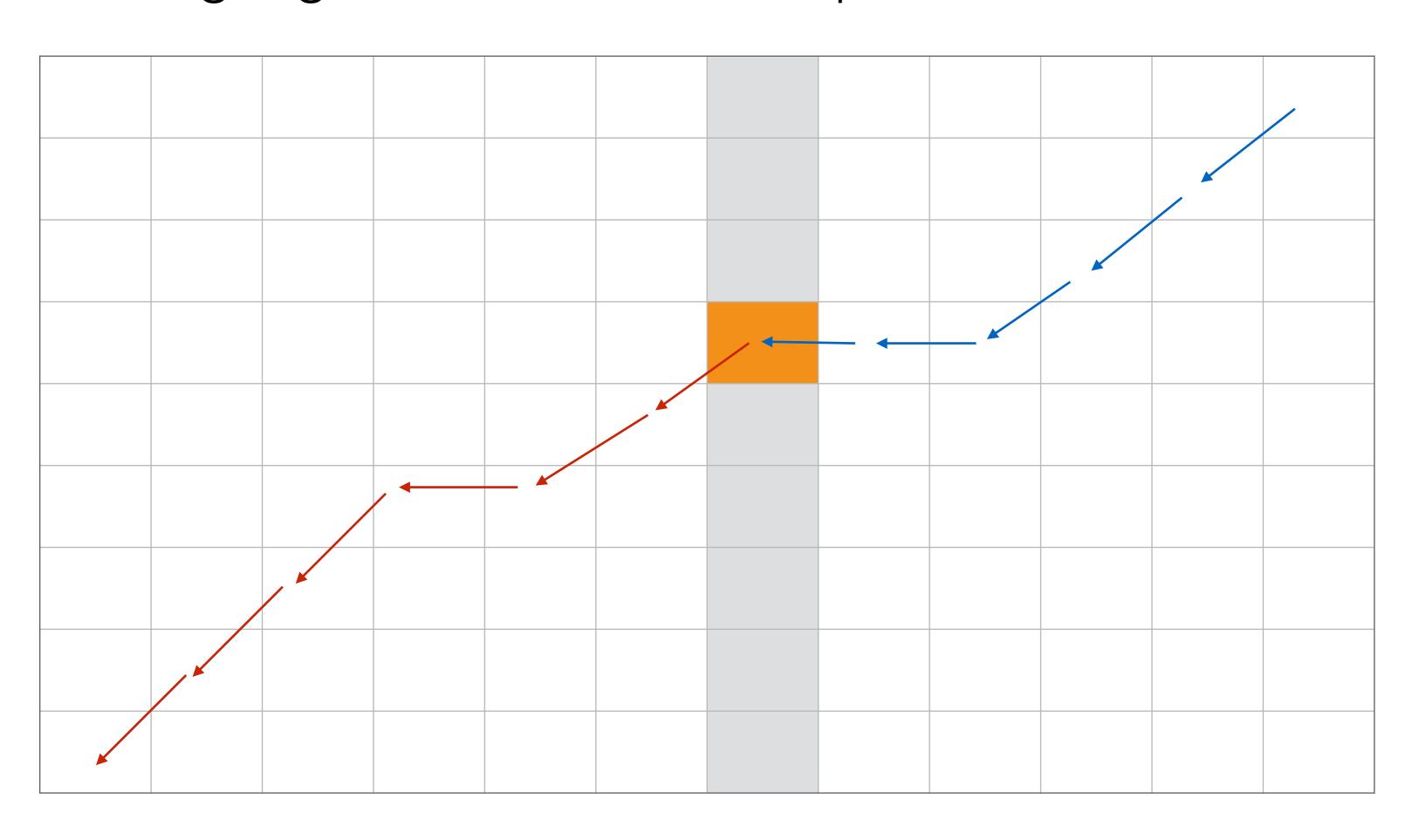


Claim: OPT[i,j] and OPT'[i,j] can be computed in linear space using the trick from above for finding an optimal **score** in linear space



Algorithmic Idea

Devise a D&C algorithm that finds the optimal alignment path recursively, using the space-efficient scoring algorithm for each subproblem.



D&C Alignment

```
DCAlignment(x, y):
    n = |x|
    m = |y|
    if m <= 2 or n <= 2:
        use "normal" DP to compute OPT(x, y)
    compute space-efficient OPT(x[1:n/2], y)
    compute space-efficient OPT'(x[n/2+1:n], y)
    let q be the index maximizing OPT[n/2,q] + OPT'[n/2,q]
    add back pointer of (n/2,q) to the optimal alignment P
    DCAlignment(x[1:n/2], y[1:q])
    DCAlignment(x[n/2+1:n], y[q+1:m])
    return P</pre>
```

D&C Alignment

How can we show that this entire process still takes quadratic time?

Let T(n,m) be the running time on strings **x** and **y** of length n and m, respectively. We have:

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

$$DCAlignment(x[1:n/2], y[1:q]) \quad DCAlignment(x[n/2+1:n], y[q+1:m])$$

$$with base cases:$$

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

 $T(2,m) \le cm$

D&C Alignment

Base:

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

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

Inductive:

$$T(n,m) \le cnm + T(n/2, q) + T(n/2, m-q)$$

Problem: we don't know what q is. First, assume both \mathbf{x} and \mathbf{y} have length n and q=n/2 (will remove this restriction later)

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

This recursion solves as $T(n) = O(n^2)$

Leads us to guess T(n,m) grows like O(nm)

Smarter Induction

```
Base:
T(n,2) \leq cn
T(2,m) \leq cm
Inductive:
T(n,m) \leq knm
Proof:
T(n,m) \le cnm + T(n/2, q) + T(n/2, m-q)
       \leq cnm + kqn/2 + k(m-q)n/2
       \leq cnm + kqn/2 + kmn/2 - kqn/2
      = [c+(k/2)] mn
Thus, our proof holds if k=2c, and T(n,m) = O(nm) QED
```

Conclusion

Trivially, we can compute the *cost* of an optimal alignment in linear space

By arranging subproblems intelligently we can define a "reverse" DP that works on suffixes instead of prefixes

Combining the "forward" and "reverse" DP using a divide and conquer technique, we can compute the optimal *solution* (not just the score) in linear space.

This still only takes O(nm) time; constant factor more work than the "forward"-only algorithm.

Doing better (in time) in practice

Can we do better in practice?

What about when we know that the edit distance is small (say e << mn)? What about when we only care about edit distances < some threshold?

Yes!

JOURNAL ARTICLE

Optimal gap-affine alignment in O(s) space $\frac{\partial}{\partial s}$

Santiago Marco-Sola ™, Jordan M Eizenga, Andrea Guarracino, Benedict Paten, Erik Garrison, Miquel Moreto

Bioinformatics, Volume 39, Issue 2, February 2023, btad074, https://doi.org/10.1093/bioinformatics/btad074

O(ns) time and O(s) space where s is the score of the optimal alignment!

Exact global alignment using A* with seed heuristic and match pruning

Ragnar Groot Koerkamp *,† and Pesho Ivanov *,†

Department of Computer Science, ETH Zurich, Switzerland

Practically even fewer comparisons
than BiWFA

https://doi.org/10.1093/bioinformatics/btad074

https://www.biorxiv.org/content/10.1101/2022.09.19.508631v2

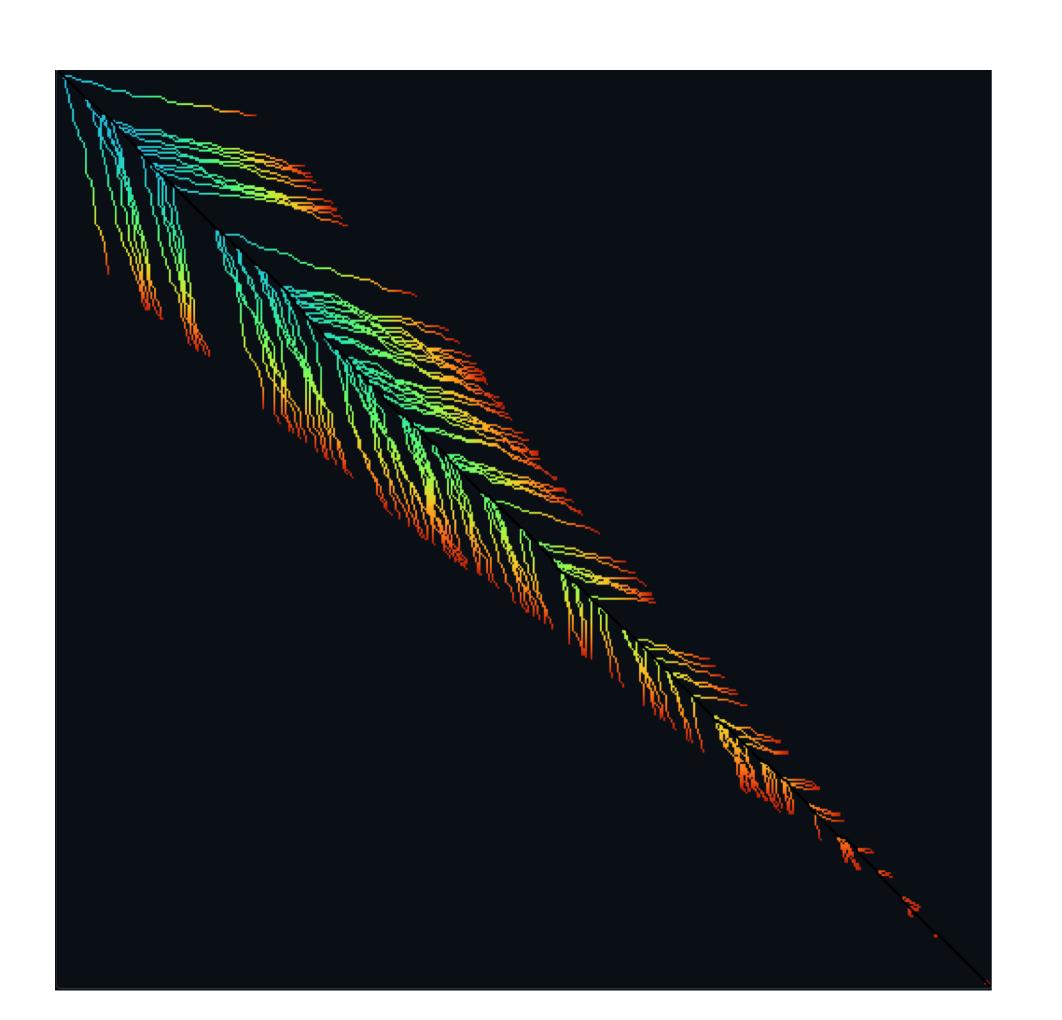
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[†]These authors contributed equally to this work.

Doing better (in time) in practice

Beautiful motivation:

https://github.com/RagnarGrootKoerkamp/astar-pairwise-aligner



Diagonal transition (WFA)