Dynamic Programming
Part Two

Announcements

- On-time Problem Set Four graded; will be returned at end of lecture.
  - Late submissions should be graded by Monday; sorry about that!
- Problem Set Five due Monday, or Wednesday using a late period.
  - Heads-up: No late days on the final project. You can a late day on Problem Set Six, but that will overlap with the final project.

Outline for Today

- **String Algorithms**
  - Processing text, genomes, etc.
- **Sequence Alignment**
  - Determining the similarity of DNA strands.
- **Levenshtein Distance**
  - Checking how close two strings are.

Recap from Last Time

Dynamic Programming

- Dynamic programming is a technique useful for solving problems exhibiting the following properties:
  - **Overlapping subproblems:** Different branches of the recursion will reuse each other's work.
  - **Optimal substructure:** The optimal solution for one problem instance is formed from optimal solutions for smaller problems.
  - **Polynomial subproblems:** The number of subproblems is small enough to be evaluated in polynomial time.

A Correction From Last Time...

Theorem: OPT(k) satisfies the previous recurrence.

Proof: If $k = 0$, no people can be covered, so OPT(0) = 0. If $k = 1$, we can choose tower 1 (value v_1) or no towers (value 0), so OPT(1) = v_1. So consider $k > 1$.

If $k \in C$, then $k - 1 \notin C$. Then all towers in C besides k are within the first $k-2$ towers, so $C(k-2) \leq \text{OPT}(k-2)$. Also, $C(k-2) \geq \text{OPT}(k-2)$; otherwise we could replace all towers in C except k with an optimal set of the first $k-2$ towers to improve C. Thus $\text{OPT}(k) = v_k + \text{OPT}(k-2)$.

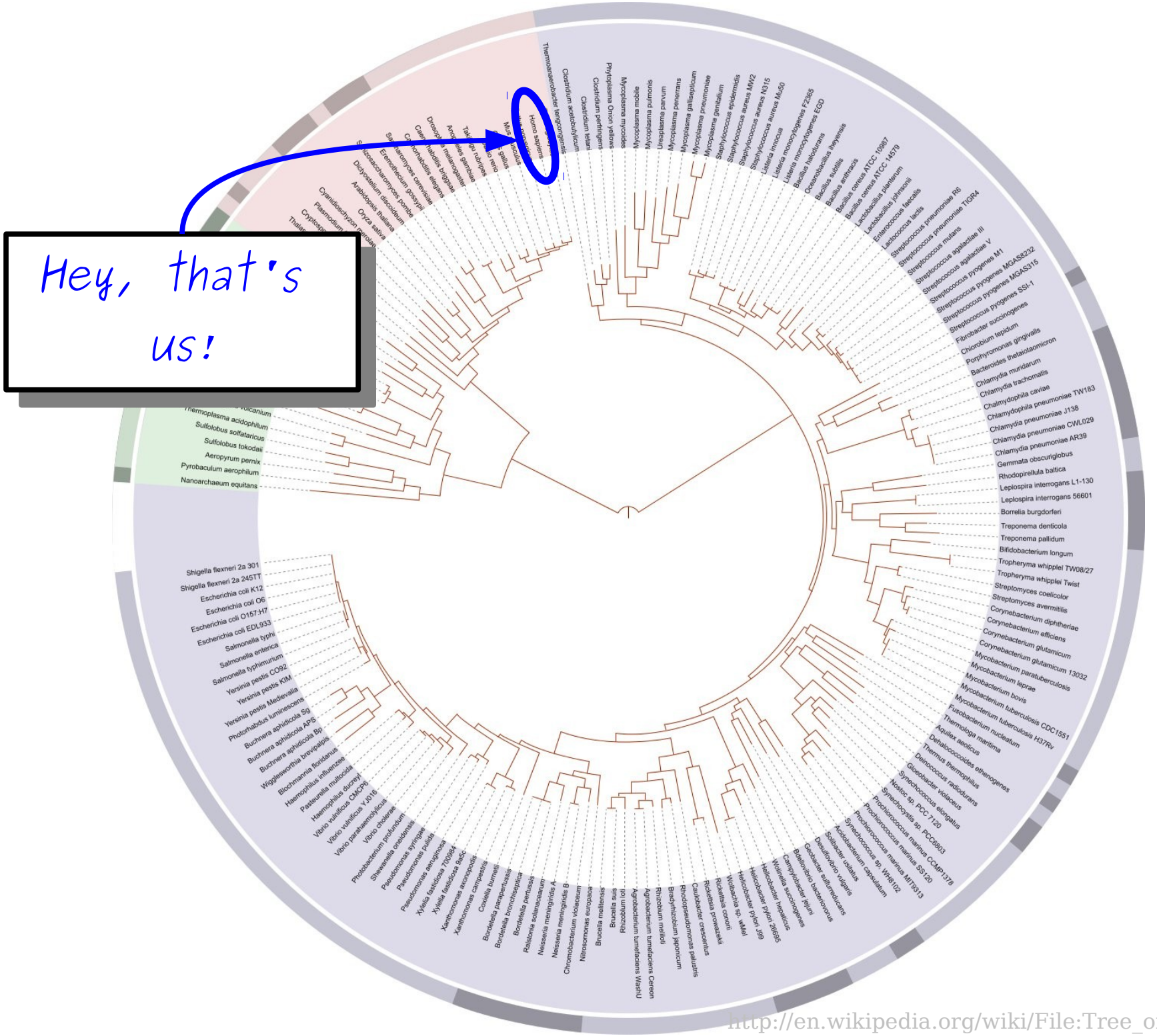
If $k \notin C$, all towers in C are in the first $k-1$ towers. Thus $C(k-1) \leq \text{OPT}(k-1)$. Also, $C(k-1) \geq \text{OPT}(k-1)$; if not, we could improve C by replacing it with an optimal set of the first $k-1$ towers. Therefore, $\text{OPT}(k) = \text{OPT}(k-1)$.

Since the optimal solution for k towers must be the better of these, $\text{OPT}(k) = \max\{\text{OPT}(k-1), v_k + \text{OPT}(k-2)\}$. ■

Sequence Alignment

DNA Structure

- DNA strands consist of strings of **nucleotides**. There are four possible nucleotides: A, C, T, and G.
- Over time, mutations can occur in DNA strands:
  - **Point mutations**, where one nucleotide is replaced by another.
  - **Insertions**, where extra DNA is spliced in.
  - **Deletions**, where DNA is removed.
- Usually, the relative order of DNA letters remains the same.



Aligning DNA Strands

- DNA from related species often are similar, though not identical.
- We can try to **align** two DNA strands by inserting blanks (denoted by -) into the DNA strand.

-	A	T	T	A	G	C	-	T	T
A	A	T	-	C	G	C	C	T	T

- There is a cost associated with pairing a letter with a blank and with pairing two mismatched letters.

Sequence Alignment

- “Cost” of an alignment determined as follows:
  - For any characters *a* and *b*, cost of matching *a* and *b* is α_{ab}. This is usually 0 if the characters are the same and nonzero otherwise.
  - Cost of inserting a gap is δ.
- Assume α_{ab}'s and δ are external, fixed parameters.
- The **sequence alignment** problem is the following: find the alignment of the sequences with the least total cost.

An Insight

- The last column in the alignment must
  - Match the last characters from both strings:

A	-	C	G	C	A	T
A	T	T	-	-	A	T

  - Insert a gap up top:

G	G	C	T	C	T	-
G	G	-	C	-	G	T

  - Insert a gap on bottom:

G	A	T	T	A	C	A
G	-	-	T	A	C	-

Some Notation

- Suppose we want to align the first i characters of A and the first j characters of B. (Denote this $A[1, i]$ and B$[1, j]$
- Let OPT(i, j) denote the optimal cost of such an alignment.
- **Claim:** OPT(i, j) satisfies the following:

$$\text{OPT}(i,j)=\begin{cases} j\delta & if\ i=0 \\ i\delta & if\ j=0 \\ min\begin{cases}\delta+OPT(i-1,j), \\ \delta+OPT(i,j-1), \\ \alpha_{A[i]B[j]}+OPT(i-1,j-1)\end{cases} & otherwise \end{cases}$$

Theorem: OPT(i, j) satisfies the previous recurrence.

Proof: If $i = 0$, the only way to match $A[1, 0]$ and $B[1, j]$ is to insert j gaps into A to match the j characters of B. This has cost δj, so OPT(i, j) = δj. By a similar argument, if $j = 0$, then OPT(i, j) = δi. Otherwise, $i > 0$ and $j > 0$. Consider an optimal alignment M^* of $A[1, i]$ and $B[1, j]$. There are three possibilities:

Case 1: M^* pairs $A[i]$ and $B[j]$. The rest of M^* aligns $A[1, i-1]$ and $B[1, j-1]$ and we claim it optimally aligns them; otherwise, changing M^* to optimally align $A[1, i-1]$ and $B[1, j-1]$ decreases the cost of M^*. Therefore, $\text{OPT}(i, j) = \alpha_{A[i]B[j]} + \text{OPT}(i-1, j-1)$.

Case 2: M^* pairs $A[i]$ with a blank. The rest of M^* aligns $A[1, i-1]$ and $B[1, j]$ and we claim it optimally aligns them; otherwise, changing M^* to optimally align $A[1, i-1]$ and $B[1, j]$ decreases the cost of M^*. Thus $\text{OPT}(i, j) = \delta + \text{OPT}(i-1, j)$.

Case 3: M^* pairs $B[j]$ with a blank. By a similar argument to the previous case, we have $\text{OPT}(i, j) = \delta + \text{OPT}(i, j-1)$.

Since the optimal solution must be one of these three options, we have $\text{OPT}(i, j) = \min\{\alpha_{A[i]B[j]} + \text{OPT}(i-1, j-1), \delta + \text{OPT}(i, j-1), \delta + \text{OPT}(i-1, j)\}$. ■

Evaluating the Recurrence

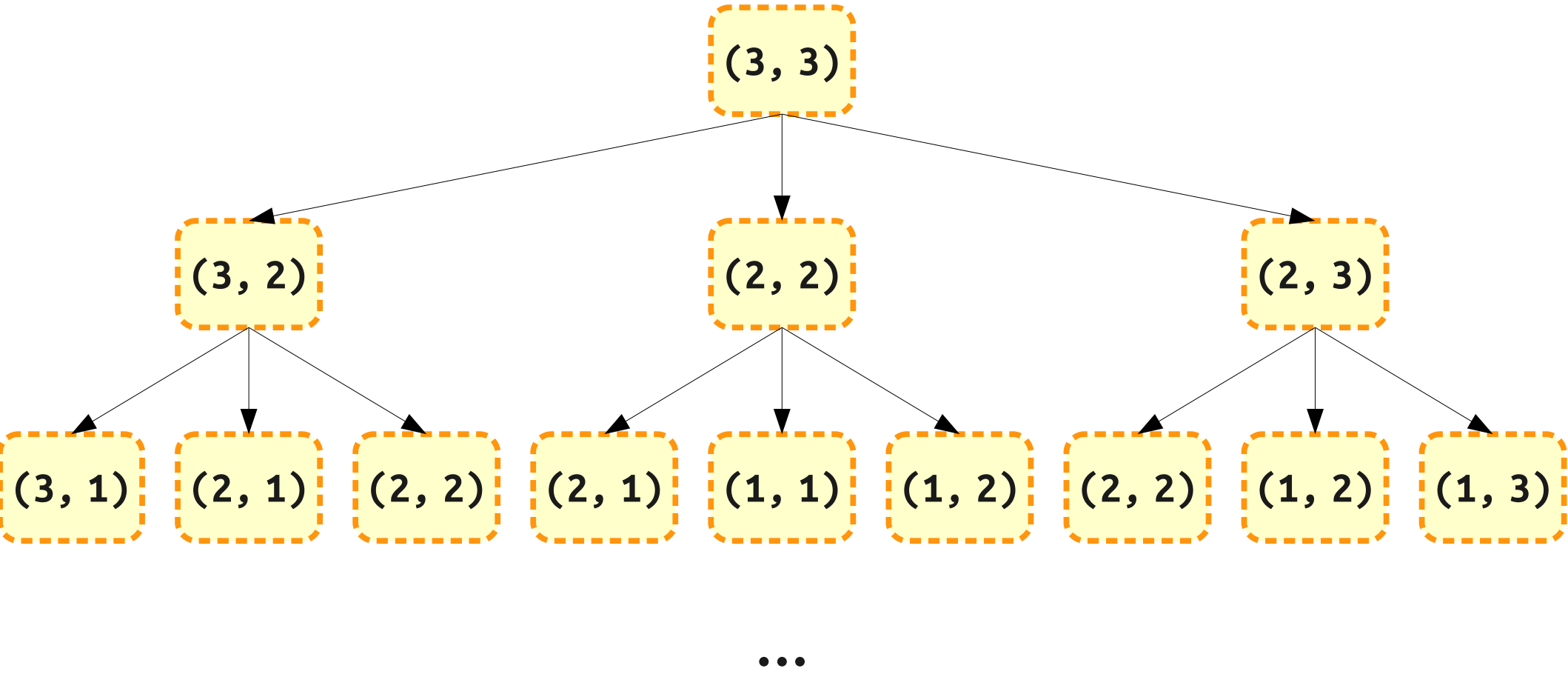
- If we can evaluate this recurrence:

$$\mathrm{OPT}(i,j)=\begin{cases} j\delta & if\ i=0 \\ i\delta & if\ j=0 \\ min\begin{cases}\delta+OPT(i-1,j), \\ \delta+OPT(i,j-1), \\ \alpha_{A[i]B[j]}+OPT(i-1,j-1)\end{cases} & otherwise \end{cases}$$

  We can evaluate the cost of an optimal alignment.

- What happens if we evaluate it directly?

The Recursion Tree



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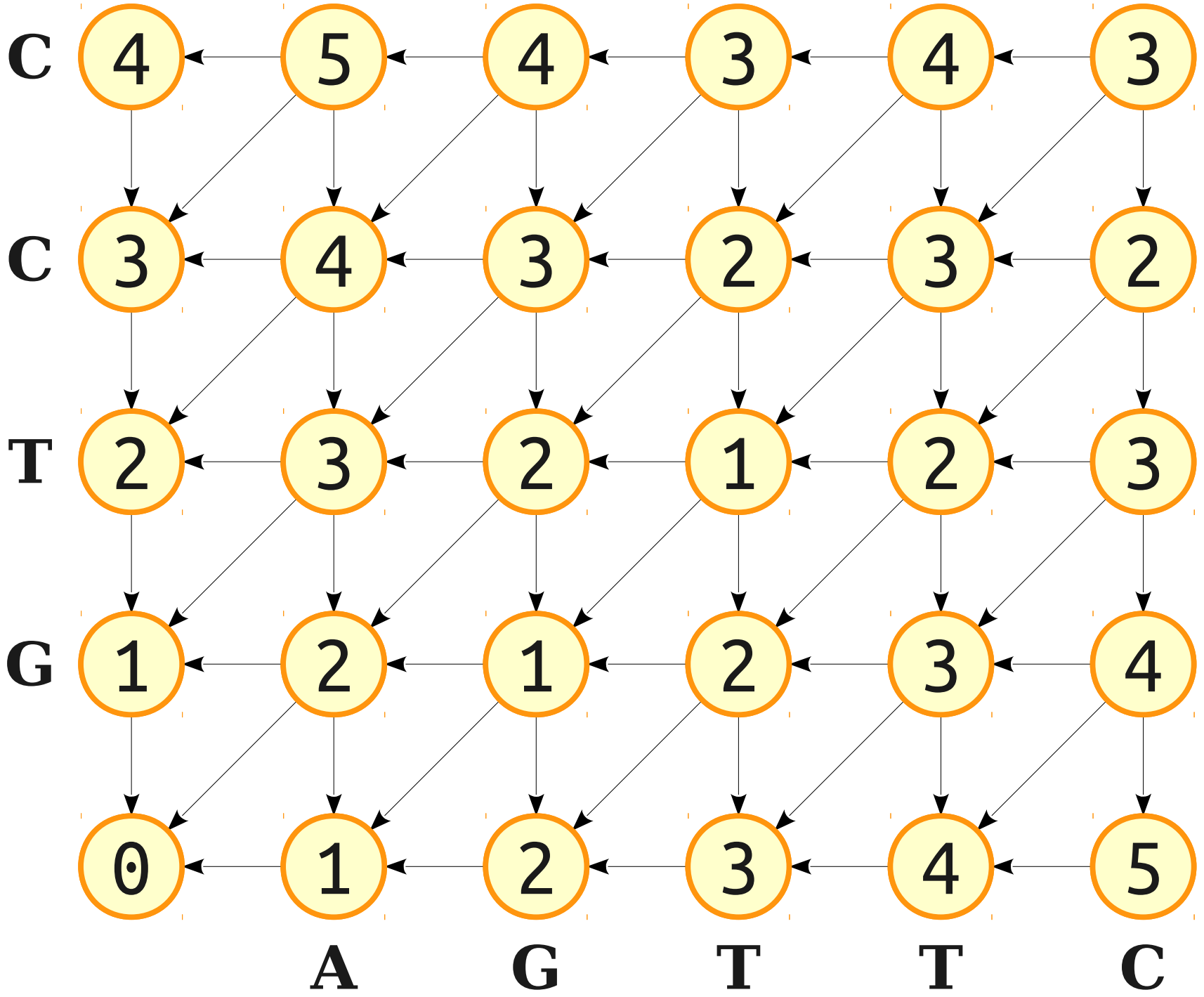
Dynamic Programming

- Do we have these three properties?
  - **Overlapping subproblems**
  - **Optimal substructure**
  - **Polynomial subproblems**
- Time to bring out the dynamic programming solution!

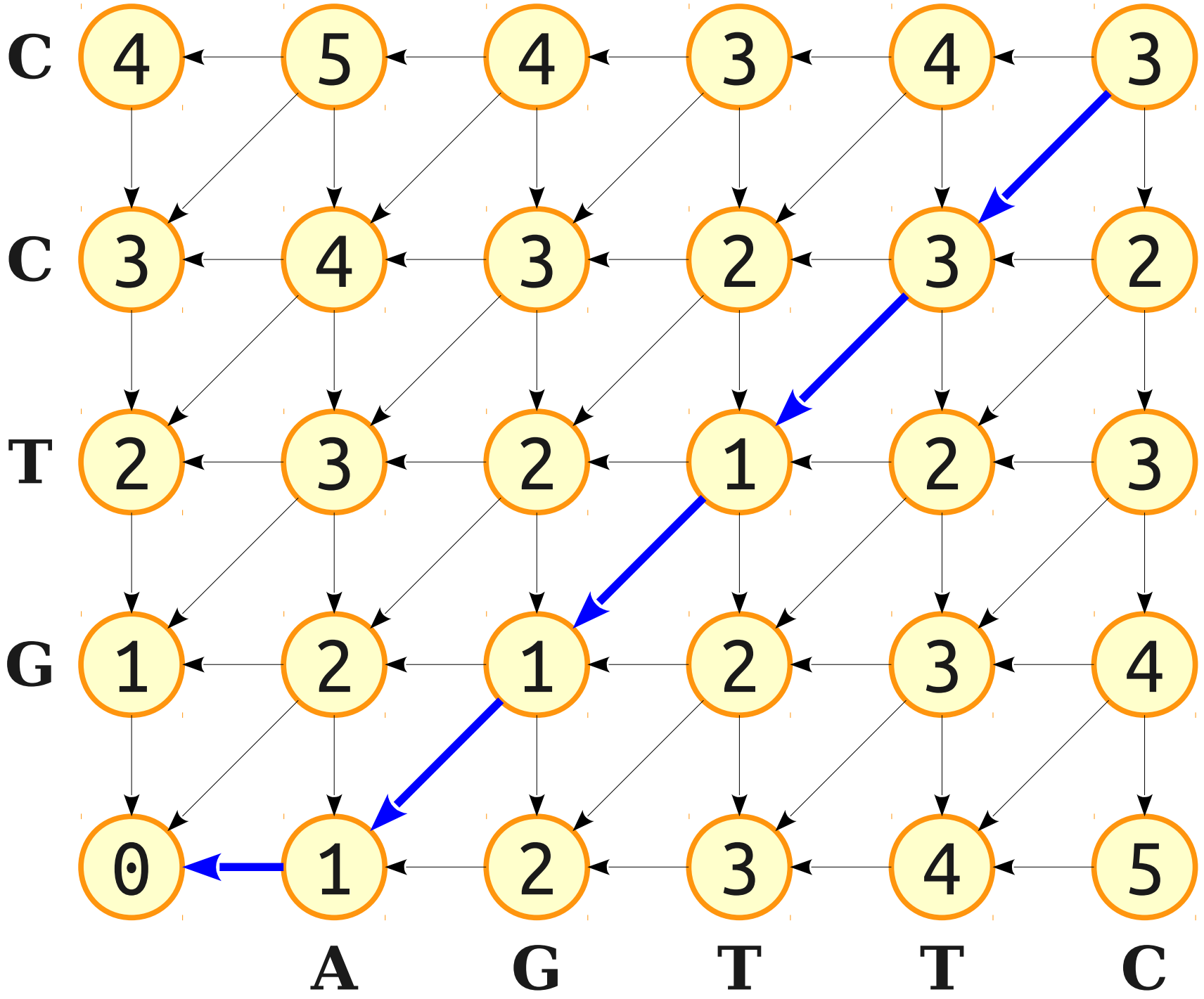

C 4 5 4 3 4 3
C 3 4 3 2 3 2
T 2 3 2 1 2 3
G 1 2 1 2 3 4
0 1 2 3 4 5
A G T T C

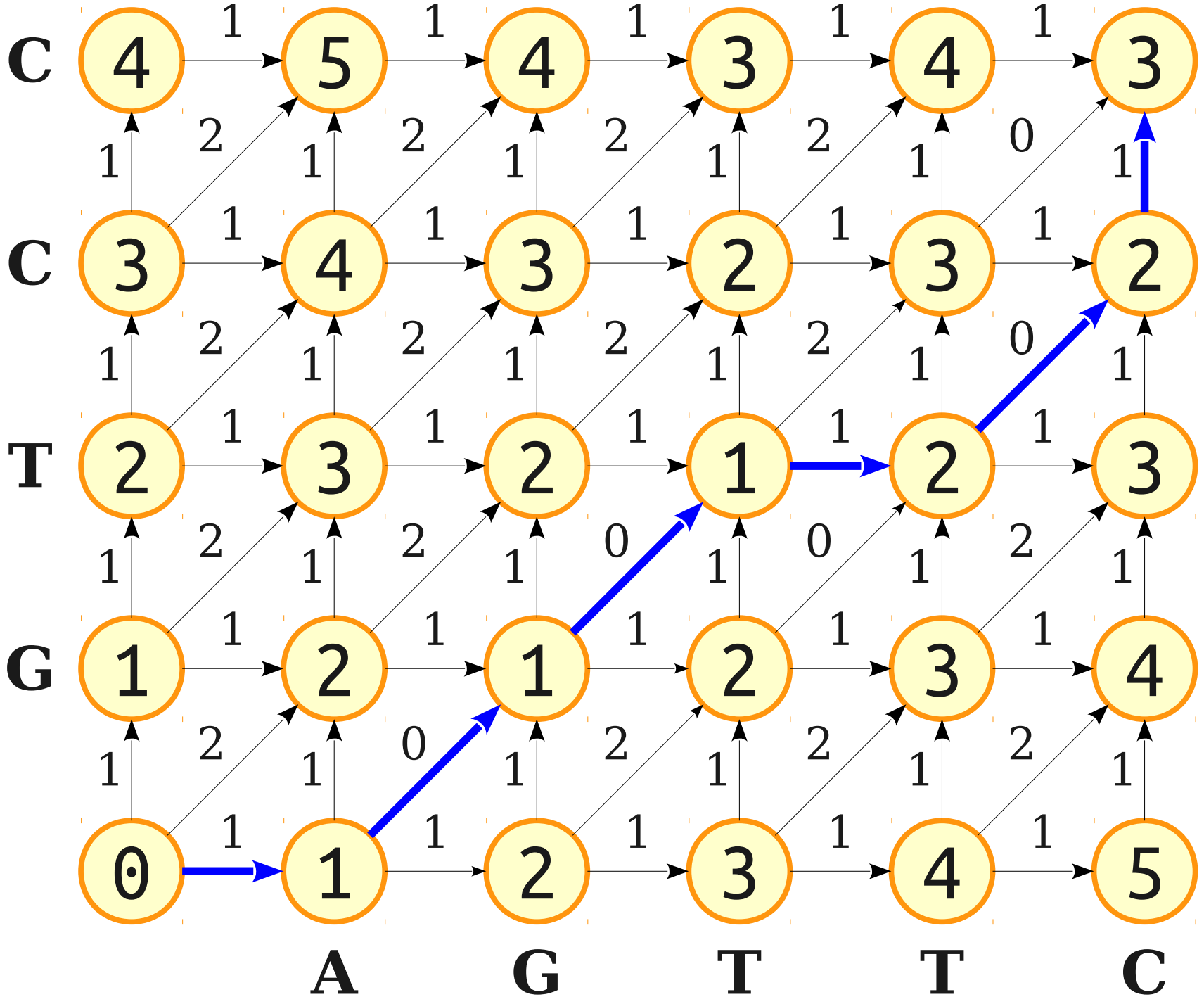
The Algorithm

- Create an $(|A| + 1) \times (|B| + 1)$ grid DP.
- For $i = 0$ to $|A|$, set DP[i, 0] = δi.
- For $j = 0$ to $|B|$, set DP[0, j] = δj.
- For $i = 1$ to $|A|$:
  - For $j = 1$ to $|B|$:
    - Set DP[i][j] to the minimum of
      - DP[i – 1][j] + δ
      - DP[i][j – 1] + δ
      - DP[i – 1][j – 1] + $\alpha_{A[i]B[j]}$

Analyzing the Algorithm

- Let $m = |A|$ and $n = |B|$.
- What is the runtime of this algorithm?
  - **O(*mn*)**
- What is the space usage of this algorithm?
  - **O(*mn*)**
- That's *way* less than the total number of possible alignments!


C
C
T
G
4 5 4 3 4 3
3 4 3 2 3 2
2 3 2 1 2 3
1 2 1 2 3 4
0 1 2 3 4 5
A G T T C


C
C
T
G
A
G
T
T
C
4 5 4 3 4 3
3 4 3 2 3 2
2 3 2 1 2 3
1 2 1 2 3 4
0 1 2 3 4 5

Finding the Alignment

- As with the DP algorithms we saw last time, we can recover the optimal sequence alignment by running the recurrence in reverse.
- Option 1: Start in the upper-left corner and walk backwards through the grid, at each point choosing a successor such that the total cost matches.
- Option 2: Treat the problem as finding the shortest path from the lower-left corner to the upper-right corner.

Reducing Space

- If you only care about the *value* of the optimal solution and not the actual solution, you can compress the DP table by only storing the last row.
- Runtime now O(mn) with space O(min{m, n}), which is better than before.
- **Clever Trick:** See Kleinberg and Tardos section 6.7 for a way to get an O(mn)-time, O(m + n)-space algorithm that does recover the optimal solution.

A Quick History Lesson

Another Algorithm: **Levenshtein Distance**

Transforming Strings

- Given a source string and target string, transform the source string into the target string by applying these edits:
  - **Insertion** of a new character,
  - **Deletion** of an existing character, or
  - **Replacement** of an existing character.
- The minimum number of edits required is called the **Levenshtein distance**.

Our Options

- Look at the first characters of each string.
- We can either
  - Match them together, if they're the same character.
  - Add in a character to the top or bottom to match the other string's character.
  - Delete a character from the top or bottom.
  - Replace the top or bottom character to match the other character.
- When one string becomes empty, the options are to add the remaining characters or delete them from the other string, both of which have the same cost.

Some Notation

- Suppose we want to transform the first i characters of A into the first j characters of B.
- Let OPT(i, j) denote the optimal cost of such an alignment.
- Let I_{ij} be 0 if $A[i] = B[j]$ and 1 otherwise.
- **Claim:** OPT(i, j) satisfies the following:

$$\mathrm{OPT}(i,j)=\begin{cases} j & if\ i=0 \\ i & if\ j=0 \\ min\begin{Bmatrix} 1+OPT(i,j-1), \\ 1+OPT(i-1,j), \\ \mathrm{I}_{ij}+OPT(i-1,j-1) \end{Bmatrix} & otherwise \end{cases}$$

Seem Familiar?

$$\mathrm{OPT}(i,j)=\begin{cases} j\delta & if\ i=0 \\ i\delta & if\ j=0 \\ min\begin{cases} \delta+OPT(i-1,j), \\ \delta+OPT(i,j-1), \\ \alpha_{A[i]B[j]}+OPT(i-1,j-1) \end{cases} & otherwise \end{cases}$$

$$\mathrm{OPT}(i,j)=\begin{cases} j & if\ i=0 \\ i & if\ j=0 \\ min\begin{cases} 1+OPT(i,j-1), \\ 1+OPT(i-1,j), \\ \mathrm{I}_{ij}+OPT(i-1,j-1) \end{cases} & otherwise \end{cases}$$

A Clever Reduction

- ***Claim:*** The Levenshtein distance between two strings is equal to their alignment cost if we set
  - $\delta = 1$.
  - $\alpha_{ab} = 0$ if $a = b$ and is 1 otherwise.
- ***Proof Idea:*** First, prove that the previous recurrence holds for Levenshtein distance, then show the recurrence is identical to that of sequence alignment with the above parameterization.

Another Intuition

- Run sequence alignment and do the following:
  - For any character matched against a blank, delete that character or insert a matching character into the other string.
  - For any character matched against a mismatched character, replace one character with the other.
- Therefore, can compute distance and transformation in $O(mn)$ time and $O(m + n)$ space, or can get value in $O(mn)$ time and $O(\min\{m, n\})$ space.

Next Time

- Shortest Paths Revisited
- The Bellman-Ford Algorithm
- Network Routing