Dynamic Programming
Statistics 650/750
Week 11 Tuesday

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Announcements

- Lecture notes available `documents/Lectures/weekBT.*`.
- Challenge milestone Tue 13 Nov: Part 2 revisions (650), Part 3 (750)
-

Introduction: Dynamic Programming

Today, we consider a useful algorithmic strategy called **dynamic programming** that is based on decomposing problems into sub-problems in a particular way.

Note: The term "programming" here is used in the old sense: referring to planning, scheduling, routing, assignment – and the optimization thereof. As with "linear programming," "quadratic programming," "mathematical programming" you can think of it as a synonym for *optimization*.

And indeed, dynamic programming is useful for a wide variety combinatorial optimization problems, as we will see.

Like other common algorithmic strategies (e.g., divide and conquer, greediness), dynamic programming is most useful in particular situations, but when it applies, it is powerful.

Illustrative Example: Fibonacci Revisited

We saw earlier a simple *recursive* algorithm for computing Fibonacci numbers.

```
fib(n):
   if n == 0: return 0
   if n == 1: return 1
   return fib(n-1) + fib(n-2)
```

Recall that this does not perform well. Why?

```
fib(7) -> fib(6) -> fib(5), fib(4) -> fib(4), fib(3), fib(3), ...
          fib(5) -> fib(4), fib(3)
```

We end up recomputing the same value multiple times.

Two key strategies:

1. Solve the problem in a particular order (from smaller `n` to larger `n`).
2. Store the values of problems we have already solved (memoization).

Together these strategies give us a performant algorithm.

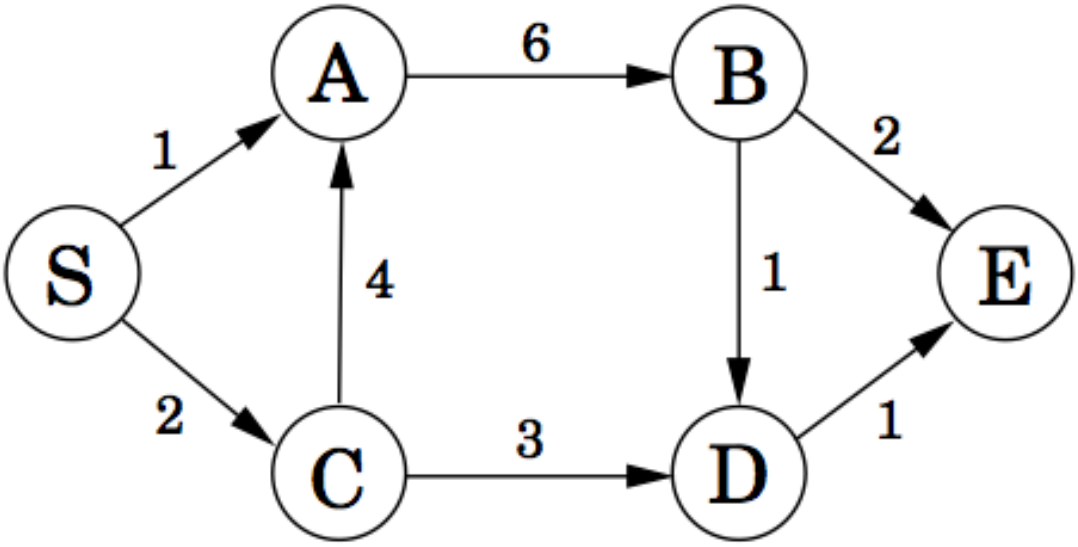
Illustrative Example: Making Change

In an earlier class, we solved the problem of how to make change in an optimal way using coins of specified denominations. How did we go about that?

Suppose we have coin denominations 1, 5, 10, and 25 and a purchase leaving 67 cents in change. What do we do?

Illustrative Example: Shortest Distance

Consider a (one-way) road network connecting sites in a town, where each path from a site to a connected site has a cost.



What is the lowest-cost path from S to E? How do we find it?

Solution

Start from E and work backward.

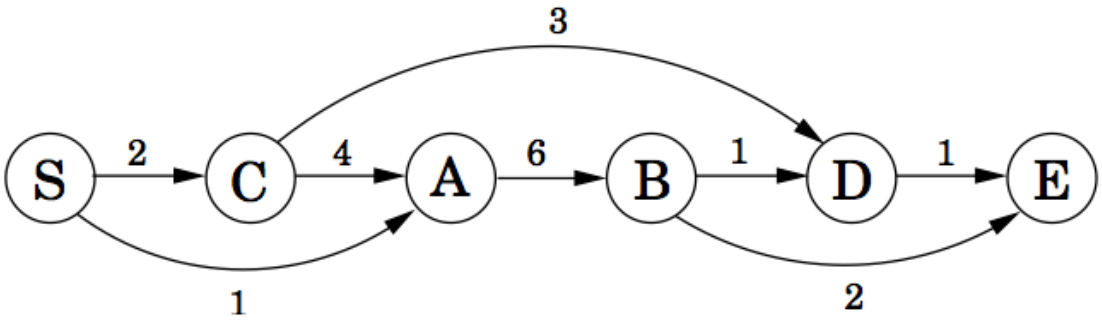
- The best route from E to E costs 0.
- The best route from D to E costs 1.
- The best route from B to E costs 2.
- The best route from A to E costs 8.
- The best route from C to E costs 4.
- The best route from S to E costs 6. [S -> C -> D -> E]

Why does this work?

The lowest-cost path from a given node to E is a *subproblem* of the original.

We can arrange these subproblems in an ordering so that we can solve the easiest subproblems first and then solve the harder subproblems in terms of the easier ones.

What ordering?



This is just the *topological sort* of the DAG that we saw above. This gives us a subproblem *dependent order*

`S, C, A, B, D, E;`

or alternatively, what we will call a *flow order*

`E, D, B, A, C, S.`

Overview: Dynamic Programming (DP)

The Key Ideas Behind Dynamic Programming

1. Decompose a problem into (possibly many) smaller (often overlapping) **subproblems**.
2. Arrange those subproblems in a **special ordering**.
3. Compute solutions to the subproblems in order, **storing** the solution to each subproblem for later use.
4. The solution to a subproblem **combines** the solutions to earlier subproblems in an essential way.

Reminder: Topological Sorting DAGS

A **topological sort** of a DAG is a linear ordering of the DAG's nodes such that if (u, v) is a directed edge in the graph, node u comes before node v in the ordering.

Example: A directed graph
network1.png
and a rearrangment showing a topological sort
network2.png
The sorted nodes are S C A B D E.
For a general DAG, how do we use DFS to do a topological sort?

```
Algorithm topological-sort:

Input: A DAG G
Output: A list of nodes representing a topological sort

Steps: Run DFS on G, configured with after_node so that
after each node is processed, we push it onto the front
of a linked list (or equivalently onto a stack).

Return the list of nodes.
```

The Key Ideas Revisited

1. Decompose a problem into smaller **subproblems**.

   Implicitly, each subproblem is a node in a directed graph, and there is a directed edge (u, v) in that graph when the result of one subproblem is required in order to solve the other.

   There are two equivalent choices for edge orientation in this graph:

   Flow orientation (u, v) is an edge when the result of subproblem u is required in order to solve subproblem v.

   Dependent orientation (v, u) is an edge when the result of solving subproblem v requires the result of subproblem u.

   As the names suggest, **flow** orientation describes how information flows through the graph during dynamic programming, whereas **dependent** orientation illustrates the dependence of each subproblem on others. Both are used. I tend to prefer the former, but the latter is more common.

   We will write $u \succ v$ or, equivalently, $v \prec u$ to denote the actual dependence relation regardless of which edge orientation we use pictorially.

   (To be specific, $u \succ v$ means that the result subproblem u is required to solve subproblem v. So both $u \succ v$ and $v \prec u$ imply that there is an edge between the two subproblems in the underlying DAG.)

2. Arrange those subproblems in the **topologically sorted** order of the graph.

   A topological sort of the underlying DAG yields an ordering of the subproblems. We will call this a *subproblem order*.

   If the DAG was defined with *flow orientation*, we will call this *subproblem flow order*, or **flow order** for short.

   If the DAG was defined with *dependent orientation*, we will call this *subproblem dependent order*, or **dependent order** for short.

3. Compute solutions to the subproblems in order, storing the result of each subproblem for later use if needed. This storing approach is called **memoization** or **caching**.

   One common scenario is when the subroblems are computed by a single function, and we store our previous solution by **memoizing** the function. That is, when we call the function, we check if we have called it with these particular arguments before. If so, return the previously computed value. Otherwise, compute the value and store it, marking these arguments as being previously computed.

4. The solution to a subproblem *combines* the solutions to earlier subproblems through a specific mathematical relation.

The mathematical relationship between a subproblem solution and the solution of previous subproblems is often embodied in an equation, or set of equations, called the **Bellman equations**. We will see examples below.

Question

For the Fibonacci example we just saw, what are the subproblems? What is the DAG? What does memoizing look like?

```
Fibonacci:
   Subproblems: computing fib for smaller, particular values
   The DAG relates the fib(n) = fib(n-1) + fib(n-2)

memoizing_table = hash_table()
memoizing_original = hash_table()

function  memoize(f):
   function f_prime(...):
       arglist = list(...)
       entry = memoizing_table.lookup(arglist)

       if entry:
           return entry
       else:
           value = f(...)
           memoizing_table.insert(arglist, value)
           return value

   memoizing_original.insert(f_prime, f)
   return f_prime

fib = memoize(fib)
```

Examples

Example #1: Shortest Path in a Graph

Given a weighted, directed graph G and a specific node s, we want to find the shortest path from s to each other node in the graph. Consider the following basic algorithm.

```
Inputs: G       a (weighted, directed) graph
        source  a node in G
Output: A list 'predecessor' specifying the shortest paths
        from source, with predecessor[w] = v if we added
        an edge from v to w to the path.

# Initialize priority queue
Q = new priority queue
foreach node n in G:
    if node is source:
        distance[node] = 0
```

```
    else:
        distance[node] = Infinity
    predecessor[node] = nil
    Q.add(node, distance[node])

# Build the path
while Q is not empty:
    closest = Q.extract_minimum()
    foreach neighbor n of closest:
        if n is in Q:
            est_dist = distance[closest] + G.weight(closest,n)
            if est_dist < distance[n]:
                distance[n] = est_dist
                predecessor[n] = closest
                Q.decrease_priority(n, distance[n])
```

Formalizing this

For nodes u in our graph, let dist(u) be the minimal cost of a path from u to E (the end node). We want dist(S). Finding dist(u) is a subproblem.

For subproblem nodes u, v with an edge $u \to v$ connecting them, let $c(u, v) \equiv c(v, u)$ be the cost of that edge.

Here is our algorithm:

1. Initialize $\text{dist}(u) = \infty$ for all u.
2. Set $\text{dist}(E) = 0$.
3. Topologically sort the graph, giving us a sequence of nodes from E to S. Call this "subproblem flow order".
4. For nodes v in subproblem *flow* order, set

$$\text{dist}(v) = \min_{u \succ v} (\text{dist}(u) + c(u, v))$$

These last equations are called the **Bellman equations**.

Let's try it.

```
Subproblem flow order is E,D,B,A,C,S, yielding:
   dist(E) =                                  0
   dist(D) = dist(E) + 1                    = 1
   dist(B) = min(dist(E) + 2, dist(D) + 1) = 2
   dist(A) = dist(B) + 6                    = 8
   dist(C) = min(dist(A) + 4, dist(D) + 3) = 4
   dist(S) = min(dist(A) + 1, dist(C) + 2) = 6
```

Exercise

Write a function `min_cost_path` that returns the minimal cost path to a target node from every other node in a weighted, directed graph, along with the minimal cost. If there is no directed path from a node to the target node, the path should be empty and the cost should be infinite.

Your function should take a representation of the graph and a list of nodes in subproblem *flow* order. You can represent the graph anyway you prefer; however, one convenient interface, especially for R users, would be:

`min_cost_path(target_node, dag_nodes_flow, costs)`

where `target_node` names the target node, `dag_nodes_flow` lists all the nodes in flow order, and costs is a *symmetric* matrix of edge weights with rows and columns arranged in flow order. Assume: costs[u,v] = Infinity if no edge btwn u,v.

Note: You can use the above as a test case. Also, be aware of the `tsort` command on the Mac or Linux command line.

```
echo "S A\nS C\nA B\nC A\nC D\nB D\nB E\nD E\n" | tsort
```

```r
constantly <- function(x) {
    return( function(z){ return(x) } )
}

min_cost_path <- function(target_node, dag_nodes_flow, costs) {
    node_count   <- length(dag_nodes_flow)
    paths        <- setNames(vector("list", node_count), dag_nodes_flow)
    dists        <- lapply(paths, constantly(Inf))
    target_index <- match(target_node, dag_nodes_flow)

    if ( !is.na(target_index) ) stop("Target node not found")

    dists[[target_node]] <- 0
    paths[[target_node]] <- c(target_node)

    for ( node_index in (target_index+1):node_count ) {
        flows_from <- target_index:(node_index-1) # indices in *flow* order

        step_cost <- unlist(dists[flows_from]) + costs[flows_from, node_index]
        best_step <- which.min(step_cost)
        min_dist  <- step_cost[best_step]

        if ( min_cost < Inf ) {
            dists[[node_index]] <- min_dist
            paths[[node_index]] <- c(dag_nodes_flow[node_index],
                                     paths[[target_index + best_step - 1]])
        }
    }
    # Note: Previous loop would be more efficient w/better graph representation
    return( list(costs=dists, paths=paths,
                 target=target_node, nodes=dag_nodes_flow, weights=costs) )
}
```

Example #2: Longest Increasing Subsequence

Given a sequence s of length n ordinals, find the longest subsequence whose elements are strictly increasing.

```
5, 2, 8, 6, 3, 6, 9, 7  ->  2, 3, 6, 9
```

Let's sketch a dynamic-programming solution for this problem. Work with a partner to answer these questions.

- What are the subproblems?
- Are they arranged in a DAG? If so, what are the relations?
- What are the Bellman equations for these subproblems?
- Sketch the DP algorithm here.
- We can find the longest length, how do we get the path?
- How would a straightforward recursion implementation perform? What goes wrong?

A Solution

- Make a graph with one node per element and a link $s_i \to s_j$ iff $i < j$ and $s_i < s_j$.
- Let L_j be length of the longest path ending in node j (plus 1 since we are counting nodes not edges).
- The sub-problems are arranged in a DAG because transitivity of $<$ implies that no path can return to a predecessor.
- Any path to node j must pass through one of j's predecessors (if it has any). Hence, $L_j = 1 + \max\{L_i : i \to j\}$.
- Initialize all the L_j's to 0, topologically sort the DAG, for every node j in subproblem order set $L_j = 1 + \max\{L_i : i \to j\}$, and return $\max(L)$
- Recursion would solve the subproblems over and over again, with many calls – exponential time in general.

  Consider the recursive approach when the sequence is sorted; then

  ```
  L_j = 1 + max(L_1, L_2, ..., L_{j-1})
  ```

  What does the tree of recursive calls look like here?

Example #3: Matrix Product Ordering

Suppose we have three matrices A, B, and C. To compute ABC, we have two choices $(AB)C$ or $A(BC)$. Which is better?

Assuming standard matrix multiplication, multiplying an $n \times p$ by a $p \times r$ takes $O(npr)$ operations.

Ex: Suppose A, B, and C are respectively 100×20, 20×100 and 100×20.

- $(AB)C$ takes $100 \cdot 20 \cdot 100 + 100 \cdot 100 \cdot 20 = 2 \cdot 20 \cdot 100^2$
- $A(BC)$ takes $100 \cdot 20 \cdot 20 + 20 \cdot 100 \cdot 20 = 2 \cdot 20^2 \cdot 100$

This is a factor of 5 difference.

Problem: Given matrices $A_1, \ldots, A_n$ and their dimensions, what is the best way to "parenthesize" them in computing the products?

There are exponentially many choices, so brute force is out.

Subproblems: For each pair $i \leq j$, parenthesize $A_i \cdots A_j$.

This gives n^2 subproblems. How long does each subproblem take to solve? Look at the Bellman equations.

```
cost(i,j) = min_{k in i..j} cost(i,k) + cost(k+1,j) + combinationCost(i,j,k)
```

This is $O(n)$ for each subproblem, giving $O(n^3)$ total. (We can improve this.)

Example #4: Text Justification

Given a paragraph and a target line length, how do we "optimally" break the text into lines that are as close to the target as possible.

```
What Orbán has done is to squash political competition. He has
gerrymandered and changed election rules, so that he doesn't
need a majority of votes to control the government. He has
rushed bills through Parliament with little debate. He has
relied on friendly media to echo his message and smear
opponents. He has stocked the courts with allies. He has
overseen rampant corruption. He has cozied up to Putin. To
justify his rule, Orbán has cited external threats - especially
Muslim immigrants and George Soros, the Jewish Hungarian-born
investor - and said that his party is the only one that
represents the real people. (David Leonhardt, NYT)
```

Suppose we want 60 character lines. One strategy could be greedy: break the first line close to 60, then the second, and so on.

```
Badness: 3242

What Orbán has done is to squash political competition. He
has gerrymandered and changed election rules, so that he
doesn't need a majority of votes to control the government.
He has rushed bills through Parliament with little debate.
He has relied on friendly media to echo his message and
smear opponents. He has stocked the courts with allies. He
has overseen rampant corruption. He has cozied up to Putin.
To justify his rule, Orbán has cited external threats -
especially Muslim immigrants and George Soros, the Jewish
Hungarian-born investor - and said that his party is the
only one that represents the real people. (David Leonhardt,
NYT)
```

Our DP strategy will be different. We will start with an *objective function*: for instance,

```
(define (badness line target)
  (let ([deviation (- (length line) target)])
    (if (<= deviation 0)
        (* deviation deviation)
        MAX-BADNESS)))
```

Given a list of words `words[0:n]`, our goal is to break the words into lines `words[0:i1]`, `words[i1:i2]`, `words[i2:i3]`, and so forth of lengths ℓ_j that minimize $\sum_j \text{badness}(\ell_j, t)$ for our target line length t.

```
Badness: 692

What Orbán has done is to squash political competition.
He has gerrymandered and changed election rules, so
that he doesn't need a majority of votes to control the
```

```
government. He has rushed bills through Parliament with
little debate. He has relied on friendly media to echo
his message and smear opponents. He has stocked the
courts with allies. He has overseen rampant corruption.
He has cozied up to Putin. To justify his rule,
Orbán has cited external threats - especially Muslim
immigrants and George Soros, the Jewish Hungarian-born
investor - and said that his party is the only one
that represents the real people. (David Leonhardt, NYT)
```

What are the subproblems?

Subproblem Structure

The j^{th} subproblem is to minimize badness for the suffix `words[j:]`. There are $O(n)$ subproblems when there are n words.

Belman equations:

- `cost[n] = 0`
- `cost[i] = min([badness(words[i:j],t) + cost[j] for j in range(i+1,n+1)])`

Solution: `cost[0]` Total time: $O(n^2)$

Example #5: Edit Distance between Strings

When you make a spelling mistake, you have usually produced a "word" that is *close* in some sense to your target word. What does close mean here?

The *edit distance* between two strings is the minimum number of edits – insertions, deletions, and character substitutions – that converts one string into another.

Example: Snowy vs. Sunny What is the edit distance?

```
Snowy
Snnwy
Snny
Sunny
```

How can we find the edit distance for any two strings edit(s,t)?

Another example: EXPONENTIAL vs. POLYNOMIAL

```
EXPONENTIAL   EXPONENTIA  EXPONENTIAL  EXPONENTIA
POLYNOMIAL    POLYNOMIA   POLYNOMIA    POLYNOMIAL

                          EXPONENTIA
EXPONENT                  POLYNOMI
POLYNOM
                          EXPONENTIA
                          POLYNOMIA

                          EXPONENTIAL
                          POLYNOMI

                          EXPONEN
```

```
                          P

edit(s, t):  s[1..i], t[1..j]
```

Questions

- What are the subproblems?
- Are they arranged in a DAG?
- How do we combine subproblems? (The Bellman Equations)

Answers

We will use a common strategy: prefixes to find subproblems.

Specifically, to find edit(s,t), we can create a subproblem by finding E_{ij} = edit(s[1..i],t[1..j]).

We can express these subproblem solutions in terms of smaller subproblems. Consider the last entry in each substring.

Either s_i is matched up with an extra character, or t_j is, or both characters are matched up with each other, in which case they can be the same or not. When there is a mismatch (insertion or deletion) the cost is one plus the cost of the smaller string; if the two are both present but there is a difference (substitution), the cost is 1 plus the cost with both smaller lists.

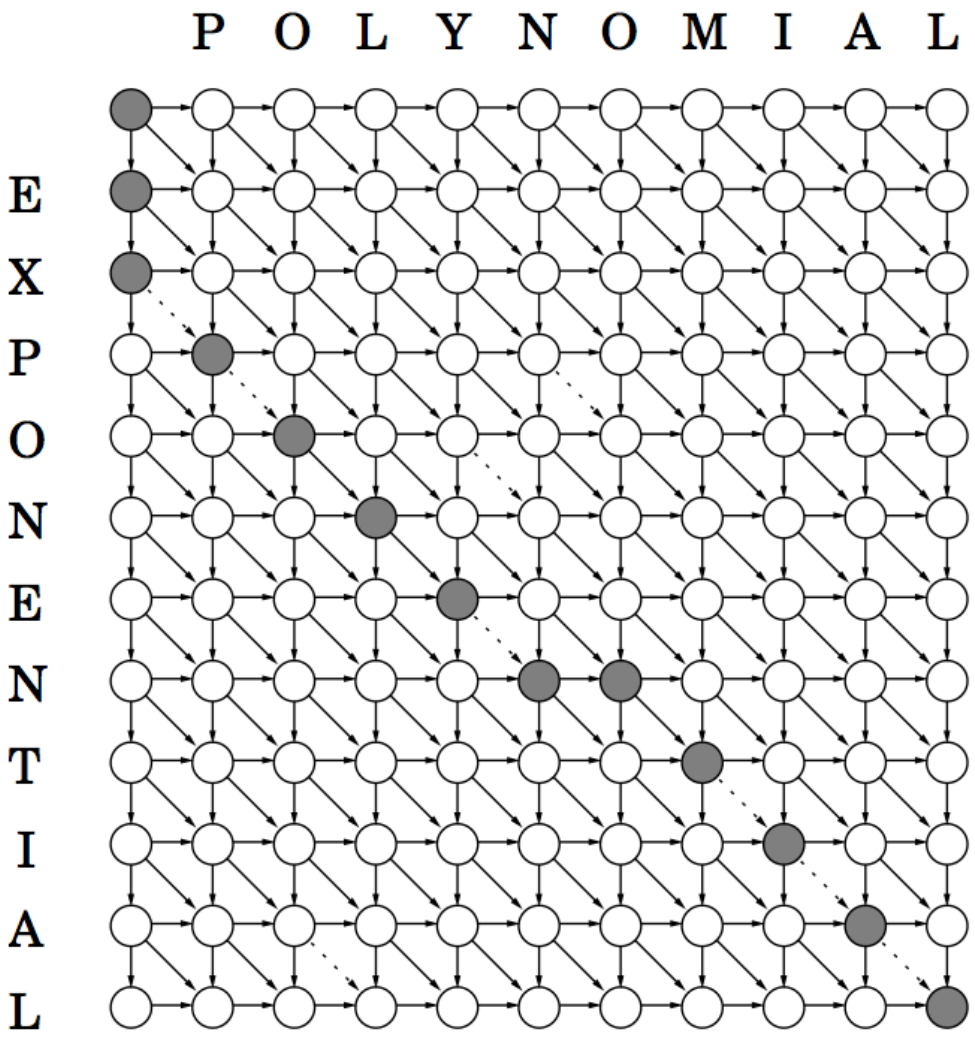
$$E_{ij} = \min(1 + E_{i-1,j}, 1 + E_{i,j-1}, (s_i \neq t_j) + E_{i-1,j-1}),$$

Notice that we have a boundary case: $E_{0j} = j$ and $E_{i0} = i$. Why? This gives us the DAG.

The elements of the DAG:

- Each pair s_i and t_j represents one node in the graph.
- Each node is linked to the three nodes corresponding to
  1. s_{i+1} and t_{j+1},
  2. s_i and t_{j+1}, and
  3. s_{i+1} and t_j.

See the Figure below for the DAG that results from comparing two specific words.



Application: Fast file differences

Programs diff, git-diff, rsync use such algorithms (along with related dynamic programming problem Longest Common Subsequence) to quickly find meaningful ways to describe differences between arbitrary text files.

Application: Genetic Alignment

Use edit distance logic to find the best alignment between two sequences of genetic bases (A, T, C, G). We allow our alignment to include gaps ('_') in either or both sequences.

Given two sequences, we can score our alignment by summing a score at each position based on whether the bases match, mismatch, or include a gap.

```
C G A A T G C C A A A
C A G T A A G G C C T T A A

C _ G _ A A T G C C _ A A A
C A G T A A G G C C T T A A
m g m g m m x m m m g x m m
```

```
Score = 3*gap + 2*mismatch + 9*match
```

With (sub-)sequences, S and T, let S' and T' respectively, be the sequences without the last base. There are then three subproblems to solve to align(S,T):

- align(S,T')
- align(S',T)
- align(S',T')

The score for S and T is the biggest score of:

- score(align(S,T')) + gap
- score(align(S',T)) + gap
- score(align(S',T')) + match if last characters of S,T match
- score(align(S',T')) + mismatch if last characters do not match

The boundary cases (e.g., zero or one character sequences) are easy to compute directly.

Question: Longest Common Subsequence

If we want to find the longest common subsequence (LCS) between two strings, how can we adapt the logic underlying this edit distance example to find a dynamic programming solution?

- Approach Again look at the last element of substring pairs. Either:
  - They both contribute to the LCS: $D_{ij} = D_{i-1,j-1} + 1$.
  - Or at least one does not: $D_{ij} = \max(D_{i-1,j}, D_{i,j-1})$.