Chapter 18

Dynamic Programming

"An interesting question is, 'Where did the name, dynamic programming, come from?' The 1950s were not good years for mathematical research. We had a very interesting gentleman in Washington named Wilson. He was Secretary of Defense, and he actually had a pathological fear and hatred of the word, research. I'm not using the term lightly; I'm using it precisely. His face would suffuse, he would turn red, and he would get violent if people used the term, research, in his presence. You can imagine how he felt, then, about the term, mathematical. The RAND Corporation was employed by the Air Force, and the Air Force had Wilson as its boss, essentially. Hence, I felt I had to do something to shield Wilson and the Air Force from the fact that I was really doing mathematics inside the RAND Corporation. What title, what name, could I choose? In the first place I was interested in planning, in decision making, in thinking. But planning, is not a good word for various reasons. I decided therefore to use the word, 'programming.' I wanted to get across the idea that this was dynamic, this was multistage, this was time-varying—I thought, let's kill two birds with one stone. Let's take a word that has an absolutely precise meaning, namely dynamic, in the classical physical sense. It also has a very interesting property as an adjective, and that is it's impossible to use the word, dynamic, in a pejorative sense. Try thinking of some combination that will possibly give it a pejorative meaning. It's impossible. This, I thought dynamic programming was a good name. It was something not even a Congressman could object to. So I used it as an umbrella for my activities".

Richard Bellman ("Eye of the Hurricane: An autobiography", World Scientific, 1984)

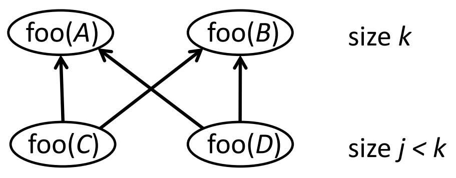
The Bellman-Ford shortest path algorithm covered in Chapter 13 is named after Richard Bellman and Lester Ford. In fact that algorithm can be viewed as a dynamic program. Although the quote is an interesting bit of history it does not tell us much about dynamic programming. But perhaps the quote will make you feel better about the fact that the term has little intuitive meaning.

In this course, as commonly used in computer science, we will use the term dynamic programming to mean an algorithmic technique in which (1) one constructs the solution of a larger problem instance by composing solutions to smaller instances, and (2) the solution to each smaller instance can be used in multiple larger instances. For example, in the Bellman-Ford algorithm, to find the shortest path length from the source to vertex v that uses at most i vertices, depends on finding the shortest path lengths to the in-neighbors of v that use at most $i-1$ vertices. As vertices can have multiple out-neighbors, these smaller instances maybe used more then once. Dynamic programming is thus one of the inductive algorithmic techniques we are covering in this course.

Dynamic programming is another example of an inductive technique where an algorithm relies on putting together smaller parts to create a larger solution. The correctness then follows by induction on problem size. The beauty of such techniques is that the proof of correctness parallels the algorithmic structure.

So far the inductive techniques we have covered are divide-and-conquer, the greedy method, and contraction. In the greedy method and contraction each instance makes use of only a single smaller instance. In the case of greedy algorithms the single instance was one smaller—e.g. Dijkstra's algorithm that removes the vertex closest to the set of vertices with known shortest paths and adds it to this set. In the case of contraction it is typically a constant fraction smaller—e.g. solving the scan problem by solving an instance of half the size, or graph connectivity by contracting the graph by a constant fraction.

In the case of divide-and-conquer, as with dynamic programming, we made use of multiple smaller instances to solve a single larger instance. However in divide-and-conquer we have always assumed the solutions are solved independently and hence we have simply added up the work of each of the recursive calls to get the total work. But what if two instances of size k, for example, both need the solution to the same instance of size $j < k$?

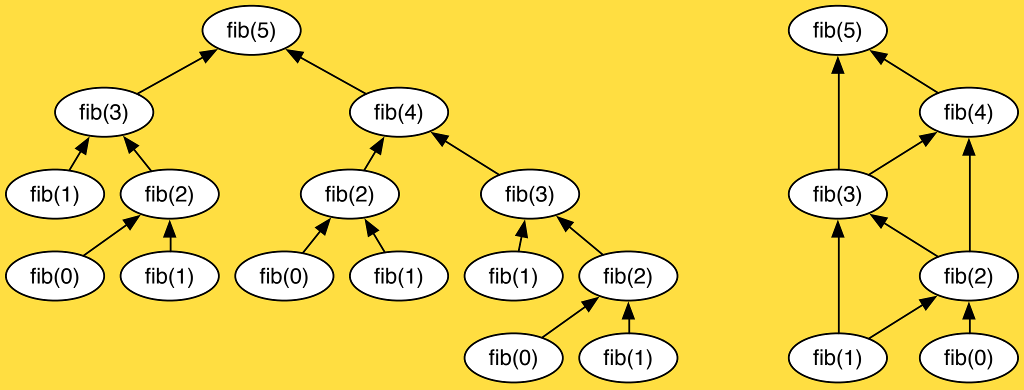


Although sharing the results in this simple example will only make at most a factor of two difference in work, in general sharing the results of subproblems can make an exponential difference in the work performed.

Example 18.1. *Consider the following algorithm for calculating the Fibonacci numbers.*

```
function fib$(n)$ =
  if $(n \leq 1)$ then $1$
  else fib$(n-1)$ + fib$(n-2)$
```

This recursive algorithm takes exponential work in n as indicated by the recursion tree below on the left for `fib`(5). *If the results from the instances are shared, however, then the algorithm only requires linear work, as illustrated below on the right.*



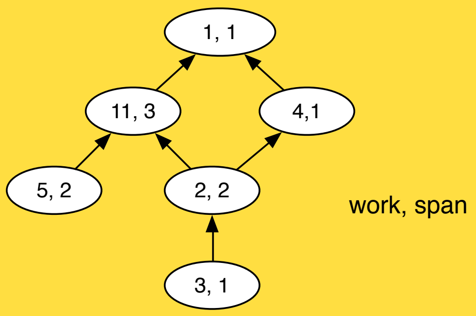
Here many of the calls to `fib` *are reused by two other calls.*

Although Fibonacci is not particularly practical, it turns out there are many practical problems where sharing results of subinstances is useful and can make a significant differences in the work used to solve a problem. We will go through several of these examples in this chapter.

With divide-and-conquer the composition of a problem instance in terms of smaller instances is typically described as a tree, and in particular the so called recursion tree. With dynamic programming the composition can instead be viewed as a Directed Acyclic Graph (DAG). Each vertex in the DAG corresponds to a problem instance and each edge goes from an instance of size j to one of size $k > j$—i.e. we direct the edges (arcs) from smaller instances to the larger ones that use them. We direct them this way since the edges can be viewed as representing dependences between the source and destination (i.e. the source has to be calculated before the destination can be). The leaves of this DAG (i.e. vertices with no in-edges) are the base cases of our induction (instances that can be solved directly), and the root of the DAG (the vertex with no out-edges) is the instance we are trying to solve. More generally we might actually have multiple roots if we want to solve multiple instances.

Abstractly dynamic programming can therefore be best viewed as evaluating a DAG by propagating values from the leaves to the root and performing some calculation at each vertex based on the values of its in-neighbors. Based on this view, calculating the work and span of a dynamic program is relatively straightforward. We can associate with each vertex a work and span required for that vertex. The overall work is then simply the sum of the work across the vertices. The overall span is the longest path in the DAG where the path length is the sum of the spans of the vertices along that path.

Example 18.2. *Consider the following DAG:*



where we have written the work and span on each vertex. This DAG does $5 + 11 + 3 + 2 + 4 + 1 = 26$ *units of work and has a span of* $1 + 2 + 3 + 1 = 7$.

Question 18.3. *Do algorithms based on dynamic programming have much parallelism?*

Whether a dynamic programming algorithm has much parallelism will depend on the particular DAG. As usual the parallelism is defined as the work divided by the span. If this large and grows asymptotically, then the algorithm has significant parallelism Fortunately, most dynamic programs have significant parallelism. Some, however, do not have much parallelism.

The challenging part of developing a dynamic programming algorithm for a problem is in determining what DAG to use. The best way to do this, of course, is to think inductively—how can you solve an instance of a problem by composing the solutions to smaller instances? Once an inductive solution is formulated you can think about whether the solutions can be shared and how much savings can be achieved by sharing. As with all algorithmic techniques, being able to come up with solutions takes practice.

It turns out that most problems that can be tackled with dynamic programming solutions are optimization or decision problems. An *optimization problem* is one in which we are trying to find a solution that optimizes some criteria (e.g. finding a shortest path, or finding the longest contiguous subsequence sum). Sometimes we want to enumerate (list) all optimal solutions, or count the number of such solutions. A *decision problem* is one in which we are trying to find if a solution to a problem exists. Again we might want to count or enumerate the valid solutions. Therefore when you see an optimization or enumeration problem you should think about possible dynamic programming solutions.

Although dynamic programming can be viewed abstractly as a DAG, in practice we need to implement (code) the dynamic program. There are two common ways to do this, which are referred to as the top-down and bottom-up approaches. The *top-down* approach starts at the root and uses recursion, as in divide-and-conquer, but remembers solutions to subproblems so that when the algorithm needs to solve the same instance many times only the first call does the work and the remaining calls just look up the solution. Storing solutions for reuse is called *memoization*. The *bottom-up* approach starts at the leaves of the DAG and typically processes the DAG in some form of level order traversal—for example, by processing all problems of size 1 and then 2 and then 3, and so on. Each approach has its advantages and disadvantages. Using the top-down approach (recursion with memoization) can be quite elegant and can be more efficient in certain situations by evaluating only those instances actually needed. Using the bottom up approach (level order traversal of the DAG) assumes it will need every instance whether or not is it use in the overall solution, but can be easier to parallelize and can be more space efficient. There is also a third technique for solving dynamic programs that works for certain problems, which is to find the shortest path in the DAG where the weighs on edges are defined in some problem specific way. *It is important, however, to remember to first formulate the problem abstractly in terms of the inductive structure, then think about it in terms of how substructure is shared in a DAG, and only then worry about coding strategies.*

In summary the approach to coming up with a dynamic programming solution to a problem is as follows.

1. Is it a decision or optimization problem?
2. Define a solution recursively (inductively) by solving smaller problems.
3. Identify any sharing in the recursive calls, i.e. calls that use the same arguments.
4. Model the sharing as a DAG, and calculate the work and span of the computation based on the DAG.
5. Decide on an implementation strategy: either bottom up top down, or possibly shortest paths.

18.1 Subset Sums

The first problem we will cover in this lecture is a decision problem, the subset sum problem. It takes as input a multiset of numbers, i.e. a set that allows duplicate elements, and sees if any subset sums to a target value. More formally:

Definition 18.4. *The* subset sum *(SS) problem is, given a multiset of positive integers S and a positive integer value k, determine if there is any $X \subseteq S$ such that $\sum_{x \in X} x = k$.*

For example, consider the multiset $S = \{1, 4, 2, 9\}$. There is no subset that sums to 8. However, if the target sum is $k = 7$, the subset $\{1, 4, 2\}$ sums to 7 and therefore is a solution.

In the general case when k is unconstrained this problem is a classic NP-hard problem. However, our goal here are more modest. We are going to consider the case where we include k in the work bounds. We show that as long as k is polynomial in $|S|$ then the work is also polynomial in $|S|$. Solutions of this form are often called *pseudo-polynomial* work (time) solutions.

This problem can be solved using brute force by simply considering all possible subsets. This takes exponential work since there are an $2^{|S|}$ subsets. For a more efficient solution, one should consider an inductive solution to the problem. As greedy algorithms tend to be efficient, you should first consider some form of greedy method that greedily takes elements from S. Unfortunately greedy does not work.

We therefore consider a divide-and-conquer solution. Naively, this will also lead to exponential work, but by reusing subproblems we can show that it results in an algorithm that requires only $O(|S|k)$ work. The idea is to consider one element a out of S (any will do) and consider the two possibilities: either a is included in X or not. For each of these two possibilities we make a recursive call on the subset $S \setminus \{a\}$, and in one case we subtract a from k ($a \in X$) and in the other case we leave k as is ($a \notin X$). Here is an algorithm based on this idea. It assumes the input is given as a list (the order of the elements of S in the list does not matter):

Algorithm 18.5 (Recursive Subset Sum)**.**

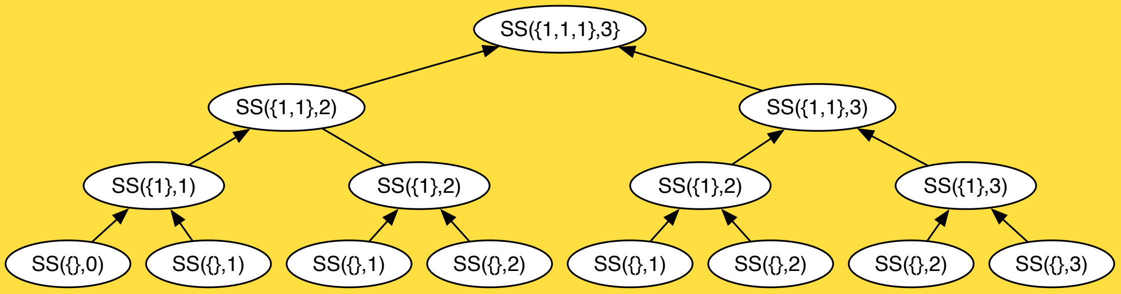
```
1 function SS($S, k$) =
2   case (showL($S$), $k$) of
3     (_, 0) ⇒ true
4   | (nil, _) ⇒ false
5   | (cons($a, R$), _) ⇒
6       if ($a > k$) then SS($R$, $k$)
7       else (SS($R, k - a$) orelse SS($R, k$))
```

Lines 3 and 4 are the base cases. In particular if $k = 0$ then the result is true since the empty set adds to zero. If $k \neq 0$ and S is empty, then the result is false since there is no way to get k from an empty set. If S is not empty but its first element a is greater than k, then we clearly can not add a to X, and we need only make one recursive call. The last line is the main inductive case where we either include a or not. In both cases we remove a from S in the recursive call R. In the left case we are including a in the set so we have to subtract its value from k. In the right case we are not, so k remains the same.

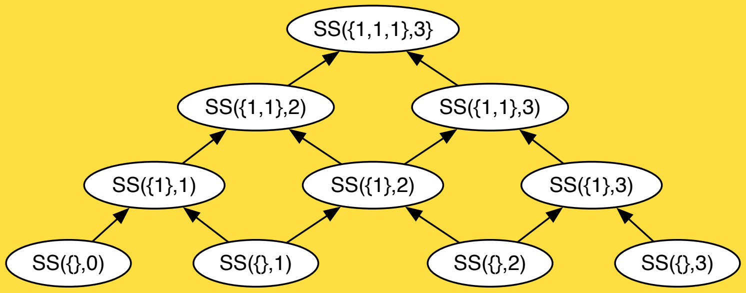
What is the work of this recursive algorithm? Well, it leads to a binary recursion tree that might be n deep. This would imply something like 2^n work. This is not good. The key observation, however, is that there is a huge overlap in the subproblems, as can be seen in Example 18.6.

The question is how do we calculate the number of distinct instances of SS, which is also the number of vertices in the DAG? For an initial instance $SS(S, k)$ there are are only $|S|$ distinct lists that are ever used (each suffix of S). Furthermore, the value of the second argument in the recursive calls only decreases and never goes below 0, so it can take on at most $k + 1$ values. Therefore the total number of possible instances of SS (vertices in the DAG) is $|S|(k + 1) = O(k|S|)$. Each instance only does constant work to compose its recursive calls. Therefore the total work is $O(k|S|)$. Furthermore it should be clear that the longest path in the DAG is $O(|S|)$ so the total span is $O(|S|)$ and the algorithm has $O(k)$ parallelism.

Example 18.6. *Consider* $\mathit{SS}(\{1,1,1\},3)$. *This clearly should return true since* $1+1+1=3$. *The recursion tree is as follows.*



There are many calls to SS *in this tree with the same arguments. In the bottom row, for example there are three calls each to* $\mathit{SS}(\emptyset,1)$ *and* $\mathit{SS}(\emptyset,2)$. *If we coalesce the common calls we get the following DAG:*



Why do we say the algorithm is pseudo-polynomial? The size of the subset sum problem is defined to be the number of bits needed to represent the input. Therefore, the input size of k is $\log k$. But the work is $O(2^{\log k}|S|)$, which is exponential in the input size. That is, the complexity of the algorithm is measured with respect to the length of the input (in terms of bits) and not on the numeric value of the input. If the value of k, however, is constrained to be a polynomial in $|S|$ (i.e., $k \le |S|^c$ for some constant c) then the work is $O(k|S|) = O(|S|^{c+1})$ on input of size $c\log|S| + |S|$, and the algorithm is polynomial in the length of the input.

At this point we have not fully specified the algorithm since we have not explained how to take advantage of the sharing—certainly the recursive code we wrote would not. We will get back to this after a couple more examples. Again we want to emphasize that the first two orders of business are to figure out the inductive structure and figure out what instances can be shared.

18.2 Minimum Edit Distance

The second problem we consider is a optimization problem, the minimum edit distance problem.

Definition 18.7. *The minimum edit distance (MED) problem is, given a character set Σ and two sequences of characters $S = \Sigma^*$ and $T = \Sigma^*$, determine the minimum number of insertions and deletions of single characters required to transform S to T.*

Example 18.8. *Consider the sequence*

$$S = \langle\, A, B, C, A, D, A \,\rangle$$

we could convert it to

$$T = \langle\, A, B, A, D, C \,\rangle$$

with 3 edits (delete the C, delete the last A, and insert a C). This is the best that can be done so the fewest edits needed is 3.

Question 18.9. *Can you think of applications of the MED problem?*

The MED problem is an important problem that has many applications. For example in version control systems such as `git` or `svn` when you update a file and commit it, the system does not store the new version but instead only stores the "differences" from the previous version[1]. Storing the differences can be quite space efficient since often the user is only making small changes and it would be wasteful to store the whole file. Variants of the minimum edit distance problem are use to find this difference. Edit distance can also be used to reduce communication costs by only communicating the differences from a previous version. It turns out that edit-distance is also closely related to approximate matching of genome sequences.

Remark 18.10. *The algorithm used in the Unix "diff" utility was invented and implemented by Eugene Myers, who also was one of the key people involved in the decoding of the human genome at Celera,*

Question 18.11. *Do you see a relationship between MED(S,T) and MED(T,S).*

The MED problem is a symmetric problem. If you have a solution for MED (S,T), you can solve MED(T,S) by reverting all the decisions, i.e., inserting instead of deleting and deleting instead of inserting.

[1] Alternatively it might store the new version, but use the differences to encode the old version.

Example 18.12. *Consider the sequence*

$$S = \langle\, A, B, C, A, D, A \,\rangle$$

and

$$T = \langle\, A, B, A, D, C \,\rangle\,.$$

We can convert S to T with 3 edits (delete the C, delete the last A, and insert a C. We can convert T to S with 3 edits, insert C, insert A, and delete C.

It is thus possible to think of MED as a sequence of characters to be inserted or deleted depending on the direction. Let's refer to this sequence as the *edits*.

A problem that is closely related to the MED problem is known as the *longest-common subsequence*, or *LCS* problem. The LCS problem requires finding the longest common subsequence of two sequences.

Example 18.13. *Consider the sequences*

$$S = \langle\, A, B, C, A, D, A \,\rangle$$

and

$$T = \langle\, A, B, A, D, C \,\rangle\,.$$

Their LCS is $\langle\, A, B, A, D \,\rangle$.

Question 18.14. *Suppose that you are given the LCS of S and T, can you find their MED?*

Given the LCS of two strings, we can compute their MED by performing the required insertions greedily. Since we never have to perform deletion, a greedy algorithm works. We can thus reduce the MED problem to the LCS problem.

Question 18.15. *Can you think of a way of reducing the LCS problem to the MED problem?*

Assuming that we are given the edits and not just the distances, we can solve the LCS problem by using a solution to the MED problem. All we have to do is simply apply the deletions specified by the edit. We can thus reduce the LCS problem to the MED problem, provided we know the edits.

Example 18.16. *Consider the sequences*

$$S = \langle\, A, B, C, A, D, A \,\rangle$$

and

$$T = \langle\, A, B, A, D, C \,\rangle\, .$$

Their MED is 3 *as witnessed by the edit (from* S *to* T*) delete the C, delete the last A, and insert a* C*. Their LCS is thus* $\langle\, A, B, A, D \,\rangle$*.*

Having established this correspondence between the two problems, from this point on, we will think of them as essentially the same and focus only on the MED problem.

Question 18.17. *Can you think of a way to solve the MED problem by using the Brute-Force method. Hint: think of the LCS problem.*

One way to solve the MED problem is to compute all subsequences of S and for any of them that are a subsequences of T return the longest one. The problem is that there are too many such subsequences to consider?

Question 18.18. *How many subsequnces does* S *have?*

Question 18.19. *Can we use a greedy algorithm?*

Another possibility would be to consider a greedy method that scans the sequences finding the first difference, fixing it and then moving on. Unfortunately no simple greedy method is known to work. The problem is that there can be multiple ways to fix the error—we can either delete the offending character, or insert a new one. If we greedily pick the wrong edit, we might not end up with an optimal solution. (Recall that in greedy algorithms, once you make a choice, you cannot go back and try an alternative.)

Example 18.20. *Consider the sequences*

$$S = \langle\, A, B, C, A, D, A \,\rangle$$

and

$$T = \langle\, A, B, A, D, C \,\rangle\, .$$

We can match the first character but when we come to C*, we have two choices, delete* C *or insert* A*, we don't know which would lead to an optimal solution because we don't know the rest of the sequences. In the example, if we insert an* A*, then a suboptimal number of edits will be required because* C *will have to be deleted.*

We shall now see how dynamic programming can help us solve the MED problem. To apply dynamic programming, we start by defining a recursive solution. We will then recognize sharing.

Question 18.21. *Any ideas about how we might define a recursive algorithm for solving the MED problem?*

To find the $\mathtt{MED}(S,T)$ in terms of the smaller problems, consider greedy solution, which gives a good hint how. Suppose $S = s :: S'$ and $T = t :: T'$. If the first characters of S and T match, then no insertion or deleted is needed, and the we only need to consider edits to the suffixes, S' and T'. If the first two characters do not match, then we have exactly two choices to consider: 1) delete s form S and 2) insert t into S. For each choice, the rest of the problem is a subproblem of the MED, which we can solve recursively.

Example 18.22. *Consider the sequences*

$$S = \langle\, A, B, C, A, D, A \,\rangle$$

and

$$T = \langle\, A, B, A, D, C \,\rangle\,.$$

We can proceed to match the first two characters. When we see C, we have two choices, delete C or insert A. We can thus consider both possibilities instead of committing to a decision like the greedy algorithm does.

Algorithm 18.23 (Recursive solution to the MED problem)**.**

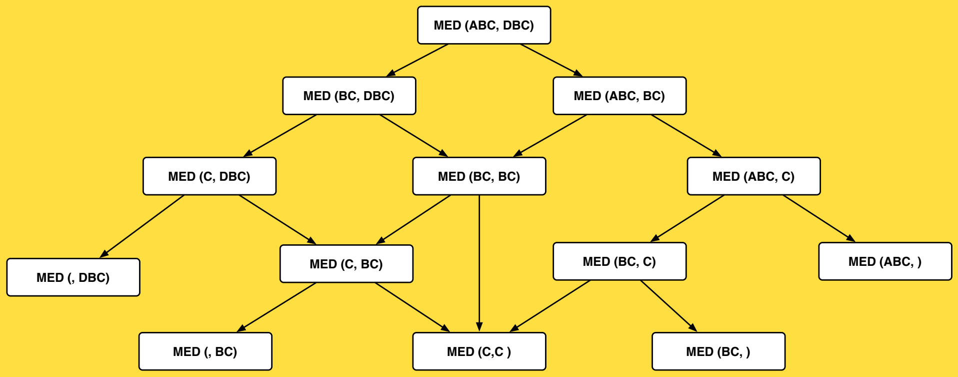
```
function MED(S,T) =
  case (showl(S), showl(T)) of
     (_, nil) ⇒ |S|
   | (nil, _) ⇒ |T|
   | (cons(s,S'), cons(t,T')) ⇒
       if (s = t) then MED(S',T')
       else 1 + min(MED(S,T'), MED(S',T))
```

In the first base case where T is empty we need to delete all of S to generate an empty string requiring $|S|$ insertions. In the second base case where S is empty we need to insert all of T, requiring $|T|$ insertions. If neither is empty we compare the first character. If they are equal we can just skip them and make a recursive call on the rest of the sequences. If they are different then we need to consider the two cases. The first case ($\mathtt{MED}(S,T')$) corresponds to inserting the value t. We pay one edit for the insertion and then need to match up S (which all remains) with the tail of T (we have already matched up the head t with the character we inserted). The second case ($\mathtt{MED}(S',T)$) corresponds to deleting the value s. We pay one edit for the deletion and then need to match up the tail of S (the head has been deleted) with all of T.

Question 18.24. *What is the work of the recursive algorithm?*

The recursive algorithm performs exponential work. In particular the recursion tree is full binary tree (each internal node has two children) and has a depth that is linear in the size of S and T. But there is substantial sharing going on.

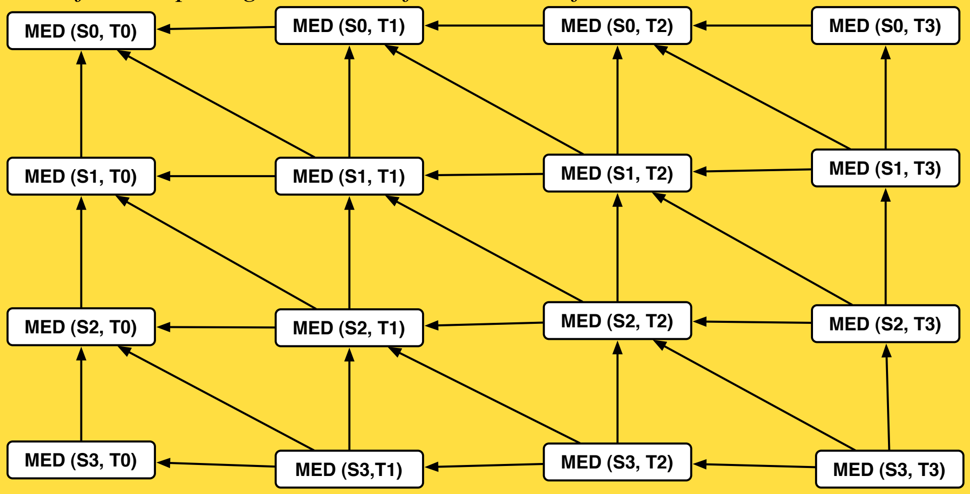
Example 18.25. *An example MED instance with sharing.*



Question 18.26. *Can you see why there is plenty of sharing?*

The reason for there is so much sharing is that the subproblems required to solve the larger problem has substantial overlap, including many of the same subproblems. It is easier to see this sharing with an abstract example.

Example 18.27. *An example MED instance with sharing. Consider two strings S and T and let Si (Ti) denote the suffix of S (T) with i characters. We can draw the top portion of the DAG for computing the MED of S and T as follows.*



More generally, we can visualize the DAG for an MED instance by considering suffixes of S and T, written $S_0 \ldots S_n$ and $T_0 \ldots S_m$ as vertices and drawing edges between vertices.

Question 18.28. *Which vertices do the edges connect? Which subproblems depend on which other subproblems?*

Edges between vertices connect subproblems. We have edges between (S_i, T_j) to and (S_{i-1}, T_j), (S_i, T_{j-1}), or between (S_i, T_j) and (S_{i-1}, T_{j-1}), depending on the case.

Question 18.29. *Can you now bound the number of vertices and edges in the DAG?*

We can now place an upper bound on the number of vertices in our DAG by bounding the number of distinct arguments. There can be at most $|S| + 1$ possible values of the first argument since in recursive calls we only use suffixes of the original S and there are only $|S| + 1$ such suffixes (including the empty and complete suffixes). Similarly there can be at most $|T| + 1$ possible values for the second argument. Therefore the total number of possible distinct arguments to MED on original strings S and T is $(|T| + 1)(|S| + 1) = O(|S||T|)$. Furthermore the depth of the DAG (longest path) is $O(|S| + |T|)$ since each recursive call either removes an element from S or T so after $|S| + |T|$ calls there cannot be any element left. Finally we note that assuming we have constant work operations for removing the head of a sequence (e.g. using a list) then each vertex of the DAG takes constant work and span.

All together this gives us

$$W(\mathit{MED}(S,T)) = O(|S||T|)$$

and

$$S(\mathit{MED}(S,T)) = O(|S| + |T|).$$

18.3 Top-Down Dynamic Programming

So far we have assumed some sort of magic recognized shared subproblems in our recursive codes and avoided recomputation. We are now ready to cover one of the techniques, the top-down approach to implementing dynamic-programming algorithms.

The top-down approach is based on running the recursive code as is, generating implicitly the recursion structure from the root of the DAG down to the leaves. Each time a solution to a smaller instance is found for the first time it generates a mapping from the input argument to its solution. This way when we come across the same argument a second time we can just look up the solution. This process is called *memoization*, and the table used to map the arguments to solutions is called a *memo table*.

The tricky part of memoization is checking for equality of arguments since the arguments might not be simple values such as integers. Indeed in our examples so far the arguments have all involved sequences. We could compare the whole sequence element by element, but that would be too expensive.

Question 18.30. *Can you think of a way to check for equality of sequences efficiently?*

You might think that we can do it by comparing "pointers" to the values. But this does not work since the sequences can be created separately, and even though the values are equal, there could be two copies in different locations. Comparing pointers would say they are not equal and we would fail to recognize that we have already solved this instance. There is actually a very elegant solution that fixes this issue called *hash consing*. Hash consing guarantees that there is a unique copy of each value by always hashing the contents when allocating a memory location and checking if such a value already exists. This allows equality of values to be done in constant work. The approach only works in purely functional languages and needs to be implemented as part of the language runtime system (as part of memory allocation). Unfortunately no language does hash consing automatically, so we are left to our own devices.

The most common way to quickly test for equality of arguments is to use a simple type, such as an integer, as a *surrogate* to represent the input values. The property of these surrogates is that there needs to be a 1-to-1 correspondence between the surrogates and the argument values—therefore if the surrogates match, the arguments match. The user is responsible for guaranteeing this 1-to-1 correspondence.

Consider how we might use memoization in the dynamic program we described for minimum edit distance (MED). You have probably covered memoization before, but you most likely did it with side effects. Here we will do it in a purely functional way, which requires that we "thread" the table that maps arguments to results through the computation. Although this threading requires a few extra characters of code, it is safer for parallelism.

Recall that *MED* takes two sequences and on each recursive call, it uses suffixes of the two original sequences. To create integer surrogates we can simply use the length of each suffix. There is clearly a 1-to-1 mapping from these integers to the suffixes. *MED* can work from either end of the string so instead of working front to back and using suffix lengths, it can work back to front and use prefix lengths—we make this switch since it simplifies the indexing. This leads to the following variant of our *MED* code. In this code, we use prefixes instead of suffixes to simplify the indexing.

```
function MED($S, T$) =
let
   function MED'($i, 0$) = $i$
          | MED'($0, j$) = $j$
          | MED'($i, j$) =
              if ($S_i = T_j$) then MED'($i-1, j-1$)
              else 1 + min(MED'($i, j-1$), MED'($i-1, j$))
in
```

```
function MED($S$,$T$) =
let
   function MED'($M$,($i$,0)) = ($M$,$i$)
          | MED'($M$,(0,$j$)) = ($M$,$j$)
          | MED'($M$,($i$,$j$)) =
              if ($S_i = T_j$) then
                 memoMED($M$,($i-1$,$j-1$))
              else let
                 val ($M'$,$v_1$) = memoMED($M$,($i$,$j-1$))
                 val ($M''$,$v_2$) = memoMED($M'$,($i-1$,$j$))
              in ($M''$,$1+\min(v_1,v_2)$) end
   and memoMED($M$,($i$,$j$)) = memo MED' ($M$,($i$,$j$))
in
   MED'({},(|$S$|,|$T$|))
end
```

Figure 18.1: The memoized version of Minimum Edit Distance (MED).

```
   MED'(|$S$|,|$T$|)
end
```

You should compare this with the purely recursive code for *MED*. Apart from the use of prefixed to simplify indexing, the only real difference is replacing S and T with i and j in the definition of *MED*$'$. The i and j are therefore the surrogates for S and T respectively. They represent the sequences $S\langle 0,\ldots,i-1\rangle$ and $T\langle 0,\ldots,j-1\rangle$ where S and T are the original input strings.

So far we have not added a memo table, but we can now efficiently store our solutions in a memo table based on the pair of indices (i,j). Each pair represents a unique input. In fact since the arguments range from 0 to the length of the sequence we can actually use a two dimensional array (or array of arrays) to store the solutions.

To implement the memoization we define a memoization function:

```
function memo $f$ ($M$,$a$) =
   case find($M$,$a$) of
      SOME($v$) ⇒ $v$
   | NONE ⇒ let val ($M'$,$v$) = $f$($M$,$a$)
              in (update($M'$,$a$,$v$), $v$) end
```

In this function f is the function that is being memoized, M is the memo table, and a is the argument to f. This function simply looks up the value a in the memo table. If it exists, then it returns the corresponding result. Otherwise it evaluates the function on the argument, and as well as returning the result it stores it in the memo. We can now write *MED* using memoization as shown in Figure 18.1.

Note that the memo table M is threaded throughout the computation. In particular every call to *MED* not only takes a memo table as an argument, it also returns a memo table as a result

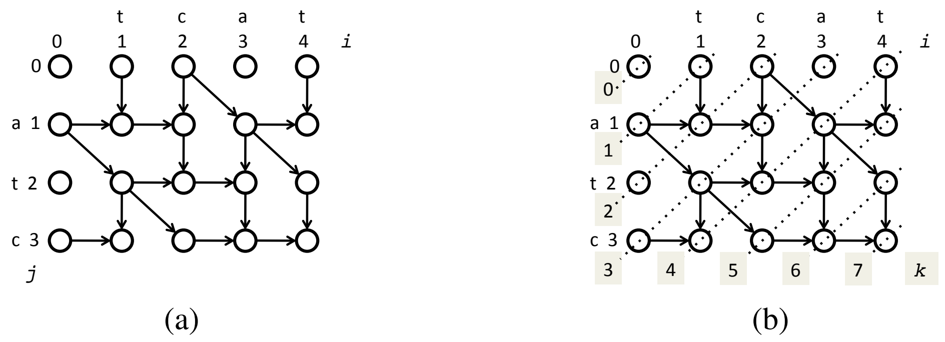


Figure 18.2: The DAG for *MED* on the strings "tcat" and "atc" (a) and processing it by diagonals (b).

(possibly updated). Because of this passing, the code is purely functional. The problem with the top-down approach as described, however, is that it is inherently sequential. By threading the memo state we force a total ordering on all calls to *MED*. It is easy to create a version that uses side effects, as you did in 15-150 or as is typically done in imperative languages. In this case calls to *MED* can be made in parallel. However, then one has to be very careful since there can be race conditions (concurrent threads modifying the same cells). Furthermore if two concurrent threads make a call on *MED* with the same arguments, they can and will often both end up doing the same work. There are ways around this issue which are also fully safe—i.e., from the users point of view all calls look completely functional—but they are beyond the scope of this course.

18.4 Bottom-Up Dynamic Programming

The other technique for implementing dynamic-programming algorithms is the bottom-up technique. Instead of simulating the recursive structure, which starts at the root of the DAG, when using this technique, we start at the leaves of the DAG and fills in the results in some order that is consistent with the DAG–i.e. for all edges (u, v) it always calculates the value at a vertex u before working on v. Because of this careful scheduling, all values will be already calculated when they are needed.

The simplest way to implement bottom-up dynamic programming is to do some form of systematic traversal of a DAG. It is therefore useful to understand the structure of the DAG. For example, consider the structure of the DAG for minimum edit distance. In particular let's consider the two strings $S = \texttt{tcat}$ and $T = \texttt{atc}$. We can draw the DAG as follows where all the edges go down and to the right:

The numbers represent the i and the j for that position in the string. We draw the DAG with the root at the bottom right, so that the vertices are structured the same way we might fill an array indexed by i and j. We Consider *MED*$(4, 3)$. The characters S_4 and T_3 are not equal so the recursive calls are to *MED*$(3, 3)$ and *MED*$(4, 2)$. This corresponds to the vertex to the left and the one above. Now if we consider *MED*$(4, 2)$ the characters S_4 and T_2 are equal so the recursive call is to *MED*$(3, 1)$. This corresponds to the vertex diagonally above and to the left. In fact whenever

```
function MED(S,T) =
let
  function MED'(M,(i,0)) = i
         | MED'(M,(0,j)) = j
         | MED'(M,(i,j)) =
             if ($S_i = T_j$) then $M_{i-1,j-1}$
             else $1 + \min(M_{i,j-1}, M_{i-1,j})$

  function diagonals(M,k) =
    if ($k > |S| + |T|$) then M
    else let
          val $s = \max(0, k - |T|)$
          val $e = \min(k, |S|)$
          val $M' = M \cup \{(i, k-i) \mapsto MED(M,(i,k-i)) : i \in \{s,\ldots,e\}\}$
        in
          diagonals($M'$, k+1)
        end
in
  diagonals({},0)
end
```

Figure 18.3: The dynamic program for *MED* based on the bottom-up approach using diagonals.

the characters S_i and T_j are not equal we have edges from directly above and directly to the left, and whenever they are equal we have an edge from the diagonal to the left and above. This tells us quite a bit about the DAG. In particular it tells us that it is safe to process the vertices by first traversing the first row from left to right, and then the second row, and so on. It is also safe to traverse the first column from top to bottom and then the second column and so on. In fact it is safe to process the diagonals in the / direction from top left moving to the bottom right. In this case each diagonal can be processed in parallel.

In general when applying *MED*(S,T) we can use an $|T| \times |S|$ array to store all the partial results. We can then fill the array either by row, column, or diagonal. Using diagonals can be coded as shown in Figure 18.3.

The code uses a table M to store the array entries. In practice an array might do better. Each round of *diagonals* processes one diagonal and updates the table M, starting at the leaves at top left. The figure below shows these diagonals indexed by k on the left side and at the bottom. We note that the index calculations are a bit tricky (hopefully we got them right). Notice that the size of the diagonals grows and then shrinks.

18.5 Optimal Binary Search Trees

We have talked about using BSTs for storing an ordered set or table. The cost of finding an key is proportional to the depth of the key in the tree. In a fully balanced BST of size n the average depth of each key is about $\log n$. Now suppose you have a dictionary where you know probability (or frequency) that each key will be accessed—perhaps the word "of" is accessed much more often than "epistemology". The goal is find a static BST with the lowest overall access cost. That is, make a BST so that the more likely keys are closer to the root and hence the average access cost is reduced. This line of reasoning leads to the following problem:

Definition 18.31. *The* optimal binary search tree *(OBST) problem is given an ordered set of keys S and a probability function $p : S \to [0:1]$:*

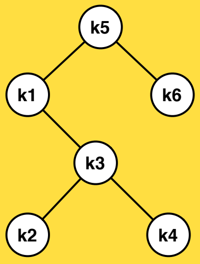
$$\min_{T \in \texttt{Trees}(S)} \left(\sum_{s \in S} d(s,T) \cdot p(s) \right)$$

where $\texttt{Trees}(S)$ is the set of all BSTs on S, and $d(s,T)$ is the depth of the key s in the tree T (the root has depth 1).

Example 18.32. *For example we might have the following keys and associated probabilities*

key	k_1	k_2	k_3	k_4	k_5	k_6
$p($*key*$)$	$1/8$	$1/32$	$1/16$	$1/32$	$1/4$	$1/2$

Then the tree below has cost $31/16$, which is optimal. Creating a tree with these two solutions as the left and right children of S_i, respectively, leads to the optimal solution given S_i as a root.



Exercise 18.33. *Find another tree with equal cost.*

The brute force solution would be to generate every possible binary search tree, compute their cost, and pick the one with the lowest costs. But the number of such trees is $O(4^n)$ which is prohibitive.

Exercise 18.34. *Write a recurrence for the total number of distinct binary search trees with n keys.*

Since we are considering binary search trees, one of the keys must be the root of the optimal tree. Suppose S_r is that root. An important observation is that both of its subtrees must be optimal, which is a common property of optimization problems: The optimal solution to a problem contains optimal solutions to subproblems. This *optimal substructure* property is often a clue that either a greedy or dynamic programming algorithm might apply.

Which key should be the root of the optimal tree? A greedy approach might be to pick the key k with highest probability and put it at the root and then recurse on the two sets less and greater than k. You should convince yourself that this does not work. Since we cannot know in advance which key should be the root, let's try all of them, recursively finding their optimal subtrees, and then pick the best of the $|S|$ possibilities.

With this recursive approach, how should we define the subproblems? Let S be all the keys placed in sorted order. Now any subtree of a BST on S must contain the keys of a contiguous subsequence of S. We can therefore define subproblems in terms of a contiguous subsequence of S. We will use $S_{i,j}$ to indicate the subsequence starting at i and going to j (inclusive of both). Not surprisingly we will use the pair (i, j) to be the surrogate for $S_{i,j}$.

Now Let's consider how to calculate the cost give the solution to two subproblems. For subproblem $S_{i,j}$, assume we pick key S_r ($i \leq r \leq j$) as a the root. We can now solve the OSBT problem on the prefix $S_{i,r-1}$ and suffix $S_{r+1,i}$. We therefore might consider adding these two solutions and the cost of the root ($p(S_r)$) to get the cost of this solution. This, however, is wrong. The problem is that by placing the solutions to the prefix and suffix as children of S_r we have increased the depth of each of their keys by 1. Let T be the tree on the keys $S_{i,j}$ with root S_r, and T_L, T_R be its left and right subtrees. We therefore have:

$$\begin{aligned}
\texttt{Cost}(T) &= \sum_{s\in T} d(s,T)\cdot p(s) \\
&= p(S_r) + \sum_{s\in T_L}(d(s,T_L)+1)\cdot p(s) + \sum_{s\in T_R}(d(s,T_R)+1)\cdot p(s) \\
&= \sum_{s\in T} p(s) + \sum_{s\in T_L} d(s,T_L)\cdot p(s) + \sum_{s\in T_R} d(s,T_R)\cdot p(s) \\
&= \sum_{s\in T} p(s) + \texttt{Cost}(T_L) + \texttt{Cost}(T_R)
\end{aligned}$$

That is, the cost of a subtree T the probability of accessing the root (i.e., the total probability of accessing the keys in the subtree) plus the cost of searching its left subtree and the cost of searching its right subtree. When we add the base case this leads to the following recursive definition:

```
1 function OBST($S$) =
2   if $|S| = 0$ then 0
3   else $\sum_{s\in S} p(s) + \min_{i\in\langle 1\ldots|S|\rangle}\left(\mathit{OBST}(S_{1,i-1}) + \mathit{OBST}(S_{i+1,|S|})\right)$
```

Exercise 18.35. *How would you return the optimal tree in addition to the cost of the tree?*

As in the examples of subset sum and minimum edit distance, if we execute the recursive program directly $OBST$ it will require exponential work. Again, however, we can take advantage of sharing among the calls to $OBST$. To bound the number of vertices in the corresponding DAG we need to count the number of possible arguments to $OBST$. Note that every argument is a contiguous subsequence from the original sequence S. A sequence of length n has only $n(n+1)/2$ contiguous subsequences since there are n possible ending positions and for the i^{th} end position there are i possible starting positions ($\sum_{i=1}^{n} i = n(n+1)/2$). Therefore the number of possible arguments is at most $O(n^2)$. Furthermore the longest path of vertices in the DAG is at most $O(n)$ since recursion can at most go n levels (each level removes at least one key).

Unlike our previous examples, however, the cost of each vertex in the DAG (each recursive in our code not including the subcalls) is no longer constant. The subsequence computations $S_{i,j}$ can be done in $O(1)$ work each (think about how) but there are $O(|S|)$ of them. Similarly the sum of the $p(s)$ will take $O(|S|)$ work. To determine the span of a vertex we note that the $\min$ and sum can be done with a reduce in $O(\log |S|)$ span. Therefore the work of a vertex is $O(|S|) = O(n)$ and the span is $O(\log n)$. Now we simply multiply the number of vertices by the work of each to get the total work, and the longest path of vertices by the span of each vertex to get the span. This give $O(n^3)$ work and $O(n \log n)$ span.

This example of the optimal BST is one of several applications of dynamic programming which effectively based on trying all binary trees and determining an optimal tree given some cost criteria. Another such problem is the matrix chain product problem. In this problem one is given a chain of matrices to be multiplied ($A_1 \times A_2 \times \cdots A_n$) and wants to determine the cheapest order to execute the multiplies. For example given the sequence of matrices $A \times B \times C$ it can either be ordered as $(A \times B) \times C$ or as $A \times (B \times C)$. If the matrices have sizes $2 \times 10, 10 \times 2$, and 2×10, respectively, it is much cheaper to calculate $(A \times B) \times C$ than $a \times (B \times C)$. Since $\times$ is a binary operation any way to evaluate our product corresponds to a tree, and hence our goal is to pick the optimal tree. The matrix chain product problem can therefore be solved in a very similar structure as the OBST algorithm and with the same cost bounds.

18.6 Coding optimal BST

As with the MED problem we first replace the sequences in the arguments with integers. In particular we describe any subsequence of the original sorted sequence of keys S to be put in the BST by its offset from the start (i, 1-based) and its length l. We then get the following recursive routine.

```
function OBST($S$) =
let
  function OBST'($i, l$) =
      **if** $l = 0$ **then** $0$
      **else** $\sum_{k=0}^{l-1} p(S_{i+k}) + \min_{k=0}^{l-1} (\texttt{OBST'}(i,k) + \texttt{OBST'}(i+k+1, l-k-1))$
**in**
   $\texttt{OBST}(1, |S|)$
**end**
```

This modified version can now more easily be used for either the top-down solution using memoization or the bottom-up solution. In the bottom-up solution we note that we can build a table with the columns corresponding to the i and the rows corresponding to the l. Each of them range from 1 to n ($n = |S|$). It would as follows:

```
  1 2 ... n
1         /
2       /
.     /
.   /
n /
```

The table is triangular since as l increases the number of subsequences of that length decreases. This table can be filled up row by row since every row only depends on elements in rows above it. Each row can be done in parallel.

18.7 Problems with Efficient Dynamic Programming Solutions

There are many problems with efficient dynamic programming solutions. Here we list just some of them to give a sense of what these problems are.

1. Fibonacci numbers
2. Using only addition compute (n choose k) in $O(nk)$ work
3. Edit distance between two strings
4. Edit distance between multiple strings
5. Longest common subsequence
6. Maximum weight common subsequence
7. Can two strings S1 and S2 be interleaved into S3
8. Longest palindrome

9. longest increasing subsequence
10. Sequence alignment for genome or protein sequences
11. subset sum
12. knapsack problem (with and without repetitions)
13. weighted interval scheduling
14. line breaking in paragraphs
15. break text into words when all the spaces have been removed
16. chain matrix product
17. maximum value for parenthesizing x1/x2/x3.../xn for positive rational numbers
18. cutting a string at given locations to minimize cost (costs n to make cut)
19. all shortest paths
20. find maximum independent set in trees
21. smallest vertex cover on a tree
22. optimal BST
23. probability of generating exactly k heads with n biased coin tosses
24. triangulate a convex polygon while minimizing the length of the added edges
25. cutting squares of given sizes out of a grid
26. change making
27. box stacking
28. segmented least squares problem
29. counting Boolean parenthesization – true, false, or, and, xor, count how many parenthesization return true
30. balanced partition – given a set of integers up to k, determine most balanced two way partition
31. Largest common subtree