

Problems in Data Structures and Algorithms

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1. Introduction

I would like to talk about various problems I have worked on over the course of my career. In this lecture I'll review simple problems with interesting applications, and problems that have rich, sometimes surprising, structure.

Let me start by saying a few words about how I view the process of research, discovery and development. (See Figure 1.)

My view is based on my experience with data structures and algorithms in computer science, but I think it applies more generally. There is an interesting interplay between theory and practice. The way I like to work is to start out with some application from the real world. The real world, of course, is very messy and the application gets modeled or abstracted away into some problem or some setting that someone with a theoretical background can actually deal with. Given the abstraction, I then try to develop a solution which is usually, in the case of computer science, an algorithm, a computational method to perform some task. We may be able to prove things about the algorithm, its running time, its efficiency, and so on. And then, if it's at all useful, we want to apply the algorithm back to the application and see if it actually solves the real problem. There is an interplay in the experimental domain between the algorithm developed, based on the abstraction, and the application; perhaps we discover that the abstraction does not capture the right parts of the problem; we have solved an interesting mathematical problem but it doesn't solve the real-world application. Then we need to go back and change the abstraction and solve the new abstract problem and then try to apply that in practice. In this entire process we are developing a body of new theory and practice which can then be used in other settings.

A very interesting and important aspect of computation is that often the key to performing computations efficiently is to understand the problem, to represent the

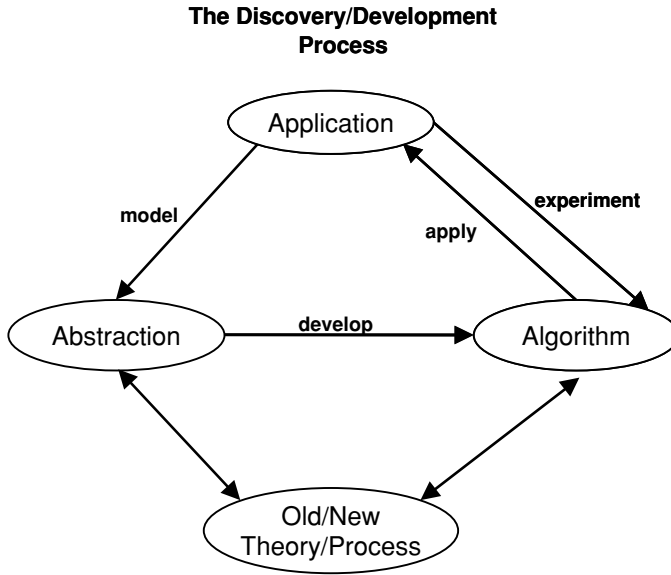


Figure 1.

problem data appropriately, and to look at the operations that need to be performed on the data. In this way many algorithmic problems turn into data manipulation problems, and the key issue is to develop the right kind of data structure to solve the problem. I would like to talk about several such problems. The real question is to devise a data structure, or to analyze a data structure which is a concrete representation of some kind of algorithmic process.

2. Optimum Stack Generation Problem

Let's take a look at the following simple problem. I've chosen this problem because it's an abstraction which is, on the one hand, very easy to state, but on the other hand, captures a number of ideas. We are given a finite alphabet Σ , and a stack S . We would like to generate strings of letters over the alphabet using the stack. There are three stack operations we can perform.

push (A)—push the letter A from the alphabet onto the stack,
emit—output the top letter from the stack,
pop—pop the top letter from the stack.

We can perform any sequence of these operations subject to the following well-formedness constraints: we begin with an empty stack, we perform an arbitrary series of *push*, *emit* and *pop* operations, we never perform *pop* from an empty stack, and we

end up with an empty stack. These operations generate some sequence of letters over the alphabet.

Problem 2.1 *Given some string σ over the alphabet, find a minimum length sequence of stack operations to generate σ .*

We would like to find a fast algorithm to find the minimum length sequence of stack operations for generating any particular string.

For example, consider the string **A B C A C B A**. We could generate it by performing: **push (A), emit A, pop A, push (B), emit B, pop B, push (C), emit C, pop C** etc., but since we have repeated letters in the string we can use the same item on the stack to generate repeats. A shorter sequence of operations is: **push (A), emit A, push (B), emit B, push (C), emit C, push (A), emit A, pop A**; now we can **emit C** (we don't have to put a new **C** on the stack), **pop C, emit B, pop B, emit A**. We got the 'CBA' string without having to do additional push-pops. This problem is a simplification of the programming problem which appeared in "The International Conference on Functional Programming" in 2001 [46] which calls for optimum parsing of HTML-like expressions.

What can we say about this problem? There is an obvious $O(n^3)$ dynamic programming algorithm¹. This is really a special case of optimum context-free language parsing, in which there is a cost associated with each rule, and the goal is to find a minimum-cost parse. For an alphabet of size three there is an $O(n)$ algorithm (Y. Zhou, private communication, 2002). For an alphabet of size four, there is an $O(n^2)$ algorithm. That is all I know about this problem. I suspect this problem can be solved by matrix multiplication, which would give a time complexity of $O(n^\alpha)$, where α is the best exponent for matrix multiplication, currently 2.376 [8]. I have no idea whether the problem can be solved in $O(n^2)$ or in $O(n \log n)$ time. Solving this problem, or getting a better upper bound, or a better lower bound, would reveal more information about context-free parsing than what we currently know. I think this kind of question actually arises in practice. There are also string questions in biology that are related to this problem.

3. Path Compression

Let me turn to an old, seemingly simple problem with a surprising solution. The answer to this problem has already come up several times in some of the talks in

¹ *Sketch of the algorithm:* Let $S[1 \dots n]$ denote the sequence of characters. Note that there must be exactly n emits and that the number of pushes must equal the number of pops. Thus we may assume that the cost is simply the number of pushes. The dynamic programming algorithm is based on the observation that if the same stack item is used to produce, say, $S[i_1]$ and $S[i_2]$, where $i_2 > i_1$ and $S[i_1] = S[i_2]$, then the state of the stack at the time of emit $S[i_1]$ must be restored for emit $S[i_2]$. Thus the cost $C[i, j]$ of producing the subsequence $S[i, j]$ is the minimum of $C[i, j-1] + 1$ and $\min \{C[i, t] + C[t+1, j-1] : S[t] = S[j], i \leq t < j\}$.

the conference “Second Haifa Workshop on Interdisciplinary Applications of Graph Theory, Combinatorics and Algorithms.” The goal is to maintain a collection of n elements that are partitioned into sets, i.e., the sets are always disjoint and each element is in a unique set. Initially each element is in a singleton set. Each set is named by some arbitrary element in it. We would like to perform the following two operations:

***find*(x)**—for a given arbitrary element x , we want to return the name of the set containing it.

***unite*(x, y)**—combine the two sets named by x and y . The new set gets the name of one of the old sets.

Let’s assume that the number of elements is n . Initially, each element is in a singleton set, and after $n - 1$ ***unite*** operations all the elements are combined into a single set.

Problem 3.1 *Find a data structure that minimizes the worst-case total cost of m find operations intermingled with $n - 1$ unite operations.*

For simplicity in stating time bounds, I assume that $m \geq n$, although this assumption is not very important. This problem originally arose in the processing of COMMON and EQUIVALENCE statements in the ancient programming language FORTRAN. A solution is also needed to implement Kruskal’s [31] minimum spanning tree algorithm. (See Section 7.)

There is a beautiful and very simple algorithm for solving Problem 3.1, developed in the ‘60s. I’m sure that many of you are familiar with it. We use a forest data structure, with essentially the simplest possible representation of each tree (see Figure 2). We use rooted trees, in which each node has one pointer, to its parent. Each set is represented by a tree, whose nodes represent the elements, one element per node. The root element is the set name. To answer a ***find*(x)** operation, we start at the given node x and follow

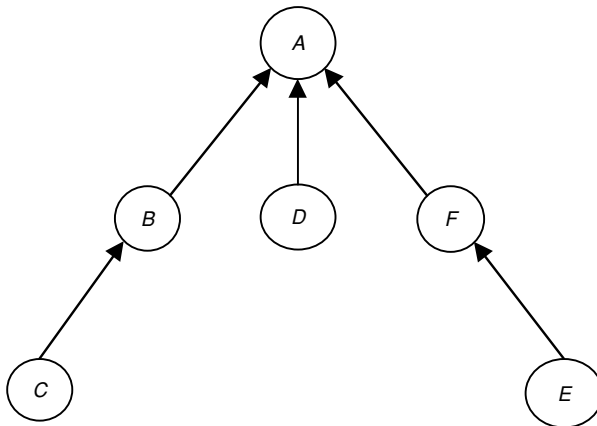


Figure 2.

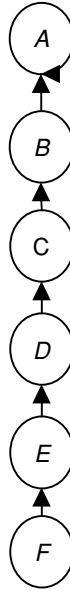


Figure 3.

the pointers to the root node, which names the set. The time of the *find* operation is proportional to the length of the path. The tree structure is important here because it affects the length of the *find* path. To perform a *unite*(*x*,*y*) operation, we access the two corresponding tree roots *x* and *y*, and make one of the roots point to the other root. The *unite* operation takes constant time.

The question is, how long can *find* paths be? Well, if this is all there is to it, we can get bad examples. In particular, we can construct the example in Figure 3: a tree which is just a long path. If we do lots of *finds*, each of linear cost, then the total cost is proportional to the number of *finds* times the number of elements, $O(m \cdot n)$, which is not a happy situation.

As we know, there are a couple of heuristics we can add to this method to substantially improve the running time. We use the fact that the structure of each tree is completely arbitrary. The best structure for the *finds* would be if each tree has all its nodes just one step away from the root. Then *find* operations would all be at constant cost. But as we do the *unite* operations, depths of nodes grow. If we perform the *unites* intelligently, however, we can ensure that depths do not become too big. I shall give two methods for doing this.

Unite by size (Galler and Fischer [16]): This method combines two trees into one by making the root of the smaller tree point to the root of the larger tree (breaking a tie arbitrarily). The method is described in the pseudo-code below. We maintain with each root *x* the tree size, *size*(*x*) (the number of nodes in the tree).

unite(x,y): If $\text{size}(x) \geq \text{size}(y)$ make x the parent of y and set
 $\text{size}(x) \leftarrow \text{size}(x) + \text{size}(y)$
 Otherwise make y the parent of x and set
 $\text{size}(y) \leftarrow \text{size}(x) + \text{size}(y)$

Unite by rank (Tarjan and van Leewen [41]): In this method each root contains a **rank**, which is an estimate of the depth of the tree. To combine two trees with roots of different rank, we attach the tree whose root has smaller rank to the other tree, without changing any ranks. To combine two trees with roots of the same rank, we attach either tree to the other, and increase the rank of the new root by one. The pseudo code is below. We maintain with each root x its rank, $\text{rank}(x)$. Initially, the rank of each node is zero.

unite(x, y): if $\text{rank}(x) > \text{rank}(y)$ make x the parent of y else
 if $\text{rank}(x) < \text{rank}(y)$ make y the parent of x else
 if $\text{rank}(x) = \text{rank}(y)$ make x the parent of y and increase the rank of x by 1.

Use of either of the rules above improves the complexity drastically. In particular, the worst-case find time decreases from linear to logarithmic. Now the total cost for a sequence of m find operations and $n - 1$ intermixed unite operations is $(m \log n)$, because with either rule the depth of a tree is logarithmic in its size. This result (for union by size) is in [16].

There is one more thing we can do to improve the complexity of the solution to Problem 3.1. It is an idea that Knuth [29] attributes to Alan Titter, and Hopcroft and Ullman [20] attribute to McIlroy and Morris. The idea is to modify the trees not only when we do **unite** operations, but also when we do **find** operations: when doing a **find**, we “squash” the tree along the **find** path. (See Figure 4.) When we perform a **find** on an element, say E , we walk up the path to the root, A , which is the name of the set represented by this tree. We now know not only the answer for E , but also the answer for every node along the path from E to the root. We take advantage of this fact by compressing this path, making all nodes on it point directly to the root. The tree is modified as depicted in Figure 4. Thus, if later we do a **find** on say, D , this node is now one step away from the root, instead of three steps away.

The question is, by how much does path compression improve the speed of the algorithm? Analyzing this algorithm, especially if both path compression and one of the **unite** rules is used, is complicated, and Knuth proposed it as a challenge. Note that if both path compression and union by rank are used, then the rank of tree root is not necessarily the tree height, but it is always an upper bound on the tree height. Let me remind you of the history of the bounds on this problem from the early 1970's.

There was an early incorrect “proof” of an $O(m)$ time-bound; that is, constant time per **find**. Shortly thereafter, Mike Fischer [11] obtained a correct bound of

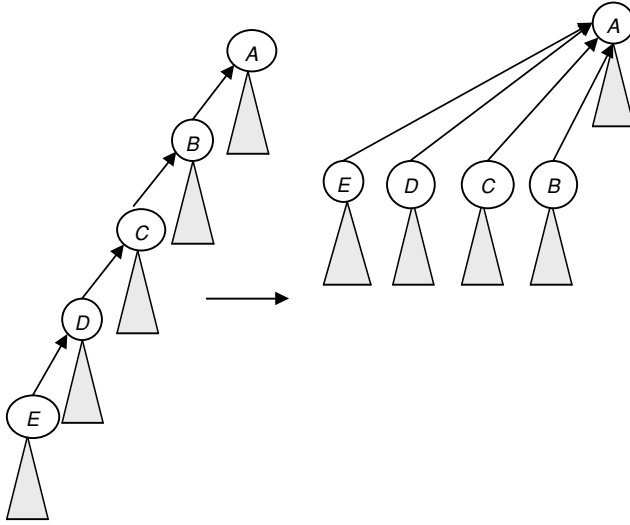


Figure 4.

$O(m \log \log n)$. Later, Hopcroft and Ullman [20] obtained the bound $O(m \log^* n)$. Here $\log^* n$ denotes the number of times one must apply the \log function to n to get down to a constant. After this result had already appeared, there was yet another incorrect result, giving a lower bound of $\Omega(n \log \log n)$. Then I was able to obtain a lower bound which shows that this algorithm does not in fact perform in constant time per *find*. Rather, its time per *find* is slightly worse than constant. Specifically, I showed a lower bound of $\Omega(n\alpha(n))$, where $\alpha(n)$ is the inverse of Ackermann's function, an incredibly slowly growing function that cannot possibly be measured in practice. It will be defined below. After obtaining the lower bound, I was able to get a matching upper bound of $O(m \cdot \alpha(n))$. (For both results, and some extensions, see [37,42].) So the correct answer for the complexity of the algorithm using both path compression and one of the *unite* rules is *almost constant* time per *find*, where *almost constant* is the inverse of Ackermann's function.

Ackermann's function was originally constructed to be so rapidly growing that it is not in the class of primitively recursive functions, those definable by a single-variable recurrence. Here is a definition of the inverse of Ackermann's function. We define a sequence of functions:

$$\text{For } j \geq 1, k \geq 0, A_0(j) = j + 1, \quad A_k(j) = A_{k-1}^{(j+1)}(j) \text{ for } k \geq 1,$$

where $A^{(i+1)}(x) = A(A^{(i)}(x))$ denotes function composition.

Note that A_0 is just the successor function; A_1 is essentially multiplication by two, A_2 is exponentiation; A_3 is iterated exponentiation, the inverse of $\log^*(n)$; after that the functions grow very fast.

The inverse of Ackermann's function is defined as:

$$\alpha(n) = \min \{k : A_k(1) \geq n\}$$

The growth of the function $\alpha(n)$ is incredibly slow. The smallest n such that $\alpha(n) = 4$ for example, is greater than any size of any problem that anyone will ever solve, in the course of all time.

The most interesting thing about this problem is the surprising emergence of $\alpha(n)$ in the time bound. I was able to obtain such a bound because I guessed that the truth was that the time per *find* is not constant (and I was right). Given this guess, I was able to construct a sequence of bad examples defined using a double recursion, which naturally led to Ackermann's function. Since I obtained this result, the inverse of Ackermann's function has turned up in a number of other places in computer science, especially in computational geometry, in bounding the complexity of various geometrical configurations involving lines and points and other objects [34].

Let me mention some further work on this problem. The tree data structure for representing sets, though simple, is very powerful. One can attach values to the edges or nodes of the trees and combine values along tree paths using *find*. This idea has many applications [39]. There are variants of path compression that have the same inverse Ackermann function bound and some other variants that have worse bounds [42]. The lower bound that I originally obtained was for the particular algorithm that I have described. But the inverse Ackermann function turns out to be inherent in the problem. There is no way to solve the problem without having the inverse Ackermann function dependence. I was able to show this for a pointer machine computation model with certain restrictions [38]. Later Fredman and Saks [12] showed this for the cell probe computation model; theirs is a really beautiful result. Recently, Haim Kaplan, Nira Shafir and I [24] have extended the data structure to support insertions and deletions of elements.

4. Amortization and Self-adjusting Search Trees

The analysis of path compression that leads to the inverse Ackermann function is complicated. But it illustrates a very important concept, which is the notion of *amortization*. The algorithm for Problem 3.1 performs a sequence of intermixed *unite* and *find* operations. Such operations can in fact produce a deep tree, causing at least one *find* operation to take logarithmic time. But such a *find* operation squashes the tree and causes later *finds* to be cheap. Since we are interested in measuring the total cost, we do not mind if some operations are expensive, as long as they are balanced by cheap ones. This leads to the notion of *amortized cost*, which is the cost per operation averaged over a worst-case sequence of operations. Problem 3.1 is the first example that I am aware of where this notion arose, although in the original work on the problem the word *amortization* was not used and the framework used nowadays for doing an amortized analysis was unknown then. The idea of a data structure in which simple

modifications improve things for later operations is extremely powerful. I would like to turn to another data structure in which this idea comes into play—*self-adjusting search trees*.

4.1. Search Trees

There is a type of self-adjusting search tree called the *splay* tree that I’m sure many of you know about. It was invented by Danny Sleater and me [35]. As we shall see, many complexity results are known for splay trees; these results rely on some clever ideas in algorithmic analysis. But the ultimate question of whether the splaying algorithm is optimal to within a constant factor remains an open problem.

Let me remind you about **binary search trees**.

Definition 4.1 A **binary search tree** is a binary tree, (every node has a left and a right child, either of which, or both, can be missing.) Each node contains a distinct item of data. The items are selected from a totally ordered universe. The items are arranged in the binary search tree in the following way: for every node x in the tree, every node in the left subtree of x is less than the item stored in x and every node in the right subtree of x is greater than the item stored in x . The operations done on the tree are **access**, **insert** and **delete**.

We perform an *access* of an item in the obvious way: we start at the root, and we go down the tree, choosing at every node whether to go left or right by comparing the item in the node with the item we trying to find. The search time is proportional to the depth of the tree or, more precisely, the length of the path from the root to the designated item. For example, in Figure 5, a search for “frog”, which is at the root, takes one step; a search for “zebra”, takes four steps. Searching for “zebra” is more expensive, but not too expensive, because the tree is reasonably balanced. Of course, there are “bad” trees, such as long paths, and there are “good” trees, which are spread out wide like the one in Figure 5. If we have a fixed set of items, it is easy to construct a perfectly balanced tree, which gives us logarithmic worst-case access time.

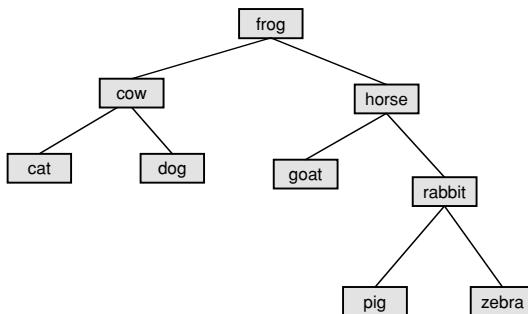


Figure 5.

The situation becomes more interesting if we want to allow *insertion* and *deletion* operations, since the shape of the tree will change. There are standard methods for inserting and deleting items in a binary search tree. Let me remind you how these work. The easiest method for an *insert* operation is just to follow the search path, which will run off the bottom of the tree, and put the new item in a new node attached where the search exits the tree. A *delete* operation is slightly more complicated. Consider the tree in Figure 5. If I want to delete say “pig” (a leaf in the tree in Figure 5), I simply delete the node containing it. But if I want to delete “frog”, which is at the root, I have to replace that node with another node. I can get the replacement node by taking the left branch from the root and then going all the way down to the right, giving me the predecessor of “frog”, which happens to be “dog”, and moving it to replace the root. Or, symmetrically, I can take the successor of “frog” and move it to the position of “frog”. In either case, the node used to replace frog has no children, so it can be moved without further changes to the tree. Such a replacement node can actually have one child (but not two); after moving such a node, we must replace it with its child. In any case, an insertion or deletion takes essentially one search in the tree plus a constant amount of restructuring. The time spent is at most proportional to the tree depth.

Insertion and deletion change the tree structure. Indeed, a bad sequence of such operations can create an unbalanced tree, in which accesses are expensive. To remedy this we need to restructure the tree somehow, to restore it to a “good” state.

The standard operation for restructuring trees is the rebalancing operation called *rotation*. A *rotation* takes an edge such as (f, k) in the tree in Figure 6 and switches it around to become (k, f) . The operation shown is a right rotation; the inverse operation is a left rotation. In a standard computer representation of a search tree, a rotation takes constant time; the resulting tree is still a binary search tree for the same set of ordered items. *Rotation* is universal in the sense that any tree on some set of ordered items can be turned into any other tree on the same set of ordered items by doing an appropriate sequence of rotations.

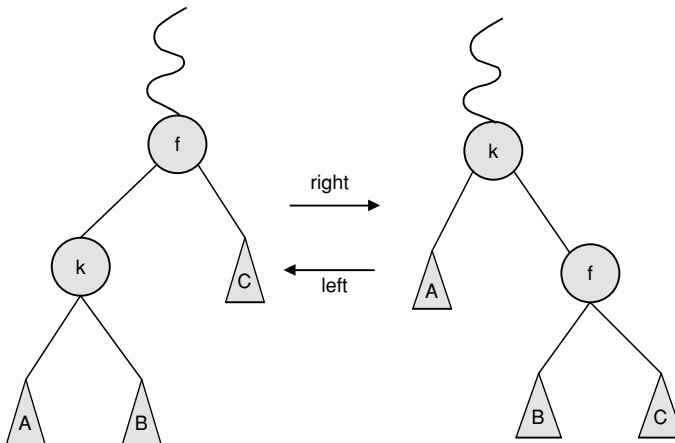


Figure 6.

We can use rotations to rebalance a tree when insertions and deletions occur. There are various “balanced tree” structures that use extra information to determine what rotations must be done to restore balance during insertions and deletions. Examples include **AVL trees** [1], **red-black trees** [19,40], and many others. All these balanced tree structures have the property that the worst-case time for a *search*, *insertion* or *deletion* in an n -node tree is $O(\log n)$.

4.2. Splay Trees

This is not the end of the story, because balanced search trees have certain *drawbacks*:

- Extra space is needed to keep track of the balance information.
- The rebalancing needed for insertions and deletions involves several cases, and can be complicated.
- Perhaps most important, the data structure is logarithmic-worst-case but essentially logarithmic-best-case as well. The structure is not optimum for a non-uniform usage pattern. Suppose for example I have a tree with a million items but I only access a thousand of them. I would like the thousand items to be cheap to access, proportional to $\log(1,000)$, not to $\log(1,000,000)$. A standard balanced search tree does not provide this.

There are various data structures that have been invented to handle this last drawback. Assume that we know something about the usage pattern. For example, suppose we have an estimate of the access frequency for each item. Then we can construct an “optimum” search tree, which minimizes the average access time. But what if the access pattern changes over time? This happens often in practice.

Motivated by this issue and knowing about the amortized bound for path compression, Danny Sleator and I considered the following problem:

Problem 4.2 *Is there a simple, self-adjusting form of search tree that does not need an explicit balance condition but takes advantage of the usage pattern? That is, is there an update mechanism that adjusts the tree automatically, based on the way it is used?*

The goal is to have items that are accessed more frequently move up in the tree, and items that are accessed less frequently move down in the tree.

We were able to come up with such a structure, which we called the **splay tree**. A Splay tree is a self-adjusting search tree. See Figure 7 for an artist’s conception of a self-adjusting tree.

“Splay” as a verb means to spread out. Splaying is a simple self-adjusting heuristic, like path compression, but that applies to binary search trees. The splaying heuristic takes a designated item and moves it up to the root of the tree by performing rotations,

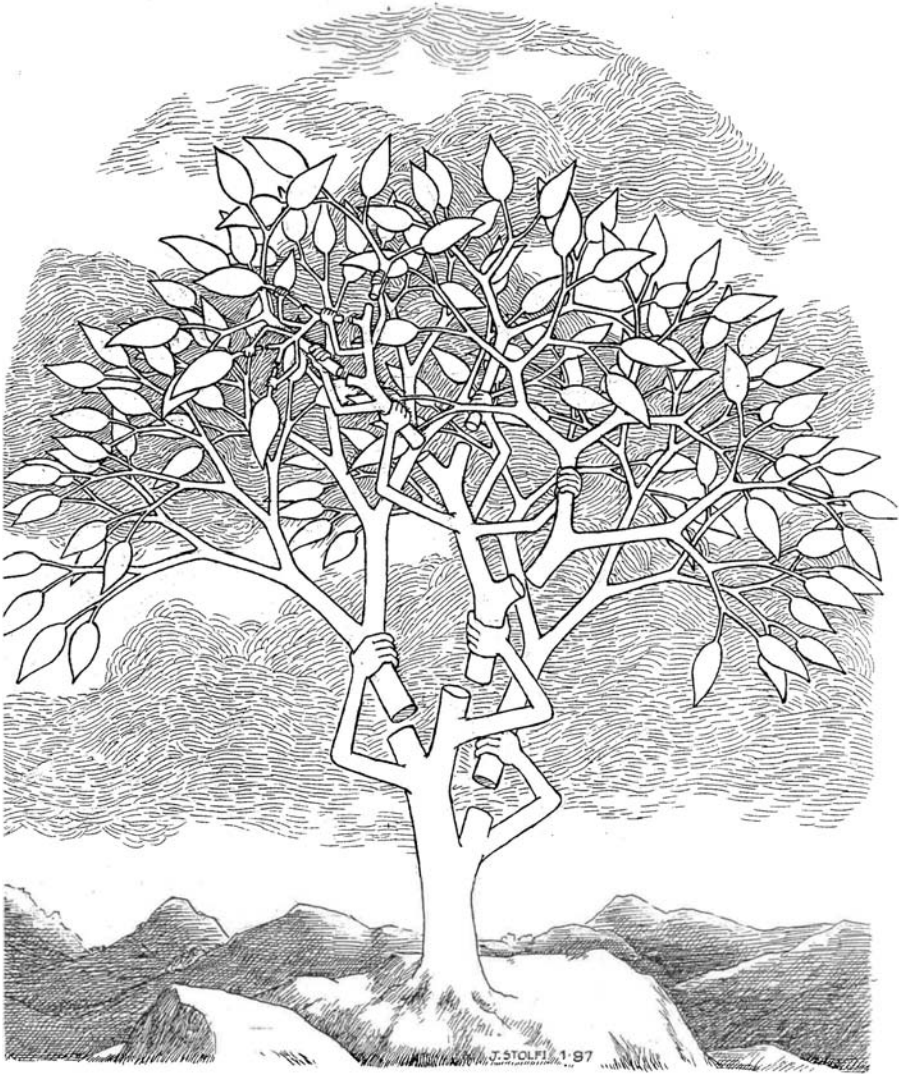


Figure 7.

preserving the item order. The starting point of the idea is to perform rotations bottom-up. It turns out, though, that doing rotations one at a time, in strict bottom-up order, does not produce good behavior. The splay heuristic performs rotations in pairs, in bottom-up order, according to the rules shown in Figure 8 and explained below. To access an item, we walk down the tree until reaching the item, and then perform the splay operation, which moves the item all the way up to the tree root. Every item along the search path has its distance to the root roughly halved, and all other nodes get pushed to the side. No node moves down more than a constant number of steps.

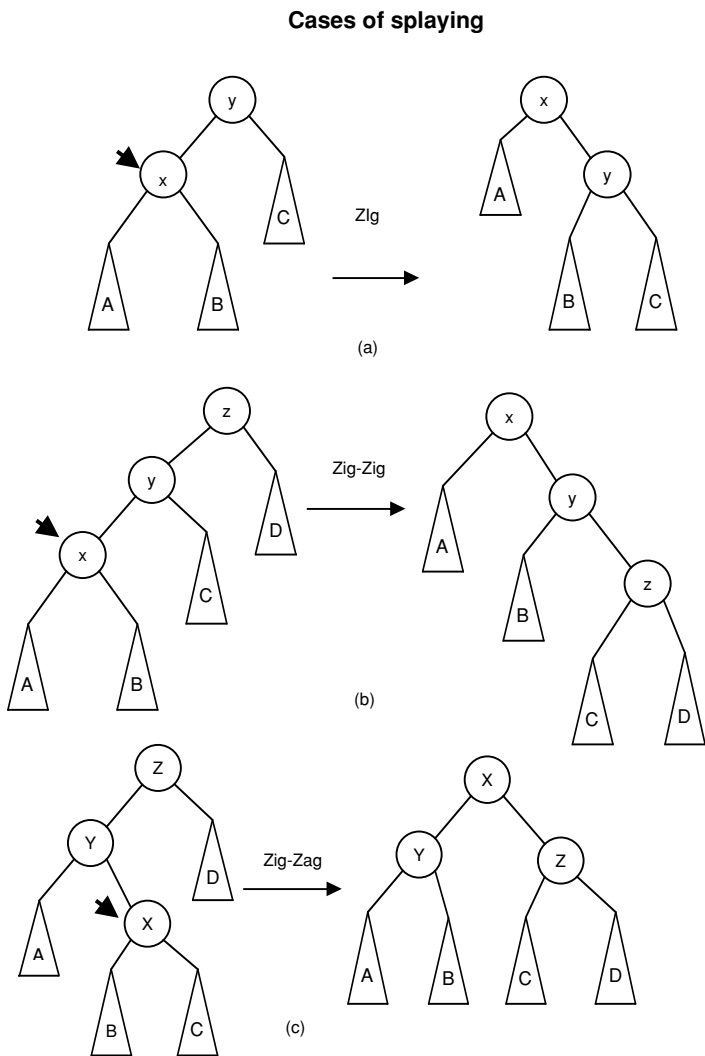


Figure 8.

Figure 8 shows the cases of a single splaying step. Assume x is the node to be accessed. If the two edges above x toward the root are in the same direction, we do a rotation on the top edge first and then on the bottom edge, which locally transforms the tree as seen in Figure 7b. This transformation doesn't look helpful; but in fact, when a sequence of such steps are performed, they have a positive effect. This is the “zig-zig” case. If the two edges from x toward the root are in opposite directions, such as right-left as seen in Figure 8c, or symmetrically left-right, then the bottom rotation is done first, followed by the top rotation. In this case, x moves up and y and z get split between the two subtrees of x . This is the zig-zag case. We keep doing zig-zag and

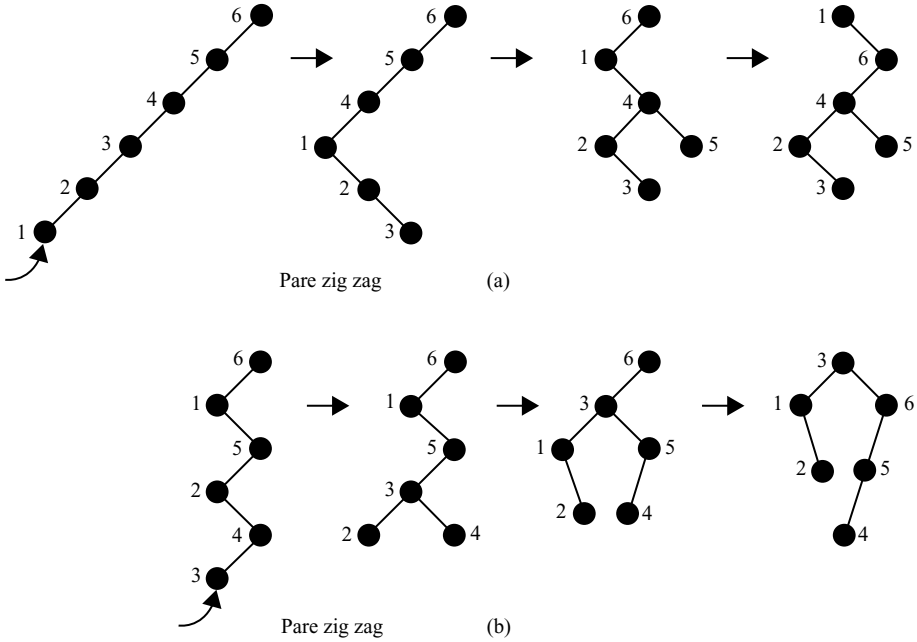


Figure 9.

zig-zig steps, as appropriate, moving x up two steps at a time, until either x is the root or it is one step away from the root. In the latter case we then do one final rotation, the zig case (Figure 8a). The *splay operation* is an entire sequence of splay steps that moves a designated item all the way up to the root.

Figure 9a contains a step-by-step example of a complete splay operation. This is a purely zig-zig case (except for a final zig). First we perform two rotations, moving item #1 up the path, and then two more rotations, moving item #1 further up the path. Finally, a last rotation is performed to make item #1 take root. Transforming the initial configuration into the final one is called "*splaying at node 1*". Figure 9b gives a step-by-step example of a purely zig-zag case.

Figure 10 is another example of a purely zig-zag case of a single splay operation. The accessed node moves to the root, every other node along the find path has its distance to the root roughly halved, and no nodes are pushed down by more than a constant amount. If we start out with a really bad example, and we do a number of splay operations, the tree gets balanced very quickly. The splay operation can be used not only during accesses but also as the basis of simple and efficient insertions, deletions, and other operations on search trees.

There is also a top-down version of splaying as well as other variants [35]. Sleator has posted code for the top-down version at [47].

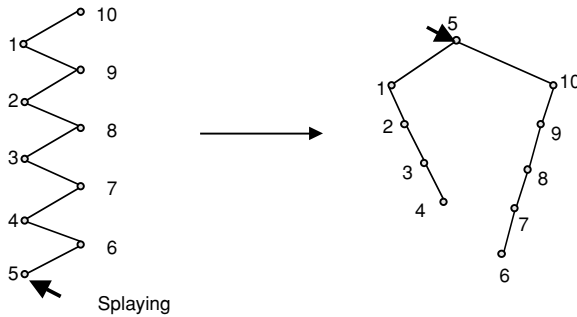


Figure 10.

4.3. Complexity Results

The main question for us as theoreticians is, “How does this algorithm perform?” Sleator and I were able to show that, in the amortized sense, this algorithm performs just as well as any balanced tree structure.

Theorem 4.3 *Beginning with an arbitrary n -node tree, suppose we perform a sequence of m accesses and ignore start-up effects; that is, we assume that $m \geq n$. The following results hold:*

- (a) The total cost of m accesses is $O(m \log n)$, thus matching the bound for balanced trees.
- (b) The splaying algorithm on any access sequence performs within a constant factor of the performance of that of the best possible static tree for the given access sequence (in spite of the fact that this algorithm does not know the access frequencies ahead of time and doesn’t keep track of them).
- (c) If the items are accessed in increasing order, each once, the total access time is linear. That is, the amortized cost per access is constant, as compared to logarithmic for a balanced search tree or for any static tree. This result demonstrates that modifying the tree as operations proceed can dramatically improve the access cost in certain situations.

It is relatively straightforward to prove results (a) and (b) above. They follow from an interesting “potential” argument that I trust many of you know. These results can be found in [35], along with additional applications and extensions. Result (c) seems to be hard to prove — an elaborate inductive argument appears in [41].

The behavior of a splay tree when sequential accesses are performed is quite interesting. Suppose we start with an extreme tree that is just a long left path, with the smallest item at the bottom of the path, and begin accessing the items in increasing order. The first access costs n . The next access costs about $n/2$, the next one costs $n/4$, and so on. The access time drops by about a factor of two with each access until after about logarithmically many accesses, at which time the tree is quite well-balanced.

Then the time per access starts behaving something like a ruler function, with a certain amount of randomness thrown in: about half the accesses take constant time; about a quarter take about twice as long; about an eighth take about three times as long; and so on. The amortized cost per access is constant rather than logarithmic.

Based on results (a)—(c) and others, Sleator and I made (what we consider to be) an audacious conjecture. Suppose we begin with some n -node search tree and perform a sequence of accesses. (For simplicity, we ignore insertions and deletions.) The cost to access an item is the number of nodes on the path from the root to the item. At any time, we can perform one or more rotations, at a cost of one per rotation. Then, knowing the entire access sequence ahead of time, there is a pattern of rotations that minimizes the total cost of the accesses and the rotations. This is the optimal offline algorithm, for the given initial tree and the given access sequence.

Problem 4.4 *Dynamic Optimality Conjecture:* *Prove or disprove that for any initial tree and any access sequence, the splaying algorithm comes within a constant factor of the optimal off-line algorithm.*

Note that splaying is an on-line algorithm: its behavior is independent of future accesses, depending only on the initial tree and the accesses done so far. Furthermore the only information the algorithm retains about the accesses done so far is implicit in the current state of the tree. A weaker form of Problem 4.4 asks whether there is *any* on-line algorithm whose performance is within a constant factor of that of the optimum off-line algorithm.

The closest that anyone has come to proving the strong form of the conjecture is an extension by Richard Cole and colleagues of the sequential access result, Theorem 4.3(c). Consider a sequence of accesses. For simplicity, assume that the items are 1, 2, 3, in the corresponding order. The distance between two items, say i and j , is defined to be $|i - j| + 2$. Cole et al. proved the following:

Theorem 4.4 [6, 7]: *The total cost of a sequence of accesses using splaying is at most of the order of n plus m plus the sum of the logarithms of the distances between consecutively accessed items.*

This result, the “dynamic finger theorem”, is a special case of the (strong) dynamic optimality conjecture. Significant progress on the weak form of the conjecture has been made recently by Demaine and colleagues [9]. They have designed an on-line search tree update algorithm that comes within a *loglog* performance factor of the optimal off-line algorithm (as compared to the *log* factor of a balanced tree algorithm). A key part of their result is a lower bound on the cost of an access sequence derived by Bob Wilber [43]. The algorithm of Demaine et al. is cleverly constructed so that its performance comes within a *loglog* factor of Wilber’s lower bound. They also argue that use of Wilber’s lower bound will offer no improvement beyond *loglog*. An immediate question is whether one can prove a similar *loglog* bound for splaying, even if the dynamic optimality conjecture remains out of reach.

To summarize, we do not know the answer to the following question:

Is the splaying algorithm (or any on-line binary search tree algorithm) optimal to within a constant factor?

Splaying as well as path compression are examples of very simple operations that give rise when repeated to complicated, hard-to-analyze, behavior. Splay trees have been used in various systems applications, for memory management, table storage, and other things. In many applications of tables, most of the data does not get accessed most of the time. The splaying tree algorithm takes advantage of such locality of reference: the splay algorithm moves the current working set to the top of the tree, where it is accessible at low cost. As the working set changes, the new working set moves to the top of the tree.

The drawback of this data structure is, of course, that it performs rotations all the time, during accesses as well as during insertions and deletions. Nevertheless, it seems to work very well in practical situations in which the access pattern is changing.

5. The Rotation Distance between Search Trees

Search trees are a fascinating topic, not just because they are useful data structures, but also because they have interesting mathematical properties. I have mentioned that any search tree can be transformed into any other search tree on the same set of ordered items by performing an appropriate sequence of rotations. This fact raises at least two interesting questions, one algorithmic, one structural.

Problem 5.1 *Given two n -node trees, how many rotations does it take to convert one tree into the other?*

This question seems to be NP-hard. A related question is how far apart can two trees be? To formulate the question more precisely, we define the *rotation graph* on n -node trees in the following way: The vertices of the graph are the n -node binary trees. Two trees are connected by an edge if and only if one tree can be obtained from the other by doing a single rotation. This graph is connected.

Problem 5.2 *What is the diameter of the rotation graph described above as a function of n ?*

It is easy to get an upper bound of $2n$ for the diameter. It is also easy to get a lower bound of $n - O(1)$, but this leaves a factor of two gap. Sleator and I worked with Bill Thurston on this problem. He somehow manages to map every possible problem into hyperbolic geometry. Using mostly Thurston's ideas, we were able to show that the $2n$ bound is tight, by applying a volumetric argument in hyperbolic space. We were even able to establish the exact bound for large enough n , which is $2n - 6$ [36]. To me this is an amazing result. The details get quite technical, but this is an example in which a

piece of mathematics gets brought in from way out in left field to solve a nitty-gritty data structure problem. This just goes to show the power of mathematics in the world.

6. Static Optimum Search Trees

A final question about search trees concerns static optimum trees. Suppose we want to store n ordered items in a fixed search tree so as to minimize the average access time, assuming that each item is accessed independently with a fixed probability, and that we know the access probabilities. The problem is to construct the best tree. There are an exponential number of trees, so it might take exponential time to find the best one, but in fact it does not. There are two versions of this problem, depending on the kind of binary search tree we want.

Problem 6.1 *Items can be stored in the internal nodes of the tree. (This is the kind of search tree discussed in Sections 4 and 5.)*

The problem in this case is: Given positive weights w_1, w_2, \dots, w_n , construct an n -node binary tree that minimizes $\sum_{i=1}^n w_i d_i$, where d_i is the depth of the i -th node in symmetric order.

Problem 6.2 *Items can be stored only in the external nodes (the leaves) of the tree.*

The problem in this case is: Given positive weights w_1, w_2, \dots, w_n , construct a binary tree with n external nodes that minimizes $\sum_{i=1}^n w_i d_i$, where d_i is the depth of the i -th external node in symmetric order.

Problem 6.1 can be solved by a straightforward $O(n^3)$ -time dynamic programming algorithm (as in the stack generation problem discussed in Section 2). Knuth[30] was able to improve on this by showing that there is no need to look at all the subproblems; there is a restriction on the subproblems that have to be considered, which reduces the time to $O(n^2)$. This result was extended by Frances Yao [45] to other problems. Yao captured a certain kind of structural restriction that she called “quadrangle inequalities”. Here we have an $O(n^2)$ dynamic programming algorithm with a certain amount of cleverness in it. This result is twenty-five years old or so. Nothing better is known. There may, in fact, be a faster algorithm for Problem 6.1; no nontrivial lower bound for the problem is known.

For Problem 6.2, in which the items are stored in the external nodes and the internal nodes just contain values used to support searching, we can do better. There is a beautiful algorithm due to Hu and Tucker [21] that runs in $O(n \log n)$ time. This algorithm is an extension of the classical algorithm of Huffman [22] for building so-called “Huffman codes”. The difference between Huffman codes and search trees is the alphabetic restriction: in a search tree the items have to be in a particular order in the leaves, whereas in a Huffman code they can be permuted arbitrarily. It turns out that

a simple variant of the Huffman coding algorithm solves Problem 6.2. The amazing thing about this is that the proof of correctness is inordinately complicated. Garsia and Wachs [17] presented a variant of the algorithm with an arguably simpler proof of correctness, and Karpinski et al. [26] have made further progress on simplifying the proofs of both algorithms. But it is still quite a miracle that these simple algorithms work. And again, there is no lower bound known. In fact, there is no reason to believe that the problem cannot be solved in linear time, and there is good reason to believe that maybe it can: for some interesting special cases the problem can indeed be solved in linear time [27].

7. The Minimum Spanning Tree Problem

Let me close by coming back to a classical graph problem—the minimum spanning tree problem. Given a connected, undirected graph with edge costs, we want to find a spanning tree of minimum total edge cost. This problem is a classical network optimization problem, and it is about the simplest problem in this area. It has a very long history, nicely described by Graham and Hell [18]. The first fully-realized algorithms for this problem were developed in the 1920's. There are three classic algorithms. The most recently discovered is Kruskal's algorithm [31], with which we are all familiar. This algorithm processes the edges in increasing order by cost, building up the tree edge-by-edge. If a given edge connects two different connected components of what has been built so far, we add it as an additional edge; if it connects two vertices in the same component, we throw it away. To implement this algorithm, we need an algorithm to sort (or at least partially sort) the edges, plus a data structure to keep track of the components. Keeping track of the components is exactly the set union problem discussed in Section 3. The running time of Kruskal's algorithm is $O(m \log n)$ including the sorting time. If the edges are presorted by cost, the running time of the algorithm is the same as that of disjoint set union; namely, $O(m \alpha(n))$, where $\alpha(n)$ is the inverse Ackermann function.

An earlier algorithm, usually credited to Prim [33] and Dijkstra [10], is a single-source version of Kruskal's algorithm. It begins with a vertex and grows a tree from it by repeatedly adding the cheapest edge connecting the tree to a new vertex. This algorithm was actually discovered by Jarník in 1930 [23]. It runs in $O(n^2)$ time, as implemented by Prim and Dijkstra. (Jarník did not consider its computational complexity at all.) By using a data structure called a heap (or priority queue) the algorithm can be implemented to run in $O(m \log n)$ time.

An even earlier algorithm, a beautiful parallel one, was described by Boruvka [3] in 1926. It also has a running time of $O(m \log n)$. (The time bound is recent; Boruvka did not investigate its complexity.) This algorithm is Kruskal's algorithm in parallel. In the first iteration, for every vertex pick the cheapest incident edge and add it the set of edges so far selected. In general, the chosen edges form a set of trees. As long as there are at least two such trees, pick the cheapest edge incident to each tree and add these

edges to the chosen set. In every iteration the number of trees decreases by at least a factor of two, giving a logarithmic bound on the number of iterations. If there are edges of equal cost, a consistent tie-breaking rule must be used, or the algorithm will create cycles, but this is just a technical detail.

All three classic algorithms run in $O(m \log n)$ time if they are implemented appropriately. The obvious question is whether sorting is really needed, or can one get rid of the log factor and solve this problem in linear time? Andy Yao [44] was the first to make progress. He added a new idea to Boruvka's algorithm that reduced the running time to $O(m \log \log n)$. He thereby showed that sorting was not, in fact, inherent in the minimum spanning tree problem. A sequence of improvements followed, all based on Boruvka's algorithm. Mike Fredman and I [13] achieved a running time of $O(m \log^* n)$ by using a new data structure called the *Fibonacci heap* in combination with Boruvka's algorithm. By adding a third idea, that of *packets*, Galil, Gabor, and Spencer [14] (see also [15]) obtained $O(m \log \log^* n)$ running time. Finally, Klein and Tarjan [28] (see also [25]) used random sampling in combination with a linear-time algorithm for verification of minimum spanning trees to reach the ultimate goal, a linear time algorithm for finding minimum spanning trees.

One may ask whether random sampling is really necessary. Is there a deterministic linear-time algorithm to find minimum spanning trees? Bernard Chazelle [4,5], in a remarkable tour de force, invented a new data structure, called the **soft heap**, and used it to obtain a minimum spanning tree algorithm with a running time of $O(m \alpha(n))$. (Our old friend, the inverse Ackermann function, shows up again!) Soft heaps make errors, but only in a controlled way. This idea of allowing controlled errors is reminiscent of the remarkable (and remarkably complicated) $O(n \log n)$ -size sorting network of Ajtai, Komlos, and Szemerédi [2], which uses partition sorting with careful control of errors.

Chazelle's ideas were used in a different way by Pettie and Ramachandran [32] who designed a minimum spanning tree algorithm that has a running time optimum to within a constant factor, but whose running time they could not actually analyze. The extra idea in their construction is that of building an optimum algorithm for very-small-size subproblems by exhaustively searching the space of all possible algorithms, and then combining this algorithm with a fixed-depth recursion based on Chazelle's approach.

In conclusion, we now know that minimum spanning trees can be found in linear time using random sampling, and we know an optimum deterministic algorithm but we don't know how fast it runs (no slower than $O(m \alpha(n))$, possibly as fast as $O(m)$). This is the strange unsettled state of the minimum spanning tree problem at the moment.

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