It is a very sad thing that nowadays there is so little useless information.

— Oscar Wilde, "A Few Maxims for the Instruction Of The Over-Educated" (1894)

Ninety percent of science fiction is crud.
But then, ninety percent of everything is crud,
and it's the ten percent that isn't crud that is important.

— [Theodore] Sturgeon's Law (1953)

⋆6 Advanced Dynamic Programming

Dynamic programming is a powerful technique for efficiently solving recursive problems, but it's hardly the end of the story. In many cases, once we have a basic dynamic programming algorithm in place, we can make further improvements to bring down the running time or the space usage. We saw one example in the Fibonacci number algorithm. Buried inside the naïve iterative Fibonacci algorithm is a recursive problem—computing a power of a matrix—that can be solved more efficiently by dynamic programming techniques—in this case, repeated squaring.

6.1 Saving Space: Divide and Conquer

Just as we did for the Fibonacci recurrence, we can reduce the space complexity of our edit distance algorithm from $O(mn)$ to $O(m+n)$ by only storing the current and previous rows of the memoization table. This 'sliding window' technique provides an easy space improvement for most (but *not* all) dynamic programming algorithm.

Unfortunately, this technique seems to be useful only if we are interested in the *cost* of the optimal edit sequence, not if we want the optimal edit sequence itself. By throwing away most of the table, we apparently lose the ability to walk backward through the table to recover the optimal sequence.

Fortunately for memory-misers, in 1975 Dan Hirshberg discovered a simple divide-and-conquer strategy that allows us to compute the optimal edit sequence in $O(mn)$ time, using just $O(m+n)$ space. The trick is to record not just the edit distance for each pair of prefixes, but also a single position in the middle of the optimal editing sequence for that prefix. Specifically, any optimal editing sequence that transforms $A[1..m]$ into $B[1..n]$ can be split into two smaller editing sequences, one transforming $A[1..m/2]$ into $B[1..h]$ for some integer h, the other transforming $A[m/2+1..m]$ into $B[h+1..n]$.

To compute this breakpoint h, we define a second function $\mathit{Half}(i,j)$ such that some optimal edit sequence from $A[1..i]$ into $B[1..j]$ contains an optimal edit sequence from $A[1..m/2]$ to $B[1..\mathit{Half}(i,j)]$. We can define this function recursively as follows:

$$\mathit{Half}(i,j) = \begin{cases} \infty & \text{if } i < m/2 \\ j & \text{if } i = m/2 \\ \mathit{Half}(i-1,j) & \text{if } i > m/2 \text{ and } \mathit{Edit}(i,j) = \mathit{Edit}(i-1,j)+1 \\ \mathit{Half}(i,j-1) & \text{if } i > m/2 \text{ and } \mathit{Edit}(i,j) = \mathit{Edit}(i,j-1)+1 \\ \mathit{Half}(i-1,j-1) & \text{otherwise} \end{cases}$$

(Because there there may be more than one optimal edit sequence, this is not the only correct definition.) A simple inductive argument implies that $\mathit{Half}(m,n)$ is indeed the correct value of h. We can easily modify our earlier algorithm so that it computes $\mathit{Half}(m,n)$ at the same time as the edit distance $\mathit{Edit}(m,n)$, all in $O(mn)$ time, using only $O(m)$ space.

Edit		A	L	G	O	R	I	T	H	M
	0	1	2	3	4	5	6	7	8	9
A	1	**0**	1	2	3	4	5	6	7	8
L	2	1	**0**	1	2	3	4	5	6	7
T	3	2	1	1	2	3	4	**4**	5	6
R	4	3	2	2	2	**2**	3	4	5	6
U	5	4	3	3	3	3	3	4	5	6
I	6	5	4	4	4	4	**3**	4	5	6
S	7	6	5	5	5	5	4	4	5	6
T	8	7	6	6	6	6	5	**4**	5	6
I	9	8	7	7	7	7	**6**	5	5	6
C	10	9	8	8	8	8	7	6	6	6

Half		A	L	G	O	R	I	T	H	M
	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞
A	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞
L	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞
T	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞
R	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞
U	0	1	2	3	4	5	6	7	8	9
I	0	1	2	3	4	5	**5**	5	5	5
S	0	1	2	3	4	5	5	5	5	5
T	0	1	2	3	4	5	5	**5**	5	5
I	0	1	2	3	4	5	**5**	5	5	5
C	0	1	2	3	4	5	5	5	5	5

Finally, to compute the optimal editing sequence that transforms A into B, we recursively compute the optimal sequences transforming $A[1\,..\,m/2]$ into $B[1\,..\,\mathit{Half}(m,n)]$ and transforming $A[m/2+1\,..\,m]$ into $B[\mathit{Half}(m,n)+1\,..\,n]$. The recursion bottoms out when one string has only constant length, in which case we can determine the optimal editing sequence in linear time using our old dynamic programming algorithm. The running time of the resulting algorithm satisfies the following recurrence:

$$T(m,n) = \begin{cases} O(n) & \text{if } m \le 1 \\ O(m) & \text{if } n \le 1 \\ O(mn) + T(m/2,h) + T(m/2,n-h) & \text{otherwise} \end{cases}$$

It's easy to prove inductively that $T(m,n) = O(mn)$, no matter what the value of h is. Specifically, the entire algorithm's running time is at most twice the time for the initial dynamic programming phase.

$$\begin{aligned} T(m,n) &\le \alpha mn + T(m/2,h) + T(m/2,n-h) \\ &\le \alpha mn + 2\alpha mh/2 + 2\alpha m(n-h)/2 && \text{[inductive hypothesis]} \\ &= 2\alpha mn \end{aligned}$$

A similar inductive argument implies that the algorithm uses only $O(n+m)$ space.

Hirschberg's divide-and-conquer trick can be applied to almost any dynamic programming problem to obtain an algorithm to construct an optimal *structure* (in this case, the cheapest edit sequence) within the same space and time bounds as computing the *cost* of that optimal structure (in this case, edit distance). For this reason, we will almost always ask you for algorithms to compute the cost of some optimal structure, not the optimal structure itself.

6.2 Saving Time: Sparseness

In many applications of dynamic programming, we are faced with instances where almost every recursive subproblem will be resolved exactly the same way. We call such instances *sparse*. For example, we might want to compute the edit distance between two strings that have few characters in common, which means there are few "free" substitutions anywhere in the table.

Most of the table has exactly the same structure. If we can reconstruct the entire table from just a few key entries, then why compute the entire table?

To better illustrate how to exploit sparseness, let's consider a simplification of the edit distance problem, in which substitutions are not allowed (or equivalently, where a substitution counts as two operations instead of one). Now our goal is to maximize the number of "free" substitutions, or equivalently, to find the *longest common subsequence* of the two input strings.

Fix the two input strings $A[1..n]$ and $B[1..m]$. For any indices i and j, let $LCS(i,j)$ denote the length of the longest common subsequence of the prefixes $A[1..i]$ and $B[1..j]$. This function can be defined recursively as follows:

$$LCS(i,j) = \begin{cases} 0 & \text{if } i = 0 \text{ or } j = 0 \\ LCS(i-1,j-1)+1 & \text{if } A[i] = B[j] \\ \max\{LCS(i,j-1),\ LCS(i-1,j)\} & \text{otherwise} \end{cases}$$

This recursive definition directly translates into an $O(mn)$-time dynamic programming algorithm.

	«	A	L	G	O	R	I	T	H	M	»
«	**0**	0	0	0	0	0	0	0	0	0	0
A	0	**1**	1	1	1	1	1	1	1	1	1
L	0	1	**2**	2	2	2	2	2	2	2	2
T	0	1	2	2	2	2	**3**	3	3	3	3
R	0	1	2	2	**3**	3	3	3	3	3	3
U	0	1	2	2	3	3	3	3	3	3	3
I	0	1	2	2	3	**4**	4	4	4	4	4
S	0	1	2	2	3	4	4	4	4	**5**	5
T	0	1	2	2	3	4	**5**	5	5	5	5
I	0	1	2	2	3	**4**	5	5	5	5	5
C	0	1	2	2	3	4	5	5	5	5	5
»	0	1	2	2	3	4	5	5	5	5	**6**

The *LCS* memoization table for `ALGORITHMS` and `ALTRUISTIC`; the brackets « and » are sentinel characters. Match points are indicated in red.

Call an index pair (i,j) a ***match point*** if $A[i] = B[j]$. In some sense, match points are the only "interesting" locations in the memoization table. Given a list of the match points, we can reconstruct the entire table using the following recurrence:

$$LCS(i,j) = \begin{cases} 0 & \text{if } i = j = 0 \\ \max\left\{LCS(i',j') \;\middle|\; A[i'] = B[j'] \text{ and } i' < i \text{ and } j' < j\right\} + 1 & \text{if } A[i] = B[j] \\ \max\left\{LCS(i',j') \;\middle|\; A[i'] = B[j'] \text{ and } i' \le i \text{ and } j' \le j\right\} & \text{otherwise} \end{cases}$$

(Notice that the inequalities are strict in the second case, but not in the third.) To simplify boundary issues, we add unique sentinel characters $A[0] = B[0]$ and $A[m+1] = B[n+1]$ to both strings. This ensures that the sets on the right side of the recurrence equation are non-empty, and that we *only* have to consider match points to compute $LCS(m,n) = LCS(m+1,n+1) - 1$.

If there are K match points, we can actually compute them all in $O(m \log m + n \log n + K)$ time. Sort the characters in each input string, but remembering the original index of each character, and then essentially merge the two sorted arrays, as follows:

```
FindMatches($A[1..m], B[1..n]$):
    for $i \gets 1$ to $m$:  $I[i] \gets i$
    for $j \gets 1$ to $n$:  $J[j] \gets j$

    sort $A$ and permute $I$ to match
    sort $B$ and permute $J$ to match

    $i \gets 1$;  $j \gets 1$
    while $i < m$ and $j < n$
        if $A[i] < B[j]$
            $i \gets i + 1$
        else if $A[i] > B[j]$
            $j \gets j + 1$
        else                    ⟨⟨Found a match!⟩⟩
            $ii \gets i$
            while $A[ii] = A[i]$
                $jj \gets j$
                while $B[jj] = B[j]$
                    report $(I[ii], J[jj])$
                    $jj \gets jj + 1$
                $ii \gets i + 1$
            $i \gets ii$;  $j \gets jj$
```

To efficiently evaluate our modified recurrence, we once again turn to dynamic programming. We consider the match points in lexicographic order—the order they would be encountered in a standard row-major traversal of the $m \times n$ table—so that when we need to evaluate $LCS(i, j)$, all match points (i', j') with $i' < i$ and $j' < j$ have already been evaluated.

```
SparseLCS($A[1..m], B[1..n]$):
    $Match[1..K] \gets$ FindMatches$(A, B)$
    $Match[K+1] \gets (m+1, n+1)$        ⟨⟨Add end sentinel⟩⟩
    Sort $M$ lexicographically
    for $k \gets 1$ to $K$
        $(i, j) \gets Match[k]$
        $LCS[k] \gets 1$                  ⟨⟨From start sentinel⟩⟩
        for $\ell \gets 1$ to $k - 1$
            $(i', j') \gets Match[\ell]$
            if $i' < i$ and $j' < j$
                $LCS[k] \gets \min\{LCS[k], 1 + LCS[\ell]\}$
    return $LCS[K+1] - 1$
```

The overall running time of this algorithm is $O(m \log m + n \log n + K^2)$. So as long as $K = o(\sqrt{mn})$, this algorithm is actually faster than naïve dynamic programming.

6.3 Saving Time: Monotonicity

Recall the optimal binary search tree problem from the previous lecture. Given an array $F[1..n]$ of access frequencies for n items, the problem it to compute the binary search tree that minimizes the cost of all accesses. A relatively straightforward dynamic programming algorithm solves this problem in $O(n^3)$ time.

As for longest common subsequence problem, the algorithm can be improved by exploiting some structure in the memoization table. In this case, however, the relevant structure isn't in the table of costs, but rather in the table used to reconstruct the actual optimal tree. Let $OptRoot[i, j]$ denote the index of the root of the optimal search tree for the frequencies $F[i..j]$; this is always an integer between i and j. Donald Knuth proved the following nice monotonicity property for optimal subtrees: If we move either end of the subarray, the optimal root moves in the same direction or not at all. More formally:

$$\boxed{\mathit{OptRoot}[i,j-1] \le \mathit{OptRoot}[i,j] \le \mathit{OptRoot}[i+1,j] \text{ for all } i \text{ and } j.}$$

In other words, every row and column in the array $\mathit{OptRoot}[1..n,1..n]$ is sorted. This (nontrivial!) observation immediately suggests the following more efficient algorithm:

```
FasterOptimalSearchTree($f[1..n]$):
  InitF($f[1..n]$)
  for $i \leftarrow 1$ downto $n$
      $OptCost[i,i-1] \leftarrow 0$
      $OptRoot[i,i-1] \leftarrow i$
  for $d \leftarrow 0$ to $n$
      for $i \leftarrow 1$ to $n$
          ComputeCostAndRoot($i, i+d$)
  return $OptCost[1,n]$
```

```
ComputeCostAndRoot($i, j$):
  $OptCost[i,j] \leftarrow \infty$
  for $r \leftarrow OptRoot[i,j-1]$ to $OptRoot[i+1,j]$
      $tmp \leftarrow OptCost[i,r-1] + OptCost[r+1,j]$
      if $OptCost[i,j] > tmp$
          $OptCost[i,j] \leftarrow tmp$
          $OptRoot[i,j] \leftarrow r$
  $OptCost[i,j] \leftarrow OptCost[i,j] + F[i,j]$
```

It's not hard to see that the loop index r increases monotonically from 1 to n during each iteration of the *outermost* for loop of FasterOptimalSearchTree. Consequently, the total cost of all calls to ComputeCostAndRoot is only $O(n^2)$.

If we formulate the problem slightly differently, this algorithm can be improved even further. Suppose we require the optimum *external* binary tree, where the keys $A[1..n]$ are all stored at the leaves, and intermediate pivot values are stored at the internal nodes. An algorithm discovered by Ching Hu and Alan Tucker[1] computes the optimal binary search tree in this setting in only $O(n \log n)$ time!

6.4 Saving Time: More Monotoniticy

Knuth's algorithm can be significantly generalized by considering a more subtle form of monotonicity in the *cost* matrix. A common (but often implicit) operation in many dynamic programming algorithms is finding the minimum element in every row of a two-dimensional array. For example, consider a single iteration of the outer loop in FasterOptimalSearchTree, for some fixed value of d. Define an array M by setting

$$M[i,r] = \begin{cases} \mathit{OptCost}[i,r-1] + \mathit{OptCost}[r+1,i+d] & \text{if } i \le r \le i+d \\ \infty & \text{otherwise} \end{cases}$$

Each call to ComputeCostAndRoot($i, i+d$) computes the smallest element in the ith row of this array M.

Let $M[1..m,1..n]$ be an arbitrary two-dimensional array. We say that M is ***monotone*** if the leftmost smallest element in any row is either directly above or to the left of the leftmost smallest element in any later row. To state this condition more formally, let $\mathit{LM}(i)$ denote the index of the smallest item in the ith row $M[i,\cdot\,]$; if there is more than one smallest item, choose the one

[1]T. C. Hu and A. C. Tucker, Optimal computer search trees and variable length alphabetic codes, *SIAM J. Applied Math.* 21:514–532, 1971. For a slightly simpler algorithm with the same running time, see A. M. Garsia and M. L. Wachs, A new algorithms for minimal binary search trees, *SIAM J. Comput.* 6:622–642, 1977. The original correctness proofs for both algorithms are rather intricate; for simpler proofs, see Marek Karpinski, Lawrence L. Larmore, and Wojciech Rytter, Correctness of constructing optimal alphabetic trees revisited, *Theoretical Computer Science*, 180:309-324, 1997.

furthest to the left. Then M is monotone if and only if $LM(i) \le LM(i+1)$ for every index i. For example, the following 5×5 matrix is monotone (as shown by the hilighted row minima).

$$\begin{bmatrix} \boxed{12} & 21 & 38 & 76 & 27 \\ 74 & \boxed{14} & 14 & 29 & 60 \\ 21 & \boxed{8} & 25 & 10 & 71 \\ 68 & 45 & 29 & \boxed{15} & 76 \\ 97 & 8 & 12 & \boxed{2} & 6 \end{bmatrix}$$

Given a monotone $m \times n$ array M, we can compute computes the array $LM[i]$ containing the index of the leftmost minimum element in every row as follows. We begin by recursively computing the leftmost minimum elements in all the odd-indexed rows of M. Then for each even index $2i$, the monotonicity of M implies the bounds

$$LM[2i-1] \le LM[2i] \le LM[2i+1],$$

so we can compute $LM[2i]$ by brute force by searching only within that range of indices. This search requires exactly $LM[2i+1] - LM[2i-1]$ comparisons; in particular, if $LM[2i-1] = LM[2i+1]$, then we don't need to perform any comparisons on row $2i$. Summing over all even indices, we find that the total number of comparisons is

$$\sum_{i=1}^{m/2} LM[2i+1] - LM[2i-1] \;=\; LM[m+1] - LM[1] \;\le\; n.$$

We also need to spend constant time on each row, as overhead for the main loop, so the total time for our algorithm is $O(n+m)$ plus the time for the recursive call. Thus, the running time satisfies the recurrence

$$T(m,n) = T(m/2,n) + O(n+m),$$

which implies that our algorithm runs in $\boldsymbol{O(m + n\log m)}$ ***time***.

Alternatively, we could use the following divide-and-conquer procedure. Compute the middle leftmost-minimum index $LM[\frac{m}{2}]$ by brute force in $O(n)$ time, and then recursively find the leftmost minimum entries in the following submatrices:

$$M\left[1 \,..\, \tfrac{m}{2}-1,\ 1 \,..\, LM[\tfrac{m}{2}]\right] \qquad M\left[\tfrac{m}{2}+1 \,..\, m,\ LM[\tfrac{m}{2}] \,..\, n\right]$$

The worst-case running time $T(m,n)$ for this algorithm obeys the following recurrence (after removing some irrelevant ± 1s from the recursive arguments, as usual):

$$T(m,n) = \begin{cases} 0 & \text{if } m < 1 \\ O(n) + \max\limits_{k} \big(T(m/2,k) + T(m/2,n-k)\big) & \text{otherwise} \end{cases}$$

The recursion tree for this recurrence is a balanced binary tree of depth $\log_2 m$, and therefore with $O(m)$ nodes. The total number of *comparisons* performed at each level of the recursion tree is $O(n)$, but we also need to spend at least constant time at each node in the recursion tree. Thus, this divide-and-conquer formulation also runs in $\boldsymbol{O(m + n\log m)}$ ***time***.

In fact, these two algorithms are essentially identical. Both algorithms examine the same subset of array entries and perform the same pairwise comparisons, although in different orders. Specifically, the divide-and-conquer algorithm performs the usual depth-first traversal of its recursion tree. The even-odd algorithm actually performs a *breadth*-first traversal of the same recursion tree, handling each level of the recursion tree in a single for-loop. The breadth-first formulation of the algorithm will prove more useful in the long run.

6.5 Saving more time: Total monotonicity

A more general technique for exploiting structure in dynamic programming arrays was discovered by Alok Aggarwal, Maria Klawe, Shlomo Moran, Peter Shor, and Robert Wilber in 1987; their algorithm is now universally known as ***SMAWK*** (pronounced "smoke") after their suitably-permuted initials.

SMAWK requires a stricter form of monotoniticy in the input array. We say that M is ***totally monotone*** if the submatrix defined by any subset of (not necessarily consecutive) rows and columns is monotone. For example, the following 5×5 matrix is monotone (as shown by the hilighted row minima), but not totally monotone (as shown by the gray 2×2 submatrix).

$$\begin{bmatrix} 12 & 21 & 38 & 76 & 27 \\ 74 & 14 & 14 & 29 & 60 \\ 21 & 8 & 25 & 10 & 71 \\ 68 & 45 & 29 & 15 & 76 \\ 97 & 8 & 12 & 2 & 6 \end{bmatrix}$$

On the other hand, the following matrix is totally monotone:

$$\begin{bmatrix} 12 & 21 & 38 & 76 & 89 \\ 47 & 14 & 14 & 29 & 60 \\ 21 & 8 & 20 & 10 & 71 \\ 68 & 16 & 29 & 15 & 76 \\ 97 & 8 & 12 & 2 & 6 \end{bmatrix}$$

Given a totally monotone $m \times n$ array as input, SMAWK finds the leftmost smallest element of every row in only $O(n+m)$ time.

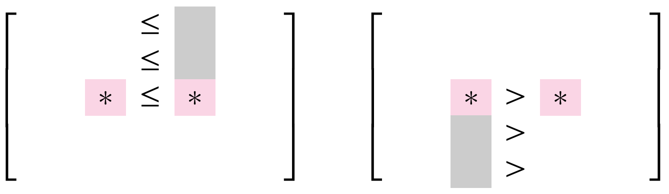
The algorithm alternates between two different subroutines, one for "tall" arrays with more rows than columns, and another for "wide" arrays with more columns than rows. The "tall" subroutine is a divide-and-conquer algorithm that already yields a significant speedup over the naive brute-force algorithm. To simplify the analysis, we assume m is a power of two, and we define the fencepost value $LM[m+1] = n$.

Wide arrays

SMAWK speeds up the recursive algorithm even further using a second procedure to handle arrays with more columns than rows. This algorithm exploits additional information gained from a single comparison between two array entries on the same row. For any row index i and any two column indices $p < q$, we have the following:

- If $M[i,p] \le M[i,q]$, then for all $h \le i$, we have $M[h,p] \le M[h,q]$ and thus $LM[h] \ne q$.
- If $M[i,p] > M[i,q]$, then for all $j \ge i$, we have $M[j,p] > M[j,q]$ and thus $LM[h] \ne p$.

Call an array entry $M[i,j]$ ***dead*** if we have enough information to conclude that $LM[i] \ne j$. Then after we compare any two entries in the same row, either the left entry and everything below it is dead, or the right entry and everything above it is dead.



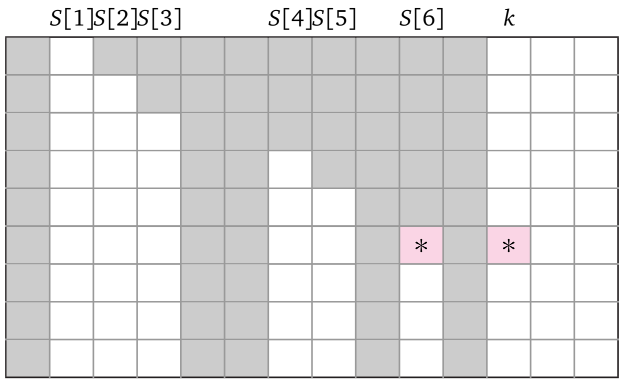
The following algorithm maintains a stack of column indices in an array $S[1..m]$ (yes, really m, the number of *rows*) and an index t indicating the number of indices on the stack.

```
REDUCE($M[1..m, 1..n]$):
  $t \leftarrow 1$
  $S[t] \leftarrow 1$
  for $k \leftarrow 1$ to $n$
      while $t > 0$ and $M[t, S[t]] \geq M[t, k]$
          $t \leftarrow t - 1$        ⟨⟨pop⟩⟩
      if $t < m$
          $t \leftarrow t + 1$
          $S[t] \leftarrow k$        ⟨⟨push k⟩⟩
  return $S[1..t]$
```

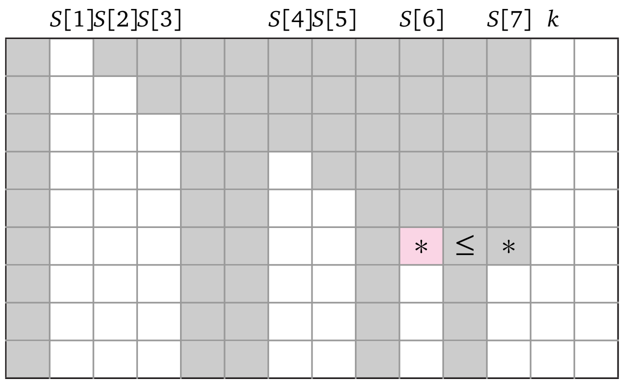
This algorithm maintains three important invariants:

- $S[1..t]$ is sorted in increasing order.
- For all $1 \leq j \leq t$, the top $j-1$ entires of column $S[j]$ are dead.
- If $j < k$ and j is not on the stack, then every entry in column j is dead.

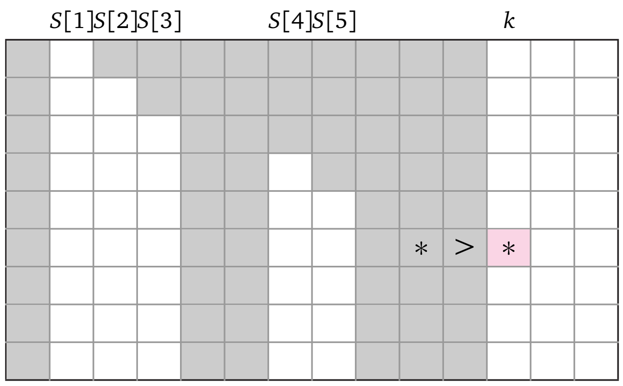
The first invariant follows immediately from the fact that indices are pushed onto the stack in increasing order. The second and third are more subtle, but both follow inductively from the total monotonicity of the array. The following figure shows a typical state of the algorithm when it is about to compare the entries $M[t, S[t]]$ and $M[t, k]$ (indicated by stars). Dead entries are indicated in gray.



If $M[t, S[t]] < M[t, k]$, then $M[t, k]$ and everything above it is dead, so we can safely push column k onto the stack (unless we already have $t = n$, in which case every entry in column k is dead) and then increment k.



On the other hand, if $M[t,S[t]] > M[t,k]$, then we know that $M[t,S[t]]$ and everything below it is dead. But by the inductive hypothesis, every entry above $M[t,S[t]]$ is already dead. Thus, the entire column $S[t]$ is dead, so we can safely pop it off the stack.



In both cases, all invariants are maintained.

Immediately after every comparison $M[t,S[t]] \geq M[t,k]$? in the REDUCE algorithm, we either increment the column index k or declare a column to be dead; each of these events can happen at most once per column. It follows that REDUCE performs at most $2n$ comparisons and thus runs in ***$O(n)$ time*** overall.

Moreover, when REDUCE ends, every column whose index is not on the stack is completely dead. Thus, to compute the leftmost minimum element in every row of M, it suffices to examine only the $t < m$ columns with indices in the output array $S[1..t]$.

Together

The main SMAWK algorithm first REDUCEs the input array (if it has fewer rows than columns), then recursively computes the leftmost row minima in the even-indexed rows, and finally fills in the rest of the row minima in $O(m+n)$ additional time. The argument of the recursive call is an array with exactly $m/2$ rows and at most $\min\{n,m\}$ columns, so the running time obeys the following recurrence:

$$T(m,n) \leq \begin{cases} O(m) + T(m/2,n) & \text{if } m \geq n, \\ O(n) + T(m/2,m) & \text{if } m < n. \end{cases}$$

The algorithm needs $O(n)$ time to REDUCE the input array to at most m rows, after which every recursive call reduces the (worst-case) number of rows and columns by a factor of two. We conclude that SMAWK runs in ***$O(m+n)$ time***.

Later variants of SMAWK can compute row minima in totally monotone arrays in $O(m+n)$ time even when the rows are revealed one by one, and we require the smallest element in each row before we are given the next. These later variants can be used to speed up many dynamic programming algorithms by a factor of n when the final memoization table is totally monotone.

6.6 Saving Time: Four Russians

Some day.

Exercises

1. Describe an algorithm to compute the edit distance between two strings $A[1..m]$ and $B[1...n]$ in $O(m \log m + n \log n + K^2)$ time, where K is the number of match points. *[Hint: Use the* FindMatches *algorithm on page 3 as a subroutine.]*

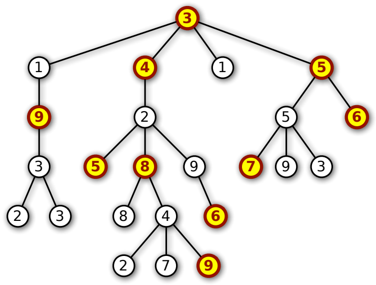
2. (a) Describe an algorithm to compute the *longest increasing subsequence* of a string $X[1..n]$ in $O(n \log n)$ time.

   (b) Using your solution to part (a) as a subroutine, describe an algorithm to compute the longest common subsequence of two strings $A[1..m]$ and $B[1...n]$ in $O(m \log m + n \log n + K \log K)$ time, where K is the number of match points.

3. Describe an algorithm to compute the edit distance between two strings $A[1..m]$ and $B[1...n]$ in $O(m \log m + n \log n + K \log K)$ time, where K is the number of match points. *[Hint: Combine your answers for problems 1 and 2(b).]*

4. Let T be an arbitrary rooted tree, where each vertex is labeled with a positive integer. A subset S of the nodes of T is *heap-ordered* if it satisfies two properties:

   - S contains a node that is an ancestor of every other node in S.
   - For any node v in S, the label of v is larger than the labels of any ancestor of v in S.



A heap-ordered subset of nodes in a tree.

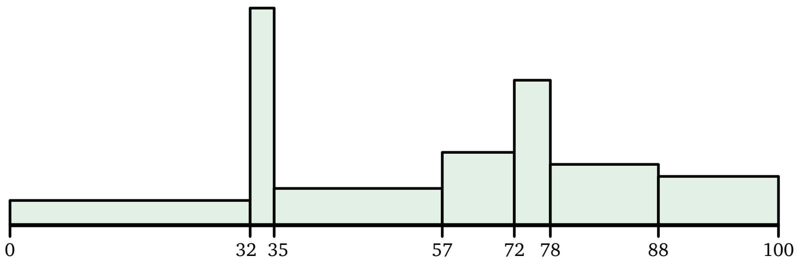
   (a) Describe an algorithm to find the largest heap-ordered subset S of nodes in T that has the heap property in $O(n^2)$ time.

   (b) Modify your algorithm from part (a) so that it runs in $O(n \log n)$ time when T is a linked list. *[Hint: This special case is equivalent to a problem you've seen before.]*

   ⋆(c) Describe an algorithm to find the largest subset S of nodes in T that has the heap property, in $O(n \log n)$ time. *[Hint: Find an algorithm to merge two sorted lists of lengths k and ℓ in $O(\log \binom{k+\ell}{k})$ time.]*

5. Suppose we want to summarize a large set S of values—for example, grade-point averages for every student who has ever attended UIUC—using a variable-width histogram. To construct a histogram, we choose a sorted sequence of ***breakpoints*** $b_0 < b_1 < \cdots < b_k$, such that every element of S lies between b_0 and b_k. Then for each interval $[b_{i-1}, b_i]$, the

histogram includes a rectangle whose height is the number of elements of S that lie inside that interval.



A variable-width histogram with seven bins.

Unlike a standard histogram, which requires the intervals to have equal width, we are free to choose the breakpoints arbitrarily. For statistical purposes, it is useful for the *areas* of the rectangles to be as close to equal as possible. To that end, define the ***cost*** of a histogram to be the sum of the *squares* of the rectangle areas; we seek a histogram with minimum cost.

More formally, suppose we fix a sequence of breakpoints $b_0 < b_1 < \cdots < b_k$. For each index i, let n_i denote the number of input values in the ith interval:

$$n_i := \#\left\{x \in S \;\middle|\; b_{i-1} \le x < b_i\right\}.$$

Then the ***cost*** of the resulting histogram is $\sum_{i=1}^{k}(n_i(b_i - b_{i-1}))^2$. We want to compute a histogram with minimum cost for the given set S, where every breakpoint b_i is equal to some value in S.[2] In particular, b_0 must be the minimum value in S, and b_k must be the maximum value in S.

Describe and analyze an algorithm to compute a variable-width histogram with minimum cost for a given set of data values. Given an array $S[1\,..\,n]$ of real numbers and an integer k, your algorithm should return a sorted array $B[0\,..\,k]$ of breakpoints that minimizes the cost of the resulting histogram.

[2]Thanks to the non-linear cost function, removing this assumption makes the problem *considerably* more difficult!