COMP 212 Spring 2022 Homework 05

This homework will focus on lists, trees, and work-span analysis. You must write purposes and tests for all functions on this assignment.

1 Trees

The type tree, with constructors Empty and Node(1,x,r) represents binary trees of integers with data stored only in the internal nodes. Here are some definitions about trees:

- The tree Empty has depth 0. The tree Node (1,x,r) has depth d if and only if
 - 1. 1 has depth d_l
 - 2. r has depth d_r
 - 3. $d = \max(d_l, d_r) + 1$.
- The tree Empty has size 0. The tree Node(1,x,r) has size s if and only if
 - 1. 1 has size s_l
 - 2. r has size s_r
 - 3. $s = s_l + s_r + 1$
- The tree Empty is balanced. The tree Node(1,x,r) is balanced if and only if
 - 1. 1 is balanced
 - 2. r is balanced
 - 3. 1 has depth d_l , r has depth d_r and $|d_l d_r| \leq 1$.
- The tree Empty is sorted. The tree Node(1,x,r) is sorted if and only if
 - 1. 1 is sorted
 - 2. r is sorted
 - 3. For every node Node(ll,xl,rl) in 1, xl < x
 - 4. For every node Node(lr,xr,rr) in $r, xr \ge x$

An expression e: tree is sorted iff it is equivalent to a value that is sorted.

These definitions are implemented in hw05-lib.sml, with a few other helper functions. Download this file and put it in the same folder as your hw05.sml file. You should feel free to write your tests in terms of these functions.

- depth : tree -> int computes the depth of its argument.
- size : tree -> int computes the size of its argument.
- isbalanced : tree -> bool evaluates to true if and only if its argument is balanced.
- issorted : tree -> bool evaluates to true if and only if its argument is sorted.
- tolist: tree -> int list computes a flattening of its argument into a list, as given in lab.
- from list: int list -> tree computes a balanced tree from a list—very useful for testing, but do **not** use it in any of your solutions, or they will not have the right span.
- treeeq : tree * tree -> bool tests whether two trees are equal

2 Contains

Task 2.1 (7 pts). Write a function contains: tree * int -> bool such that for any sorted tree t, contains(t,i) returns true if i is an element of t and returns false if not. For full credit, your solution should have $O(\log n)$ work and span when t is a balanced tree of size n.

The listToTree function from lab is called fromlist: int list -> tree in the homework code, and can be used to write tests.

3 Tree Induction

Recall the size and depth functions on trees:

```
(* size t computes the natural number which
  represents how many Nodes are in a tree *)
fun size (t : tree) : int =
    case t of
        Empty => 0
        | Node (l, x, r) => 1 + size l + size r

(* depth t computes the natural number which
  represents how many levels are in a tree *)
fun depth (t : tree) : int =
  case t of
    Empty => 0
        | Node (l, x , r) => 1 + max (depth l, depth r)
```

Task 3.1 (15 pts). Prove the following relationship:

Theorem 1. For all trees t, depth $t \leq size t$.

The function $\max(x, y)$ returns the maximum of x and y; i.e. if x is bigger it returns x and if y is bigger it returns y. You may want to use some of the following properties of \max :

- $x \le \max(x, y)$ and $y \le \max(x, y)$
- $\max(x, y) \le z$ if $x \le z$ and $y \le z$
- $\max(x, y) \le \max(x', y')$ if $x \le x'$ and $y \le y'$

4 QuickSort

In last week's homework, you implemented QUICKSORT on lists. As we've discussed in lecture, there is not a lot to be gained by using parallel sorting algorithms on lists: there are dependencies inherent in the structure of a list that get in the way of real parallelism.

In that spirit, you'll now implement QUICKSORT on trees. Assuming the pivots yield subproblems of equal size (which can be achieved using randomness), this algorithm will have $O(n \log n)$ work and $O((\log n)^3)$ span. The logarithmic span means significant speedups can be gained by running the algorithm in parallel.

We'll represent trees with the tree type defined at the beginning of this assignment. In specs, we will say that x is an element of a tree t when Node(...,x,...) appears somewhere in t.

4.1 Combine

First, we will need a function to combine two trees into one. Unlike merge from lecture, we will not require that the inputs are sorted, but we will also not ensure that the outputs are sorted, or that the outputs are in the same order as in the original trees. Because this function will be used prior to sorting, the elements can be in any order we choose. This means the following code suffices:

You may wish to draw **combine**'s output on some examples to understand how it works. More formally, this code meets the following specification:

- Functionality: For all trees T1 and T2, combine (T1,T2) is valuable, and contains every element of T1 and every element of T2 and no other elements.
- Depth: For the analysis of quicksort, we need the following bound on the depth of combine's result:

```
Lemma 1. For all values t1 t2: tree, depth (combine (t1, t2)) \leq 1 + max(depth t1, depth t2).
```

• Running-time: Let d_1 be the depth of T1, d_2 be the depth of T2. The work and span of (combine (T1,T2)) are both $O(d_1)$.

4.2 Filter

Task 4.1 (15 pts). Implement a tree analogue of filter_less and filter_greatereq:

```
filter_less : tree * int -> tree
filter_greatereq : tree * int -> tree
```

Your implementation must satisfy the following specs:

- Functionality: If T is a value of type tree, p is a value of type int, then:
 - filter_less(T,p) contains all and only the elements of T that are less than p.
 - filter_greatereq(T,p) contains all and only the elements of T that are greater than or equal to p.
- Depth: For all T:tree, p:int, depth (filter (T,p)) ≤ depth T.
- Running-time: If d is the depth of a tree T, your implementation of each (filter (T,p)) should have $O(d^2)$ span. On a balanced tree, your implementation of each filter should have O(n) work, where n is the size of the tree.

4.3 Quicksort

Task 4.2 (15 pts). Finally, put all the pieces together to write

```
quicksort_t: tree -> tree
```

which implements QUICKSORT values of type tree.

- Functionality: quicksort_t T is sorted and contains all and only the elements of T.
- Running-time: If T is a balanced tree with size n, (quicksort_t T) should have $O(n \log n)$ work and $O((\log n)^3)$ span, assuming the pivots yield balanced subproblems.

You may want to use the fromlist : int list -> tree and issorted functions to test your implementation of quicksort_t.

5 Balancing

To mergesort trees, we needed to *rebalance* a tree after manipulating it. Rebalancing takes a tree that is not necessarily balanced, and computes a balanced tree with the same elements.

We have provided most of an implementation of a simple rebalancing algorithm in the handout. The key helper function is unimplemented. You will implement this helper and then analyze the complexity of rebalance.

In all of the tasks, you should assume that the function size: tree -> int, which computes the size of a tree, runs in constant time on all inputs. This happens to be obviously false. However, it's easy to make binary trees whose size can be computed in constant time by storing the size at each node—so this is a relatively harmless lie.

Task 5.1 (15 pts). Implement the function

¹If you use the tree method to try to prove this, you will run into a sum that we have not yet seen in the course; see the next problem for its big-O.

```
takeanddrop : tree * int -> tree * tree
```

takeanddrop(T,i) separates a tree T into "left" and "right" subtrees, T1 and T2 respectively. T1 contains the leftmost i elements of T, in their original order, and T2 the remaining elements, also in their original order. For example, if we define

then we have

```
takeanddrop (test,3) ==
  (Node (Node (Empty,1,Empty),2,Node (Empty,3,Empty)),
  Node (Empty,4,Node (Node (Empty,5,Empty),6,Empty)))
```

More formally, suppose T is any tree, and $0 \le i \le size$ T. Then takeanddrop (T,i) evaluates to a pair of trees (T1,T2) such that

- max(depth T1, depth T2) ≤ depth T
- \bullet size T1 \cong i
- (tolist T1) @ (tolist T2) \cong (tolist T)

This last condition ensures that T1 contains the leftmost elements, and that the elements of T1 and T2 are in the appropriate order.

If d is the depth of T then your implementation of (takeanddrop (T,i) must have O(d) work and span.

Hint: use the **splitAt** function from mergesorting trees as a model; the difference is that instead of splitting based on the values stored in the tree, here we are splitting based on the number of elements in the tree.

Task 5.2 (18 pts). Your implementation of takeanddrop is necessary for the helper function halves, which is used by rebalance; see the starter code. The following tasks ask you to analyze these functions:

- 1. Give a recurrence that describes the work of your implementation of takeanddrop, $W_{\mathsf{takeanddrop}}(d)$, in terms of the **depth** d of the input tree. Argue that $W_{\mathsf{takeanddrop}}(d)$ is O(d).
- 2. Give a recurrence that describes the span of your implementation takeanddrop, $S_{\text{takeanddrop}}(d)$, in terms of the **depth** d of the input tree. Argue that $S_{\text{takeanddrop}}(d)$ is O(d)

Note: the remaining tasks will be graded assuming that $W_{\sf takeanddrop}(d)$ and $S_{\sf takeanddrop}(d)$ are O(d), even if that is not true for your code, or if your recurrence above is incorrect.

- 3. Give a recurrence that describes the work of halves, $W_{\text{halves}}(d)$, in terms of the depth of the input tree. Give a tight big-O bound for $W_{\text{halves}}(d)$.
- 4. Give a recurrence that describes the span of halves, $S_{\text{halves}}(d)$, in terms of the depth of the input tree. Give a tight big-O bound for $S_{\text{halves}}(d)$.
- 5. Give a recurrence that describes the work of rebalance, $W_{\text{rebalance}}(n)$, in terms of the size n of the input tree. You should assume that the input is roughly balanced—that is to say, there exists some constant c such that the depth of the input is $c \log n$. This will be true when rebalance is called from mergesort, because the merging will only have unbalanced the tree by a known amount.

Give a closed form and a tight big-O bound for $W_{rebalance}(n)$.

6. Give a recurrence that describes the span of rebalance, $S_{\text{rebalance}}(n)$, in terms of the size of the input tree. You should assume that the input is roughly balanced—that is to say, there exists some constant c such that the depth of the input is $c \log n$. This will be true when rebalance is called from mergesort, because the merging will only have unbalanced the tree by a known amount.

Give a closed form and a tight big-O bound for $S_{rebalance}(n)$.

The recurrences for the later tasks should be defined in terms of the recurrences defined in the earlier tasks for the helper functions.

You may use the following tight bounds:

$$\log n + \log \frac{n}{2} + \log \frac{n}{4} + \log \frac{n}{8} + \ldots + 1 \quad \text{is} \quad O(\log n)^2)$$
$$\log n + 2\log \frac{n}{2} + 4\log \frac{n}{4} + 8\log \frac{n}{8} + \ldots \text{ (with log } n \text{ terms)} \quad \text{is} \quad O(n)$$

6 NON-COLLABORATIVE CHALLENGE PROBLEM: Transcription Errors

Remember that non-collaborative challenge problems are to be done independently. You are not allowed to communicate with anyone about the problems, except to ask the instructor or TAs clarification questions (not hints). Additionally, you are not allowed to search for help on the specific problem from any sources besides the course materials. You are free to ask clarification questions about the concepts involved.

DNA strings are sequences of four bases, written A,T,C,G. We can represent a DNA string as a list of strings, e.g. AGGCT as the list

Many tasks in computational biology involve modeling the replication of DNA, i.e. copying a DNA string to a new one. Ideally, the replication would produce a perfect copy of the original, but sometimes errors are introduced.

In this problem, your goal is to write a function that takes two DNA strings and counts how many errors were introduced while copying the first to the second. For simplicity, we assume that the only possible errors are adding and dropping a base. Since many different sequences of errors can produce the same string, this function should (optimistically) report the fewest number of errors that could possibly have occurred while transcribing the first string to the second.

For example:

string 1	string 2	fewest errors
ATCG	ACG	1
ATCC	ATCGC	1
ATCC	ACG	3
GATC	GGATC	1

- For the first example, the fewest errors that could turn ATCG into ACG is 1 (delete the T). The first string could be turned into the second in other ways with more errors e.g. delete the T, delete the C, and then add a C would be 3 errors. But we will assume that these detours don't happen and count the fewest errors.
- For the second example, the fewest errors that could turn ATCC into ATCGC is 1 (add the G).
- For the third, the fewest errors that could turn ATCC into ACG is 3 (delete the T, delete one of the C's, and add the G).
- For the fourth, the fewest errors that could turn GATC into GGATC is 1 (delete one of the G's).

Task 6.1 (10 pts). Write a function errors that, when given two DNA strings reports the fewest errors that could turn the first string into the second.

Task 6.2 (6 pts). Analyze the work and span of your errors function.