These must be completed and shown to your TA either by the end of this lab, or at the start of your next lab. You may work in groups of up to two people.

1. Start an SSH session on one of the department servers.

2. Download the modified version of the AVL tree code you have already used (along with associated files) from the course web page under this lab's entry or, better yet, just copy all the lab files from: `/home/c/cs221/public_html/current/handouts/labs/lab9/`.

3. Complete the function `findMaxHelper`, which is called by `findMax` in order to find the maximum element in the tree using divide-and-conquer fork/join style parallelism.

   Your solution should fork off tasks to handle subtrees until you can guarantee by looking at the root node of a subtree that it has at most 1100 nodes, at which point it should switch to the provided sequential version instead. Be prepared to briefly justify your cutoff to your lab TA.

   If you can't get the code to speedup try modifying REPS at the head of the file.

   Hint: findMaxHelper is essentially a modification of findMaxSequential, so you may find it useful to start by copying that code.

4. Time your solution on that machine using the two sample text files in:

   `/home/c/cs221/public_html/current/handouts/labs/lab9/parallel-lab-resources`

   (We provide the King James Bible because it's a *big* file available from Project Gutenberg and one tiny piece of Google's ngram corpus from its scanned collection of texts, because it's *bigger*.) Note that you do *not* need to copy these files! Just pass the path to one of the files as the command line argument to your `avl` program. What is the most common word in these files?

5. For each sample file that we provide, find a cutoff for which the sequential algorithm performs better (in terms of runtime) than the parallel verion, and vice-versa. (Work with the Bible first, as it's a much more manageable size. Then, spend a few minutes getting the data points you need for the Google ngrams file.)

6. Be sure to show your work to your TA, or you will not receive credit for the lab!