

CSCI 335 – Spring 2021

Homework #3

C++ programming assignment (100 points)

Due March 12, 11:00pm

This is an individual assignment

1. Please follow the Blackboard instructions on writing and submitting programming assignments. The functions you provide should compile and run to receive any credit.
2. Read and follow the contents Programming Rules document on Blackboard ('Course Information' Section). Design and documentation is worth 25 points.
3. Read the assignment description below.
4. Submit **only** the files requested in the deliverables at the end of this document to Gradescope by the deadline.

Learning Outcome: The goal of this assignment is to become familiar with lists and trees and compare the performance of the self-balancing AVL tree. You will also work with a real-world data set and construct a generic test routine for comparing several different implementations of the tree container class. You are encouraged to use the book's implementation for AVL trees. Acknowledge the sources you use in the README.AVL file.

AVL Trees

Files provided: avl_tree.h, query_tree.cc, test_tree.cc, test_tree_mod.cc, dsexceptions.h, a README.txt, a Makefile and more text (.txt) files. The output should look exactly as described below to obtain the full grade (consider this part of an exact API specification).

Part 1 (15 points)

First, create a class object named SequenceMap that has as private data members the following two:

```
string recognition_sequence_ ;  
vector<string> enzyme_acronyms_;
```

Other than the big-five (note that you can use the defaults for all of them), you have to add the following:

- a) A constructor SequenceMap(const string &a_rec_seq, const string &an_enz_acro), that constructs a SequenceMap from two strings (note that after the constructor is called the vector enzyme_acronyms_ will contain just one element, the an_enz_acro).
- b) bool operator<(const SequenceMap &rhs) const, that operates based on the regular string comparison between the recognition_sequence_ strings (this will be a one line function).

- c) Overload the << operator in order to print out the enzyme_acronyms vector, for a given recognition sequence. Refer to assignment 1 for example of overloading the operator signature.
- d) void Merge(const SequenceMap &other_sequence). This function assumes that the object's recognition_sequence_ and other_sequence.recognition_sequence_ are equal to each other. The function Merge() merges the other_sequence.enzyme_acronym_ with the object's enzyme_acronym_. The other_sequence object will not be affected.

This class (which is non-templated) will be used in the following programs. First test it with your own test functions to make sure that it operates correctly.

Part 2

Introduction to the problem

For this assignment you will receive as input two text files, rebase210.txt and sequences.txt. After the header, each line of the database file rebase210.txt contains the name of a restriction enzyme and possible DNA sites the enzyme may cut (cut location is indicated by a ') in the following format:

enzyme_acronym/recognition_sequence/.../recognition_sequence//

For instance the first few lines of rebase210.txt are:

```
AanI/TTA'TAA//
AarI/CACCTGCNNNN'NNNN/'NNNNNNNNGCAGGTG//
AasI/GACNNNN'NNGTC//
AatII/GACGT'C//
AbsI/CC'TCGAGG//
AccI/GT'MKAC//
AccII/CG'CG//
AccIII/T'CCGGA//
Acc16I/TGC'GCA//
Acc36I/ACCTGCNNNN'NNNN/'NNNNNNNNGCAGGT//
...
```

That means that each line contains one enzyme acronym associated with one or more recognition sequences. For example on line 2:

The enzyme acronym `AarI` corresponds to the two recognition sequences `CACCTGCNNNN'NNNN` and `'NNNNNNNNGCAGGTG`.

Part 2.1 (25 points)

You will create a parser to read in this database and construct an AVL tree. For each line of the database and for each recognition sequence in that line, you will create a new `SequenceMap` object that contains the recognition sequence as its `recognition_sequence_` and the enzyme acronym as the only string of its `enzyme_acronyms_` and you will insert this object into the tree. This is explained with the following **pseudo code**:

```
Tree<SequenceMap> a_tree;
string db_line;
// Read the file line-by-line:
```

```

while (GetNextLineFromDatabaseFile(db_line)) {
    // Get the first part of the line:
    string an_enz_acro = GetEnzymeAcronym(db_line);
    string a_reco_seq;
    while (GetNextRecognitionSequence(db_line, a_rego_seq){
        SequenceMap new_sequence_map(a_reco_seq, an_enz_acro);
        a_tree.insert(new_sequence_map);
    } // End second while.
} // End first while.

```

In the case that the `new_sequence_map.recognition_sequence_` equals the `recognition_sequence_` of a node X in the tree, then the search tree's `insert()` function will call the `X.Merge(new_sequence_map)` function of the existing element. This will have the effect of updating the `enzyme_acronym_` of X. Note, that this will be part of the functionality of the `insert()` function. The `Merge()` will only be called in case of duplicates as described above. Otherwise, no `Merge()` is required and the `new_sequence_map` will be inserted into the tree.

To implement the above, write a test program named **query_tree** which will use your parser to create a search tree and then allow the user to query it using a recognition sequence. If that sequence exists in the tree then this routine should print all the corresponding enzymes that correspond to that recognition sequence.

Your programs should run from the terminal as follows:

```
% ./query_tree <database file name>
```

For example you can write on the terminal:

```
% ./query_tree rebase210.txt
```

The user should enter THREE strings (supposed to be recognition sequences) for instance:

```

CC'TCGAGG
TTA'TAA
TC'C

```

Your program should print in the standard output their associated enzyme acronyms. In the above example the output will be

```

AbsI
AanI PsiI
Not Found

```

We will test it with a file containing three strings and run your code like that:

```
% ./query_tree rebase210.txt < input_part2.1.txt
```

Part 2.2 (20 points)

Next, create a test routine named **test_tree** that does the following in the sequence described below:

1. Parses the database and construct a search tree (this is the same as in Part 2.1).
2. Prints the number of nodes in your tree n .
3. Computes the average depth of your search tree, i.e. the internal path length divided by n .
 - a. Prints the average depth.
 - b. Prints the ratio of the average depth to $\log_2 n$. E.g., if average depth is 6.9 and $\log_2 n = 5.0$, then you should print $\frac{6.9}{5.0} = 1.38$.
4. Searches (find()) the tree for each string in the sequences.txt file and counts the total number of recursive calls for all executions of find().
 - a. Prints the total number of successful queries (number of strings found).
 - b. Prints the average number of recursion calls, i.e. #total number of recursion calls / number of queries.
5. Removes every other sequence in sequences.txt from the tree and counts the total number of recursion calls for all executions of remove().
 - a. Prints the total number successful removes.
 - b. Prints the average number of recursion calls, i.e. #total number of recursion calls / number of remove calls.
6. Redo steps 2 and 3:
 - a. Prints number of nodes in your tree.
 - b. Prints the average depth.
 - c. Prints the ratio of the average depth to $\log_2 n$.

The output of Part 2.2 should be of the exact form:

```
2: <integer>
3a: <float>
3b: <float>
4a: <integer>
4b: <float>
5a: <integer>
5b: <float>
6a: <integer>
6b: <float>
6c: <float>
```

If you didn't complete a step, just print after the step number: Not Done

Your program should run from the terminal as follows:

```
% ./test_tree <database file name> <query file name>
```

For example you can write on terminal

```
% ./test_tree rebase210.txt sequences.txt
```

Part 2.3 (15 points)

You will use the `avl_tree.h` code you have written for Part 2.2 and you will modify it in order to implement double rotations directly instead of calling the two single rotations. Name your modified implementation `avl_tree_mod.h`. Run the exact same routines as in Part 2.2, but now with your modified AVL implementation. The executable should be named `test_tree_mod`. The results should be the same as in Part 2.2.

For example you can write on terminal

```
% ./test_tree_mod rebase210.txt sequences.txt
```

You will be given a mandatory Makefile, along with some code to start (start of main functions)
`query_tree.cc test_tree.cc test_tree_mod.cc`

Gradescope Deliverables: You should only submit these files:

- `README.AVL` file
- **Part 1:**
`sequence_map.h`: Your original `sequence_map.h` will be reused for all further sections.
- **Part 2.1: (Modify `avl_tree` code by adding functions)**
`query_tree.cc`
`avl_tree.h`
- **Part 2.2:**
`test_tree.cc`
`avl_tree.h`
- **Part 2.3:**
`test_tree_mod.cc`
`avl_tree_mod.h`