

Report for Assignment # 2

CS 5500

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Status

The current status of the assignment is as follows:

- Genomes have been defined in terms of unsigned character strings (`unsigned char*`).
- Facilities for generating random genomes of a given size exist (`generate_random_gene`).
- A serial version of the mutation scoring algorithm has been implemented (`serial_mutation_score`).
- A parallelized version of the above algorithm has been implemented using SIMD instructions (`serial_mutation_score`).
- A `Node` type has been defined for the construction of phylogenetic trees.
- The implementation of a library for working with phylogenetic trees is partially completed.
- The current version of the code compiles, running the code demonstrates the serial and parallel scoring algorithms on pair of random genomes (execute `bin/collateral-monk`).

Plan

The project could be completed with the following steps:

- Complete the implementation of the phylogenetic tree library. This includes writing a tree destructor and finishing the algorithm used to build a phylogenetic tree, followed by refactoring and debugging.
- Complete the algorithm used to pick a near-optimum phylogenetic tree. The algorithm currently planned is brute force in nature.
- Write top-level code to demonstrate the phylogenetic tree and for the purpose of timing the mutation scoring algorithms.
- General refactoring and commenting over the whole codebase.

Conclusion

It should be possible to complete this assignment in a way that exceeds expectations with probability %95 by Sunday, and with certainty by Monday.