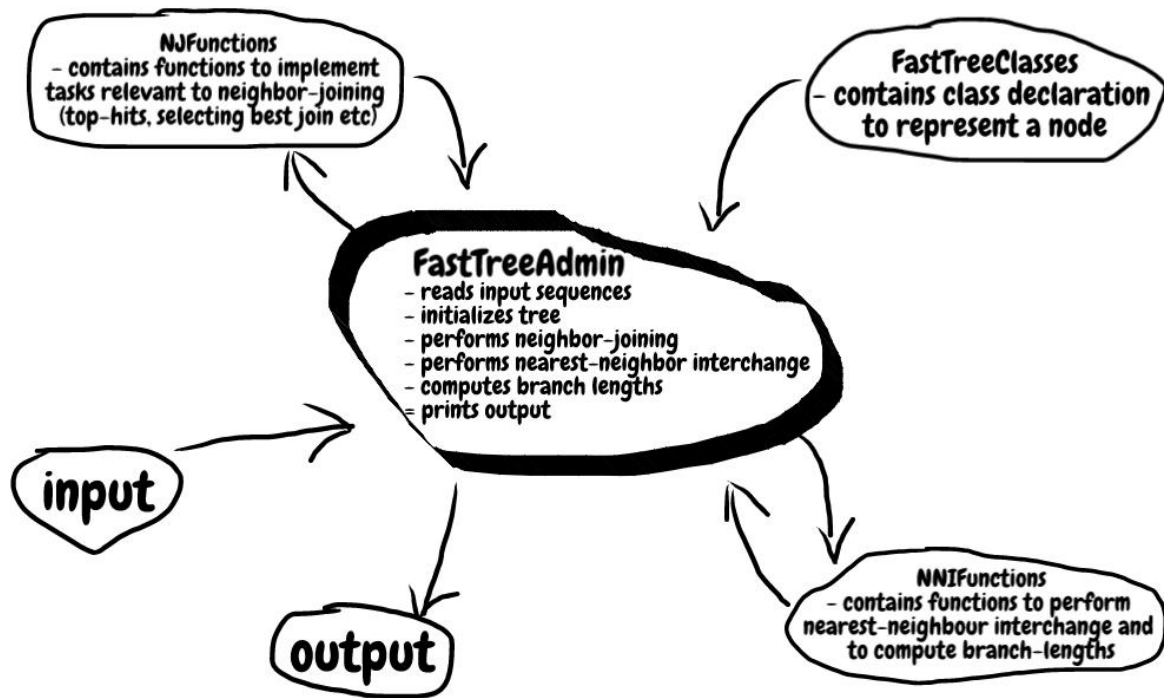


FastTree Implementation Overview

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Hello! This document contains an overview of the way this fasttree implementation works and instructions to run this on python.



There are 4 python files in this package – FastTreeAdmin, NJFunctions, NNIFunctions, and FastTreeClasses. General role of each file is displayed in the figure above. For more details, please refer to the documentation in the files themselves.

Instructions to run this implementation:

- Unzip the FastTree.zip file in the folder *"folder_location/folder_name"*
- Save the input sequences file (.txt format) in the above folder. Format for the input file should be the same as *"TestSequences.txt"* file present in the same folder. This format is essentially the same format as present on the github page for test sequences.
- Import the contents of this folder as a python project in an IDE.
- Open FastTreeAdmin.py from the project files.
- Change the name of input file in the line: *'mainFile: TextIO = open("TestSequences.txt")'*
- Run FastTreeAdmin.py, the results will be printed in the terminal

Note: I did not dedicate enough time to figure out how the Newick format works. As a result, I am printing the final tree in a simple format indicating a node, its children, distance (branch-length) from children, its parent, and distance (branch-length) from parent. I apologise in advance if this causes any inconvenience in evaluating my results against a standard.