BUILD:
Compilation requires all four files:
main.cpp, suffixTree.cpp, includes.h, genomics.cpp
Everything is included in main, so it should be the only thing you have to compile.

RUN:
Running
>Project2 in.fasta alphabet.txt
Will output the BWT index to outfile.txt and the DFST to DFST.clock().out.txt for input strings under 100000 characters. You can set the global variable FORCEPRINT(found in main) to 1 to force it to output regardless of input size.
It will also print information to the terminal including construction time and other stats of the tree.