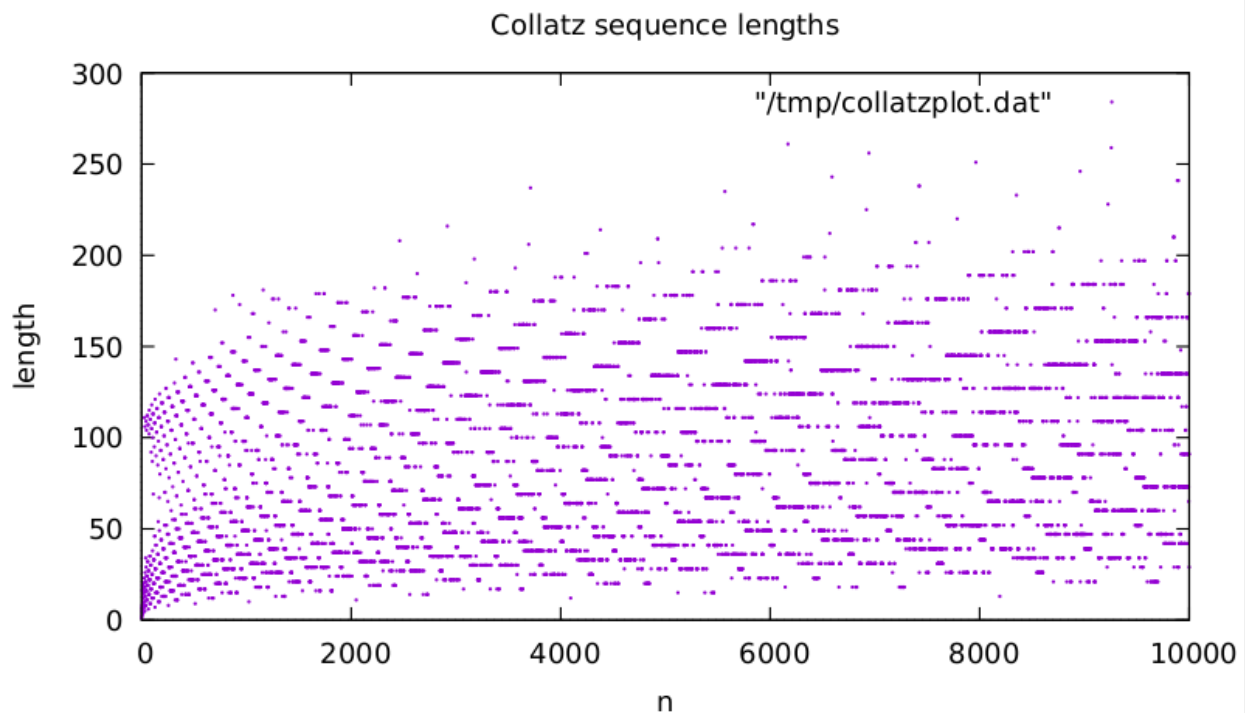


WRITEUP

The creation of each of these graphs will be explained below.

1. Collatz Sequence Lengths

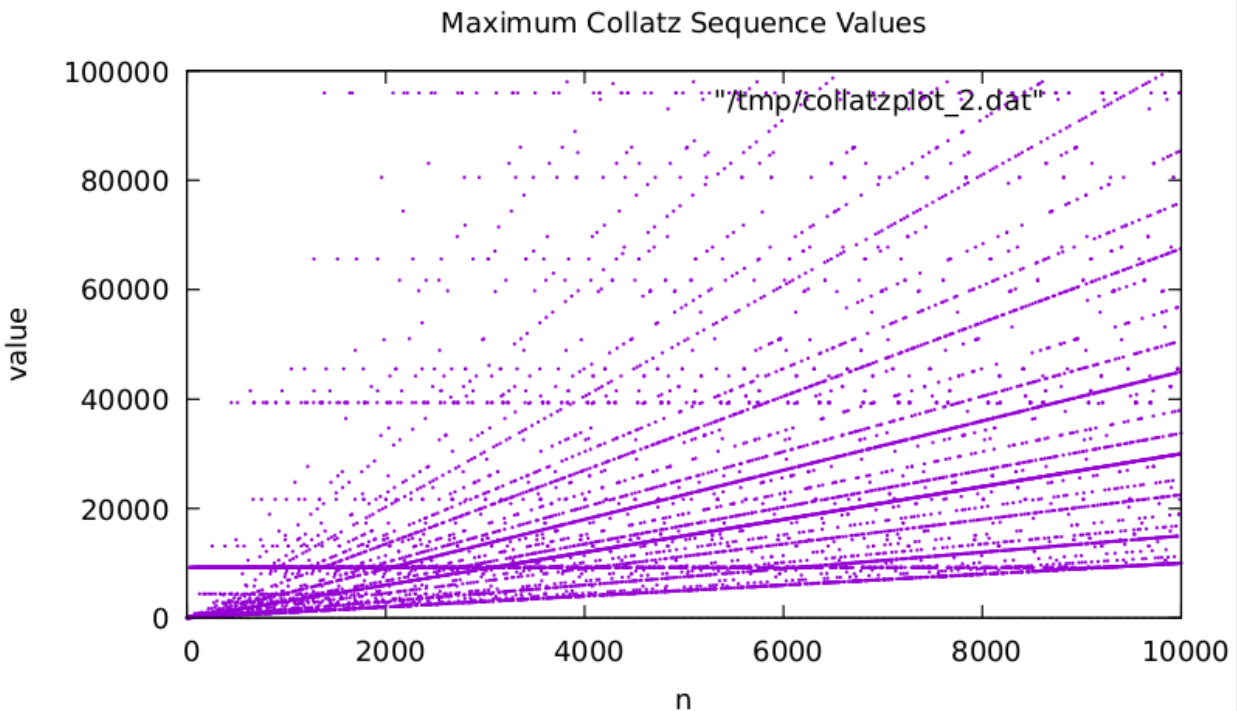


Collatz Sequence Lengths (Graph 1)

- A. I will list the commands used to create the graph as seen above.
- "wc -l": This command is used to count the number of lines in the collatz.dat file each time it is executed. The -l in the command is the option to specifically count the number of new lines. The number of lines, each time the collatz.c program is executed and sequence of numbers that are put in the file, represents the length of the sequence. Let's say we run collatz.c for 2 and output everything to a file. We want to get down to the number 1. Since 2 is an even number, divide it by 2, and 1 is the result. Therefore 2 and 1 are printed on the file, separated by a newline. Note that for each iteration, the file is overwritten by another sequence of numbers for the next iterator.

- b. “echo”: The “echo” command is used for standard output of the command. The modifier “>>” is used to redirect the output. This command is used to input all the plotting data into a .dat file.

2. Maximum Collatz Sequence Values

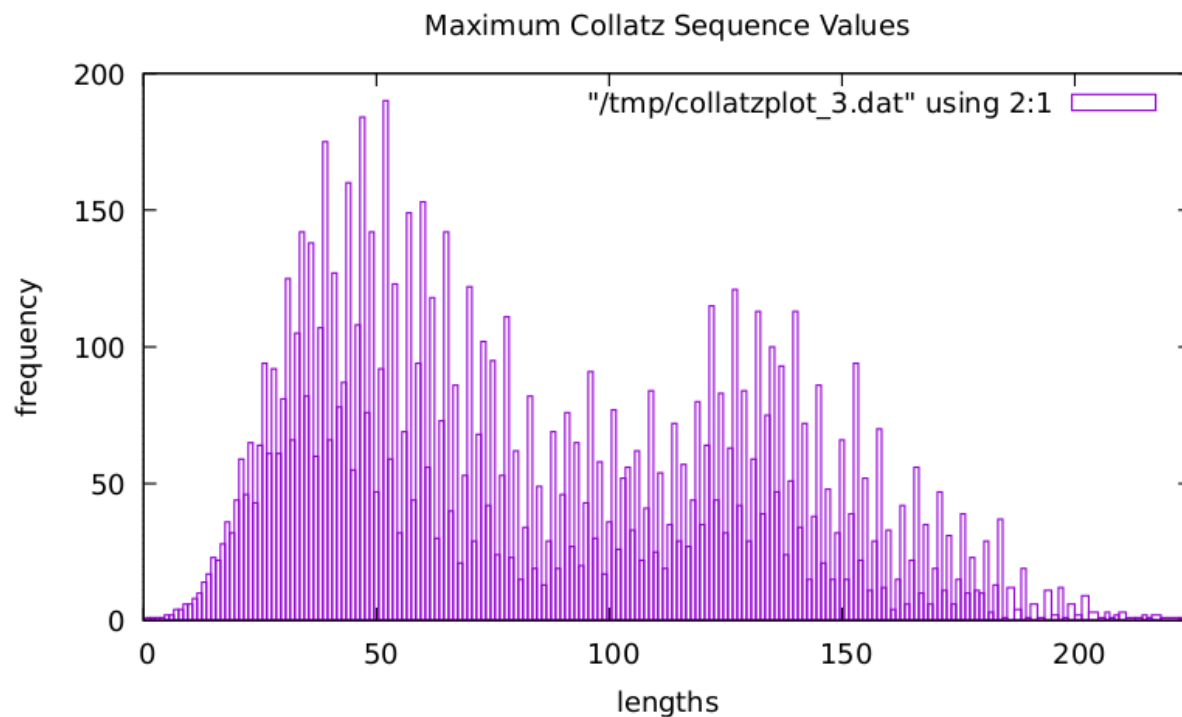


Maximum Collatz Sequence Value (Graph 2)

- A. I will list the commands used to produce graph 2.
- a. “sort -n -r -o”: This command is used to sort the collatz sequences generated by each number (iterator) by line. The option “-n” means to sort the file by numerical value. The second option “-r” means to reverse the sort. By default, the file will be sorted from least to greatest, but I wanted the file to be sorted from greatest to least. The third option -o means to output the command of the sort command into a file instead of outputting it to the command line (standard output).
 - b. “head -n 1”: This command is used to read the lines from a file. Because I have already used a sort command to sort the collatz sequences from greatest to least, I would only have to read the top line of the file to get the maximum value out of a collatz sequence. The number modifier after the -n modifier tells bash the numbers of lines to read from a file. In this case, I wanted to read only 1 line, so I put the “1” modifier.

- c. “echo”: This command is used to input all the plotting data into a .dat file.

3. Collatz Sequence Length Frequencies



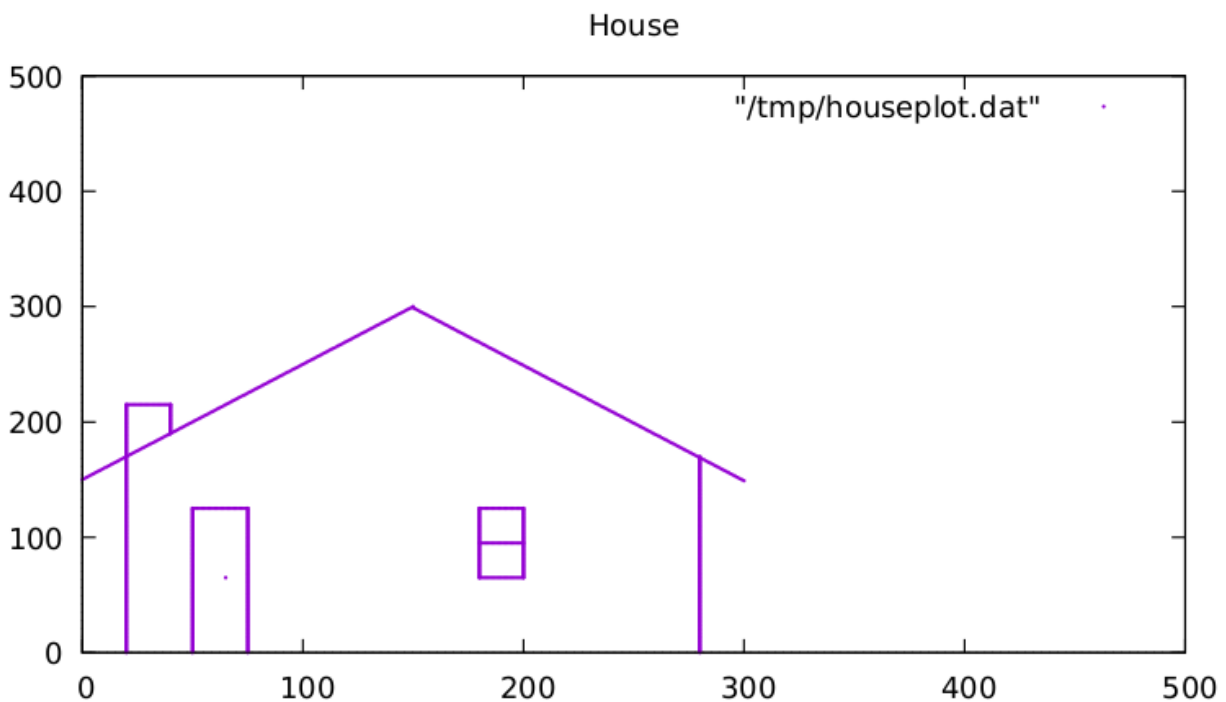
Collatz Sequence Length Frequencies

- A. I will list the commands that are used to produce graph 2.
- a. “echo”: There are two instances where this command is used.
 - i. “echo \$count >>”: Note that the count variable, as used in the “wc” command, will put all sequence lengths obtained into a file. The “echo” command is used for standard output of the command. The modifier “>>” is used to redirect the output.
 - ii. “echo \$count >>”: Note that the count variable, as used in the “wc” command, will put all sequence lengths obtained into a file. The “echo” command is used for standard output of the command. The modifier “>>” is used to redirect the output.
 - b. “sort -n -o”: This command is used to sort the collatz sequence lengths generated by each number (iterator) by line. The option “-n” means to sort the file by numerical value. The “-o” modifier is used to redirect the output

instead of using the standard output. I redirected the output to the same file, so the file itself has been sorted numerically.

- c. “Uniq -c”: This command is used to filter the number of duplicate occurrences in a file. Specifically this command is used to do that and also print the number of occurrences of each number next to each number that appears a certain number of times in a file as with the “-c” modifier. This command will not work properly unless the file has been sorted first.

4. House



House (Graph 4)

- A. I will list the commands that are used to produce graph 4
 - a. “echo”: The “echo” command is used for standard output of the command. The modifier “>>” is used to redirect the output. This command is used to put all data into a .dat file to plot the house.