Write a Perl/Python script to:

1. Recursively find all FASTA files in a directory and report each file name and the number of sequences in that file that are greater than 300 bp long to an output file.

2. For each FASTA file, report the 10 longest and the 10 shortest sequences (with sequence headers) to an output file.

3. For each FASTA file, report the GC% and N50 size to an output file.

NOTE:
       - Sample input files have been provided.
       - Please make sure the script can run on the command line.
       - In the spirit of assessing your programming abilities, please avoid using 3rd-party tools (e.g. bioPerl/bioPython) to solve the problem, but Linux/Unix commands are fine.