

1. Download CheckGene zip from <https://github.com/xieyuxi1107/CheckGene>
2. Unzip CheckGene-master and put the folder that contains the CSV files into CheckGene-master folder
3. Open the command prompt and navigate to the CheckGene-master folder
for example: (for windows)
`cd Downloads/CheckGene-master`
4. Compile findRecur.cpp with command (for windows)
`g++ -o findRecur findRecur.cpp`
* Only need to compile the first time the code is downloaded or when code is changed locally
5. Execute project with command (for windows)
`findRecur.exe`
6. When the project is running; it will prompt user inputs:
Please enter csv files folder path: //enter the name of the folder that contains the csv files, for example: `CSVfiles`
Please enter number of csv files in folder:
Look at ___ number of most frequently occurred genes:
7. The output of the program will be saved in output.txt in the CheckGene-master folder