

# User manual

## Run the Program

To download and run this program, firstly, you have to be equipped with a computer in Linux system. Then go to the github link <https://github.com/yipang/sysc5709-project> to clone or download to local repository. Then open the terminal to run this program.

1. Use command “cd” to the folder that you save the repository.
2. Use “make” command to compile
  - a. Type in “make project” if the user wants to compile only the project.
  - b. Type in “make tests” if the user wants to compile the tests.
  - c. Type in “make all” if the user wants to compile both the program and tests.
3. If the user has done a. and c. in step 2, then he/she can type in “./bin/project” to start the program. If the use has done b. and c. in step 2, then he/she can type in “./bin/tests” to run the tests.
4. If the user runs the tests, then he/she will be able to find a log file stored in test/data, which records all the test results. (we only have successful tests, so we include all the test results)
5. If the user runs the program, he/she will start by select a way to input the data. If the user chooses 1, he/she can simply type the inputs. If the user chooses 2, then he/she needs to type the filename he/she wants to use. There is a file stored in ./data called data1, or the user can have their own input file if they can create it and put it in the same directory as data1 as the path has set in the main function. There are restrictions of inputs for both method, the length of two sequences cannot be more than 10, and they can only contain letters “G”, “U”, “A”, “C”, the rest of three inputs match\_score, mismatch\_score and gap\_penalty accept both integer and float type, but a float type input will be automatically converted to integer type. After inputs collection, the program will provide six options for user to choose:
  - a. If choose 1, the program will call matrix\_builder function to modify a matrix based on Needleman-Wunsch Algorithm, then output the matrix.
  - b. If choose 2, the program will call get\_align function to output optimal alignment of two RNA sequences along with number of matches, gaps and alignment length.
  - c. If choose 3, the program will save all the information above to a text file. The filename should be input by the user.
  - d. If choose 4, the program will be back to step 1.
  - e. If choose 5, the program will read the next inputs from file. If it reaches the end of the file, the program will output an error message ask user to re-choose.
  - f. If choose 6, the program will exit.
  - g. If else, the program will output an error message and asks user to make a new decision.
6. The program will provides the above options repeatedly until the option 6 is chosen by the user.