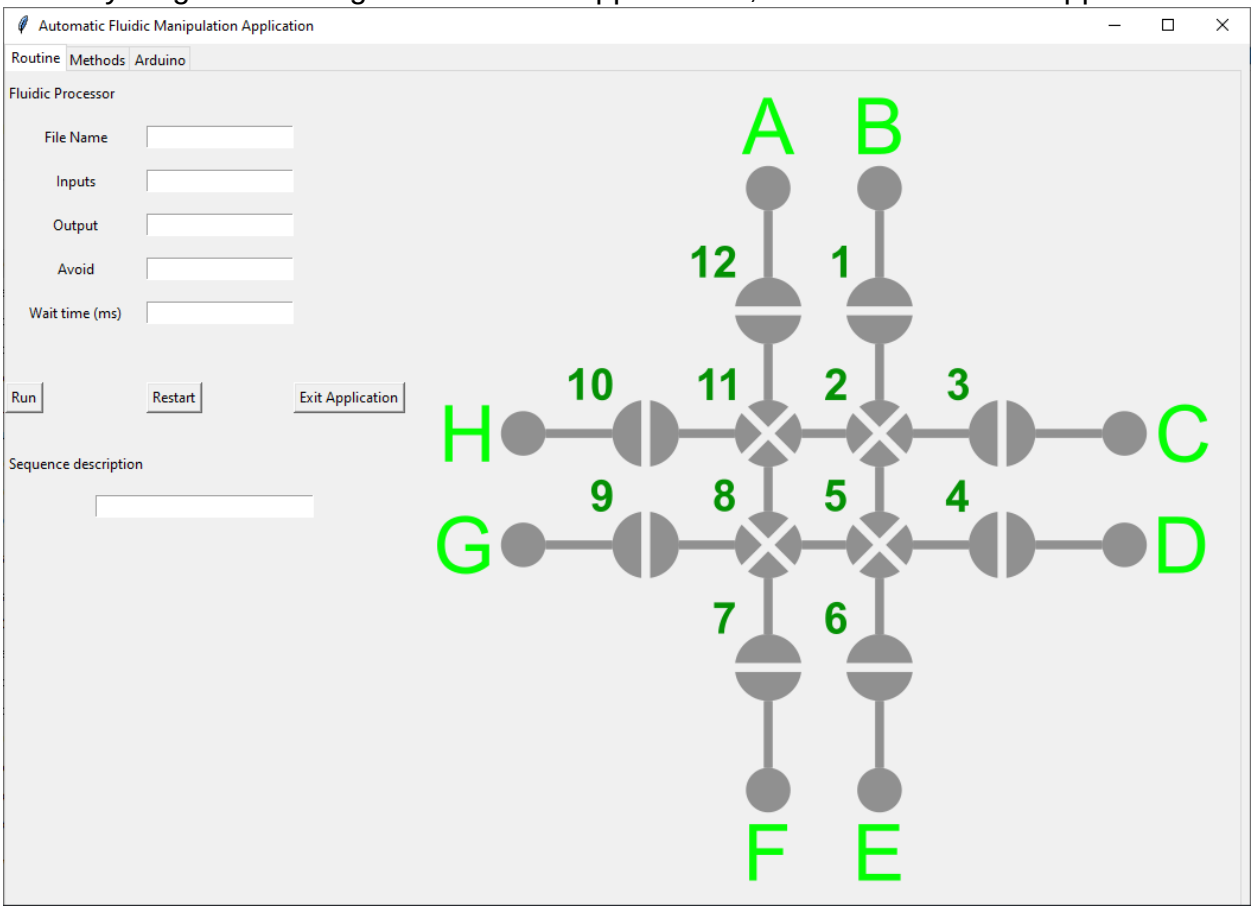
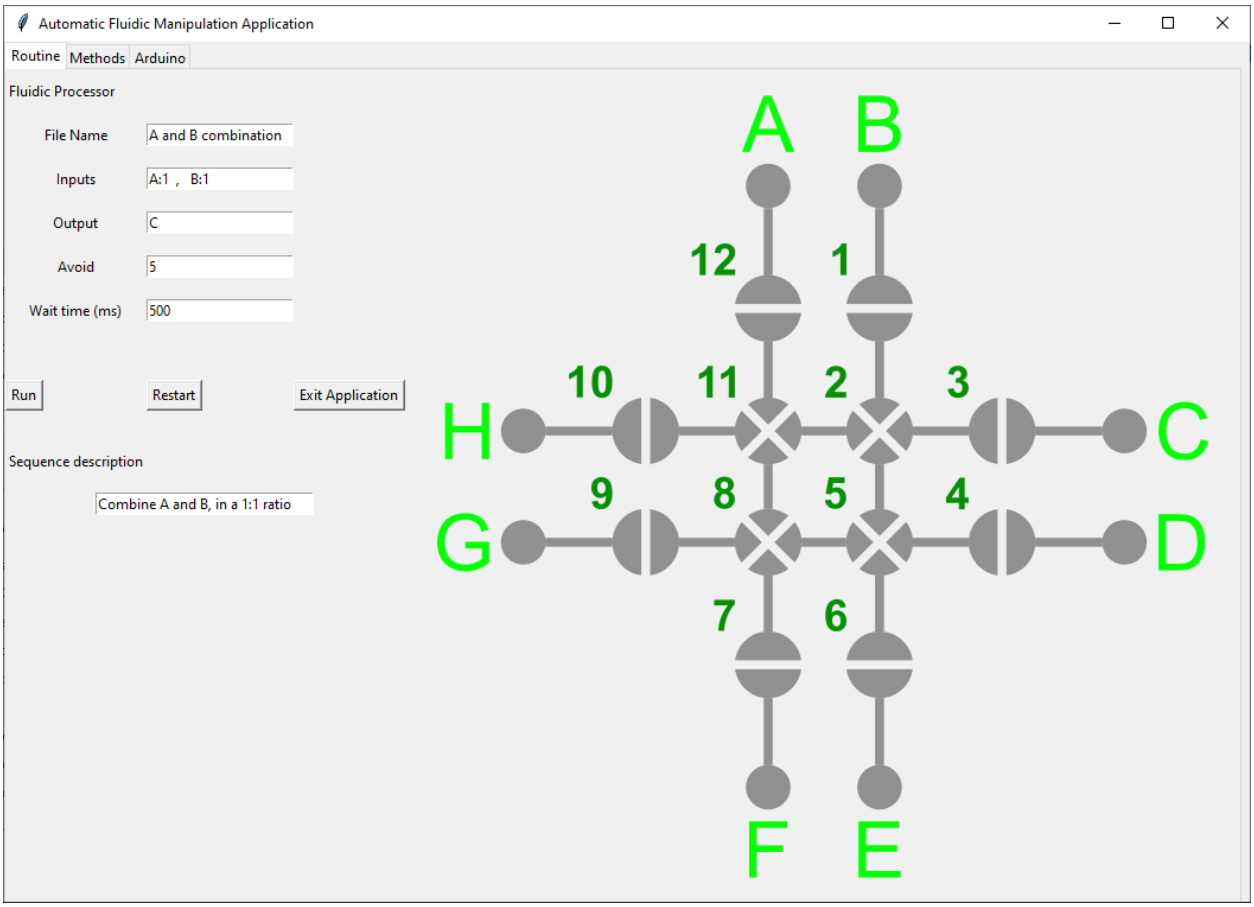
How to use the Fluidic Manipulation Application

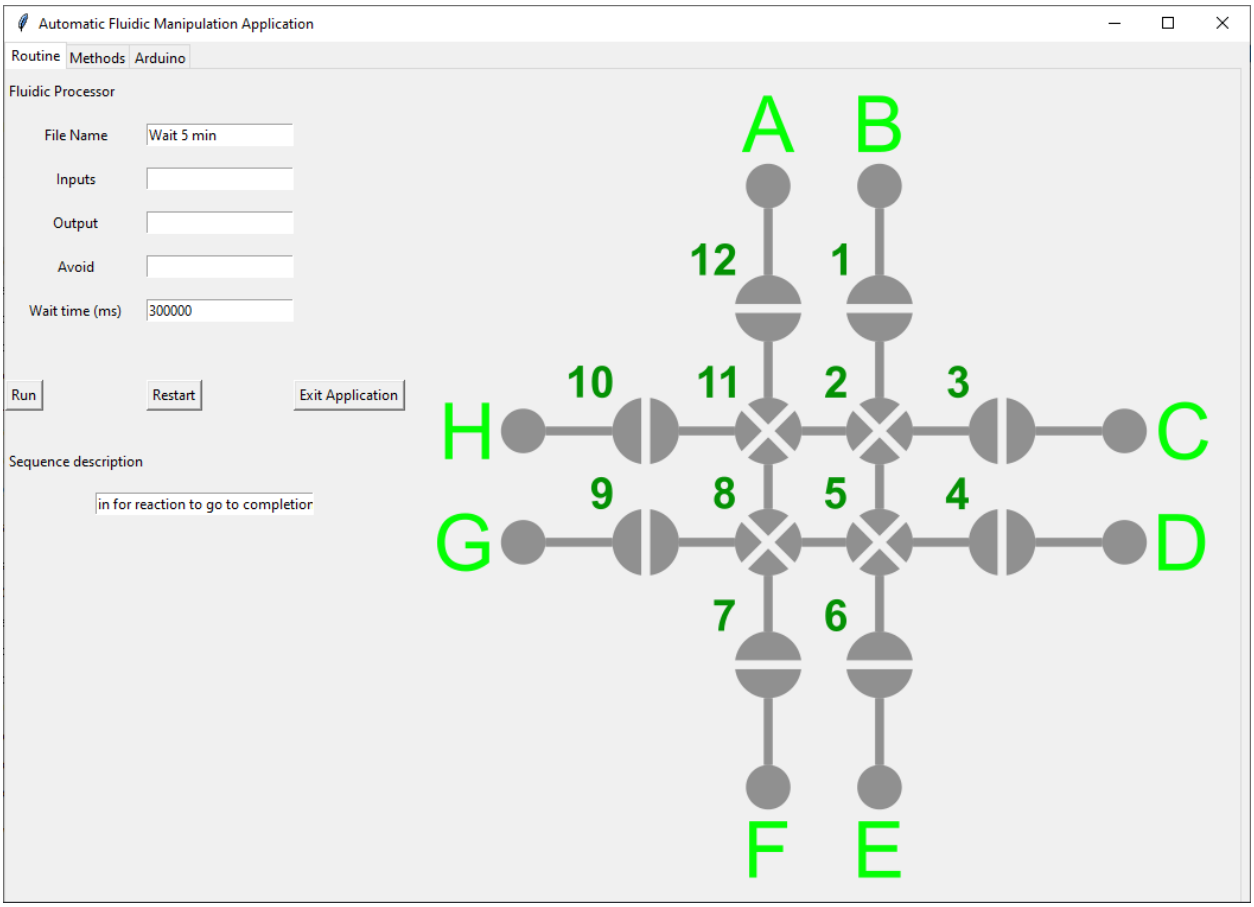
1. Install a Python IDLE in your computer. I suggest the Anaconda package. If you already have it installed in your computer, skip to step 2.
2. Download the Fluidic Manipulation Application at Github.
3. Open the Anaconda command prompt (or the command prompt of your IDLE), and install the PyFirmata protocol using pip.s
    a. Copy and paste this on your command prompt: pip install pyfirmata
    b. Hit enter.
4. Open the Fluidic Manipulation Application on Python. You can do that either by:
    a. the command prompt:
    cd C:\Users\Desktop\Fluidic_Manipulation_Application (or where you have placed the folder)
    python Fluidic_Manipulation_Application.py
    b. By dragging and dropping the Fluidic_Manipulation_Application.py file into the IDLE window, and hitting Run file (or F5).
5. If everything is working as it was supposed to, this window will appear:



6. In this window you can give your Routine a name (File name box), and write a brief description of what this routine does (Sequence description box), but this step is not mandatory.
    a. Example: File name: A and B combination
       Sequence description: Combine A and B, in a 1:1 ratio
7. To include which input fluid reservoirs are going to be used, go to the Inputs box, and add the reservoir letter, followed by a colon and the number of valves worth of fluid to be used. If more than one reservoir is to be used, just add a comma between instructions.
    a. Example: I want to move 1 valve worth of fluid A and 1 valve worth of fluid B to an output. Inputs: A:1,B:1
        i. The inputs are not case sensitive, so a:1,b:1 also works.
        ii. There is no need to add spaces between instructions, but you can do so to ease visualization. This is specially useful if using multiple reservoirs. The code will remove the extra spaces.
            Example: A:1 , B:1
8. Add the Output reservoir (*i.e.* the reservoir that will receive the fluids transferred from the input reservoirs), by typing the corresponding letter into the Output box.
    a. Example: Output: C
    b. Also not case-sensitive
9. If, for any reason, a valve (or valves) become inoperative, you can indicate to the program which valve(s) to avoid. If none, leave it blank.
    a. Example: Avoid: 5
10. You can change the wait time between open and close operations. If you want a faster pumping rate, this number would be lower; conversely, lower pumping rates require higher numbers. The valve actuation time is an important parameter, meaning that it is not an arbitrary choice, and there are things to be considered when choosing it. We recommend some testing to optimize it to each system.
    a. Example: Wait time (ms): 500
    b. The time is expressed in milliseconds
    c. The default time is 300 ms, but this can be changed in the code (line 714: value_e4 = 300).
11. Hit Run, and this routine sequence will be saved in the Routines folder. All fields will be cleared out, and you can design another routine.

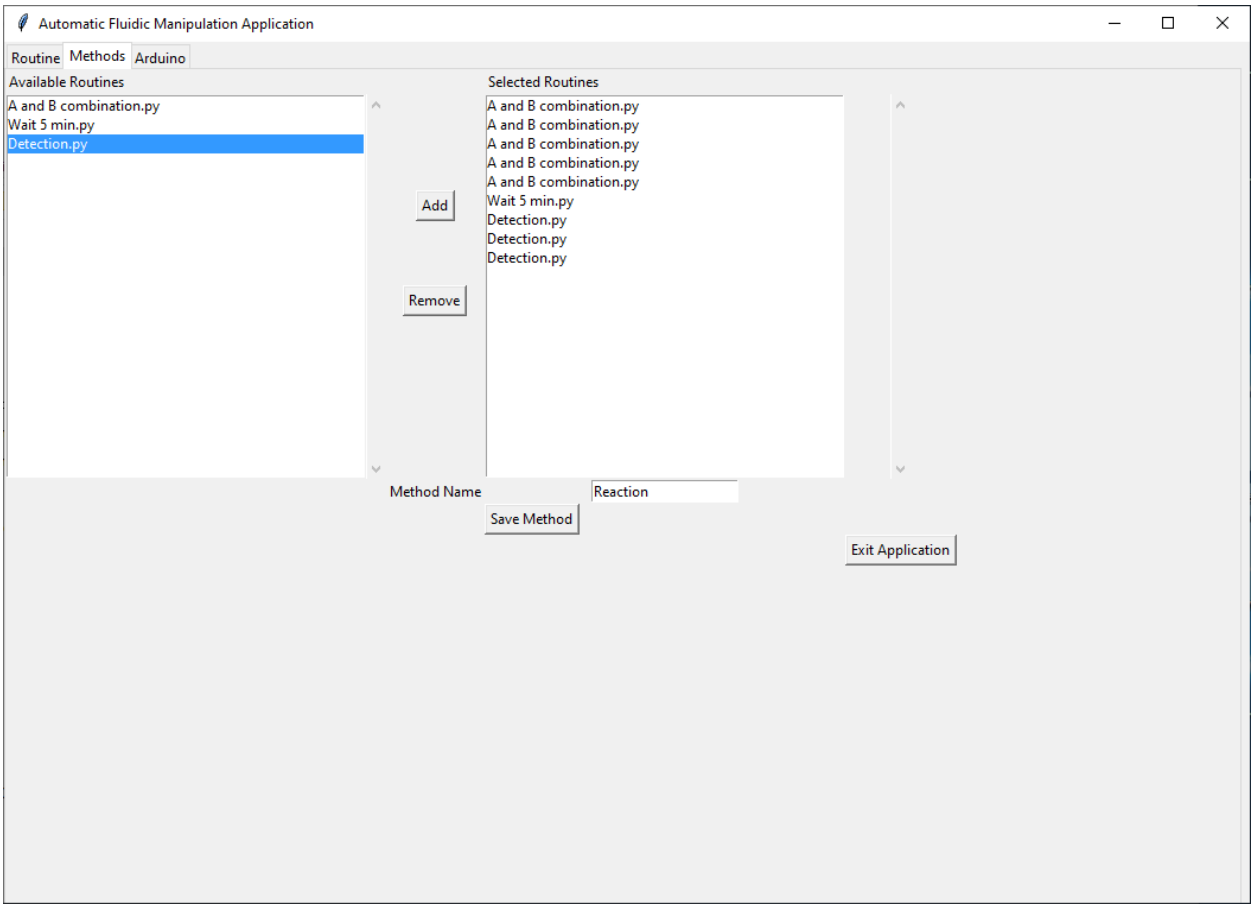


12. A waiting routine is also very useful.
    a. Example: You want to mix 2 reagents together (as described above), and you want to store them in reservoir C for 5 min, which is the time required for your reaction to go to completion. For that, you must populate only the Wait time (ms) box, with the appropriate time.
        i. Example: Wait time (ms): 300000
        ii. (5 min x 60 s/min x 1000 ms/s) = 300000

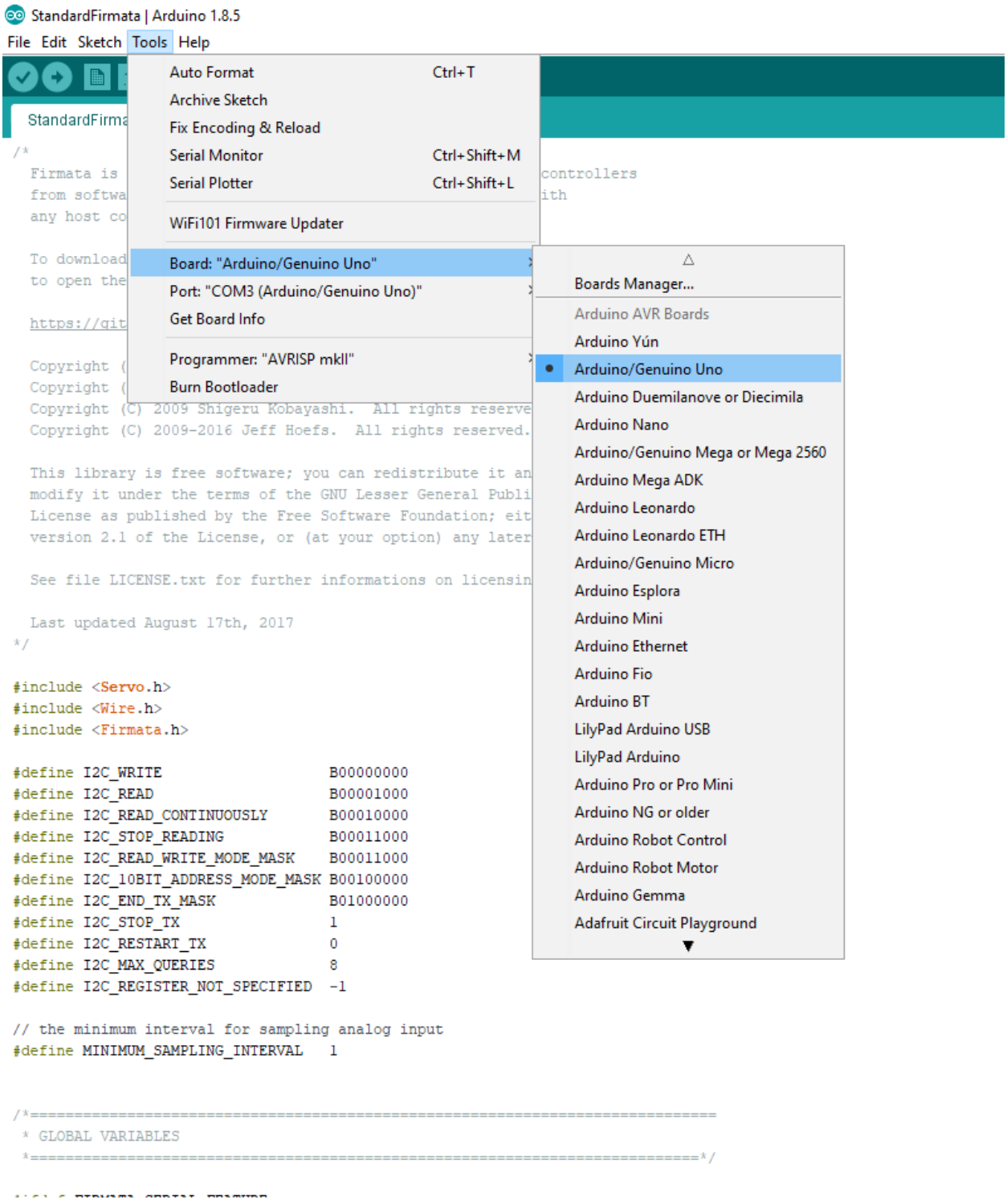


13. After creating different routines, you can combine them into methods.
    a. Example: You want to combine the A and B reagents in a 1:1 ratio, then wait 5 min to the reaction to go to completion, and then send the products to the detector, which is connected to reservoir F. You go into the Methods tab, and add the different methods into a routine.
    b. IMPORTANT: each routine is executed once by the program, meaning that the volume transported will be a result of one repetition of the routine. If larger volumes are to be transported, you just need to add the same routine multiple times in a row.
        i. Example: highlight the A and B combination.py file from Available Routines, and click on 'Add' 5 times, to repeat this sequence 5 times. You can see how many times this routine will be repeated on the Select Routines box. If a wrong number of routines was added, just highlight the wrong routine and hit 'Remove'.
    c. Then add the other routines
        i. Example: highlight the wait 5 min.py file and click on 'Add'; highlight the Detection.py file and click on 'Add' 3 times, to repeat this sequence 3 times.
    d. Give a name to your Method (not necessary, but very useful to do so).
        i. Example: Method name: Reaction

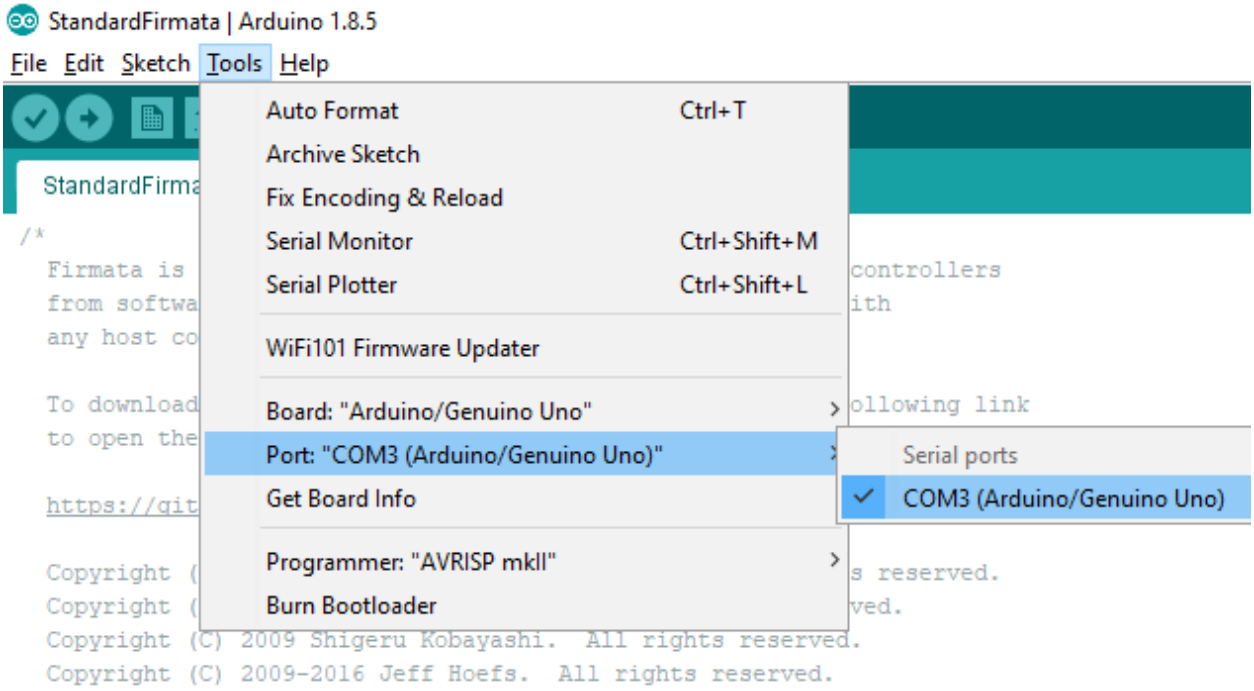
14. Hit Save Method, and this method will be saved in the Methods folder. All fields will be cleared out, and you can design another method.



15. If you have an Arduino-based system connected to your computer, you need to connect it using the Standard Firmata protocol.
    a. In the Fluidic_Manipulation_Application folder, there is a folder named StandardFirmata. In that folder, there is a StandardFirmata.INO file. Open that file using the Arduino program, and select the board you are using (in this case, an Arduino/Genuino Uno).

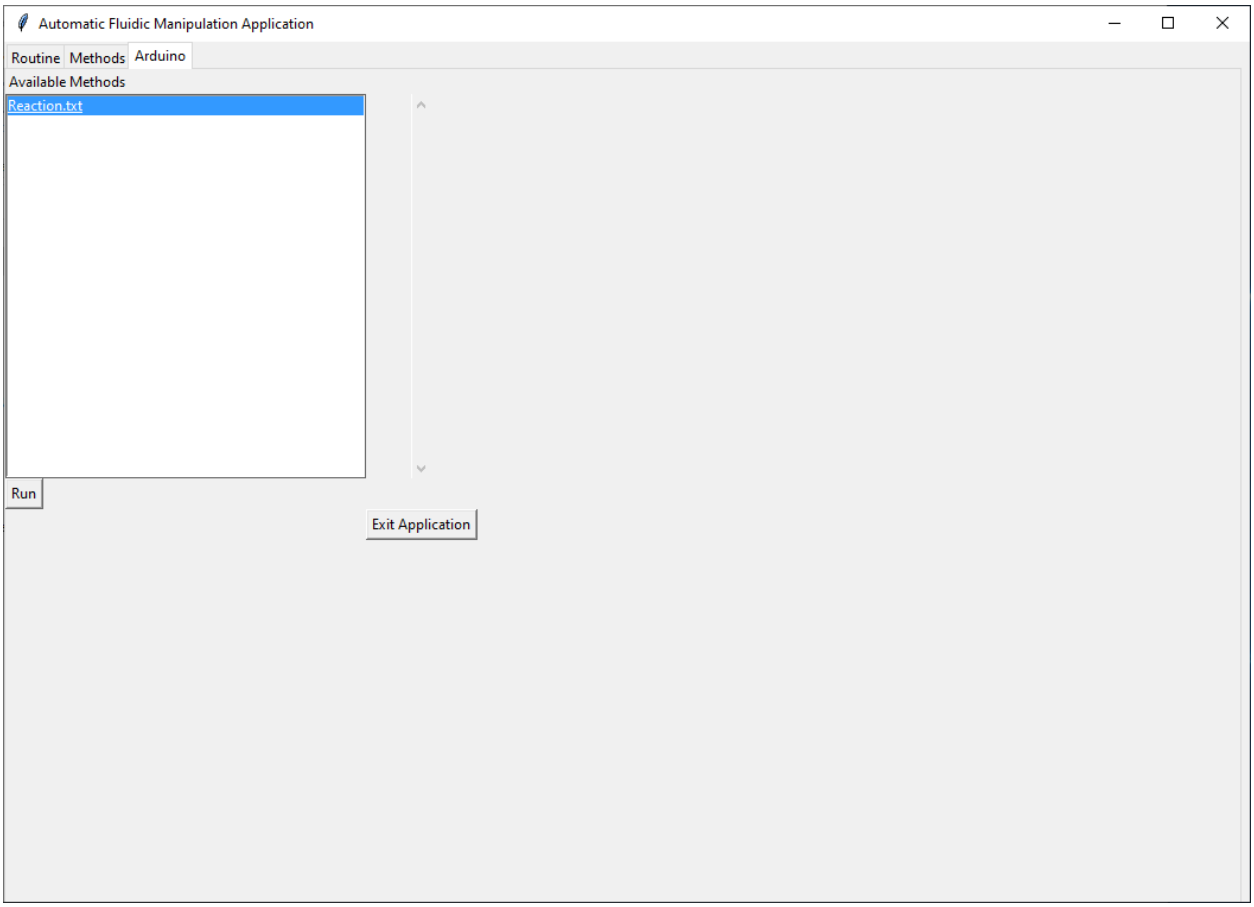


16. Then, select the port being used (in this case, port COM3).

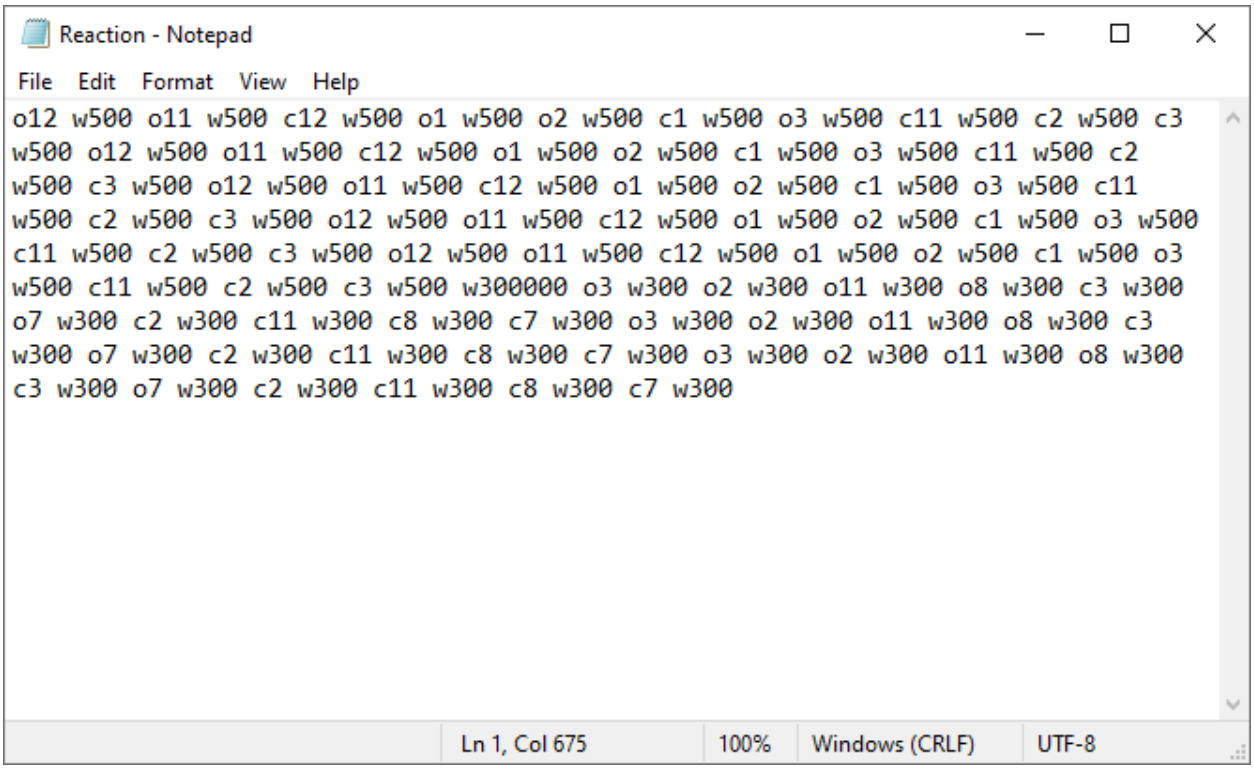


17. Then, hit the upload arrow, located at the upper left corner of the screen, to upload the Firmata protocol to operate the Arduino board from the Fluidic Manipulation Application.

18. Once the Arduino board is all set, you can open the Arduino tab and select the available methods you created. Highlight the method you want to perform from the Available Methods list, and hit Run, to run your method in your microfluidic system.



19. If you are using a LabView system, or any other systems that operate on a long list of commands, you can simply copy and paste the commands from the Methods .txt file generated.


Reaction - Notepad
File Edit Format View Help
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