How to Use `itm.r`
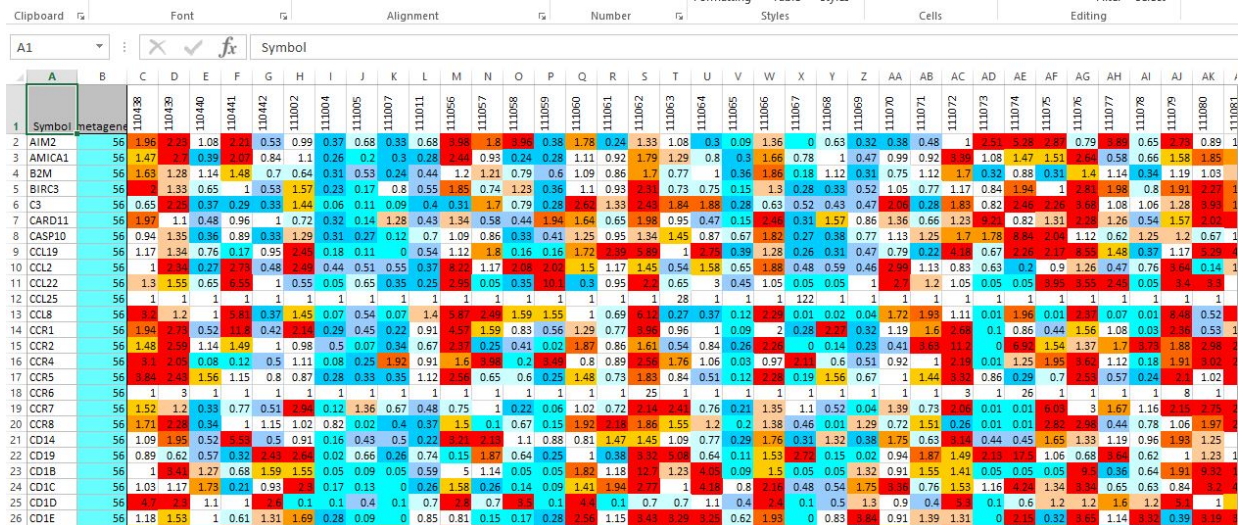
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1. The only essential file for the program to work is `itm.r`. Place it in a new directory named, say, `ITM`. Other files that can be placed in the same directory include:

    - `itm_doc.r`: This is `it.r` with comments added to explain how the program works.
    - `itm_usage.pdf`: This file.
    - Data files as explained in §2.

2. Prepare the data file. Suppose that the raw data is stored in an excel file.

    - Copy the data into a new excel file. Give it a short name, such as `MPF.xlsx` or `AB2.xlsx`, with no spaces or special characters in the name. Delete extra information, leaving only the labels of the cancer cases in Row 1, the gene names in Column A, and metagene in Column B as shown below.
    - Make sure that the word metagene in cell B1 is spelled exactly like that.

    - Save the excel file using `File -> Save As` in a CSV format, to produce a new file `MS.csv`. Place that in the same directory as the project.

3. Start RStudio and create a new Project using `File -> New Project ...` and choose the directory `ITM`.

4. Use the command

        source('itm.r')

    to load the program. You only need to do this one time for the Project.

5. To analyze the data stored in `MS.csv`, use the command

        mmsc('MS')

    The first iteration uses the cutoff 20%, and the other iterations uses 0.6.

    The output will be in the file `MS20_0.6_output.csv`. This file can be viewed using Excel, and then re-saved in the `.xlsx` format.