

Readme\_file.pdf: Modified on 14/01/2022

This directory contains all input data files and codes to identify metabolic influences between each pair of microbial entities. All the required Input files have been provided in the “Input\_files” folder and all output files will be generated in the “Output\_files” folder upon successful execution of source code and executable file

**Instructions and System requirement:**

In order to run the executable code, you need to have a Linux operating system with GCC compiler installed. One can use a different compiler (other than GCC) that supports the execution of C++ code. Within the terminal, move to the “code” directory. Write the command: “make” to create the executable file, then run the command “. / getWxy\_matrix” to run the executable code. The output files will be generated in the ‘Output\_files’ directory.