A Manual for installing FASTCORE, COBRA Toolbox V3 & IBM CPLEX 12.10 for Windows 10

Windows version: 10.0.19042 Build 19042

1- Installing MATLAB
Version: 2021b
MATLAB toolboxes are checked during installing:

       Bioinformatics Toolbox (required)
       Curve Fitting Toolbox (required)
       Optimization Toolbox
       Parallel Computing Toolbox
       Signal Processing Toolbox
       SimBiology
       Statistics and Machine Learning Toolbox
       Symbolic Math Toolbox

2- Installing CPLEX Optimization Studio 12.10 :
    1- Downloading CPLEX Optimization Studio 12.10 :
- Go to https://www.ibm.com/academic/topic/data-science
- Register an IBM account with an academic email.
- Go back to https://www.ibm.com/academic/topic/data-science, and sign in with your account.
- Scroll down then click on "Software" on the Left
- Click on the arrow below "ILOG CPLEX Optimization Studio"
- Click on "Download"
- Click on "Search for Software" on the left side.
- Search for "IBM ILOG CPLEX Optimization Studio 12.10.0 for Windows x86-64 Multilingual"
- Click on "HTTP", then click on the checkbox for the Windows version.
- Choose "I agree", then "Download Now"

    2- Install CPLEX pre-requisites:
      a. The latest Git for Windows:
        https://git-scm.com/download/win

      b. Visual Studio for Windows:
        https://visualstudio.microsoft.com/
      c. Oracle Java SDK/JRE/JDK

For Windows pre-requisites, check: https://www.ibm.com/support/pages/detailed-system-requirements-ibm-ilog-cplex-optimization-studio#1210

➢ Made sure to uninstall other CPLEX versions installation, before beginning installing CPLEX 12.10

    3- Install the CPLEX from the downloaded installer:

So check the parent folder manually (C:\Program Files\IBM\ILOG\CPLEX_Studio1210\cplex\bin\x64_win64), and if the @Cplex folder is missing, Please uninstall, then reinstall Cplex

Then run these lines in MATLAB to add the CPLEX path

```
> addpath(genpath('C:\Program Files\IBM\ILOG\CPLEX_Studio1210\cplex\matlab\x64_win64'))
> setenv('ILOG_CPLEX_PATH','C:\Program Files\IBM\ILOG\CPLEX_Studio1210\cplex\matlab\x64_win64')
```

If CPLEX is correctly installed, you should find "Cplex" command in MATLAB.

4- Installing COBRA Toolbox V3:

4.1. Run MATLAB as administrator

4.2. Double check that the setfield command has only this path "/Applications/MATLAB_R2020a.app/toolbox/matlab/datatypes/setfield.m" by running:

```
> which –all setfield
```

If there are other paths, remove them such as these examples:

```
> rmpath('C:\Program Files\MATLAB\R2021b\toolbox\finance\ftseries\')
> rmpath('C:\Program Files\MATLAB\R2021b\toolbox\sl3d\sl3d\')
```

4.3. Download COBRA toolbox from https://github.com/opencobra/cobratoolbox either using Git (Start > open Git Bash) then run
> git clone --depth=1 https://github.com/opencobra/cobratoolbox.git cobratoolbox
Or manually (not recommended):
> from « Code », click on "Download ZIP"

4.4. Add Cobratoolbox folder to paths using
➢ addpath(genpath('/PATH OF THE DOWNLOADED cobratoolbox/'))

4.5. From MATLAB, go to the downloaded "cobratoolbox" folder, then run
➢ initCobraToolbox.m

4.6 Check if CPLEX is correctly installed and detected by the COBRA Toolbox:

by finding this line during installation **"ibm_cplex   active   1   1   1   1"**
And also "changeCobraSolver('IBM_CPLEX')" should return logical 1

4.7. If MATLAB crashes and closes during installation, open MATLAB and run again the initCobraToolbox.m and you might want to doublecheck that cobratoolbox is still added to the path using which –all initcobratoolbox. If the command is not found, repeat step 4.4.

4.8 In case of failed installation, you may need to remove *cobratoolbox* and *cplex* paths, and add them again using
```
% Restoring all default paths, please note this would remove paths for other non-default MATLAB tools
restoredefaultpath
```

```
% Adding the CPLEX path
addpath(genpath('C:\Program
Files\IBM\ILOG\CPLEX_Studio1210\cplex\matlab\x64_win64'))
setenv('ILOG_CPLEX_PATH','C:\Program
Files\IBM\ILOG\CPLEX_Studio1210\cplex\matlab\x64_win64')
Cplex % should return Logical 1
% Checking if there is only this path for setfield command:
"/Applications/MATLAB_R2020a.app/toolbox/matlab/datatypes/setfield.m "
which -all setfield
% Saving permanently the new paths
savepath
```

5- Download FASTCORE:
   Either using Git Bash:
   ➢ git clone https://github.com/sysbiolux/rFASTCORMICS
   Or manually:
       from « Code », click on "Download ZIP"

   From MATLAB:
   ```
   addpath(genpath('/PATH OF THE DOWNLOADED rFASTCORMICS/'))
   ```

   If you are able to call the following functions (and more related functions) in the command window of MATLAB then the installation is done.

   - fastcc_fastcore   *(from the fastcore folder)*
   - fastcc_4_fastcormics *(from the fastcormics for microarray data folder)*
   - fastcormics_RNAseq *(from the fastcormics for RNA-seq data folder)*