**A Manual for installing FASTCORE, COBRA Toolbox V3 & IBM CPLEX 12.9 for macOS**

**macOS version**: macOS Monterey 12.0.1

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

1. Installing CPLEX Optimization Studio 12.9 :
2. Downloading CPLEX Optimization Studio 12.9 :

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 12.9 for OSX Multilingual (CNZM6ML ) “

Click on “HTTP”, then click the checkbox for the OSX version.

Choose “I agree”, the “Download Now”

1. Install CPLEX pre-requisites:

**Visual Studio for Mac :**[**https://visualstudio.microsoft.com/**](https://visualstudio.microsoft.com/)

**Install Python3 through HomeBrew as documented here:**[**https://docs.python-guide.org/starting/install3/osx/**](https://docs.python-guide.org/starting/install3/osx/)

**Oracle Java SDK/JRE/JDK**

The complete list pre-requisites can be found here:

<http://pic.dhe.ibm.com/infocenter/prodguid/v1r0/clarity-reports/report/html/softwareReqsForProduct?deliverableId=E57328F0919E11E8A5E6A380334DFF95&osPlatform=Mac%20OS>

For Windows pre-requisites, check: <https://www.ibm.com/support/pages/detailed-system-requirements-ibm-ilog-cplex-optimization-studio#1290>

1. Install the CPLEX from the downloaded installer:

-Sometimes a folder (/Applications/CPLEX\_Studio129/cplex/matlab/x86-64\_osx/@Cplex) is deleted during installation into the *Bin* folder.

So check the parent folder manually (/Applications/CPLEX\_Studio129/cplex/matlab/x86-64\_osx), and if the @Cplex folder is missing, Please uninstall then reinstall Cplex

Then run this line in MATLAB

addpath(genpath('/Applications/CPLEX\_Studio129/cplex/matlab/x86-64\_osx/'))

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

1. Install COBRA Toolbox
2. Download COBRA toolbox from <https://github.com/opencobra/cobratoolbox>

either using git:

* git clone --depth=1 https://github.com/opencobra/cobratoolbox.git cobratoolbox

Or manually:

> from « Code », click on “Download ZIP”

1. From MATLAB  
   addpath(genpath('/PATH OF THE DOWNLOADED COBRA TOOLBOX /'))

initCobraToolbox

If CPLEX is correctly installed and detected by COBRA Toolbox, you should find this line

**“ibm\_cplex active 1 1 1 1 ”**

1. Download FASTCORE:

Either using git:

* + 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)*