

Instructions for IGM App

REQUIREMENTS

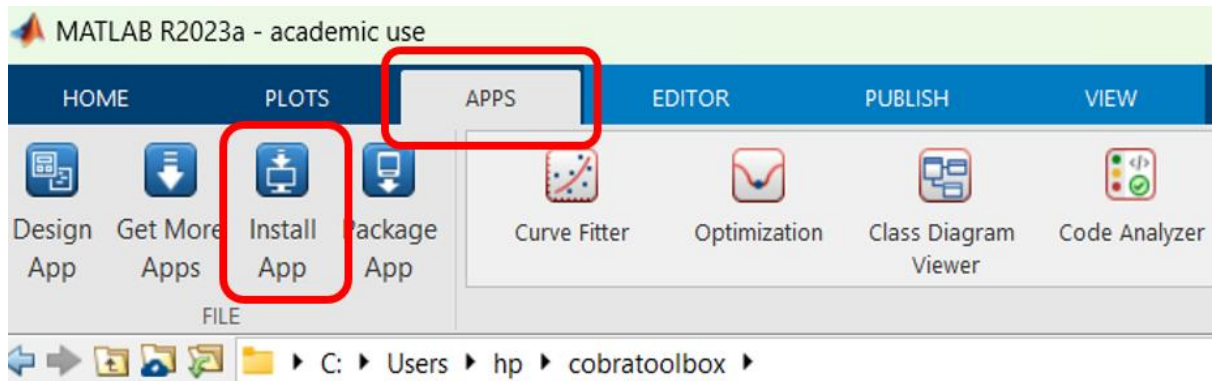
1. **Matlab** (version R2023a or better)
2. **CobraToolbox** ([Installation Guide] <https://opencobra.github.io/cobratoolbox/stable/installation.html>)
3. **Gurobi solver** (version 11.0.3 or better, free academic)
4. **Genome scale metabolic model** ([Download from BiGG Models] <http://bigg.ucsd.edu/> and iML1515 can be downloaded from <http://bigg.ucsd.edu/models/iML1515>)
5. **Gene expression data file**
6. **Uptake rates data file**

***Notes

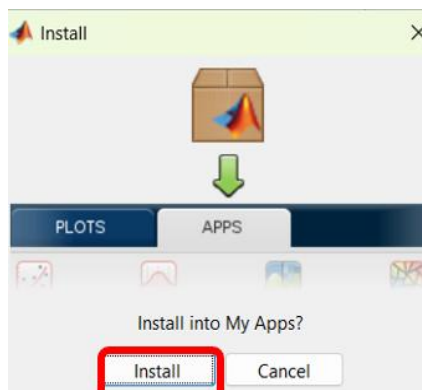
- Files in 4, 5, and 6 are in the same directory.
- The first column of the gene expression file must contain **gene symbols/names** used in the genome-scale metabolic model.
- The first column of the uptake rates file must contain **reaction IDs** used in the model.
- The first row in both files must contain the **condition names**, and these names should match between files.

Installation of IGM App

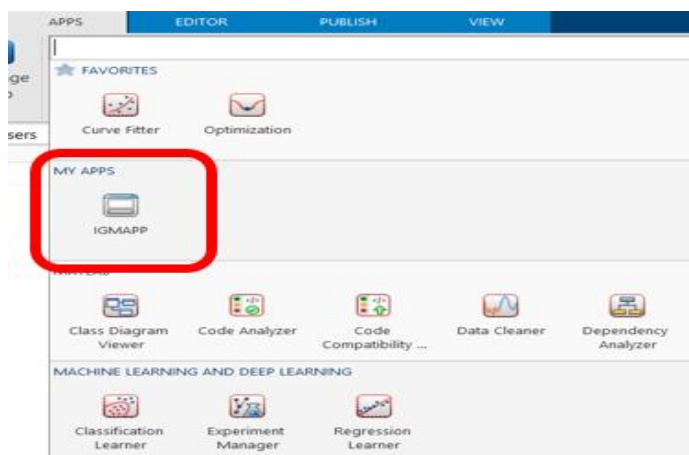
1. Download the **IGMAPP** installer from GitHub.
2. Open **MATLAB** and go to the **APPS** tab.



3. Click **Install App**, select the **IGMAPP** installer you downloaded from GitHub, and press **Open**.
4. Click **Install** to install **IGMAPP**.



5. **IGMAPP** will now appear in the **APPS** tab.




How to Run IGM

1. Type **initCobraToolbox** in the MATLAB command window and run it.
2. Open IGMAPP .
3. Click **Current Directory** to check the current working directory. If this is not your working directory, click **Choose Directory** and select the desired folder.
4. Select the **genome-scale metabolic model file**, then click **Read Model**. Wait until the status changes to Finished and the lamp turns green.

Genome Scale Metabolic Model

File Name (Model)

status:



5. Select the **gene expression table file**, then click **Read Table**. Wait until the status changes to Finished and the lamp turns green. You can verify your data in the displayed table.


Gene Expression Table

Note: The first column of the gene expression file must contain gene symbols/names used in the genome-scale metabolic model.

| Var1 | RF | pgm | |
|-------|---------|-------|---|
| b0957 | 45.2787 | 27.11 | ▲ |
| b0929 | 42.1731 | 20.90 | |
| b1480 | 38.3515 | 63.77 | ▼ |

File Name (gene expression)

status:




6. Select the **uptake rates table file**, then click **Read Table**. Wait until the status changes to Finished and the lamp turns green. You can verify your data in the displayed table.

Uptake Rate Table

The first column of the uptake rates file must contain reaction IDs used in the model.

| Var1 | RF | pgm |
|------------|---------|------|
| EX_glc_D_e | -2.9300 | -3.1 |
| EX_o2_e | -5.7900 | -5. |
| EX_co2_e | 4.1100 | 6. |

File Name (uptake rate)

status: 

7. Select **optional inputs**:
 - a. Select the conditions for calculation in IGM (more than one condition).
 - b. Select the normalization method.
 - c. Select the method for calculating IGM.

Optional Inputs

Conditions

☒ All condition
☒ RF
☒ pgm
☒ pgi
☒ gapC


Note** select more than 1 condition

Normalization methods

Select method

Methods for Flux Calculation

Select method

 File Name

8. Click **Run IGM Model** and wait until the status changes to Finished and the lamp turns green.
9. **(Optional)** To save the flux results, enter a file name (e.g., filename.csv) and click Save Results. The output file will be saved in the selected directory.

Visualization using IGM Framework

1. After running the IGM model, you can visualize the results by selecting two conditions for flux change analysis. In the plot settings, you can filter flux values within a specified range (between the upper and lower bounds of the fluxes), then select the number of top-changing fluxes to display. Click **Plot** to generate the visualization.

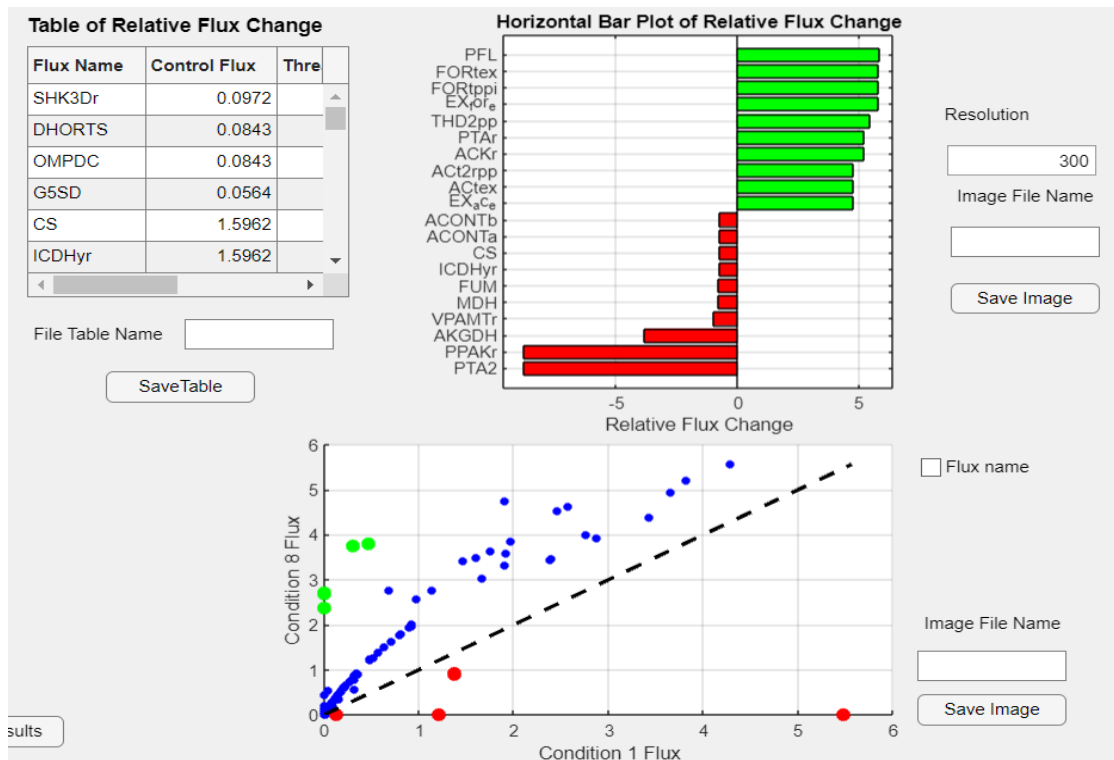
Visualization of Flux Change Analysis

Control Condition
RF
Filter (upper bound)
100
Top change fluxes
10

Threat Condition
RF
Filter (Lower bound)
-100

Plot

2. The visualization includes:
 - a. A table of relative flux changes (you can save this table by entering Filename.csv and clicking **Save Table**).
 - b. A horizontal bar plot of the top-changing reaction fluxes.
 - c. A scatter plot of fluxes between the two selected conditions.



3. You can change the conditions, adjust parameters, or check the **Flux Name** box to display flux labels in the scatter plot. After making adjustments, click **Plot** again to update the visualization automatically.
4. To save the visualization image, enter a file name (e.g., imagename.png) and click **Save Image**.