# Instructions for IGM App

## REQUIREMENTS

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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**

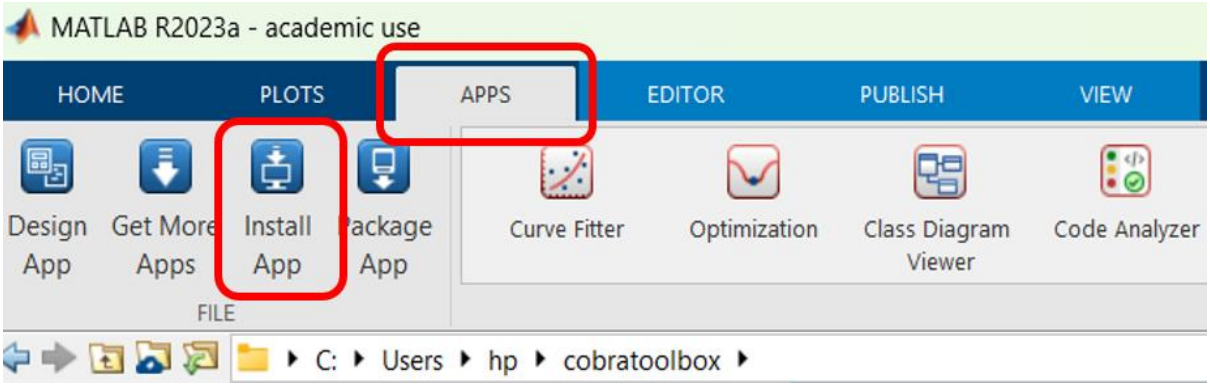
6. **Uptake rates data file**

***Notes

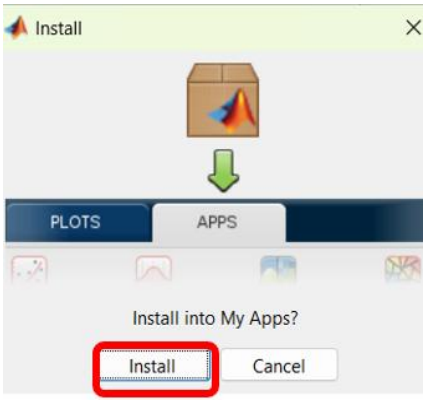
- Files in 4, 5, and 6 are in the same directory.
- The first column of the gene expression file must contain **gene symbols/names** used in the genome-scale metabolic model.
- The first column of the uptake rates file must contain **reaction IDs** used in the model.
- The first row in both files must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

**Installation of IGM App**

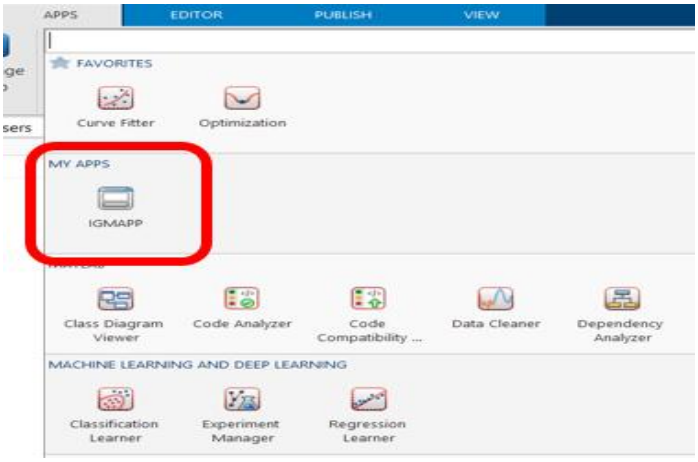
1. Download the **IGMAPP** installer, IGM function which consists of **IGMRUN.m**, **IGM_function.m**, **IGML1.m**, and **IGML2.m** from GitHub and save in your working directory.
2. Open **MATLAB** and go to the **APPS** tab.




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

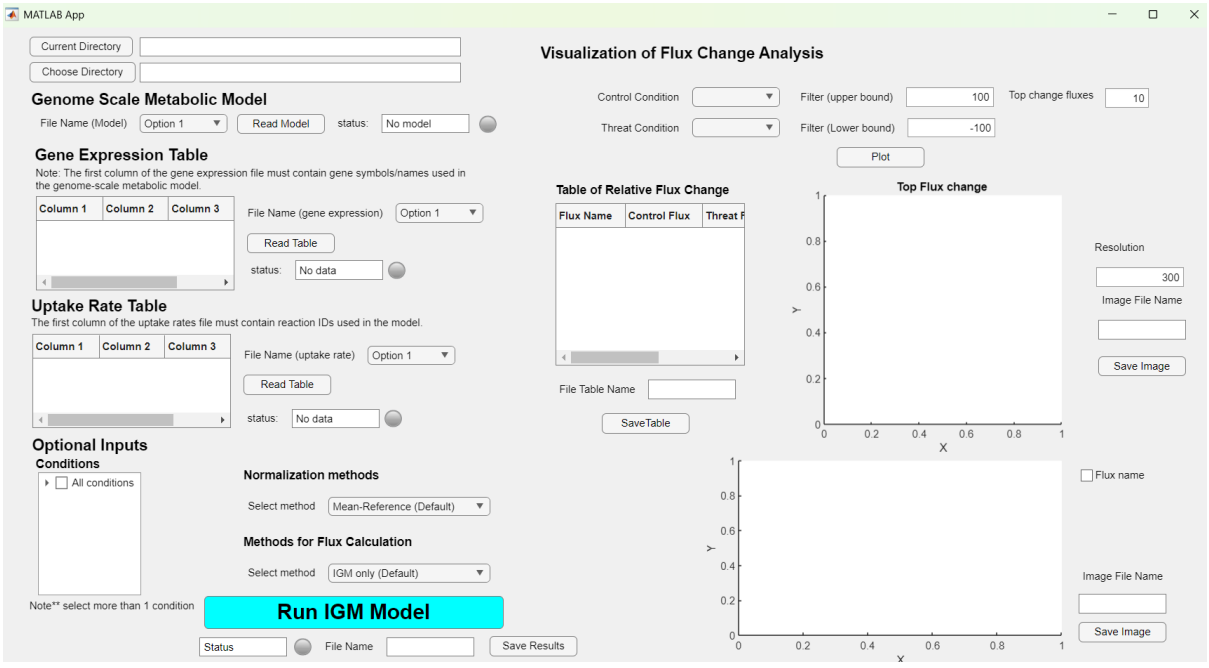



5. **IGMAPP** will now appear in the **APPS** tab.



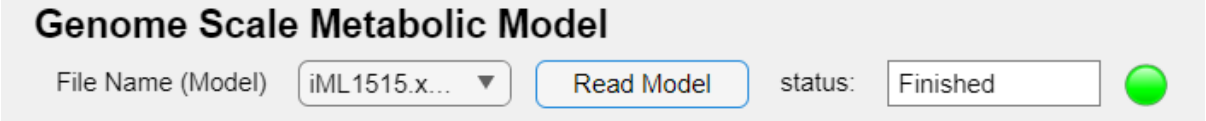

## How to Run IGM

1. Type **initCobraToolbox** in the MATLAB command window and run it.
2. Open IGMAPP .

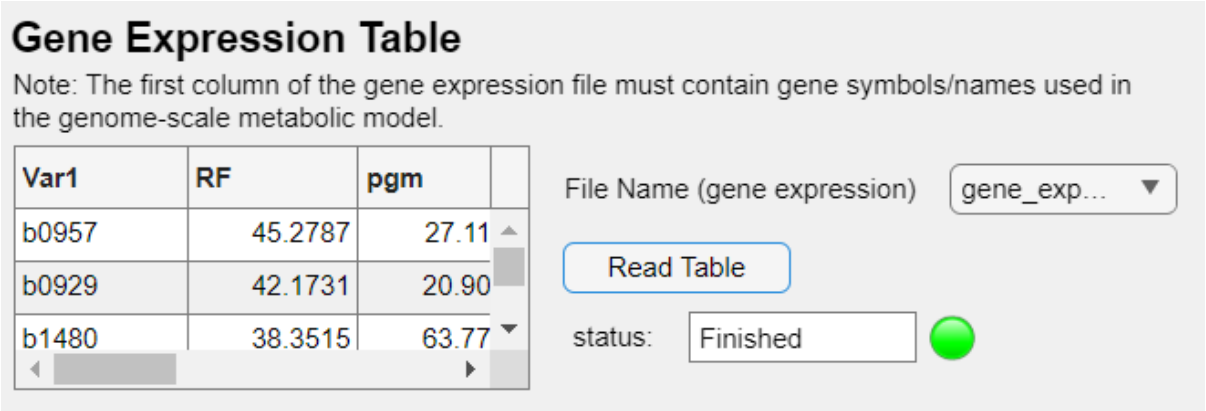



3. Click **Current Directory** to check the current working directory. If this is not your working directory, click **Choose Directory** and select the desired folder.

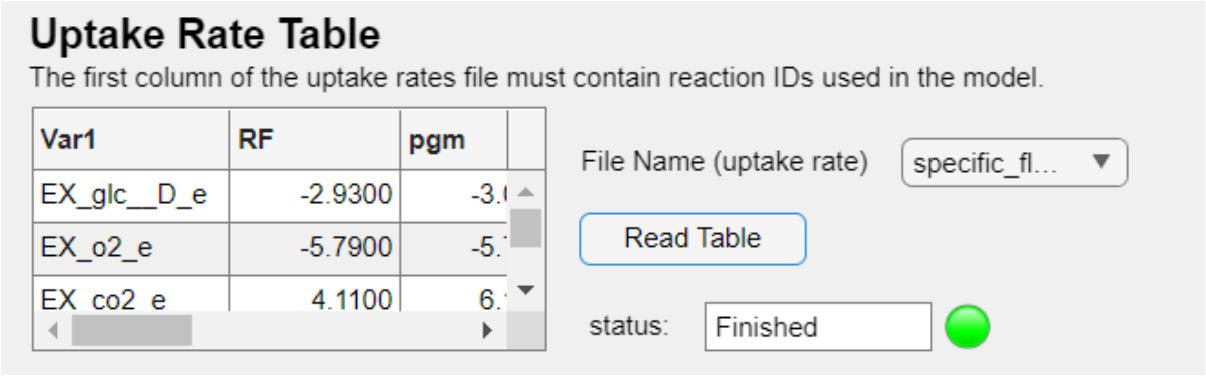
4. Select the **genome-scale metabolic model file**, then click **Read Model**. Wait until the status changes to Finished and the lamp turns green.




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.




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.

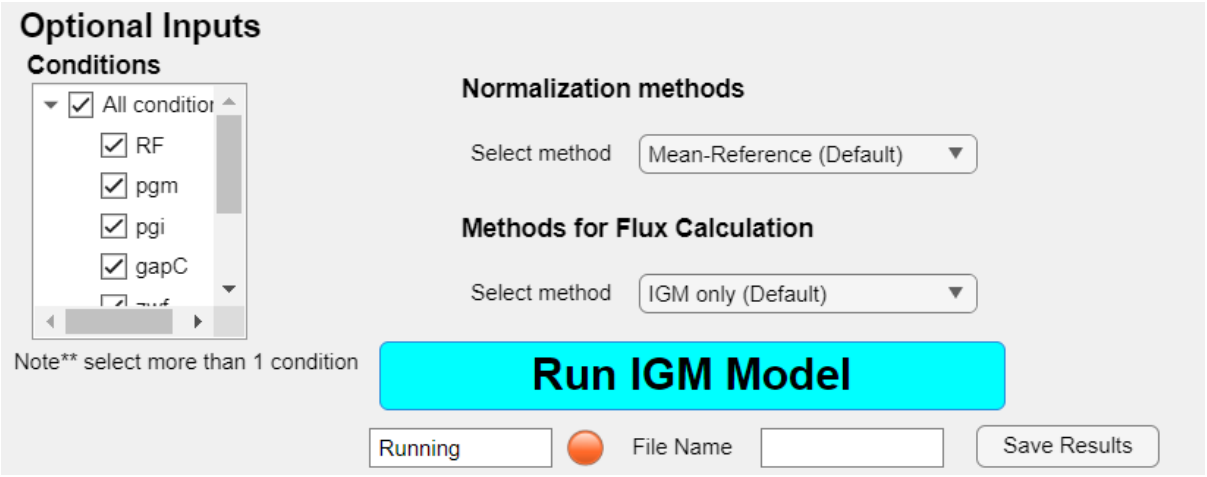



7. Select **optional inputs**:

   a. Select the conditions for calculation in IGM (more than one condition).

   b. Select the normalization method.

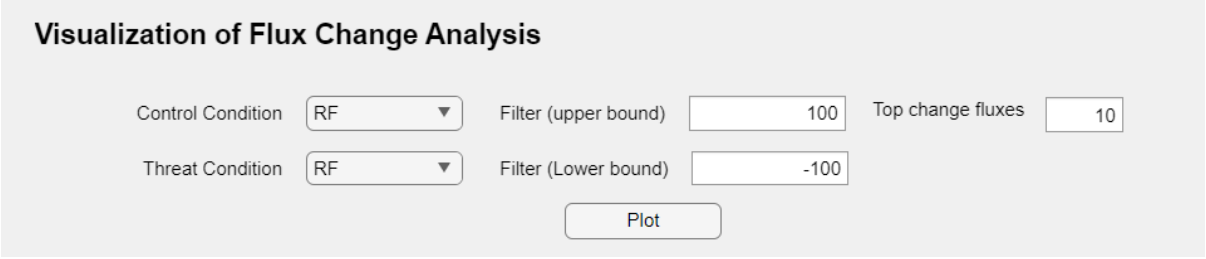
   c. Select the method for calculating IGM.




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.

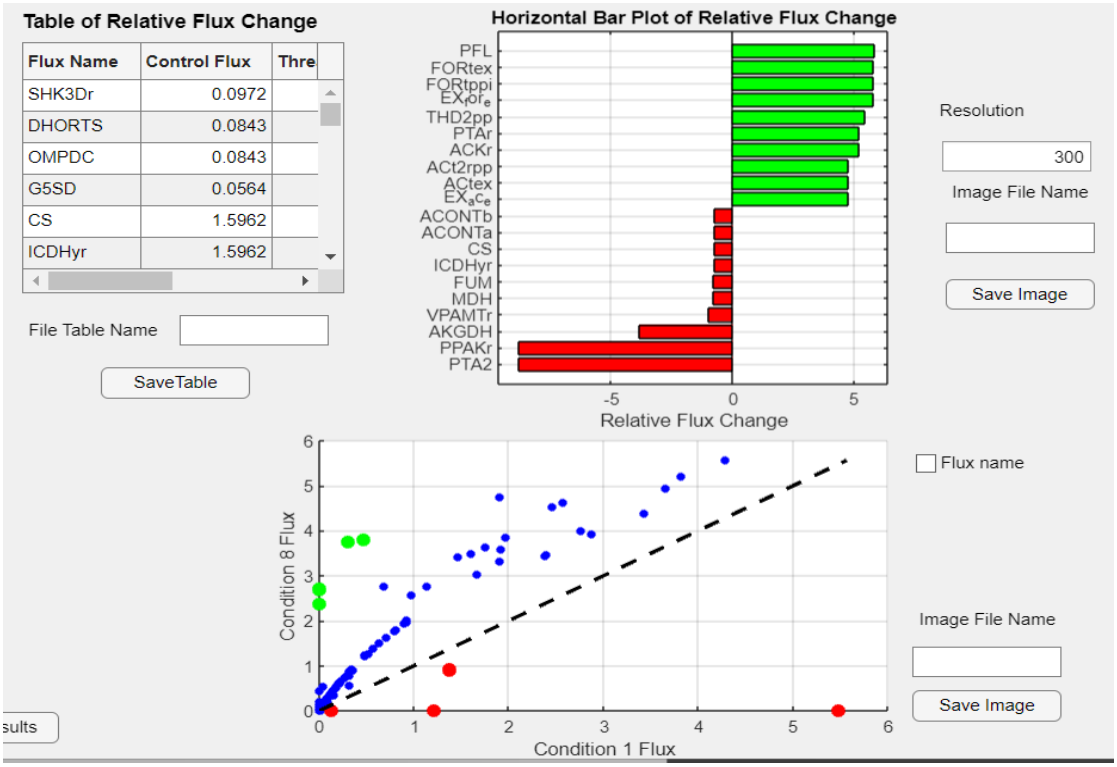



2. The visualization includes:

   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**.