**README**

**Required Software to Run Liver\_glycogen\_model:**

**MATLAB WinRAR(Windows) UnRarX (Mac OS X)**

**How to Run Liver\_glycogen\_model:**

1. Download and unrar Liver\_glycogen\_model.rar.
2. Open runmain.m under MATLAB editor and click on ‘run’ button; or type ‘runmain’ in the command window.
3. In runmain.m, two functions are called: main.m is the main program file and plot\_conc.m is the plot function for generating enzyme (glycogen synthase a and glycogen phosphorylase a) and substrate (glycogen) concentrations over time. The four concentrations 0.2 mM/min, 0.4 mM/min, 0.6 mM/min and 1.4 mM/min are consistent with those presented in our paper.
4. main.m takes two inputs: ‘state’ and ‘gluc\_input’. ‘state’ takes the value of ‘fed’ or ‘fasted’, which determines the fasting time from fed steady state. There are 3 runs in main.m: the first run is for the system to reach fed steady state with a constant feeding rate in the blood; the second run is the post-adsorption state with a decreasing glucose feeding rate from the fed steady state (drops below 5% in 140 mins.) Here, two fasting times are chosen to represent a fed and fasted livers: tmax = 250 mins or tmax = 1200 mins. The third run is for a glucose stimulus to enter the system as a step function. This rate is stored in the input variable ‘gluc\_input’.
5. plot\_conc.m generates figures for GPa, GSa and glycogen after the glucose stimulus enters the system.
6. Data are stored in the folder ‘./results’ in the form of ‘y\_fasted\_XpX.mat’ or ‘y\_fed\_XpX.mat’ where ‘XpX’ is the glucose feeding rate in the blood. For example, ‘y\_fasted\_0p2.mat’ means glucose input rate = 0.2 in a fasted liver.

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# UNC Software: << *Liver\_glycogen\_model* >>

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