You are studying the induction of a *lacZ*-controlled, GFP-tagged gene in E. coli, after induction with IPTG. You record the fluorescence of an induced culture, of a non-induced culture (negative control), and of LB medium alone (blank) every 5 min for 300 min.

Load the matrix "realdata" from the workspace timecourse.mat. Its first row contains the raw data for the IPTG-induced culture. The second row contains the raw data for the negative control. The third line contains the measurement for the blank.

Subtract the blank for each corresponding measurement (both in induced and non-induced time-courses). Plot the negative control and the IPTG-induced data on the same plot. Add labels for data and axes.

In the presence of IPTG, the induction of the GFP-tagged gene is represented by the following ODE model:

$$\frac{d[mRNA]}{dt} = 0.9$$

$$\frac{d[GFP]}{dt} = 0.3[mRNA]^2 - 0.5[GFP]$$

Simulate the production of GFP protein in the time frame of the experiment, with

[mRNA] = *[GFP]* = 0 mM

and compare the result with your data.

Make another plot of the simulation superimposed on real data (with nice labels and a title ☺)