

Simulations of glycolysis using GUI simply

Susana Vinga, 2008

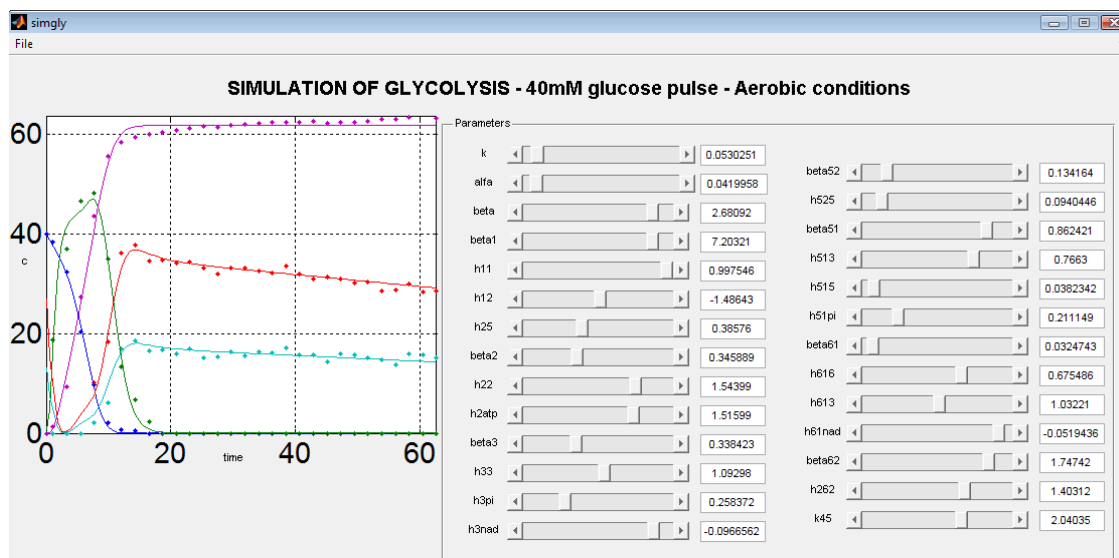
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This document presents some snapshots of MATLAB scripts that simulate glycolysis in *L. lactis* under aerobic conditions. This GUI allows the user to change the parameters of the differential equations and test in silico what would happen if the kinetic properties of the enzymes were different, according to this model.

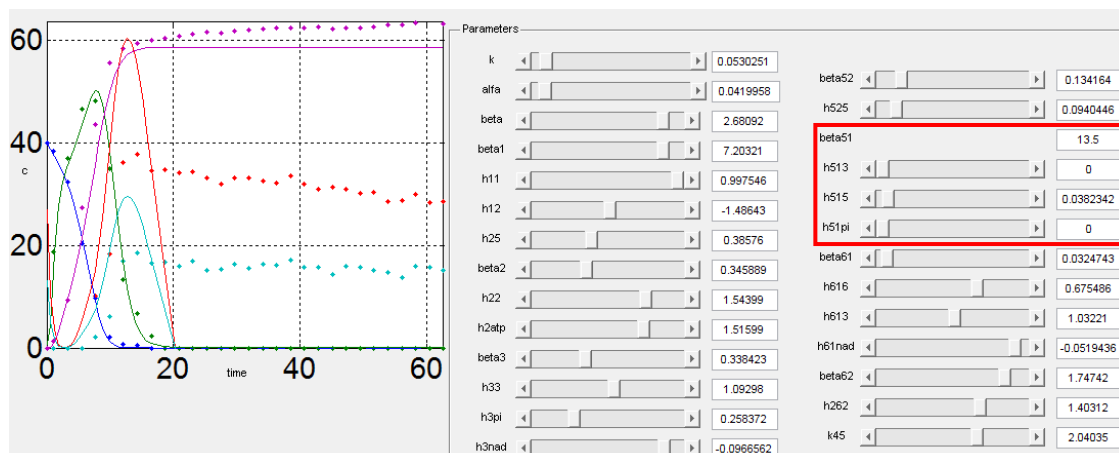
See also: Vinga S., Thomaseth K., Lemos J.M., Neves A.R., Santos H. and Freitas A.T. (2008) [Structural analysis of metabolic networks: a case study on *Lactococcus lactis*](#). In Proc. of the 8th Portuguese Conference on Automatic Control ([CONTROLO'2008](#)). July 21-23, Vila Real, Portugal.

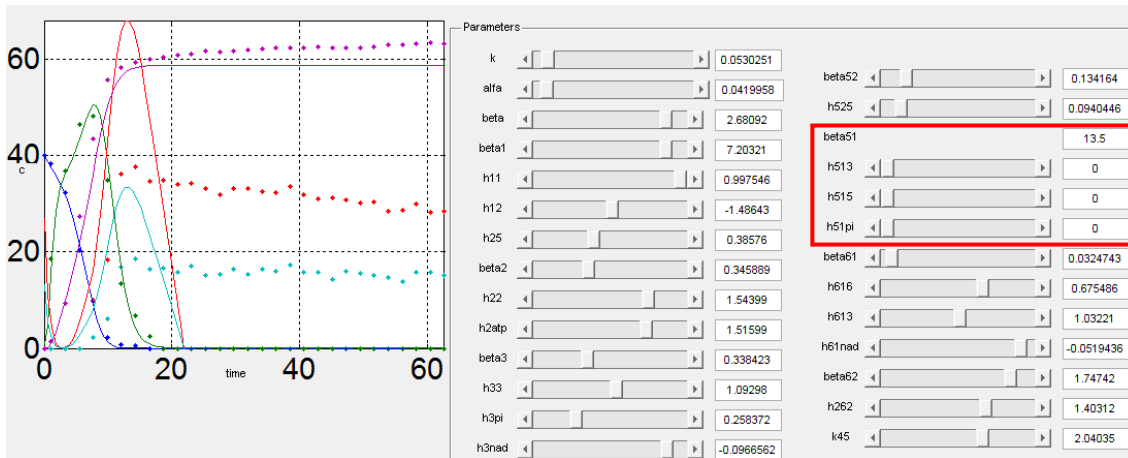
Accompanying files: simply.m, simply.fig, gly.m and Lactococcus_Data.mat

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>> simply
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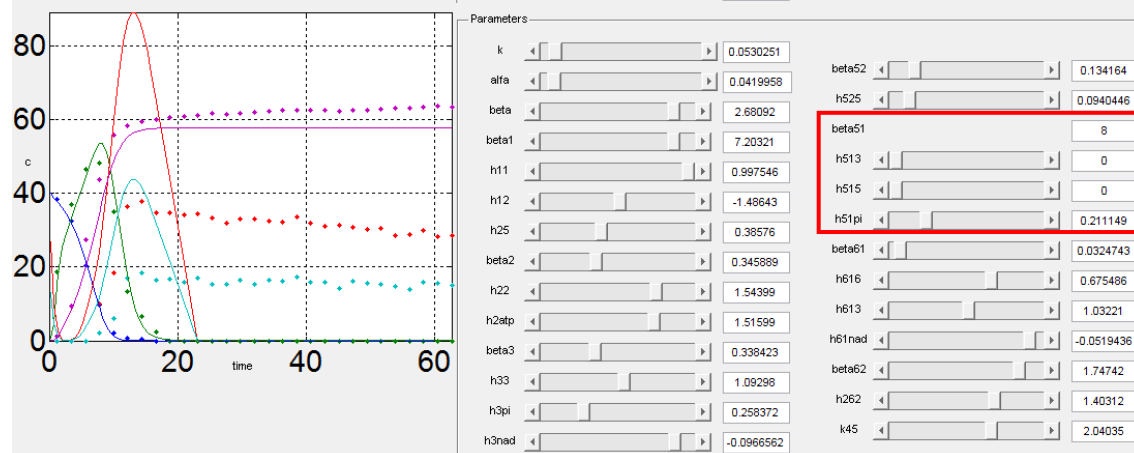
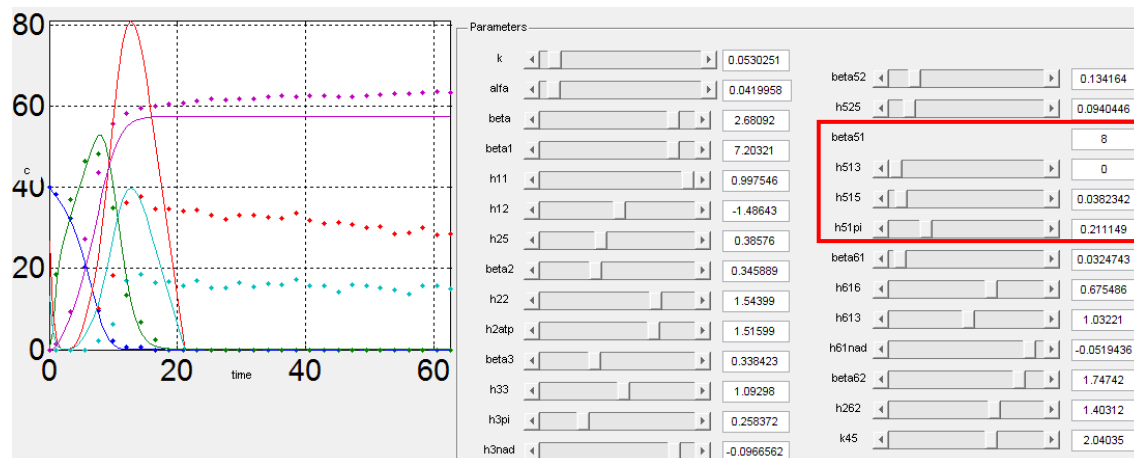


1) No regulation by PK (h513=0, h515=0, h51pi=0, adjust beta51 accordingly to FPBmax).





2) Exclusive inhibition by Pi (h513=0)



3) Exclusive activation by FBP (h51pi=0, h515 variable, b51 ajusted)

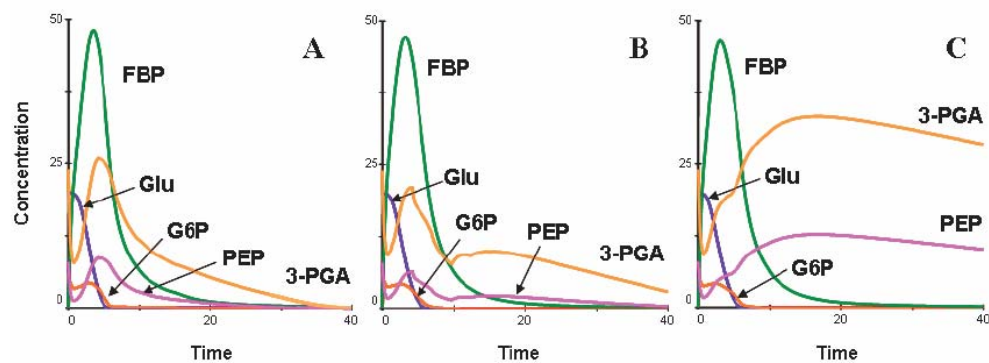
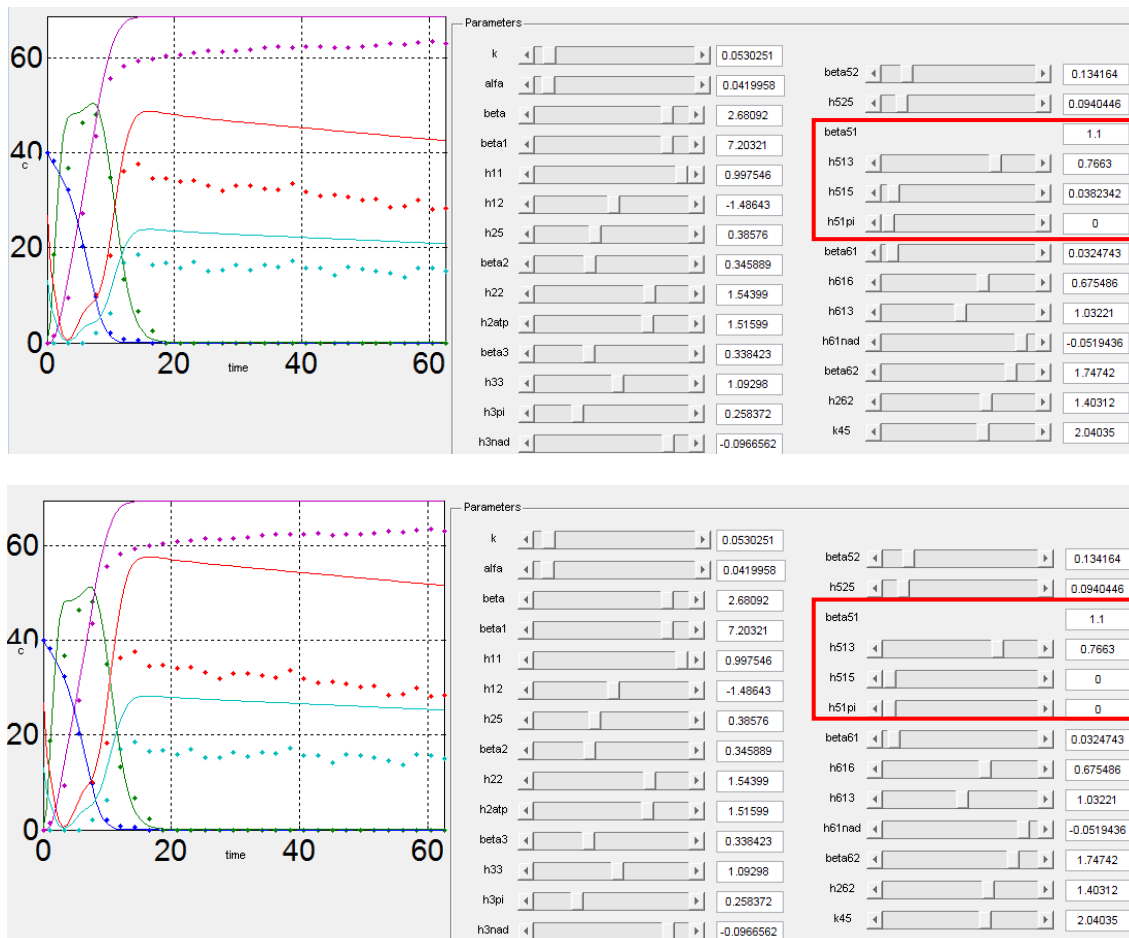


Figure 7: Comparison of the dynamics of PEP and 3-PGA in alternative system designs with no regulation of PK (A), exclusive inhibition by P_i (B), or exclusive activation by FBP (C). While (C) is very similar to the fully regulated system (Figs. 2, 5), the designs in (A) and (B) fail to generate and hold enough PEP to restart glycolysis after a period of starvation. The somewhat jagged appearance is due to the fact that P_i enters the system as off-line variable, which is given in the form of raw data (see Fig. 2).

In: Voit et al. Syst Biol (Stevenage). 2006 Jul;153(4):286-98.