Quantitative Analysis of the Effective Functional Structure in Yeast Glycolysis

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Table S1: Model parameter values

Symbol	Value	Exp. References
V_{m1}	1.3×10^{-3} M/min	Ref. [1]
V_{m2}	1.2×10^{-2} M/min	Ref. [2]
V_{m3}	1.4×10^{-3} M/min	Ref. [3]
K_{m1}	10.0×10^{-5}M	Ref. [4]
K_{m2}	5.0×10^{-5}M	Ref. [5]
K_{m3}	3.0×10^{-5}M	Ref. [6]
K_2	6.3×10^{-5}M	Ref. [4]
K_3	10.0×10^{-5}M	Ref. [4]
K_{d2}	3.5×10^{-5}M	Ref. [7]
K_{d3}	2.9×10^{-5}M	Ref. [8]
K_{d4}	22.5×10^{-5}M	Ref. [9]
L_1	6.0×10^{5}	Ref. [10]
L_2	10^{3}	Ref. [9]
c	10^{-5}	Ref. [2]
q_1	8.0×10^{-4}Hz	Free parameter
q_2	6.9×10^{-2}Hz	Free parameter
ω	7.6×10^{-3}Hz	Free parameter
λ_1	2.0 sec	Free parameter
λ_2	0.6 sec	Free parameter

To the date the kinetics of individual enzymes in cellular conditions cannot be yet accurately determined. However, in-vitro studies give very precise quantifications of the enzymatic rate equations and their kinetic parameters. When in metabolic models it is considered the kinetics of irreversible enzymes, the kinetic laws observed in-vitro might work in-vivo as well. This does not mean that the in-vivo behavior is fully explained by in-vitro studies. But if one accounts for the dissipative conditions, as it can be done in numerical simulations, the in-vitro kinetic laws might be valid in physiological conditions. For these reasons, it is advisable to use dynamical models to study metabolism in which the molecular mechanisms of the irreversible enzymes are gathered by the in-vitro kinetics. These models take into account the dissipative mechanisms which are generating the instability present in far-from-equilibrium systems.

Therefore, an alternative to investigate the dynamics of metabolic pathways is to use the biochemical knowledge, gathered by the in-vitro kinetics of the irreversible enzymes, to predict the system catalytic behavior to eventually compare the prediction with experimental data [11].

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