

MATHEMATICAL MODELING OF CELL SIGNALING REGULATORS DYNAMICS

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Common approach to mathematical modeling of cell signaling is biochemical reaction description via ordinary differential equations (ODE) using either the mass action law, or Michaelis-Menten kinetics, or Hill equation [1]. Regardless the type of chemical reaction and the way of its description there is always a rate constant coefficient before each equation term. The rate constant coefficients are usually considered constant.

In normal cell at physiological conditions there are multiple signaling pathways regulated by hormones, metabolites, calcium ions, and others. No regulators levels are constant, their concentrations and activity is continuously changing depending on cell state [2]. Along the way, rate constants of processes they activate or suppress are changing too. Although researchers usually single out two distinct states of the regulated process – either active or inactive, there is still somewhat sharp but rather continuous change in regulators concentrations and hence rates of regulated processes.

Thus, it is natural to describe cell signaling regulators dynamics and their effect in terms of fuzzy logic approach [3], or in terms of activation function commonly used in neural networks modeling.

We adapt this approach to construct a dynamical model of glucose and lipid metabolism signaling pathways in hepatocyte [4]. Our model allows to qualitatively estimate the role of certain signaling dysfunctions to hepatocyte functioning pathology development.

References:

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