

Summary of the doctoral dissertation - Methods for energy metabolism modeling using queueing theory

The text discusses the use of queueing theory methods in computational biology, specifically in the modeling of biological pathways like the Krebs cycle, pentose phosphate pathway (PPP), and the insulin signaling pathway. Computational biology models can be used to simulate the behavior of biological systems and predict the outcomes of different treatments or interventions. The queueing theory method is used to track the relationships between individual metabolites formed at different stages of the pathway and to observe changes caused by fluctuations in metabolite concentrations and their impact on the entire pathway. This type of model can be used to predict the impact of therapy, which in turn will lead to an increase in its effectiveness. The text also mentioned that the model obtained stability based on the data derived from scientific papers.

Computational biology models can be extremely useful in precision medicine, as they can help predict how a patient will respond to a particular treatment. By simulating the patient's biology, these models can identify the specific genes, proteins, and pathways that are driving a disease and predict which drugs or other treatments will be most effective. This can lead to improved patient outcomes, reduced side effects, and reduced healthcare costs. These models can be used to simulate the interactions between metabolites, proteins, and other biomolecules.

The developed models were based on different kinetics equations that describe the rate of enzyme-catalyzed reactions. The models of the Krebs cycle and PPP used Michaelis-Menten kinetics equations, which are commonly used to describe enzyme kinetics and take into account the substrate and product concentrations and kinetic properties of given enzymes. On the other hand, the model of the insulin signaling pathway was based on mass action law, which describes the rate of reactions based on the concentrations of the reactants and products. This choice of kinetics equation reflects the specific characteristics of each pathway and the goals of the presented research.