

Abstract

English

Obesity is nowadays one of the most severe health problems. It causes different diseases that reduce life quality. The existence of a mathematical model that could simplify the testing of new research ideas, before time and costs consuming *in vitro* and *in vivo* experiments are employed, is of major interest and importance.

Here three different models of adipogenesis are presented. One model consists of a system of ordinary differential equations and is able to reproduce the gene expression profiles of some of the well known adipogenesis regulators, inhibitors and markers like Ppar γ , Cebp α , Gilz, Gata2, Fabp4 and Scd1. Another model is based on an echo state network that models the interactions between the key players of adipogenesis. This model is capable of predicting the gene expression levels in response to a certain adipogenic cocktail out of the gene expression levels in response to other adipogenic cocktails. The third model is based on so called "essential genes". From these genes a subset is chosen to be employed in the parameter estimation of the model. The "impact" of each gene on the dynamic behavior of the model is computed. In this way a list of new genes, sustained by biological research, is proposed for further studies. These genes could play an important role in the process of adipogenesis.

Keywords: adipogenesis, mathematical model, *in silico*, differential equation, neural network, "essential" genes