Hybrid Models for Gene Expression Dynamics

In Systems Biology, microarray technology has made it possible to derive timed measurements of gene expression levels for different genes under specified environmental conditions. Two basic classes for modelling of the gene expression dynamics coexist: discrete valued models reflecting quantized measurement sequences, and continuous valued models.

A hybrid modelling approach based on Zhegalkin polynomials is presented, that tries to combine the advantages of both classes. Parameter identification of these hybrid models can be formulated as quadratic mixed integer programming with constraints given by the so called canalizing property. First results on hybrid modelling of yeast gene dynamics are discussed.