REDUCTION OF GENE NET DYNAMIC MODELS USING PROPER ORTHOGONAL DECOMPOSITION

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Key words: *plant growth, auxin, gene net, differential equations, model reduction, proper orthogonal decomposition.*

Motivation and Aim: One of the problem in analysis of gene net differential equation models is a large amounts of high-dimensional data (tens and hundreds variables and parameters as well as hundreds and thousands time points). But real model dimension may be much lower as a result of intrinsic system regularity. One may well do a regularity detection with the aid of proper orthogonal decomposition (POD). The POD-transformation is the way of the reduction of system differential equations to the one with much less dimension. Such system may be more simple than initial. POD is rare used in biology, but is usual practice in technical sciences [1-2].

Methods and Algorithms: The essence of POD is the singular value decomposition (SVD) of matrice "time points – variables", i.e. trajectory of dynamic system in multidimensional space, and truncation of axes (factors) with small or null variations. The remain factors are a linear combinations on the whole set of variables and are the new integral variables describing the same dynamic system with minimal waste of information. The reverse is true also, source variables are the linear combinations of new factors. The substitution of these combinations in the source differential equations result to a system of differential equations via new factors.

Results: We investigated a family of the trajectories of the plant root growth under the auxin influence gene net dynamic model with 30 variables and different sets of initial parameters. The first factor had 68% total variation, four first factors – 80% and the ten first factors – 99%. All source variables made basic contributions in first factor except "chloroplast cytolasm cell membrane TOP" and "peroxisome cytolasm cell membrane TOP". These variables made basic contributions in the next three factors. Thus, ten integral variables quite enough for this system formal description. Nevertheless, a biological interpretation of these factors is necessary. It is a difficult but interesting task.

Conclusion: POD-transformation of gene net differential equation models is new perspective tool for such systems studies. Further investigations in this direction are need.

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