SOFTWARE AUTOMATED PACKAGE FOR ANALYZING THE DYNAMICS OF CONTROL GENE NETWORKS

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Resume

Motivation:

Control gene networks (CGN) are structured most intricately and have a variety of possible behavior regimes, leading to considerable problems in studies of their properties on the level of analytical constructions exclusively. For this reason it seems necessary to invoke some additional investigation techniques, particularly computer modeling and computer experiments.

Results:

The present program complex realizes the method of generalized threshold models (GTM) for the analysis of the dynamics of the molecular genetic control systems (MGCS) and is intended to analyze the eukaryotic CGN dynamics with regard to cellular divisions and phases of a cellular cycle.

Availability:

This application software is available on request from the author.

Introduction

The CGN computer modeling expects the solution of two relatively independent problems. On the one hand, one should formulate the description of CGN as a dynamic system made up of many interacting elements, which are different by their nature and occupy different levels of the internal hierarchy, and the interactions themselves (regulatory bonds). On the other hand, this is the program realization of mathematical methods to study the dynamics of CGN functioning on qualitative and quantitative levels. In this work the solution of both formulated problems are presented.

Program structure

The system comprises five principal modules (Fig. 1): CME, DataBase, MGCS/MGTM, IDV and ODV.

1. The CME-module supports the construction and modification environment for CGN models with an arbitrary complexity.
2. The IDV-module provides a visual representation of the characteristics of the CGN model.
3. In the MGCS/MGTM-module the GTM method has been directly realized, and it allows to plot the diagrams of gene activities, kinetic curves for concentrations of gene products (mRNA and proteins), “phase portraits” in the plane (for two genes), and exact values of respective variables.
4. The ODV-module provides a visual representation of output data in the graphical and tabulated forms.
5. The DataBase-module is meant to store computer experimental data (with the required set of operations: insertion, deletion, extraction and automatic allocation of an element like the CGN model in the program environment).

Methods and algorithms

The program has been developed in terms of object-oriented programming based on peculiar features of the problems on portrait modeling of the behavior of biological systems. The concept of describing an MGCS-type object is based on the gene network mathematical model in the GTM method [1]. With the aim to retain a biological meaning of actual MGCS properties at the level of program realization a direct correlation is

Figure 1. Main components of the program and the diagram of their interactions.
established between the elements and functions of the real MGCS and the components of data structures it is described with. To accomplish this a correlation is made among the objects from different conceptual, logical and functional systems. Thus, MGCS genes are correlated with genetic blocks of its mathematical model; on the basis of the description of the model elements some abstract classes of program realization are elaborated ("MGCS", "Genetic Block", "Genetic Block Control System", "Genetic Block Controlled System", "Regulatory Zone", "Regulatory Interaction"), which classes are a combination of fields, methods and properties reflecting the structure and functional association of the MGCS elements. The arrangement of interaction procedures among the objects with the specific types of abstract classes in question makes it possible to model the behavior of arbitrary MGCS more or less complex (MGCS/MGTM-module). In the DataBase-module the representation is based on tables in the database format "Paradox 7.0" ("MGCS", "Gene", "Site") and their interrelations. The "MGCS" table stores the data of computer experiments on the models; structures of the "Gene" и "Site" tables agree with the fields of the lowest hierarchic levels of the "Regulatory Interaction" and "Genetic Block" classes respectively. In the CEM-module the CGN model is realized through the bidirectional self-connected list, thus making it possible to "collect" its structure in the dynamic manner from an arbitrary number of standard-type elements ("Genetic Block" and "Regulatory Relation").

Implementation and results

With the aid of the developed software an attempt has been made to analyze the dynamics of control subsystem for morphogenesis of Arabidopsis thaliana flower [2], and also the efficiency of the GTM method has been estimated as compared with a specific algorithm [3]. Preliminary data have been got on the dynamics of the system controlling the plane development of the Dr. melanogaster plant. The proposed approach is also good in analyzing the dynamics of other CGN.

References