**THE EQUATIONS OF DYNAMICS OF GENES ACTIVITIES IN A GENERAL VIEW.**

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During last 30 years numerous attempts to study dynamics of great multicomponent molecular-genetic control systems have been made by means of mathematical modeling using various mathematical theories [1-5]. The method of generalized threshold models enables to obtain kinetic curves for macromolecular components (DNA, RNA, proteins) of both pro- and eucariotic molecular genetic control systems of varying complexity [4,6]. However, during investigation of processes of inheritance, determination and differentiation it would be necessary to have a more simple formalism for modeling qualitative features of genetic networks, that would be invariant for details of specific molecular mechanisms of control of genes expression. An example of such formalism is given in this report.

http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image1.gif

Let’s name gene *j* switched on, if the subprogram of formation of primary genetical products is realized, otherwise we shall name gene *j* switched off. Let’s assign to each gene *j* binary value http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma_j.gif, and  
The value http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma_j.gif we shall interpret as ***activity of gene j***.  
Let’s take the basic premises necessary for the further constructions.

***Postulate 1.*** The activity of each controlled gene of the genome is identically determined by regulatory molecular products of genes from this genome.

***Postulate 2.*** If gene is active, the concentration of its product increases until maximal value; if gene is inactive, the concentration of its product decreases up to the minimal value.

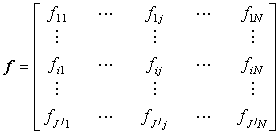
***Postulate 3.*** For each regulatory substance specific to some gene (genes) there exists such an effective concentration, which changes the activity of a gene this regulatory substance is specific to.

For the control processes of a genetic level we shall accept the following premise.

***Postulate 4.*** The activity of regulatory gene cannot change instantly (principle of "inertia").  
Thus, as well as in a general case, the processes of genetic control are discrete.  
Further we shall consider genetic blocks *Gj*, i.e. gene j, which is taken in combination with mechanisms of transcription, processing, transport, translation and depot of its final product [7]. In cell genetic network let’s isolate control subnet Sc(*G*) which can be presented as finite loaded oriented graph with genetic blocks from finite set http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image2.gif on its tops and with the arches that are information channels of connection between outputs of one block and inputs of other genetic block. According to a postulate 4 the activity of a gene can’t change instantly, and the processes of control are discrete, therefore we choose a discrete temporary scale, i.e. http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image14.gif. Let’s notice that the segment between two adjacent moments of time that is measured in terms of physical time, is not so necessary to be equal to an interval between two other adjacent moments of discrete time. If each genetic block *Gj* contains only one gene *j*, the set of genetic blocks G unequivocally can be characterized by cortege  
http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image3.gif,  
which we shall name as a http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma.gif***-vector of genes activities***, where every component of a http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma.gif-vector – the function from time http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma_j.gif=http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma_j.gif(*t*), thus ***Г***=***Г***(*t*). Let’s notice that values of components of http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma.gif-vector can be observed experimentally by fixing presence or absence of products of the appropriate genes in the given moment of the time. Therefore we shall call function ***Г***(*t*), which at any moment of time *t* puts in correspondence to each element (genetic block) of subnet Sc(*G*) its activity in this moment:  
http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image4.gif,  
where http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma_j.gif – activity of an element *Gj* at the moment of time *t*, ***observable behavior of a control genetic network.***

Let’s choose an segment of time http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image15.gif, where http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/nju.gif – intermediate value of discrete variable *t*, and http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image16.gif. With reserve we shall accept the following rule.

***Postulate 5.*** Neither elements (genetic blocks), nor functional relations between them do not change during time of observation, i.e. during a segment of time http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/teta.gif the structure of genetic network Sc(*G*) does not change.

After formalization of these postulates by simple layings out the generalized equations of activities dynamics for ***autonomous*** (i.e. not having entrance channels) and ***non-autonomous*** genetic networks are obtained. For autonomous control net http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image13.gif, where the bottom index "e" means eucariotical nets, the equation of dynamic for http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma.gif-vector is:  
http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image6.gif, (1)  
where http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image7.gif – http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma.gif-vector of activities of all elements of a network http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image13.gif; ***F*** – column of dimension *N*x 1, which elements are Boolean functions (***"composition" of logic structures***);  
,  
where each element *fij* of a matrix ***f*** is a restrictedly-determinated operator which link internal variable v*ij* with a sequence of input signals e*ij*, entering on *i* input channel of *j* genetic block; http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image9.gif – value of the output signal maximal delay among all *G*-blocks, affecting the given one (*Gi*).

As activities of genes frequently depend on influences that are external for control system, the case of autonomous subnet is not real. Therefore we shall consider non-autonomous subnet http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image13.gif which also consists of *N* elements but has *H* input channels which are not connected to any output channel of any element from subnet itself. Then for non-autonomous control network http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image13.gif it is easy to receive the equations of dynamics similar to expression (1):  
http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image11.gif (2),  
where http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image12.gif – 0,1 word of length *H*, and *H* – number of output channels of subnet http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image13.gif.

So, for knowing the valuation of a http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/gamma.gif-vector of activities ***Г***(*t*) of control genetic network Sc(*G*) at the moment of time http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image17.gif, and http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image18.gif, it is necessary to know the observable behavior of this network and values of input signals on a finite time segment with length of n discrete time units, where http://www.bionet.nsc.ru/meeting/bgrs/thesis/26/Image19.gif – length of a such half-segment, in which values of any input variable e*ij* of arbitrary genetic block *Gj* are equalized according to postulates 2,3.

When interpreting this result it is possible to make the following untrivial conclusion.

*If the observable behavior of control genetic network and values of input influences during a final time segment is known, it is possible to identically predict behavior of a network in every subsequent moment of time irrespective of the concrete molecular mechanism of regulation of expression of genes (at a level of transcription, processing, translation, etc.).*

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