

Proceedings  
of

# ITAFE'05

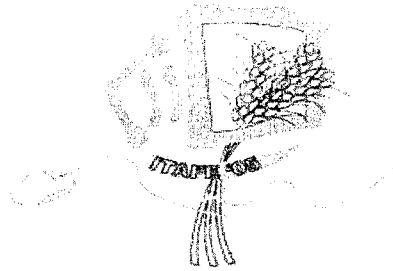
International Congress  
on  
Information Technology  
in  
Agriculture, Food and Environment

October 12-14, 2005  
Çukurova University, Adana, Turkey

## VOLUME I

Editors

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ISBN 975-487-125-6

## Development of Dynamic Model for a Biological System Under Conditions of Insufficient Information

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**Abstract.** Methodology for development of dynamic model for a biological system under conditions of insufficient information is developed including algorithm and description of methods. Methodology is orientated to create a model, which can be used later for development of artificial control system (ACS) for the biological system. Therefore the biological system is analysed as a set of control loops of biological control system (BCS), which later has to collaborate with control loops of ACS.

Methodology includes 2 stages: 1) creation of topological model to find out the structure of the object as a BCS and 2) implementation of functional relationships between structural elements to develop a dynamic model of BCS and verify it by experimental data.

Methodology is described by an algorithm, which includes following methods:

- the surveys of experts and "brainstorming" experiments to obtain the necessary information for the development of the model and testing,
- development of dynamic model of the biological system with the software package Powersim Constructor 2.51. linking it to Microsoft Excel software for the purpose of the data exchange,
- verification by means of the software package Powersim Solver 2.0 using genetic algorithms.

Big attention is paid to the application of methods of expert survey and data mining because modelling takes place under conditions of insufficient information about a biological system.

Verified dynamic model of BCS can be used as a final product to analyse behaviour of biological system or as a first step to create efficient ACS to control the biological system.

**Keywords.** *dynamic model, biological system, topology, experts*

### Introduction

The unsuccessful examples of the control systems of the biological systems despite the rapidly growing possibilities of the computer technology prove that insufficient and incomplete methodology of the development of computer control becomes the factor disturbing the development of the computer prediction and control systems of biological systems.

The weak item is insufficient methodology base in the meaning of the operation of biological systems and their simulation. This can be especially seen in the case of multiparameter control with insufficient information on the object. Insufficient understanding of the processes taking place in the biological system leads to the development of unsuitable control system.

The approaches to the simulation of the biological systems found in the literature are quite specific and focused on particular directions because the term of simulation in the biology is very wide (Antamonov, 1977; Lisenkov, 1979; Renshaw, 1995; Schmidt, 2000). In the literature no methodology or algorithms of the simulation or research of the biological systems from the viewpoint of the control of the biological systems and transitional processes during control have been found.

The simulation of biological system from the system control viewpoint is related to several problems and these are the problems not characteristic of the technical systems. In the case of the biological systems there is no unambiguous information on the principles of the construction, relations of causes – consequences and interaction with the environment because this system has not been constructed by a man for particular targets by the means selected by a man. This factor restricts the possibilities of application of the simulation methods of the technical systems where methodologies are more developed.

As the dynamic model of biological system is related in this paper to the later possible use to create the artificial control system (ACS), the biological object is analysed as a set of control loops of biological control system (BCS).

The goal of the paper is to create the methodology for the development of the dynamic model of biological system under the conditions of incomplete information on the regularity of the operation of the biological system.

### Methodology of Model Development of BCS

It is assumed that no model of the biological system is available and it has to be developed from the very first stage. As the system is assumed to be complex the model is built starting with the structure of biological system in a static model and continued by adding to the static model functional relationships at a later stage.

The algorithm for the development of the BCS model is shown in Figure 1.

### Development of Static Topological Model of BCS

The development of the model starts with the application of the topological simulation (Ore, 1962; Osis, 1969, 1970, Osis et al. 1991). Use of topological modelling is caused by its flexibility regarding implementation of changes. That is very important in circumstances of insufficient amount of information, which requires possibility of easy and quick structure change of the model.

The operation of the set of the parameters  $B$  of the biological system existent in the nature under the conditions of set of environmental parameters  $V$  can be described in the form of the model

$$M_b = F_b(b_1, \dots, b_k; v_1, \dots, v_s; t), \quad (1)$$

$$b_k \in B, v_s \in V, B \cap V = \emptyset,$$

where  $b_1, \dots, b_k$  – the variables characterising the biological system (internal control loop) belong to the set of the parameters  $B$  of the biological system,  
 $v_1, \dots, v_s$  – the variables characterising the environment, belong to the set of the parameters  $V$  characterising the environment,  
 $t$  – time.

Reproduction and metabolism is a common feature of all the biological systems. The description of these processes can be used as the initial point for the simulation when the biological system is viewed in totality as a population.

When a process within the biological system or its part is viewed, the food, energy, heat, time or other balance can be used as the initial data. These can be viewed independently of each other or in relation.

As it is necessary to take into consideration many functional correlations relating the variables of the biological system  $b_1, \dots, b_k$  to the variables of the biological system and environment  $b_1, \dots, b_k$  and  $v_1, \dots, v_s$ , the initial model is developed by means of the topological modelling. In this stage of the development of the model cooperation of the experts of the biological system and knowledge engineers is necessary.

The algorithm for the development of the BCS model  $M_b$  is shown in Figure 1. The description of the operations contained in the algorithm (**in bold**) has been provided for every step of the algorithm.

**Definition of the control targets** is intended for the specialisation of the model from the point of view of control system to be developed.

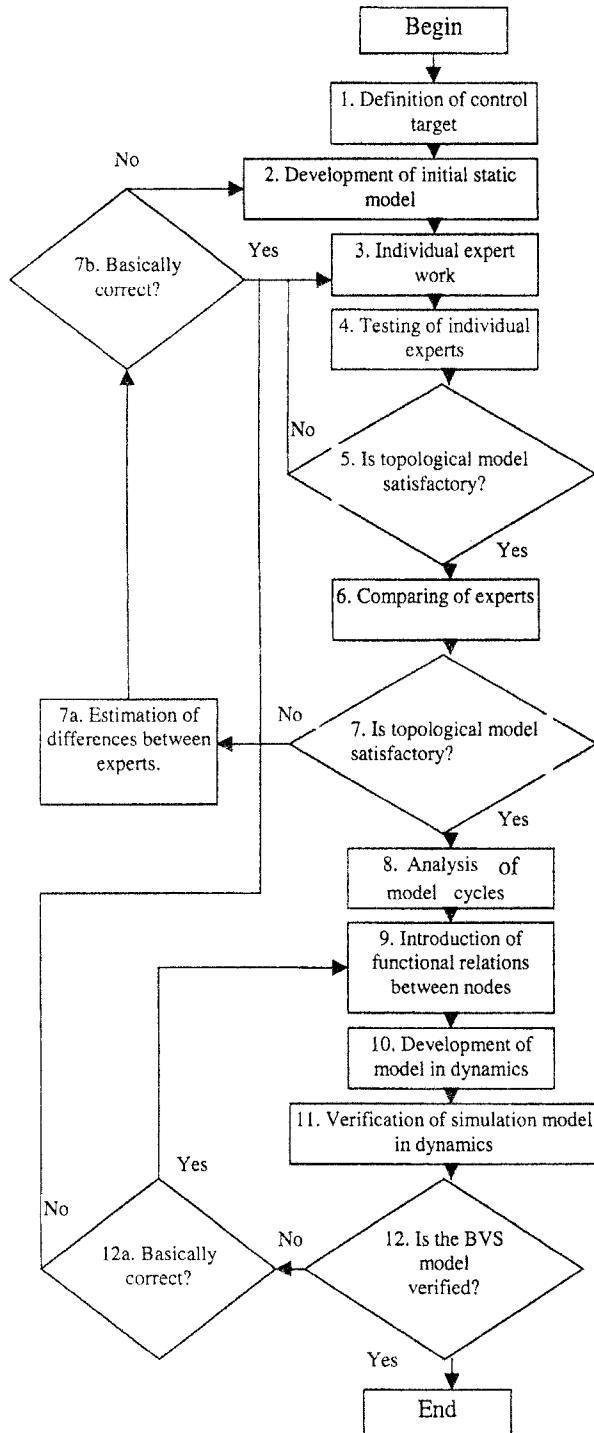


Figure 11. Development algorithm of BCS model.

The control task is being solved to satisfy the set of the control targets  $G\{g_1, \dots, g_q\}$

$$G = F_g(b_k, v_s, t), \quad (2)$$

where  $k=1, K; s=1, S$ .

The control targets  $G$  can be clearly defined in the definition of the control task, or these should be reduced to the particular parameters characterising the system when the targets have been defined generally. Further detailed study of the system will be devoted only to the processes related to the control target thus permitting to reduce the extent of the model to the minimum required.

**The initial static topological model** is the first iteration of the following topological model

$$M_t = F_t(b_1, \dots, b_K; v_1, \dots, v_S; \dots, v_S). \quad (3)$$

It is necessary as the basis for further statements by the experts at the stage of the expert survey. The initial model is developed referring to the data in the literature or with the participation of some of the experts to be invited later on.

Further improvement of the model is done by the experts introducing the changes to the model  $M_t$  (Stalidzans and Markovics, 2000, Stalidzans 2005). Incidence matrix and the topological model as the kinds of the information reflection are applied for making the model more precise by experts in iterative process first individually (cycle: **individual expert work, testing individual experts, satisfactory model**). Individual expert work is followed by **comparing of experts**. If the result is not **satisfactory model** and after **estimation of differences between experts** does not appear **basically correct** the initial topological model can be changed.

The evaluation of the information provided by the experts based upon the level of the concord of the experts is made depending on the type of the survey: direct estimation or comparison of pairs.

In case of the direct estimation of the parameters the level of concord of the experts is evaluated based upon the concordation coefficient  $W_t$  (Kendall, 1955, Djakova and Krug, 1966) in compliance to the following formula:

$$W_t = \frac{12 \sum_{i=1}^n \left\{ \sum_{j=1}^m r_{ij} - \frac{1}{2} m(n+1) \right\}^2}{m^2 (n^3 - n)}, \quad (4)$$

where  $n$  - number of estimated objects in the group,  
 $m$  - number of experts,  
 $r_{ij}$  - rank of object  $i$  accordingly to estimation of expert  $j$ .

In case of the comparison of the pairs the level of concord of the experts is determined based upon the concordation rate  $W_p$  in compliance to the following formula (Kendall, 1955, Djakova and Krug, 1966):

$$W_p = \frac{4(\sum \partial_{lk} - m \sum \partial_{lk} + C_m^2 C_s^2)}{m(m-1)s(s-1)} \quad (5)$$

where  $\partial_{lk}$  - numbers in the table of pair comparison;  
 $l=1, \dots, s; k=1, \dots, s$  - indexes of comparable objects;  
 $s$  - number of comparable objects;  
 $m$  - number of experts;  
 $C_m^2$  - number of conformities from  $m$  each 2;  
 $C_s^2$  - number of conformities from  $s$  each 2.

The value of the concordation coefficients  $W_t$  and  $W_p$  varies within the scale  $0 \leq W \leq 1$ , and  $W=0$  of there is no relation between the ranks and it is 1, if all the experts have rated the objects the same. The value  $W \geq 0,5$  is considered sufficient for the concordation rate when it is considered that the concord

between the experts is sufficiently high. In case when the concordation coefficients are satisfactory the obtained average values or the weight rates can be used.

When the number of the experts  $m$  is small the role of every expert increases. Consequently the inaccuracy of any single expert's view strongly influence the average arithmetic value. Another methodology for obtaining the resulting assessment is applied for the prevention of this effect. It is known that the essence of the evaluation by the experts is obtaining an unknown value as an incidental value the distribution of which is judged based upon the individual evaluations by the experts. Thus the initial data massive of the experts' views should be processed based upon the mathematical statistics concepts. In case when the number of experts is small the average arithmetic value is not the best way for obtaining the resulting assessments.

Therefore the evaluation of every  $i$  parameter should be defined as the mathematic expectation of the average value  $C$  which is calculation on iterative bases where the formula for  $q$  iteration is (Voronin, 1974).

$$C_q = \frac{\sum_{j=1}^m C_j \exp\left[-\frac{1}{2\delta^2}(C_{q-1} - C_j)^2\right]}{\sum_{j=1}^m \exp\left[-\frac{1}{2\delta^2}(C_{q-1} - C_j)^2\right]} \quad (6)$$

where  $C_j$  - evaluation of expert  $j$  of the object  $i$ ,  
 $C_{q-1}$  - result of previous iteration,  
 $q=1, \dots, \mu$  - iterations,  
 $\delta$  - standard deviation,  
 $m$  - number of experts.

On the first iteration it is recommended to apply the average arithmetic value

$$C_1 = \frac{1}{m} \sum_{j=1}^m C_j \quad (7)$$

Then in compliance to the procedure of iterations the exact value should be found. The iterative process has been completed when the changes of the value between iterations are lower than the permitted error.

Following the development of the topological model **the analysis of the cycles of the model** should be performed defining the particular BCS loops in the biological system itself.

#### Development of Dynamic Model of BCS and Its Verification

If the experts decide that the topological model  $M_t$  sufficiently well depicts the relation of the biological system and the environment parameters the study of the system should be continued in the dynamics and **the introduction of the functional relations between the nodes** is required. The topological model and its incidence matrix developed for the application case (the model for the temperature control of wintered bee colony) can be seen in Figure 2 and Table 1 respectively.

The static topological model  $M_t = F_t(b_1, \dots, b_k, \dots, b_K; v_1, \dots, v_s, \dots, v_S)$  is homomorphly changed into the dynamic model  $M_b = F_b(b_1, \dots, b_k, \dots, b_K; v_1, \dots, v_s, \dots, v_S; t)$  applying the software package *Powersim Constructor 2.51* (POWERSIM). The parts of the dynamic model can be seen in Figure 3.

Choice of *Powersim Constructor 2.51* dynamic modelling software is determined by its flexibility in relation to the changes in a model, simple user interface and possibility to connect with the *Microsoft Excel* program for information exchange.

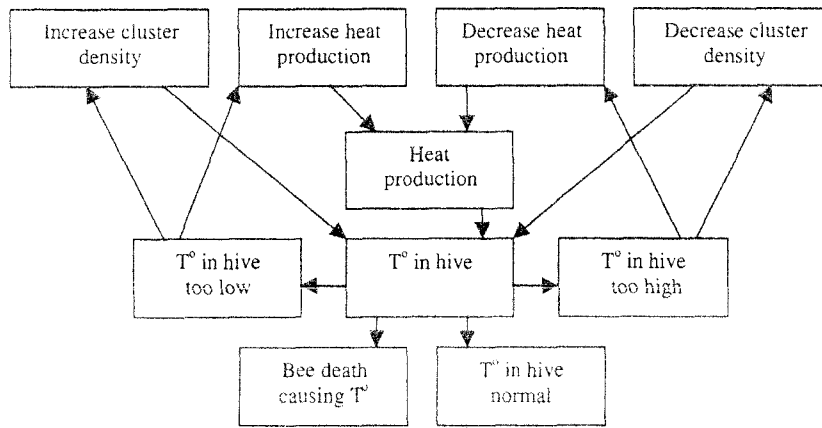


Figure 12. The topological model for the temperature BCS of wintered honeybee colony.

Table 1. Incidence matrix for the temperature BCS of wintered honeybee colony.

		1.	2.	3.	4.	5.	6.	7.	8.	9.	10.
1.	Increase cluster density	X						1			
2.	Increase heat production		X			1					
3.	Decrease heat production			X		1					
4.	Decrease cluster density				X		1				
5.	Heat production					X		1			
6.	T° in hive too low	1	1				X				
7.	T° in hive						1	X	1	1	1
8.	T° in hive too high			1	1				X		
9.	Bee death causing T°									X	
10.	T° in hive normal										X

Under the conditions when sufficient information on the relations between the nodes is not available the surely known data to be expressed in the form of equation become the most valuable basic information of the model. These can become the tools for turning down the low quality data as deficient. Instead of the unknown relations it is necessary to introduce very approximate functions initially and they can be updated in the process of simulation.

**Development of the simulation model in dynamics** (model  $M_b$ ) comprises one of the most important stages of the work - tuning the model on which the level of similarity of the model to the simulated processes in the biological system depends.

**Verification of the simulation model in dynamics** should be performed by the data collected in the nature and registered.

The verification operation is intended for checking the correctness of the simulated data of the model. It is necessary to minimise the deviations of the model from the measurements obtained in the field tests  $M_i = F_i(b_1, \dots, b_k, \dots, b_K; v_1, \dots, v_s, \dots, v_S; t)$ .

$$\Delta_{ver} \geq |M_b - M_i| = F_b(b_k, v_s, t) - F_i(b_k, v_s, t), \quad (8)$$

where  $\Delta_{ver}$  - difference between the field measurements  $M_i$  and the system model  $M_b$ ,  $k=1, K; s=1, S$ .

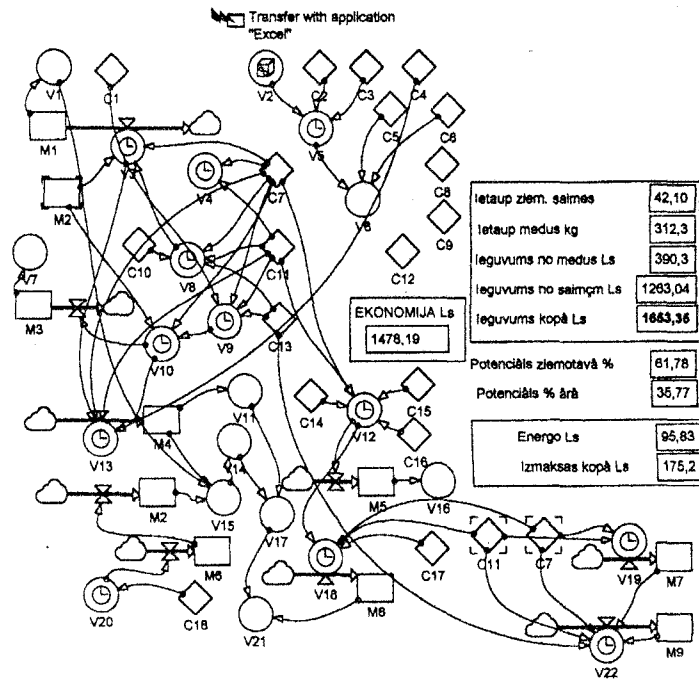


Figure 13. Part of microclimate BCS model of bee colony in form of diagram (Powersim Constructor 2.51).

The maximum permitted verification error  $\delta_{mver}$  can be specified separately for every parameter of the set B:

$$\delta_{ver k} \geq |F_0(b_k) - F_1(b_k)|, \quad k=1, K. \quad (9)$$

It is necessary to attempt to minimise the deviations from the measurements performed in the nature paying major attention to the comparison of the tendencies (growth, decrease, stagnation). When the difference between the test data  $M_1$  and the model data  $M_0$  has become lower than the permitted  $\Delta_{ver}$ , the **BCS model verification** has been performed and the model of the biological system  $M_b = F_b(b_1, \dots, b_K; v_1, \dots, v_S; t)$  can be considered as established. In the further operations this will replace the biological system.

Verification is done by software *Powersim Solver 2.0*, which works with model created on *Powersim Constructor 2.51*. It provides flexibility and modifications done in the BCS model do not need to be changed for *Powersim Solver 2.0* (POWERSIM). This software optimise coefficients in the functional relationships of the model, which are permitted to be changed (limits can be set for each coefficient) using genetic algorithms thus allowing fine tuning of model to match the verification criteria or to find out, that a modification is necessary.

### Discussion

The way of creating the static model depends on knowledge quality about the biological object. "Brainstorming" has to be used in case if there is small amount of information about process to be modelled to get more versions about the structure of the object.

It can turn out, that there are several models of the biological object and group of experts divides into several groups. In that case there is sense to examine and develop all the models to find out the best of them in later stages.



Verification of dynamic model using Powersim Solver has no sense if the parameters, which satisfy verification criteria are impossible for the BCS. That can be adjusted by changeable parameter settings during tuning operations.

### Conclusions

Methodology for development of dynamic model for a biological system under conditions of insufficient information is developed. Methodology consists from an algorithm and description of methods to use it in practice.

It is suggested to use topological modelling to fix the structure of biological object and find out the control loops of biological control system (BCS).

Creation of a model in dynamics and its verification with experimental data is suggested to do using programs *Powersim Constructor* and *Powersim Solver*.

Structure of the model is adapted for its later implementation in the model with artificial control system (ACS) to perform the control process of several parameters of biological object.

The conclusions of the value of the paper and the development perspectives have been summarised: On the simulations based development of control system in case of the biological system diminishes necessary time and resources and carries considerable part of tuning of control system from the field experiments on computer simulations. Not of less importance is a complex understanding for the problem of control, which a model gives for each particular case.

The developed methodology is especially important in cases when the complexity of the system or lack of information to be studied determines the necessity for the collaboration and coordination of a big number of the computer experts and biologists. The algorithms for developing the models allow both the knowledge engineer and the biological expert to perform their model development procedure minimising the subjective influence by other experts.

The developed methodology has wide area of application in industries – biotechnology, pharmacy, food processing industry and agriculture.

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### Acknowledgement

This work has been partly supported by the European Social Fund within the National Programme "Support for the carrying out doctoral study programs and post-doctoral researches" project "Support for the development of doctoral studies at Riga Technical University"