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EVOLUTIONARY MODELING PROBLEMS IN STRUCTURAL SYNTHESIS OF INFORMATION NETWORKS OF AUTOMATED CONTROL SYSTEMS

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Abstract

This paper provides a new approach for solving a problem of modeling and structural syntheses of information networks of automated control systems by applying fuzzy sets theory, fuzzy logic and genetic algorithms. The procedure of formalizing structural syntheses of multi-level dispersed information networks of automated control systems is proposed. Also, the paper proposes a conceptual model of evolutionary syntheses based on genetic algorithms, which do not require additional information about the characteristics and features of target function. Modified genetic operators of crossover, mutation and algorithms of evolutionary syntheses of information networks systems are developed. Finally, the results of computational experiments on researching the influence of probability of the use of crossover and mutation operators, method of choosing parental pairs, and the size of initial population on the speed and precision of final results are provided.

Keywords:

Information Networks, Soft-Computing, Fuzzy Set Theory, Genetic Algorithms, Automated Control Systems

1. INTRODUCTION

The problem statement of designing the DCN (Data-computing network) in automated control systems as the problem of synthesizing a system with the specified quality is a complicated multi-step iterative process. It is impossible to know in advance all the circumstances to be faced in the design of the system and its operation [1, 2, 3, 4, 7, 12]. In addition, DCN designing is carried out mainly in conditions of uncertainty and vagueness of the initial information and it requires consideration of many factors, intractable rigorous quantitative assessment and engineering intuition of the decision maker (DM).

Complexity of accounting for such requirements is that, not being a specialist in the field of information technology, the customer usually formulates a number of conditions to the network performance, reliability and security, the possibility of its expansion and modernization, as well as the cost of its construction in the form of hard formalizing verbal assessments [3, 4, 5, 7]. All of this makes one learn the system in some simple, standard and non-standard situations and formulate specific functional requirements of the system, i.e. to make the first attempt to set a task-synthesis system with desired properties in terms of fuzzy initial information and uncertainty [3, 7, 8, 9, 11].

In general, any design process of DCN from local to corporate is implemented in the following sequence:

1) Problem identification of designing and selection of a standard network that best meets a number of set requirements.
2) The optimal structure determination of DCN, establishing composition and spatiotemporal interaction component modules of network. At the same time the amount and location of the subscribers' functional network stations as well as the structure of connections between them is revealed.
3) Choice of hardware and software implementation of the network from a set of alternative units, which perfectly provides task performance.

We will consider the problem of synthesis of optimal topological structure of DCN based evolutionary modeling in more details.

2. PROBLEM STATEMENT

Assume, there are geographically distributed DCN of automated systems, presented in the form of an undirected graph

$$G = (V, R), \tag{1}$$

where, $V = A \cup K$ - set of graph nodes, which corresponds to nodes of a network, R- set of edges of graph, which corresponds to communication channel of a network; $A = \{a_1, a_2,\dots,a_n{}^a\}$ - subset of user parts of a network and $K = \{k_1, k_2,..,k_n{}^k\}$ - subset of switching points of a network. Each element of the set $V = \{v_1, v_2,\dots,v_n\}$ is characterized by a collection of speeds of data transfer, on which given node can work with intensity of an information exchange $Q_i(\mu)$ where, $\mu = \{\mu_1, \mu_2, ..., \mu_{n_q}\}$ - set of network technologies.

The coordinates of user parts $A = \{a_1, a_2,\dots,a_n{}^a\}$ and switching points' coordinates $K = \{k_1, k_2,..,k_n{}^k\}$ data streams $Q_i(\mu)$ distance between network nodes $D^{ak} = \left\langle d_{ij}^{ak} \right\rangle, i = \overline{1, n_a}, j = \overline{1, n_k}$ and $D^{kk} = \left\langle d_{ij}^{kk} \right\rangle, i = \overline{1, n_k}, j = \overline{1, n_k}$ are given. There is a set of switching equipment of different types $H = \{h_1, h_2, ..., h_{n^h}\}$, various types of communication channels between user parts and switching points with data throughput $P^{ak} = \left\langle p_{ij}^{ak} \right\rangle, i = \overline{1, n_a}, j = \overline{1, n_k}$, $P^{kk} = \left\langle p_{ij}^{kk} \right\rangle, i = \overline{1, n_k}, j = \overline{1, n_k}$, cost of construction of communication channels $C^{ak} = \left\langle c_{ij}^{ak} \right\rangle, i = \overline{1, n_a}, j = \overline{1, n_k}$, $C^{ak} = \left\langle c_{ij}^{kk} \right\rangle, i = \overline{1, n_k}, j = \overline{1, n_k}$ and switching points $C^h = \left\langle c_j^h \right\rangle, j = \overline{1, n_k}$ are given. It is required to define structure of a network and its parameters, which minimizes efficiency function of many variables:

$$F = \sum_{i=1}^{n_a} \sum_{j=1}^{n_k} x_{ij} c_{ij}^{ak}(\lambda_{ij}, Q_i^a(\mu), d_{ij}^{ak}) + \sum_{i=1}^{n_k-1} \sum_{j=i+1}^{n_k} y_{ij} c_{ij}^{kk}(\lambda_{ij}, Q_{ij}^r(\mu), d_{ij}^{kk}) + \sum_{i=1}^{n_k} c_i^h, \tag{2}$$

under restrictions on: network topology and types of switching equipment (SE); data throughputs of communication channels amount of ports of switching points (SN- switching node); and values of their speed; delay of transfer of a package in communication channels; productivity in the frames of the switching equipment (SE) and maximal productivity of its system bus and size of the address table of switchboards.

Direct solution of this problem requires a numerical solution of the case with $n(n-1)/2$ variables. Since the structure of the network is defined as a graph, it is advisable to apply a mathematical apparatus of the theory of graphs. However, standard methods of graph theory cannot solve the problem of synthesis of optimal tree structure of the network due to the following reasons: first, for networks with a large number of subscribers and switching devices to find the optimal skeleton graph of many possible orders is not feasible. Second, the optimal tree structure of the network is not the shortest skeleton graph. This is because the cost of the network depends not only on the length of the communication channels, but also on their capacity, type and capacity of the switching equipment. Problem of synthesis is particularly complicated readability criterion function, in which acceptable switching devices and bandwidth of communication channels are taken from a fixed discrete set. Thus, we conclude that it is necessary to find a suboptimal solution based on evolutionary modeling methods, in particular by means of genetic algorithms.

3. SOLUTION OF THE PROBLEM ON THE BASIS OF EVOLUTIONARY SEARCH METHODS

It is necessary to determine the potential solutions in the chromosome space to solve the problem of structural synthesis using genetic algorithms.

S is the set of all possible space structures of potential solutions, designed network represented as a graph Eq.(1) and constraints on the system: the network topology and types of *SE*, bandwidth of communication channels, the number of ports *SN* and values of their speed, the delay in packet transmission communication channels, the performance in frames of *SE* and maximum performance of its system bus and address table size and switches.

Space of representations *Z*, which corresponds to all possible structures of a network from space S, shall present as:

$$Z = concat\,(Z^*,\ Z^{**}),$$

where, $Z^*=(z_1^*,z_2^*,\ldots,z_{n_a}^*)$ - part of chromosome, representing the information on interrelations between the users and switching points of a network; $Z^{**}=(z_1^{**},z_2^{**},\ldots,z_{n_k(n_k-1)/2}^{**})$ - part of chromosome, carrying the information on interrelations only between switching points of a network.

These parts of chromosome, we shall name respectively *FP* (First Part of Chromosome) and *SP* (Second Part of Chromosome) – parts of chromosome.

The elements of *FP* -part vector of chromosome, submitted by a vector Z^*, are strictly ordered according to numbers of the users of a network $a_i \in A, i=\overline{1,n_a}$. Every i^{th} element of a vector $z_i^* \in Z^*$ contains the number of switching point $k_j \in K$, by which the i^{th} user of a network is connected $a_i \in A$:

$$z_i^* = \begin{cases} k_j, & if\ \ a_i \in A\ connected\ to\ k_j \in K \\ 0, & if\ \ a_i \in A\ not\ connected\ to\ k_j \in K \end{cases} \tag{3}$$

SP- part of chromosome submitted by vector Z^{**} is concatenation of rows of adjacency matrix *Y*, laying above of the main diagonal,

$$z_{l^{**}}^{**} = y_{ij}\,,\ l^{**} = i + (i-1) * n_k - \sum_{\eta=1}^{i} \eta + |i-j|\,, \tag{4}$$

where, $i=\overline{1,n_k-1},\ j=i+\overline{1,n_k}\quad i<j$

Obviously, the length of the chromosome in such a coding is:

$$L = n_a + n_k\,(n_k - 1) / 2. \tag{5}$$

As a result of application of genetic operations of crossing or mutation there can be formed dead chromosomes, i.e. decisions which are not satisfying to parametrical and structural conditions of network $F(Z) = \infty$. For elimination of possible cases of dead chromosomes formation the modified crossover and mutation operators are offered.

4. MODIFIED OPERATOR OF CROSSOVERING

Let’s have two parental structures Z_1 and Z_2, submitted by the graphs $G_{cp1} = (V_{cp1}, R_{cp1})$ and $G_{cp2} = (V_{cp2}, R_{cp2})$. On the basis of these graphs it is necessary to receive graph $G_{cn} = (V_{cn}, R_{cn})$ appropriate to structure of descendant Z_3 formed as a result of applying crossovering operator.

For this purpose, we shall assign sub-graphs on the graph G_{cp1} and G_{cp2}

$$G_{cp1}^{ak} = \left(V_{cp1}, R_{cp1}^{ak}\right), G_{cp1}^{kk} = (K_{cp1}, R_{cp1}^{kk})\,, \tag{6}$$

$$G_{cp2}^{ak} = (V_{cp2}, R_{cp2}^{ak})\,, G_{cp2}^{kk} = (K_{cp2}, R_{cp2}^{kk})\,, \tag{7}$$

where,

$$G_{cp1} = G_{cp1}^{ak} \cup G_{cp1}^{kk},\quad R_{cp1}^{ak} \cap R_{cp1}^{kk} = \varnothing,\quad V_{cp1} \supset K_{cp1}\,,$$

$$G_{cp2} = G_{cp2}^{ak} \cup G_{cp2}^{kk},\quad R_{cp2}^{ak} \cap R_{cp2}^{kk} = \varnothing,\quad V_{cp2} \supset K_{cp2}\,.$$

Let's form the sets of communications channels that have no coincidence at G_{cp1} and G_{cp2}:

$$R_{ak}^* = (R_{cp1}^{ak} \cup R_{cp2}^{ak}) \setminus (R_{cp1}^{ak} \cap R_{cp2}^{ak})\,, \tag{8}$$

$$R_{kk}^* = (R_{cp1}^{kk} \cup R_{cp2}^{kk}) \setminus (R_{cp1}^{kk} \cap R_{cp2}^{kk})\,. \tag{9}$$

We introduce the following notation:

- $R_{ak_{cp1}}^*$, $R_{kk_{cp1}}^*$ - accordingly the subset of edge types <subscriber.node> → <switch.node> and <switch.node> → <switch.node>, belonging only to parental structure G_{cp1} $R_{ak_{cp1}}^* \subseteq R_{cp1}$ and $R_{kk_{cp1}}^* \subseteq R_{cp1}$;
- $R_{ak_{cp2}}^*$, $R_{kk_{cp2}}^*$ - accordingly the subset of edge types <subscriber.node> → <switch.node> and <switch.node>

$\rightarrow$ <switch.node>, belonging only to parental G_{cp2} $R^{*}_{ak_{cp2}} \subseteq R_{cp2}$ and $R^{*}_{kk_{cp2}} \subseteq R_{cp2}$, then

$$R^{*}_{ak} = R^{*}_{ak_{cp1}} \cup R^{*}_{ak_{cp2}}, \quad R^{*}_{kk} = R^{*}_{kk_{cp1}} \cup R^{*}_{kk_{cp2}} \qquad (10)$$

We define vertex set V_1^* and V_2^*, incidental edges out of the sets R^*_{ak} and R^*_{kk}. The position of edge components from sets V_1^* and V_2^*, respectively in vectors Z_1 and Z_2, the point of corssovering is defined.

We form set of weight factor of edges $W^{ak}\left(R^{ak}\left(V_1^*\right)\right)$ <subscriber.node> $\rightarrow$ <switch.node> types, incidental to users' part from the sets V_1^* and the set of weight factor $W^{kk}\left(R^{kk}\left(V_2^*\right)\right)$ which is <switch.node> $\rightarrow$ <switch.node> type, incidental to switch node from the sets V_2^* such as:

$$W^{ak}\left(R^{ak}\left(V_1^*\right)\right) = \left\{w_\gamma^{ak}\left(r_{ij}^{ak}(v_i)\right)\right\}, \qquad (11)$$

where, $w_\gamma^{ak}(r_{ij}^{ak}(v_i)) = \dfrac{F(Z_1) - F(Z_2)}{\sum_{l=1}^{N_p} F(Z_l)} + 0{,}5 - divide(d^{ak}_{sp1_{ij}} - d^{ak}_{sp2_{ij}})$,

$\gamma = 1, m_1^*, \forall_{v_i}, v_i \in V_1^*$, m_1^* - power of set V_1^*; d^{ak}_{cp1} – length of communication channel (CCh) (edge) $r^{ak}_{cp1_{ij}} \in R^*_{ak_{cp1}}$; d^{ak}_{cp2} – length of CCh (edge) $r^{ak}_{cp2_{ij}} \in R^*_{ak_{cp2}}$; divide($x$) $\in$ [0, 1] – brought (normalized) length value of CCh.

Weight factors of $W^{kk}\left(R^{kk}\left(V_2^*\right)\right)$ is computed by using the following formulae

$$W^{kk}(R^{kk}(V_2^*)) = \left\{w_\eta^{kk}(r_{ij}^{kk}(v_j))\right\}, \qquad (12)$$

where, $w_\eta^{kk}(r_{ij}^{kk}(v_j)) = \dfrac{F(Z_1) - F(Z_2)}{\sum_{l=1}^{N_p} F(Z_l)} + 0{,}5 - divide\,(d^{kk}_{cp1_{ij}} - d^{kk}_{cp2_{ij}})$,

$\eta = 1, m_2^*, \forall_{v_i}, v_j \in V_2^*$, m_2^* - respectively the power of set V_2^*; d^{kk}_{cp1} – length of CCh (edge) $r^{kk}_{cp1_{ij}} \in R^*_{kk_{cp1}}$; d^{kk}_{cp2} – length of CCh (edge) $r^{kk}_{cp2_{ij}} \in R^*_{kk_{cp2}}$; divide($x$) $\in$ [0, 1] – brought (normalized) length value of communication channels.

The formation Structure descendant G_{cn} = (V_{cn}, R_{cn}) is realized stage by stage solving the task of formation *FP* and *SP* - parts of chromosome descendant.

1) We form *FP* - parts of chromosome by way of section graph :

$$G^{ak}_{cn} = (V_{cn}, R^{ak}_{cn}),\ V_{cn} \subseteq V_{cp1} \text{ and } V_{cn} \subseteq V_{cp2}. \qquad (13)$$

Since all the network nodes are to be present in the structure of descendant, then set point of graph of the descendant G_{cn} is equal to the set point of graph, presented by any parent structure, i.e., $V_{cn} = V_{cp1} = V_{cp2}$. We determine subsets of edges R^{ak}_{cn} of the graph G^{ak}_{cp}, connecting user parts of a network to its switching point:

a) Let $R^{ak^0}_{cn}$ - empty set of edges of a <user part>$\rightarrow$< switching point> type. We add a subset of edges to set $R^{ak^0}_{cn}$, that coincide at parental structures G^{ak}_{cp1} and G^{ak}_{cp2}:

$$R^{ak'}_{cn} = R^{ak^0}_{cn} \cup (R^{ak}_{cp1} \cap R^{ak}_{cp2}). \qquad (14)$$

User parts which belong to a subset $A^{**} = A \backslash A^*$ remain not connected to the switching points after performance of the given operation in the sub-graph G^{ak}_{cn}, where A^* - subset of user parts of a network, that incident to the edges of the set $R^{ak'}_{cn}$.

b) In a random way let's choose number $\xi \in$ [0, 1] and form a subset of edges $R^{ak''}_{cn} = \left\{r^{ak''}_{ij}\right\}$, that incident to user parts $v_i \in A^{**}$, where,

$$r^{ak''}_{ij} = \begin{cases} r^{ak}_{ij_{cp1}} \in R^*_{ak_{cp1}}, \textit{if } w_\gamma(r^{ak}_{ij}(v_i)) < \xi, \\ r^{ak}_{ij_{cp2}} \in R^*_{ak_{cp2}}, \textit{if } w_\gamma(r^{ak}_{ij}(v_i)) \geq \xi,\ \gamma = 1, m_1^*, \end{cases} \qquad (15)$$

c) We unite subsets of edges $R^{ak'}_{cn}$ and $R^{ak''}_{cn}$: $R^{ak}_{cn} = R^{ak'}_{cn} \cup R^{ak''}_{cn}$.

The result is the sub-graph $G^{ak}_{cn} = (V_{cn}, R^{ak}_{cn})$ that displays the structure of *FP* -part of chromosomes of descendant, representing the information on connection of user parts of the network with the appropriate switching points (Fig.1).

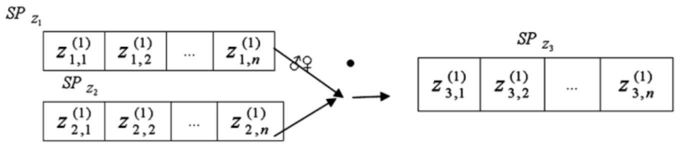

Fig.1. Structure *SP*- parts of descendants

2) We form *SP* - part of chromosomes as sub-graph:

$$G^{kk}_{cn1} = (K_{cn}, R^{kk}_{cn}), \qquad (16)$$

where, $K_{cn} = K_{cp1} = K_{cp2}$ and $K_{cn} \subseteq V_{cp1}$, $K_{cn} \subseteq V_{cp2}$.

From $V_{cn} = V_{cp1} = V_{cp2}$, we obtain $K_{cn} = K_{cp1} = K_{cp2}$. Granting this, the decision of the second subtask can be reduced to definition of a subset of edges $R^{kk}_{cn} \subseteq R_{cn}$:

a) Let $R^{kk''}_{cn}$ - empty set of edges of <switching point> $\rightarrow$ <switching point> type. We define a subset of edges, that coincide at parental structures G^{kk}_{cp1} and G^{kk}_{cp2}:

$$R^{kk'}_{cn} = \left(R^{kk}_{cp1} \cap R^{kk}_{cp2}\right) \qquad (17)$$

We divide the subset of switching points K_{cn} to two nonintersecting subsets K^*_{cn} and K^*_{cn}:

$$K_{cn} = K^*_{cn} \cup K^{**}_{cn},\ K^*_{cn} \cap K^{**}_{cn} = \varnothing,\ K^{**}_{cn} = K_{cn} \setminus K^*_{cn}, \tag{18}$$

where, K^*_{cn} - subset of switching points of the network, that incident to the edges of set $R^{kk'}_{cn}$, K^{**}_{cn} - subset of weighted switching points.

b) Casually choosing switching point $k_i \subseteq K^{**}_{cn}$, we find an edge r^*_{ij} from subset of the edges R^*_{kk}, that connects it with any other switching point $k^*_j \subseteq K^*_{cn}$ on minimum expense criterion, i.e. $r^*_{ij} = \min\{R^*_{kk}\}$. We shall add found edge in a subset $R^{kk''}_{cn}$, and translate switching point k_i from subset K^{**}_{cn} to K^*_{cn}:

$$K^*_{cn} = K^*_{cn} \cup k^*_i,\ K^{**}_{cn} = K^{**}_{cn} \setminus k^*_i. \tag{19}$$

The search of an edge r^*_{ij} from a subset of edges R^*_{kk} is carried out as long as the subset of the weighed vertexes will not be empty, i.e. $K^{**}_{cn} = \varnothing$.

c) We unite subsets of edges $R^{kk'}_{cn}$ and $R^{kk''}_{cn}$:

$$R^{kk}_{cn} = R^{kk'}_{cn} \cup R^{kk''}_{cn}. \tag{20}$$

d) In case of $K^{**}_{cn} = \varnothing$ in graph $G^{kk}_{cn1} = (K_{cn}, R^{kk}_{cn})$ there are formed isolated sub-graphs. These sub-graphs is sequentially united with the help of the casually chosen edge r^{**}_{ij} from set of all possible edges R.

After performance of the given operations we have *SP* - part of chromosomes of descendant, representing information on connection of switching points among themselves as a sub-graph:

$$G^{kk}_{cn} = (K_{cn}, R^{kk}_{cn}). \tag{21}$$

We can define the graph $G_{cn} = (V_{cn}, R_{cn})$ that represents the chromosome structure of descendant Z_3, as:

$$G_{cn} = G^{ak}_{cn} \cup G^{kk}_{cn}, \tag{22}$$

where, $R_{cn} = R^{ak}_{cn} \cup R^{kk}_{cn}$, $V_{cn} = V_{cp1} = V_{cp2}$, $V_{cp} \supset K_{cp}$.

Thus, we get the graph $G_{cn} = (V_{cn}, R_{cn})$ representing structure descendant of Z_3, which forms as the result of crossover operator application.

5. MODIFIED OPERATOR OF MUTATION

Let the parental structure Z_{cp}, presented in the graph $G_{cp} = (V_{cp}, R_{cp})$. We get the graph $G_{cn} = (V_{cn}, R_{cn})$ as the result of application of mutation operator, corresponding the structure descendant Z_{cn}, forming from the graph $G_{cp} = (V_{cp}, R_{cp})$.

To solve this problem at initial stage we suppose that:

$$G_{cn} = G_{cp}. \tag{23}$$

Taking in to account Eq.(8) and Eq.(9), in the graph $G_{cn} = (V_{cn}, R_{cn})$ we determine sub-graphs:

$$G^{ak}_{cn} = (V_{cn}, R^{ak}_{cn}),\ G^{kk}_{cn} = (K_{cn}, R^{kk}_{cn}), \tag{24}$$

Such as,

$$G_{cn} = G^{ak}_{cn} \cup G^{kk}_{cn}, V_{cn} = A_{cn} \cup K_{cn}, R_{cn} = R^{ak}_{cn} \cup R^{kk}_{cn},$$
$$A_{cn} \cap K_{cn} = \varnothing, R^{ak}_{cn} \cap R^{kk}_{cn} = \varnothing, V_{cn} \supset K_{cn}.$$

From set of edges R_{cn} we choose casual edge $r_{ij} \in R_{cn}$ and delete it

$$R'_{cn} = R_{cn} \setminus r_{ij}. \tag{25}$$

If this edge falls in the edge type of <subscriber.node> → <switch.node>, i.e. $r_{ij} \in R^{ak}_{cn}$, i.e., subscriber node $v_i \in A_{cn}$ remained switched off the network, we connect to switching node according to the following rule:

$$R''_{cn} = \begin{cases} R'_{cn} \cup r_{i^* j^*} \in R^{ak}_{cn} & if \quad \xi > 0{,}5, \\ R'_{cn} \cup r_{i^* \eta^*} \in R^{ak}_{cn} & if \quad \xi \le 0{,}5, \end{cases} \tag{26}$$

where, i^* is the number of subscriber node network $v_{i^*} \in A_{cn}$ remaining as the result of operation Eq.(24); j^* is the number of subscriber node network $v_{j^*} \in K_{cn}$ defined on the minimum cost criteria $d_{i^* j^*} = \min_j \{d^{ak}_{i^* j}\}$; η^* is a random natural number, corresponding the number of switching node of the network $v_{\eta^*} \in K_{cn}$, $\eta^* \in [1, n_k]$; ξ is a random number, lying in interval [0.1], $\xi \in [0,1]$

In this way the changes will be made in FP - parts of chromosomes Z_{cn}.

If the remote edge belongs the class of edge types <switch.node> → <switch.node>, i.e., $r_{ij} \in R^{kk}_{cn}$, then at the result of the operation Eq.(25) in graph $G_{cn} = (V_{cn}, R_{cn})$ there form isolated sub-graphs:

$$G^*_{cn} = (V^*_{cn}, R^*_{cn}),\ G^{**}_{cn} = (V^{**}_{cn}, R^{**}_{cn}), \tag{27}$$

Such that,

$$V_{cn} = V^*_{cn} \cup V^{**}_{cn},\quad V^*_{cn} \cap V^{**}_{cn} = \varnothing,$$
$$V_{cn} \supset V^*_{cn},\quad V_{cn} \supset V^{**}_{cn},$$
$$R_{cn} = R^*_{cn} \cup R^{**}_{cn} \setminus r_{ij},\quad R^*_{cn} \cap R^{**}_{cn} = \varnothing,$$
$$V_{cn} \supset K_{cn} = K^*_{cn} \cup K^{**}_{cn},\quad K^*_{cn} \cap K^{**}_{cn} = \varnothing.$$

In this case the isolated sub-graphs are connected as follows:

$$R''_{cn} = \begin{cases} R'_{cn} \cup r_{i_k^* j_k^*} \in R_{cn}^{kk} & if \quad \xi_k > 0{,}5; \\ R'_{cn} \cup r_{i_k^{**} j_k^{**}} \in R_{cn}^{kk} & if \quad \xi_k \le 0{,}5; \end{cases} \tag{28}$$

where, i_k^* , j_k^* - respectively, the rooms and the network switching nodes $v_{i_k}^* \in K_{cn}^*$ and $v_{j_k}^* \in K_{cn}^{**}$, defined by a minimum cost; $d_{i_k^* j_k^*} = \min_{ij} \left\{ d_{ij}^{kk} \right\}$; i_k^{**} , j_k^{**} - respectively, random integers, corresponding to the numbers of switching nodes - $v_{i_k}^{**} \in K_{cn}^*$ and $v_{j_k}^{**} \in K_{cn}^{**}$, $i_k^{**} \in [1, n_k]$, $j_k^{**} \in [1, n_k]$; ξ_k - a random number in the range [0,1], $\xi \in [0,1]$.

As a result of this procedure there will be changes in *SP*-part of a chromosome Z_{cn}.

Thus, assuming $R_{cn} = R''_{cn}$, we obtain a graph $G_{cn} = (V_{cn}, R_{cn})$, that represents the structure of the new offspring chromosomes Z_{cn}.

6. MODIFIED GENETIC ALGORITHM FOR STRUCTURAL SYNTHESIS OF INFORMATION NETWORKS

DCN can be represented on the basis of the above theoretical assumptions and the proposed genetic operators generalized algorithm for structural synthesis as follows:

1) We encode the network structure $G(1)$ in the form of chromosomes Z_3, determine the maximum and minimum boundaries of power $m_n^{\max}, m_n^{\min}$ that will change dynamically during the evolutionary search of the maximum value to the mean average of the minimum and then in reverse order.
2) We randomly generate an initial population with a capacity of $m_n^{\max}$:

$$\Im = \{Z_1, Z_2, \cdots, Z_{m_n^{\max}}\}. \tag{29}$$

3) We assess population fitness under:

$$P_i^{Ch} = F(Z_i) \Big/ \sum_{j=1}^{m_n^{\max}} F(Z_j) \tag{30}$$

4) We choose a selection method:
   - If $P_{sel}(\xi) \ge 0, 6$ and $P_{sel}(\xi) \ge 0, 7$ then, as a selection method we select the proportional method and individuals from the previous generation transfer to a new population based on their fitness, wherein $P_{sel}(\xi)$ is the random number is in the interval [0, 1];
   - If $P_{sel}(\xi) \ge 0, 3$ and $P_{sel}(\xi) \ge 0, 4$ then, we choose an elite method by using selective method and the best adapted individuals from the previous generation will move to the new population;
   - In other cases, individuals passing into a new population, determined by roulette rule method.
5) We calculate the total number of individuals eligible for the transition to the next generation m'_n and the number of individuals who need to get through the application of genetic operators $m''_n = m_n^{\max} - m'_n$. .
6) We sort out the existing m'_n individuals according to the principle of increasing fitness.
7) We solve the problem of the choice of genetic operators and the formation of a new population:
   - If $0, 7 \le P_{gen}(\xi) \le 0, 8$, then we choose the modified operator of crossovering as a genetic operator. Further by using of inbreeding and outbreeding methods we choose parents parent pairs and perform the operation of crossing.
   - If $0, 2 \le P_{gen}(\xi) \le 0, 3$, then we select a modified mutation operator as a genetic operator and make changes in a parent chromosome genes selected by roulette rule method.
8) We move chromosome, resulting from the application of the modified operators of crossovering and mutations in to a new population.
9) We check the power of the new population, if it is less than $m_n^{\max}$ or, $m_n^{\min}$ then go to point 7, otherwise go to point 10.
10) We solve the problem of the choice of models and types of switching devices, bandwidth of communication and assess the value of fitness function.
11) If the value of fitness function satisfies specified accuracy or number of epochs exceeds its limit value, the evolutionary search process is complete, otherwise we go to step 3 of this algorithm.

On the basis of the proposed algorithm special software has been developed and computing experiments have been conducted in order to explore the influence on the rate of convergence of the algorithm and the quality (accuracy) of the obtained solutions of different genetic operators, selection schemes individuals-parents and the initial population size (Fig.2).

Experiments were conducted on a number of network nodes from 20 to 100. For each network in ten solutions average values were calculated, and rated as the decision itself and the search speed of the decision. Results of computing experiments showed that the use of the proposed modified genetic operators leads to an improvement of the solution found by an average of 9 - 14%, and reduces the search time for a solution to 21 - 27%.

Improving search results and search time reduction is explained with that when using classical genetic operators, structures are formed outside the region of feasible solutions, which is typically a small fraction of the area of all possible solutions generated in the evolutionary process. The additional computing resources are required for their processing when "repairing" the chromosomes corresponding cyclic compounds and isolated sub-graphs.

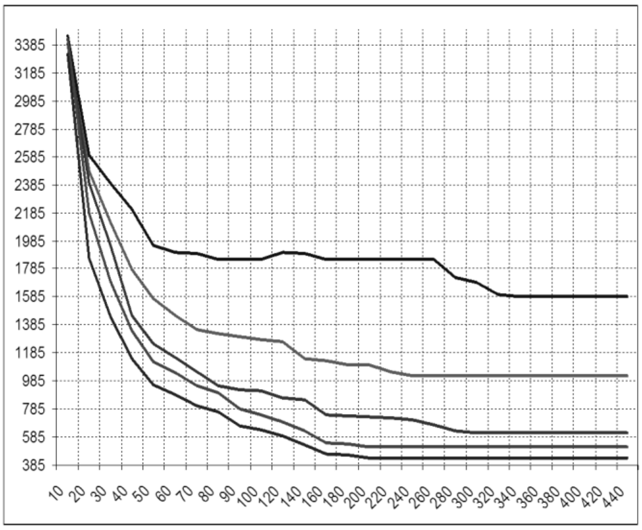

Fig.2(a). The convergence diagram of fitness function values

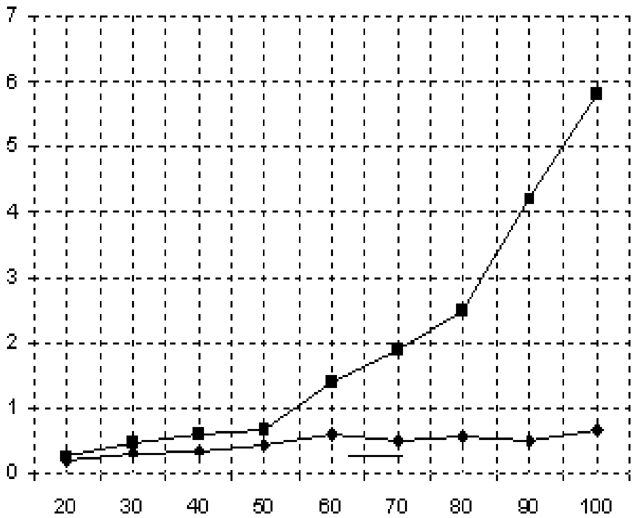

Fig.2(b). Efficiency estimation of the found decision

Fig.2. The results of computing experiments

7. INVESTIGATION OF THE INFLUENCE OF GENETIC ALGORITHM PARAMETERS ON THE EFFICIENCY OF THE SEARCH FOR SOLUTIONS

The main parameters of genetic algorithms (GA), affecting the efficiency of evolutionary search are: power of the population, probability of the usage of genetic operators, selection circuit of parental pairs and method of selecting individuals in the new generation.

As you know, one of the most important parameters of GA is the power of the population. Studies have shown that the detection power of the population, depending on the type of objective function and the setting of the optimization problem is a rather complicated task [2, 5, 11]. Power of the populations primarily strongly influences on the search time and accuracy of solution. A small number of individuals in the population is reduced during the search for solutions, and the quality of the solution obtained in this case is much worse. Conversely, the best result of the search is achieved when the number of individuals in the population is increased significantly and the search time is greatly increased. Optimum power for every task is different and single method of calculating its value is not yet available.

Hereupon, there has been proposed an approach of dynamic power variation within the population of maximum and minimum power limits during the whole search process for solutions. The computing experiments have shown that the best results are achieved in the two-stage power changes, when the power varies from the maximum value to the average of the minimum, then in reverse order. As is has been shown in [5, 9, 10], the crossover is the main generating operator, so the definition of the optimal probability of crossover seems to be quite important task.

Optimal probability of crossover has been defined by experimental way. The results of the experiments are shown in Fig.3. As can be seen from the graph, the best solutions occur at values 0, 7 < *pcross* < 0, 8.

Taking into account the fact that the smaller the probability of crossover, the faster the algorithm we accepts *pcross* = 0, 7. This result is slightly different from those of other researchers, for example in [9] it is recommended to use *pcross* = 0, 6. This difference can be explained by the specificity of the problem and features of used crossover operator.

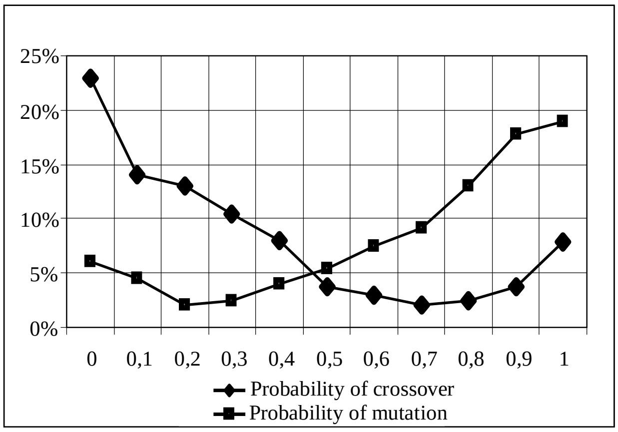

Fig.3. Graph of the dependency accuracy of the search for solutions on the probabilities of crossover and mutation

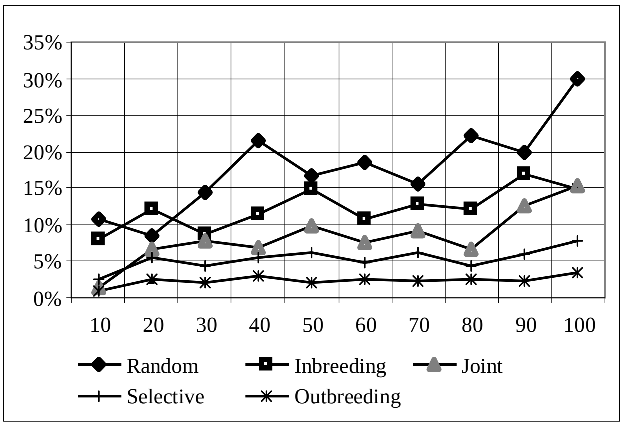

Fig.4. Graph of the dependency efficiency of finding solutions from the parental pair selection method for different amount of subscribers

The mutation operator plays the role of fine-tuning of the found solution where the solution converges to the nearest local or global optimum. The operator is different from the conventional one in the proposed algorithm of the application scheme of mutation, in which all the bits of the chromosome is mutated with some probability. In our case, initially P_{mut} is determined whether to apply an operator to chromosome mutations, and then, if the chromosome is mutated, each edge of this chromosome with probability P_r is replaced by another in accordance with the modified mutation algorithm. Selection of edge replacement occurs only among the edges of the form "user-switch" and "switch-to-switch". As can be seen from Fig.3, the optimum value of the probability of mutation lies in the range $0.2 < P_{mut} < 0.3$, the optimal value of the edge replacement is located in the range of $0.03 < P_r < 0.04$. Scheme selection of parental pairs for genetic crossover operator is one of the main parameters affecting on the efficiency of evolutionary search. The most well-known methods of selecting parental pairs are inbreeding, outbreeding, random method, and selective method [5, 7].

The Fig.4 and Fig.5 show the results of a comparative analysis of different methods for selecting parental pairs for the crossover operator. The graphs represent the relationship of differences resulting from the optimal solutions for different values of number of subscribers. According to the results of the comparative analysis, we can conclude that the selective and random selection methods be have inefficiently. Using the method of inbreeding reduces search time, but the search results are worse. This is explained by the fact that the algorithm converges to local minima, without having to scrutinize the scope of all possible solutions for new extreme. Selection of parental pairs by outbreeding method leads to slower performance of the algorithm, but yields more accurate solutions. The most effective result on convergence and accuracy is achieved in joint application of inbreeding and outbreeding methods.

The selection methods of individuals for new generation i.e. selection of chromosomes shows significant influence on efficiency of the evolutional search. Selection takes place among individuals, resulting from the use of genetic operators from individuals of the previous generation.

We allocate proportionate and elite selection method among the existing methods of selection. In proportional method the transition probability into the next generation of individuals depends on its fitness Eq.(29). Elite selection method creates a new population of the fittest among special populations and individuals of the previous generation, resulting from the application of genetic operators.

The Fig.5 and Fig.6 show the results of a comparative analysis of these methods. As it can be seen from the results of computational experiments using a proportional sampling method will lead to long search for solutions, and solutions are not effective enough. There is a possibility of a significant reduction of search time when using the elite selection method, but there is a greater likelihood of premature convergence to a local minimum, which leads to solutions that deviate quite strongly from the optimal.

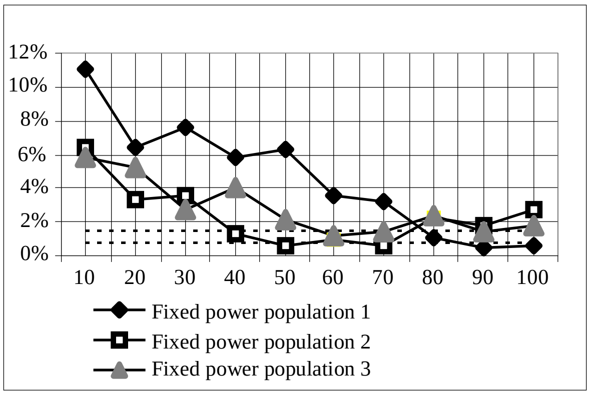

Fig.5. Graph of efficiency dependency search for decisions from selection method of parental pairs

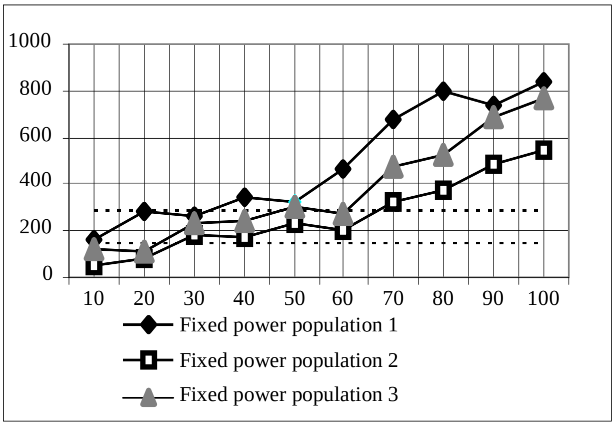

Fig.6. Graph of time dependency search for decisions from selection method of parental pairs

Analysis of the results allows us to draw a conclusion that these methods are necessary to use with a certain probability. As the results of computer simulation, periodic use of elite selection provides faster convergence of evolutionary search algorithm and a proportional sample - a detailed study of the search area. Results of computing experiments show that the best solution is to use elite method with a probability of 0.3-0.4, with a probability proportional method 0.7-0.6.

8. CONCLUSION

Thus, in this study we have solved the problem of formalization of structural synthesis of multi-levelly distributed DCN ACS and conceptual model of the evolutionary synthesis based on genetic algorithms has been suggested that does not require additional information on the nature and properties of the target function. There have been proposed modified genetic operators of crossovering, mutations and evolutionary synthesis algorithms structure DCS of automated systems.

There has been suggested a joint-application and elite selection method of individuals to improve the efficiency of the genetic algorithm in the new generation. As a result, periodic use of elite selection (with probability 0.2-0.3) led to the convergence of the algorithm to speed up the solution, and a proportional sample (with probability 0, 8-0, 7) allowed to carry out a detailed analysis of the area and improve the search results. Optimal use of the probability of crossover operators (0.6-0.7) and mutation (0.4-0.3) determined experimentally for different networks with the number of nodes from 20 to 100.

The computing experiments have established that the application of the proposed modified genetic operators leads to an improvement in the average of the obtained solution at 9-14% as well as to reduce the search time solutions for 21-27%. Improving search results and the search time reduction is explained with the fact that when using classical genetic operators therefore, some structures that are not in the area of feasible solutions, which typically make up a small part of the area of all possible solutions generated in the evolutionary process. The additional computing resources to process them when "repairing" of chromosomes corresponding cyclic compounds and isolated sub-graphs.

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