

UOT 681.332

# Giving an approach for selecting active nodes in Wireless sensor networks by using genetic algorithms\*

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*Wireless sensor networks are used as an appropriate and efficient approach for controlling and monitoring. The main issues in these networks are saving energy and appropriate sensor covering of environment, so that the link between nodes and final connection of whole network are stable. There are approaches for solving these problems which select subset of nodes in each moment and keep them in active mode and other nodes remain in sleep mode. The problem of these approaches is that they cannot select subsets appropriately in large scale networks. In other words selecting active node is a np-problem. So in this article in order to solve this problem, we use a genetic algorithm that has better efficiency than previous algorithms according to previous evaluations and results.*

**Key words:** covering, sensor networks, genetic algorithm, active nodes.

## 1. Introduction

**W**ireless sensor networks are new discussions and subset of case networks. Sensor networks include sets of nodes that spread in environment and communicate with each other so that they monitor given environment by appropriate cover and process the data that are sensed from environment and at the end deliver the desirable information data sets to sink node by exchanging the data sets between nodes.

The sensors that are used in these networks have limitations like energy and lifetime that for this reason the density of the used nodes should be much enough [20] (more than 20 nodes in one square meter). In order to increase the lifetime of network in such networks with high density and limitation of nodes' energy, it is not necessary that all the nodes should be in active mode at the same time, but it is better that the subset of nodes be in active mode at the same time so that if all the nodes be in active mode simultaneously, the amount of energy consumption would be high and also much additional information would be collected from environment. So one of the main issues is controlling of network's density (that is the subset of those nodes that are in active mode simultaneously). Controlling of density should be done in a way that the active nodes should first cover whole the network properly and second the connection between two neighbour node in network is stable.

In order to communicate the nodes, the neighbor nodes should be stand in transmission radius  $r$  and according to sensory radius  $R$  of each node, selecting of nodes should be done in a way that environment is sensed completely and also nodes communicate with each other. In article [7] was proved that if  $r = 2R$ , means connection radius is twice sensory radius of nodes and if nodes cover the environment, in this way the nodes can communicate with each other. Therefore we can use sensory radius for covering environment so that the connection between nodes remains unchanged. In article [3, 9] was proved that the problem of selecting subset of active nodes for appropriate covering of given area among all the existing nodes is an npcomplete problem and there are approaches for solving this problem in articles [9, 4, and 5]. Each one of these approaches selects subset of nodes among all the existing nodes in network so that each subset covers the given area. In each moment only one of these nodes is in active mode and others are in sleep mode. According to this note that when the density of nodes is high in the network or the scale of network expands, the complexity of selecting subsets is high, in this case previous algorithms can not select these subsets properly.

So in this article we offer a genetic algorithm to solve the problem of selecting subsets which selects subsets with minimum number of nodes by correct selection of nodes. Because of using minimum number of nodes at each subset, the number of subsets also increases and results in saving energy and increasing of network's lifetime. In second section of

\* Статья дана в авторской редакции.

article the related works have been presented and in the third section the proposed approach will be explained completely. In the fourth section we state the evaluation of proposed approach and in the last section the final conclusion is presented.

**2. Related works**

PEAS algorithm [2], [6] is a density controlling algorithm that was presented in order to strong sensory covering in sensor networks. In PEAS, subset of nodes acts in active mode in order to preserve the covering of environment and other nodes are in sleep mode. One node in sleep mode becomes active at specific time intervals in order to check that whether active nodes are in their own sensory range. If there is not any node, it remains in its active mode, otherwise it returns to sleep mode again.

In article [4], Heinzelman and Perillo have been stated an approach that divide nodes to subsets so that each one of the subsets covers the environment. At each moment only one of the nodes is in active mode. The aim of this approach is proper scheduling to activate subsets at different times. In article [5], Cardie and Du have been divided the existing nodes to distinct sets, so that each set covers the given environment individually and at each moment only one of these nodes is in active mode. In this approach unlike article [4], the sets are scheduled by Round Robin technique.

**3. The presented genetic algorithm to solve this problem**

The genetic algorithms are approaches that by randomly searching the representation try to find the existing best solution in representation, but this randomly searching is conducted toward finding the best solution by some kinds of operators (driven from nature), so we can not think that these algorithms are completely random. According to these specifications, genetic algorithms have more capability to search in complex and large representations [8]. Fig. 1 shows the generic structure of genetic algorithms.

**3.1. Definition of chromosome's structure.** The first step to define a genetic algorithm is defining the chromosome's structure. The chromosome's structure that is given in this article is a set of two dimensional coordinates of the nodes' location in geographical zone. If N is the number of subset of existing nodes in geographical zone, in this case each chromosome include N pair number that shows the location coordinates of each node in geographical zone according to current chromosome.

**3.2. Initialization.** In order to initiation in each chromosome, the coordinates of node (each node has two dimensional coordinates) is selected randomly and is based on remained energy of each node from

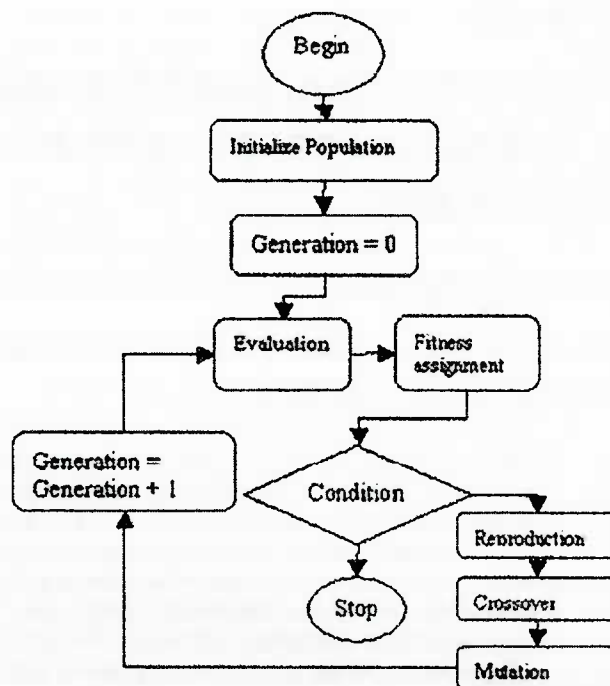


Fig. 1. The generic structure of genetic algorithms

the list that has the location coordinates of all the existing nodes in the network, is the number of subset nodes that cover the geographical zone.

**3.3. Evaluation Function.** In each genetic algorithm we should present the definition of better and worse. These principles are presented by evaluation function [8]. The parameters of presented evaluation function are as follow: Proper covering of entire zone Discordance of nodes (In order to have minimum active nodes, the nodes should have discordance). If one node with radius R is in coordinates P, in this case all the nodes that are at distance R from point P, will be under covering of node. Since the studying of point to point covering of geographical zone at each chromosome is time consuming and has more calculations, we select some points as index points at geographical zone and for each chromosome we study the covering of these points by nodes. In order to calculate coordination between two nodes, we suppose that N<sub>1</sub> is the first node in coordinates P<sub>1</sub> (with sensory radius R) and N<sub>2</sub> is a second node in coordinates P<sub>2</sub> (with sensory radius R). In this case the distance between two nodes is calculated by equation

$$D(N_1, N_2) = \sqrt{(P_1x - P_2x)^2 + (P_1y - P_2y)^2}, \quad (1)$$

where P<sub>1</sub>x, P<sub>1</sub>y are coordinates of N<sub>1</sub> and P<sub>2</sub>x, P<sub>2</sub>y are coordinates of N<sub>2</sub> and D(N<sub>1</sub>, N<sub>2</sub>) is the distance between two nodes. And if D(N<sub>1</sub>, N<sub>2</sub>) ≥ 2R, in this case



there is not any coordination between two nodes, but if  $D(N_1, N_2) < 2R$  in this case there is a coordination between two nodes that the coordination between them is calculated by equation

$$OV(N_1, N_2) = |2R - D(N_1, N_2)|. \quad (2)$$

Final evaluation function: In order to calculate the final evaluation function we should use entioned criterions in a way, so the pseudo code of fig. 2 was given for this purpose:

```

Int PNC; Number of points that not covered by sensors
Int P; The constant value as penalty
Double fitness S;
Set A1, A2; A1 = A2 set of sensors positions
For Each Sensor (i) In A1
{
For each Sensor (j) In A2
S+ = D(Ni, Nj);
A2- = Ni;
}
Fitness = S + PNC*P;
    
```

Fig 2: Pseudo code of evaluation function. In above code, PNC is the number of index points that were not covered, P is the penalty per uncovered point, fitness is evaluation function and S is the sum of OV parameter that is defined in equation (2) for all the nodes.

**3.4. Crossover operators.** In this article, we use Crossover operator of Uniform [10] so that we create binary array of T with the size of chromosomes' length randomly. Then we create child C from two parents A, B: if  $T[i] = 0$ , so  $C[i] = A[i]$  and if  $T[i] = 1$  in this case  $C[i] = B[i]$ .

**3.5. Mutation operators.** The Mutation operator plays an important role in scaping from local optimums and increasing the speed of convergence of ge-

netic algorithms. In the proposed algorithm, three mutation operators are presented for creating diversity and increasing the speed of convergence. Random mutation operator in this random operator, the coordinates of one node in chromosome is selected and is replaced by one random coordinates from list. Special-purpose random mutation operator in this operator, first, one search is done and two nodes are selected which have minimum distance Among others, then one of these nodes is selected randomly and is given new random coordinates from coordinate list of existing nodes.

This operator tries to use other nodes at the other side of geographical zone instead of active nodes that are concentrated at the other side of geographical zone. Special-purpose random mutation operator of Creep Like Special-purpose random mutation operator, this operator also selects two nodes with minimum distance in comparison with other nodes. Then calculates the linear slope that connects the centres of two nodes and according to driven slope replaces one of these two nodes with one new close node so that the distance between two nodes become more than before.

**3.6. Selection operators.** The role of selection operator is convergence of chromosomes' population toward better chromosomes (based on evaluation function). In this article the selecting method of Tournament with parameter 2 is presented as a selection operator [8].

**4. Evaluation of efficiency**

For evaluation, the proposed algorithm was implemented in c programming environment and was compared with PEAS and MC-MIP methods and the results were represented by diagram.

*Used parameters:* In this simulation, the represented energy model in article [2] is used so that we suppose that each node has 10 meters sensory radius and its lifetime in idle mode is 5000 seconds. And also we ignore the energy consumption in sleep mode because the energy consumption is very low. For every transmission packet in a state that density of wireless connection is 40 kb per second and the length of packet is 34 byte, the lifetime of node reduces 6.9 seconds. The area of simulation is 50 m<sup>2</sup>. The comparison parameters are covering percent (the rate of covered environment relative to entire environment) and the number of active nodes that are used for proper covering of environment.

The diagram of fig. 2 shows the proper covering of environment by active nodes related to all the existing nodes in network. Proposed method has better covering in most situations in comparison with and MC-MIP. The diagram of fig. 3 shows more required active nodes for covering related to all the nodes in

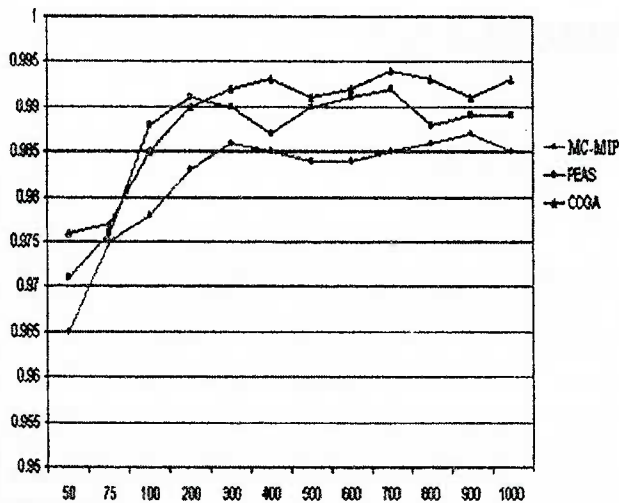


Fig. 2. Covering percent

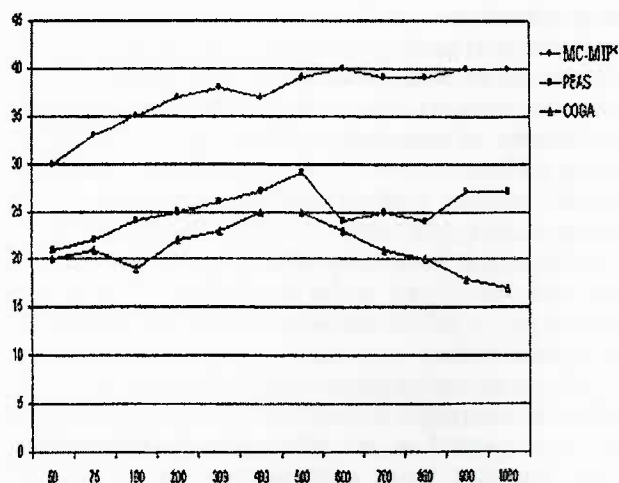


Fig. 3. Number of active nodes

three methods. It is seen that proposed algorithm reduces active used nodes by selecting correct location of active nodes, so it acts more successful than other two algorithms.

### 5. Conclusion

In this article, an approach is presented by using genetic algorithm to select proper subsets among all the existing nodes in the network that at each moment only one subset is in active mode. By proper selecting of each subset's nodes, the number of nodes in each subset is reduced, so the number of subsets is increased and resulted in saving energy and increasing the lifetime of network. This proposed approach in networks with high density of nodes and

in large scale networks is proper than other algorithms. In future works we will reduce complexity of proposed algorithm by presenting better methods of initial encoding and more appropriate evaluation function.

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УДК 004.773.5

## Работа врачей — узких специалистов в системе телемедицины

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*Описано разработанное авторами автоматизированное рабочее место врачей — узких специалистов, содержащее модуль "Телемедицина", с помощью которого можно проводить удаленное консультирование врачей.*

**Ключевые слова:** автоматизированное рабочее место, медицинская информационная система, специализированное программное обеспечение.

**Н** а сегодняшний день в медицинских учреждениях вся информация, необходимая для работы с пациентами, хранится и циркулирует в бумажном виде и минимальное внимание уделяется защите информации о паци-

енте. При существующем положении дел практически невозможно провести удаленное консультирование специалиста, затрудняющегося в постановке предварительного либо окончательного диагноза, так как для этого необходимо