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Design and Analysis of Soft Computing Based Improved Routing Protocol in WSN for Energy Efficiency and Lifetime Enhancement

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Abstract: Mobile wireless sensor networks have been developed as a result of recent advancements in wireless technologies. Sensors in the network are low-cost and have a short battery life, in addition to their mobility. They are more applicable in terms of the essential properties of these networks. These networks have a variety of uses, including search and rescue operations, health and environmental monitoring, and intelligent traffic management systems, among others. According to the application requirements, mobile wireless sensor nodes are energy limited equipment, so energy conservation is one of the most significant considerations in the design of these networks. Aside from the issues posed by sensor node mobility, we should also consider routing and dynamic clustering. According to studies, cluster models with configurable parameters have a substantial impact on reducing energy usage and extending the network's lifetime. As a result, the primary goal of this study is to describe and select a smart method for clustering in mobile wireless sensor networks utilizing evolutionary algorithms in order to extend the network's lifetime and ensure packet delivery accuracy. For grouping sensor nodes in this work, the Genetic Algorithm is applied initially, followed by Bacterial Conjugation. The simulation's results show a significant increase in clustering speed acceleration. The speed of the nodes is taken into account in the suggested approach for calibrating mobile wireless sensor nodes.

Keywords: WSN, Cluster, Node Energy, Node lifetime, Genetic Approach, Routing Protocol

1. INTRODUCTION

There are two key parts to the WSN:

1. Sensor Nodes
2. Base Station (Central Gateway)

1.1 Sensor Nodes

In most cases, sensors nodes are made up of a few sensors and a mote unit, as depicted in Figure 1.1. There are sensors that collect data and transmit it to the mote. Physical ambient characteristics such as temperature, pressure, humidity, sound, and vibration and changes in the health of a person are often measured by sensors. Sensor nodes have made significant use of MEMS-based sensors.

All of the components of a mote are contained in a single device: a processor, memory, battery, A/D converter, and radio transmitter. A sensor node consists of a mote and a sensor. In a sensor network, each sensor node is connected to a wireless ad-hoc network. Multi-hop routing algorithms can be supported by each node and used to forward data packets to the base station.
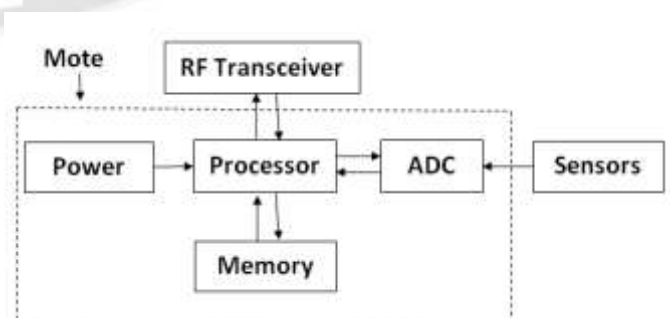

Figure 1.1 Block Diagram of Sensor Node

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1.2 Base Station

The sensor network is connected to another network via a base station. All of these components are housed in a single case. Low-power mesh networking software is preinstalled to facilitate communication among the system's numerous wireless sensor nodes. All sensor nodes send their data to the base station for processing and decision-making, hence the location of the base station is critical to the success of a wireless sensor network. A sensor network base station is installed to conserve energy, protect sensor nodes, and ensure network resilience. It's common to think of base stations as a fixed object, although this isn't always the case.

Figure 1.2 Base Station Node

1.3 Radio Model

For the sake of consistency, we've used the same radio model as previous studies. Fig.1.3 illustrates how the transmitter and receiver expend energy to run their radio electronics and power amplifiers, respectively, for radio hardware purposes. As part of this project, both the free space (d2 power loss) and multi path fading (d4 power loss) channel models were used depending on the transmission distance. Free space (fs) and multi path (mp) models are utilised for distances greater than a certain threshold.
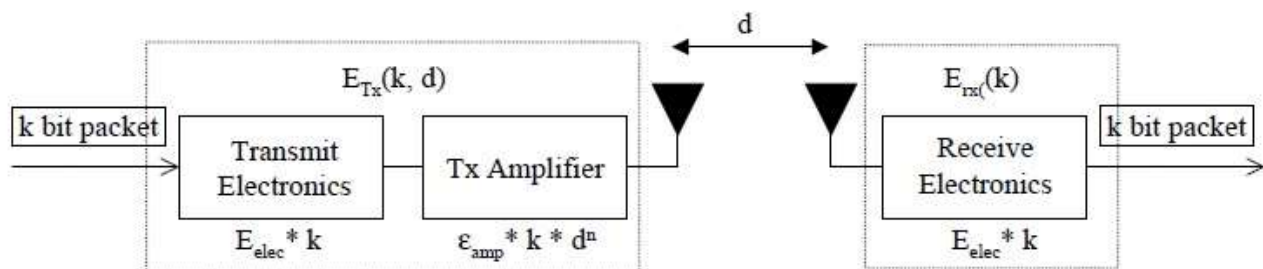

Figure 1.3 Radio Model

An overview of the energy-aware WSN routing algorithms that have been studied in the past.

- Trying to find routing algorithms that can enable WSN technologies that are more energy efficient.
- Defining metrics for analysis.
- Using the MATLAB programme to write the code for the simulator.
- Simulation of the network for the routing algorithms that were selected.

- Results from the simulation situations are analysed in terms of their behavioural outcomes.
- Merged layer node deployment with node activation procedure for lifespan improvement in Homogeneous and Heterogeneous protocols.
- Node activation procedure in Homogeneous and Heterogeneous protocols can be improved by using the optimal cluster head selection in the merged layer node deployment technique.

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1.4 Motivation

Based on simulations of current routing protocols, such as the major clustering-based hierarchical routing protocol, this research is derived. Simulated wireless sensor networks can be used to examine more aspects and investigate more parameter values than can be done with real-world wireless sensor networks. With simulations, a wide range of alternative algorithms or protocols and a wide range of implementation approaches can be evaluated. The accuracy of each simulation, however, is dependent on the accuracy of the simulation models employed in the routing protocols that have been developed. For this reason, we want to test our most promising algorithms and techniques in real sensor networks to improve our simulation results.

2. LITERATURE REVIEW

Z. Al Aghbari, A.M. Khedr, W. Osamy (2020) , and others Wireless sensor networks (WSNs) have been a major improvement in wireless communication during the past few decades (WSNs). There is a limited quantity of energy in sensor nodes, which are utilised to relay data. Depletion of energy occurs during transmission. WSNs face substantial issues in terms of energy usage and network lifespan. Researchers have done a lot of effort recently to find the most efficient route between source and destination nodes, which will help a network conserve energy. As a result, the goal is to devise a routing algorithm that minimises energy use and maximises network longevity. There are a variety of ways to find the best route between a source node and a destination node. WSN routing is examined in detail utilising a variety of optimization approaches in this article. All past WSN research investigations from 2010 to 2019 are summarised in one article. The findings presented in this study will help researchers fill in the gaps in the WSN research field and discover new research trends in this area [1].

Gui, T., Ma, C., Wang, F., and Wilkins, D. E. (2016) - Swarm intelligence (SI) is discussed first in this work, and many interesting meta-heuristics are then surveyed in terms of research efforts. Termite colonies and fission-fusion social structures based on spider monkey clustering in WSNs are discussed in the second section of the paper. To wrap up, we conduct a comparative analysis, highlighting key difficulties and possible future paths [2].

If you're looking for a way to get your hands on some of the most important data in the field of neuroimaging, go no further than Parwekar, Rodda, and Kalla. This decade, WSNs have risen to the top of the technology heap. Wireless sensor networks face a huge difficulty in terms of energy consumption. A number of challenging WSN issues are impossible to solve in deterministic time. Optimization techniques can be used to overcome these difficult challenges. Nodes' location and maintenance, routing and clustering, and so on are some of the issues that could be solved. Techniques like these try to give a solution in a predetermined amount of time while also reducing the network's overall energy consumption, therefore extending the network's lifespan. The implementation of many existing optimization approaches in the field of WSN [3] is fully described in this study.

Saranraj, G., & Selvamani, K. (2017) - PASO (Particle with Ant Swarm Optimization) was proposed in this paper to create stable clusters with the best possible cluster heads. The pheromone-guided exploration of an ant colony is used locally to synchronise the particle positions in the PSO in order to reach the possible domain of the fitness function more quickly. " For picking the cluster head, the PASO's fitness function considers residual energy, distance and node degree as well as other factors. According to the results of the NS2 tool, the suggested approach outperforms existing clustering approaches in terms of energy usage, network longevity, and packet delivery ratio [4].

Mathivanan, V., and K. V. K. Stephen (2018) - It is common for wireless sensor networks (WSNs) to lack a central network. In order to gather information about an environment, a large number of sensor nodes work together. There are two sorts of WSNs: structured and unstructured. Sensor nodes are abundant in an unstructured WSN. These sensors are compact, don't require a lot of processing power, and cost next to nothing. It is capable of sensing, measuring, and gathering information from the environment, and then transmitting it to the user via a local decision process. In a sensor network, the security and life span of each sensor node are critical considerations. Data security is critical since the sensor nodes in these networks have a limited battery life and are frequently deployed in risky situations. Adding a new node to a secure WSN requires a significant amount of time and effort. Mobile sinks and Particle Swarm Optimization for combined WSN are proposed in this paper. [5] The new algorithm outperforms the standard convergence algorithm both in terms of efficiency and quality of solutions.

3. OBJECTIVE OF RESEARCH

By merging energy management with information management, this study intends to find an efficient way to reduce the energy consumption of a WSN (and thus increasing network lives). Small-scale industrial and commercial applications are the primary focus of the target networks. Despite the fact that scalability (the network's capacity to run effectively as the number of nodes increases) is not a major concern for this study, local techniques should be used to evaluate their scalability. Simulations should be used to test and validate the appropriateness of aspects that are directly relevant. For energy research and data management, this comprises appropriate modelling of energy structure components, sensing systems (accuracy and information values), communications, and timekeeping (both of which

heavily affect node operation and data communication).

The themes of this research are as follows:

- **Energy-aware operation**

This study focuses on the energy-controlled operation of the nodes and the network as a whole. Resource use, including energy collecting [5,] was also added. This generates energy dynamics that must be efficiently exploited at the nodes because energy supply is frequently intermittent and recurring.

- **Information-aware operation**

The nodes and the network as a whole are taken into account in this analysis. It is important to take into account the specifics of each packet while assessing the usefulness of data..

- **Modeling and simulation**

The established method is tested using a simulation. In order to be useful, the simulation models must be used effectively and accurately. It is crucial to model parts of this study that have a direct impact on energy and understanding.

4. PROPOSED METHODOLOGY

This study proposes an efficient evolutionary technique that could be used to Robotics applications, for example, can be used to solve real-time challenges. The only variable is the ''Population Size" of the suggested algorithm is what makes it work. The single operator used during the method is similar to parameter-less algorithms. The bacterial conjugation operator is used to carry out the algorithm. It makes the suggested algorithm's implementation considerably simpler. The technique for performing the bacterial conjugation operator utilised in this algorithm is distinct from the operators used in other algorithms. A moniker that has been used in various evolutionary algorithms before, such as the pseudo. The bacterial genetic algorithm, also known as the microbial genetic algorithm, is a type of genetic algorithm that uses

bacteria to solve problems. For a total of 23 items, the benchmark functions, as well as a few other well-known optimization tasks,   Experiments show that the proposed algorithm outperforms the competition compared to a simple genetic method and particle swarm optimization. The genetic algorithm (GA) has been widely used in recent decades to solve a variety of problems.

4.1 Improved HPGA (High Performance Genetic Algorithm)

The HPGA (high performance genetic algorithm) is proposed in this study as an efficient evolutionary algorithm. The bacterial conjugation operator is used in a high-performance genetic algorithm. HPGA makes use of   Bacterial conjugation is another genetic mechanism that can be used as an optimization operator.   This occurs when genes are transferred directly between bacterial cells. Bacterial conjugation is a process in which bacteria join together to form a   model a genetic material transfer method between bacterial cells that are   in a direct cell-to-cell link this operator is one of the horizontal operators. Mechanisms of gene transfer [4]. In the suggested approach, this operator is employed in a way that accelerates the evolutionary process other algorithms [5–7] include this process as a major component Operator. The microbial genetic algorithm simplified the traditional genetic algorithm.   To its simplest form, representing the horizontal gene transfer operator, which was inspired by   Bacterial conjugation in its natural state. The genetic algorithm of a fictitious bacterial (PBGA)   incorporates a bacterial mutation operator that is based on a modified mutation operator.   Microbial evolution is a biological phenomenon [8]. The evolution of microorganisms the BEA algorithm has the same features as the PBGA, but adds an additional operation. The operation is known as gene transfer, and it is also inspired by microbial evolution. Occurrence [9]. BEA, in reality, combines two activities in order to

evolve its population: the bacterial mutation and the operation of gene transfer while the bacterial mutation is occurring, within the confines of a single chromosome, the gene acts as a local enhancement.   The transfer operation allows chromosomes to send data straight to the nucleus. The population's other chromosomes one bacteria can use this technique to communicate with another.   Its genetic information propagated quickly to other cells [8]. Despite the fact that BEA is inspired,   its implementation approach suffers from an unusually large number of gene transfer procedures. It has a high number of parameters, which adds to its complexity. Furthermore, it looks could be a memory-intensive approach with a total of ninf sorting steps for each Ninf is the number of infections each generation [8], and this results in For real-time optimization challenges, it is pointless.

4.2 Description of Proposed Algorithm

The main operator of the proposed algorithm is discussed in this part, as well as the procedure is described.   The following are the primary characteristics of the suggested algorithm.

The bacterial conjugation operator is described in detail in next section.

There are two key phases in the bacterial conjugation (BC) operator.

- Gene transfer that occurs horizontally
- There is a competition

Two parent chromosomes are used in the horizontal gene transfer method.

The donor chromosome has a higher fitness level than the recipient chromosome. The recipient has a lower level of fitness. The highest and worst fitness values throughout the   Execution of algorithms is well-known. The recipient is the one who receives the gene once it has been transferred.   In the first stage, the chromosome and the newly formed chromosome are entered.   Step one of the competition. The BC operator output is the

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chromosome that results. As a result, the BC operator's input arguments are as follows:

- The chromosome of the donor (CHDonor)
- Chromosome of the recipient (CHRecipient)
- The highest level of fitness ever attained (FitnessBest)
- Worst fitness ever acquired (FitnessWorst)

Figure 4.1 depicts the BC operator's entire procedure, whereas Figure 4.2 depicts the BC operator's entire procedure. On two sample chromosomes, this operator was applied. A string of genes from the donor is picked in the first phase of the BC operator. Chromosome and inserting it in the identical spot on the recipient chromosome. The beginning A random position on the donor chromosome's gene string is chosen. It has a length of proportional to the fitness gap between parent and child chromosomes the population as a whole Horizontal gene transfer begins with the donor's continuous gene string being chosen.

Two parameters are used in this procedure:

- The string to be copied's length (L)
- The starting position of the copied string (P)

The length of the string will be determined by the fitness gap between the two athletes. Two parent chromosomes and their ratio, as well as the difference between the best and worst results

During the execution of the algorithm, fitness was attained. The value of L is determined by Equation.

$$L = \frac{|\text{Fitness}\,(CH_{\text{Donar}}) - \text{Fitness}\,(CH_{\text{Rexpient}})|}{|\text{Fitness}_{\text{Eist}} - \text{Fitness}_{\text{wors}}|} \times \text{Length Of Chromosome}$$

$$P = \text{Uniform Random}\,(0, \text{Length Of Chromosome})$$

A random value with a uniform distribution was used to determine the start point of the gene string. The chromosome length is utilised as a distribution between zero and the length of the chromosome.

Following the determination of these two characteristics, the donor's gene string is determined. chromosome with a length of L, starting at position P, substitutes the corresponding string in the chromosome of the recipient If the operator reaches a certain point during the gene transfer, before L number of donor chromosomal genes are replicated, the end of the chromosome onto the receiving chromosome; after that, the copying process starts over. Chromosomes are a group of chromosomes that make up a person's It should be noted that because the copy operation's start point is random, the Each time the operator is used to the same chromosome, the resulting chromosome will be different parents.
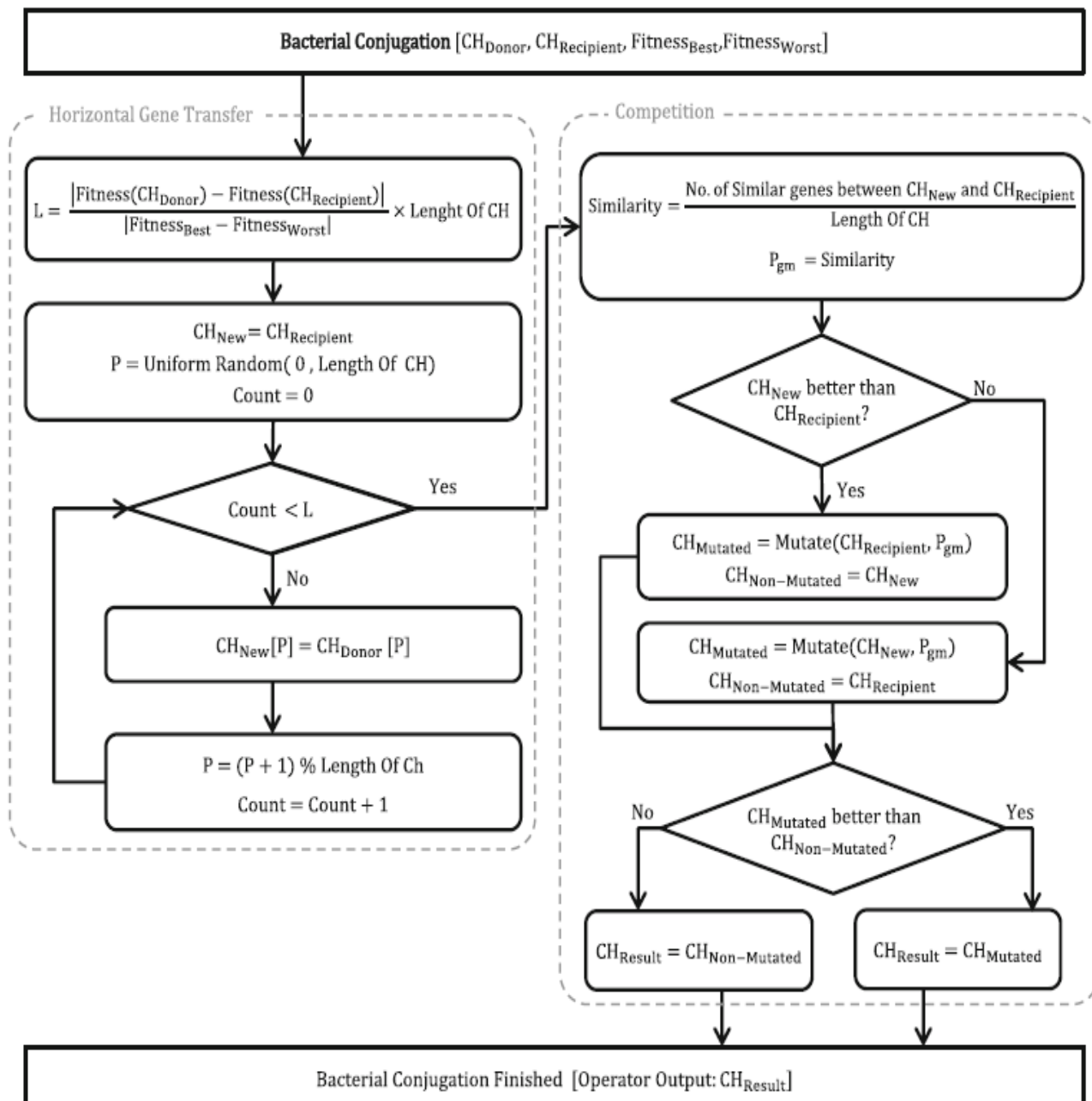
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Figure 4.1 Block Diagram of Bacterial

Conjugation Operation

The chromosome from the gene transfer operation is used in the second phase of the BC operator. Competes with the receiver in a competition the mutation operator is used on the data. To the chromosome with the lowest fitness value in order to improve the likelihood of its occurrence winning. Mutated and non-mutated chromosomes have different fitness values. When the winning chromosome is compared, it replaces the receiver in the population. The number of genes that should be modified is specified in the mutation operator. The ''Per Gene Mutation Rate" (Pgm) is a chromosome-by-chromosome calculation. The number of comparable genes in the operand chromosomes determines the value of Pgm. As a result, it has a self-adaptive rate while the algorithm is running.
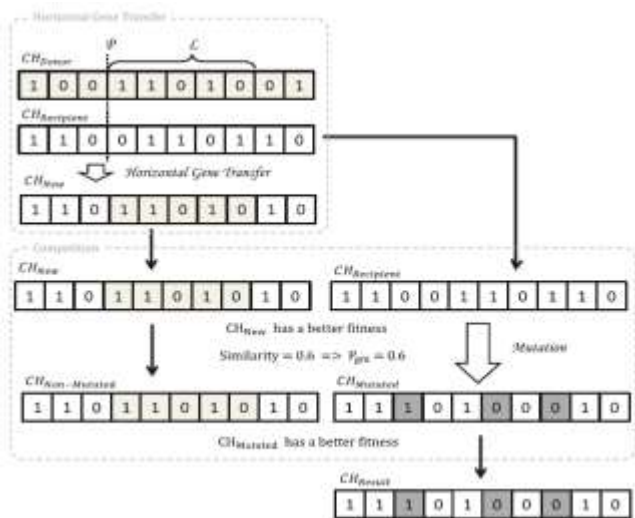
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Figure 4.2 Example of Bacterial Conjugation Operation for Two Sample Parent Chromosomes with Length Of 10

A random number between zero and one is created for each gene, and when this number reaches one, the gene is said to be active.   If the value is less than Pgm, the mutation is used. The more chromosomes that are similar, the better.   The more mutations required on the chromosome with the lowest fitness value, the lower the fitness value improves itself and the other way around. The criterion for chromosomal similarity is: The ratio of similar genes in analogous places on two chromosomes is defined as to the overall chromosomal length, which will be a number between 0 and 1.

$$\text{Similarity} = \frac{\text{Number of similar genes between two chromosomes}}{\text{Length of chromosome}}$$

$P_{gm} = \text{Similarity}$

The value of L decreases as the chromosome length decreases, and the beneficial genes decrease. Not be able to transfer to the recipient chromosome; as a result, the closer the recipient chromosome fitness value is to the value of the operator, the better.   The greater the donor chromosome, the higher the mutation rate.

4.3 Procedure of HPGA Algorithm

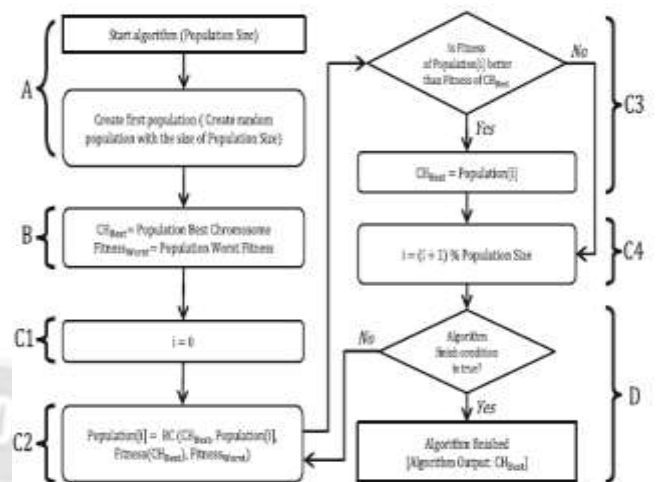The suggested algorithm's steps are depicted in Figure 4. 3

Figure 4.3 Block Diagram of HPGA

- The algorithm begins by producing a chromosomal population to work with. For Random chromosomes are generated up to the ''Population'' level for this purpose.   Size''— the algorithm's input argument equals the size of the data set. The starting population is made up of this population.

- The suggested algorithm's only operator is bacterial conjugation, and the donor chromosome will be the most fit chromosome ever found. The Best Chromosome will be the most common in the population. As a result, it's important to remember the BestChromosome. In addition, as previously stated, the best and worst fitness values must be used to calculate L. Best Fitness and Worst Fitness values will 'e used in this article. Best Fitness may be obtained by merely looking at the Best Chromosome. Worst-case scenario throughout the algorithm's execution, fitness must be kept in mind. At this point, the initial population's Best Chromosome and Worst Fitness are saved. Separate from the general public .

- When the BC operator is used in the suggested algorithm, one generation is finished. Applied to the entire population's chromosomes As a result, the steps that follow are necessary. For each generation, the following tasks are completed:

19

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- The population's first chromosome is chosen.
- As the donor, the BC operator is used to Best Chromosome. Chromosome, as well as to the chromosome chosen as the recipient.
- The operator's fitness of the produced chromosome is compared. It will be picked as the Best Chromosome if it is better. Best Chromosome. It's important to notice that the chromosomes that result are not identical. When compared to the BC operator, the BC operator always has superior or equivalent fitness. It is not essential to update the prior ones in the population. Worst Fitness is a metric that measures how fit you are. The BC loser chromosome, on the other hand, The Worst Fitness value has not been updated because the operator has not been assessed. Either this is due to the fact that this chromosome will never be implanted in the body. If the Worst Fitness value has been changed in accordance with the population, the fitness value of the chromosomes in the chromosomes in the chromosomes in the chromosomes in the chromosomes in the chromosomes in the chromosomes. The population will approach the Best Fitness value in the future. Worst Fitness and Best Fitness are two fitness levels. As a result, the value of the currency has increased. The L parameter in the BC operator's gene transfer process will be become nearly zero, lowering the algorithm's performance.
- In this generation, the surgery on the targeted chromosome is completed, and With the selection of the next chromosome, the algorithm returns to older step in the general population
- The suggested algorithm's termination condition is similar to that of the SGA.
- The number of generations, which is referred to as max-generation, can be any number of generations.
- The number of fitness function calls is used to define the termination condition. The The

algorithm ends when the fitness function is called n times, or in other words, when the fitness function is called n times.

- In other words, it comes to an end after n chromosomes—n state spaces—have been examined.

5. RESULT ANALYSIS
5.1 System Architecture

In this simulation, the ratings of Mica nodes has been used to simulate the equivalent sensor network. All sensors have the same arteries in terms of internal structure and hardware features are. Capability sensor nodes change the angle to reach the goals of the algorithm and as long as their energy storage energy is not eliminated.

After several simulations, the results show that the proposed method is very efficient because reduces communication distance and energy consumption. For a different number of nodes from the following parameters in the table express the specification of the network-

Table 5.1
Number and Specifications of Nodes

Parameters	Ratings
Network size	433 ×433
Number of sensor nodes	13
The sensory radius of the node	43 meters
The communication radius of the node	3 meters

The distribution of nodes is completely linear. Nodes × Nodes in an environment with dimensions 433.The sensor is mobile and the energy stored in the nodes at the beginning of the algorithm can be completely the same. Also, the physical structure of the nodes is quite similar. The parameters of the process simulation of Genetic algorithm parameters and bacterial composition is explained in table 5.2.

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Table 5.2
Genetic Algorithm Parameters and Bacterial Composition

Parameters	Genetic algorithm	Bacterial Composition Algorithm
Population size	13	13
Crossover rate	0.2	-
Crossover type	Single point	-
Mutation rate	0.3	Sim Genes / (Ch_Length*10)
Generation size	433	433

In the mutation rate calculation formula that genome the number of identical genes between two chromosomes and chromosome length. The chromosome is steady and it staples with stratospheric stratigraphy of these two algorithms in stratospheric stratigraphy of MATLAB to achieve new protocol outputs.

5.2 Simulation and Analysis

After the simulation with the proposed strategy it was evident that the proposed algorithm improved energy consumption throughout the simulation time.

After the clustering phase, it also indicates a favourable situation at this stage of the network. The practical implementation of clustering is explained in figure 5.1. The sensor nodes have been distributed in area of 433 meters with a uniform distribution of 50 sensor nodes. Ordinary nodes due to optimization performed with different colors with mark, live nodes with mark and some nodes that have more energy than other nodes are also differentially marked.
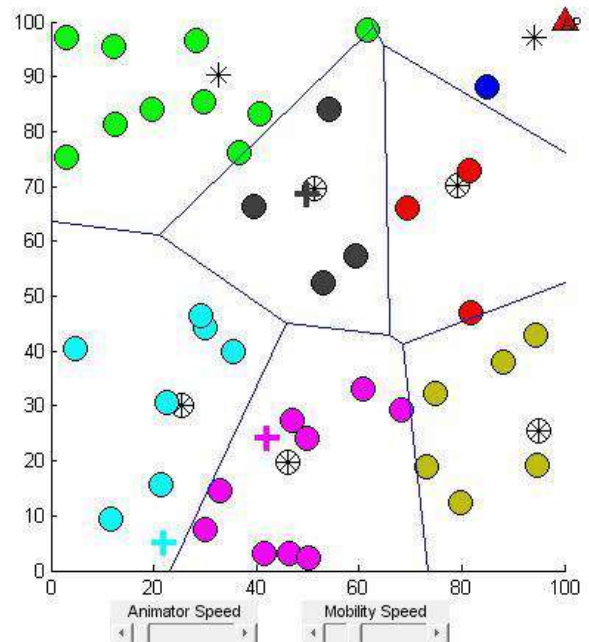

Figure 5.1 Routing Representation

We considered the duration of the simulation same and the number of sensors or the number of the initial population to be 13, and also Energy consumption is calculated based on the energy model presented below.

$$E_{Tx}(k, d) = E_{elec} \times k + \varepsilon_{amp} \times k \times d^2$$
$$E_{Rx}(k) = E_{elec} \times k$$

It shows the radio model used in this study, n this model, the energy consumption to send k bits is calculated. The energy sent to receive k bit is obtained. $\varepsilon_{amp} = 10pJ/(bit \times m^2)$, $E_{elec} = 50J/bit$ in the given calculation. Here the data is considered to be one bit long. Since the communication distance d is an influential factor. It is energy consumption, it is clear that with increasing distance, the amount of energy consumption increases and vice versa.

For Evaluation of residual energy of all sensor nodes the residual energy does not form nodes for both the Genetic Algorithm and the bacterial composition. It is assumed here that all nodes can be selected as headers and grounding through the nearest plot line for each node or grating through the nearest neighbour node.

The Comparison of residual energy reduction of sensor nodes after clustering with genetic

21

algorithms and bacterial composition is shown in figure 5.2.

According to the performed experiments, it is determined that sending to the node have more energy than the neighbouring node Sending through a neighbouring node distributes the energy load over the path nodes with uniform energy in the lattice. By examining the diagram, we find that the algorithm combines bacteria with optimal tuning of sensor nodes can reduce the power consumption of the grid, thus resulting in a longer lifespan.

The grid lifetime has increased with decreasing energy consumption. Next goal is to evaluate the number of times to refer to the fitness function the bacterial composition algorithm is used with the comparative analysis with genetic algorithm of the number parameter to refer to the fitness function. The graph shown in figure 5.3 explains both algorithms as a function of fitness function. The diagram of the bacterial composition algorithm has been able to achieve better results in the same clustering round than genetic algorithm.
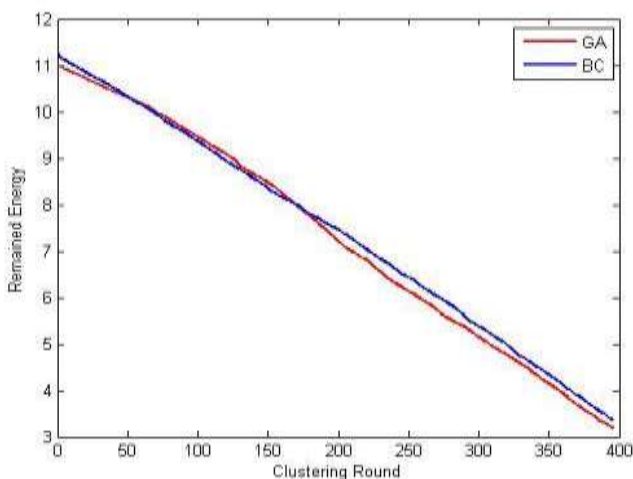

Figure 5.2 Comparison of Residual Energy Reduction of Sensor Nodes after Clustering with Genetic Algorithms and Bacterial Composition
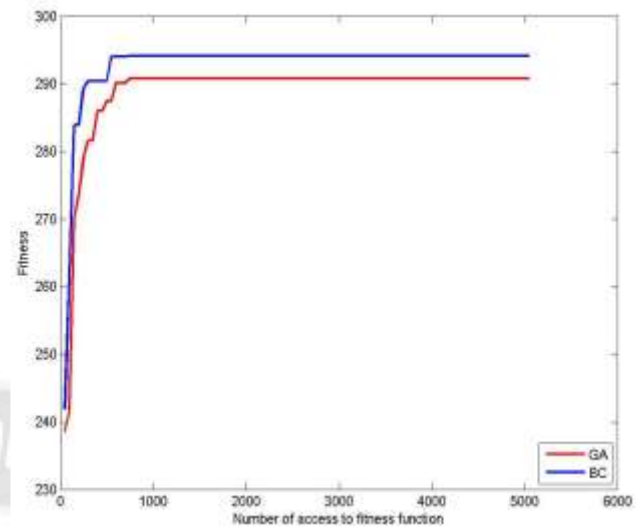

Figure 5.3 Comparison Fitness Function of Sensor Nodes after Clustering with Genetic Algorithms and Bacterial Composition

In this section, the lifetime analysis of network sensor has been analysed for different rounds for the comparative assessment between bacterial conjugate and genetic algorithm. It is evident that the long network life is the best result in bacterial conjugate method due to improved energy consumption throughout the simulation. After the clustering phase, it also indicates a favourable situation at this stage of the network.
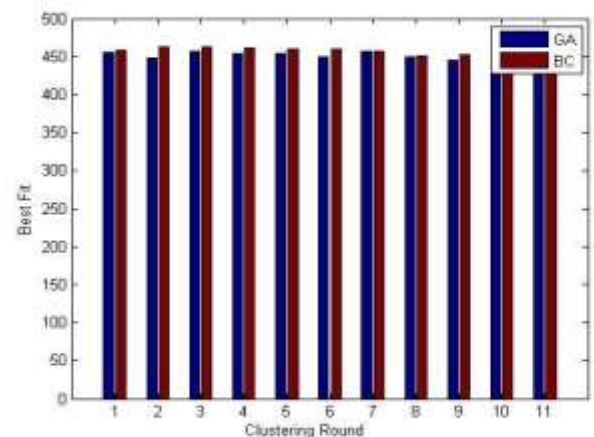

Figure 5.4 Lifetime Analysis

6. CONCLUSION AND FUTURE SCOPE
6.1 Conclusion

Recent advances in wireless technologies has led to the development of mobile wireless sensor networks. In addition to mobility of sensors,

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sensors in the network are low-cost and have limited amount of battery. With regard to fundamental characteristics of these networks they are more applicable. Among different characteristics of these networks they have many applications, such as: search and rescue operations, health and environmental monitoring and intelligent traffic control systems. According to the application requirements with regard to the act that mobile wireless sensor nodes are energy limited equipment's, which saving energy is one of the most important issues in the designing of these networks. Beside all of the challenges caused by the mobility of the sensor nodes, we can note to the routing and dynamic clustering. Studies show that cluster models, which have adjustable parameters have significant impact in minimizing energy consumption and extend the lifetime of the network. Therefore, the main objective of this research is to present and select the smart way using evolutionary algorithms for clustering in mobile wireless sensor networks for increasing Lifetime of the Network and correct delivery of packets. In this thesis, firstly, Genetic Algorithm, and then Bacterial Conjugation is used for clustering sensor nodes. The results of the simulation represents substantial growth in accelerating the clustering speed.In the proposed method for calibration of mobile wireless sensor nodes, the speed of nodes is considered

6.2 Future Works

The problem is assumed that clustering is done periodically and periodically redefined optimism. Among the future works for this dissertation, the following can be noted-

- Use of Hybrid Optimization Techniques
- Comparative Assessment can be done with respect to other evolutionary optimization techniques.

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