



Cluster Optimization in Mobile Wireless Sensor Networks

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ABSTRACT

This study describes an ideal evolutionary strategy that could be applied to address real-world problems in Mobile Wireless Sensor Networks (MWSN), like energy conservation. The algorithm is executed using simply the bacterial conjugation operator, which makes the offered approach simpler to use and put into practice. When compared to other evolutionary algorithms with the same name, such as the pseudo bacterial genetic method or the microbial genetic method, this technique's use of the bacterial conjugation operator is different. In this study, we aim to broaden the optimisation issues for wireless mobile sensor networks. First, use genetic algorithms to improve orthogonal, orthopedic, and sensor node optimisation Reduce the distance between network nodes for communication by splitting the installment. The fact that this approach does not personalize the amount of clusters is one of its problems. Greater flexibility, which enables the placement of sensor nodes in various contexts, presents this difficulty. As with earlier algorithms, it is also assumed that the nodes are sensor nodes because they are not uniform. As a result, MWSNs have a limitation on non-uniformity. This enables the usage of this kind of wireless sensor network in many settings.

Keywords: Contour Detection, Disease Detection, Median Filter, Mean Filter

1. Introduction

The emergence of MWSNs has caused the focus to move from conventional stationary WSNs to networks with mobile sensor nodes capable of sensing a variety of activities. They can also routinely change their location in a sensing area. MWSN applications include time-driven, event-driven, on-demand, and monitoring apps. Mobile sensor node design, residual energy utilisation, motion, topologies, adaptability, localization, data collection routing, Quality of Service (QoS), and other factors are crucial when creating an energy-efficient MWSN for a particular application.

The MWSN is a collection of alleged sensor nodes that have the ability to move and alter their positions in order to interact with actual objects. Movable sensor nodes have the same abilities as fixed sensor nodes, including the capacity to recognise, compute, and communicate with one another. The ability of the movable sensor nodes to move around the network is the primary distinction. They can move around and gather information. Presented to you is information. It is possible to transmit data from one mobile sensor node to another. The distribution of the data is another distinction. While routing is dynamic in mobile wireless sensor networks, it is predetermined and fixed or dispersed by CSS in fixed wireless sensor nodes.

A few of the characteristics are error tolerance, wireless connection, scheduling, protection, condition monitoring, wireless communication, automation, and protection. There are many important architecture issues for MWSNs, including hardware cost, network architecture, implementation, memory and battery sizes, information processing, topology changes, sensor node/sink movement, exposure, power depletion, protocol scheme, extensibility, positioning, data and node based, network differences, hardware failures, QoS, data coalition and repetition, auto configured, inter-layer system, and equitable traffic (Rathee, 2016). Typically, a sensor network will have one or more sensors to monitor temperature, brightness, wetness, compression, glow, proximity, and other variables. Additionally, it contains an antenna, battery, radio transmission, (ADC) analogue to digital converter, and CPU. The nodes' small size results in insufficient integrated storage, battery capacity, computing power, and radio capacity (Nabil, 2017). A mobile sensor node's structure is nearly comparable to that of a traditional sensor node. On the other hand, extra parts like localization-location discoverers, mobilizers, and energy producers are taken into consideration for mobile sensor nodes. The mobilizer gives the sensor node its mobility, and the location or site finder unit establishes its position. The power generator device is capable of producing electricity using any specialised techniques, such as solar cells, to satisfy the sensor node's additional power requirements.

2. Related Work

In the modern period, the genetic algorithm (GA) has been successfully used to numerous optimisation problems. Numerous algorithms have been evolved using biological operators like combinations and mutations. The growth of operators has been a persistent focus of much research. While minimising clutter, other algorithms change their focus to create uniformity. . The evolutionary explanation of the aforementioned techniques did provide some difficulties, though. The fact that many of these algorithms have numerous input parameters is another significant issue. They need to be decommissioned and recommissioned, which necessitates a specialised study for each trainer. Even for a surface algorithm genetic technique, population size, composition

rate, and mutation rate can be input parameters at a level of Different equations, including the sales rectangle, were discovered by pedestrians. These algorithms can be implemented in a variety of ways and accept multiple input operators. Additionally, each lengthy step requires time to locate the best inputs. This operator is regarded as a genetic surface transfer method. This operator boosts network connection speed.

By combining data, clustering promotes network extensibility and minimises power consumption. Numerous additional advantages (Çakıcı, 2014) are proportionate to the additional objectives, including: Concentrate and localise the size of the rectilinear table and the rectangular planar surface. While extending the range of intergroup contacts to clusters, it can sustain communication bandwidth. restricts and prevents the interruption of sensor message exchange. Clustering can reduce overhead and overall maintenance costs while maintaining the stability of the sensor network design. Reduce the topology, which means that only when the sensors are linked to their headers are they preserved. When the levels between the heads alter, they are both influenced and unaffected. Increased network enactment and node battery life lengthen the network's operational life.

3. Network Design

For data to be transferred from mobile sensor nodes to the sink/base/central station in MWSNs, the network structure is essential. Then, the washbasin is connected to the remote user or server over the internet. huge Performance of MWSN only depends on topology organisation or data collection technique. The architecture guarantees a robust network with enhanced QoS for motion traffic and full connectivity as a result. Additionally, in MWSNs, topologies define the size of the sensor node group, manage the addition of new members, and deal with the removal of members who leave the cluster. The creation of an upgraded MWSN and effective data collection with low energy consumption might result from taking into account various network topology elements. To ensure the best data collection and network implementation, different network topologies are employed depending on the features of the MWSNs. To maximise data collection, a variety of network topologies are used depending on the properties of the network.

4. Procedure

The bacterial synthesis algorithm separates the base layers of the traditional genetic algorithm from the surface transfer operator Genetics that makes use of a mixture of bacteria in a manner that is inspired by nature. A chromosome with a high degree of appropriateness will act as a donor chromosome for the population because it has been demonstrated using this way that the genetic information of the donor chromosome is helpful for the recipient chromosome. The complexity of implementation and the use of computational resources during implementation are reduced in this way, making it an evolutionary strategy as well. The bacterial composition algorithm's superior performance compared to other developed algorithms means that it can be used for a variety of applications without the need to modify its basic parameters. It starts working right away because it doesn't waste time looking for the best parameters. The implementation strategy prevents early convergence and produces precise outcomes.

The orthogonal nature of the orthogonal algorithm is typical of the orthodontic elimination and synthesis algorithm in the orthodontic approach. The only masters are the bacteria. It should be noted that this operator is flexible and does not require any other input parameters, therefore the initial population parameter value serves as the algorithm's sole input. This method is quicker and includes an input parameter despite the genetic algorithm's various branches. This algorithm's procedures are less expensive, and research shows that they combine the effectiveness and high accuracy of PSO and SGA approaches. For the first time, the bacterial composition method was applied in this research to cluster moveable sensor nodes, and promising results were attained. Before discussing the outcomes of modelling this algorithm, we experiment with how it functions and how it is applied to portable wireless sensor nodes to determine its usefulness for clusters.

5. Bacterial Composition Process

The lifespan of the network and time are determined by the sensor nodes in the MWSN. In sensor networks used for sensing applications, network longevity is one of the most important service quality characteristics. The electricity they consume directly correlates with the lifespan of nodes (Sharma, 2015). We want to set up enough sensors in sensor networks to cover a target for remote monitoring. A data collection centre must receive all the data the sensors have compiled. Information transmission requires more energy at longer intervals. Information is sent to the central from each sensor. In contrast to multi-hop communication methods, direct transmission networks are very easy to create but require a lot of power from the centre because of the high sensitivity of the communication (Bhatia, 2016). Multi-step connections are more practical and economical in these networks because of the high degree of compactness of the sensor nodes in surface units and, as a result, their close proximity to one another. However, because each sensor has a finite amount of energy and communication with additional sensors uses more energy, they are less effective than single-step connections. Additionally expensive is the utilisation of multi-step connections. The life of the sensor network is further shortened by the significant power depletion in sensors.

The advantages of short distance for the majority of nodes are increased by using clusters for each year of information to a base central station by requiring only a few nodes for communication from long distance to central station. The installation has a line-by-line node that gathers all the data from its line-by-line nodes. Clustering is such that we link the network to a number of dependent clusters that each have their own clustering. This method uses fewer steps and only threaded nodes to get to the main centre (Lobiya, 2019). Since most nodes prefer to send information to nearby sources rather than the main centre, optimisation can greatly lower communication costs for most nodes. This example demonstrates how tempered reduces communication header in both multi-step and single-step communication.

To comprehend the quantity of clusters There have been attempts to establish the ideal number of clusters in various contexts. The authors (Sabo, 2014) proposes a distributed algorithm for wireless sensor networks in which each sensor, given a chance, selects itself as a hint and contributes to its generalisation. With this algorithm, one-step clusters can be made. To determine the ideal number of headers, every step is examined, and an analytical model is developed. It offers functions for a number of variables, including sensory field size, turbulence, and node count.

5.1 Clustering based on evolutionary procedures

Researchers have recently used evolutionary algorithm-based clustering approaches widely. By locating the fewest number of clusters in the network, these methods offer the energy-optimal model and determine the best distribution of sensor nodes inside the lattice region. In this field of stimulation, a variety of optimisation techniques have been used, including GA, ant and bee colony algorithms, PSO algorithms, and others. Each of these strategies uses unique fitness-related aspects to accomplish their objectives. Quadratic processes are more efficient when they use different approaches and NP-hard quadrants. Due to the need for general information, which is provided at the network's central station, these methods are typically centralised and operated there.

5.2 Bacterial composition procedure

Surface gene transfer and competition make up the two components of the bacterial composition operator. Applying the technique of superficial gene transfer to paternal chromosomes. chromosome that fits its chromosomes the best The recipient chromosome is the one that fits the least well with the donor chromosome. During algorithm execution, the best and worst fit in values are known. After the gene transfer phase, a receptor chromosome and a new chromosome are created. They enter the competition stage from the first stage. The generated chromosome is the output of the bacterial composition algorithm. The input arguments of the bacterial composition algorithm are: Donor chromosome,

Receiver chromosome, the best fit and worst fit. The process of the algorithm combines the bacterium and the pressure shows application on two chromosomes.

5.3 Genes surface transfer

The sequencing of genes from the chromosome does not contribute to the chromosome in the first stage of the BC algorithm. The receiver is put in the exact same spot. The start of the pertinent gene string is chosen at random. Surface transfer of genes and competition are the two main components that make up how this algorithm functions. The donor chromosome's gene sequences are continuously chosen by the bacterial composition algorithm. The two input parameters for this procedure are the length of the string to be cloned (L) and the starting point of the gene strand to be cloned (P). The algorithm results in the length of the line that should be duplicated from the difference in the amount of parental fitness, divided by the difference between the best and the worst fit. A value that is randomly distributed between zero and the length of the chromosome is used to determine the starting point of a gene strand. P's value is discovered. The donor chromosome's gene strand is stretched starting at position P and length L after these two parameters have been set. In the same place, the receiver is changed. If the process of replicating all the genes during the transfer fails. The operator continues to copy genes from the chromosome's start all the way to the receptor chromosome's end on the barrier. This point should also take into account the fact that consecutive performances of the gene copying process will produce different chromosomes because the starting point is chosen at random.

The chromosome excised from the gene transfer step enters the second stage of the bacterial synthesis operator. The chromosomal mutation operator behaves in a way that has the worst fit to the likelihood of winning the competition with the receiving chromosome. Expand it. The winning chromosome replaces the receiving chromosome in the population because the suitability values of mutant and non-mutated chromosomes are connected to one another. The number of genes to be mutated is known as Pgm in the mutation operator, and it will be counted for each chromosome. The number of similar genes shared by two chromosomes determines the amount of Pgm. For each gene, a jump is applied if the number between zero and the A stroke generation is smaller than the Pgm value. The more mutations there are for a chromosome, the bigger the number of chromosomes, and the worse fit. The number of genes located on two half-length chromosomes that are single-stranded serves as the formula's criterion for chromosome similarity. A chromosome with a value between zero and one is obtained. By altering the genes on the recipient chromosome, it becomes incredibly effective. There is also a chance for this. The beneficial genes have a chance to transfer to the chromosome if the amount of L is insufficient for the length of the chromosome. The operator is therefore created to suit as many chromosomes as possible. More mutations will occur the closer the receiver gets to the donor's chromosome's eligibility.

- Creating a main population of chromosomes is the first step in the technique. In order to achieve this goal, chromosomes are used to build a random assortment of populations from our starting population.
- The bacterial composition serves as the lone operator in the predisposing algorithm, and the donor chromosome with the highest Fitness stands out from the rest.
- The worst and best values, which are referred to as the worst fit and the best fit called, are needed for calculation L. The best chromosomes produce the best match. When the Shattood storage algorithm is running, the worst chromosomes must be present. The ideal and undesirable chromosomes are produced at this stage. They are separated from the general populace one by one.

- When the BC operator is applied to every chromosome, a string in the stringed algorithm comes to an end. Consequently, each chromosome goes through the following stages: The first chromosome from the population is chosen. The receiver chromosome as well as the best chromosome are both affected by the BC operator.
- The best chromosome and the chromosome formed by the BC operator are compared for fit. Being chosen as the best chromosome was preferable. It is vital that the chromosome produced by the BC operator always fits the members of the prior population better or equally. The previous chromosomes need not fit perfectly with this operator. The proverb's meaning is believed to be that the BC operator evaluates the loser chromosome to replace the worst chromosome. Because this chromosome has never been assigned to a population, updating the poorest fit with it will bring the fit of the chromosome among the population closer to the best value. Consequently, the parameter L's value is about equal. will be 0, which will make the algorithm less effective.
- Chromosome operation: Choose the entire line and proceed to step 2 of the algorithm to choose the subsequent chromosome.
- The greatest need can be known as the need for finishing the algorithm, similar to the genetic algorithm.

6. Performance Evaluation

The flexibility and lifespan of the network have been increased by the optimisation of mobile sensor nodes. The inexpensive frame has received a lot of scientific attention recently. The leader of each cluster is frequently referred to as a red head. It has been determined how saturated mobile WSNs are. The problem's title is regarded as having a high time complexity. In these kinds of networks, exploratory algorithms perform well. It will be quite challenging to determine the ideal number of surface lines among moving sensors. If there are 433 sensor nodes, then we need to use a different combination to solve the problem in the appropriate way. As was already explained, the algorithm. In order to improve network stability, the combination of bacteria successfully responds to the orthostatic planet and to the orthostatic genetic algorithm, as shown by (Zhao, 2004), which schedules tasks for multiple processors, determines the ideal number of eclipses, minimises power consumption, and increases network life. The technique that has been used consists of several distinct phases. It has a stage 2 starting point that serves as the central hub for eclipses generated by the bacterial composition algorithm. finds and common sensor nodes join these rows in the following phase, which is the steady state. The sensor nodes send the clusters their acquired data frames, which are then transmitted to the clusters and clustered. They transfer this data to the central station after processing it.

6.1 Start Phase

The ideal number of clusters is looked for and tested in the initial stage. In the initial round, the central station delivered brief messages to all sensor nodes in the desired distance to wake them up and capture their positions, energy levels, and identification numbers. The sensors from the central station and the map's surface are gathered, and an ideal number of sensor nodes are marked with the Blocked Block - Selects sensor nodes as red bacterial method. The members of each branch are also chosen by the central station, which also creates the clusters. None of these nodes transmit data to the central station directly. When the headlines were chosen, the individuals in each cluster that were found had to be linked to this heading. A message to all sensors that had this header then had to be sent. The brief message from the central station states that each line has a schedule based on the protocol. TDMA is created, and each cluster member is given a unique set of time intervals utilising these intervals. It occasionally updates the nodes. Malformations are less likely to be prevented using TDMA scheduling. When the data for the goal is not delivered, the possibility of shutting off the sensors stores the energy between the data transmissions. Use the CSMA protocol with a single code that uses distinctive and comprehensive details to encode and cancel your data in order to prevent cross-linear interactions. The next paragraph provides a detailed explanation of how to optimise sensor nodes using the algorithm for bacterial composition.

6.2 Steady Stage

The awake sensor nodes in this case are awake to gather data. Sensitise the data and deliver it to the cluster head based on the TDMA timing. To receive data from other nodes, the link line node must maintain its receiver. The threaded node turns the signal into a unified signal after processing the data when it is received. Eventually, this consolidated signal is transmitted to the central station. It has already been established that the network has returned to startup mode after a predetermined period of time, and new headers are chosen based on the bacterial composition.

Our goal is to shorten the distances between the sensor nodes and the nodes next to them as well as between those nodes and the central station. Additionally, the objective function often benefits from the number of headers. Because the cluster head performs a lot of work on regular nodes and uses more energy as a result, reduced energy dissipation and greater surface area cause nodes to dissipate more energy; Therefore, the bacterial composition algorithm is illustrated as follows to find the ideal value of the headers and raise the value of the objective function:

$$fitness = w * (D - distance_i) + (1 - w) * (N - H_i) \quad (1)$$

The two Distance factors—the total of all nodes—that are employed determine the objective function. With their cluster heads and how far away they are from the central station, it is typical. H_i is the total number of network heads. The process for bacterial composition need to use the fewest headers and Distance_i. The direct distance between each node and the central station is the objective function mentioned above. With N Number of sensor nodes and a default weight of 0, the method can be further evaluated, for instance. This indicates that while $w = 1$ is a communication component for us, the number of clusters is essential to us. One set of random systems is used to begin the genetic algorithm. Chromosomes can identify the number of nodes

in a cluster once they have found the ideal match. A very successful and efficient method for locating solutions in networks with uniform and non-uniform topology is the objective function in (Tsai, 2006), which has been utilised for long distance communication with nodes. The findings indicate that 43% of sensor nodes are equivalent to the number of headers. The communication distance between the sensors is also reduced by 13% in this way compared to the direct shipping option. The article (Tsai, 2006) is where the objective function for this dissertation was taken. It is particularly effective at optimising the problem due to its low computation requirements and high improvement. The number of times the algorithm must run is specified at the start of the variable procedure. The method stops if the number of created cluster heads is more than this starting point.

The results of various simulations show how effective the suggested technique is in reducing communication distance and power consumption. The following parameters in table 1 are shown for network and sensor nodes for a variable number of nodes. Nodes are scattered around a 433 metre square region. The nodes are distributed in a wholly linear fashion. Nodes Nodes in a 433-dimensional world. The energy that was initially stored in the nodes at the start of the algorithm can be exactly the same because the sensor is mobile. The nodes' physical makeup is also extremely similar. Table 2 provides examples of genetic algorithm parameters and bacterial composition. Ch_length is the length and the number of identical genes between two chromosomes in SimGenes' algorithm for calculating mutation rates. A stable chromosome is present. The new protocol outputs produced by MATLAB. The optimal outcome is a long network life. Throughout the year, there has been a decrease in energy usage. It also denotes a favourable state at this point of the network after the clustering phase.

With 50 nodes evenly distributed across 433 by 33 metre areas, we get a MWSN (fig. 1). We have some standard nodes as well as some extra-powerful (43 J) nodes. Energy equal to $E_0 = 31$ is present at the plane of the sensor nodes. These sensors are typical ones. Due to the usage of heterogeneous sensors, this combination of energy affects behaviour.

We took into account that the simulation would run for 2333 times, that there would be 13 sensors or beginning population members, and that energy depletion would be calculated by the energy model from [7]. After clustering, it is evident that the persistent energy does not create nodes for either the Genet One method or the Bacterial Composition. Here, it is expected that: All nodes can be chosen as headers; each node can be grounded through the closest plot line or can grate through and be the closest neighbour node. The results of the trials show that sending a node 100% more energy than it consumes from its neighbours is effective. Sending through a nearby node distributes the energy load over the path nodes, whereas sending straight to the node sends 100 times as much energy to the sender each year, resulting in 0% energy use. By looking at the picture below, we can see that the method that mixes bacteria with the best sensor node tuning can only lessen the network's power depletion, leading to a longer lifespan. Fig. 2 shows that the grid has grown as energy demand has decreased. The chromosome composition calculation portion is removed from the bacterial composition method; thus, any calculations relating to this operator, such as selection, comparison, etc., have also been removed. As a result, from the number of reference parameters to the fit function, the genetic algorithm uses this approach for comparison numbers. Both algorithms are displayed as a fit function in the set. The algorithm of bacterial composition's diagram (fig. 3) shows that the better the solution, the fewer trips are required.

7. Conclusion

Two genetic algorithms and bacterial composition are employed in this study to optimise sensor node mobile wireless. To cluster sense nodes, the genetic algorithm from the past is widely utilised. The algorithm for bacterial composition that has been applied in this field thus far was employed. The chromosome with the best fit, the chromosome with no best fit, and the chromosome with the worst fit are the recipients in the Bacteria composition algorithm. The best and worst fit values are determined during the algorithm's execution. Receptor chromosomes and newly generated chromosomes enter the competition stage from the first stage chromosome following the stage of gene transfer. A bacterial compound is the algorithm's output. This algorithm simply requires one input, responds quickly, and when the fitness function is referred to 11% of the time, it returns the best possible result. It's genetic. The results of the genetic algorithm with 13 matched sensors and fixed network parameters in 43 successive runs are shown and compared to the findings of the algorithm's simulation, which reveal a 441 percent growth. A growth rate greater than 423% can also be supplied for optimisation by altering the number of sensors.

Table 1: Number and stipulations of nodes

Parameters	Values
Network size	433 m ²
Number of sensor nodes	13
The sensory radius of the node	1 Meter
Node communication radius	3 meters

Table2: GA Values and Bacterial Composition

Parameter	Bacterial composition algorithm	Genetic algorithm
Population size	13	13
Crossover rate		3.1
Crossover type		Single point
Mutation rate	SimGenes / (Ch_Length*10)	3.2
Generation size	433	433

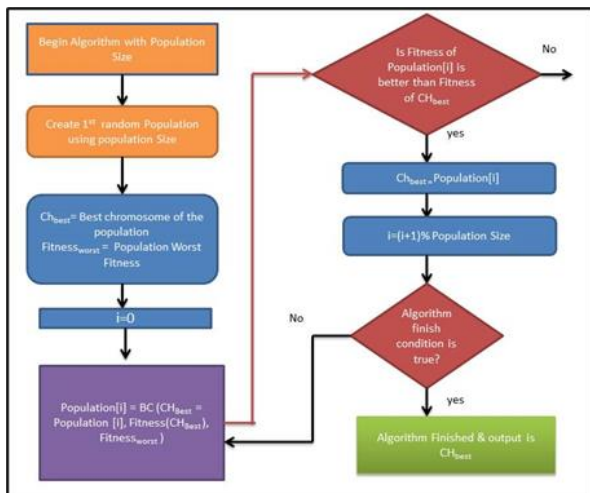


Fig. 1: Anticipated Method

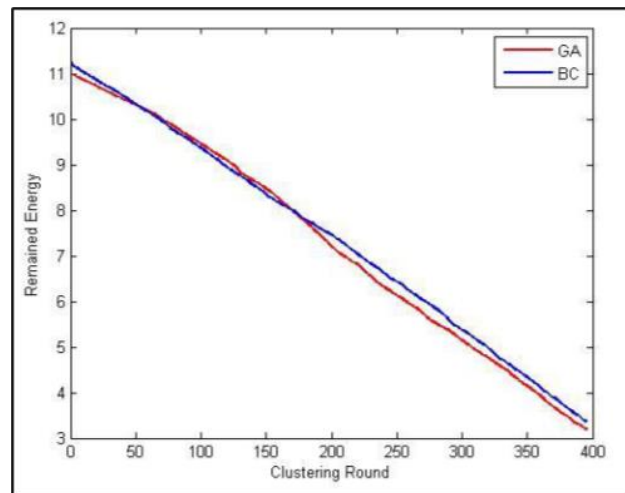


Fig. 2: Residual Energy of Network

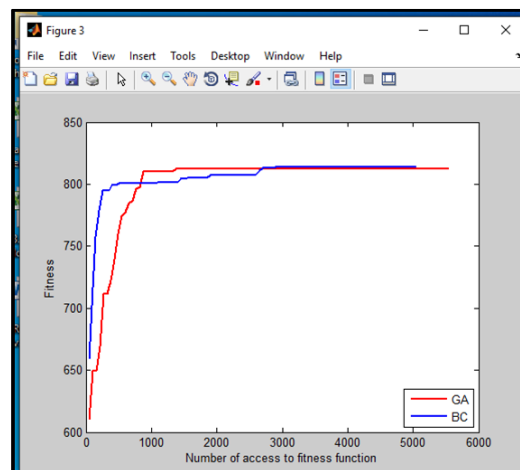


Fig. 3: Evaluation of Fitness of Network

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