Analysis of the Genetic Algorithm Operators for the Node Location Problem in Local Positioning Systems

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Abstract. The node location plays a critical role in the LPS performance capabilities. Due to the complexity of this problem, the implementation of heuristic methodologies such as genetic algorithms (GA) has been widely proposed in the literature. However, the performance of GA is heavily dependent of the consistency of its foundation and its adaptation to the nature of the optimization problem. In this paper, we analyze and compare a variety of different selection and crossover techniques in search for the most suitable configuration for the node location problem. Results show that although some combinations achieve adequate results, the concept of a hybrid GA that takes advantage from different configurations depending on the problem requirements can surpass any fixed individual combination.

Keywords: CRLB, Hybrid Genetic Algorithms, Localization, Local Positioning Systems, Node Location Problem.

1 Introduction

Local Positioning Systems (LPS) have supposed an active topic of research over the last few years. They rely on the deployment of sensors in a well-defined area in which the accuracy demands are higher than the Global Navigation Satellite Systems (GNSS) can provide. GNSS devices suffer distortion in the quality of their signals by crossing large buildings [1], by facing obstacles in their paths [2], by ionospheric effects [3] or by unstable synchronization among the system elements [4].

For these reasons, a new solution to mitigate these adverse effects is required for high-demanded applications such as autonomous navigation in indoor and outdoor environments. LPS have proven to enhance localization accuracy based on the ad-hoc deployment of sensors to avoid negative phenomena on signals. This requires an exact knowledge of the environment and a technique to correctly distribute the sensors in space.

However, the distribution of sensors in space in LPS, known as the node location problem, is a complex problem which has been proven to be NP-Hard [5] [6]. Therefore, heuristic solutions to the node location problem has been widely proposed in the literature. Tabu search methodologies [7], the firefly algorithm [8], the dolphin swarm algorithm [9], simulated annealing [10] but especially genetic algorithms (GA) [11] [12] [13] have been used to solve this problem.

Authors have previously addressed this problem by achieving reductions in the signal noise [14], algorithm coverage enhancements [15], clock errors [4] or mitigating adverse phenomena such as multipath or sensor failures [16] in Wireless Sensor Networks. This requires the computation of a fitness function to measure the beauty of the node distributions. Generally, the Cramer Rao Lower Bound (CRLB) estimator has been used to provide an evaluation of the quality of a sensor deployment in LPS [14] [17] [18] [19] [20]. CRLB is a maximum likelihood estimator which defines the minimum localization error achievable by any positioning algorithm in a target location given a defined node distribution in a particular operation environment. In this way, the overall reduction of the CRLB in every possible target location, Target Location Environment (TLE), produces the better node configuration in the space among the possible node distributions considered in the optimization, Node Location Environment (NLE) [11].

We showed in [11] that the beauty of the sensor configuration in Line-of-Sight environments is a heuristic complex problem in which the configuration of the hyperparameters of the Genetic Algorithm was crucial to achieve actual and valuable solutions. In this sense, the purpose of this study was to describe the methodology for constructing a valid GA for the node location problem, considering a further discussion to the genetic operators (selection, crossover and mutation techniques) in order to achieve better results.

In this paper, we study different configurations for the genetic operators of the node location problem in an Asynchronous Time Difference of Arrival (A-TDOA) [21] positioning architecture in order to improve the quality of the heuristic search of our previous studies. We also look for providing a common framework for the discussion of the genetic operators used in the node location problem as well as the combination of these functions in a hybrid GA configuration to enhance the overall performance.

The remaining of the paper is organized as follows: the steps of the GA for the node location optimization in LPS are introduced in Section 2, the results are presented in Section 3 and Section 4 concludes the paper.

2 Genetic Algorithm for the Node Location Problem

The node location problem is crucial for LPS. The freedom of the designer to locate sensors in space allows the reduction of the errors produced by signal noise [18], algorithm coverage enhancement [15], clock errors [4], multipath effects [13] or sensor failures [16]. This requires a heuristic approach since the problem has been characterized as NP-Hard [5] [6].

Among the different metaheuristics, the GA have proven to specially fit the requirements of this complex problem. GA were first introduced by Holland [22] and later refined by Goldberg [23] built on the theory of evolution. By this postulate, the best adapted individuals are the most probable to survive and produce offspring for the next generations, where descendant individuals will present better adaptation to the environment.

The general steps followed in a GA computation problem are described in Figure 1. These steps include the generation of the initial population for which a codification of the individuals is required, a fitness function definition for the evaluation of the individuals, a stop condition that can be based on a pre-defined number of generations or the definition of a suitable convergence criteria for the problem; and the genetic operators (selection, elitism, crossing and mutation) which are deeply discussed in this paper.

2.1 Codification of individuals

GA are composed by generations of individuals. Every of these individuals are a possible solution of the node location problem among all the combinations considered for the optimization (NLE). The codification is usually binary since it allows the better performance of the genetic operators. Therefore, it requires the escalation of the variables implied in the definition of the individuals into the binary coding. In this problem, these variables are the Cartesian coordinates of each node used in the positioning architecture displayed.

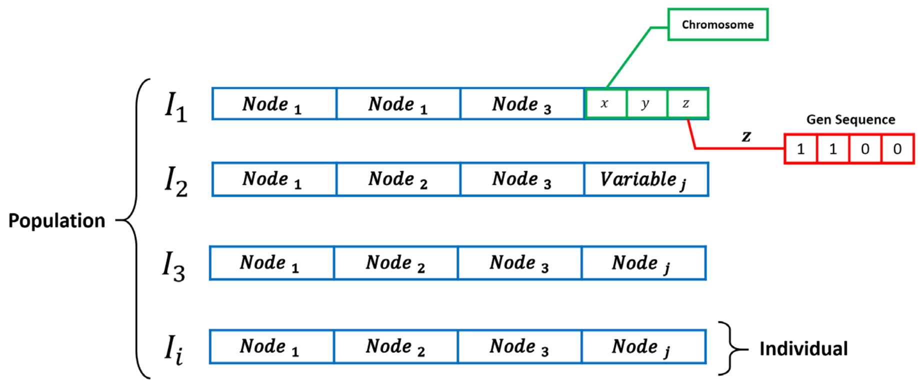

Fig. 1. Genetic Algorithm Codification of Individuals

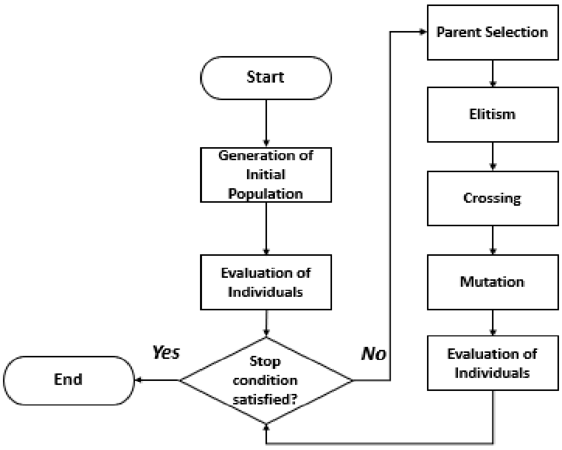

Fig. 2. Flux diagram of the GA.

As it is shown in Figure 1, the population consists of a number *i* of individuals which must be defined as one of the hyperparameters of the GA. Each individual carries a number *j* of nodes to locate, consisting every node of the gene sequences used for the escalation in binary codification of the position of a node for each defined Cartesian coordinate. In this paper, the initial population of the GA is randomly defined for guaranteeing the diversity of the initial population.

2.2 Evaluation of individuals

The beauty of each individual must be determined through a fitness function in order to detect the better adapted individuals of the population which are the best candidate solutions for the node location problem. Over the last few years, in the localization field, the CRLB parameter has been used as fitness function for the node location problem [14] [17] [18] since it allows the introduction of the uncertainties present in the communications channel in the covariance matrix of the system. Particularly, Kaune et al. [14] proposed a CRLB matrix form in which Huang et al. [17] introduced a heteroscedastic noise model consideration which especially fits for LPS applications:

$$FIM_{mn} = \left[\frac{\partial h(TS)}{\partial TS_m}\right]^T R^{-1}(TS)\left[\frac{\partial h(TS)}{\partial TS_n}\right] + \frac{1}{2} tr\left\{R^{-1}(TS)\left[\frac{\partial R(TS)}{\partial TS_m}\right] R^{-1}(TS)\left[\frac{\partial R(TS)}{\partial TS_n}\right]\right\} \tag{1}$$

where **FIM** is the Fisher Information Matrix (the inverse of the CRLB), **h(TS)** a vector containing the travel of the signal in the positioning architecture at study (in this case

the A-TDOA [18] [21]), **R(TS)** the covariance matrix of the system containing the information of the signal noise uncertainties as we introduced in [11], TS the target sensor position expressed by its Cartesian coordinates through the *m* and *n* estimated parameters.
The Root Mean Square Error (RMSE), which is used as the fitness function of the GA, with the minimum achievable error in the TS location, can be directly obtained through the trace of the inverse of the FIM (CRLB) as follows:

$$RMSE = \sqrt{trace\ (FIM^{-1})} \quad (2)$$

2.3 Selection techniques and elitism concept

Once evaluated, the selection procedure for the population is started. The main goal of this step of the GA is to arrange the individuals for the crossover in a way that optimizes the final solution, relying on the fitness value as a beauty estimator.

However, numerous selection methodologies are available, depending on the particular behavior of the specific characteristics of the problem. Therefore, in search for the most suited technique, we will analyze the behavior of tournament selection, with 2 and 3 individuals, roulette and ranked roulette selection [24].

The proportional and ranked roulette methodologies base their selection probability on the fitness value obtained by each individual. Although any individual can be selected, it is common for the most adapted individuals to dominate the selection criteria, resulting in a loss of diversity and a premature convergence.

The ranked-roulette pursues to prevent this phenomenon by establishing a selection probability based on the rank or position of each individual in the overall population. However, this methodology demands additional computation time, as it is required to rearrange the individuals multiple times and it is heavily dependent on the rank assignment which hinges on the specific problem characteristics.

On the other hand, the tournament selection methodologies rely heavily on the fitness values and may present problems of diversity for large number of contestants. However, being the selection of the contestants random, techniques such as tournament 2 or 3 stand out as well rounded and balanced selection methodologies.

Furthermore, the use of elitism along the selection criteria has been widely used through the GA literature. Although this particular step is optional, its improvement of the obtained solution by increasing the selection pressure is quite remarkable.

In this research we have opted for a persistent elitism where a certain percentage of the most adapted individuals are preserved for the next generation. The adequate selection of this percentage is critical for the GA's stability. An excessive value of elitism will result in a loss of genetic diversity and will incur a worse solution, thus we will analyze the appropriate value for each configuration we propose.

2.4 Crossover techniques

The crossover techniques, as well as selection criteria, play a decisive role in the performance of the GA in the exploration and optimization of the solution. The objective of this step is to create the next generation of individuals in a way that optimizes the algorithm search for the optimal solution. Three different methodologies have been studied, the single point crossover, multipoint crossover and the uniform crossover.

These three techniques differ from one another in the amount of crossover points of the procedure, as shown in Figure 2. By increasing the number of crossover points, up to the uniform technique, we enhance the genetic diversity and the probability of a productive new individual [25].

Nevertheless, a methodology with a lower number of crossover points, such as single point crossover, promotes the convergence of the algorithm by preserving most of the gene sequence of the most adapted individuals.

In search for the best appropriate methodology for the node location problem, we will study the single point crossover (SP), the multipoint crossover for 2 (MP2) and 3 (MP3) points and the uniform crossover.

2.5 Mutation techniques

The mutation function in a GA provides an additional source of genetic diversity to the configuration, playing a main role in the exploration of the environment in search for the optimal solution.

In this step of the GA, we artificially create entropy in the optimization of the solution by randomly modifying the genetic sequences of some individuals. Although it may seem futile to sabotage some of the individuals, the addition of the right amount of chaos is favorable for the optimization process, especially when close to a local or global maximum of the solution.

However, it is crucial to select an appropriate value for the mutation parameter, being an excessive value adverse for the convergence of the GA.

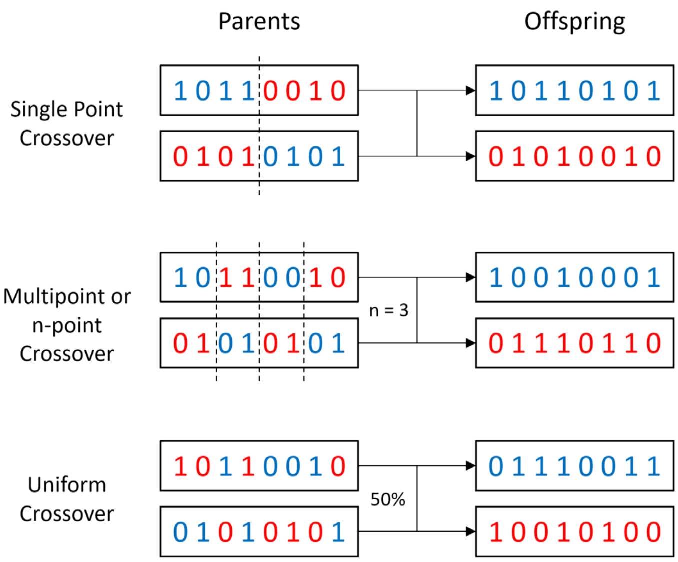

Fig. 3. Crossover methodologies

3 Results

The simulations were executed in the Python programing language, in an environment with the following characteristics.

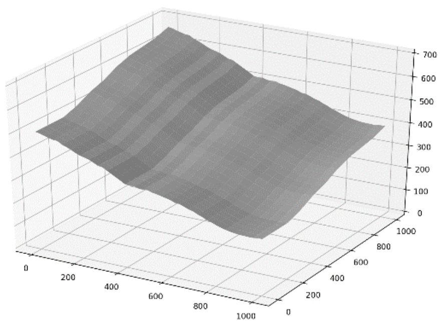

Fig. 4. Environment selected

Parameter	Value
Transmission Power	400 W
Mean Noise Power	-94 dB
Frequency of Emission	1090 MHz
Bandwidth	100 MHz
Path Loss Exponent	2.1
Antennae gains	Unity
Time - Frequency Product	1
Communication Type	Full-Duplex

Table 1. LPS Parameters [4]

In order to obtain the most suited methodology, we have studied a variety of possible combinations between the previously explained techniques. All simulations were executed with the same parameters of elitism, mutation and individuals, which were experimentally obtained based on previous simulations. The results of these different configurations over 10 simulations are listed below.

As shown in Table 2, three methodologies stand out, tournament 3 with 3-point crossover and tournament 2 and 3 with single point crossover. Once selected the best possible configurations, it is possible to optimize the mutation and elitism parameters for each configuration, as shown in Figure 4.

	T2		**T3**		**R**		**RR**	
	Max	Mean	Max	Mean	Max	Mean	Max	Mean
Single point	**2546**	1832	**2002**	1436	1510	560	684	361
Two-point	815	623	1413	1016	785	531	859	321
Three-point	867	589	**2277**	1532	1637	735	1547	1065
Uniform	424	213	722	468	631	453	421	226

Table 2. Comparison of the selection methodologies of tournament 2 (T2) and 3 (T3), roulette (R) and ranked roulette (RR) with the corresponding crossover techniques. All simulations were run equally with a 15% percentage of mutation and elitism.

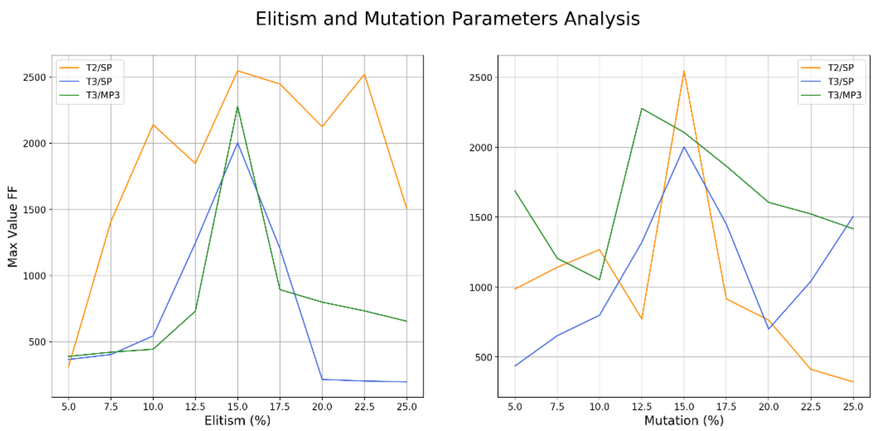

Fig. 5. Comparison between the best combinations of Table 2, in each graph the parameter at study is modified, remaining constant the second variable with a fixed value of 15%.

The best values are obtained from the T2/SP (tournament 2 and single point crossover) combination.

Therefore, we consider this value to be the optimal solution as no other combination obtains a greater result. However, in the T2/SP configuration, the single point crossover is considered to be an elitist technique that provides a quick and strong convergence, however the genetic diversity could be compromised.

On the other hand, in the T3/MP3 (tournament 3 and 3-point crossover) technique features a more chaotic approach which is favorable for the exploration of the environment but can difficult the convergence to the optimal solution.

Hence, we have assembled a hybrid genetic algorithm that combines these two methodologies in the pursuit of a superior solution. This hybrid algorithm present two different stages: an exploration-heavy phase and a solution intensification phase. The first phase relies on the T3/MP3 configuration for searching the optimal solution in the whole environment, after a certain number of generations, the algorithm would switch to the second stage. This last phase pretends to favor the convergence to the optimal solution encountered in the previous phase, through the elitist configuration of T2/SP.

In each phase of the program, the parameters of elitism and mutation are adapted to the optimal configuration of each technique in charge, obtained from Figure 4.

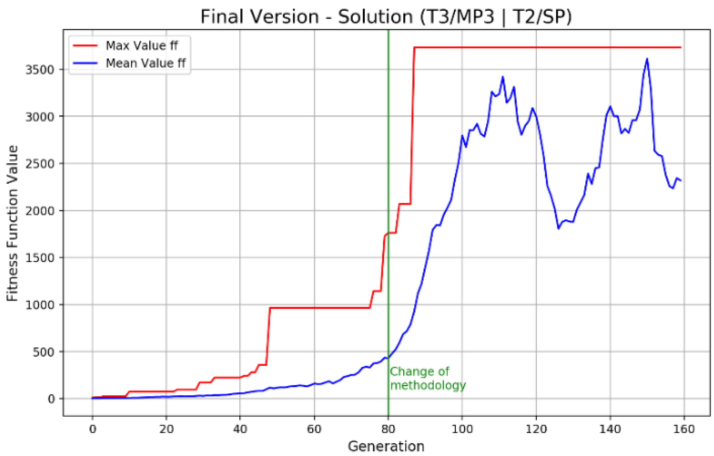

Fig. 6 Performance of the hybrid configuration of the GA

As seen in Figure 5 the result obtained is greater than the maximum obtainable for each configuration individually. The optimal node distribution obtained for this configuration can be obtained from the most adapted individual, displayed in Figure 6.

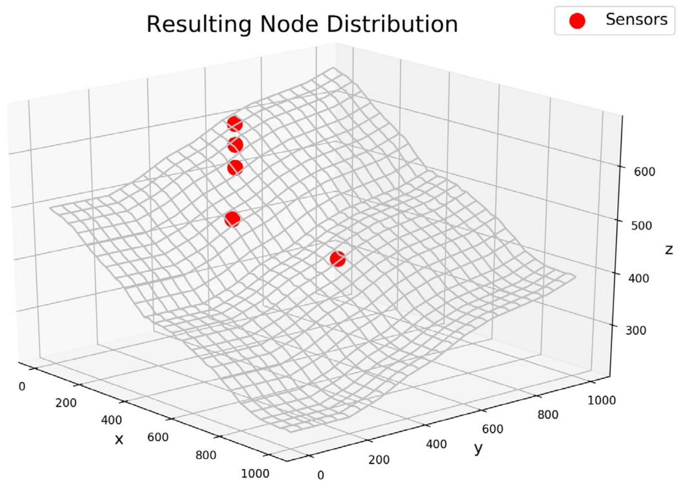

Fig. 7. Sensor positioning obtained from Figure 5

4 Conclusions

LPS have proven to be a well-suited alternative to GNSS for certain applications, thus its renown in the research community. However, LPS have shown to be heavily dependent on the environment characteristics and its particular distribution on it. Nonetheless, this problem has been defined as NP-Hard, thus the use of heuristic methodology, such as GA, has been widely expanded throughout the literature.

In this paper, we have studied and compared the use of different methodologies of selection, crossover, mutation and elitism in order to obtain the most suited combination to find the optimal solution to this particular problem.

Results show that a strong elitism favors the convergence to the desired solution. Also, the entropy generators in the GA, such as mutation and multiple points crossovers play a decisive role to achieve valuable results. The use of these operators is critical in order to explore the environment selected in search for the optimal solution.

Therefore, the hybrid configuration proposed, which relies on multiple phases in the optimization procedure, achieves a greater solution than any possible individual combination of the most expanded genetic operators analyzed, thus fulfilling the main objective of this paper.

The conclusions achieved on this paper present a different perspective in the node location problem incorporating hybrid genetic configurations, opening new opportunities for future investigations.

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