

GENETIC ALGORITHM OPTIMIZED DCM POSITIONING

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ABSTRACT

Database Correlation Methods estimate the mobile station location by comparing a measured radio frequency fingerprint with a set of previously collected or generated reference fingerprints. This set is referred to as the search or correlation space. Genetic algorithms can be used to optimize both the location accuracy and the time required to produce a position fix, reducing the size of the search space. This paper proposes an innovation in such application of genetic algorithms, restricting the first generation population to the predicted best server area of the serving sector measured by the mobile station. In field tests in a GSM cellular network in a dense urban environment, this approach achieved reductions of 20% and 15% in the 50-th and 90-th percentile location errors, respectively, in comparison to the original formulation, where the initial population is randomly distributed throughout the whole service area. An average reduction of 91% in the time to produce a position fix was also observed.

I. INTRODUCTION

Different levels of location awareness are inherent to any metropolitan area network (MAN) with wireless radio access. These allow packet routing to any mobile station (MS) and session continuity when the MS moves from one base transmission station (BTS) coverage area to another. These built-in location capabilities can be extended to provide added value location services (LCS) to the subscribers, which include, among others, location based billing and emergency call location. This latter application has been receiving much attention from government authorities and is already mandatory for cellular networks in some countries [1][2].

It seems that, in a near future, the winner technology for MS positioning will be based on the Global Positioning System (GPS), due to its accuracy and to the cost reduction in GPS receivers as its deployment scales up. Nonetheless, even in such scenario, there are still situations in which network based methods should be employed: **i)** unavailability of GPS signals (such as in indoor environments) and **ii)** location of MS without built-in GPS receivers. In addition, these methods serve as *fallback* when more precise ones can not be used due to systemic limitations, increasing LCS availability [3]. This latter improvement is of the highest importance when considering the positioning of MS originating emergency calls in cellular networks [4]. Network based methods use information already available at the serving BTS or periodically sent by the MS through the network measurement reports (NMR). The NMRs are used for call or session management - power control, handover, etc.

The location method presented in this work is a radio frequency (RF) fingerprinting method - or database correlation

method (DCM). It is a network based method which correlates measured RF fingerprints with RF fingerprints previously stored in a correlation database (CDB) to estimate the MS location [5]. Those fingerprints contain RF parameters measured by the MS and reported through the NMR. The CDB might be built from field measurements or from propagation modeling [6].

The service area - i.e., the region where a LCS based on the DCM solution is provided - is represented by a digital elevation model (DEM). The DEM is divided into non-overlapping elements with a $r \times r$ m² surface each, referred to as *pixels*. Each *pixel* has an associated RF fingerprint stored in the CDB. The *correlation space* is the set of *pixels* whose associated RF fingerprints are compared, by means of an evaluation function, to the RF fingerprint measured by the MS which is to be localized. Each *pixel* within the correlation space is a *candidate solution* for the MS location problem. It is not feasible to include all service area *pixels* in the correlation space, as this would cause a very high computational load, resulting in a long time to produce a position fix. In order to optimize the search for the MS estimated position, some techniques can be applied to reduce the correlation space. In this work, this is done by a genetic algorithm (GA). GA has already been used together with DCM solutions in [7]. However, we propose an alternative for the population initialization, restricting the random distribution of candidate solutions in the first generation to the predicted best server area of the serving cell (also referred to as sector). The proposed innovation reduced both the average location error and the average time to produce a position fix, in comparison to the original formulation presented in [7].

The remaining of this paper is organized as follows: in Section II, the measured and predicted RF fingerprints used in the MS location are presented, as well as the process of building the CDB from propagation modeling; in Section III, the correlation function used to evaluate each position candidate is introduced; in Section IV, the genetic algorithm used to optimize the MS location process is presented; in Section V, results for field tests in a 850 MHz GSM network are analyzed; Section VI brings the conclusions.

II. RF FINGERPRINTS AND THE CDB

Many DCM solutions in the literature employ CDBs built from field tests [8][9]. To keep those CDBs up-to-date, drive tests must be carried out after any change in radio access network elements, making this solution impractical for MANs. The detrimental effects due to the use of out-of-date network parameters in the correlation process in cellular networks has been demonstrated in [10] and [9]. To prevent those problems, and to allow for a quick and inexpensive CDB upgrade, a CDB built from propagation modeling has been used [11][12]. However, to maximize the accuracy of the DCM algorithm, additional efforts might be required in initial stages to tune the propagation models [13].

The propagation model used in this work to build the CDB is Okumura-Hata [14], which is largely applied to RF planning in cellular networks. It computes the average propagation loss using:

$$L_p = k_1 + k_2 \log(d) + k_3 \log(h_b) + k_4 L_f + k_5 \log(h_b) \log(d) \quad (1)$$

where d is the distance in meters from the BTS to MS, h_b is the BTS antenna effective height and L_f is the diffraction loss attenuation, calculated by the Epstein-Peterson method [15]. The MS height is assumed to be 1.5 m. The model coefficients k_i depend on the area morphology and transmission frequency. As the field test in Section V was carried out in the 869-881 MHz band, the model was applied at the central frequency of 875 MHz. The coefficients values are $k_1=-12.1$, $k_2=-44.9$, $k_3=-5.83$, $k_4=0.5$, $k_5=6.55$. All those values are the standard Okumura-Hata values for urban environment, except k_4 , which was empirically defined by the authors in [6].

The topography of the region where the LCS is to be offered is represented by a matrix $\mathcal{T} = (a_{i,j})_{I \times J}$, where $a_{i,j} \in \mathbb{R}_+$ for any $i \in \{1, 2, 3, \dots, I\}$ and $j \in \{1, 2, 3, \dots, J\}$. Each matrix element $a_{i,j}$ stores the terrain height averaged over a $r \times r$ m² square, where r is the \mathcal{T} matrix planar resolution. The \mathcal{T} matrix might also contain, added to the terrain height, the buildings heights. If the region covers a total surface of $L \times W$ m², then \mathcal{T} has $\lceil \frac{L}{r} \rceil \times \lceil \frac{W}{r} \rceil$ elements. Here, each element of \mathcal{T} will be referred to as a *pixel*.

The received signal strength (RSS) prediction for a single sector, as shown by Fig. 1, is obtained by the application of Eq. (1) to the terrain profile between the BTS antenna position and each element in \mathcal{T} . The transmitting antenna characteristics - geographical coordinates, azimuth, radiation pattern, effective isotropic radiated power, etc. - are considered in the propagation prediction.

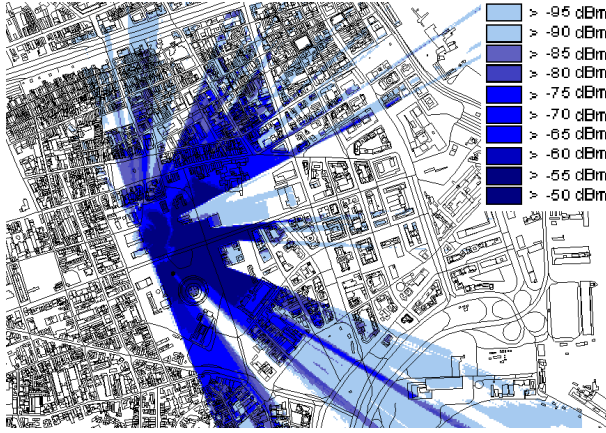


Fig. 1. RSS prediction for a serving antenna.

Each *pixel* in \mathcal{T} has an associated predicted RF fingerprint, obtained by the superposition of the RSS predictions of all sectors in the service area. The predicted RF fingerprint of the i -th *pixel* is given by the matrix [11]:

$$\hat{\nu}_{P,i} = \begin{bmatrix} \text{ID}_{P,1} & \text{RSS}_{P,1} \\ \vdots & \vdots \\ \text{ID}_{P,V} & \text{RSS}_{P,V} \end{bmatrix} \quad (2)$$

The $\hat{\nu}_{P,i}$ matrix has $V \times 2$ elements, where V is the number of sectors in the service area. Each line of $\hat{\nu}_{P,i}$ contains a sector identification (ID) and the correspondent predicted RSS. The lines

are organized in descending order of RSS. The RSS dynamic range and quantization step vary depending on the wireless access technology. The CDB is completed after $\hat{\nu}_P$ has been calculated for all *pixels* in \mathcal{T} . The predicted RF fingerprints in the correlation space are compared to the measured RF fingerprint, obtained from a subset of the parameters listed in the NMR. The measured RF fingerprint is given by the matrix:

$$\nu_M = \begin{bmatrix} \text{ID}_{M,1} & \text{RSS}_{M,1} \\ \vdots & \vdots \\ \text{ID}_{M,N} & \text{RSS}_{M,N} \end{bmatrix} \quad (3)$$

The ν_M matrix has $N \times 2$ elements, where N ranges from 1 to n_{max} , which is the maximum number of sectors that the MS can report in the NMR.

III. THE CORRELATION FUNCTION

In order to estimate the MS location, it is necessary to compare the measured RF fingerprint with the predicted RF fingerprints in the correlation space, which are stored in the CDB. The higher the similarity or correlation between a measured RF fingerprint and a predicted RF fingerprint, the higher the probability that the MS is located at coordinates associated with that predicted RF fingerprint. This similarity is assessed by means of an evaluation or correlation function.

Let $\mathcal{I}_{P,i}$ be the set of IDs listed in $\hat{\nu}_{P,i}$ and let \mathcal{I}_M be the set of IDs listed in ν_M . The set \mathcal{C}_i contains the IDs listed both in $\hat{\nu}_{P,i}$ and ν_M , i.e., $\mathcal{C}_i = \mathcal{I}_{P,i} \cap \mathcal{I}_M$. Let $\mathcal{S}_{P,i}$ and \mathcal{S}_M be the sets containing the predicted and measured RSS values, respectively, of the sectors listed in \mathcal{C}_i . The value of the correlation between the measured and predicted RF fingerprints at the i -th *pixel* is defined as:

$$f_i^{-1} = 2\alpha (n_{max} - \#\mathcal{C}_i) + \sum_{j=1}^{\#\mathcal{C}_i} \left[\frac{|s_{M,j} - s_{P,i,j}|}{\delta} \right] \quad (4)$$

where δ represents the MS inherent RSS measurement inaccuracy in dB units [11], n_{max} is the maximum number of sectors which can be listed in the NMR, $\#\mathcal{C}_i$ is the cardinality of \mathcal{C}_i , α is the dynamic range of RSS, $s_{M,j}$ and $s_{P,i,j}$ are the j -th elements of \mathcal{S}_M and $\mathcal{S}_{P,i}$, respectively. In GSM networks, $n_{max} = 7$, $\alpha = 63$ dB and $\delta = 6$ dB [16].

The first term in Eq. (4) is the penalty due to the absence in $\hat{\nu}_{P,i}$ of sectors that are in ν_M . The second term calculates the absolute cumulative difference between the elements of $\mathcal{S}_{P,i}$ and \mathcal{S}_M . If all sectors listed in ν_M are also in $\hat{\nu}_{P,i}$, i.e., $\mathcal{C}_i \equiv \mathcal{I}_{P,i} \equiv \mathcal{I}_M$, then $\#\mathcal{C}_i = n_{max}$, and the first term in Eq. (4) is null. In the worst case scenario, where $\mathcal{C}_i = \emptyset$, the first term in Eq. (4) reaches its maximum value and the second term is null. Regarding the penalty term, consider the i -th and j -th *pixels*. For each sector listed in ν_M and not in $\hat{\nu}_{P,i}$ or $\hat{\nu}_{P,j}$, a 2α value is added to f_i or f_j , respectively. As α is equal to the maximum variation of RSS, the first term in Eq. (4) ensures that if $\#\mathcal{C}_i > \#\mathcal{C}_j$, then $f_i > f_j$, regardless of the second term value.

IV. REDUCING THE CORRELATION SPACE WITH GA

GA is an adaptive search technique based on the principle of natural selection and genetic reproduction [17]. Each candidate solution is an individual, represented by a numeric sequence called chromosome. When using binary representation, each bit in a chromosome is referred to as a gene. The set of individuals at

each cycle or generation is called population. The individuals of a population are modified and combined by means of genetic operators - crossover, mutation, elitism - producing a new population for the following generation. Crossover mixes segments of chromosomes of two individuals (parents), producing two new individuals (crossover children) for the next generation. Mutation is a random modification of one or more genes of a chromosome. Elitism is the technique of cloning the best individual of a generation into the next cycle [18]. The aptitude or fitness of an individual is assessed by means of an evaluation function. Better fitted individuals have higher probability of being selected for reproduction (crossover). The best individual in a population is the one who achieves the highest value at the evaluation function. This cycle continues until a stop criterion - maximum number of generations, fitness of the best individual, processing time, etc. - has been reached. The best individual of the last generation gives the problem sub-optimal solution [17].

GA might be used to reduce the *correlation space* of a DCM algorithm, optimizing the search for the MS position. The correlation space is the set of *pixels* whose associated RF fingerprints are compared to the RF fingerprint measured by the MS. Each *pixel* within the correlation space is a *candidate solution* for the MS location problem. The set of candidate solutions in a DCM algorithm, without applying the GA, is the *original correlation space*. The set of candidate solutions, after applying the GA, is the *optimized correlation space*, which is a subset of the original correlation space. A GA *correlation space reduction factor* γ can be defined as the ratio between the number of elements in the optimized correlation space and the number of elements in the original correlation space.

In [7], the original correlation space is the full service area, represented by \mathcal{T} . At the first generation, p_a individuals, i.e., *pixels*, are randomly selected throughout \mathcal{T} . If there are g generations, the optimized correlation space is a set with $p_a \times g$ elements, so $\gamma_a = (p_a \times g) / \#\mathcal{T}$, where $\#\mathcal{T}$ is the cardinality of \mathcal{T} .

The probability of a MS being located within the predicted best server area of its serving sector is higher than in any other *pixels* in the service area. Therefore, the original correlation space is restricted to the predicted best server area of the serving sector, defined by the set of *pixels* $\mathcal{X} = \{i \in \mathcal{T} \mid \text{ID}_{P,i,1} = \text{ID}_{M,1}\}$, where $\text{ID}_{P,i,1}$ is the predicted best server ID at the i -th *pixel* and $\text{ID}_{M,1}$ is the measured best server ID, reported in the NMR. So, when initializing the first generation population, instead of randomly selecting individuals throughout the whole service area, the individuals should be randomly selected among the *pixels* within \mathcal{X} . In such conditions, if the population size is p_b individuals and there are g generations, the correlation space reduction factor is $\gamma_b = (p_b \times g) / \#\mathcal{X}$. Two assumptions can be made regarding the proposed innovation in the initialization of the first generation population:

- 1) $\mathcal{X} \subset \mathcal{T}$, so $\#\mathcal{X} \leq \#\mathcal{T}$. In practice, $\#\mathcal{X} \ll \#\mathcal{T}$, because the whole service area is much wider than a single sector best server area. As a result, for $\gamma_a = \gamma_b$, $p_b < p_a$, which means that, in comparison to [7], less individuals will be required per generation to find the sub-optimal solution;
- 2) As the probability of a MS being located within the *pixels* in \mathcal{X} is higher than in any other subset of \mathcal{T} , the average fitness of the first generation population will be higher - i.e., in average, the first generation individuals will be closer

to the real MS location - which means that, in comparison to [7], less generations will be required to find the sub-optimal solution;

Therefore, it is expected that the use of the proposed innovation in the initialization of the first generation population, will result in higher accuracy and lower time to produce a position fix. This will be verified in Section V.

The proposed GA steps can be summarized as:

- 1) Initialize first generation population, randomly selecting individuals - i.e., *pixels* or candidate locations - within the original correlation space, which can be the full service area, represented by matrix \mathcal{T} , or the predicted best server area of the serving sector, represented by matrix \mathcal{X} ;
- 2) Evaluate the fitness of each individual in current population, using the evaluation function in Eq. (4);
- 3) Create chromosomes, converting the individuals coordinates to binary format;
- 4) Apply genetic operators - crossover, mutation and elitism - to create a new generation;
- 5) Convert chromosomes to integer format;
- 6) If stop criterion has been met, provides MS location, given by the coordinates of the fittest individual; otherwise, returns to step 2.

If the service area is a square with $L \times W$ m², then \mathcal{T} is a square matrix with $\lceil \frac{L}{r} \rceil \times \lceil \frac{W}{r} \rceil$ elements. If the service area is geographically represented by means of a rectangular projection, like Universal Transverse Mercator (UTM) [19], and the UTM coordinates of one *pixel* are known, then it is possible to obtain the UTM (x, y) coordinates of any other element in \mathcal{T} . The length of each chromosome will be the number of bits required to identify the position of a *pixel* - i.e., its line and column in \mathcal{T} - and is given by $\lceil (\log_2 \lceil \frac{L}{r} \rceil + \log_2 \lceil \frac{W}{r} \rceil) \rceil$.

V. FIELD TESTS IN A 850 MHZ GSM NETWORK

V-A. Drive Test Scenario

Field tests were performed in a 850 MHz GSM network in the downtown area of Rio de Janeiro. The test area characteristics are summarized in Tab. I. The test set was composed of a GSM phone and a GPS receiver, both connected to a laptop placed inside a moving vehicle. The MS was in active mode and for each transmitted NMR the current location was calculated by the GPS receiver. Every NMR and GPS measurement were recorded for further processing. A total number of 4501 NMRs has been collected. The large number of samples ensures a reasonable confidence for statistical analysis. The GPS location was assumed to be the reference position, so, for each NMR and each location method, the positioning error is the Euclidean distance between the GPS position and the location provided by the respective method.

V-B. GA Parameters

The parameters used in the genetic algorithm are summarized in Tab. II. Parameters g_{max} , ϵ and ϕ define the stop criterion. The GA stops when one of the two conditions occurs: **i)** the maximum number of generation g_{max} is reached; **ii)** the fitness of the best individual during ϕ consecutive generations does not improve by a value higher than ϵ . The second condition is an improvement of the stop criterion based only on the maximum number of generations: if the aptitude of the best individual reaches a steady state, it might

mean that the algorithm has reached a local maximum and therefore there is no use in creating new generations [20]. Parameter γ is the correlation space reduction factor, defined in Section IV.

Table I. Characteristics of the test area

Characteristic	Value
Morphology	Dense Urban
Area	4.84 km ²
Cell Density	24 cells/km ²
DEM planar resolution (r)	10 m
DEM with building heights?	Yes

Table II. Summary of GA parameters

Parameter	Value
Crossover ratio	60%
Selection type	Roulette
Mutation ratio	1%
Elitism	Yes
Chromosome length	16 genes (bits)
g_{max}	20 generations
ϵ	0.00001
ϕ	5 generations
γ	3%

V-C. Experimental Results

Fig. 2 shows the cumulative distribution function (CDF) of the MS location error achieved by the DCM using the original (Method I) and proposed (Method II) initialization methods for the first generation population. Both have used the parameters and stop criterion described in Section V-B. Method I has achieved location errors of 197 and 426 meters, for the 50-th and 90-th percentiles. Method II has achieved location errors of 156 and 362 meters for the same percentiles, which represents an error reduction of 20% and 15%, respectively.

Fig. 3 shows the average fitness of the first population for each positioning fix, i.e. per collected NMR. As expected, Method II achieved a higher average fitness in the first generation population, what results in less generations to reach the suboptimal solution: Method I requires in average 9 generations, while Method II requires only 7 generations - a 23% reduction.

The reduction in the average number of generations, coupled with the fact that the population size in Method II is much smaller than in Method I, results in a significant reduction in the time required to produce a position fix, as shown in Fig. 4. To allow for a fair comparison, both methods were tested using the same hardware and software. The average time required to produce a position fix using Method II was 91% lower than in Method I. This makes Method II a more suitable option for real time MS location applications, like MS tracking.

In MS tracking applications, a moving average filter might be helpful in reducing the location error, by filtering out abrupt variations in location estimations between adjacent position fixes along a route [21]. Applying a moving average filter with length 20 - i.e., the current MS location estimate is given by the arithmetic mean of the previous 20 estimated positions - to the results obtained by Method II, the 50-th and 98-th location error percentiles become 119 and 342 meters. This precision is slightly better than the one achieved in the third route in [22] - 125 and 349 meters for the

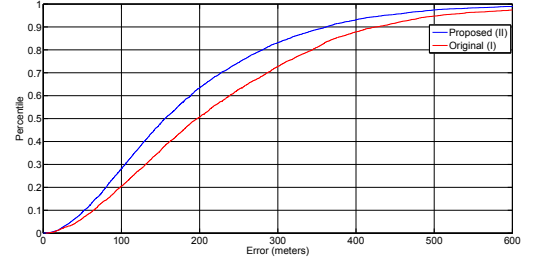


Fig. 2. CDF of MS location error in meters.

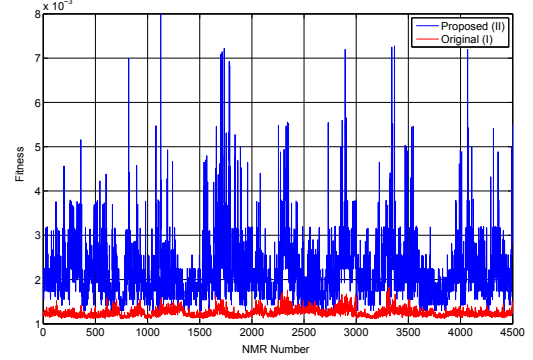


Fig. 3. Average fitness of first generation per NMR.

same percentiles - where a GA has been used for MS tracking. However, in [22] the test has been carried out in a 1800 MHz GSM network with 41 cells/km². This cell density is considerably higher than in the test area described in Tab. I. Therefore, it is expected that the DCM algorithm presented here, using GA with the proposed first generation population initialization, would achieve an even higher precision if applied to the same environment described in [22].

VI. CONCLUSION

This paper proposes an alternative for the initialization of the first generation population of a genetic algorithm, used to reduce the correlation space in a RF fingerprinting location method. The proposed alternative consists in restraining the randomly selected first population individuals to the predicted best server area of the serving sector, instead of selecting individuals throughout the whole service area. The proposed innovation produces smaller and better fitted initial populations, which results in location accuracy improvement and in significant reduction of the average time to

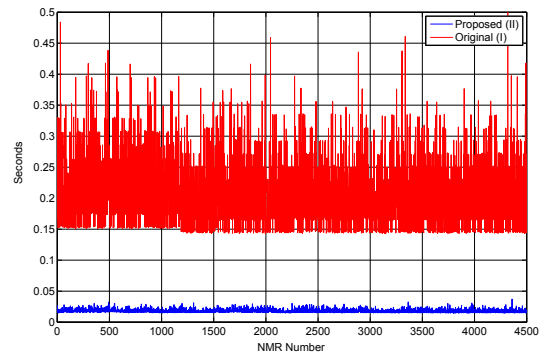


Fig. 4. Time in seconds to produce a position fix per NMR.

produce a position fix. The method has been tested in a 850 MHz GSM network, but its application is extensible to different types of wireless metropolitan area networks. The achieved precision shows that the DCM+GA proposed location method is suitable for MS positioning in urban environments.

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