OPTIMISATION OF CELLULAR BASE STATIONS PLACEMENT IN TERRITORY WITH URBAN AND ENVIRONMENTAL RESTRICTIONS BY MEANS OF GENETIC ALGORITHMS

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INTRODUCTION

The realization of new cellular networks needs the mobile phone operator to choose optimal location for Base Stations (BSs) placement to reach the wider coverage of a considered territory and the minimum cost of the net itself, that is the minimum number of BSs.

In the most situations, and in particular inside the cities, there are a lot of restrictions due to the limited number of available site for BSs placement and due to the limits about electromagnetic field emissions, that impose to reduce, as more as possible, overlapping of fields radiated from different BSs.

The solution of this optimisation problem is not so simple and immediate since it is necessary to deal with a lot of restrictions.

The purpose of this paper is to illustrate a Genetic Algorithms (GAs) based technique that allows to find an optimal resolution to the mentioned problem ensuring the desired coverage of the considered territory with the minimum number of BSs, using only the allowed locations and reducing to the minimum level the superposition of emission diagrams of the BSs.

DEFINITION OF THE PROBLEM

The use of GAs for optimal BSs placement has already been studied (Calegari *et al.*,1997;. Han *et al.*, 2001;. Laki *et al.*, 2001;. Lieska *et al.*, 1998; Park *et al.*, 2002) but in the most of cases it has been considered only the best coverage of territory, without considering the typical restrictions of limited sites available for BSs placement and the typical restrictions of avoiding overlapping of coverage diagrams of BSs that increases the level of emitted electromagnetic fields, which, on the contrary, we consider in this paper.

Further it has been considered BSs ideal circular coverage diagram instead of more real and common three lobes coverage diagram, with the results that the ideally optimized coverage of cellular service does not provide a good quality of service when it is practically realized.

In this paper we consider only the 2D problem, that is to place correctly the different BSs on the territory with the given restrictions, properly rotating the BSs so that their coverage lobes help to reach the desired goal.

The extension to the related 3D problem can be rapidly implemented considering also the height of the different zones of the territory and the tilt of the radiative diagram but this is out of the scope of this paper that is to study a fast method to have first level solutions to the BSs placement, which can be refined in a second time with more detailed optimization GAs, adding further variables to be optimised.

In the following we describe how the problem is coded and solved in term of GAs, that allows to solve rapidly the considered problem.

GENETIC ALGORITHMS

Genetic algorithms are considered wide range numerical optimisation methods, that use the natural processes of evolution and genetic recombination (Davis, 1987, 1991; Dias and de Vasconcelos, 2002; Goldberg, 1989, 1991; Holland, 1992; Winter *et al.*, 1995). Thanks to their versatility, they can be used in different fields and they also find a lot of applications in wireless network optimization problems (Calegari *et al.*,1997;. Han *et al.*, 2001;. Laki *et al.*, 2001;. Lieska *et al.*, 1998; Park *et al.*, 2002).

GAs are particularly useful when the goal is to find an approximate global minimum in a high-dimension, multi-modal function domain, in a near-optimal manner. Unlike the most optimisation methods, they can easily handle discontinuous and non-differentiable functions.

The algorithms encode each parameters of the problem to be optimised into a proper sequence (where the alphabet used is generally binary) called a gene and combine the different genes to constitute a chromosome. A proper set of chromosomes, called population, undergoes the Darwinian processes of natural selection, mating and mutation, creating new generations, until it reaches the final optimal solution under the selective pressure of the desired fitness function.

GA optimisers, therefore, operates according to the following nine points:

1) encoding the solution parameters as genes;
2) creation of chromosomes as strings of genes;
3) initialisation of a starting population;
4) evaluation and assignment of fitness values to the individuals of the population;
5) reproduction by means of fitness-weighted selection of individuals belonging to the population;
6) recombination to produce recombined members;
7) mutation on the recombined members to produce the members of the next generation;
8) evaluation and assignment of fitness values to the individuals of the next generation;
9) convergence check.

The flow chart of GAs operative process is schematised in fig.1.

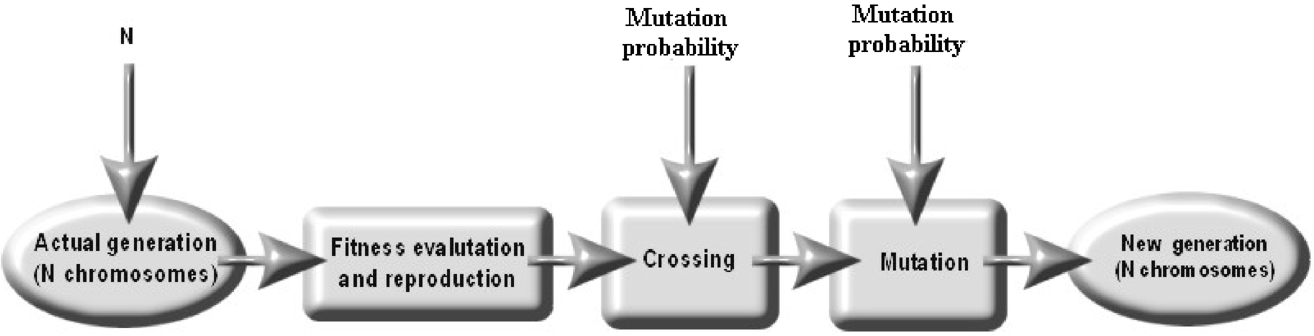


Fig. 1. Flow chart of GAs operative process

The coding is a mapping from the parameter space to the chromosome space and it transforms the set of parameters, which is generally composed by real numbers, in a string characterized by a finite length. The parameters are coded into genes of the chromosome that allows the GA to evolve independently of the parameters themselves and therefore of the solution space.

The parameters can be discrete or continuous. If they are continuous, it is generally necessary to fix some limits on them or to restrict the values that they can assume in a handful possible range. In both cases a binary representation is generally used since it can be shown (Goldberg, 1989**)** that coding has a underlying relevance in producing improved results and that it is better to use the shortest possible useful alphabet as the binary one.

If g_i is the i-th coded gene representing the i-th parameter of the N solution parameters, encoded by means of M_i bits b, its structure is:

$$g_i=[b_1\ b_2\ b_3\ \ldots\ldots b_{Mi-1}\ b_{Mi}] \quad (1)$$

and the general chromosome c shows the following structure:

$$c=[g_1\ g_2\ g_3\ \ldots\ldots g_{N-1}\ g_N]=[b_1\ b_2\ b_3\ \ldots\ldots b_{M-1}\ b_M] \quad (2)$$

being M the sum of the bits that compose each gene, that is $M=M_1 + M_2 + \cdots + M_{N-1} + M_N$.

The greater the number of bits used to represent a certain parameter and the greater is the accuracy but the slower is the convergence: the correct number of bits must therefore result as a compromise between the real precision required and the velocity of convergence.

Once created the chromosomes it is necessary the choose the number of them which composes the initial population. This number strongly influences the efficiency of the algorithm in finding the optimal solution: a high number provides a better sampling of the solution space but slows the convergence. A good compromise consists in choosing a number of chromosomes varying between 5 and 10 times the number of bits in a chromosomes, even if in the most of situations, it is sufficient to use a population of 40-100 chromosomes and that does not depend of the length of the chromosome itself. The initial population can be chosen at random or it can be properly biased according to specific features of the considered problem.

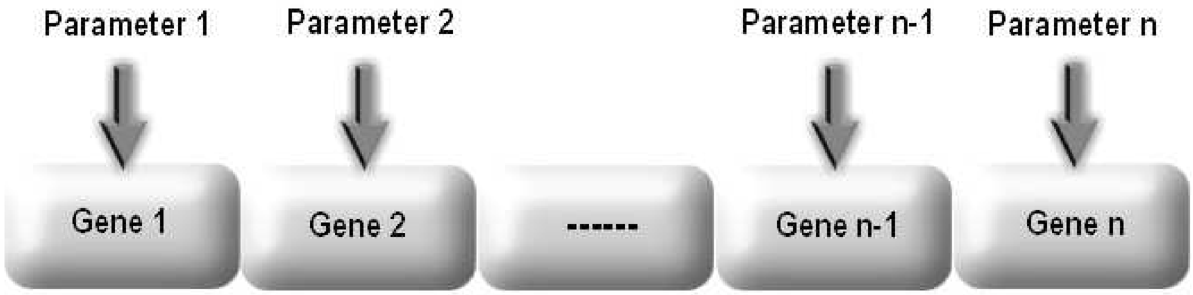


Fig. 2. Scheme of coding of problem parameters into chromosomes

Fitness function, or cost function, or object function provides a measure of the goodness of a given chromosome and therefore the goodness of an individual within a population. Since the fitness function acts on the parameters themselves, it is necessary to decode the genes composing a given chromosome to calculate the fitness function of a certain individual of the population. The fitness function is the only connection between the physical problem being optimized and the genetic algorithm. The only constraints on the form and content of the fitness function, imposed by GAs, are that the fitness value returned by the fitness function is in some manner proportional to the goodness of a given trial solution and that the fitness value is positive (even if this last constraint is not always required).

The reproduction takes place utilising a proper selection strategy which uses the fitness function to choose a certain number of good candidates. The selection process cannot be based only on choosing the best individuals, since they cannot be very close to the optimal solution: for this reason there must be some chances that some unfit individuals are preserved, to be sure that the genes carried by them are not lost prematurely from the population. A very common selection strategy is represented by the proportionate selection, where individuals compete on the basis of their fitness. The individuals are assigned a space of a roulette wheel that is proportional to they fitness: the higher the fitness, the larger is the space assigned on the wheel and the higher is the probability to be selected at every wheel tournament. The tournament process is repeated until a reproduced population of N individuals is formed.

The recombination process selects at random two individuals of the reproduced population, called parents, crossing them to generate two new individuals called children. The simplest technique is represented by the single-point crossover, where, if the crossover probability overcome a fixed threshold, a random location in the parent's chromosome is selected and the portion of the chromosome preceding the selected point is copied from parent A to child A, and from parent B to child B, while the portion of chromosome of parent A following the random selected point is placed in the corresponding positions in child B, and vice versa for the remaining portion of parent B chromosome. If we point out with c_p^A and c_p^B the chromosomes of parents A and B respectively, and if R is the random location:

$$c_p^A = [b_1^A\ b_2^A\ b_3^A \dots b_{R-1}^A \mid b_R^A \dots . b_{M-1}^A\ b_M^A] \tag{3a}$$

$$c_p^B = [b_1^B\ b_2^B\ b_3^B \dots b_{R-1}^B \mid b_R^B \dots . b_{M-1}^B\ b_M^B] \tag{3a}$$

their children c_c^A and c_c^B , generated by the crossover, are:

$$c_c^A = [b_1^A\ b_2^A\ b_3^A \dots b_{R-1}^A \mid b_R^B \dots . b_{M-1}^B\ b_M^B] \tag{4a}$$

$$c_c^B = [b_1^B\ b_2^B\ b_3^B \dots b_{R-1}^B \mid b_R^A \dots . b_{M-1}^A\ b_M^A] \tag{4a}$$

If the crossover probability is below a fixed threshold, the whole chromosome of parent A is copied into child A, and the same happens for parent B and child B. The crossover is useful to rearrange genes to produce better combinations of them and therefore more fit individuals. The recombination process has shown to be very important **(**Goldberg, 1989**)** and it has been found that it should be applied with a probability varying between 0.6 and 0.8 to obtain the best results.

The mutation is used to survey parts of the solution space that are not represented by the current population. If the mutation probability overcomes a fixed threshold, an element in the string composing the chromosome is chosen at random and it is changed from 1 to 0 or vice versa, depending of its initial value. To obtain good results, it has been shown **(**Goldberg, 1989 that mutations must occur with a low probability varying between 0.01 and 0.1.

The converge check can use different criteria such as the absence of further improvements, the reaching of the desired goal or the reaching of a fixed maximum number of generations.

IMPLEMENTATION OF THE PROBLEM

Once given a certain territory to be covered (with a desired percentage p_T), whose area is A_T, and once given the coverage diagram of a BS (which is the diagram that indicates where the emitted signal is above a minimum receivable threshold and that is obviously related to the irradiation diagram and the emitted power), whose area is A_{BS}, the minimum number N^{BS}_{min} of base stations is equal to:

$$N^{BS}_{min} = \text{round}\ (p_T\ A_T / A_{BS}), \tag{5}$$

where the rounding operation is made towards the nearest integer equal or greater than the argument of the operation.

The number obtained from eq.(5) is obviously ideal since it can be really reached if all the territory is available for base stations placement and if the coverage diagram is characterized by a regular shape (i.e. triangular, etc.) that allows to ensure a not-superposed coverage. It is evident that in real conditions, the minimum number of base stations necessary to ensure the desired coverage percentage of the considered territory is obviously greater than the value calculated by means of eq.(5), due to the not perfect matching of coverage diagrams of near BSs and due to the limitation of territory for placing BSs.

For this reason, given a certain territory, it is considered an initial number $n*N^{BS}_{min}$, of BSs (where n is a parameter, greater than 1, to be chosen at will) greater than the minimum number N^{BS}_{min}, leaving to the GA the duty of optimising and reducing their number, according to the availability of installation places, up to reaching theoretically the value of N^{BS}_{min} in ideal conditions.

Depending of the desired goal, it is also possible to choose an initial number of BSs lesser than N^{BS}_{min}, knowing that this doesn't allow the desired coverage of the considered territory.

Once defined the initial number $n*N^{BS}_{min}$ of BSs, it is necessary to define the parameter to be optimised for each BS, represented by its coordinates. To increase the optimization capability of used GA, it is also considered the rotation of each BS, so that the GA is capable of realizing a fine matching of coverage diagram of near BSs.

Since not all the initial BSs are used to perfectly cover the considered territory, it is necessary to add, for each BS, an information that indicates if the BS is active of not.

These considerations lead to four solution parameters, for each BS, that are:

1) x coordinate;
2) y coordinate;
3) rotation of the coverage diagram;
4) activity of the BS.

Let's discuss now the variability range of the parameters indicated above and the relative accuracy necessary to represent them in term of binary strings.

Concerning the x and y coordinates, if we choose a 1 meter resolution and we consider ordinary territory extension (≈ 50-100 km), 17 bits are enough to represent a distance between 1 and 131.072 meters (i.e. ≈ 130 km). If it is necessary to consider a wider territory, it is sufficient to add further bits, considering that each bit allows to double the considered distance.

The rotation angle of the coverage diagram can vary between 0 and 360°: we choose to use 9 bits that allow to represent 512 numbers. Since the necessary numbers to codify the phase with a resolution equal to 1° are only 360, the remaining 152 values are used to represent the corresponding phase values between 0° and 152°, maintaining them active in the evolution process. A 8 bit encoding is not possible since it allows to represent only 256° with a resolution of 1° that is not enough for our purposes. Since in the most of real cases the coverage diagram of BS is symmetric (i.e. composed by three equal spaced lobes), it could be enough lo limit the rotation to 120° only: we choose to consider total rotation of 360° to consider even not symmetric coverage diagram.

The activity of each BS is coded using a single bit, where a 1 indicates that the BS is active while a 0 indicates that the BS is not active, even if it is located in a given (x,y) position.

4 genes are therefore used to encode the parameters of each BS whose total length is equal to 44 bits. The genes features are summarized in Table 1.

TABLE 1. Features of the 4 genes used to identify a BS

Base Station parameters			
Gene	**Feature**	**Number of bits**	**Range**
1	x coordinate	17	0 ÷ 131.071 meters
2	y coordinate	17	0 ÷ 131.071 meters
3	Rotation of coverage diagram	9	0 ÷ 360°
4	Activity of BS	1	0 ÷ 1

Each chromosome, or individual, representing a solution of the problem, is composed by a string representing all the $n*N^{BS}_{min}$ BSs and the related 4 parameters (whose total length is equal to 44 bits). The total length of each chromosome is therefore equal to $44*\ n*N^{BS}_{min}$ bits.

It is now necessary to define the fitness function f. This function must consider all the desired optimization goals that are:

1) coverage of the desired percentage of considered territory with the minimum number of BSs;
2) absence or minimum value of overlapping of coverage diagram, to reduce as more as possible the value of electromagnetic field;
3) placement of BSs only in the allowed zones.

Points one and two are synthesized with a proper function while point three is considered using a proper territorial array.

The considered fitness function of the generic individual I, can be expressed as:

$$f(I)=\alpha\frac{\text{coverage area}(I)}{\text{desired coverage area}}-\beta\frac{\text{overlapping area}(I)}{\text{desired coverage area}}-\chi\frac{N^{BS}(I)-nN^{BS}_{min}}{nN^{BS}_{min}} \quad (6)$$

where “coverage area (I)” is the area covered by the BSs distribution related to the chromosome I, or individual I, $N^{BS}(I)$ is the number of active BSs related to the individual I and “overlapping area (I)” is the total area of overlapping of the different coverage diagrams of BSs.

The mentioned function keep into consideration the performances of the individual I (BSs distribution) in term of coverage area (first term), in term of reduced number of BSs (second term), and in term of reduced value of overlapping (third term), with a variable weight selectable at will by means of coefficient α, β, γ respetively, variable between 0 and 1.

The information relative to the not allowed zones for BSs placement is stored in a proper binary array, characterized by the same dimensions and resolution of (x,y) coordinates of BSs (i.e. 2^{17}x2^{17} metres). Each element of the array (representing a cell of the territory whose dimensions are 1 m x 1 m) that can be used for BSs placement is marked with a binary 0 while if it cannot be used for BSs placement, it is marked with a binary 1. Since in the most of real situation, the considered territories have not a regular profile (square, circular, etc.) using this representation it is also possible to design correctly the border of the considered territory, out of which the BSs placement is not allowed. In this way it is also possible to consider territories whose extension is reduced with respect to the maximum extension considered in this paper, that is a square territory of about 131 x 131 kms.

The control about the BSs placement in not allowed zones is made at any genetic operation (reproduction, crossing, mutation), checking in the proper array if the coordinates of the BSs of the actual chromosome, or individual, are marked with a binary 1: if this happens, the related chromosome is deleted.

Once generated the initial population at random, the individuals characterized by BSs not allowed placement are eliminated, and the selection is operated only on the remaining individuals, until attaining a reproduced population characterized by the same number of individuals of the initial population.

Since the initial population is generated at random, there is generally a portion of it that is eliminated at the begin, but after the first iterations more fitting individuals are generated and it is not necessary to eliminate any of them.

Once recombined and mutated the population, the fitness function of the population is again calculated with the same criteria illustrated above, considering only fitting individuals. The converge test is made controlling if the difference between the mean value of fitness functions of the valid individuals belonging to the actual generation and the mean values of the last N_G generations is lesser than a certain percentage value p_{stop}.

Good results and rapid converge are obtained with population composed by 40-50 individuals, with converge test parameters N_G and p_{stop} equal to 20 and 0.1 respectively.

The use of the mentioned array allows to realize more refined methods that can consider also undesired coverage zones inside the territory. This situation takes place when a partial BSs placement has already been realized and it is necessary to add further BSs to reach a complete coverage of the territory: in this situation the new BSs must cover only the zones that are not covered by the already installed BSs. To consider this situation the zones already covered by already installed BSs are marked, for example, with the number two: during the mentioned GA optimization process if a BS emission diagram covers one the these marked zones it is immediately deleted, ensuring only the survival, in the next generation, of BSs that respect this restriction.

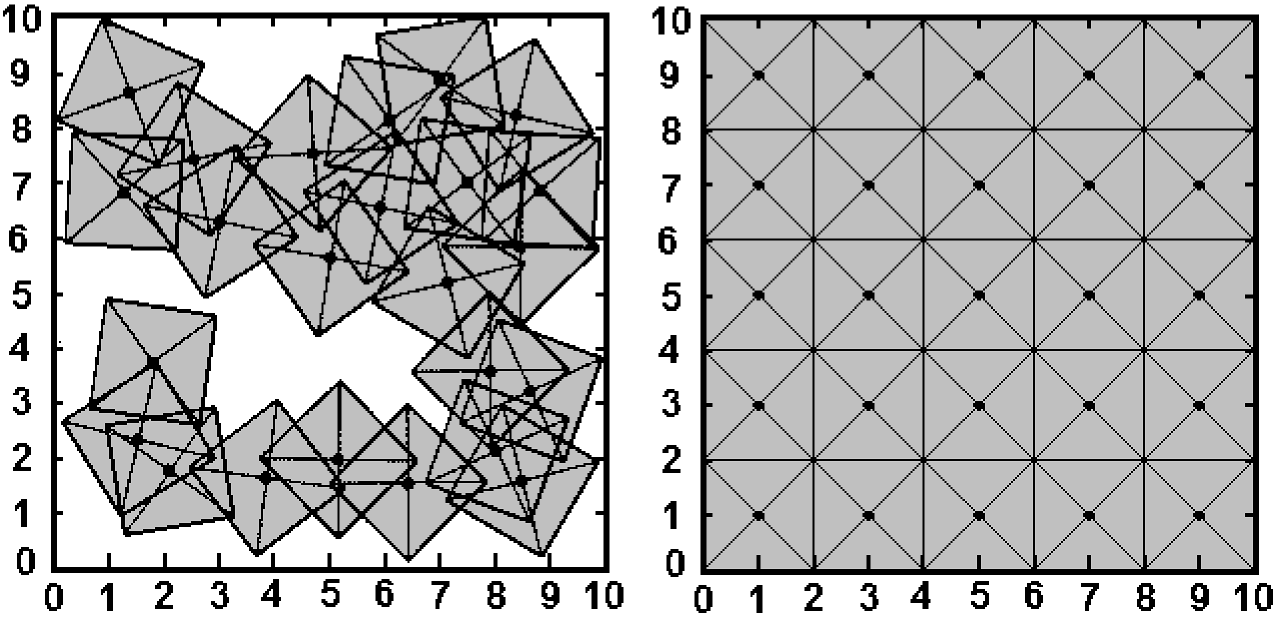
RESULTS

The proposed GA has demonstrated to be extremely versatile in BSs optimal placement in territory with urban and environmental restrictions.

The optimal solutions are generally obtained after a limited number of generations that rarely overcomes 100 generations. The computation time strictly depends of the number of BSs considered since each of them adds 44 bits to each chromosome and therefore 44 bits of information to be handled by the GA. The number of BSs grows not only with the extension of the considered territory but also with the reduction of coverage area: the wider this area and the lesser the number of BSs (and therefore the time necessary to reach the final optimal solution).

As a simple test it has been considered a 10 km x 10 km square territory and BSs characterized by 4 triangular radiation lobes, as the ones showed in figures 3.

Due to the regularity of territory, to the regularity of coverage diagrams of BSs and to the absence of forbidden installation zones the GA is capable of finding an optimal placement of BSs on the territory, reaching a 100% coverage with the minimum number of BSs and without overlapping of coverage areas, as shown in figures 3.



(a) (b)

Figs.3. Example of optimal placement (dimensions are expressed in kilometres). 4 triangular radiation lobes BSs have been considered. (a) one initial random distribution before the optimization, where generally about 50% of territory is covered. (b) optimal placement after GA operations where always 100% of territory is covered (this solution is obtained in no more than 30-40 generations starting from any initial random distributions).

In real situations, where the territories are not regular and the BSs can be installed only in some limited zones, the proposed algorithm is always capable of ensuring optimal results.

As an example it is considered a certain portion of territory, characterized by a connected and not regular contour and an initial number of 8 BSs, characterized by the typical three lobes diagram. In the initial situation, since the BSs position is selected randomly, the most of BSs is located out of the considered zone or overlapped each other, as it si shown in fig.4.

After the optimization process, generally obtained for this configuration after 40-55 generations, the BSs are positioned on the territory to reach a coverage of more than 85%.

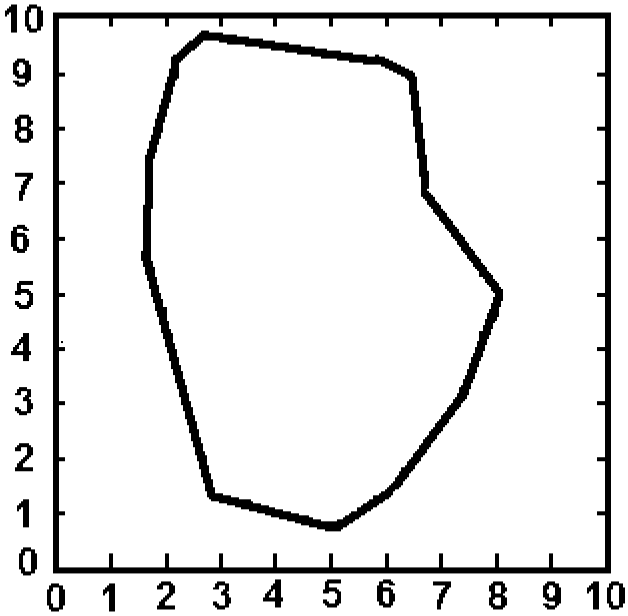


Fig.4(a)

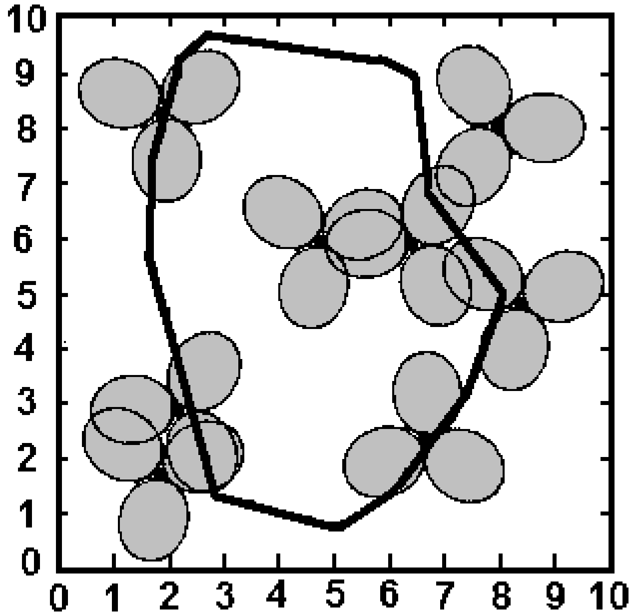


Fig.4(b)

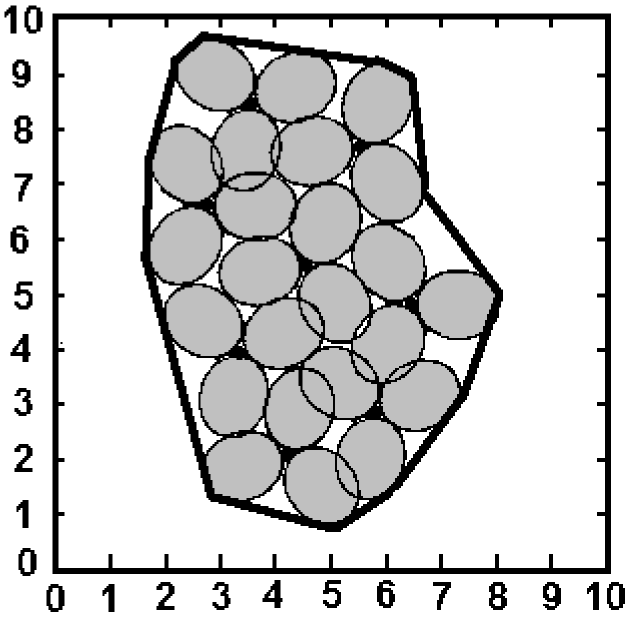


Fig.4(c)

Figs.4. Example of optimal placement (dimensions are expressed in kilometres). 3 real radiation lobes BSs have been considered. (a) a considered initial territory (inside the contour). (b) one initial random distribution of 8 BSs before the optimization. (c) optimal placement after GA operations. More than 85% coverage of territory is always covered (this solution is obtained in no more than 40-55 generations starting from any initial random distributions).

CONCLUSIONS

A new technique for BSs placement in territory with urban and environmental restrictions using Genetic Algorithms optimisation has been presented. It is capable of operating on any kind of real situations, reaching optimal results.

It can be used in the initial planning phase of cellular networks, adding in a second time further restriction that has been identified, to refine the found solutions in an optimal way.

Further improvement can be added considering 3D situations but this is out of the scope of the paper that is to study a fast method to have first solutions to the BSs placement, which can be refined in a second time with more detailed GAs optimization, adding further variables to be optimised such as the height of the different zones of considered territory and the tilt of the coverage diagram of BSs.

The use of GA techniques on this kind of problem ensures to find, always and efficiently, quasi-optimal solutions, that would otherwise be impossible to be located due to the considerable numbers of parameters involved in the optimisation problem.

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