

# WIRELESS LAN OPTIMAL DESIGN IN THE UNDERGROUND GRAN SASSO MOUNTAIN NATIONAL LABORATORIES OF ITALIAN INSTITUTE OF NUCLEAR PHYSICS

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## INTRODUCTION

Wireless LANs, thank to their capability of reaching data transmission velocities comparable with cable LANs, without the restrictions imposed by the cable itself, are actually having a considerable development which tends to be more rapid with time. The technologies that use wireless LAN are also named Wi-Fi, an acronym that stands for Wireless Fidelity.

Due to the possibilities of transmitting data with a high velocity between mobile or fixed devices without using cables, this technology allows of realizing extremely advanced services and functionalities.

Wireless LANs use electromagnetic waves at the microwave frequencies (2.5 GHz or 5 GHz). To allow point to point connections or multipoints connections. In both cases one of the device can be represented by an access point (AP) that allows the wireless devices to connect to the fixed LAN where the AP is connected.

The extremely low emitted powers (of the order of milliWatts) are considerably lesser than the power emitted by a cellular phone, which can reach peaks above 1 watt. These low emitted powers surely respect any international safety standard for exposition of people to electromagnetic fields but do not allow of reaching distances above 100 meters.

The most common technology used worldwide is based on IEEE 802.11X protocol, developed by International Institute of Electrical and Electronical Engineers. The final X is used to point out the different versions (a, b, g, etc.) that were realised, characterized by growing communications velocities (variable from 11 Mbit/s up to 54 Mbit/s, reaching 108 Mbit/s in fast modality, which is the same velocity of wire LAN) and growing security levels (cryptographic protocols).

The transmission velocity decreases both with distance and with background electromagnetic noise level in the used frequency band, passing from 11 Mbit/s at 35 meters of distance (for a medium performances 802.11b AP) until reaching 1 Mbit/s at a distance of 100 meters

The 802.11g protocol allows of reaching 54 Mbit/s in standard mode and 108 Mbit/s in fast mode.

It is evident that the design and the realization of a wireless LAN that must guarantee an optimal working from the velocity and the benefits/costs ratio point of view (avoiding of installing an excessive number of APs that would increase the costs and decrease the reliability of the LAN due to excessive number of installed devices) needs a preliminary analysis from the service and the electromagnetic environmental point of view. In fact this last term can represent a potential source of electromagnetic noise and it can provoke a decrease of the performance of the LAN.

This activity must be executed with an extreme care when we deal with environments which impose severe restrictions, such the considered one.

The purpose of this paper is to illustrate the optimal design procedure that has been used in the considered underground Gran Sasso mountain national laboratories using advanced techniques such as Genetic Algorithms (GAs).

## THE UNDERGROUND GRAN SASSO MOUNTAIN NATIONAL LABORATORIES OF ITALIAN INSTITUTE OF NUCLEAR PHYSICS

The underground Gran Sasso mountain National Laboratories (GSNL) of Italian Institute of Nuclear Physics (INFN) are located in Assergi, in the L'Aquila city province and about 120 km est of Rome (Italy). The underground laboratories are located inside the Gran Sasso Mountain (about 3000 meter above the sea level), 1400 meters under the central rocky mass, named Eagle Mountain.

The offices and the directional centre are located 1 km away from the Assergi highway exit and they extend on a 12.000 square meters surface.

Under the Gran Sasso mountain there is a separate double highway tunnel (one tunnel for traffic in the L'Aquila – Teramo direction and one tunnel in the Teramo – L'Aquila direction).

The entrance of GSNL is located in the Teramo – L’Aquila direction tunnel using a passage reserved to the laboratory traffic and created by means of a narrowing of about 1 km of the tunnel road in the correspondence of underground laboratories.

The GSNL are the biggest and most important underground laboratories of the world characterized by a unique environment for the kind of research that is made inside them. Further, they have been realized on purpose and not recovering or adapting already existing structures, such as active or closed mine (KAMIOKANDE in Japan and SNO in Canada).

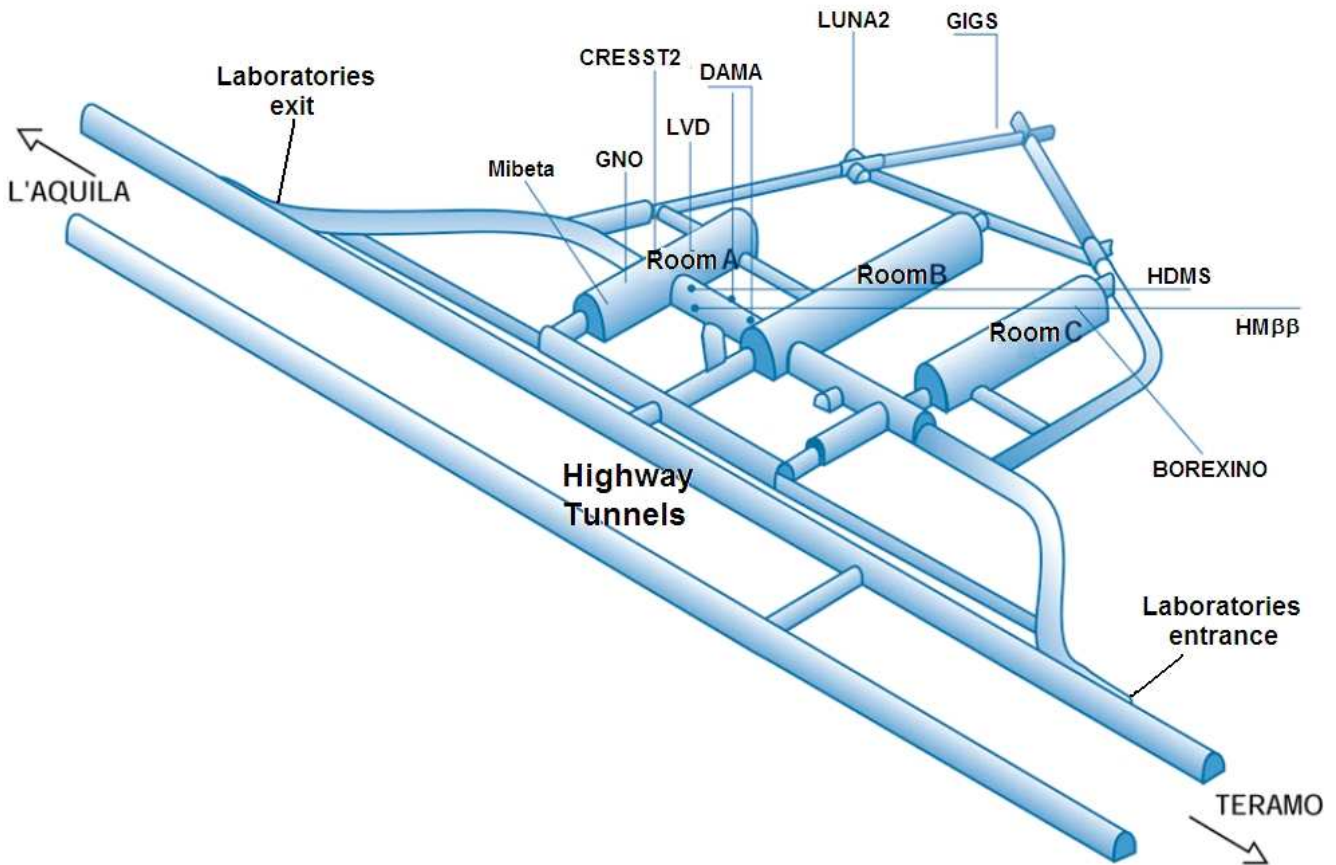


Fig.1 3D view of the laboratories with the existing experiments.

The design, the approval and the public financing have been possible thanks to the simultaneous drilling and construction, in '70-'80 years, of the highway tunnels in the same zone. The GSNL realization started in 1982 and the construction of the first experimental apparatus started only 4 years later, in 1986, when the first tunnel was opened to the public traffic. The underground laboratories are mainly constituted by 3 experimental rooms, whose dimensions are about 100 x 20 x 20 meters, and by a series of connection tunnels that are used for the installations necessary for the correct functioning of the laboratories and for hosting secondary and reduced dimension experimental devices. The total internal volume is about 180.000 m<sup>3</sup>.

Actually there are about 15 experiments currently working in the 3 experimental rooms and in some connection tunnels.

TABLE 1. Main experiments that are actually running inside the laboratory

BOREXINO experiment <i>Room C</i>	Aimed at revealing sub-nuclear particles (neutrins).
LVD experiment <i>Room A</i>	Aimed at working such as an advanced neutrino telescope, capable of observing star collapse in our galaxy.
GNO experiment <i>Room A</i>	Aimed at providing a more accurate observation and measure of the intensity of solar electronic neutrins. This experiment have terminated its vital cycle and it is actually in a dismantlement phase.
Moon 1 and Moon 2 experiments <i>Connection galleries</i>	Aimed at studying the thermo-nuclear processes of the sun by means of a 400 kV accelerator.
LENS experiment <i>Connection galleries</i>	Aimed at making a research and develop program, not yet started, with Pseudocumene cells, properly confined and

	whose volume is relatively reduced.
$\beta\beta$ Milan experiment <i>Rooms A and C</i> Haidelberg-Moscow experiment <i>Connection galleries</i> Cresst experiment <i>Room A</i>	They constitute a family of experiments aimed at observing the interaction of rare particles with lattice such as tellurium oxide, germanium, sapphire at extremely low temperature (close to the absolute zero).
Dama experiment <i>Connection galleries</i>	Aimed at researching particle candidate to be obscure matter of the universe.
Opera experiment <i>Room C</i>	Aimed at researching $\tau$ neutrins with photographic emulsions.

In the Gran Sasso mountain are present other subjects that makes specific activities (highway, aqueduct, etc.) and for this reason the GSNL represented only one important component of a wider and complex system where each component interacts, unavoidably, with the other components. In fact, for example, the highway represents the only entrance to the laboratories, where not only people but also all the installations (such as electrical, fanning, cooling, telecommunications, etc.) that guarantee the correct functioning and the safety of laboratories must pass through it. This implies that a possible accident inside the highway tunnels can compromise not only the stability and reliability of the installations of laboratories but also the capability for fire brigades, highway tunnel personnel and emergency teams of reaching the laboratories. The same happens if an accident takes place inside the laboratories. For this reason the emergency plans related to one of the subjects which operates inside the Gran Sasso mountain must consider also the other subjects present.

This characteristic gives to GSNL an extreme iniquity at the international level.

Due to the multitude of systems, devices and installations that must be controlled, it is evident that the laboratories, to be managed securely in the best way, need to use intensively advanced technologies finalized to obtain a high and efficient quality of services.

For this reason it is planned the realization of a wireless LAN, to be installed inside GSNL, that could ensure the communication between any devices, fixed or mobile, without using cables that would unavoidably increase the complexity of the system and reduce the reliability of it.

The wireless LAN will allow, in future, the realization of new and efficient functionalities, mainly in terms of safety and security of people and surrounding environment.

## DEFINITION OF THE PROBLEM

The use of genetic algorithms for optimal APs placement has already been studied (Maksuriwong *et al.*, 2003, Nagy and Farkas, 2000, Rong-Hou *et al.*, 2001, Shih-An *et al.*, 1999) but in the most of cases it has been considered only the best coverage of a given area, considering eventually the attenuation of walls and other obstacles (keeping into account also their composing materials) that are present inside the considered area.

In our problem we deal with peculiar restrictions such as the possibility of installing the APs only on the lateral sides of the galleries of GSNL and not in a any position, and the unavailability of some installation zones due to the presence of other devices or installations. This implies that the coverage diagram of AP restricts from circular shape to half circular shape.

Further we need a full redundancy of the whole coverage area, that is each point of the laboratory must be covered by almost two APs. Since the wireless LAN must be characterized by a high reliability, each zone of the laboratory have two LANs located on opposite sides and the APs are alternatively connected to them, so that a malfunctioning of one LAN, and of the related wireless APs, is immediately recovered by the other LAN and the related wireless APs connected to it.

Further it is necessary to consider the background noise that could be present inside the laboratories and that could reduce the coverage area of each AP and the related transmission velocity.

In the following we describe how this peculiar problem is coded and solved in term of GAs, that allow to solve it rapidly and in an efficient way.

## 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 (Maksuriwong *et al.*, 2003, Nagy and Farkas, 2000, Rong-Hou *et al.*, 2001, Shih-An *et al.*, 1999).

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.2.

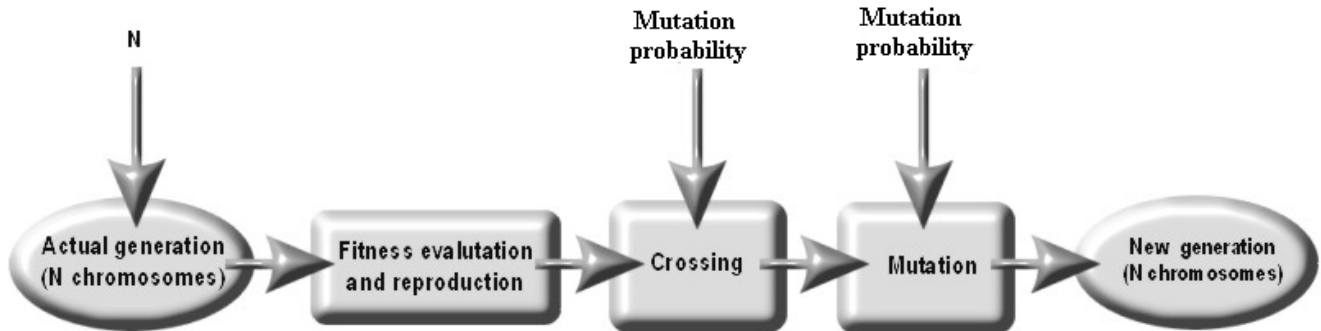


Fig. 2. Flow chart of GAs operative process

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:

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

and the general chromosome  $c$  shows the following structure:

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

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

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.



Fig. 3 Scheme of coding of problem parameters into chromosomes.

Once created the chromosomes it is necessary to 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 chromosome, 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.

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 their 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 overcomes 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:

$$c_p^A = [b_1^A \ b_2^A \ b_3^A \ \dots \ b_{R-1}^A \ | \ b_R^A \ \dots \ b_{M-1}^A \ b_M^A] \quad (3a)$$

$$c_p^B = [b_1^B \ b_2^B \ b_3^B \ \dots \ b_{R-1}^B \ | \ b_R^B \ \dots \ b_{M-1}^B \ b_M^B] \quad (3a)$$

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

$$c_c^A = [b_1^A \ b_2^A \ b_3^A \ \dots \ b_{R-1}^A \ | \ b_R^B \ \dots \ b_{M-1}^B \ b_M^B] \quad (4a)$$

$$c_c^B = [b_1^B \ b_2^B \ b_3^B \ \dots \ b_{R-1}^B \ | \ b_R^A \ \dots \ b_{M-1}^A \ b_M^A] \quad (4a)$$

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

The 2D map of GSNL is shown in figure 4. In the same map the zones where are present some obstacles that do not allow the installation of APs are also shown.

The analysis and measurement of background noise that could be present inside the laboratories and that could reduce the coverage area of each AP and the related transmission velocity was made (Garzia *et al.*, 2004) and it did not reveal particular critical points to be considered inside the design procedure.

Once calculated the area to be covered, whose value is  $A_T$ , and once given the maximum coverage distance  $R_{AP}$  of an AP (which is the circular 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  $A_{AP} = \pi R_{AP}^2$ , the minimum number  $N_{min}^{AP}$  of access points is equal to:

$$N_{min}^{AP} = 2 \cdot \text{round} \left( \frac{A_{GSNL}}{\pi R_{AP}^2} \right) \quad (5)$$

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

The number two is present due to the installation of AP on the side of the laboratories that reduces the coverage area since only half circle of the coverage diagram is used inside the laboratories and the other half is lost inside the rocks, due to the absence of nearby rooms.

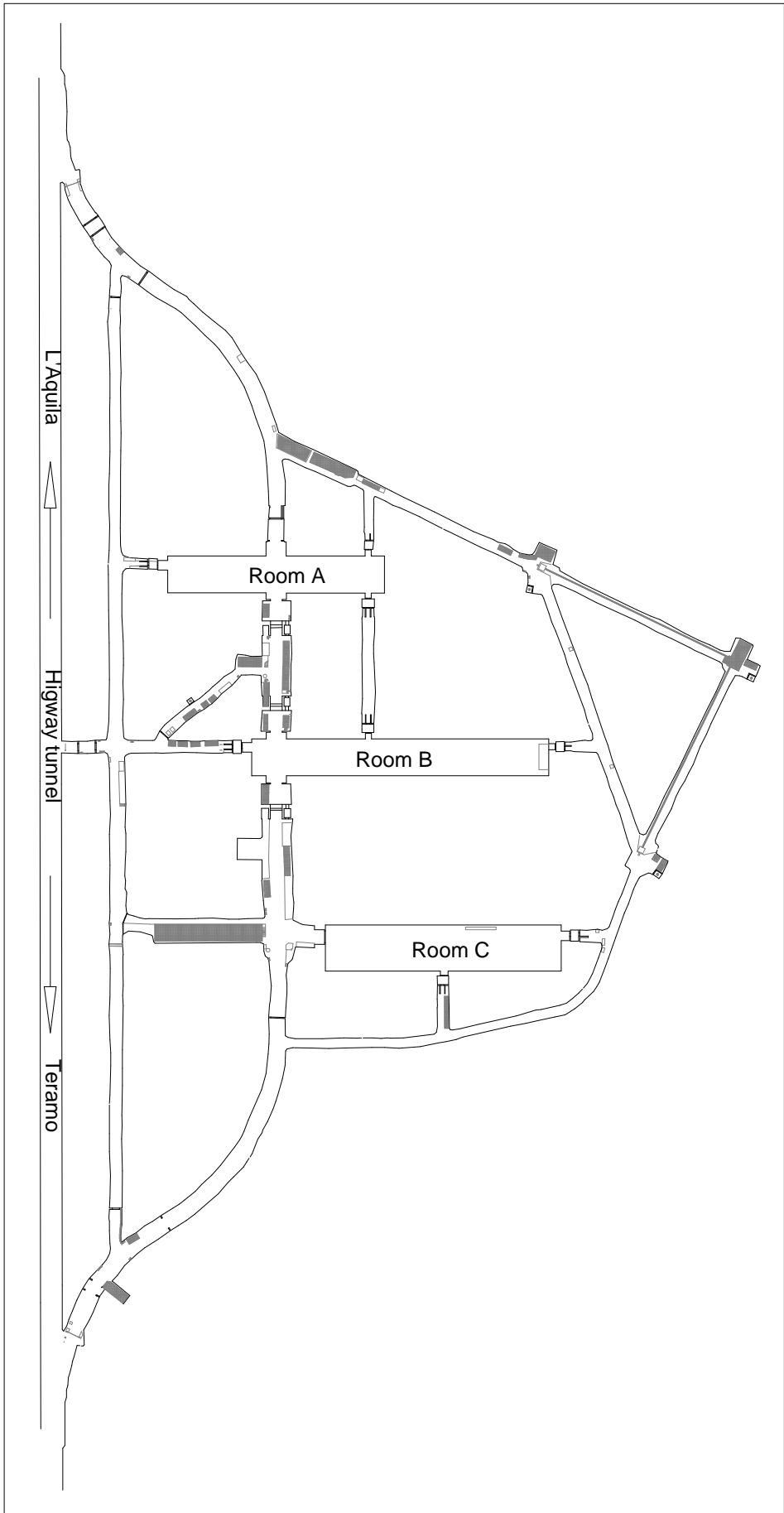


Fig.4 2D map of Gran Sasso mountain National Laboratories.

The number obtained from eq.(5) is obviously ideal since it can be really reached if all the internal area is available for APs placement and if the coverage diagram is characterized by a regular shape (i.e. square, etc.) that allows to ensure a perfect matching between the coverage of nearby APs. It is evident that in real conditions, the minimum number of APs necessary to ensure the complete coverage of the GSNL with the desired redundancy is obviously greater than the value calculated by means of eq.(5), due to the not perfect matching of coverage diagram of near APs and due to the limitation of places for APs installation.

For this reason, given the internal area, it is considered an initial number  $n \cdot N_{min}^{AP}$ , of APs (where  $n$  is a parameter, greater than 1, to choose at will) greater than the minimum number  $N_{min}^{AP}$ , leaving to the GA the duty of optimising and reducing their number, according to the availability of installation places, reaching eventually the value of  $N_{min}^{AP}$  in ideal conditions.

Once defined the initial number  $n \cdot N_{min}^{AP}$  of APs, it is necessary to define the parameter to be optimised for each AP, represented by its coordinates. To increase the optimization capability of used GA, it is also considered the trimmer of emitted power of each APs that allows to reduce linearly the maximum radius of coverage radius  $R_{AP}$  up to zero, so that the GA is capable of a fine matching of coverage diagram of near APs.

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

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

- 1) x coordinate;
- 2) y coordinate;
- 3) activity of the AP;
- 4) reduction of maximum coverage distance  $R_{AP}$ .

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 the maximum extension of laboratories ( $\approx 1$  km), 9 bits are enough to represent distance between 1 and 1.023 meters (i.e.  $\approx 1$  km).

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

The reduction of maximum coverage distance can vary between 0 and 100%: we choose to use 7 bits that allow to represent 127 numbers. Since the necessary numbers to codify the percentage with a resolution equal to 1% are only 100, the remaining 27 values are used to represent the corresponding percentage values between 0% and 27%, maintaining them active in the evolution process. A 6 bits encoding is not possible since it allows to represent only 64 numbers with a resolution of 1 that is not enough for our purposes.

4 genes are therefore used to encode the parameters of each AP whose total length is equal to 26 bits. The genes features are summarized in Table 2.

TABLE 2. Features of the 4 genes used to identify an AP

<b>Base Station parameters</b>			
<b>Gene</b>	<b>Feature</b>	<b>Number of bits</b>	<b>Range</b>
1	x coordinate	9	0 ÷ 1.023 meters
2	y coordinate	9	0 ÷ 1.023 meters
3	Activity of AP	1	0 ÷ 1
4	Reduction of maximum coverage distance $R_{AP}$ of AP	7	0 ÷ 100 %

Each chromosome, or individual, representing a solution of the problem, is composed by a string representing all the  $n \cdot N_{min}^{AP}$  APs and the related 4 parameters (whose total length is equal to 26 bits). The total length of each chromosome is therefore equal to  $26 \cdot n \cdot N_{min}^{AP}$  bits.

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

- 1) integral coverage of laboratories with the minimum number of APs;
- 2) overlapping of coverage diagram by means of almost 2 APs belonging to different fixed LANs, to increase as more as possible the reliability of the wireless LAN;
- 3) placement of APs 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 chromosome  $C$  can be expressed as:

$$f(C) = \frac{\frac{\text{coverage area}(C)}{\text{total coverage area}} \cdot \frac{\text{redundant overlapped area}(C)}{\text{total coverage area}}}{\frac{N^{AP}(I) - N_{\min}^{AP}}{N_{\min}^{AP}} + 1} \quad (6)$$

where “coverage area (C)” is the area covered by the APs distribution related to the chromosome C, or individual I,  $N^{AP}(C)$  is the number of active APs related to the chromosome C and “redundant overlapped area (C)” is the total area of redundant overlapping of the different coverage diagrams of APs to increase the reliability of the wireless LAN.

The mentioned function keep into consideration the performances of the chromosome C (APs distribution) in term of coverage area (first term of numerator), in term of respecting of redundant overlapping (second term of numerator) and in term of reduced number of APs (denominator). The number 1 that has been added as second term of denominator is necessary to avoid divergence towards infinity when the fitness function is used to evaluate a chromosome C that uses a minimum number  $N_{\min}^{AP}$ , of APs.

The information relative to the allowed zones for APs placement is stored in a proper binary array, characterized by the same dimensions and resolution of (x,y) coordinates of APs (i.e.  $2^9 \times 2^9$  meters). Each element of the array (representing a cell of the laboratory whose dimensions are 1 m x 1 m) that can be used for APs placement is marked with a binary 0 while if it cannot be used for APs placement, it is marked with a binary 1. Practically inside the mentioned array the internal profile of the laboratories is stored, with the exception of the zones occupied by devices that do not allow the installation of APs.

The control about the APs placement in not allowed zones is made at any genetic operation (reproduction, crossing, mutation), checking in the proper array if the coordinate of the APs of the actual chromosome C, or individual I, 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 APs 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 initialised 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  $p_{\text{stop}}$ .

Good results and rapid converge are obtained with population composed by 50-60 individuals, with converge test parameters  $N_G$  and  $p_{\text{stop}}$  equal to 25 and 0.08 respectively.

## RESULTS

The proposed GA has demonstrated to be extremely versatile in APs optimal placement in areas, such as the one of GSNL, where a plenty of restrictions are present. The optimal solutions are generally obtained after a limited number of generations that rarely overcomes 150 iterations.

The computation time strictly depends of the number of APs considered since each of them adds 26 bits to each chromosome and therefore 26 bits of information to be handled by the GA. The number of APs grows with the reduction of maximum coverage  $R_{AP}$  of APs: the longer this distance and the lesser the number of APs and therefore the time necessary to reach the final optimal solution.

Since the proposed design technique must be independent from any particular commercial devices, different optimizations were made considering variable values of maximum reachable distance  $R_{AP}$  of APs to know for which values the maximum reduction of initial number of APs is obtained. The n value to be multiplied for  $N_{\min}^{AP}$  was chosen to be equal to 2. The results are shown in figure 5.

It is possible to see that the maximum reduction of number of APs is obtained if are used devices that ensure a maximum coverage distance greater than 60 meters. This can explained with the geometry of laboratories. In fact, due to the absence of wide spaces (with the exception of the main rooms) and to the presence of numerous long galleries and reduced spaces, a short-medium range coverage of APs is preferable with respect of a long coverage, thanks to the possibility of GA of optimising, in the better way, their position to respect the restrictive design condition imposed. Even if long range APs are used, since the GA can control also the coverage range, the APs are always placed in the same position, reducing properly their coverage distance. This also implies that it is not necessary to choose more expensive long range APs, since a coverage of only 60 meters ensures optimal results in term of reduction of number of APs and therefore in term of increasing of reliability of the wireless LAN.

It is obvious that different design solutions were obtained, each of them characterized by a different placement of APs inside the laboratories and all respecting the design conditions. Their are not shown for brevity.



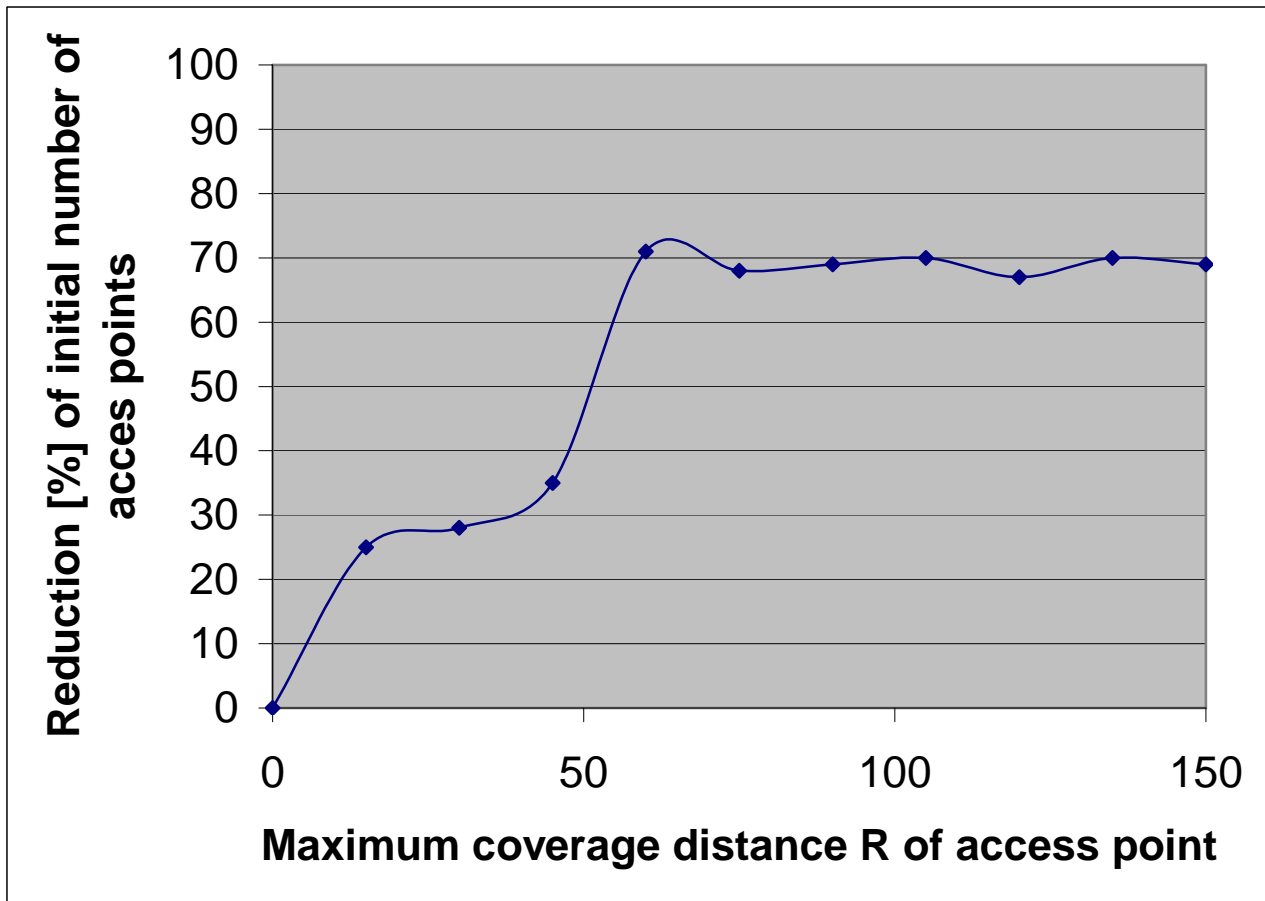


Fig.5 Reduction [%] of the initial number of access points as a function of the maximum coverage distance  $R_{AP}$  of access point to be installed.

## CONCLUSIONS

An efficient technique that uses Genetic Algorithms for APs placement in areas with different kind of restrictions, such as Gran Sasso underground National Laboratory of Italian Institute of Nuclear Physics, has been presented. It is capable of operating on any kind of real situation, reaching optimal results.

It can be used in the initial planning of wireless LAN, adding later further restrictions, which has been identified, to improve the found solutions.

It gives not only different optimal solutions for access points placement inside the laboratories but also the maximum coverage requested to the APs to reach the minimum cost of installation.

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 and due to the numerous vinculum to be considered in the resolution of the problem.

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