Spectrum Optimization in Cognitive Radio Networks using Genetic Algorithms

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Abstract:

The rapid revolution in wireless communication in past years has increased the demand of radio spectrum to fulfill quality of service (QoS) requirements of wireless applications, leading to spectrum overcrowding. To solve the spectrum overcrowding problem, cognitive radio (CR) has emerged as a leading technology because it can intelligently sense an unused spectrum without creating any harm to authorized users. Once the spectrum is sensed, to fulfill QoS requirement of the application and to utilize the radio resources more efficiently, an intelligent decision to allocate an optimum spectrum is a prime requirement.

In this thesis work a spectrum allocation procedure is proposed. Genetic Algorithms (GA) an evolutionary computational technique is used which works on Darwin theory of evolution. It defines the radio in the form of chromosomes and genes. The procedure is modeled using Matlab, and the application’s QoS requirements are given as input to the GA procedure, which results in an optimum solution after several evolutions.
Acknowledgement:

Read! In the name of the Lord who createth

All the praises and thanks to Allah almighty, who is the Cherisher and Sustainers of the Universe.

We would like to acknowledge and express our heartiest gratitude to our supervisor Maria Erman for her supervision and examiner Jörgen Nordberg for their support during this thesis work. Furthermore, we really appreciate the facilities and environment provided by Blekinge Tekniska Högskola, Karlskrona.

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<th>Description</th>
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</thead>
<tbody>
<tr>
<td>EM</td>
<td>Electromagnetic</td>
</tr>
<tr>
<td>FCC</td>
<td>Federal Communications Commission</td>
</tr>
<tr>
<td>CR</td>
<td>Cognitive Radio</td>
</tr>
<tr>
<td>QoS</td>
<td>Quality of Service</td>
</tr>
<tr>
<td>GA</td>
<td>Genetic Algorithms</td>
</tr>
<tr>
<td>SDR</td>
<td>Software Defined Radio</td>
</tr>
<tr>
<td>EC</td>
<td>Evolutionary Computation</td>
</tr>
<tr>
<td>GP</td>
<td>Genetic Programming</td>
</tr>
<tr>
<td>DSP</td>
<td>Digital Signal Processors</td>
</tr>
<tr>
<td>FPGA</td>
<td>Field-Programmable gate array</td>
</tr>
<tr>
<td>BER</td>
<td>Bit Error Rate</td>
</tr>
<tr>
<td>RF</td>
<td>Radio Frequency</td>
</tr>
<tr>
<td>FM</td>
<td>Fitness Measure</td>
</tr>
<tr>
<td>BPSK</td>
<td>Binary Phase Shift Keying</td>
</tr>
<tr>
<td>QPSK</td>
<td>Quadrature-Phase Shift Keying</td>
</tr>
<tr>
<td>GMSK</td>
<td>Gaussian Minimum Shift Keying</td>
</tr>
<tr>
<td>16 QAM</td>
<td>16 Quadrature Amplitude Modulation</td>
</tr>
<tr>
<td>DPSK</td>
<td>Differential Phase Shift Keying</td>
</tr>
<tr>
<td>MSK</td>
<td>Minimum Shift Keying</td>
</tr>
<tr>
<td>OFDM</td>
<td>Orthogonal Frequency-Division Multiplexing</td>
</tr>
<tr>
<td>OOK</td>
<td>On-Off Keying</td>
</tr>
<tr>
<td>GW</td>
<td>Associated weight of gene</td>
</tr>
<tr>
<td>FP</td>
<td>Fitness Point</td>
</tr>
<tr>
<td>ABS</td>
<td>Absolute Difference</td>
</tr>
<tr>
<td>AWS</td>
<td>Aggregated Weighted Sum</td>
</tr>
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Chapter 1

1.1. Introduction

During the past two decades use of wireless applications has increased rapidly, which has eventually increased the demand of bandwidth. This higher demand of bandwidth has resulted in spectrum scarcity. Studies show that this spectrum scarcity is due to inefficient use of electromagnetic (EM) spectrum which is in fact available in abundance. EM spectrum is “a collective name of arranged electromagnetic radiations emitted from different sources according to their respective frequencies and wavelengths.” The EM spectrum is controlled by government authorities like Federal Communications Commission (FCC). Under the Federal Radio Act of FCC “only licensed users are allowed to use the EM spectrum”. It has been seen that at some places this spectrum is fully utilized, at some it’s partially and at some places it’s completely underutilized. This misuse of the EM spectrum results in a decrease of the spectral efficiency of the wireless networks. To solve the spectrum underutilization problem cognitive radio (CR) has been introduced. CR is defined as a kind of smart radio and the term was first used by Mitola and Magurire (Doyle 2009). It is a device which can adapt and change its behaviour according to the radio environment. In CR networks the secondary users can borrow the unused spectrum from the primary user for some time but this must be done by creating no harm to the primary user’s communication. The spectrum is then released after the completion of communication.

In this lending process of EM spectrum to secondary users there are several issues to be considered, as described in (Doyle 2009). A CR device must have four qualities: firstly this device should have an understanding of the radio environment it is operating in (i.e. the device should have to be intelligent enough to sense the spectrum holes in radio environment for secondary user). Secondly this device must be capable to understand the communication requirements of the application; study shows that for an efficient wireless communication process QoS constraints of an application are of great importance, therefore to maintain the QoS requirements of the application proper management of the unlicensed spectrum is required. Thirdly this device must have an understanding of regulatory polices enforced by the licensing authorities (i.e. the proper sharing of unlicensed spectrum on basis of agreement with the licensing authorities to make possible the use of spectrum without harming the communication of licensed users). Fourthly the device must have an understanding of its own operational capabilities such as radio parameters.
In this thesis work we have considered the spectrum management issue of cognitive radio. As CR is a self organizing system and it has been stated earlier that for efficient wireless communication control of QoS requirements is very important, the EM spectrum needs to be organized accordingly. According to (Doyle 2009), spectrum management is defined as a process of organizing the EM spectrum in terms of its usage. This organization involves how, when and by whom this spectrum is used. This organization of spectrum involves complex decisions, and the term used in the CR world for this process is called “Spectrum Allocation”.

In this thesis work a spectrum allocation process is introduced in which decisions to assign the spectrum is made according to the QoS requirements of the application, using genetic algorithms (GA); an evolutionary computing technique use to solve complex optimization problem. The evaluation is done by proper simulation of this model in Matlab.

1.2. Thesis Layout

Chapter 2 gives a brief introduction on the fundamental concepts of cognitive radios explaining its need and use in the communication world, and its technical requirements. In chapter 3 an overview of genetic algorithms is described, including its history and background and its usage in engineering sciences. Chapter 4 gives a detail description of the proposed model. Results and conclusions are given in chapter 5.
Chapter 2 Fundamental Concepts in Cognitive Radio

2.1. Introduction

During the past years it has been seen that the interoperability, seamless connectivity and increasing QoS requirements for applications are of high demand in wireless communication due to their diversity.

The QoS of a network application is defined as “the set of quantitative and qualitative characteristics of the communication system required to achieve desired functionality of that application” (Andreas Vogel 1995). Further, as described by (Yan Chen 2004), an application’s QoS can base on human perception of different kinds of media (e.g. voice, text, video etc.) and its technological attributes, such as time-dependence (real time and non real time) and symmetry (symmetric and asymmetric).

In 1991-92 Joseph Mitola introduced a radio called "Software Defined Radio (SDR)” (Mitola 1993). SDR is defined as a radio terminal competent enough to operate with different bandwidths, that can a have wide range of operating frequencies and can use different modulation techniques and waveform formats. These capabilities make SDR able to support different communication standards like GSM, CDMA, OFDMA, WIMAX etc. SDR at times has provided the most promising solution for the interoperability and seamless connectivity problem, but QoS requirements of an application has still been under consideration. Thus, the increasing demands of QoS have introduced Cognitive Radio (CR) (B. Fette 2007).

So, in 1999 J. Mitola again stepped forward and together with G. Maguire coined the term CR. In their research they described CR as “a radio that understands the context in which it finds itself and as a result can tailor the communication process in line with that understanding” (Doyle 2009).

Basically the following are three prime applications required to be added in a SDR to make it a CR (B. A. Fette 2009):

- Optimization and management of spectrum.
- Interface with a wide variety of wireless networks, leading to management and optimization of network resources.
- Interface with a human, providing electromagnetic resources to aid the human in his or her activities.
Studies show that the EM spectrum is available in abundance but is not being utilized intelligently to meet today’s needs in wireless communications where high bandwidth is in great demand which has resulted in increased QoS requirements of the applications. This higher demand of bandwidth has resulted in spectrum scarcity, and the ‘cognitive radio’ also known as a very smart radio is the best purposed solution to control this spectrum misuse and to provide QoS requirements of the application (Doyle 2009). The proceeding sections briefly describe some fundamental concepts of cognitive radios.

2.2. Behaviour and Cognition Capabilities

It is seen that in order to have efficient communication, all the wireless systems in today’s world use their capabilities of adaptation and can change their behaviours in certain ways. For example a 3G communication device has the capability to nullify the power imbalance between different users by proper alteration of output power; furthermore a mobile phone can adapt the incoming signal regardless of the added noise in it and also a WIMAX network in order to maintain good throughput and link stability has the ability to adapt the characteristics of its transmitted signals such as different modulation techniques (Doyle 2009).

2.2.1. Behaviour of Cognitive Radio

The behaviour of CR is also adaptive but unlike the above mentioned communication systems its level of adaptively is very much increased and it can adapt as many operating parameters as possible, e.g. pattern of antenna beam, operating frequency, power, modulation and coding technique, battery and processor usage etc. This adaptation can itself happen in either a planned or an unplanned way. Further to make the communication more potential a CR can recognise the radio environment, can learn from previous behaviours and can predict the future events (Doyle 2009).

2.2.2. Cognition Capabilities

The aforementioned adaptive ability pave the way to define the capabilities a cognitive radio must have and collectively these capabilities are known as cognition capabilities; these are learning, sensing, awareness and reasoning (B. Fette 2007). With these adaptive capabilities in consideration, CR can very precisely be defined as “Radio capable to comprehend; the operating environment it is working in, the requirements of its users, the regulatory policies and its own potentials” (Doyle 2009).
Simply we can say that cognitive radio has full knowledge of the environment and framework. Cognitive radio executes the received information and makes self-directed decisions on how to arrange and put together itself with the communication process (Doyle 2009).

2.3. The Cognitive Cycle: observe, decide and act

A Radio capable of learning and sensing the radio environment, that has awareness of its own potential and user requirements, and that has the ability of reasoning with the regulatory polices, is known as cognitive radio. If we take these capabilities as observations for CR still there is a need to take a proper decision and on the basis of which an action is taken. Keeping this in mind we can simply say that cognitive radio works in a cycle i.e. observe, decide and act (Doyle 2009).

Observation involves the learning and sensing of the outer world (i.e. whole radio environment) and these observations are given as input to the CR where a decision is made on the basis of a mechanism and finally an action is taken.

According to (Doyle 2009), the complexity of a process depends upon the type of observations and decisions are made accordingly, it further states that a decision making process may be of a very simple kind or it may have a very complex procedure with involvement of some past knowledge or future analysis and probabilities. So the decision process must be properly designed in order to make intelligent decisions. With these possibilities in consideration a cognitive cycle is described in Figure 2.1.
Theoretically it looks like a cognitive cycle starts at ‘observation’ end and goes further in a traditional way. But actually this cycle starts at ‘act’ end with a logical reason, and that is to first know what actions are of significance and certainly possible, before we can understand what observations need to be made and what decision need to be taken (Doyle 2009).

So its three steps would be as following

- Act (Taking an Action)
- Observe (Making an Observation)
- Decide (Making a Decision)

Next, to better understand the above three steps, they are described in more detail in coming sections.

2.3.1. Taking an Action

‘Taking an action’ implicitly defines all the possibilities of alterations or actions that can be set to attain a desirable performance from a CR. It depends on the observation part of the cycle as it provides the indications for alterations. By altering certain parameters like frequency, bandwidth, pattern of the antenna beam, power, modulation technique etc. a CR
can be made efficient enough to achieve the desirable goal. This has been chosen as the first step of the cognitive cycle because before making an observation and take a possible decision a CR must be aware of the possibility of actions it can take to perform a certain job. It also involves the understanding of the radio environment CR is working in (Doyle 2009). Next is the observe part of the cycle and how this part plays its role in the cycle.

2.3.2. Making an Observation

As was described in the preceding part, radio parameters are altered to attain a certain performance, thus it is natural that the alteration of these parameters need some clues and hints etc. These clues are provided by the observation part of the cycle. This part works as the input and it indicates the state the radio is currently working in and after that the decision is made and action is taken. It involves the comprehension of the operating environment, understanding of the user requirements and regulatory polices; finally the awareness of its own capabilities. CR is capable of either getting observations from other entities or it can make its own observations (Doyle 2009).

In (Doyle 2009) four general approaches described for observations are as following.

- A CR can get the observational data naturally.
- An extra hardware device can be used to observe certain kind of information, such as a GPS device etc.
- By using a special signaling analysis technique.
- Learning from the environment it is operating in.

The last discussed approach is the most critical one in a CR. Learning the environment involves the proper understanding of the other systems operating in that environment, so to know what spectrum is available and for this a “spectrum sensing” mechanism is needed. Generally, the observation part of the cognitive cycle is considered synonymous with spectrum sensing (Doyle 2009).

2.3.2.1. Spectrum Sensing

According to (Doyle 2009), “spectrum sensing” involves the detection of a transmitted signal of interest by a CR receiver. It involves the ability of a CR to detect white spaces and sense the existence of other radios in the radio environment. To achieve the desirable goal certain
factors are needed to be considered; like accurate sensing of the spectrum, sensing on the appropriate range and sensing in time.

2.3.2.1.1. Accurate Sensing

A CR must be made smart enough so that it can detect the spectrum accurately. According to (Doyle 2009), there are two possible scenarios for an inaccurate detection: a “false alarm” and “missed detection”. When there is no primary user present in the radio environment but the CR observes that there is a primary user present, this is known as “false alarm”. The other scenario is the opposite of this, that a CR observes that a primary user is not present but actually the primary user is present. Both of these scenarios lead to an inefficient communication, as in first case the CR will miss the opportunity to communicate and in the second case interference will occur.

2.3.2.1.2. Sensing in the Appropriate Range

This is a process to improve the accurate sensing described above. In a communication system every transmitter has a defined range of the spectrum, and with this range a receiver can properly receive and decode the transmitted signal. This range depends upon the transmitter’s power and the receiver’s sensitivity. So both the primary and secondary users have receivers of such level of sensitivity that they can sense within the appropriate range (Doyle 2009). Sensing within this proper range is a remedy to the problems of “false alarm” and “missed detection”.

2.3.2.1.3. In Time Sensing

The in time sensing involves sensing of primary user in the spectrum. This can be divided into two terms white spaces and return of primary user. The first term, white spaces, addresses the vacation of primary users which in result create spectrum holes, therefore an in time sensing of spectrum holes is required to avail the opportunity to communicate. If it takes too long to sense the white spaces then there is a chance to lose the communication opportunity. The second term, return of primary user, addresses the return of licensed user of the spectrum, therefore an in time sensing of the return of primary user is required to avoid unwanted interference between primary and secondary users. If it takes too long to observe the primary user then there is a possibility of interference between primary and secondary users which may not be acceptable for efficient communication (Doyle 2009).
2.3.3. Making a Decision

In the previous section we have seen how a CR makes observations. These observations are fed as the input to the decision making process in order to select the action to take. The decision making process is said to be the “heart of cognitive radios”. In CR the very important decision is about the distribution and usage of the radio resources; and for a fair communication an optimal resource distribution is required (Doyle 2009).

2.3.3.1. Optimization

According to (Doyle 2009) (Mitchell 1998), “An optimization process can be defined as the process involved in selecting the ‘best’ choice from the list of available choices in order to reach some kind of goal or at least get as near as possible to the goal”.

The above mentioned definition leads to three scenarios that need to be discussed in detail, and these are ‘optimization goal’, ‘available choices’ and determining the ‘best choice’.

The ‘optimization goal’ involves the selection of such solutions by which simultaneously efficiency of a communication system can be maximized and any inefficiency can be minimized (Doyle 2009).

‘Available choices’ refer to the set of all possible solutions for a certain goal and list of these choices is called a search space and each choice within that list is a possible solution (Doyle 2009).

To obtain the ‘best choice’ from the search space, a proper fitness test is set and base on that fitness test the best available solution is selected (Doyle 2009).

The optimization depends on the nature of tasks involved in the process, some of which are described here.

Allocation of the spectrum is an optimization task; it involves the procedure of assigning the white spaces found in the spectrum sensing process to the secondary users. Another one is the proper control of power; every user or application in CR controls the power by itself and provide feedback. This proper power control helps to reduce the signal noise and guarantee the required QoS for the communication. Furthermore proper toggling of modulation and coding schemes plays an important role in optimization; a CR should have the ability to toggle between modulation schemes to compensate for any variations in the channel of
communication and the characteristics of traffic. For example, when the accessible bandwidth reduces, the system should toggle to a modulation scheme that has high bandwidth efficiency and vice versa. Lastly the carrier frequency of the operation has a vital importance in the optimization process; a CR has the ability to change its carrier frequency with the help of its radio environment information. Cognitive radio determines the most appropriate operating frequency and does the vibrant communication over that selected frequency.

According to (Doyle 2009), many optimization tasks involved in CR has a very large search space, so a probabilistic method is required to solve the task. It further states that ‘heuristics’ and ‘meta-heuristic’ approaches are used to find the solutions from large search spaces. The heuristic approach works in simple approximation manner, but in a meta-heuristic approach several kinds of tricks are used to get rid of any possible mess, like local minima or maxima etc. So to perform optimization tasks in CR, meta-heuristic approaches are best suitable (Doyle 2009). There are several meta-heuristic approaches, like hill climbing, greedy algorithms, tabu search, simulated annealing and genetic algorithms and few more (Doyle 2009).

For this thesis work we used a genetic algorithm approach which is totally different from all discussed above as it works on Darwin’s theory of evolution and takes a population of chromosomes. Later several genetic operations like selection, crossover and mutation are performed. Only the best chromosomes survive to reproduce and mutate, and the weak are discarded which certainly yields the best possible solution. Genetic algorithms and their applications are discussed in detail in the coming chapter.
Chapter 3 Genetic Algorithms and their Applications

3.1. Brief History of Evolutionary Computations

Evolutionary computation (EC) was introduced between the 1950s and 1960s. During the studies of EC, researchers came to know that this computation technique can be used to obtain an optimal solution in engineering science problems. “Evolution strategies” (Evolutionsstrategie in the original German) were first described by Rechenberg in 1960. It was a method he used to optimize real-valued parameters for devices such as airfoils (Mitchell 1998).

In 1960 John Holland together with his colleagues and students developed an evolutionary algorithm at University of Michigan, which is known as the genetic algorithms (GA). The GA is an evolutionary computational technique for an optimized problem solution. Darwin theory is the base for these algorithms and in order to get the optimal solution it involves all the methods described in Darwin’s theory like mutation, crossover, inheritance and selection (Mitchell 1998). John Koza was the first who did Genetic Programming (GP) in 1992.

3.2. Methods of Optimization

According to (Doyle 2009), optimization refers to finding a global maxima or minima of an object function and avoids finding a local maxima or minima. For computation problems, an optimum solution is required. But the search towards optimum solution may lead to complications and loss of an important individual because of a very large search space. There are several meta-heuristic techniques to find an optimum solution like hill climbing searches, greedy algorithm searches, tabu searches, simulated annealing searches, and genetic algorithms etc. The main advantage of using a meta-heuristic approach is its tricky nature which really prevents the search space from getting stuck into a local minima or maxima. These techniques can lead to a better solution but for network applications we can not define an optimum solution in practical words. This is because there is always a possibility that a global maxima or minima may never be found in desired time, and hence almost all network applications are time-dependent therefore the process should be terminated at a given time. For a CR it is required to apply a termination criteria because of certain reasons, for example in case of dynamic spectrum access in a CR, time plays vital role and if decisions are not made in timely fashion then the opportunity to communicate may pass.
Hill climbing is a search approach in which a move is made when the successor state is better than present state. If there is no better state than the present state, the process of hill climbing is terminated. The main disadvantage of this approach is that it finds only a local maxima or minima. The greedy algorithm is a meta-heuristic approach to find the global optimum by finding the state that looks best at the moment. It makes an optimal choice locally in the hope to find a global optimal solution; a disadvantage of this approach is that it quickly delivers a solution which is perhaps not the best (Doyle 2009).

In tabu search all the tested solutions are stored in a list called “tabu list”, and a new solution is only possible if all the tested solutions are present in the list; for example if all downhill are in tabu list then uphill moves can occur. This storing mechanism of tabu search prevents the algorithm from cycling back to already tested solutions (Gendreau 2003).

Like tabu search, simulated annealing can also search in downhill and uphill. This technique is inspired by the method of annealing used in metallurgy. The annealing in metallurgy involves the heating and control cooling of materials to increase the size of its crystal and reduce their defects. By heating the material, atoms leave their initial positions and move around randomly, thus creating a search space. If the system is allowed to become very hot then the search will be uphill and if the temperature is decreased then the search will be downhill (Doyle 2009).

### 3.3. Uses and Advantages of Genetic Algorithms

Fields from engineering, computer sciences and economics to bio-informatics are using GA to solve optimization problems. Non-deterministic finite automaton, machine learning, evolution of music as well as image processing are some problems which are effectively solved by using GA. The main advantage of using GA over other techniques is the parallelism, which can really speed up the simulation results (Haupt and Haupt 2004).

Due to the generation of a completely new population for each search space GA have considerably less chances to get stuck in local extremes as compared to other discussed techniques. Fast convergence is another main advantage of the GA and it can converge quickly on a problem’s specific solution. Implementation of the GA can be done on semiconductors devices like Digital Signal Processors (DSP) and FPGA, and with the help of this it can be integrated with wireless technology (Haupt and Haupt 2004).
This easy implementation and re-usage make the GA more significant than other heuristic search schemes. If a basic GA is implemented, then a new object like other chromosomes can be added to it, in order to solve a new problem. However we can face some difficulties during an encoding scheme and fitness measures etc. Some other problems can also be faced at the time of computation i.e. these algorithms can be slower than that of other techniques available. But this factor can be ignored if a number of generations and longer simulations can be controlled or performed using faster hardware resources (Rondeu, et al. 2004).

The following are some other significant advantages of the GA (Haupt and Haupt 2004):

- Continuous or discrete variables can be optimized with the GA.
- It doesn’t require derivative information.
- It can deal with a large number of variables.
- It suits well with parallel computers.
- It does not only provide a single solution but a list of optimum solutions.
- It may encode the variables so that the optimization is done with the encoded variables.
- It works with numerically generated data, experimental data, or analytical functions.

### 3.4. The GA Approach

The computation of the GA starts from the assortment of the chromosomes which are randomly generated. These chromosomes have certain characteristics and they follow the computation through generations. Chromosome fitness at a generation is calculated on the basis of stochastic calculation and mutation. The fitness is evaluated on individual basis and thus it gives rise to a new population of chromosomes. After this, an iterative algorithm will be used for the continuation of a process to several generations to generation, unless or until the most optimum solution is received (Withall, et al. 2003).

In (Withall, et al. 2003), it is stated that a GA can be implemented using the following steps

1. **Initialization:** A random initial population of n chromosomes is generated. This population contains the available solutions for the specified problem.

2. **Fitness measures:** Evaluation of the fitness of an initial population’s chromosomes.
3. **Construction of a new population:** Try the following steps to reproduce, until the production of the next generation completes:

   i. **Selection:** A selection of chromosomes will be done in a way such that these chromosomes have the better level of fitness in the current available population.

   ii. **Crossover:** The crossover is done to make new individuals for the incoming generation. So with the defined probability of crossover, selected chromosomes reproduce to form new individuals.

   iii. **Mutation:** The new created individual will be mutated at a definite point.

4. **Stopping Criteria:** The process is repeated with all the above mentioned steps until a desired optimum solution is obtained or a set of maximum numbers of the population are generated.

To implement the GA there are still several factors to consider, like creation of chromosomes, types of encoding used to perform the genetic algorithms, selection of the optimum chromosomes, and different criterion such as defining the fitness measure. (Withall, et al. 2003).

**3.4.1. Configuration of Chromosome**

Chromosomes are basic building blocks of the GA:s they should be represented in a way that they give out information about the solution of the problem. The most common and popular representation is the binary string representation. In this type, a bit in the whole population represents the characteristics of each chromosome in the generation. Representation through a real number or that of an integer can also be used for this task (Haupt and Haupt 2004).

Some important radio parameters are selected to contribute as ‘genes’ in the chromosomes, a chromosome can consist of several genes. This selection plays an important role in the chromosome’s basic structure, because without these parameters the structure of the chromosome is incomplete. The chromosome’s initial population will be generated randomly to give a collection of chromosomes. This collection will be the possible optimized solution of the problem. After this the transformation of chromosomes is done and we get several generations after performing specific operations like selection of chromosomes, crossover.
and mutation. The operations are performed at every generation of chromosomes. This newly constructed population is then used as the input population (Haupt and Haupt 2004).

3.4.2. Fitness Measure

This function is defined as the quality measurement of each chromosome involved in the genetic process. The definition of this fitness varies as the problem differs. This applicability of the fitness measure will lead towards the production of a new generation in the next iteration. The fitness measure function acts as a filter, which takes out those individuals (chromosomes) which are below a specific level of fitness from the current population, so the chromosomes which are away from the optimized solution will be taken out and only optimum chromosomes are transferred to the next generation. It is thus important to apply a fitness function on every generation of chromosomes. After the specification of the fitness measure and a genetic representation, the GA will perform the other tasks like selection, crossover and mutation (Haupt and Haupt 2004).

3.4.3. Selection, Crossover and Mutation

After the definition of the structure of the chromosome and that of the fitness function, the genetic algorithms will perform certain operations like selection, crossover and mutation to find an optimum solution. These operations are executed in a clear and distinct way and the developers have the right to select the selection mechanism of their own choice and define the rates of both crossover and mutations.

The selection of fit chromosomes depends upon the defined fitness measures, thus fitness measures and selection are related to one another. In GA:s there are several techniques used to select fit chromosomes; these are elitism, roulette wheel and tournament selection.

In elitism, two or more chromosomes with highest fitness measures are carried forward to the next generation without reproduction or mutation. Roulette wheel selection works with a probability distribution in which each chromosome is compared with the sum of the fitness of all the chromosomes and the chromosomes with higher probability has the greater chance of selection. In tournament selection a tournament is run between several randomly selected chromosomes and winner of that tournament is selected; this process is repeated to obtain the desired number of fit chromosomes (Reeves and Rowe 2003).
After the selection of fit chromosomes with either of the above mentioned procedures the selected chromosomes reproduce to give birth to new off-springs. If the crossover procedure is carried out on two parents in order to make an offspring then a group of random crossover points will be chosen in the chromosomes. These points will separate them into parts having parametric values. This process might divide the individual genes into two. To have an increment in the probability of the operation occurrence, the crossover rates are usually set high (Haupt and Haupt 2004).

After the crossover operation, the mutation process is done. This process is performed in all or some bits of the chromosome. A random value will be generated and if the value is lesser than that of the mutation probability which was defined by the user, than an inversion of one of the bits in the gene will be performed. The rate of this process is generally kept low because otherwise it can affect the fitness level and the structure of the offspring under production. In a case where the fitness of the gene is not improved, then the rate of the mutation process can be increased to reach the required optimization level (Haupt and Haupt 2004).

3.5. GA in the Radio Frequency (RF) Environment

As we studied in the previous chapter, the CR works in an observe, decide and act cycle, so the knowledge observed from the radio environment needs a proper representation in the GA to get an optimized solution. This representation will allow the CR to accommodate the GA into them and this will help developing the CR adaptation ability (Rondeu, et al. 2004). In the spectrum allocation optimization problem in CR, the convergence behaviour of the GA is of great benefit.

3.5.1. A Definition of Chromosomes for the RF Environment

For optimization task the most important step in the GA is to develop a fitness measure to find the total fitness of a chromosome. Hence a proper definition of a chromosome is required.

In GAs the chromosomes can be represented with the help of simple data structure vectors. These structures have different data types which defines their genes respectively. The chromosome of a radio can have many parameters that can be represented as genes of a chromosome; these parameters could be the data rate, bandwidth, frequency, error rate,
modulation/coding scheme, and antenna gain etc.

3.5.2. A Definition of Fitness Measures for the RF Environment

After the construction of the chromosome, the definition of a fitness measure for the radio environment is the next step. For the observed radio environment, the definition of a fitness function based on the performance parameters, is to be defined.

In radio or wireless communications, QoS requirements of a user or application have great importance. The fitness measure should be designed in such a way that radio resources can be used efficiently and there shouldn’t be any resource wastage. A possible way to make this happen is to ask the secondary user about its preferences, like frequency, power, data rate etc. and by the allocation of spectrum with requested values a misuse of the spectrum resources will be stopped.

For this procedure stochastic processes are used. The corresponding associated weights to each of the chromosome are of great help. For example, the error rate in loss sensitive applications will be having a higher weight as compared to that of data rate because of the indication of its importance in QoS as specified by the user. In case of applications which are time sensitive, higher weight will be assigned to data rate than that of error rate.

With a proper definition of fitness measure, only better chromosomes will have the chance to survive. So in fact this is a filtration process to get the optimized individuals at each generation (Rondeau, et al. 2006).

3.6. The Process of Spectrum Allocation

The main theme of our thesis work is the optimization and management of spectrum in CR. This involves the secondary user to enter the QoS requirements of the application it is using. The RF environment is sensed by the CR receiver and after that the radio is involved in the procedure to allocate a spectrum hole for the requesting user keeping in mind the QoS requirements.

The observed spectrum status is given as input to the spectrum allocator by the sensor and after that a test is performed. If the resultant parameters satisfy the user’s QoS requirements, the process is terminated; otherwise several tests are performed until an optimum solution is achieved. To perform spectrum allocation tests, an important factor that must be considered is

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“Spectrum allocation regulations” prescribed by the regulatory authorities. These regulations help to reduce the interference of the spectrum bands and also help to satisfy the QoS requirements of the applications; another factor that must be considered is the preference given to the primary user on detection.

An important thing to remember is that, it is complex to get an exact solution with GA:s but the main benefit of using the GA for this task is that it is giving multiple solutions for a single problem. Consequently the GA:s are saved from being stuck at any level of the optimization process. This also shows that if the GA does not give an exact solution for a problem, it will actually give the best possible solution among a variety of different solutions.

The next chapter will describe the GA development for this spectrum optimization process in more detail. The evaluation of these techniques will be performed with the help of mathematical tools; i.e. MATLAB.


Chapter 4 METHODOLOGY

4.1. Introduction

The wireless or mobile devices should be able to adapt to the varying RF conditions, for this cognitive radios are being developed which automatically configure the communication system to optimize for and take advantage of the prevailing RF environment (Hauris 2007).

This thesis work discusses the application of GA to solve the optimization of RF parameters for wireless networks with main emphasis on the issues related to spectrum optimization of the CR networks, regarding the QoS requirements for the applications. We consider that a radio environment has been sensed already and desired spectrum information has to be requested by the secondary user. Now the CR receiver will have to make a decision to accommodate the secondary user, who is requesting for allocation of spectrum, specifying its application needs. This Spectrum allocation decision requires some factors or parameters for consideration like operating frequency, data rate, transmitting power, modulation/coding scheme, signal bandwidth, error rate etc. The desired spectrum information by the secondary user is the QoS requirements for the application it is going to use. These specified values will be given to the CR that also has the sensed information about the whole radio environment. This sensed information about the radio environment makes a pool of available solutions for spectrum allocation to a secondary user, and from this pool of available solutions the initial population for the GA will have to be selected randomly. After the selection of an initial population the decision for the allocation of the spectrum takes place after certain processes discussed in detail further in the report.

It is stated in (Hauris 2007), that the design of RF communication links and network configuration depends on multiple parameters like operating frequency, noise figure, various antenna types, signal power, data rate, interference levels and modulation/coding scheme etc. For spectrum allocation and management tasks for a radio network, in this report we will only consider five RF parameters and these are Data Rate, Signal Power, Error Rate, Operating Frequency and Modulation Technique.

To obtain a simultaneous optimal solution for these parameters is very difficult and complex using a probabilistic approach as the solution space for each of the equations governing the parameters varies and overlaps with each other. One solution to this problem is to apply Evolutionary Computing and in particular the GA (Hauris 2007). The QoS requirements of
the application are compared with several available solutions in the pool and then the best possible and optimized solution is to be taken. The GA uses biological concepts of chromosomes or the genotype of the genome and genes. In particular, a Fitness Measure (FM) is derived which provides a figure of merit for the performance of the GA in relation to overall RF performance. The GA:s have some operations or functions like selection, crossover (recombination) and mutation. The performance of the GA depends on these functions. From the initial population of chromosomes, the best are selected in the selection operation and new population is generated by applying crossover and mutation functions on the chromosomes. It is generally considered that the new generation has more optimal solutions than the old one but in practical there is also a possibility that new population’s chromosomes are worse than parent chromosomes.

As described in section 3.4 a general GA works in some defined steps. For our thesis work these steps are as following.

1. Construct the proper chromosome structure.

2. Generate the initial population from random chromosomes.

3. Calculate the fitness measure for each chromosome.

4. Construct a new population using the following steps

   - Selection: Choose the fit chromosomes based on specified fitness measure and discard others, among the fit chromosomes select the best two and save them as elite chromosomes.
   - Crossover: Apply the crossover function on the selected chromosomes other than the elite chromosomes with a determined crossover function and rate.
   - Mutation: The chromosomes are mutated with a determined probability of mutation. In mutation every gene of the chromosomes is represented in form of binary bit strings.

Put the chromosomes into the new generation.

5. Return to Step 3 until the new generation contains the desired individuals. Replace the old population with the newly generated population.
6. Terminate: When a good enough solution is achieved or a number of defined generations is produced.

The procedure of genetic algorithm is shown in Figure 4.1 (Pohlheim 2006).

![Figure 4.1 The GA Procedure](image)

### 4.2. The Chromosome Structure

For the GA to act accurately a proper chromosome structure is required. A chromosome is the problem solver for the GA which consists of different genes. In this thesis work each gene is representing some aspect or parameter of the RF environment. We have considered five important RF parameters, and this is done to keep the size of chromosome as small as possible so that the complications of computing do not affect our optimization model.

The parameters we consider for this thesis work are stated below in the order they are going to be considered in the chromosome.

1. Data Rate
2. Signal Power
3. Error Rate
4. Operating Frequency
5. Modulation Technique
Once we have decided the number of genes for the chromosome, next is the encoding of the chromosome. Study shows that the most critical part in the GA is to find a suitable encoding for a chromosome to solve the given problem. The proper representation of the chromosome will increase the performance of the GA by limiting the search space. The most commonly used encoding techniques are binary encoding, permutation encoding, value encoding and tree encoding. In this thesis work we will consider value encoding and binary encoding. The value encoding is done for the whole GA process mainly selection and cross over, in this each gene of a chromosome is represented by a decimal number. But for mutation process chromosomes are converted into binary and each gene is now represented by bit strings. This is because in mutation an alteration of a single bit will form a new chromosome, whereas if we use decimal representation this will alter the whole gene and result will be worse. Each gene of the chromosome is defined in detail in the proceeding sections of this report.

4.2.1. Value Encoding of the Chromosome

In value encoding the chromosome can have any type of value connected to the problem, these values can be in decimal number form, real number form or these can be some characters describing the problem. For this work the decimal representation is used.

4.2.1.1. Data Rate in decimal form

Data rate is the first gene of the chromosome used for the generation of the population. In communications it is “the rate bits are transferred in per unit of time” so it is calculated in bits per seconds. In this thesis work the data rate is ranging from 0-2Mbps and the step size is 125Kbps. This will provide the algorithm with 16 decimal values for representation. The decimal value ‘0’ is assigned to the 1st data rate band, ranging from 0Kbps to 125Kbps the decimal value ‘1’ is assigned to the 2nd data rate band of range 126Kbps to 250Kbps and so. In the end the decimal value ‘15’ is assigned to 1.876Mbps to 2Mbps data rate band. The assignment of decimal values to specific data rates are shown in Table 4.1.

<table>
<thead>
<tr>
<th>Decimal Values</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>......</th>
<th>......</th>
<th>7</th>
<th>8</th>
<th>......</th>
<th>......</th>
<th>13</th>
<th>14</th>
<th>15</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Rate Kbps</td>
<td>125</td>
<td>250</td>
<td>375</td>
<td>0.876</td>
<td>1.001</td>
<td>......</td>
<td>......</td>
<td>1.626</td>
<td>1.751</td>
<td>1.876</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Data Rate Mbps</td>
<td>1.000</td>
<td>1.125</td>
<td>1.750</td>
<td>1.875</td>
<td>2.000</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 4.1 Data Rate Gene in Decimal Form
4.2.1.2. **Signal Power in decimal form**

Signal power is the second gene of the chromosome used for the generation of population. Power is a very important radio parameter for communication. For valuable communication a certain amount of power is required for specific applications; a very high power or a lower than the desired power value may affect communication. A specific power range permits users to correspond without any error and boosts the probability of successful communication. The number of errors can also be decreased by increasing the signal power.

For this particular thesis work we will take the power range from -31 dBm to 31 dBm. Now setting the step size of 1 dBm will return us the total of 63 values to represent this gene of the chromosome in decimal format. Now if we start from 0, we will have the values 0 to 62. Where the '0' decimal value represents the -31 dBm to -30 dBm power band, '1' represents the -30 dBm to -29 dBm power band and so on and in the end the decimal value '62' represent the 30 dBm to 31 dBm power band. The whole power band is shown in Table 4.2.

To have the desired power band for an application, the user will input a decimal value which is assigned to it. For Example, if the application desires 30 dBm of power then the user can input the decimal value 61.

<table>
<thead>
<tr>
<th>Decimal Values</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>......</th>
<th>......</th>
<th>31</th>
<th>......</th>
<th>......</th>
<th>61</th>
<th>62</th>
</tr>
</thead>
<tbody>
<tr>
<td>Signal Power</td>
<td>-31 dBm</td>
<td>-30 dBm</td>
<td>-29 dBm</td>
<td>-28 dBm</td>
<td>......</td>
<td>......</td>
<td>0 dBm</td>
<td>......</td>
<td>......</td>
<td>30 dBm</td>
<td>31 dBm</td>
</tr>
</tbody>
</table>

*Table 4.2 Signal Power Gene in Decimal Form*

4.2.1.3. **Error Rate in decimal form**

Error Rate is the third gene of the chromosome in this thesis work. For error rate we mean bit error rate (BER) and it can be defined as when “the transmitter’s sent bits are not received by the receiver in a specific time interval”. Error rate depends on the type of application to be used. Simply, each and every application requires specific error rate. Like video applications can tolerate higher error rates but they do not compromise on bandwidth but on the other hand a VoIP application does not require high bandwidth but it is very sensitive to error and can not tolerate the error rate. In contrast to the wired network error rates are higher in wireless communication systems. These errors should be reduced in radio and wireless...
communication by using some techniques or procedures. By using a specific coding scheme or increasing the signal power these errors can be reduced.

In our thesis work, the error rate is ranging from $10^{-1}$ to $10^{-16}$ and the step size is $10^{-1}$, which has resulted into 16 decimal values required for the chromosome representation. The detailed decimal representation of the error rate gene is shown in Table 4.3.

<table>
<thead>
<tr>
<th>Decimal Values</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>…..</th>
<th>…..</th>
<th>…..</th>
<th>…..</th>
<th>14</th>
<th>15</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error Rate (BER)</td>
<td>$10^{-1}$</td>
<td>$10^{-2}$</td>
<td>$10^{-3}$</td>
<td>$10^{-4}$</td>
<td>…..</td>
<td>…..</td>
<td>…..</td>
<td>…..</td>
<td>$10^{-15}$</td>
<td>$10^{-16}$</td>
</tr>
</tbody>
</table>

*Table 4.3 Error Rate Gene in Decimal Form*

4.2.1.4. Operating Frequency in decimal form

The fourth gene of the chromosome used for the generation of population is the Operating Frequency. For communication, every application uses a specific frequency to transmit and receive information. The range of the operating frequency band we are using in this thesis work is from 0-20Mhz. The number of users that can be facilitated simultaneously in the communication using this frequency band can be calculated by defining the step size. For this thesis work we considered the step size 40 KHz producing 500 frequency bands. This means that the 500 users can use this frequency band simultaneously with each of them having a 40 KHz band for communication. These 500 frequency bands are also the decimal representation for the frequency gene in the chromosome, this decimal representation is discussed in more detail below.

The decimal value ‘0’ is assigned to the 1st frequency band, ranging from 0 to 40 KHz. In the same way, the ‘1’ decimal value is assigned to the 2nd frequency band, ranging from 41 KHz to 80 KHz and so on. In the end the decimal value ‘499’ is assigned to the 19.961 MHz to 20 MHz frequency band. The assignment of decimal values to specific frequency bands is provided in Table 4.4.

<table>
<thead>
<tr>
<th>Decimal Values</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>…..</th>
<th>249</th>
<th>…..</th>
<th>496</th>
<th>497</th>
<th>498</th>
<th>499</th>
</tr>
</thead>
<tbody>
<tr>
<td>KHz</td>
<td>KHz</td>
<td>KHz</td>
<td>KHz</td>
<td>MHz</td>
<td>MHz</td>
<td>MHz</td>
<td>MHz</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Table 4.4 Operating Frequency Gene in Decimal Form*
4.2.1.5. **Modulation Technique in decimal form**

Our fifth gene to be considered in the chromosome is the "modulation technique". In telecommunication the modulation defines the varying relationship of two different waveforms. So the modulation technique for each and every application is required for communication. In our thesis work we will use a total eight (8) modulation techniques for communication. Those modulation techniques are BPSK, QPSK, GMSK, 16 QAM, DPSK, MSK, OFDM and OOK. To define the chromosome these techniques should be represented in decimal form. The corresponding decimal value for each modulation technique is shown in Table 4.5. For QoS the required modulation technique for the application user needs to enter the relevant decimal number.

<table>
<thead>
<tr>
<th>Decimal Values</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Modulation Technique</td>
<td>BPSK</td>
<td>QPSK</td>
<td>GMSK</td>
<td>16 QAM</td>
<td>DPSK</td>
<td>MSK</td>
<td>OFDM</td>
<td>OOK</td>
</tr>
</tbody>
</table>

Table 4.5 Modulation Technique Gene in Decimal Form

4.2.1.6. **Configuration of the Chromosome in decimal form**

Next is the configuration of the chromosome based on these five genes or parameters. In this configuration, the orders of genes are the same as mentioned earlier. It can be seen in the Table 4.6; the data rate is the 1st parameter or gene in the configuration of the chromosome and has decimal values ranging from 0 to 15. Signal power is the 2nd parameter or gene in the configuration of the chromosome and has decimal values ranging from 0 to 62. Error rate is the third gene in the configuration of the chromosome and has decimal values ranging from 0 to 15. The operating frequency is the 4th gene or parameter in configuration of the chromosome and has values ranging from 0 to 499. Finally the last gene is the modulation technique which has 8 decimal values ranging from 0 to 7.

<table>
<thead>
<tr>
<th>Order No.</th>
<th>Gene</th>
<th>Decimal Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Data Rate</td>
<td>0-15</td>
</tr>
<tr>
<td>2.</td>
<td>Signal Power</td>
<td>0-62</td>
</tr>
<tr>
<td>3.</td>
<td>Error Rate</td>
<td>0-15</td>
</tr>
<tr>
<td>4.</td>
<td>Frequency Band</td>
<td>0-499</td>
</tr>
<tr>
<td>5.</td>
<td>Modulation Technique</td>
<td>0-8</td>
</tr>
</tbody>
</table>

Table 4.6 Configuration of the chromosome in Decimal Form
The secondary user will ask for the desired spectrum for the application it is using based on these decimal values of the gene and the best possible spectrum will be allotted.

4.2.2. Binary Encoding of the Chromosome

In the mutation operation of the GA, the binary encoding of the chromosome is required. So now each gene is converted from decimal representation to a binary representation for the mutation operation. After the mutation process the genes are converted back to their respected decimal forms.

4.2.2.1. Data Rate in binary form

For mutation operation of the genetic algorithms the decimal value of data rate gene has to be converted into binary form. From 4.2.1.1 we know that to represent data rate in decimal form for this thesis report we have total of 16 decimal values. To represent 16 decimal values we require total of 4 bits for binary representation. Same would be the case for each gene discussed in the proceeding sections. An error message for the function should come if the range of value exceeds from 16 this.

4.2.2.2. Signal Power in binary form

For 63 values of signal power, a total of 6 bits are required to represent it in the binary form. This is because 6 bits can represent 64 decimal values, which accommodates 63 power bands. An error message for the function should appear if the range of value exceeds from this.

4.2.2.3. Error Rate in binary form

The same is required for the error rate gene. For the error rate we have 16 decimal values which require only 4 bits to represent it in the binary form for the mutation operation of the GA. An error message should come if the range of value exceeds this.

4.2.2.4. Operating Frequency in binary form

The binary form of the operating frequency gene is required for mutation, in which the frequency is converted from the decimal to the binary form. As mentioned earlier, for an operating frequency of 20 MHz with the step size of 0.04 MHz, we will have 500 frequency bands. Thus, to represent a total of 500 frequency bands in binary form, 9 bits are required. 9 bits can represent a total of 512 decimal values, which accommodate the required 500 frequency bands.
4.2.2.5. **Modulation Technique in binary form**

As we have 8 different modulation techniques, a total of three (3) bits are required to represent them into binary form. So the modulation gene will be converted to 3 bits for the mutation operation and after that it will be converted back to decimal. An error message for the function should appear if the range of value exceeds this.

After the mutation process, all the binary values are reconverted to their respective decimal forms for further manipulation.

4.2.2.6. **Configuration of the Chromosome in binary form**

The spectrum allocation optimization procedure discussed in this report requires a 26-bit-chromosome to perform the mutation operation in the GA. This 26-bit-chromosome consists of a 4-bit data rate gene, a 6-bit signal power gene, a 4-bit error rate gene, a 9-bit operating frequency gene and a 3-bit modulation gene.

Table 4.7 shows the chromosome’s binary configuration depending upon the number of bits assigned to each gene.

<table>
<thead>
<tr>
<th>No. of gene</th>
<th>Gene</th>
<th>Number of bits</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Data Rate</td>
<td>4</td>
</tr>
<tr>
<td>2.</td>
<td>Signal Power</td>
<td>6</td>
</tr>
<tr>
<td>3.</td>
<td>Error rate</td>
<td>4</td>
</tr>
<tr>
<td>4.</td>
<td>Operating Frequency</td>
<td>9</td>
</tr>
<tr>
<td>5.</td>
<td>Modulation Technique</td>
<td>3</td>
</tr>
</tbody>
</table>

Table 4.7 Configuration of the chromosome in Binary Form

4.3. **Initial Population Generation**

So far in this report we have constructed the basic unit of the GA population called “the chromosome”. The next step is the generation of a pseudorandom initial population for further operations like selection, crossover and mutation. According to (Hill 1999), a good initial population facilitates a GA’s convergence to good solutions while poor initial populations can hinder it. Usually, to cover the whole range of possible solutions, the initial population is generated arbitrarily without having any size limitations and to attain satisfactory results, the defined size of the initial population can be increased or decreased accordingly.
In this thesis work we have considered an initial population of 100 chromosomes with a breeding rate of 50 generations. Research source shows that the optimum solution typically converges within 50 generations. This initial population can have the very best and the worst solutions for the problem. To select the best among this initial population a fitness measure is needed to be defined before the selection operation of GA can take place. Afterwards, operations like selection, crossover and mutation are performed. This will lead us to the new generation of chromosomes. The process is repeated up to a certain number of generations as in this case 50. After that the process is terminated and the optimum solution is selected.

4.4. Fitness Measure

The next step after the construction of the chromosomes and generation of the initial population; is to derive a Fitness Measure (FM) for each chromosome. According to (Haupt and Haupt 2004), the Fitness measure is also known as the survival evaluation, and in GA it determines how well an individual (i.e. the chromosome) from a population is at solving the given problem. The fitness is traditionally given as some integer or real number value, where the higher the value, the greater the fitness.

In the generated initial population of the chromosomes there is a number of possible solutions which satisfies the application's requested requirements (i.e. QoS requirements). Some of these may fully satisfy the requested requirements and some may be less close. But the possibilities of the solution with the most terrible values are also in the solution set. So concerning the optimization, the selection of the best and the rejection of the worst are required, and therefore a certain fitness measure is needed to be derived for each chromosome. This fitness measure must be derived in such a way that it minimizes the chances of the selection of the most terrible chromosomes for the next generation of population. After the derivation of the fitness measure, each chromosome will be evaluated accordingly and the best will be selected for the next generation by operations like selection, elitism, crossover and mutation. All these genetic operations are discussed in later sections of this report.

As was defined in an earlier part of this chapter, we have five parameters i.e. data rate, signal power, error rate, operating frequency and modulation technique. These five parameters act as genes of a chromosome in the GA. Each gene will have a specific weight associated in the chromosome. The weight for each gene is calculated as the number of bits need for its
representation in the binary representation. Now to represent the operating frequency in binary form, 9 bits are required and the whole chromosome is a total of 26 bits.

Thus the operating frequency gene will have approximately 35% of the total weight of the chromosome. The weights for all other genes are calculated in the same manner, keeping in mind that the sum of all the associated weights is equal to 100. This weight of the gene is represented by $GW1, GW2, GW3, GW4$ and $GW5$ for the data rate, the signal power, the error rate, the operating frequency and the modulation technique respectively to use in the fitness equations and detailed weights for all the genes are shown in Table 4.8.

<table>
<thead>
<tr>
<th>Representation</th>
<th>Gene Name</th>
<th>Percentage Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>GW1</td>
<td>Data Rate</td>
<td>15%</td>
</tr>
<tr>
<td>GW2</td>
<td>Signal Power</td>
<td>23%</td>
</tr>
<tr>
<td>GW3</td>
<td>Error rate</td>
<td>15%</td>
</tr>
<tr>
<td>GW4</td>
<td>Operation Frequency</td>
<td>35%</td>
</tr>
<tr>
<td>GW5</td>
<td>Modulation</td>
<td>12%</td>
</tr>
</tbody>
</table>

Table 4.8 Calculate percentage weight of chromosome's genes

Like the weight of each gene in the chromosome, there is a fitness point (FP) for each gene, this point will have an integer value within the range defined for each gene in their respective decimal representation part in the preceding report. As for the operating frequency gene there are a total of 500 decimal values ranging from 0 to 499. So the FP can have any value within this range of 0 to 499. This value is purely the developers own choice. We check different values within their respective ranges and came up with the values given in Table 4.9; these values showed better results as compared to other values. As we can see that these fitness points have values almost half of their respective decimal ranges such as decimal range of operating frequency is from 0 to 499 and its FP is set as 200, this is because to find an optimal value for operating frequency the GA will consider 200 values in each direction of the secondary user’s requested value which in any case will cover the whole search which is 500 in case of operating frequency. For example, if the required frequency band has decimal value 300 then the GA will take the chromosome with decimal value 300 for Operating Frequency as a central point and will consider 200 chromosomes in each direction for the search space, now the search space will have the chromosomes with values 101 to 499 for operating frequency. This will ultimately cover the whole decimal range and hence the chance to select the chromosome with optimal values increases. In Fitness measure equations,
for each gene these fitness points are represented by $FP_1, FP_2, FP_3, FP_4$ and $FP_5$. Each fitness point value with their respective genes is stated in Table 4.9.

<table>
<thead>
<tr>
<th>Fitness Point No.</th>
<th>Name of the Gene</th>
<th>Fitness Point Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>FP1</td>
<td>Data Rate</td>
<td>6</td>
</tr>
<tr>
<td>FP2</td>
<td>Signal Power</td>
<td>20</td>
</tr>
<tr>
<td>FP3</td>
<td>Error rate</td>
<td>7</td>
</tr>
<tr>
<td>FP4</td>
<td>Operation Frequency</td>
<td>200</td>
</tr>
<tr>
<td>FP5</td>
<td>Modulation</td>
<td>1</td>
</tr>
</tbody>
</table>

Table 4.9 Assigned fitness point of chromosome’s genes

Next, each entered value of a gene by the secondary user is compared with the respective gene of the chosen chromosome from the initial population and the fitness measure will be calculated as following.

First of all an absolute difference of the application requested parameter or gene with the relative parameter of the chosen chromosome will be calculated, shown in Eq. 4.1.

$$\text{Absolute Difference} (ABS) = |(\text{Chromosome's gene} – \text{Application's gene})| \quad \text{Eq. 4.1}$$

Furthermore, the value of this absolute difference ‘ABS’ is compared with the respective Fitness Point ‘FP’ for each parameter or gene which has already been defined. Now if the defined value of the respective fitness point is greater than the absolute difference calculated in Eq. 1 the Fitness Measure for the gene will be calculated as shown in Eq. 4.2, and if the defined value of the fitness point is less than or equal to the absolute difference, the fitness measure of the gene will be the weight of that respective gene as shown in Eq. 4.3.

$$\text{Fitness Measure of the Gene} = \left( (GW \times ABS) \div FP \right) \quad \text{if } FP > ABS \quad \text{Eq. 4.2}$$

$$\text{Fitness Measure of the Gene} = GW \quad \text{if } FP \leq ABS \quad \text{Eq. 4.3}$$

In the end the total fitness of the chromosome is calculated by summing up all the fitness of the genes and then taking their percentage.

Next the fitness measures for each gene are shown with their respective fitness points and weights.
4.4.1. Fitness Measure of the Data Rate Gene

To calculate the fitness of a Data rate gene, we will first calculate the absolute difference 'ABS' of the data rate requested by the application with the data rate of the chosen chromosome, as said in the preceding section and it is shown in Eq. 4.4.

\[
ABS = |(\text{Chromosome's data rate} - \text{Application's data rate})| \quad \text{Eq. 4.4}
\]

To meet the desired QoS requirement of the application, fit chromosomes are needed to be selected and we know that the fitness of the chromosome depends upon the fitness of each gene. From randomly selected chromosomes for the initial population the algorithm will select the fittest in the following manner. For the decision of the fittest chromosome as per its data rate gene we already have defined a Fitness Point 'FP1' which is an integer variable. This 'FP1' will limit the search process of the algorithm on both side of the required data rate band. Now the algorithm will look for the empty bands within this limit.

Using the same general equation and concept defined earlier in this report if the value of 'FP1' is less than the value of \(ABS\), the fitness of the modulation gene will be calculated as shown in Eq. 4.5.

\[
FM \text{ of the Data Rate Gene} = \left[ (GW1 \times ABS) \div FP1 \right] \quad \text{if } FP1 > ABS \quad \text{Eq. 4.5}
\]

Otherwise the fitness of the modulation gene is the respective associated weight described in Table 4.8 and Eq. 4.6 shows how to calculate it.

\[
FM \text{ of the Data Rate Gene} = GW1 \quad \text{if } FP1 \leq ABS \quad \text{Eq. 4.6}
\]

From Table 4.8 and Table 4.9 it is known that the associated gene weight \(GW1\) and fitness point \(FP1\) for modulation gene are 15% and 6 respectively. Hence, the value for \(GW1\) in decimal is equal to 15 for the data rate gene.

Next to better understand the above mention scenario let us consider 2 cases.

**Case 1:** An application’s required data rate is 900Kbps, now within the band of 2Mbps with a step size of 125Kbps there is a total of 16 bands. Table 4.1 shows that the requested data rate band is 7, now from the randomly generated initial population of chromosomes two chromosomes with decimal value 8 and decimal value 15 are chosen for comparison. We already know that the associated weight of the gene is 15 and the defined fitness point is 6.
Now the fitness of the frequency gene will be calculated for both chromosomes one by one using Eq. 4.4 and either Eq. 4.5 or Eq. 4.6.

**Chromosome 1:**

\[ ABS = |8 - 7| = 1 \]

Now \( FP1 > ABS \), so using Eq. 4.5 and putting the values of \( ABS, GW1 \) and \( FP1 \) we get

\[ FM \text{ of Data Rate Gene} = \left[ (15 \times 1) \div 6 \right] \]

\[ FM \text{ of Data Rate Gene} = 2.5 \]

**Chromosome 2:**

\[ ABS = |15 - 7| = 8 \]

Here \( FP1 < ABS \), so the Fitness of the data rate gene is calculated by using Eq. 4.6

\[ FM \text{ of Data Rate Gene} = 15 \]

**Case 2:** For this case the application required data rate is the same i.e. 900Kbps and has the decimal value 7, but this time there are different chromosomes, chromosome 1 has decimal value 6 and chromosome 2 has decimal value 11. Now using the same three equations, the fitness of the frequency gene is calculated. \( FP1 \) and \( GW1 \) have same values.

**Chromosome 1:**

\[ ABS = |6 - 7| = 1 \]

\( FP1 > ABS \), so using Eq. 4.5 the fitness measure is

\[ FM \text{ of Data Rate Gene} = \left[ (15 \times 1) \div 6 \right] \]

\[ FM \text{ of Data Rate Gene} = 2.5 \]

**Chromosome 2:**

\[ ABS = |11 - 7| = 4 \]

Here again, \( FP1 > ABS \) so fitness measure \( FM \) is calculated using Eq.4.4 as well
\[ FM \text{ of Data Rate Gene} = \left( 15 \times 4 \right) \div 6 \]

\[ FM \text{ of Data Rate Gene} = 10 \]

From both cases above we see that the chromosome with a low fitness measure has the data rate band somewhere near to the requested data rate band. So from this result we conclude that the fitness measure result approaching zero will give us the best answer. In both cases, chromosome 1 is selected because of its low fitness value, as it is the best fit for the problem.

For all the other genes almost the same process is repeated, depending upon their respective values of Fitness Points, Associated Weights and Requested Bands.

### 4.4.2. Fitness Measure of the Signal Power Gene

Now for the signal power gene, the absolute difference of the power band requested by the application with the power band of the chromosome is given in equation Eq. 4.7.

\[ ABS = |(Chromosome's \text{ power} - Application's \text{ power})| \quad \text{Eq. 4.7} \]

Now the same pattern as described in the preceding section of the data rate gene, a fitness point 'FP2' is already set that can have any value from 0 to 62. For this thesis work the value of 'FP2' is set to 20 as shown in Table 4.8 and this was done after examining the results with different values.

Just as we had in the data rate frequency measure; if the value of 'FP1' is less than the value of the absolute difference, to calculate the fitness of the power gene we will use Eq. 4.8.

\[ FM \text{ of Signal Power Gene} = \left( GW2 \times ABS \right) \div FP2 \quad \text{if} \ FP2 > ABS \quad \text{Eq. 4.8} \]

Otherwise the fitness measure is calculated using Eq. 4.9

\[ FM \text{ of Signal Power Gene} = GW2 \quad \text{if} \ FP2 \leq ABS \quad \text{Eq. 4.9} \]

Here 'GW2' is the associated weight of the power gene in the chromosome, which has an integer value of 23 as it contains 23% of the total chromosome.

To better understand the scenario let us see two of many possible cases for the power gene.
Case 1: Let us consider an application requiring a signal power of \(-12\text{dBm}\) to transmit, from the power description shown in Table 4.2 we know that the decimal value representing this power value is 19. Now the two randomly selected chromosomes 1 and 2 for this particular example have the decimal values 36 and 23 respectively. Fitness point \('FP2'\) has integer value 20 as mentioned earlier in this part. Now the fitness of the power gene will be calculated for each chromosome using equations 4.7, 4.8 and 4.9 as follows.

Chromosome 1:

\[
\text{ABS} = |36 - 19| = 17
\]

\(FP2 > \text{ABS}\), using Eq. 4.8 and putting the value of \(ABS, GW2\ and FP2\) we get

\[
\text{FM of Signal Power Gene} = \left\lceil \frac{(23 \times 17)}{20} \right\rceil
\]

\(\text{FM of Signal Power Gene} = 19.55\)

Chromosome 2:

\[
\text{ABS} = |23 - 19| = 4
\]

Again \(FP2 > \text{ABS}\) so using Eq. 4.8 and putting the respected values we get

\[
\text{FM of Signal Power Gene} = \left\lceil \frac{(23 \times 4)}{20} \right\rceil
\]

\(\text{FM of Signal Power Gene} = 4.6\)

Case 2: Considering again the same band with a decimal value of 19, let this time the chosen chromosomes 1 and 2 have values 9 and 42 respectively. The values of \('GW2'\ and \('FP2'\) are the same as before. Now by using equations 4.7, 4.8 and 4.9 we get

Chromosome 1:

\[
\text{ABS} = |9 - 19| = 10
\]

\(FP2 > \text{ABS}\), so Eq.4.8 will give us

\[
\text{FM of Signal Power Gene} = \left\lceil \frac{(23 \times 10)}{20} \right\rceil
\]

\(\text{FM of Signal Power Gene} = 11.5\)
Chromosome 2:

\[ ABS = |42 - 19| = 23 \]

Here \( FP2 < ABS \), so using Eq. 4.9 we get

\[ FM \text{ of Signal Power Gene } = 23 \]

Just as the results for the data rate genes, the results for the power gene are the same. It is clearly seen here as well that that the chromosome with the less fitness value for the power gene has the less difference and more resemblance with the requested value of power by the application in both cases. So for the first case chromosome 2 is selected and in the second case chromosome 1 is selected as the best fit chromosomes.

4.4.3. Fitness Measure of the Error Rate Gene

To calculate the fitness of the error rate gene, (here the error rate is the bit error rate (BER) as mentioned in section 4.2.1.3) we will first calculate the absolute difference of the error rate requested by the application with the error rate of the chosen chromosome, as said in the preceding section and it is shown in Eq. 4.10.

\[ ABS = |(\text{Chromosome's Error Rate} - \text{Application's Error Rate})| \quad \text{Eq. 4.10} \]

To meet the desired QoS requirements for the application, fit chromosomes are needed to be select and we know that the fitness of the chromosome depends upon the fitness of each gene. From randomly selected chromosomes for the initial population, the algorithm will select the fittest in the following manner: For the decision of the fittest chromosome as per its error rate gene we already have defined a Fitness Point 'FP3' which is an integer variable.

Using the same general equation and concept defined earlier in this report, if the value of 'FP3' is less than the value of \( ABS \), the fitness of the error rate gene will be calculated as shown in Eq. 4.11.

\[ FM \text{ of Error Rate Gene } = \left( \frac{GW3 \times ABS}{FP3} \right) \quad \text{if } FP3 > ABS \quad \text{Eq. 4.11} \]

Otherwise the fitness measure is the respective associated weight of the gene described in Table 4.8 and Eq. 4.12 shows how to calculate this.

\[ FM \text{ of Error Rate Gene } = GW3 \quad \text{if } FP3 \leq ABS \quad \text{Eq.4.12} \]
From Table 4.8 and Table 4.1 it is known that the associated gene weight 'GW3' and fitness point 'FP3' for the error rate gene are 15 and 7 respectively. Now let us consider 2 cases to explain the above scenario.

**Case 1:** Let us consider that an application requiring a BER of $10^{-7}$ to transmit, and from the error rate description shown in Table 4.3, we know that the decimal value representing this value is 8. Now the two randomly selected chromosomes 1 and 2 for this particular example have the decimal values 12 and 10 respectively. Next the fitness of the error rate gene will be calculated for each chromosome, using equations 4.10, 4.11 and 4.12 as follows.

Chromosome 1:

\[ ABS = |12 - 6| = 6 \]

\[ FP3 > ABS, \quad \text{Eq. 4.11 will give us} \]

\[ FM \ of \ Error \ Rate \ Gene = [(15 \times 6) \div 7] \]

\[ FM \ of \ Error \ Rate \ Gene = 12.85 \]

Chromosome 2:

\[ ABS = |10 - 6| = 4 \]

Again \( FP3 > ABS \) so using Eq. 4.11 and putting the respected values we get

\[ FM \ of \ Error \ Rate \ Gene = [(15 \times 4) \div 7] \]

\[ FM \ of \ Error \ Rate \ Gene = 8.57 \]

**Case 2:** Consider the same error rate with decimal value 6; this time let the chosen chromosomes 1 and 2 have values 15 and 8 respectively. The values of GW3 and FP3 are the same as before.

Chromosome 1:

\[ ABS = |15 - 6| = 9 \]

\[ FP3 < ABS, \quad \text{so Eq. 4.12 will give us} \]
FM of Error Rate Gene = 15

Chromosome 2:

\[ \text{ABS} = |8 - 6| = 2 \]

\[ FP3 > ABS, \text{ using Eq. 4.11 we get} \]

\[ FM \text{ of Error Rate Gene} = \left[ (15 \times 2) \div 7 \right] \]

\[ FM \text{ of Error Rate Gene} = 4.28 \]

Like the data rate gene and the power gene here it's concluded that from these results, the chromosome with less fitness value for the error rate gene has less difference and more resemblance with the requested value of the error rate by the application in both cases. So for both cases chromosome 2 is selected as best fit chromosomes.

4.4.4. Fitness Measure of the Operating Frequency Gene

Now for the frequency gene, the absolute difference of the operating frequency band requested by the application with the operating frequency band of the chromosome, is given in equation Eq. 4.13

\[ \text{ABS} = |(\text{Chromosome's Frequency} - \text{Application's Frequency})| \quad \text{Eq. 4.13} \]

For this thesis work the value of \( 'FP4' \) is set to 200 as shown in table 4.9 and this was done after examining the results with different values.

Just as we had in data rate, power and error rate measures; if the value of \( 'FP4' \) is less than the value of the absolute difference, to calculate the fitness of the frequency gene we will use Eq. 4.14.

\[ FM \text{ of Frequency Gene} = \left[ (GW4 \times \text{ABS}) \div FP4 \right] \quad \text{if } FP4 \leq \text{ABS} \quad \text{Eq. 4.14} \]

Otherwise the fitness measure is calculated using Eq. 4.15

\[ FM \text{ of Frequency Gene} = GW4 \quad \text{if } FP4 > \text{ABS} \quad \text{Eq. 4.15} \]

To better understand the scenario, let us have a look at two of many possible cases for the Operating Frequency gene.
**Case 1:** Let us consider an application requiring a frequency of 11.320-11.360 MHz to operate. From the operating frequency description shown in Table 4.4 we know that the decimal value representing this operating frequency value is 283. Now the two randomly selected chromosomes 1 and 2 for this particular example have the decimal values 347 and 399 respectively. Fitness point 'FP4' has an integer value of 200 as mentioned earlier in this part. Now the fitness of the operating frequency gene will be calculated for each chromosome using equations 4.13, 4.14 and 4.15 as follows.

**Chromosome 1:**

\[
ABS = |347 - 283| = 64
\]

\[FP4 > ABS,\text{ using Eq. } 4.14\text{ and putting the value of } ABS, GW4 \text{ and } FP4 \text{ we get}\]

\[
FM\text{ of Frequency Gene } = \left\lfloor \frac{(35 \times 64)}{200} \right\rfloor
\]

\[
FM\text{ of Frequency Gene } = 11.20
\]

**Chromosome 2:**

\[
ABS = |399 - 283| = 116
\]

Again \( FP4 > ABS \) so using Eq. 4.14 and putting the respected values we get

\[
FM\text{ of Frequency Gene } = \left\lfloor \frac{(35 \times 116)}{200} \right\rfloor
\]

\[
FM\text{ of Frequency Gene } = 20.30
\]

**Case 2:** Consider the same band with decimal value 283; this time let the chosen chromosomes 1 and 2 have values 489 and 300 respectively.

**Chromosome 1:**

\[
ABS = |489 - 283| = 206
\]

\[FP4 < ABS,\text{ so Eq. } 4.15\text{ will give us}\]

\[
FM\text{ of Frequency Gene } = 35
\]
Chromosome 2:

\[
\text{ABS} = |300 - 283| = 17
\]

\[FP4 > \text{ABS},\text{ so using Eq. 4.14 we get}\]

\[FM\ of\ Frequency\ Gene = [(35 \times 17) \div 200]\]

\[FM\ of\ Frequency\ Gene = 2.975\]

Just as the results we had for the data rate genes, the power gene and the error rate gene. It is clearly seen here as well that that the chromosome with the less fitness value for the Operating Frequency gene has the less difference and more resemblance with the requested value of the Operating Frequency by the application in both cases. So for the first case chromosome 1 and the second case chromosome 2 are selected as the best fit chromosomes.

4.4.5. Fitness Measure of the Modulation Technique Gene

Finally, the fitness measure for the Modulation Technique gene; for this we will first calculate the absolute difference (ABS) of the modulation scheme requested by the application with the modulation scheme of the chosen chromosome, as said in the preceding section and it is shown in the Eq. 4.16.

\[\text{ABS} = |(\text{Chromosome's Modulation} - \text{Application's Modulation})|\]  

\[\text{Eq. 4.16}\]

From randomly selected chromosomes for the initial population the algorithm will select the fittest in the following manner: for the decision of the fittest chromosome as per its Modulation Technique gene we already have defined a Fitness Point 'FP5' which is an integer variable. Together with its original purpose of limiting the search process, this fitness point 'FP5' will also give us the optimal solution. It is understood from the previous sections that the fitness measure approaching to zero is optimum which is somehow acceptable because of the random values generated in the GA. But in the modulation technique all the techniques have their own pros and cons so assigning of the same technique as requested by the application or secondary user is the optimum solution. Fitness point 'FP5' is given the integer value 1 and this is done because for the optimum solution, modulation gene required by the application and the chosen chromosome’s gene must have exactly the same value.
Using the same general equation and concept defined earlier in this report if the value of \( FP_5 \) is greater than the value of \( ABS \), the fitness of the modulation gene will be calculated as shown in Eq. 4.17.

\[
FM \text{ of Modulation Gene} = [(GW_5 \times ABS) \div FP_5] \quad \text{if } FP_5 > ABS \quad \text{Eq. 4.17}
\]

Otherwise the fitness of the modulation gene is the respective associated weight described in Table 4.8 and Eq. 4.18 shows how to calculate this.

\[
FM \text{ of Modulation Gene} = GW_5 \quad \text{if } FP_5 \leq ABS \quad \text{Eq. 4.18}
\]

From Table 4.8 it is known that the associated gene weight \( GW_5 \) is 12 and the fitness point \( FP_5 \) has been discussed earlier in this part.

**Case 1:** An application’s required modulation technique is DPSK and Table 4.5 shows that the decimal value assigned to the requested Modulation Technique band is 4. Now from the randomly generated initial population of chromosomes two chromosomes with decimal value 4 and decimal value 5 are chosen for comparison. We already know that associated weight of the gene \( GW_5 \) is 12 and defined fitness \( FP_5 \) is 1. Now fitness of modulation gene will be calculated for both chromosomes one by one using Eq. 4.16 and either Eq. 4.17 or Eq. 4.18.

**Chromosome 1:**

\[
ABS = |4 - 4| = 0
\]

Now here \( FP_5 > ABS \), so using Eq. 4.17 and putting the values of \( ABS, GW_5 \) and \( FP_5 \) we get

\[
FM \text{ of Modulation Gene} = [(12 \times 0) \div 1] 
\]

\[
FM \text{ of Modulation Gene} = 0
\]

**Chromosome 2:**

\[
ABS = |5 - 4| = 1
\]

Here \( FP_5 = ABS \), so fitness of the modulation gene is calculated by using Eq. 4.18

\[
FM \text{ of Modulation Gene} = 12
\]
**Case 2:** For this case the application requires the same Modulation Technique i.e. DPSK and has the decimal value 4; but this time there are different chromosomes, chromosome 1 has decimal value 6 and chromosome 2 has decimal value 7. Now using the same three equations the fitness of the Modulation Technique gene is calculated. FP5 and GW5 have the same values.

**Chromosome 1:**

\[ ABS = |6 - 4| = 2 \]

\[ FP5 > ABS, \] so using Eq. 4.18 the fitness measure is

**FM of Modulation Gene = 12**

**Chromosome 2:**

\[ ABS = |7 - 4| = 3 \]

Here again, \( FP5 < ABS \) so fitness measure FM is calculated using Eq.4.18 as well

**FM of Modulation Gene = 12**

For modulation technique fitness we have a slightly different result. The only optimum result found in the above mentioned cases is of the chromosome’s 1 in case 1. So that would be carried forward to the solution set. For case 2 both chromosomes have the same fitness measure so it doesn’t make any difference if any of them is carried forward. In all other genes the communication is not disturbed if we have a slight difference, but matching the exact modulation technique is always required.

So the chromosome with fitness measure 0 is the optimum in the case of modulation gene.

**4.4.6. Total Fitness Measure of a Chromosome**

So far we have derived the fitness measure for each gene. The next step is to derive the total fitness measure of a chromosome which is used to guide us to an optimal solution. To achieve this optimal solution we have used an aggregated weighted sum approach (Newman, et al. 2007). This aggregated weighted sum (AWS) is the cumulative sum of all the individual fitness measures as shown in Eq. 4.19
\[ \text{AWS} = \text{FM}_D + \text{FM}_P + \text{FM}_E + \text{FM}_F + \text{FM}_M \]

\text{Eq. 4.19}

Where, \( \text{FM}_D \) = fitness measure of data rate gene

\( \text{FM}_P \) = fitness measure of signal power gene

\( \text{FM}_E \) = fitness measure of error rate gene

\( \text{FM}_F \) = fitness measure of operating frequency gene

\( \text{FM}_M \) = fitness measure of modulation gene

As the maximum fitness measure of a chromosome can be 100 so the total fitness of a chromosome is calculated by using Eq. 4.20.

\[ \text{Total Fitness Measure of Chromosome} = 100 - \text{AWS} \]

\text{Eq. 4.20}

From (Withall, et al. 2003), we came to know that the traditional representation of the fitness measure is in some integer or real number value, where the higher the value, the greater the fitness.

To better understand this aggregated weighted sum approach and total fitness measure let us consider an example using the same input values and received fitness measures for each gene of the chromosome from the earlier parts of this report.

The chromosome structure based on the parameter requested by the application and two possible chromosomes from the solution set with their respective fitness measures are shown in Table 4.10.

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Data Rate Value</th>
<th>Signal Power Value</th>
<th>Error Rate Value</th>
<th>Frequency Value</th>
<th>Modulation Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Application Requested</td>
<td>7</td>
<td>19</td>
<td>6</td>
<td>283</td>
<td>4</td>
</tr>
<tr>
<td>Chromosome 1</td>
<td>8</td>
<td>23</td>
<td>8</td>
<td>300</td>
<td>4</td>
</tr>
<tr>
<td>Chromosome 2</td>
<td>15</td>
<td>36</td>
<td>15</td>
<td>489</td>
<td>5</td>
</tr>
</tbody>
</table>

Table 4.10 Respective parameters of requested and resultant chromosomes
Using the information given in section 4.4.1, 4.4.2, 4.4.3, 4.4.4 and 4.4.5 the calculated fitness measures for both the chromosomes are given in Table 4.11.

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Data Rate (FM_DG)</th>
<th>Signal Power (FM_PG)</th>
<th>Error Rate (FM_EG)</th>
<th>Frequency (FM_FG)</th>
<th>Modulation (FM_MG)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chromosome 1</td>
<td>2.5</td>
<td>4.6</td>
<td>4.28</td>
<td>2.97</td>
<td>0</td>
</tr>
<tr>
<td>Chromosome 2</td>
<td>15</td>
<td>19.55</td>
<td>15</td>
<td>35</td>
<td>12</td>
</tr>
</tbody>
</table>

**Table 4.11 Gene’s fitness measures of resultant chromosomes**

First the $AWS$ is calculated by using equation 4.19, and then by using equation 4.20 the percentage of total fitness of these chromosomes are calculated for both the chromosomes.

**Chromosome 1:**

$$AWS = 2.5 + 4.6 + 4.28 + 2.97 + 0$$

$$AWS = 14.35$$

**Total Fitness** $= 100 - 14.35$

**Total Fitness** $= 85.65$

**Chromosome 2:**

$$AWS = 15 + 19.55 + 15 + 35 + 12$$

$$AWS = 96.55$$

**Total Fitness** $= 100 - 96.55$

**Total Fitness** $= 3.45$

These results show that the 1st chromosome is best fit for the optimization solution as all parts of its respective genes have the values approaching zero in comparison to the 2nd chromosome and these results have confirmed our earlier fitness measure calculations for each gene.
4.5. Construction of New Population

Once the Fitness measures for all the genes in the chromosomes are defined and a total fitness has been evaluated for each chromosome, the next step is the construction of the new population. This construction of a new population involves certain genetic operations like selection, crossover and mutation.

4.5.1. Selection

To construct the next generation “Selection” is the first step. According to (Reeves and Rowe 2003) the selection should be related to the fitness measure of the chromosomes. The selection step is the most significant in the GA as the other two steps i.e. crossover and mutation are performed on the chromosomes selected during the selection step. In general it is required that the selection should favour chromosomes which have better fitness measures, but due to randomly generated values poorer chromosomes also have a chance to contribute. Among many well-defined selection methods; roulette wheel selection and tournament selection are used more often. For this thesis work we use "roulette wheel selection" with added "elitism".

4.5.1.1. Elitism

To make the GA converge efficiently a record of the best individual found so far must be maintained throughout the genetic process. Elitism is stated as “the process of selecting ‘the best’ chromosome from the given solution set according to the total fitness measure and adding it to the new solution set without performing crossover and mutation”. Any genetic algorithm can be made elitist by the following alterations (Reeves and Rowe 2003).

1. Record the current best chromosome $k$ in the solution set.
2. If there is nothing better than $k$ in the new solution set, add $k$ to the new solution set, replacing the worst individual.

The best of the previous generation are inserted in place of the worst in the current generation. The number of elite chromosomes is user defined, and for this thesis work by using elitism we have considered only the two best chromosomes to be carried forward to the next generation. The GA will record the best two from the solution set by using a swap operation.
4.5.1.2. **Roulette Wheel Selection**

According to (Reeves and Rowe 2003), the roulette wheel selection method uses a probability distribution in which the selection probability of a given chromosome is directly proportional to its fitness. The probability of selection is given as, if \( f(i) \) is the fitness measure of a chromosome then \( p(i) \) is the probability of the selection for this chromosome and it is given by the fitness measure \( f(i) \) of the respective chromosome divided by the sum of the fitness measures of ‘n’ number of chromosomes present in the solution set as shown in Eq. 4.21.

\[
p(i) = \frac{f(i)}{\sum_{j=1}^{n} f(j)} \quad \text{Eq. 4.21}
\]

Once the probabilities of the selection are calculated, these selection probabilities are allocated slots or shares on the roulette wheel according to their percentage. The roulette wheel is then spun ‘n’ times for n numbers of chromosomes in the population or solution set.

<table>
<thead>
<tr>
<th>Chromosome No.</th>
<th>Total Fitness ( f(i) )</th>
<th>Probability of Selection ( p(i) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>93</td>
<td>29%</td>
</tr>
<tr>
<td>2</td>
<td>55</td>
<td>16%</td>
</tr>
<tr>
<td>3</td>
<td>88</td>
<td>26%</td>
</tr>
<tr>
<td>4</td>
<td>25</td>
<td>8%</td>
</tr>
<tr>
<td>5</td>
<td>70</td>
<td>21%</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>331</strong></td>
<td><strong>100%</strong></td>
</tr>
</tbody>
</table>

*Table 4.12 Solution set with their fitness measures and probabilities of selection*

To better understand the selection process, take the initial population or a possible solution set of 5 chromosomes with their respective total fitness measures and calculated probabilities of selection as an example, as given in Table 4.12. It shows that the Chromosome No. 1 has the maximum fitness value 93 among the pool and Chromosome No. 4 has the minimum fitness value 25 so the corresponding selection probabilities are 29% and 8% respectively.

The possible available share on the simulated roulette wheel for each chromosome in the solution set is shown in Figure 4.2.

From the figure it can be seen that Chromosome No. 1 with the maximum selection probability has occupied the largest space on the wheel whereas Chromosome No. 4 with the minimum selection probability has the smallest share on the wheel. During the spin the
chance to select the chromosome with a large area is always higher than one with a small area. This whole process makes the selection of worst chromosomes nearly impossible.

Using elitism, the two best solutions have already been preserved.

Figure 4.2 Roulette Wheel Section Diagram

4.5.2. Cross Over

Once the fit chromosomes are selected, the next step is to perform crossover (also known as reproduction) on randomly selected chromosomes. Crossover is such a process by which characteristics of any two chromosomes can be exchanged with each other to form two new chromosomes (Hasancebi and Erbatur 2000).

There are several crossover techniques like single point, 2-point, multi-point and uniform crossovers. Furthermore (Hasancebi and Erbatur 2000) stated that numerical testing of mentioned crossover techniques show that 2-point crossover technique produces better solutions as compared to other techniques. So for this thesis work we applied the 2-point crossover technique. As described in section 4.2.1, we used value encoding for our
chromosome structure so we have to develop some crossover specifications. The crossover points are defined at the connection of the genes in the chromosome. Possible crossover cases for the chromosomes with 5 genes are shown in Figure 4.3.

For a proper crossover technique, the crossover rate is also important. Usually the crossover rate is set at 80% to 90%. For this thesis work we consider a 90% crossover rate, which means that the randomly selected 45 pairs of chromosomes (other than the elite) will perform a 2-point crossover process to produce new results. These results are then transferred to the next generation.

From case 1 shown in Figure 4.3, the generation of 2 new children will be done in the following manner: For the first child genes from the beginning of the chromosome to crossover point 1 are copied from chromosome 1, the part from crossover point 1 to crossover point 2 is copied from chromosome 2 and the rest is again copied from chromosome 1. The generation of the second child is the complete reverse of this process, as shown in Figure 4.4.

As the case shown in Figure 4.4, random crossovers will be performed. This will definitely increase the diversity for the new solution set to solve the problem more efficiently.
Figure 4.3 Crossover Cases
4.5.3. Mutation

In GA to maintain the genetic diversity from one generation to the next, mutation is another important operation like selection and crossover discussed earlier. Mutation is applied on the genes of the child just produced after recombination or crossover, altering a binary bit of 0 to 1 or vice versa (Reeves and Rowe 2003). In section 4.2 we described two encodings, value encoding and binary encoding of chromosome for this particular thesis work. Crossover was performed on value encoded (i.e. decimal form) chromosomes but for mutation the chromosomes are needed to be converted to binary form. So the chromosomes after crossover are converted to binary form and mutation is performed. Like crossover, mutation also has a mutation rate i.e. out of 100 chromosomes how many chromosomes are going to mutate. To avoid severe damage on the chromosomal structure of child the mutation rate is kept low, normally around 1% to 5% (Reeves and Rowe 2003). For this research work we have considered a mutation rate of 2%. This means that from the children just created by crossover only 2 will undertake the mutation process. This mutation process with all its possibilities is shown in Figure 4.5. Part (a) shows a child with its decimal representation, in part (b) converted child in the binary representation and the mutation bit is shown by a red arrow. In part (c) the chromosome with the mutated bit is shown which is indicated by a green arrow, and in part (d) the mutated chromosome after the reconversion to decimal is shown.
Figure 4.5 An example of the Mutation Operation

From the above figures it is seen that after the mutation a new chromosome has been produced for the solution set.

The three steps discussed in this section conclude the construction of a new population. A randomly selected initial population of 100 chromosomes for this process is shown in Figure 4.6; chromosomes are assigned colours to differentiate them.
Figure 4.6 Randomly Generated Initial Population

Figure 4.7 shows a newly constructed population, which is completely different from the initial population as the colours shows. This happens because of the genetic operations discussed earlier in this section. The resultant population is diverse and a general assumption is that it will have better individuals than the initial one.

The construction of the new population ends the GA cycle but does not end the process. The process goes on unless a stopping criterion is met (Reeves and Rowe 2003).

This newly constructed population then replaces the previous population and now this population becomes the initial population for the GA. The GA cycle will repeat itself with these steps: fitness measure, selection, crossover and mutation in the same manner as discussed earlier in detail.
### 4.6. Stopping Criteria

The stopping criteria depend upon the user’s own choice depending upon the problem. The optimum stopping criteria is when a solution with best values is achieved. Another stopping criterion is to set a number of generations the GA should produce and after that it is terminated. It is generally observed that a GA usually gives an optimum solution in 50 to 100 generations, and the increase in the number of generation slowdowns the genetic process (Hauris 2007). For this thesis work we have considered 50 generations with a population size of 100 chromosomes per generation. The fitness measure on the final generated population is performed and the best among this population is chosen as the optimum and the final spectrum for the requested application or user.

GA deals with random values so there is always a possibility to choose wrong answers because of the random behaviour. The chosen result may not exactly match the requested values but the values chosen would indubitably be the optimum among the available solution set. There is also a possibility that the resultant values match exactly with the desired values.

The application or user is then allocated the spectrum to use, which can have different values on every request with the same input because of random behaviour.

![Newly constructed population](image)

**Figure 4.7 Newly constructed population**
Chapter 5 Results and Conclusions

This chapter will demonstrate the simulated results and an evaluation of the proposed solution described in the previous chapter. Furthermore the behaviour of genetic algorithms is also discussed in 5.2. The thesis work is concluded in 5.3.

5.1. Simulated Results

To test the proposed solution, a simulation in Matlab is done. For the evaluation of the proposed solution, several inputs are tested. The QoS requirements for the application that a user wants to use are given in Table 5.1. These values are given as the input to the simulation model. It has been stated in 4.1 that a communication link already exists and this work concentrate on the spectrum adaptation mechanism. To better evaluate the simulated model, the same inputs were given 10 times and the results obtained are shown in Table 5.2.

<table>
<thead>
<tr>
<th>Data Rate</th>
<th>Power</th>
<th>Bit Error Rate (BER)</th>
<th>Frequency Band</th>
<th>Modulation scheme</th>
</tr>
</thead>
<tbody>
<tr>
<td>6</td>
<td>30</td>
<td>6</td>
<td>300</td>
<td>4</td>
</tr>
</tbody>
</table>

Table 5.1 QoS requirements of an application given as input to the process

<table>
<thead>
<tr>
<th>Results</th>
<th>R1</th>
<th>R2</th>
<th>R3</th>
<th>R4</th>
<th>R5</th>
<th>R6</th>
<th>R7</th>
<th>R8</th>
<th>R9</th>
<th>R10</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Rate</td>
<td>8</td>
<td>6</td>
<td>9</td>
<td>6</td>
<td>9</td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>9</td>
</tr>
<tr>
<td>Power</td>
<td>34</td>
<td>32</td>
<td>30</td>
<td>30</td>
<td>42</td>
<td>30</td>
<td>37</td>
<td>30</td>
<td>21</td>
<td>30</td>
</tr>
<tr>
<td>Bit Error Rate (BER)</td>
<td>6</td>
<td>3</td>
<td>6</td>
<td>2</td>
<td>6</td>
<td>3</td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>8</td>
</tr>
<tr>
<td>Frequency band</td>
<td>369</td>
<td>300</td>
<td>300</td>
<td>251</td>
<td>300</td>
<td>300</td>
<td>310</td>
<td>320</td>
<td>300</td>
<td>300</td>
</tr>
<tr>
<td>Modulation Scheme</td>
<td>4</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>4</td>
<td>5</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Fitness (%)</td>
<td>82%</td>
<td>79%</td>
<td>93%</td>
<td>74%</td>
<td>79%</td>
<td>82%</td>
<td>81%</td>
<td>98%</td>
<td>90%</td>
<td>88%</td>
</tr>
</tbody>
</table>

Table 5.2 Resultant chromosomes with their fitness measures
Figure 5.1 Fitness measures for each gene of resultant chromosomes

It is noticeable that input values should be in the defined range, as described for each gene in chapter 4. If the value is not in the defined range, an error message will be displayed and the user has to re-enter the values. Figure 5.1 and Figure 5.2 shows the fitness measure plots for the resultant chromosomes and are discussed in 4.4.
Part (a) of Figure 5.1 shows that the fitness of the data rate gene is between 90 to 100 and from 10 results it can been seen that a 100% fitness of the data rate gene is achieved 6 times. In part (b) the fitness of the power gene is shown and we can see that the resultant power values are a little bit less than that of the data rate but this just happens two times out of 10, that the fitness value is below 90 but still there are 5 chromosomes with a 100% result. Like the results for the data rate gene, the error rate (BER) gene is between 90 to 100, with 7 resultant chromosomes with 100% result as shown in part (c). The Operating frequency gene has fitness values between 90 and 100, with 6 chromosomes having a 100% result shown in part (d). The fitness criterion for the modulation gene is slightly different from all the others, and a modulation gene can either have a fitness value of 100. If less, it will have the value hundred minus its associated weight as described in detail in 4.4.5. It is very clearly seen from Figure 5.1(e) that the modulation gene has only two fitness values i.e 100 or 88. Still we have 7 chromosomes with 100% modulation gene fitness.

**Figure 5.2 Total fitness measures of resultant chromosomes**
Figure 5.2 shows the total fitness measures of 10 resultant chromosomes. From the fitness measures for all the resultant chromosomes shown in Figure 5.2, it can be seen that total fitness of the chromosomes is between 70 and 100. Although an ideal solution demands for 100% results, an optimum solution can have values between this range. The results shown in Table 5.2 are the best among the available pool of solution generated in the GA process. In comparison we see that the fitness measures of each gene is almost 90 to 100 for every chromosome. A possible reason for this result is the presence of different genes in the chromosome with their associated weights; another reason is the random behaviour of the GA and due to that at each input with the same values, the GA will generate a totally different result from the previous one which could be better or worse for the problem, but among the solution set the optimum value is chosen each time.

5.2. Analysis of the GA behaviour

To solve an optimization task, the given problem is needed to have a well defined mathematical statement. Many problems can be solve in traditional ways but in cases with a very large solution set and no deterministic solution for a given problem, then an evolutionary computing approach like GA is required.

Still GA does not give a 100% solution of a problem, but it does give a solution which is one of the best for the problem. Due to the random behaviour of GA, no one can predict a 100% solution and its execution time at any stage. The premature convergence of GA is also a big problem in finding a 100% result; in which GA may only find a local minimum and the algorithm just stays in that limit may ignore the optimum solutions. A poor definition of the fitness measure (FM) may also produce a bad solution. In the FM of the chromosome each gene contributes according to their specified gene weight (GW) and fitness point (FM). The FM and GW directly affects the total fitness of the chromosomes and hence the total process.

5.3. Conclusion

The allocation of spectrum bands according to QoS requirements of the applications is one of the main challenges in CR networks. It is not always possible to assign the perfect band due to certain radio and environmental factors. Still the capability to assign the best band among the available bands is an open research topic in CR networks. Keeping these things in mind we proposed a spectrum allocation solution for CR networks that provided the optimum
solution among the available solution set, assuring that the QoS requirements of the application are met.

In the earlier part we discussed the behaviour of GA and its effects. We concluded that a GA does not give a 100% result but it surely gives an optimum solution most of the time, yet there is a possibility that its random behaviour somehow can give a worse solution due to the behaviour discussed in 5.2. There are several steps that can remedy the GA behaviour up to some extent. Starting with the first challenge in consideration, if instead of a random population a proper seeded population is used then the problem of unpredictable results can be minimized. In a seeded initial population, the first half of the population is generated randomly and the second half is generated using the information of the first half. This will result in a less random initial population. Seeding of the population can also become a reason for a second challenge i.e. premature convergence. The premature convergence of GA can be controlled in several ways:

- An increase in the initial population will decrease the chances of premature convergence of the algorithm, but the execution time will increase accordingly.
- The use of more crossover and mutation will also decrease the chances of premature convergence but still this will also randomize the new generations and will also increase the computation time.

The above mentioned possible solutions are very easy to implement but still there is an ambiguity in radio communications, as the time plays an important role and the QoS requirements of an application may put a limit on the required time. Keeping all these aspects in mind it is concluded that the proposed design is a somehow favourable solution for this spectrum allocation problem in a CR. It gives the best solution among the available solutions in time.

5.3.1. Future Work

This thesis work has the research opportunities in both CR and GA fields. In the future, to get a more optimum solution a proper seed for the population can be proposed also a different crossover or mutation mechanism can be designed to increase the performance. Furthermore, a chromosome with more or less genes can be used in which all or a few genes can be interdependent on each other. This work can also be extended from a single secondary user to
multi secondary users. A mechanism can also be defined that can smartly reallocate the spectrum on the detection of a primary user.
Works Cited


