Dynamic Spectrum Allocation for Cognitive Radio
Using Genetic Algorithm

V.Amudha\textsuperscript{1}, G.P.Ramesh\textsuperscript{2}

\textsuperscript{1}Professor Department. of E.C.E, St. Peters University, Avadi, Chennai
\textsuperscript{2}Professor, Department of E C E St. Peters University, Avadi, Chennai

Abstract ——— Cognitive radio (CR) has emerged as a promising solution to the current spectral congestion problem by imparting intelligence to the conventional software defined radio that allows spectrum sharing through opportunistic spectrum access. The principal objective of CR is to optimize the use of under-utilized spectrum through robust and efficient spectrum sensing (SS). In this paper genetic algorithm is used for SS and based on the fitness value primary or secondary users are accessing the spectrum. False alarm found to be only present while secondary user occupying the spectrum with a classification of 100\% for primary and 60\% for secondary

Index Terms—— cognitive radio, false alarm, spectrum sensing.

INTRODUCTION

The higher demand for bandwidth has resulted in spectrum scarcity. Studies show that the spectrum scarcity is due to inefficient use of electromagnetic (EM) spectrum which is in fact available in abundance. This underutilization of the EM spectrum results in a decrease of the spectral efficiency of the wireless networks. To solve this problem cognitive radio has been introduced. CR is defined as a kind of smart radio and the term was first used by Mitola and Magurire\textsuperscript{3}. 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 disturbance to the primary user’s communication. The spectrum is then released after the completion of secondary user communication.

In this paper the spectrum optimisation issue of cognitive radio is considered. As CR is a self organizing system, the EM spectrum organizes according to the Radio Frequency (RF) environment. The organization of EM spectrum involves complex decisions, and the term used in the CR world for this process is called “Spectrum Allocation”. In this paper a spectrum allocation process is introduced in which decisions to assign the spectrum is 802.22, using Genetic Algorithm (GA); an evolutionary computing technique use to solve complex optimization problem. IEEE 802.22 is a standard for Wireless Regional Area Network (WRAN). Development of IEEE 802.22.

WRAN is aimed at using CR technique to allow sharing of unused spectrum utilisation.

The paper is organized as follows, Section I describes why to choose GA for cognitive radio sensing, in Section II, the chromosome is framed. Section III explains how to evaluate GA. Section IV gives the channel assignment using Euclidean distance method. Results of the channel classification is presented in Section V . Conclusion and future scope is discussed in Section VI.

I. PROBLEM FORMULATION

The aim in case of optimization problems is to get an optimal solution but the difficulty is that the search may get complex and one may not identify where to come across for the solution or where to begin with conventional cognitive approaches derived from rule based systems, expert systems, fuzzy logic, and neural networks.

Each approach has severe limitations that reduce their operational value in real-time cognitive radio functions, particularly in changing wireless environments. Rule based systems are limited to predetermined capabilities intended into their own rule set. While fuzzy logic permits approximate solutions to be found in uncertain inputs, the logic has used to locate the approximations does not have a natural evolutionary ability that permits the logic to change in time. The most popular technique for CR modeling is the neural networks, is uncontrollable in that may or may not participate within a set of constraints. Most neural networks involve extensive training to reproduce observed behaviors and usually behave in unexpected ways when problem to solve. The GA inspired cognitive radio model presented in this paper has developed to distribute self-evolution and learning
capabilities in terms of the human cognitive development process.[5]

It has been shown that a genetic algorithm-based engine can provide awareness-processing, decision-making, and learning elements of cognitive functionality [7]. Genetic algorithms (GA) rely upon evolving a set of parameters of the channels are represented in the form of chromosomes.

The main advantage of GA is its random nature and flexibility. Unlike HMM , it does not need any channel prediction state to allot the spectrum. So, the input given to the algorithm will be a trained set of chromosomes. The genetic algorithm approach starts with the definition of the structure of a chromosome. This structure is a sets of genes i.e. frequency, modulation, power and BER in this particular each genes will be considered for the decision-making process fact that a part of the solution. We shall consider the genes from parameters of CR network as IEEE 802.22 discussed in paper[1]. The chromosomes and their ranges are described as follows in table I.

<table>
<thead>
<tr>
<th>Gene parameter</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Frequency (MHz)</td>
<td>40 to 910</td>
</tr>
<tr>
<td>Power (dbm)</td>
<td>-90 to -40</td>
</tr>
<tr>
<td>BER</td>
<td>$10^{-3}$ to $10^{-7}$</td>
</tr>
<tr>
<td>Modulation</td>
<td>BPSK, QPSK, 8-QAM, 16-QAM</td>
</tr>
</tbody>
</table>

For the simplicity of frequency gene, we assumed BW=800 MHz and $B(\text{channel})=8$ MHz frequency band is able to transmit and receive for a particular CR network. The frequency band that we shall consider for this research would range from 40-840 MHz, with a step size = 8MHz, gives integer values ranging from 0 to 100, as provided by the following table II

| Frequency band MHz | 40-48 | 48-56 | ... | 832-840 |

One of the important parameters is power gene that we will consider in the chromosome structure definition. This is required by application to give for a high quality transmission, a power less than that may result in poor transmission. The range of power values specified in IEEE802.22 varies from -90dBm to -40dBm. Chromosome structure definition contains the power gene that would be the 2nd one in the order ranges from -90dBm to -40dBm with a step size of 1 dBm is characterized in the corresponding integer values shows in the following table II.

<table>
<thead>
<tr>
<th>Decimal value</th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>50</th>
</tr>
</thead>
<tbody>
<tr>
<td>Power dBm</td>
<td>-90</td>
<td>-89</td>
<td>...</td>
<td>-40</td>
</tr>
</tbody>
</table>

Another parameter in chromosome’s structure is the bit error rate (BER) defined as ratio of erroneous bits to total transmitted bit. BER may vary depends upon certain service applications. The bit error rates can either be reduced by the use of certain modulation and coding schemes at the receiver and transmitter. One more way to reduce the bit error rates is to increase the transmission power of the device that is limited by FCC. In this paper we will consider the bit error rates ranges $10^{-1}$ to $10^{-9}$ with a step size of $10^1$. This will give us 9 different values of BER. The following table IV shows these values are mapped adjacent to their corresponding BER.

<table>
<thead>
<tr>
<th>Decimal value</th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>9</th>
</tr>
</thead>
<tbody>
<tr>
<td>BER</td>
<td>$10^{-1}$</td>
<td>$10^{-2}$</td>
<td>...</td>
<td>$10^{-9}$</td>
</tr>
</tbody>
</table>

The last of the 4 genes to be considered in structure of definition chromosome is the modulation gene. This paper considers four modulation schemes. These are Binary Phase shift Keying(BPSK), Quadrature Phase Shift Keying (QPSK), Quadrature Amplitude Modulation (8QAM), and 16QAM. To represent these four schemes needs 4 integers as shown in table V.

<table>
<thead>
<tr>
<th>Decimal value</th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>100</th>
</tr>
</thead>
</table>

Table V

Modulation gene representation
The four genes as discussed above, all together define structure of chromosome. The arrangement of all genes in the chromosome structure is shown in table VI.

## Table VI

<table>
<thead>
<tr>
<th>Gene</th>
<th>Frequency</th>
<th>Power</th>
<th>BER</th>
<th>Mod</th>
</tr>
</thead>
<tbody>
<tr>
<td>Order</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>BPSK</td>
<td>QPSK</td>
<td>8QAM</td>
<td>16QAM</td>
<td></td>
</tr>
</tbody>
</table>

III. EVALUATION OF GA

Let us assume that the generation of an initial population size is 10 chromosomes. Further, this population size can be increased up to ‘n’ numbers, if the outcomes are not acceptable, in the supplied solution set. The fitness in the decision-making process is test over randomly generated 1st population of chromosomes, if results are not satisfactory then goes to a number of operations like selection, crossover and mutation to produce the next generation of fittest chromosomes and process repeats until optimal solution found.

The training procedure:

- Generating a set of 20 chromosomes for primary
  - fitness for genes is evaluated
  - fitness for chromosomes is evaluated
  - check for criteria
  - perform crossover and selection
- Iterate the process for certain generations
- Obtain the best chromosome for primary
  - Repeat the procedure to obtain best chromosome for secondary

These four parameters as genes in a chromosome need total of 19 bits. After defining the chromosome structure the next problem is generating the first generation population of chromosomes. A training procedure was implemented to generate 40 chromosomes for the initial population. These chromosomes were trained according to pre assumed primary and secondary users characteristic.

This initial population can have the very best and the worst solutions for the problem. A fitness measure was defined to select the best chromosome from the initial population. Afterwards, selection and crossover were performed that lead us to the new generation of chromosomes. The process was repeated up to a certain number of generations. After that, the process was terminated and the optimum solution was selected.

In this paper, assumption has been made that fitness function that is equally dependent on all the four parameters. The fitness function uses weighted sum approach in GA. All the four parameters set as an equal weight each. The input is given by SU or application for QoS requirements are compared against the population of chromosomes. As discussed earlier, GA has capability of multi objective optimization, so that overall fitness is computed as the cumulative sum of the individual fitness of each parameter (gene) according to the procedure described.[1]

Let parameters x1, x2, x3 and x4 be the frequency gene, power gene, BER gene and modulation gene respectively.

Therefore the fitness function $f_i$ for each gene is calculated by

$$f_i = w_i \frac{|x_i - x_i^d|}{x_i^d}$$

Where $x_i^d$ is the secondary user demand and the value for $d$ taken are 2,4,8. where $i=1,2,3$ and 4 be the gene order of concern parameter as given in table VI. Note that each gene having equal weight i.e. $w = 25\%$, however in true practical case, this will vary according to user’s choice. The overall fitness function value of chromosome $F$ can be calculated as cumulative sum of individual fitness value of all the genes.
The overall fitness value of chromosome in percentages is given by

$$F = \sum_{i=1}^{4} f_i$$

After finding fitness the next step to perform the crossover operation. The crossover operation is carrying out on a pair of chromosomes, selected arbitrarily. A novel method for crossover is performed as follows:

After Cross Over

<table>
<thead>
<tr>
<th>Chromosome 1</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Fre1</td>
<td>Pow1</td>
<td>BER1</td>
<td>Mod1</td>
</tr>
<tr>
<td>Chromosome 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fre2</td>
<td>Pow2</td>
<td>BER2</td>
<td>Mod2</td>
</tr>
</tbody>
</table>

If $t_{o1} < t_{o2}$,
unknown chromosomes are classified to primary.
Same procedure has been repeated for chromosomes with secondary characteristics.

V. RESULTS

The following parameter values of chromosomes have been trained for primary and secondary channel:

For primary:
Frequency band = (49-56) MHz,
Power = -60 to -40 dBm,
BER = $10^{-6}$ to $10^{-9}$,
Modulation = BPSK.

For secondary:
Frequency band = (49-56) MHz,
Power = -90 to -70 dBm,
BER = $10^{-1}$ to $10^{-4}$,
Modulation = BPSK.

Ten iterations were run and results are verified. The output consists of final optimized gene values. It has been verified that the best solution with the fitness value of the gene converging to 0.315 for primary and 0.1 for secondary as shown in figure 2 and 3. It has been also verified that, the larger the fitness value, the better the solution obtained and vice versa, result shows that the best total fitness value (%) turn out to be 68.5% for primary and 90% for secondary.
The performance of GA was compared by substituting different weights and different ‘d’ values for genes of the chromosomes with primary and secondary characteristics. The false alarm rate for 10 unknown chromosomes to primary and secondary was obtained with the help of the euclidean distance method. It is shown in figure 4.

VI. CONCLUSION & FUTURE SCOPE

This work shows that the fitness function of the individual parameters or genes increases with increase in number of generations, but this performance is always not linear. This is due to the existence of other genes in the chromosome structure that affect the decision-making process, to reach an optimal solution. A gene with lesser ‘d’ value gave highest fitness percentage and as the increase in the ‘d’ value the fitness percentage went on decreasing. The optimum solution is achieved with 10 number of generations of the algorithm and the false alarm rate is found. Classification of unknown chromosomes to be primary and secondary was achieved at a success rate of 100% for primary and 60% for secondary using the optimum solution. The possible future work of the research can be the consideration other parameters i.e. Noise, channel coding, throughput, delay, packet error loss, free space loss, data-rate, fading and multipath.

References


Author Biography

Dr. V. Amudha, completed her B.E (ECE) from Madurai Kamaraj University in the year 1994 and M.E in Communication Systems during 2000. Her PhD thesis work is optimization of speech recognition system using FPGA. She authored 4 journal papers and 5 IEEE conference papers. She was sponsored as women scientist by department of Science and Technology, New Delhi during 2005 – 2008, as a part of her PhD thesis work.