# ENHANCING SPECTRUM PRODUCTIVITY THROUGH COGNITIVE RADIOS FACILITATING CELL-BY-CELL DYNAMIC SPECTRUM ALLOCATION

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### ABSTRACT

The cognitive radio technology has been identified as one solution to the apparent spectrum scarcity problem and the deployment of the cognitive radios in a particular cell at a given time depends on the availability of low priority spectrum opportunities. Network operators can generate such opportunities by allocating the spectrum dynamically on a cell by cell basis, considering spectrum as a function of time and space. The cell-by-cell dynamic allocation problem is considered as a NP hard class combinatorial optimisation problem and is very hard to solve by conventional optimisation techniques. Therefore, a genetic algorithm assisted method is proposed in this paper for the cell-by-cell dynamic spectrum allocation. A system level simulator referred "GENEDYSA" has been developed for dynamic spectrum allocation and also for comparison with fixed spectrum allocation scheme. The new scheme outperformed the conventional method in terms of spectral efficiency in both uniform and non-uniform traffic conditions.

### **1. INTRODUCTION**

The ever growing need for mobile communication systems that provide high data rates entrails a significant demand for new spectrum and more efficient use of existing limited spectrum. Several spectral measurement studies conducted in the recent past indicated that frequency spectrum in the range 30 MHz - 3 GHz is most of the time unused and consequently resulting low spectral occupancy. Latest claims by Defiance Advanced Research Projects Agency (DARPA) indicated that in the United States at any given time only 3% of the spectrum is used. Moreover the same claimed has been made by the UK regulator [1]. However, the situation is not critical, if the spectrum is viewed dynamically, as a function of time and space and allocate spectrum according to temporal and spatial traffic demand. Such allocation would increase the overall spectral efficiency of the system and additionally release spare spectrum for deployment of other radio technologies including cognitive radios (CR). As cognitive radios seek

unoccupied spectrum white spaces or secondary unused spectrum of networks for communication, the efficiency of the CR technology is primarily depend on the availability and accessibly of such spectrum bands. A dynamic spectrum allocation (DSA) is a primary means of generating such spectrum holes.

Several dynamic spectrum allocation techniques have been published in the literature [2]-[3] and most of the techniques consider either temporal or spatial traffic variations. However, cell-by-cell DSA method considers both variations simultaneously and therefore indicate better performance over published DSA techniques.

The fundamental idea behind the cell-by-cell scheme is that it only assigns the actual amount of spectrum required in each individual cell. The proposed scheme allocate spectrum every predefined DSA interval based on the anticipated temporal and spatial demands.

The cell-by-cell DSA problem can be considered as a NP-hard class combinatorial optimization problem. For instance, consider an operator with three spectrum carriers, these carriers can be allocated to a base station in seven ways ( $\gamma$ =7), in a multi-base station environment, the possible feasible allocation combinations for twenty base stations (M=20) would be 7<sup>20</sup> ( $\gamma^{M}$ ) and analyzing all these combinations would take several years [4]. However, Genetic algorithms (GA) [5] which are developed based on Darwinian theories have been successfully applied in many NP hard optimization problems [6], and its potential in solving complex optimization problems provided the motivation for this paper.

### 2. GA ASSISTED DYDNAMIC SPECTRUM ALLOCATION

Genetic algorithms are conceptually based on the method that living organisms use to adapt to their environment, known as the process of evolution. They are programmed to work the same way populations solve problems by changing and organizing their component parts using the processes such as reproduction, mutation, and natural selection. The flowchart of the genetic algorithms invoked for spectrum allocation in a WCDMA system is depicted in Figure 1.

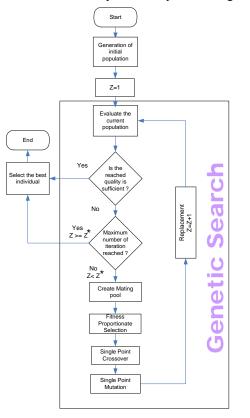


Figure 1: A flowchart depicting the structure of the genetic algorithm

Genetic algorithms work by representing information as a string of digits known as a chromosome. They provide methods of searching all possible combinations of digits to identify the right chromosome representing the best possible structure of the problem. A genetic algorithm commences by generating an initial population of legal chromosomes; each chromosome corresponds to one of the possible solutions in the problem domain. Then individual chromosome in the population is evaluated using a predefined fitness function and ranked them according to their level of desirability as possible solutions. Next, the top best chromosomes that survived (i.e., chromosomes with fitness above a threshold value) are selected to create a mating pool for selection. Thereafter a loop is processed to simulate generations. In each generation, chromosomes are selected probabilistically according to their fitness and then subjected to crossover and mutation to produce new chromosomes to maintain the population size. This process continues until convergence is achieved or it exceeds the maximum number of generations  $(Z^*)$ . The best chromosome in the population is selected and then decoded to obtain the optimal solution. The main components of

genetic algorithms in relation to the dynamic spectrum allocation are described in the following sections.

### 2.1. Chromosome Encoding

The process of mapping solutions into artificial chromosomes is known as encoding, and it has a significant impact on the performance of the genetic algorithm; different encoding schemes leads to dissimilar performances in terms of accuracy and computation time. Several encoding schemes have been proposed in the literature including binary encoding, permutation encoding and value encoding. In this paper, a novel 2D (two dimensional) encoding scheme is used to represent the DSA solutions. Figure 2 illustrates representing a feasible carrier allocation of an eight cell system with three carrier bands (1, 2 and 3).

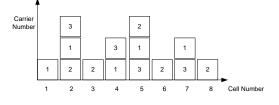


Figure 2: 2D chromosome encoding

#### 2.2. Seeding

Seeding is the process of setting the initial population to some initial configuration. If the population is seeded properly, the performance of a genetic algorithm can be greatly improved. As a genetic algorithm works by probabilistically combining and mutating, the number of iterations could be significantly reduced if the population is initially preset to good solutions.

### 2.2. Fitness Function

A fitness function plays a major role in genetic algorithms and serves as the only link between the problem and the algorithm. It evaluates each chromosome and assigns a numerical value, which is used to rank solutions in the population: the higher the value the better the solution. Moreover, better individuals have a better chance for survival and engage in reproduction to generate far better solutions. The fitness function (Z) proposed for the cell-bycell DSA scheme can be expressed as:

$$Z = \varphi \sum_{m=1}^{M} e^{\frac{|\lambda_m - d_m|}{-\gamma}}$$

where  $\lambda_m$  and  $d_m$  are the allocated capacity and projected demand of the  $m^{th}$  cell for the next DSA period respectively. *M* is the total number of cells in the system and  $\varphi$  and  $\gamma$  are constants that control the degree of scaling and must be selected appropriately, otherwise the fitness values would

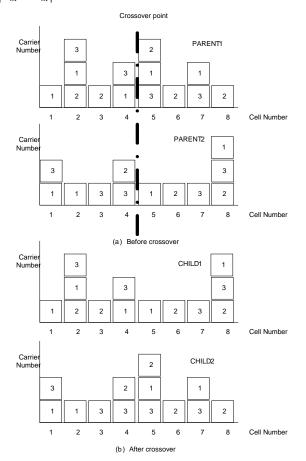


Figure 3: Single-point crossover process

Assuming closed loop power control, the projected uplink cell capacity ( $\lambda_m$ ) considering both same cell and other cell interferences can be estimated using the following equation [7].

$$\lambda_m = 1 + \frac{(W/R)}{\alpha (E_b/N_0)} - 0.047 \sum_{q=1}^6 M_q \qquad \forall m$$

where W is the bandwidth R is the data rate.  $\alpha$  is the voice activity factor,  $E_b$  is the energy per bit and  $N_0$  is the noise power spectral density.  $M_q$  is the number of terminals in  $q^{th}$ neighbouring cell in the first tier of the considered cell.

#### 2.3. Selection

There are many ways in which a new population can be generated from the previous population. However, regardless of what method is used, it is imperative that chromosomes having higher fitness values in a given mating pool must be offer a better chance of reproducing offspring in the subsequent generations, than the lower-fitness chromosomes in the same pool. The task of selecting these individuals for reproduction is performed by a selection mechanism. There are many different selection strategies available to implement the selection process. The most widely used selection scheme, the roulette wheel selection [8] is employed in the simulator.

#### 2.4. Crossover

A crossover process combines two chromosomes (parents) and produces entirely new chromosomes (children). The idea behind crossover is that the new chromosomes may be better than both of the parents, if it takes the better attributes of the both parents. Numerous crossover methods have been proposed in the GA literature and the simplest crossover method called single point crossover [8] is used in this study. Figure 3 illustrates an example of the single point crossover process for the proposed 2D chromosomes. As the name implies, a single point crossover operation uses one randomly chosen cross-over point and once it is selected, two parents are then interchanged at this point to produce new chromosomes Fig. 3(b). The newly generated chromosomes consist of some attributes of both parents and they are significantly different to their parents. Generally, crossover occurs during evolution according to a specified probability and typically the value lies between 0.8 and 0.9.

#### 2.5. Termination

The exact structure of the search domain is often unknown in optimization problems. Hence in the search algorithms, with the exception of an exhaustive search, it is typically difficult to ensure that the optimum solution can be found. There are numerous ways of determining the termination criterion for genetic algorithms. In this case, generation number is used as the termination criterion.

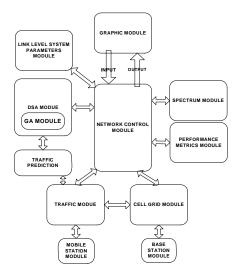


Figure 4: Block diagram of the cell-by-cell system simulator

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#### **3. SYSTEM SIMULATOR**

In order to evaluate the performance of the GA base cell-bycell DSA algorithm, a system simulator referred "GENEDYSA" (Genetic based Dynamic Spectrum Allocation) has been developed and implemented in MATLAB<sup>®</sup>. The simulator consists of several functional modules and Figure 4 shows the general block diagram of the system simulator.

SPECRITHUM BANDS	GA PARAMETERS	CELL GRID	
Casas Bendwidth UTBMId)   01 5 1520 1524   01 5 1525 1525   01 5 1525 1524   04 5 1525 1525   05 5 1505 1526   05 5 1505 1526   06 5 1505 1562   07 1.25 1587 1560.25   08 1.27 1587 1500.25   09 2.75 1574 1577.75	Pop Size 100   Elicen(%) 5   Cross Podi (%) 100   Mutation Prob (%) 1   No of Generations 100   Generation No. 100	No of Cells (s) 5 No of Cells (s) 2 UMTS cell radiu(tin) 1 Cell Geometry Cellslar 4 Hotspot selection Robinsetty 4	Simulation Clock, Min.) 145.121 Test Eligored (Min.) 173.251
08 1/5 19/4 19/7/5   10 5 1900 1904   11 5 1905 1909   12 5 1900 1994   13 20 2000 2020   14 20 2040 2060	PERFORMANCE METHICS Overal Blocking rate 440009 Overal Dispong rate 11,61489 Overal unitarities units 10,005	SYSTEM PARAMETERS   Dr Rule 122   Eb/NO 6.5	INITIALIZE SPECTRUM CELL GRID
TRAFFIC PARAMETERS	Overall satisfaction ratio 80.695 Spectrum Utilisation 90.1209 factor (31)	Voice Activity 0.67 factor	TRAFFIC
Anival rate 6000	Spectral efficiency (1) 84.96/96	DSA PARAMETERS	FSA
al Duration 120 No. of Hotipute 3 Demand(1) HS 10 Handaver (3) 10	Handover nationality sate(%)	DSA Interval 15 Min Sexulation period 2 Hourt Current DSA 0	DSA RESET

Figure 5: Screenshot of the GENEDYSA program front end

### 4. EXPERIMENTAL RESULTS

The results presented in this section were obtained from GENEDYSA system simulator. A screen shot of the front end of the simulator is shown in Figure 5.

#### 4.1. Simulation Parameters

Performance of the cell-by-cell DSA was investigated against the conventional fixed spectrum allocation (FSA) in a WCDMA cellular network comprising 20 transmitters (cells) and three carriers of each 5 MHz bandwidth (3x 5MHz). The reason for selecting only three carriers is twofold: firstly, the maximum number of carriers an operator owned based on the current UK allocation is three, and secondly to maintain an acceptable computational load. Two types of mobile terminals namely moving and stationary were considered and the number of moving terminals was set to 20% of the total mobiles in the system and they were subjected to handover to neighboring cells during the course of simulation. The initial location of the users was defined at the beginning of the simulator, which specifies the geographic traffic weighing. The other network parameters are listed in Table 1. GENEDYSA supports both static and dynamic hotspots, which are referred to as unexpected rise of traffic density of a cell. A cellular network with three dynamic hotspots was considered in this study, particularly to measure the performance benefits that the proposed DSA could gain over the conventional FSA.

Parameter	Value	
No. of base stations	20	
Cell radius	1km	
Path loss exponent	-3.5	
Threshold $E_b/N_0$ (uplink)	6.5dB	
Antenna type	Omni-directional	
Number of carriers	3	
Carrier bandwidth	5MHz	
Handover percentage	10%	
Average call duration	120sec.	
Voice activity factor	0.66	
Chip rate	3.84Mchip/s	
Traffic class	Voice	
Bit rate	12.2kbps	
Mobile transmit power	24dBm	
Simulation time	8hrs	
DSA interval	15min.	
Number of hotspots	3	
Hotspot type	dynamic	

Table 1: Network simulation parameters

As the proposed DSA scheme is based on the GA, a proper configuration of GA parameters is crucial for better performance. In the context of genetic algorithms, there are several parameters that are important. These parameters and the selected values based on the pervious experiments are listed in Table 2.

Parameter	Value
Individual initialization method	random
Selection method	Roulette wheel
Cross-over operation	Single-point
Mutation operation	single point mutation
Elitism	5%
Population size	100
Mating pool size (P)	0.8*P
Crossover probability	0.80
Mutation probability	0.01
Number of Generations	1000

Table 2: Configuration of the GA

Several performance metrics can be used to compare the two spectrum allocation schemes. Previously defined measures including quality of service (QoS) [9] and spectral efficiency gain ( $\Lambda$ ) [10] were used in this study and mathematically expressed as follows:

$$\Lambda = \left(\frac{\zeta_{DSA}^{98\%} - \zeta_{FSA}^{98\%}}{\zeta_{DSA}^{98\%}}\right) \times 100$$

where  $\zeta_{DSA}^{98\%}$  is the user density of the dynamic spectrum allocation at 98% quality of service measured in users/cell/hour, and  $\zeta_{FSA}^{98\%}$  is the user density of the fixed spectrum allocation at 98% QoS

#### 4.2. Simulation Results

Fig. 6 shows the QoS variation verses offered traffic load under non-uniform traffic distributions. Three randomly selected dynamic hotspots were considered and they were alive for 1-2 hours, commencing at different DSA intervals during the eight hour simulation period. Both DSA and FSA exhibits decrease in QoS as the traffic load increases; however, the rate of decrease of DSA is much lower than the FSA. According to the Fig. 6, the maximum user densities that can be supported by DSA and FSA schemes at 98% QoS are 170 and 100 Ms/cell/hour respectively. This indicates that the cell-by-cell DSA can support extra 70 more users/cell/hour than the FSA scheme giving a spectral efficiency of 42%. This is a 4% higher than the previously studied contiguous dynamic spectrum allocation [10].

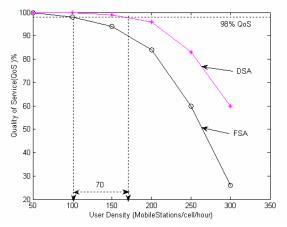


Figure 6: QoS variation verses user density (with hotspots)

Fig. 7 displays the spectrum allocation with respect to time and space for the dynamic hotspot scenario. As the DSA interval is 15 minutes, there were thirty two DSA allocations during the eight hour period. As expected, the cell-by-cell scheme has allocated the minimum enquired amount of spectrum closely following both temporal and special traffic variations. For the three hotspots (cell 5, 11 and 18), maximum available spectrum of 15MHz (3x5MHz) were assigned at 15, 20 and 24 DSA periods. These allocations can be clearly visible in the contour plot with bright white patches. In addition to that, there are number of cells where only two carriers (2x5MHz) were used depending on the number of handovers, which were scattered in space and time domain. According to the plot, it seems that most of the cells required only one carrier (5MHz) to provide the required QoS. This clearly indicates the amount of spare spectrum could be used for secondary usage with the advent of the proposed genetic based cell-bycell DSA scheme.

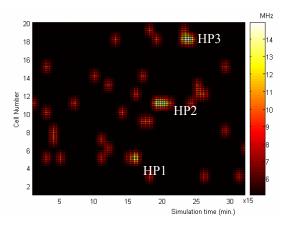


Figure 7: Spectrum allocation map (HP-hotspot)

### 5. CONCLUSIONS

A genetic algorithm based cell-by-cell DSA scheme has been studied in this paper to enhance system spectral efficiency while minimizing the spectrum usage, specifically to release network's spare spectrum for the benefit of cognitive radios. A novel 2D encoding scheme was proposed to map the DSA problem into artificial chromosomes, which significantly increase the convergence time as scheme prevents forming illegal chromosomes. The DSA scheme showed a spectral efficiency gain of 42% over FSA under a non-uniform traffic distribution. This study presents the first step towards understanding the application of genetic algorithms as a solution approach to the cell-bycell dynamic spectrum allocation. The developed simulator, GENEDYSA at this stage only supports a single radio access network and in future, the simulator will be extended to handle multi radio technologies.

#### 6. ACKNOWLEDMENT

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