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Cognitive Radio Networks (CRN): Resource Allocation Techniques based on DNA-inspired Computing

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***Abstract*—**Spectrum is a scarce commodity, and considering the spectrum scarcity faced by the wireless-based service providers led to high congestion levels. Technical inefficiencies from pooled, since all networks share a common pool of channels, exhausting the available channels will force networks to block the services. Researchers found that cognitive radio (CR) technology may resolve the spectrum scarcity. A CR is a self-configuring entity in a wireless networking that senses its environment, tracks changes, and frequently exchanges information with their networks. However, CRN facing challenges and condition become worst while tracks changes i.e. reallocation of another under-utilized channels while primary network user arrives. In this paper, channels or resource reallocation technique based on DNA-inspired computing algorithm for CRN has been proposed.

***Keywords*—**Ad hoc networks, channels reallocation, cognitive radio, DNA local sequence alignment**.**

I. Introduction

THE unlicensed 2.4 GHz and 5 GHz wireless bands are limited by the number of non-interfering channels available, and most wireless-based networking equipment use the same frequency band. These bands seem to be over-crowded by different players of wireless networks. The most of the exploitable frequency spectrum already has been assigned for licensed user, resulting in a scarcity of spectrum for new players. To resolve this problem, the U.S. Federal Communications Commission (FCC) classifies the problem in three ways [1]: spectrum reallocation, spectrum leases, and spectrum sharing. In spectrum reallocation, bandwidth from long-standing users is reassigned to new wireless services such as mobile phone, broadband Internet and video streaming. Where as spectrum reallocation focused on improving the efficiency of spectrum usage. The FCC is considering a new spectrum-sharing pattern, where licensed bands are opened to unlicensed operations on a non-interference basis. Because some licensed bands (such as TV bands) are under-utilized, spectrum sharing in empty sections of these licensed bands can fill the spectrum scarcity problem. This spectrum-sharing model frequently referred to as dynamic spectrum access (DSA). Licensed users are referred to primary users (PU), whereas unlicensed users that access spectrum opportunistically are referred as secondary users (SU). The under-utilized spectrum can be views as spectrum holes [2]: A spectrum hole is a frequencies band assigned to a primary user, but, at a particular time and particular geographic location, is not utilizing the band. The spectrum utilization can be improved particularly by making it possible for a secondary user to access a spectrum hole. The spectrum holes have been utilized to encourage the efficient use of the spectrum by the use of cognitive radio technology. This new research domain of cognitive radio (CR) networks to promote spectrum efficiency. The idea of CR networks is that the secondary users (SUs) need to vacate the band once as the arrivals of primary user (PU). CR networks, however, facing difficulty due to the variation in the spectrum holes as well as unlike quality of service (QoS)[3]. A suitable description is also found in paper [4]: "Cognitive radio is an intelligent wireless communication system that is aware of its surrounding environment i.e. its outside world, and uses the methodology of understanding-by structure to learn from the surroundings and adapt its internal states to statistical variations in the incoming radio frequency (RF) stimuli by making corresponding changes in certain operating parameters e.g. transmit power, carrier frequency, and modulation strategy in real time. A CR is a Software defined radio (SDR) that additionally senses its environment, tracks changes, and possibly reacts upon its findings. The technology of cognitive radio (CR) plays an important role in realizing the DSA paradigm. In addition, a CR can learn from its environment and intelligently adjust its operating parameters based on what was learned. In DSA, CR users (SU) must be able to scan a certain spectrum range and intelligently decide which spectrum band to use for its transmission. During spectrum sensing, if a SU detects the presence of PU's at particular band, it stops accessing that band and searches for another empty band or spectrum hole that is accessible called channel reallocation. If no PUs is detected, the SU coordinates with other SU to share the spectrum holes. Depending on the operation scenario, the SU can employ either cellular network architecture or an ad hoc network architecture [5]. The

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intelligence of CR is embedded in physical [PHY] and medium access control [MAC] layers of SU to work effectively. A cellular CR network architecture is employed in the IEEE 802.22 standard that specifies the air interface for a CR-based wireless regional area network (WRAN). A WRAN cell is composed of a base station and a number of consumer premise equipments, and the coverage of a WRAN cell can range from tens of kilometers to a hundred kilometers. In contrast, a CRAHN is comprised of low-energy mobile computing devices equipped with CRs, and they interact with each other via multihop wireless links. Although these two types of CR networks have different network architectures, spectrum sensing and reallocation is an essential component of both, and it represents one of the key technological hurdles that must be overcome before the widespread deployment of CR networks is possible.

This paper presents a channels reallocation optimization method for user of CRN (SU) based on DNA-inspired computing by means of DNA local sequence alignment algorithm, which is most computationally efficient, compare to other existing complex and crushing technique.

The rest of the paper is organized as follows: Section-II discusses the problems of game theoretic optimization methods of spectrum reallocation and section-II describes DNA local sequence alignment optimization method for channels reallocation and mat lab simulation results with discussions. Finally conclusion and future work are discussed in Section IV.

II. Problem formulation

In this section we first review and analyze the problems of general model of game theory for spectrum of channels reallocation optimization method used in cognitive radio. The objective in of optimization tasks is to achieve an optimum solution but the problem is that the search may get complex and one may not recognize where to come across for the solution or where to start with. There are many methods of game theory that can help finding a fitting solution but the result might not be the best one [5].

Game theory is used for interactive decision conditions provide systematic tools to predict the outcome of composite interactions between the rational entities based on apparent result. It works on predictions of probabilities but stress for a precise awareness of the total number of nodes, but the dynamic nature of real-time networks one doesn't even have the knowledge of what users of CRN do enter or disappear the network and at real time. Also, the definition of a steady state and fear form an undesirable flow with increasing number of user of CRNs may cause suspicions and may make the realization of game theory concept in the cognitive radios is very complicated. The dimension of the system state in a stochastic game is exponential to the number of users of the system, so that the convergence speed of algorithm suffers badly when the system has large number of users of CRN for channel reallocation. The game theoretic approaches can achieve the Nash equilibrium, they cannot guarantee the Pareto optimum, leading to lower network capacity [5]-[7].

Although condition will be worst in above model while SU has already allocated a channel of spectrum hole and suddenly PU arrives then SU has to relinquish that channel as soon as possible and reallocates to another channel of spectrum holes. As shown in Figure 1 [4], Dynamic spectrum-sharing for four channels, and the way in which the spectrum manager allocates the channel bandwidths for three time instants $t_1 > t_2 > t_2$, depending on the availability of spectrum holes. Here once channel has allocated to SU but at next moment PU arrives then reallocation of SU to another band is very complicated task in order to avoid interference or collision.

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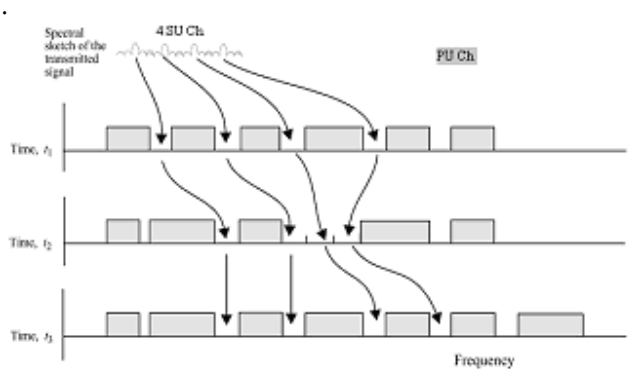


Fig. 1 Dynamic spectrum sharing for four channels

This reallocation task in the cognitive radio research area is still challenging [8]. A novel robust and less computational algorithm based on DNA local sequence alignment scheme for this task has been proposed in next section.

III. Problem solution

In this section we first discuss the background of DNA local sequence alignment algorithms and then implementation of proposed solution model on the signal processing of CRNs along with simulation results.

A. Background of DNA local sequence alignment scheme

Sequence alignment is an important tool in bioinformatics, text, and signal processing. It is capable of identifying the similar and diverged region between two biological DNA sequences or text string. The recent availability of new, less expensive high-throughput DNA sequencing technologies frequently analyses sequence data. From the biological point of view matches may be turn out to be similar function i.e. homology pairs and conserved region while mismatches may detect functional differences [9]. The standard local sequence alignment algorithm, referred to as Smith-Waterman (SW) Algorithm derived from dynamic programming approach [10]-[12]. Before discussing this algorithm, it's important to first understand the basic DNA (deoxyribonucleic acid) molecule that are used in computational biology. DNA sequences are strings from a 4-letter alphabet of nucleotides: adenine (A), thymine (T), guanine (G), and cytosine (C)[11].

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Let us denote DNA sequence as $S = \{s_1, \ldots, s_n\}$ and assume that a nucleotide s occurs at random with probability p_s, independent of all other nucleotides in the sequence. Then the probability ρ of the occurrence of such a sequence of length n is given by

$$\prod_{i=1}^{n} \rho \tag{1}$$

A local sequence alignment is the best (highest scoring) alignment of a sub-string of X to a sub-string of Y. It is usually the case that only part of two sequences is notably similar, so those parts must be recognized.
Given two sequences X = AACCCTA and Y = AGCCTT can be expressed mathematically as;

$$X = \{x_i\}_{i=1}^{m} \text{ and } Y = \{y_j\}_{j=1}^{n} \tag{2}$$

Where *m* and *n* is the total length of string sequence X and Y respectively, where as x and y is the nucleotides. The comparison between two sequences using a SW algorithm approach [12], the initial step is to align one of the sequences across the columns of the matrix, and the other sequence across the rows. The pseudocode of the Smith-Waterman algorithm is as follows which gives the scoring matrix that is used to find the optimal alignment between X and Y.

Input: Two sequences X and Y of length m and n, respectively;

Scoring matrix $\sigma(a, b)$; linear gap penalty W.

Output: matrix M.

Initialization:

$$M(0, 0) = 0.$$

for $i = 1$ **to** m

$$M(i, 0) = 0.$$

for $j = 1$ **to** n

$$M(0, j) = 0.$$

Recursion:

for $i = 1$ **to** m

for $j = 1$ **to** n

$$M(i, j) = \max\{0, M(i-1, j-1) + \sigma(x_i, x_j),$$

match/mismatch in the diagonal.

$$M(i-1, j) - W, \quad \text{\# gap in sequence } X.$$

$$M(i, j-1) - W.\} \quad \text{\# gap in sequence } Y.$$

If gaps are allowed in the sequences, then the potential length of both the first and second sequences is *m+n*. This method needs three steps to finish i.e. initialization step, matrix fill step, and trace-back step respectively for local sequence alignment as desired. Since it is likely to begin an alignment with a gap, the algorithm builds an $(n+1) \times (m+1)$ matrix M. With this pseudocode and the scoring function given in Table 1, the entire first row and first column of the comparison matrix, M, will attain a value of zero and a sample of results at the selected iteration shown in Fig. 2 gives the final comparison matrix, M, based on the penalty and scoring criteria in Table 1 [13].

TABLE 1
SCORING FUNCTION

$\sigma(x_i, x_j)$	Score
Match ($x_i = y_j$)	+1
Mismatch ($x_i \neq y_j$)	0
Gap (W)	-1

M		A	A	C	C	C	T	T
	0	0	0	0	0	0	0	0
A	0	1	1	0	0	0	0	1
G	0	0	1	1	0	0	0	0
C	0	0	0	2	2	1	0	0
C	0	0	0	1	3	3	2	1
T	0	0	0	0	2	3	4	3
T	0	0	0	0	1	2	4	4

Fig. 2 Final comparison matrix

Once the M matrix is computed, from Figure 2, one can observed that the highest score for any alignment of nucleotides in the lower right hand side corner of the matrix. To take out the alignment information, one begins from the right side of bottom cell, and compare the value with the immediate left, immediate top, and upper left diagonal to see which it came from. A general rule of thumb is to track the diagonal path whenever possible in the case of a tie. If trace back is reached on an upper left diagonal cell, then x_i and y_j are aligned, if it is the immediate left cell, then x_i is aligned with a gap, and in the case of immediate top, y_j is aligned with a gap. If we trace back the highlighted path in Fig. 2, then the resultant alignment is shown in Fig. 3.

It can easily observe that how the local sequence alignment tool based on Smith-Waterman algorithm aligned the two sequences for analysis of their performance and characteristics. Since string of sequence *X* can be views as channels (Ch1 to Ch7) of PUs and sequence *Y* as channels (Ch1 to Ch6) of SUs, shown in Fig. 3.

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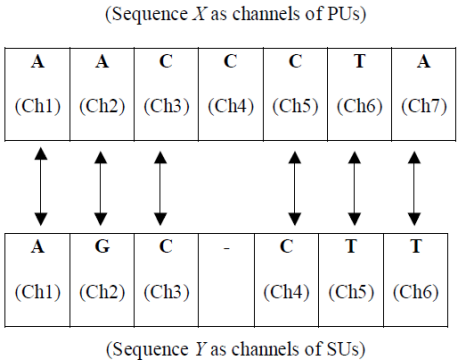


Fig. 3 Alignment of two sequences

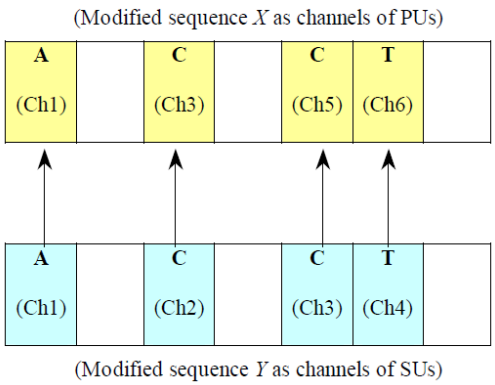


Fig. 4 Modified sequence for SUs and PUs

Therefore this algorithm can be little modified to gives the results as CR desired, shown in Figure 4. This is easily implemented on CRNs to set-up knowledgeable relation between PUs and SUs in terms of channel reallocation has been explained in next following section.

B. Proposed solution model and assumptions

We consider PUs as inheritance device that accesses a block of spectrum through assigned stationary channels. This is a universal tender in various licensed spectrum bands. For example, a TV channel has a bandwidth of 6 MHz and there are more than 100 TV channels [14]. By use of spectrum sensing technique [15], it has been observed that at any instant, each channel can be in either an active or idle state, which refers respectively to times when a PU occupies the channel or does not. From equation (1), we can assume that the channel states are statistically independent and having total of *m* frequency channels $S = \{s_1, ..., s_n\}$ can be views the total primary users $\mathrm{PU} = \{PU_1, ..., PU_m\}$ in the frequency channels. These primary users can only engage their respective assigned frequency channels. Since the primary users are licensed users, they are provided with an interference-free environment [4]. Similarly, we can assume that the *n* secondary users $\mathrm{SU} = \{SU_1, ..., SU_n\}$ transmitting their own data in the system. From equation (2), **PU** and **SU** can be viewed as DNA sequences **X** and **Y** respectively. Averaged power of the frequency channels $\{PU_1, ..., PU_m\}$ and $\{SU_1, ..., SU_n\}$ can be mapped with nucleotides A, C, G and T of DNA sequence as CRNs desired [16]. In IEEE 802.22 a CR terminal is allowed to use a radio communication channel with a bandwidth of channel ranges 6 to 8 MHz in the frequency range between 41 MHz and 910 MHz [17], but in CRNs, channel ranges can be up to 22 MHz. In Fig. 5 the received signal power per frequency averaged over a sensing period *t* is depicted and wide frequency ranges are characterized by very low average signal energy [17].

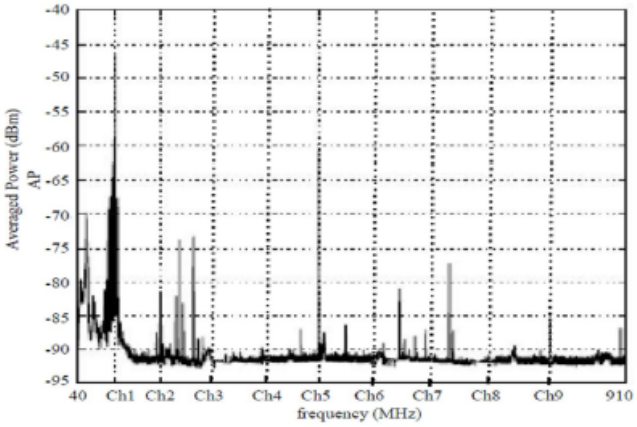


Fig. 5 Received signal power per frequency

During this period the channel is not allocated by the licensed user and is thus an attractive candidate for CR usage. In order to detect such periods that are also known as white spaces a suitable observation of wide frequency ranges has to be provided. As can be observed in Fig. 5, the depict signal possesses a high dynamic range. During measurements a maximum signal power of − 41.8 dBm at channel 1 was observed. The general noise level measured in unallocated sub-bands is − 92 dBm. Therefore, all the channels are mapped with A, C, G and T.

TABLE II
MAPPING CHANNELS WITH NUCLEOTIDES

Channels $i = 1, 2, \ldots, m.$	Nucleotides	Value	Averaged power range
Ch_i	A	1	AP ≤ -90 dBm (Channels are idle or may contains noise);
Ch_i	C	2	-90 dBm < AP ≤ -80 dBm
Ch_i	G	3	-80 dBm < AP ≤ -70 dBm
Ch_i	T	4	AP> -70 dBm

From Fig. 5, assumption has been made for channels of PUs as given in Table 2, so that the PUs channel can be transformed to DNA sequence *X* depicted in Fig. 6.

T	C	A	A	G	A	A	A	G
Ch1	Ch2	Ch3	Ch4	Ch5	Ch6	Ch7	Ch8	Ch9

Fig. 6 PUs channel transformed as DNA sequence

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Here nucleotide A is most required candidate for SUs channels. The availability of channel for SUs depends upon idle state of PUs with respect to time *t*. On the SUs point of view, transmitter power of channels can be mapped with A, C, G, and T according to required power but should not exceed as direction of FCC [1], so that sequence of SUs channel can be formed as *Y*. Therefore, these two sequences has been aligned using S-W algorithm and can be adopted in physical [PHY] and media access control [MAC] layer of CRN to work efficiently for reallocation of SUs channel [18]. Matlab simulation and results are demonstrated in next following section.

C. Simulation and results

In this section we have analysed the simulation and its result based on S-W optimisation algorithm.

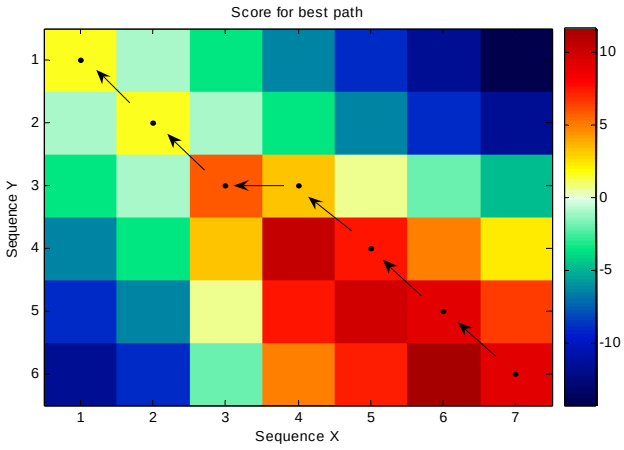


Fig. 7 Previous examples depicted in Fig. 2 are realized by matlab simulation

Let us consider at time instant t_1, PUs sequence assumed to be initially 9 available channels as sequence X = TCAAGAAAG and simulation results shown in Fig. 8 has compared with Fig. 5 and Table 2. It has been observed that there are 5 unused channels on PUs side. SUs sequence assumed to be as sequence Y = AAAAA for convenience and simulation of resultant alignment of X and Y in terms of channels allocation for SUs has been shown in Fig. 9. We observed that unused 5 channels of PUs are allocated to SUs channels where as solid lines represents SUs channels and broken line viewed as busy channels of PUs.

Now at time instant t_2, it is assumed that the PUs has changes dynamically as X = TAAAGAGAG and simulation of resultant alignment of X and Y in terms of channel reallocation for SUs shown in Fig. 10. It can be easily observe that the availability of unused channels has been changed dynamically and reallocated to SUs on unused channels.

Similarly, at time instant t_3, assumed that again PUs has changes dynamically as X = AACAGATAG and simulation of resultant alignment of X and Y in terms of channel reallocation for SUs shown in Fig. 11, which gives the same result as explained above.

We also examine a case where unused channels on PUs are less than the channels required by SUs. Let at time instant t_4, X = ACGATAGTC, resultant simulation is shown in Fig. 12. We observed that only 3 channels for SUs has been reallocated and remaining two channels has either not allowed or to be wait until PUs have enough unused channel sensed by spectrum sensing technique discussed in [15].

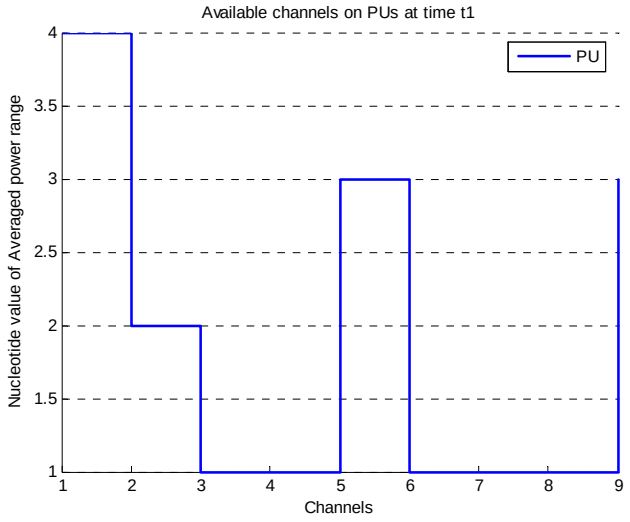


Fig. 8 Available channel on PUs at time instant t_1

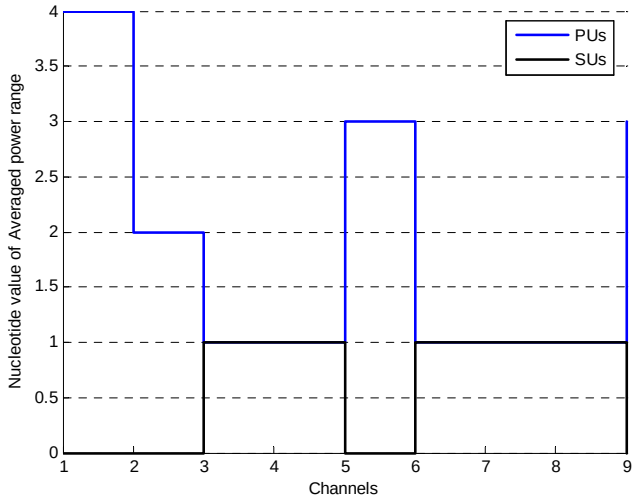


Fig. 9 SU's Channel allocation at PUs at time instant t_1

IV. Conclusions

Researchers all over the world are trying to find out the best solution to develop a wireless communications system that would be able to realize the requirements for a cognitive radio system. It has been seen that CR is the emerging spectrum sharing technology and can be the best option for next generation wireless networks as CRN, since present spectrum crisis and uneven use of spectrum.

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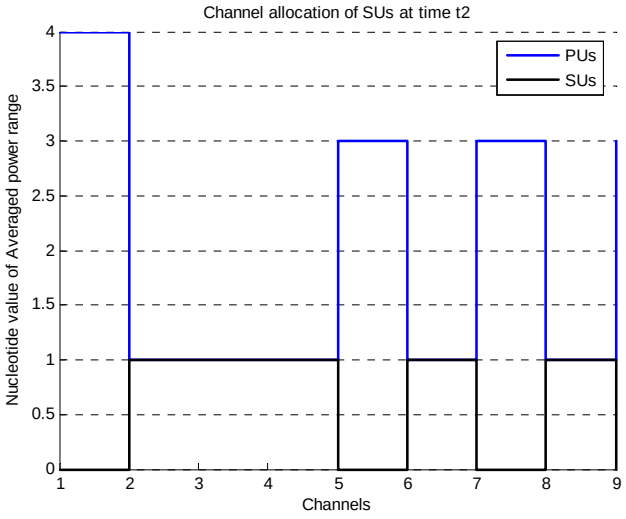


Fig. 10 SU's Channel allocation at PUs at time instant t_2

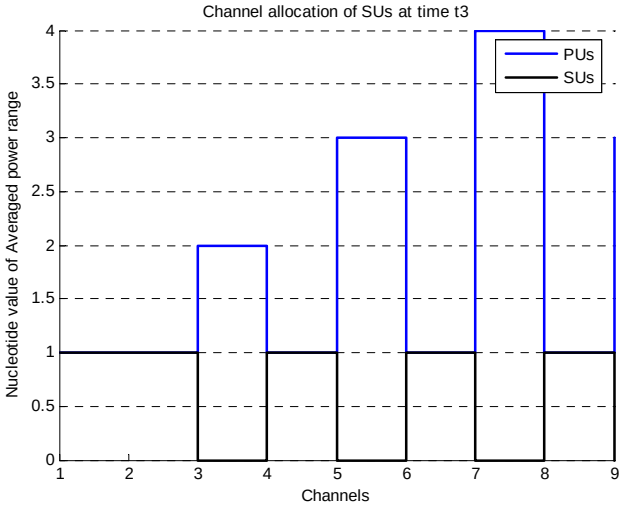


Fig. 11 SU's Channel allocation at PUs at time instant t_3

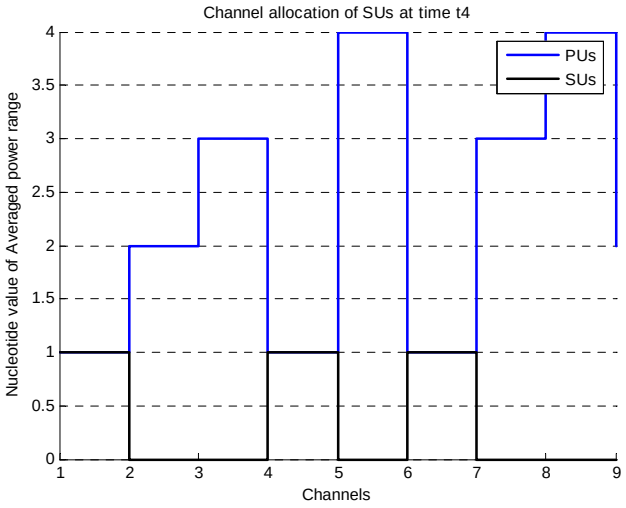


Fig. 12 SU's Channel allocation at PUs at time instant t_4

In this paper, a DNA-inspired computing based opportunistic spectrum access scheme is proposed which is found to work fine and can be implemented on CRNs. The best part is that spectrum allocation and reallocation condition in given Haykin's paper [4] as shown in Fig. 2 has been precisely recognize through Fig. 9, 10 and 11. The simulation programs for the proposed system are neither complex nor consume much time to respond. Hence, it can be easily embedded into physical [PHY] and media access control [MAC] layer of CRN to work efficiently. In this paper, however, difficulty arises while SUs is greater than unused channel of PUs has been ignored are proposed in future research work.

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