Evaluation of Parameters and Techniques for Genetic Algorithm based Channel Allocation in Cognitive Radio Networks

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Abstract—**Genetic Algorithm is a promising optimization technique for solving the problem of Channel Allocation in Cognitive Radio Networks(CRNs). This work involves exploration of various parameters and techniques used in Genetic Algorithm(GA). The selection of parameters and techniques influence the run-time and ability of genetic algorithm to arrive at a globally optimal solution. Therefore, this paper validates various crossover and mutation techniques to be fit/unfit for use and their effect on convergence of genetic algorithm for optimum channel allocation strategy. Extended version of current genetic algorithm for channel allocation using partial mapped crossover(PMX) is proposed. The simulation results show that PMX crossover is a robust method for dealing with the interference problem encountered in the extended version of the genetic algorithm.**

Keywords—Genetic Algorithm, Channel Allocation, Cognitive Radio Networks, Heuristic algorithms, Biologically-inspired AI.

I. INTRODUCTION

Cognitive Radio (CR)[1] is the enabling technology which empowers us to do dynamic spectrum access: technology that provides a way out of spectrum scarcity problem which is a rising concern across the globe. Therefore, CR is thought to be a promising technology for next generation wireless communication networks. Making radios and wireless networks truly cognitive, however, is an uphill task[15]. The research involves ideas from communications, graph and game theory, networking engineering, machine learning, signal processing, and re-configurable antenna and radio-frequency design for building network with capabilities of observing the surrounding environment by the means of sensing, re-configuring itself and its knowledge base to adapt the changes in network.

The fixed spectrum access and allocation strategy has been used traditionally by the spectrum regulation agencies. Each part of frequency-spectrum with fixed bandwidth is assigned to one or more dedicated users called Primary User (PU). By doing so, only the assigned (licensed) users get to access the spectrum which is allocated to them, and no other users can access the spectrum without permission, regardless of whether the spectrum is available for use at a given instance. As the spread of wireless technology has continued in the last few decades, in several countries, most of the available spectrum has been exhausted. This has lead to the scarcity of available spectrum. Whereas the recent studies that were done for measuring actual utilization of available spectrum show that a large chunk of spectrum allocated to a licensed user remains free but is not allocated to other users resulting in scarcity of spectrum [3][4][5]. This inefficient and permanent channel allocation technique has led to this scarcity in physical spectrum available for use. To continue the wide spread of wireless communication, new paradigm for channel allocation strategy must be considered.

A. Dynamic Spectrum Allocation

Dynamic Spectrum Access(DSA) is widely proposed as an alternative solution for the access and utilization of the spectrum in a much efficient manner [1], [2]. In DSA, certain part of spectrum is assigned to one or more than one user, which are called Primary (licensed) Users. However, it should be noted that PUs do not hold exclusive rights for that spectrum. The spectrum is available for use by others called as Secondary Users (SUs). SUs can access the allocated spectrum in an opportunistic manner till primary users do not start to communicate again using same allocated spectrum. Secondary users are also allowed to share the spectrum with the PUs till PUs are protected, that is, the transmission by SU should not interfere with the transmission of PU. This allows network to reuse the radio spectrum opportunistically and even share it all the time. Traditionally, radio spectrum is divided into different frequency-bandwidths. Each bandwidth is defined by its range of frequencies i.e. the frequencies between its upper and lower limit. A band is assigned to a licensed user exclusively and hence no interference arises. In a CRN, the outcome of spectrum sensing i.e. available channels for transmission is given as input to resource allocation function. A function or algorithm then allocates available channels to the competing users such that the utility function is maximized. Utility function is a quantitative measure of goodness of the allocation strategy. Channel availability is both time and space dependent because channels may not be permanently available for secondary users. This makes the problem an interesting and challenging area of research.

In this paper, study of parameters and techniques used in genetic algorithm which has been used to propose a solution for channel allocation in CRNs is done. The paper contains information about related works in section II. Section III talks about modelling the channel allocation problem and the extension which implements genetic algorithm to find a strategy for complete network centrally. Section IV gives

introduction about genetic algorithms and a study of techniques and parameter involved.

II. Related Works

In this section, the work closely related with our study on optimization and heuristic based algorithms for channel allocation and power control in a CR Network has been listed. In [14], EZ tragos el al. provide a detailed overview of present challenges, approaches and techniques used to solve the problem of spectrum assignment for cognitive radio networks. The techniques which authors discuss are heuristics based, graph-theory, game-theory, fuzzy logic and evolutionary algorithms based. The approaches include centralized, distributed, multi-channel selection, PU considered or PU not considered. In [6], Antonio et al. give a survey on current research, future-scope and new challenges in Cognitive Radio(CRs).

In [7], Shi and Hou formulate a model for the cross layer power control. The model designed gives a solution for scheduling and flow routing problem, which supports a given set of user communication session in the network. They then use branch and bound and convex hull relaxation on their model. With this model they approach an estimate that their solution is $(1 - \epsilon)$ optimal, where ϵ is the amount of accuracy required. In [8], Ma and Tsang give cross layer model including channel allocation and power control. In their work a formulation based on binary integer using linear programming for cross layer problem has been proposed. Assumptions were made that the power levels at which all nodes transmit are same. This makes the model simplified but it limits the efficiency simultaneously. The works detailed above implement a centralized approach for giving the strategy.

In [9]-[10], El Nainay et. al. talk about the islandic genetic algorithm which is the main focus of work done in this paper. Their current model for formulation in localized islandic genetic algorithm is studied for multiple techniques and parameters labelling them as fit for use in current model and comparing their convergence rates with the standard ones. The next section explains the model for allocation and power control problem. In [11], excellent work regarding modelling of cognitive radio network on island Genetic Algorithms was done. It provides a solution to incorporate learning methods in cognitive radio architecture. Author also suggests reinforcement learning techniques to overcome slow convergence and manual configuration issues.

Other biologically inspired AI based optimization algorithms are also being explored by researchers to find out means to get best spectrum assignment strategy in Cognitive Radio Networks. For example, Jian-Ping et. al. in [13] explore the optimal strategy for spectrum assignment using Ant Colony Optimization Algorithm. Li et. al. in [12] use bee colony algorithm for spectrum allocation.

III. Channel Allocation and Power Control Model

This is an introduction to the model for localized iGA by El. Nainay et. al. for understanding the background of the channel allocation and power control problem which are addressed as follows.

A. Channel Allocation Modelling

The model proposed in [10] considers a CRN with set of nodes, $\mathcal{N}$. A node in the network $n_i \in \mathcal{N}$ can both transmit and receive data simultaneously on separate channels. Defining $l_{i,j}$ as the link for communication where the transmitting node is n_i and the receiving node is n_j. The author considers full duplex mode of communication.

Assuming that each node n_i senses $\mathcal{C}_i$ called its set of available channels amongst the set of all non overlapping channels $\mathcal{C}$ present in the spectrum. For every link say $l_{i,j}$ to be established between two nodes,the available common intersection for transmission between two nodes is called $\mathcal{H}_{i,j} \in \mathcal{C}_i \cap \mathcal{C}_j$. Channel assignment vector is defined as the Cartesian product of the available channel set over the links of communication. The assignment vector is called **h** and $h_{i,j}$ is the element of the vector which is the channel allocated to the link $l_{i,j}$.

B. Power Control Modelling

The model in [10] follows the protocol interference model [16] where interference is modelled as a Boolean condition, which means that any two links either interfere or there is no interference. With the following model this can be generalized that a node n_i can communicate on any power level up to to a maximum transmission power $\mathcal{P}_i$, which is influenced by factors like node capabilities and even battery level. Denoting $\mathcal{R}_i^{Tmax}$ to be the maximum transmission range for the node whilst it transmits at maximum power. Similarly, $\mathcal{R}_i^{Imax}$ defines the range of maximum interference for a node whilst the node transmits data at maximum power. Consider $g_{i,j}$ as channel gain for transmitting from i^{th} node to j^{th} node.

$$g_{i,j} = \frac{1}{d_{i,j}^\gamma} \tag{1}$$

In eq.(1) the distance from i^{th} node to the jth node is called $d_{i,j}$ and path loss index i.e. the exponential loss in the gain as distance increases is called γ. The result from derivation process in [10] for set of allowable transmission values are discussed. $p_{i,j}^{min}$ is defined as minimum power needed for transmission by node n_i to transmit without much loss due to noise to node n_j. The results are:

$$p_{i,j}^{min} = \left(\frac{d_{i,j}}{R_i^{Tmax}} \right)^\gamma . P_i \tag{2}$$

For successful transmission between node n_i and node n_j, we have:

$$p_{i,j}^{min} \le p_{i,j} \le P_i \tag{3}$$

$\mathcal{P}_{i,j}$ is the set of all the power values allowed for transmission for link $l_{i,j}$, i.e. it is equal to $\{p : p_{i,j}^{min} \le p \le P_i\}$. The $\mathbf{p} \in \times \mathcal{P}_{i,j}$ is an assignment vector of the transmission power levels. $\times \mathcal{P}_{i,j}$ refers to the Cartesian product of the set of admissible transmission power levels with the links.

C. Cross Layer Modelling

$\mathcal{L}_c$ can be defined as the set of directed communication links to which a given node can set up link with its maximum transmission power. Then the model defines $\mathcal{G}_c = (\mathcal{N}, \mathcal{L}_c)$ as

a graph of communication links. Similarly, to establish interference, $\mathcal{G}_I = (\mathcal{N}, \mathcal{L}_I)$ is defined as the graph of interfering links where $\mathcal{L}_I$ is defined as the set of interference links that can be present given maximum transmission power of each node. $l_{i,j} \in \mathcal{L}_I$ if and only if node n_j is within the node n_is range of interference i.e. (R_i^{Imax}). L_i^C is defined as the set of those links which originate from any node within node i's interference range R_i^{Imax} in the outward direction. This also includes the i^{Th} node itself, i.e. $\mathcal{L}_i^C = \{l_{i,j} \in \mathcal{L}_C, i \neq j\} \cup \{l_{k.m} \in \mathcal{L}_C : \exists l_{i.k} \in \mathcal{L}_i, k \neq i, m \neq k\}$ Denoting the $\mathcal{H}_{j,k}^i$ as available channel set from which channels can be allocated to link $l_{j,k}$ where $l_{j,k} \in \mathcal{L}_i^C$. The $\mathcal{Q}_{j,k}^i$ defines the available power transmission levels for $l_{i,j} \in \mathcal{L}_i^C$. The channel assignment vector is defined as $\boldsymbol{hq_i}$ of length $\left| \mathcal{L}_i^C \right|$ as $\boldsymbol{hq_i} \in (\mathcal{H}_{j,k}^i \times \mathcal{Q}_{j,k}^i)$.

The localized objective of each node is to optimize the following:

$$\max_{\boldsymbol{hq_i} \in \times (\mathcal{H}_{j,k}^i \times \mathcal{Q}_{j,k}^i)} \left[f(\boldsymbol{hq_i}) = \sum_{l_{j,k} \in \mathcal{L}_i^C} \left(\frac{w_{j,k}.p_{j,k}}{1 + \left| \mathcal{L}_i^C \right|} \right) \right] \quad (4)$$

The term $w_{j,k}$ defines the bandwidth of channel allocated to link represented in $h_{j,k}$. Alterations in model are made to change the channel assignment vector length to all the links to be allocated in the network. Therefore, strategy for channel assignment for all network can be searched using genetic algorithm running once instead of running on multiple islands. The next section deals with the problem of interference that was encountered during the crossover and mutation and also describes that the iGA model is optimal in that regard. It also evaluates the model on multiple crossover and mutation techniques.

D. Notations and Terminology

Symbols	Definition
$\mathcal{N}$	Number of nodes present in the CRN
n_i	i^{th} node in network
$l_{i,j}$	Link between i^{th} node and j^{th} node
$\mathcal{C}$	Set of all channels
$\mathcal{C}_i$	Set of available channels for n_i
$\mathcal{H}_{i,j}$	Set of available channels for link $l_{i,j}$
$\mathcal{P}_i$	Maximum transmission power
R_i^{Tmax}	Maximum transmission range while transmitting at maximum power
R_i^{Imax}	Maximum interference range while transmitting at maximum power
$g_{i,j}$	channel gain
$d_{i,j}$	distance from n_i to n_j
γ	exponential path loss
$\mathcal{L}_c$	The set of directed communication links to which a given node can set up link with its maximum transmission power
$\mathcal{L}_i$	The set of interference links that can be present given maximum transmission power of each node
$\mathcal{L}_i^C$	Set of those links which originate from any node within node is interference range R_i^{Imax} in the outward direction including the ith node.

IV. Applying Genetic Algorithm and Evaluation

The genetic algorithm [17] rests on the principle based on natural evolution. The algorithm is widely used in optimization and heuristic based search for results in various scientific and engineering problems. Genetic algorithms are population based where each element of the population is a unique individual defined by its chromosome and the population evolves after each iteration where evolution is based on a quantifiable metric which defines how 'good' a candidate solution is for the problem. Therefore, genetic algorithms incorporate randomness using genetic operators to search the solution space that may contain multiple local maxi-ma and exhaustive search might be computationally intractable. The details for the genetic algorithm are defined as follows and their effect on convergence of GA is evaluated:

A. Crossover and mating

There are multiple crossover techniques for which information-DNA of parents or elements of the population can be taken and are mixed in a particular way to form new individuals of the population.

- *Single-point Crossover*: The parent is randomly searched for a pivot and broken into two-halves where complementary halves are taken from parents and concatenated.

- *Two-point Crossover*: The parent is randomly searched for a sub-string of chromosome i.e. broken using two pivots and then the complementary parts from both parents are concatenated.

- *Uniform Crossover*: The parents have their contribution to the lowest level of information rather than substring levels. Uniform crossover makes this possible by having a mixing ratio between parents. A mixing ratio of 0.5 says that both parents contributed the same to the child.

The above techniques involve unordered mixing and replacement in the chromosome of the population. Therefore, the model in [10] performs perfectly in the above crossover techniques and converges in finite number of steps. But when genetic algorithm is run where channel assignment vector $\boldsymbol{hq_i}$ has length equal to all the links in the graph at any instance, the alternate model doesn't adhere to the interference condition. The issue being that when channel assignment vector length is equal to all the links in the network, the interference conditions make the chromosome ordering sensitive. Therefore, on performing one-point crossover on the ordered chromosome and concatenating the complementary parts from both the parents, the child may or may not follow the conditions. So the ordered crossover techniques explored are listed below:

- *Partially matched Crossover(PMX)*: The crossover involves parent one to donate a swath of genetic material to the child. The corresponding swath from the second parent which has no intersection with the material from the first parent is sprinkled about the child and rest of the alleles are copied from the second parent into the child. The evaluation for ordered technique serves no useful insight into the model but it works

even when channel assignment vector hq_i has length equal to all the links in the graph. Picking any node n_i randomly, $\mathcal{L}_I^C$ for the node is calculated. This set acts as our swath from first parent, which is copied into the child. Now the channels allocated in second parent are considered which are not present in the swath of first parent and sprinkled in the child. This does not generate any interference as the channels were allocated to any link in $\mathcal{L}_I^C$. The alleles are then copied from second parent to the child.

- *Order matched Crossover(OX1)*: The crossover involves one parent to donate the swath of genome and then the second parent is scanned from right to left populating the child with the entries other than those present in the swath of the first parent. The technique fails on the extended model as there can be multiple entries of same channel being allocated in the chromosome when it does not interfere with some other link. Thus the total number of entries remaining in the second parent may not be able to populate the child completely.

- *Cycle Crossover (CX)*: The crossover involves finding 'cycles' in the parents. A cycle refers to a set of genes in both parents that are just permutations of one another. The resulting child can inherit a cycle from either of the parents and in case of multiple cycles, the child can have any possible combination of cycles. The technique works properly when both parents have the same genes, just in different orders. In the extended model, such a situation is rare and thus the technique fails to be applicable.

B. Mutation and Mutation Rate

Mutation is the operation which adds diversity to the population. The process of mutation involves replacing the channel allocated to the link in chromosome with some other channel available such that the overall extended model doesn't encounter interference. The base model caters to the island only during the mutation. Hence, single-point replacement doesn't make the chromosome invalid. Therefore there was no need to check that the chromosome is valid after the mutation has been applied.

The mutation rate was studied for model by varying them for multiple different values to note the convergence and quality of population for a given mutation rate after multiple iterations. Few results are given in later sections discussing the mutation rates.

C. Selection

Selection or mating is the mechanism by which potential solutions for recombination are selected to give new set of population of solutions. The two types of selection mechanisms used in this work are:

- *Fitness Proportionate Selection*: The selection is based on picking up elements proportionately with their fitness scores. The fitness proportion is a roulette wheel based mechanism where each chromosome has a set of numbers in its favour in proportion with its
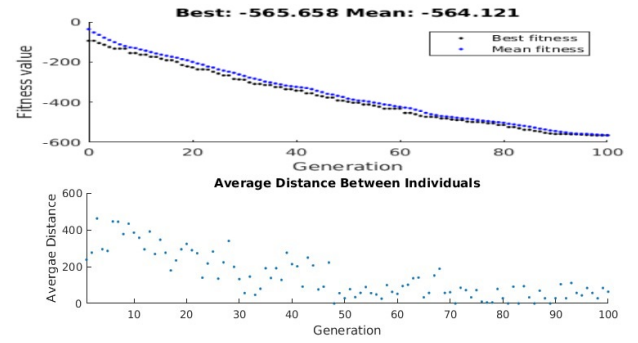
Fig. 1.   iGA One-point crossover Mutation rate 0.01
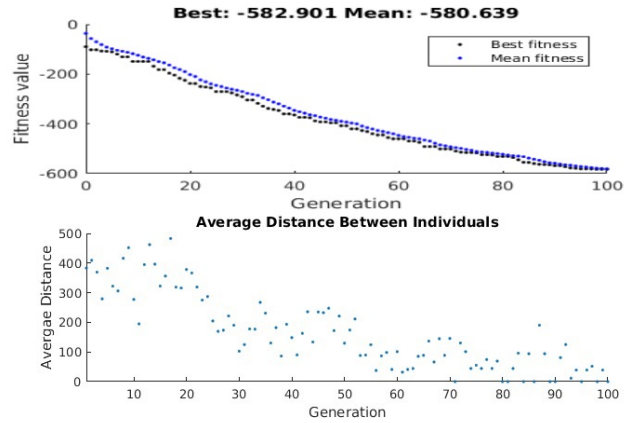
Fig. 2.   Extended GA PMX Crossover Mutation rate 0.01

fitness value. The two ways to implement it are: a pool based method, where among all the entries in the pool the number of entries of each chromosome are in proportion with their fitness scores. Then a random draw is made to find the candidate. The other method involves rejection sampling which is a faster way to draw samples based on fitness proportions.

- *Tournament Based Selection*: The selection is based on picking up individuals by running several "tournaments" among the randomly chosen chromosomes from the population. The candidate for crossover is selected by choosing winner among them.

V. SIMULATION AND RESULTS

The simulation was done for channel allocation using genetic algorithm to study its results and convergence by applying different types of genetic operators as listed above, both on standard iGA model and the extended version. The results depict the convergence of genetic algorithm's best fitness value. The simulation uses method to simulate similar behaviour for finding the strategy with maximum fitness values by finding the minimum amongst the negative of fitness values. The first graph in every figure depicts the current value of best fitness and mean fitness on y-axis versus generations on x-axis. Best fitness is the fitness value of most fit chromosome and mean fitness is average fitness value of all chromosomes. Therefore, in every Figure, the first result has a negative slope
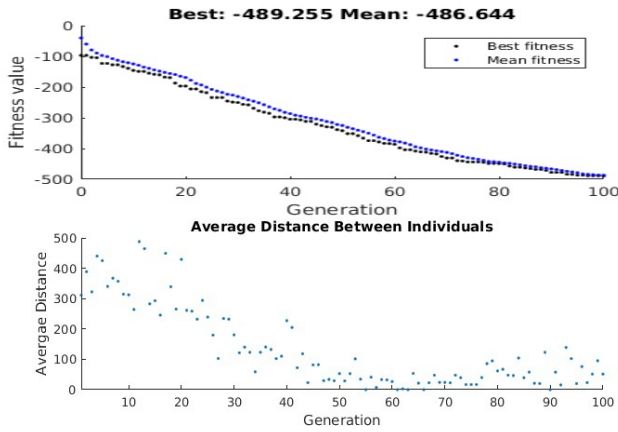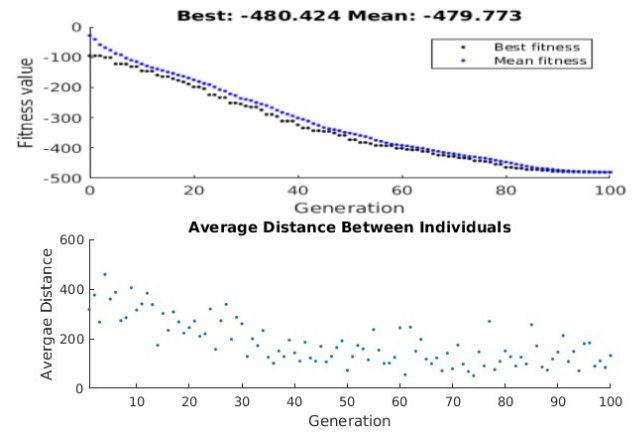
Fig. 3.   iGA Two-point Crossover Mutation rate 0.01

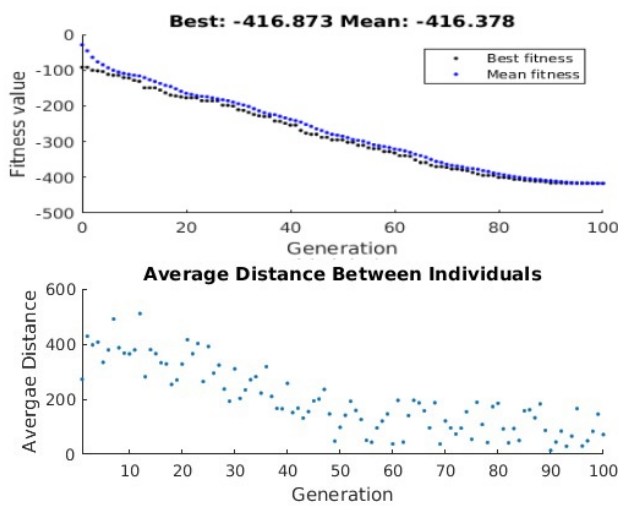

Fig. 4.   iGA One-point Crossover Mutation rate 0.05

Fig. 5.   Extended GA PMX crossover Mutation rate 0.05

Fig. 6.   iGA Two-point Crossover Mutation rate 0.05
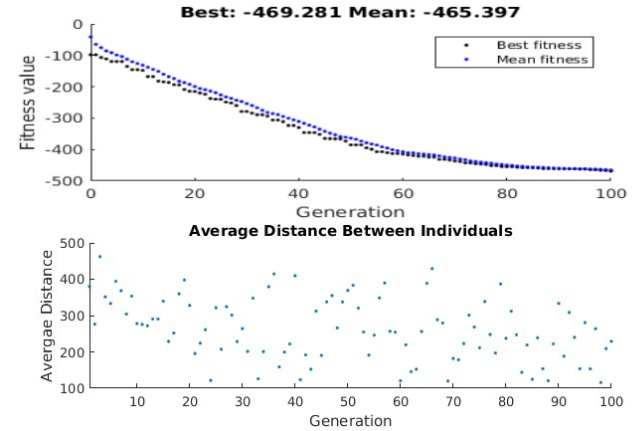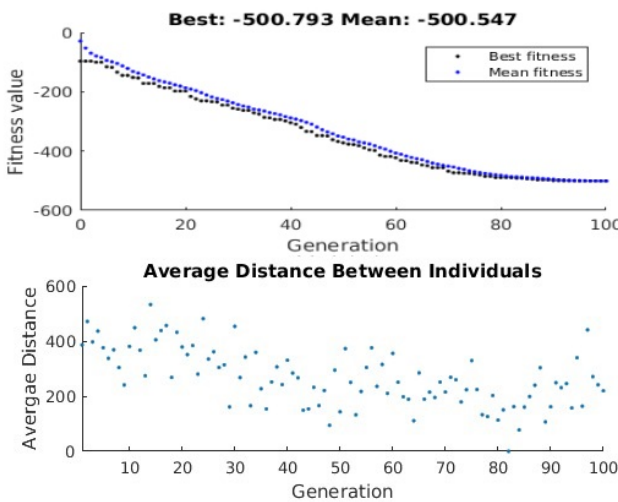

Fig. 7.   iGA One-point Crossover Mutation rate 0.1

Fig. 8.   Extended GA PMX Crossover Mutation rate 0.1
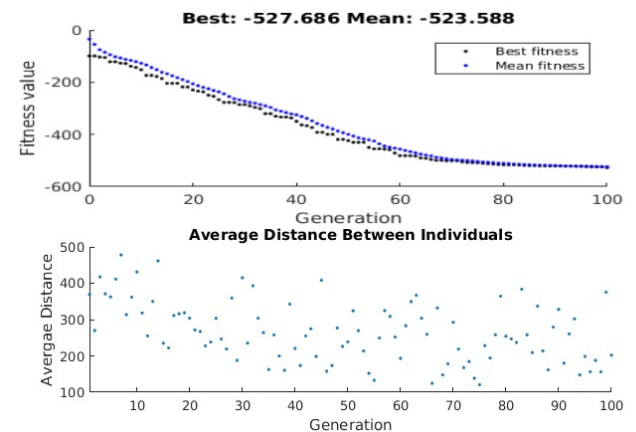
The second result in every figure defines the average distance between the population. More the mutation rate, more likely it is that the population will have variation and hence the average distance will be high. For an ideal mutation rate, as generations pass the average distance comes down, since all solutions become close to the global solution.

The graphs were generated multiple times and their aver-

mostly until it finally converges. This depicts that after each generation the mean and best fitness of the population improve.
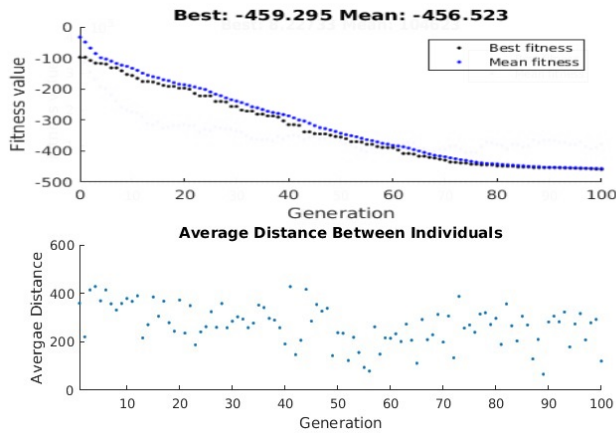
Fig. 9.   iGA Two-point Crossover Mutation rate 0.1

ages were taken to find out which of crossover techniques, mutation rates and selection mechanism do better. The two selection mechanisms, fitness proportional selection and tournament based selection, were found to be equally optimal. Mutation rates were studied among which the results can be divided in three groups. The rates in each group produce almost equal effect on convergence. The three main rates from each can be 0.01, 0.05 and 0.1. The sets will consist of values around these main rates.

The figures depict result of one point and two point crossovers on iGA method where standard one point crossover produced better results. The extended version of GA which runs on all the network uses PMX crossover. It converges in finite number of steps showing results similar to iGA considering the optimization runs on all the channels.

VI.   Conclusion

In this paper, efforts were made to find an extension of current iGA model which runs the genetic algorithm on the entire network. The channel assignment vector (hq_i) used is of the length of all the active links in the network at a given instance of time. It was discovered that invalid candidate solutions are present in the population as they will not be able to adhere to the interference condition during the mating and mutation process for any of the crossover and mutation techniques except for PMX crossover. Simulation results validate that the current model for iGA applied to channel allocation method executes and terminates in a finite number of steps in multiple combinations of cross-over and mutation techniques. Results also show that the overall fitness and best fitness of the population improve with each iteration, which implies that within finite steps GA will converge to an optimal strategy.

In future, a new set of adaptive genetic algorithms and other heuristic based optimization for finding the best techniques and parameter values automatically can be used. Another area left unexplored is to study spectrum analysis and feature selection methods so that the channels can be separated qualitatively while sensing them. This will help to design a heuristic for better initialization of population rather than random initialization, eventually improving the convergence and network's throughput.

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