A Mutation factor based Clonal Selection Algorithm for Data Clustering

Suresh Chittineni[1], *Professor, Dept. IT, ANITS Visakhapatnam*

Prasad Reddy PVGD[2] *Professor, Dept. CS&SC, AU Visakhapatnam*

Suresh Chandra Satapathy[3] *Professor, Dept. CSE, ANITS Visakhapatnam*

Summary
The Clonal Selection hypothesis is a widely accepted model for the immune system's response to infection in human body. Clonal Selection Algorithms (CSA) is a special class of Immune algorithms (IA), inspired by the Clonal Selection Principle. To improve the Algorithm's ability to perform better, this CSA has been modified by implementing two new concepts called Fixed Mutation Factor and Ladder Mutation Factor. Fixed Mutation Factor maintains a constant Factor throughout the process, where as Ladder Mutation Factor changes adaptively based on the affinity of antibodies. This paper compared the conventional CLONALG, with the two proposed approaches are tested on twelve datasets.
The proposed method applied on the data clustering, which is an important task of data mining. Experimental results empirically shows that the proposed Ladder Mutation based Clonal Selection Algorithm (LMCSA) and Fixed Mutation Clonal selection Algorithm (FMCSA) significantly out performs the existing CLONALG method in terms of quality of the solution.

Key words:
Data Clustering, Clonal Selection, Mutation Factor, Ladder Mutation Factor, Fixed Mutation Factor.

1. Introduction

Data clustering is the most important unsupervised learning problem, which deals with finding a structure in a collection of unlabeled data. Clustering is the process of organizing objects into groups according to the similarity in some way, so that the cluster is collection of objects which are similar between them and are dissimilar to the objects belongs to other clusters.
The main goal of clustering is to set similar objects together. Hence, the main target of clustering is to provide clusters, which must be as compact as possible and as separable as from other compact clusters. It means, the intra cluster distance must be minimized and inter cluster distance must be maximized.
Partitioning based clustering methods are confined in the work to find optimal results due to its nature of trapping local optimal solutions. The most popular partitioning based techniques are K-means and its variants. These algorithms normally initialization of cluster centers, number of clusters to be known prior. To over these challenges, implementing Artificial Immune System based techniques are applied in this work.
Artificial Immune System (AIS) is one of the bio-inspired approaches for solving the real complex and difficult optimization problems. The AIS is greatly reinforced by the human immune system. In humans, the immune system is responsible for protection from pathogens.
De Castro proposed a Clonal selection algorithm (CSA) based on the Clonal selection principle and the affinity maturation process [1]. CLONA LG (Clonal Algorithm) is an artificial Immune algorithm [7] based on Clonal selection principle. CLONA LG is used to optimize inter cluster and intra cluster distances [1]. CLONALG has global searching ability as it uses the principle of Clonal expansion.

Data clustering process is an optimization problem. In this point of view given a chance to Artificial Immune System (AIS) is one of the bio-inspired approaches to solve clustering challenges like to give candidate cluster centroids, find better optimal partitioning of given data set.
This paper, present an improved version of the immune system model based on the Clonal selection theory. Two algorithms LMCSA (Ladder Mutation factor based Clonal Selection Algorithm) and FMCSA (Fixed Mutation factor based Clonal Selection Algorithm) are proposed by introducing two novel immune mutation factors and are applied to unimodal and multi-modal optimizations. The results illustrate that the proposed algorithm shave are mark-able performance over basic CLONALG. The proposed methods are applied on partitioning based clustering method k-means and gets optimized results.
The remainder of this paper is organized as follows: Section2 briefly discusses the basic steps in Clonal selection optimization algorithm (CLONA LG) and antibody diversity maintaining principles. Section-3 describes modified versions of immune optimization algorithm with the introduction of mutation factor and its details. Section 4 gives further explanations, experimental analysis, simulation results to twelve datasets like Iris, Wine,Pima Indian, Hayes etc.. and comparisons of our proposed algorithms with the conventional CLONALG. Section5 concludes with remarks and conclusions.

Manuscript received April 5, 2016
Manuscript revised April 20, 2016

2. Basic Immune Optimization Algorithm (Clonalg)

A CLONALG is a population based Meta heuristic algorithm whose search power relies on its mutation operator. In our proposed work the main thrust is given to these mutation operators while developing better algorithms. The Clonal Selection Algorithm (CSA) reproduces individuals with high affinities and selects improved maturate progenies. This strategy suggests that the algorithm performs a greedy search, where single members will be locally optimized and the newcomers yield a broader exploration of the search space. This characteristic makes the CSA very suitable for solving optimization tasks. The basic steps and working of Immune Optimization algorithm (CLONA LG) is described as follows:

Step1. Anti-body Pool (AB) Initialization

Initially, an Antibody Pool (AB) is created with N antibodies chosen randomly in the search space. Antibodies are represented by the variables of the problem (ab1, ab2,...,abN) which are potential solutions to the problem.

Step2. Selection:

For each Antibody (abi), its corresponding affinity is determined. These antibodies are then sorted according to the affinity calculated. And n antibodies are selected having highest affinity.

Step3. Cloning:

Cloning is one of the key aspects in AIS. It is the process of producing similar populations of genetically identical individuals. The selected best n antibodies will be replicated in proportionate to their antigenic affinity. The replicated antibodies i.e., Clones are maintained as a separate clone population C. The Number of Clones for each antibody can be calculated by the following equation:

$$N_c = \sum_{i=1}^{n} round\left(\frac{S.N}{i}\right) \quad \text{.....(1)}$$

Where Nc is the total number of clones[6] generated, β is a multiplying factor, N is the size of Antibody Pool (AB) and round(.) is the operator that rounds its argument towards the closest integer. Clone size of each selected antibody is represented by each term of this sum. Higher the affinity, the higher becomes the number of clones generated for the selected antibody [2].

Step4. Affinity Mutation:

The Clone Population C is now subjected to mutation process which is inversely proportional to its antigenic affinity measurement methods. This Mutation helps for low affinity antibodies to mutate more in order to improve its affinity. The mutations always result in better affinity antibodies. For gray coding uniform mutation, Gausion mutation or Cauchy mutation using Gaussian distribution is used for matching a search in the area surrounding the cell with high probability. And it has an outstanding ability of both local and global searching.

$$\left\{\begin{array}{l} \theta_i^j = \theta_i^j \times \exp\left(\tau_1 \times N(0.1) + \tau_2 \times N_j(0.1)\right) \\ ab_i^j = ab_i^j + \theta_i^j \times N_j(0.1) \\ \tau_1 = \left(\sqrt{2 \times \sqrt{D}}\right)^{-1} \\ \tau_2 = \left(\sqrt{2 \times D}\right)^{-1} \\ \theta_i = \{\theta_1, \theta_2, \ldots, \theta_D\} \end{array}\right\} \text{.....(2)}$$

The Gaussian mutation operator [7] can be described as follows:

where, i=1,2,3...Nc, j=1,2,....,D, The parameter is the mutation step of antibody ab_i^j, τ_1 and τ_2 is the whole step and the individual step respectively. Then, the affinities of the mutated clones are calculated. The better affinity mutations are stimulated while the worse are restrained when antibody undergoes affinity mutation. The higher affinity values are taken for next generation while the Lower affinity antibodies are deleted.

Step5. Antibody Diversity Maintenance:

Inspired by the vertebrate immune system mechanism called antibodies restraint, the process of suppression and supplementation are defined in CLONALG. This step maintains diversity and helps to find new solutions that correspond to new search regions by eliminating some percentage of the worst antibodies in the population and replacing with the randomly generated new antibodies. This helps the algorithm to avoid being trapped to local optimal solutions. In antibodies restraint [3], for every iteration, the similar antibodies are removed and randomly generated antibodies are introduced in the place of removed antibody of the Antibody Pool (AB).

3. Proposed Fixed Mutation Factor And Ladder Mutation Factor Based Clonal Selection Algorithm (FMCSA and LMCSA)

In the basic CLONALG, initially best and worst antibodies are identified; the process of cloning is applied to the both best and worst antibodies such that cloning rate is high to the best antibodies and less to the worst antibodies [2]. Therefore, more clones are produced for the antibody that has highest affinity. Then, worst antibodies are mutated in order to make them better. By doing this, the worst antibodies can improve; however, no care is taken to the best antibodies. Since, more population of best antibodies also exists in that pool; there is a chance of faster convergence if best antibodies are also taken care properly. Otherwise, these can lead to local optima and the low convergence rate, resulting poor performance of the Algorithm.

In this paper, two novel methods are introduced to solve this problem by properly nurturing the best antibodies. The basic flowchart for these methods is given in fig.1.

3.1. Fixed Mutation Factor based Clonal Selection Algorithm (FMCSA):

Like in CLONALG, the best antibody is cloned according to the cloning rate (β) and clones of best antibodies are generated. In this process, mutation is done to some of the best antibodies also along with the worst antibodies. A few percentages of best antibodies that are cloned are taken and are mutated along with the worst antibodies. So, a fixed mutation factor (γ) is defined and stated as: the percentage of best cloned antibodies in Clone population (C) that are to be considered for mutation. This mutation factor (γ) is fixed throughout the process. The Number of best anti bodies to be considered for mutation in each antibody's Clone Population (CMUTAB) is calculated as follows:

$$CMUTAB=Ceil(\gamma * CAB) \quad \text{.....(3)}$$

Where: CMUTAB=. The Number of best anti bodies to be considered for mutation in each antibody's Clone Population, γ = Fixed Mutation Factor, CAB= Total Number of antibodies in each clones Population of an antibody and Ceil (.) is the operator that rounds its argument towards the nearest integers towards infinity.

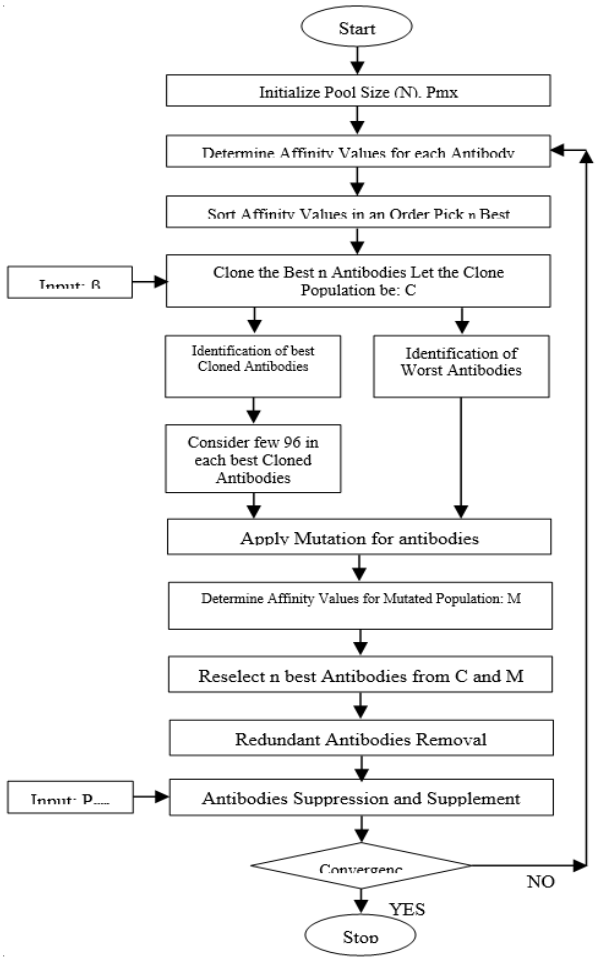

Fig. 1. Basic Flow chart for FMCSA and LMCSA

For example: For 5 Initial antibodies after performing steps from 1 to 3, let the clone population be: [5, 4, 3, 2, 1]. Let the fixed Mutation factor γ be: 0.3. So, upon using the above Eq. 3, CMUTAB= 2. Hence, 2 best antibodies are considered out of 5 initial cloned antibodies for Mutation, similarly 2 best antibodies out of 4 and 1 out of 3 best antibodies. As the worst antibodies are having less antigenic affinity, they are cloned less in number and all the worst antibodies as in basic CLONALG [1]. In general, for FMCSA algorithm, the fixed mutation factor (γ) is chosen to be very small.

3.2. Ladder Mutation Factor based Clonal Selection Algorithm (LMCSA):

In the Fixed Mutation Factor approach, the mutation factor remains constant. When the affinity difference between the worst antibody and the best antibody is high, then the Worst antibodies try to go and follow the best as in any other Evolutionary Strategies. But, when their affinity

difference is very less, all the worst and best antibodies are in the same surrounding area of the search space or in other words, worst antibody has come closer to best antibody's area [8]. At this time, the further improvement may not achieve at faster rate. This can be enhanced by considering few additional antibodies for mutation. A chance of better convergence can be attained by adaptively incrementing the percentage of best cloned antibodies for mutation as explained. The mutation factor can be incremented adaptively based on the affinity measure. This mutation factor is proportional to the affinity of the antibodies i.e., if the ratio of the affinities between the best and worst antibody is less than the threshold value (μ), then mutation factor should be incremented.

The following pseudo code is included in the step [4] of the basic CLONALG:

If (aff [ab_b]/aff[ab_w]) <μ

$$\gamma = \gamma \times \rho$$

ρ is a parameter, changed dynamically as follows:

$$\rho = \left(\frac{iter}{maxiter}\right) * \alpha \text{.....(4)}$$

Where: μ is the Threshold value,
ab_b is The best antibody in the Antibody Pool.
ab_w is the Worst antibody in the Antibody Pool.
α *is a* Constant multiplier depends on the problem type.
γ is the Mutation Factor.
Iter stands for current Iteration.
Maxiter stands for Maximum number of Iterations.
Aff(.) is a function used for calculating the affinity of the antibody.

4. Results and Analysis:

A. Data sets for Simulation

A suite of twelve standard and well-known data sets [4], [5], [9], [10] are taken into consideration to test the effectiveness and efficiencies of the proposed approaches FMCSA and LMCSA with the basic CLONALG.

B. Experimental Setup:

The approaches that are described earlier have been coded using the MATLAB Scripting language and all experiments took place on a 1.8 GHz Intel Core 2 Duo processor, 2GB of RAM and on Windows XP operating system. Each algorithm is evaluated for 1000 iterations as the termination criteria.

The following simulation conditions are used.

- Initial population or Antibody Pool Size, *AB* = 50
- Clone Multiplying factor′*s Range* β=[0.5-1]
- Type of mutation used: Gaussian
- Gaussian mutation probability P_{mg}= 0.01
- Percentage of Suppression P_{sup}= 0.2
- The affinity threshold $\sigma = 10^{-3}$.
- Number of Iterations=1000
- Fixed Mutation factor (γ) in FMCSA=0.20
- μandα varies from problem's Domain Range.
- Number of Dimensions taken for each Benchmark value=10

5. Partitioning Clustering Methods:

The main focus of work is to study clustering using evolutionary techniques. From the analysis of partitional clustering, it is evident that optimization is an inherent property of a good cluster. To achieve compact and separable clusters the intra cluster distance and inter cluster distance must be optimized properly

Given a data set, a desired number of clusters, k, and a set of k initial starting points, the k-means clustering algorithm finds the wanted number of distinct clusters and their centroids. A centroid is well-defined as the point whose coordinates are obtained by computing the average of each of the coordinates (i.e., feature values) of the points of the jobs assigned to the cluster [1]. Formally, the k-means clustering algorithm follows the following steps.

1. Choose a number of clusters, *k*.
2. Choose *k* starting points to be used as initial estimates of the cluster centroids. These are the initial starting values.
3. Examine each point (i.e., job) in the workload data set and assign it to the cluster whose centroid is nearest to it.
4. When each point is assigned to a cluster, recalculate the new *k* centroids.
5. Repeat steps 3 and 4 until no point changes its cluster assignment, or until a maximum number of passes through the data set is performed.

Tweleve datasets with a variety of complexity are used to evaluate the performance of the proposed approach. The datasets are Iris, Wine, Pima Indian Diabates, Hayes roth,, Zoo,seeds,glass,balance scale,, Haberman's Survival , Ecoli , Vowel and Fertility ,which are available in the repository of the machine learning databases [2]. Table 1 summaries the main characteristics of the used datasets.

The performance of the LMCSA algorithm is compared against well known and the most recent algorithms reported in the literature, including K-means , FMCSA,Basic clonalg The performance of the algorithms is evaluated and compared using two criteria:

Sum of intra-cluster distances as an internal quality measure: The distance between each data object and the center of the corresponding cluster is computed and summed up, as defined in Eq. (5). Clearly, the smaller the sum of intra-cluster dis- tances, the higher the quality of the clustering. The sum of intra-cluster distances is also the evaluation fitness in this work.

A summary of the intra-cluster distances obtained by the clustering algorithms is given in Table 2. The values reported are best, average, worst and the standard deviation of solutions over 50 independent simulations.
As seen from the results in Table 2, the LMCSA algorithm achieved the best results among all the algorithms.

Table 1: Unconstrained optimization (all minimization)

Data sets name	Algorithm Used	Mean and Standard Deviation of number of cluster	Mean and Standard Deviation of CS Measure	Exact cluster number for dataset
Iris data	FMCSA	2.89±0.0382	0.6643±0.097	3
	LMCSA	2.15±0.443	0.6261±0.131	
	Basic Clonalg	2.25±0.0958	0.7282±2.003	
Wine data	FMCSA	3.05±0.0391	0.9249±0.032	3
	LMCSA	2.95±0.0352	0.8721±0.037	
	Basic Clonalg	3.01±0.0112	1.5842±0.328	
Breast cancer data	FMCSA	2.00±0.00	0.4532±0.034	2
	LMCSA	1.85±0.0632	0.3854±0.009	
	Basic Clonalg	2.00±0.0083	0.6089±0.016	
Glass data	FMCSA	6.05±0.0148	0.3324±0.487	6
	LMCSA	5.55±0.0093	0.2642±0.073	
	Basic Clonalg	5.75±0.0346	1.4743±0.236	
Vowel data	FMCSA	5.65±0.0751	0.9089±0.051	6
	LMCSA	5.10±0.0183	0.5827±0.331	
	Basic Clonalg	5.35±0.0075	1.9978±0.966	

Table 2: (Mean and Standard deviation over 40 independent runs) after each algorithm was terminated after running for 1200 FEs with the quantization error-based fitness method for real dataset

	Iris Dataset		
Agorithms	**Fitness value**	**Intra cluster distance**	**Inter cluster distance**
Basic Clonalg	0.2800±4.8905e-4	2.1824±0.0622	2.1025±0.1629
FMCSA	0.2800±0.0010	2.2251±1.3492e-15	2.1422±2.2487e-15
LMCSA	0.2789±7.9006e-4	2.2251±1.3492e-15	2.0022±2.2487e-15
	Wine Dataset		
Basic Clonalg	337.6825±0.0596	338.1072±2.1419	329.5147±7.9801
FMCSA	337.8922±0.3097	337.7693±1.6820	328.6101±8.0570
LMCSA	337.6299±3.7834e-4	377.2333±0.3612	325.5560±8.2283
	Pima Indian Diabates Data		
Basic Clonalg	14.4565±0.0037	729.5871±0.4613	29.7691±1.0354
FMCSA	14.4556±0.0026	729.5668±0.2204	29.4928±0.5097
LMCSA	14.4545±0.0029	729.6685±0.3566	29.1699±0.5900
	Hayes roth Dataset		
Basic Clonalg	0.2192±0.0055	3.7616±0.1877	1.2809±0.1812
FMCSA	0.2224±0.0098	3.7954±0.0033	1.2275±0.0465
LMCSA	0.2093±1.0580e-14	3.795±4.6181e-16	1.2001±0
	Zoo Dataset		
Basic Clonalg	0.0076±4.1273e-04	1.6121±1.1244e-15	2.6875±2.2386e-15
FMCSA	0.0088±7.8519e-05	1.6121±1.1244e-15	2.6875±2.1976e-15
LMCSA	0.0024±0.0012	1.6121±1.1244e-15	2.5875±2.2284e-15
	Seeds Dataset		
Basic Clonalg	0.3181±6.2355e-04	5.2342±0.5141	2.8766±0.3456
FMCSA	0.3187±0.0019	4.8379±0.0182	3.0890±0.0249
LMCSA	0.3186±0.0025	4.8154±0.0169	3.0386±0.0132
	Glass Dataset		
Basic Clonalg	0.0399±8.9169e-4	5.3671±0.5035	2.5420±4.4456
FMCSA	0.0406±0.0011	5.1841±0.4340	3.4537±5.2102
LMCSA	0.0376±0.0012	4.9219±0.4339	3.1766±5.8815
	Balance Scale Dataset		
Basic Clonalg	0.4735±0.0050	5.7278±0.0125	1.3667±0.0745
FMCSA	0.4673±0.0080	5.7334±0	1.3333±0
LMCSA	0.4444±8.6750e-13	5.7334±0	1.3333±0
	Haberman's Survival Dataset		
Basic Clonalg	5.0498±0.0518	39.8499±1.9999	3.4172±3.8449
FMCSA	4.9697±2.2633e-4	40.9948±0.2782	5.1623±2.3668
LMCSA	4.9618±0.0052	41.0388±0	4.5462±9.3622 e-16
	Ecoli Dataset		
Basic Clonalg	0.0591±7.2137e-04	0.6850±0.0580	0.2060±0.1082
FMCSA	0.0600±0.0019	0.6508±0.0979	0.2477±0.1739
LMCSA	0.0525±0.0045	0.6883±0.1348	0.2317±0.1534
	Vowel Dataset		
Basic Clonalg	33.8605±1.4882	841.2638±143.7361	528.9102±260.6815
FMCSA	34.1437±2.0720	877.6941±144.9632	595.9829±261.8246
LMCSA	25.6672±1.0023	790.0012±140.1121	583.1102±236.1129
	Fertility Dataset		
Basic Clonalg	0.2187±8.4747e-05	3.0702±6.9111e-04	0.4604±0.0145
FMCSA	0.2186±5.2678e-06	3.0699±0	0.4540±0
LMCSA	0.2186±0	3.0699±0	0.4540±0

From Table 2 it is shown that the algorithm LMCSA is keeping 1st position in clustering the dataset among all algorithms in all dataset except seeds dataset, where Basic Clonalg algorithm keeping the 1st position. In Iris dataset LMCSA is giving better result than other algorithms, whereas Basic Clonalg is giving second best and BASIC CLONALG is giving 3rd best solution. In Glass dataset LMCSA is giving better result than other algorithms and Basic Clonalg is giving second best and Basic Clonalg is giving 3rd best solution. In Wine dataset LMCSA is giving 1st best solution and Basic Clonalg is giving second best and BASIC CLONALG is giving 3rd best solution. Similarly in Haberman's Survival Data set LMCSA is giving 1st best solution and FMCSA is giving second best and Basic Clonalg is giving 3rd best solution. In Pima Indian Diabates Data LMCSA is giving better result than other algorithms and FMCSA is giving second best and BASIC CLONALG is giving 3rd best solution. In Hayes roth Dataset LMCSA is giving better result than other algorithms and Basic Clonalg is giving second best and BASIC CLONALG is giving 3rd best solution. Balance Scale DataSet LMCSA is giving 1st best solution and FMCSA is giving second best and BASIC CLONALG is giving 3rd best solution. In Ecoli dataset LMCSA is giving 1st best solution and Basic Clonalg is giving second best and elitist BASIC CLONALG is giving 3rd best solution.

In Zoo dataset LMCSA is keeping 1st position, FMCSA is in 2nd position whereas FMCSA is keeping 3rd position. In Vowel dataset LMCSA is giving 1st best solution and Basic Clonalg is giving second best and elitist BASIC CLONALG is giving 3rd best solution. In Seeds dataset Basic Clonalg is giving 1st best solution and elitist BASIC CLONALG is giving second best and BASIC CLONALG is giving 3rd best solution. In Fertility dataset, LMCSA is giving 1st best solution and Basic Clonalg is giving second best and BASIC CLONALG is giving 3rd best solution.

6. Conclusions

In this work proposed two novel approaches, Fixed Mutation Clonal Selection Algorithm (FMCSA) and Ladder Mutation Clonal Selection Algorithm (LMCSA). Our objective is to increase the searching area by increasing a few numbers of antibodies that undergo mutations as to further improve the performance of basic CLONALG. On solvinga suite of data sets, FMCSA performs better than CLONALG and LMCSA outperforms both FMCSA and CLONALG. Simulation results on Standard Datasets have shown that the proposed methods are useful techniques to solve complex Clustering problems.

References

[1]. Data Mining: Concepts and Techniques , Jiawei Han, MichelineKamber, Simon Fraser University , Morgan Kaufmann Publishers.

[2]. Leandro N. deCastro andFernandoJ.VonZuben LearningandOptimizationUsing theClonal Selection Principle", IEEE Transaction Evolutionary Computation, Vol. 6, No. 3, JUNE 2002, pp. 239-251.

[3]. De Castro andJonathan Timmis "An Introductionto Artificial Immune Systems: A New Computational Intelligence Paradigm, SpringerVerlag, 2002.

[4]. Lijun Pan andZ Fu,A Clonal Select ion Algorithm for Open Vehicle RoutingProblem: Proceedings of third International Conference on Genetic and Evolutionary Computing, 2009.

[5]. Suganthanand S. Baskar, "Comprehensive Learning Particle Swarm Optimizer for Global Optimization of Multimodal Functions", IEEE Trans. on Evolutionary Computation,Vol.10,No.3,June2006.

[6]. S.H.LingandC. Iu," Hybrid Particle Swarm Optimization With Wavelet Mutation and Its Industrial Applications", IEEE Tran. On Systems,Man and Cybernetics-PartB:Cybernetics,Vol.38,No.3,June2008.

[7]. XuesongXu and Jing Zhang,"An Improved Immune Evolutionary Algorithm for Multimodal Function Optimization": proceedings of third International Conference on Natural Computation, ICNC 2007.

[8]. JonathanTimmis,C.Edmonds and Kelsey, "Assessing the Performance of Two Immune Inspired Algorithms and a Hybrid Genetic Algorithm for Function Optimization," Proceedings of the Congress on Evolutionary Computation, 2004, pp.1044-1 051.

[9]. Khaled, A.M. Abdul-Kader and Nabil A Is mail ,"Artificial Immune Clonal Select ion Algorithms : A Comparative Study of CLONA LG, opt -IA, and BCA with Numerical Optimization Problems ", IJ CS NS International Journal of ComputerScience and Network Security, VOL.10 No.4, April 2010.

[10]. JingqiaoZhang and Arthur C. Sanders on, "JADE: Adaptive DifferentialEvolutionwith OptionalExternalArchive" IEEE Tran. On Evolutionary Computation, Vol.13, No.5 October 2009.

Suresh Chitteneni HOD of IT ANITS, full time PhD scholar in CSSE department,AU.He has 18 years of experience in teaching and research. His research areas are soft computing, data mining, computer networks, security etc.

Prasad Reddy PVGD HOD of CSSE AU College of engineering.He has 30 plus years of experience in teaching and research. His research areas are soft computing, data mining etc.

Suresh Chandra Satapathy HOD of Department of CSE ANITS, .He has 26 years of experience in teaching and research. His research areas are soft computing, data mining, image processing etc.