Digital Database for Screening Mammography Classification Using Improved Artificial Immune System Approaches

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Abstract: Breast cancer ranks first in the causes of cancer deaths among women around the world. Early detection and diagnosis is the key for breast cancer control, and it can increase the success of treatment, save lives and reduce cost. Mammography is one of the most frequently used diagnosis tools to detect and classify abnormalities of the breast. In this aim, Digital Database for Screening Mammography (DDSM) is an invaluable resource for digital mammography research, the purpose of this resource is to provide a large set of mammograms in a digital format. DDSM has been widely used by researchers to evaluate different computer-aided algorithms such as neural networks or SVM. The Artificial Immune Systems (AIS) are adaptive systems inspired by the biological immune system, they are able of learning, memorize and perform pattern recognition. We propose in this paper several enhancements of CLONALG algorithm, one of the most popular algorithms in the AIS field, which are applied on DDSM for breast cancer classification using adapted descriptors. The obtained classification results are 98.31% for CCS-AIS and 97.74% for MF-AIS against 95.57% for original CLONALG. This proves the effectiveness of the used descriptors in the two improved techniques.

1 INTRODUCTION

Breast Cancer is malignant tumor that develops from breast cells; it is becoming one of the major causes of death among women in the whole world, according to the World Health Organization (WHO) the incidence rate of breast cancer between 2008 and 2012 was more than 20% with 14% of mortality rate (Ferlay and al., 2013), and as there is no prevention techniques, the only way to help patients survive is by early detection. If cancerous cells are detected before they spread other organs, the survival rate of patient is more than 97% (American cancer society homepage 2008).

There is no doubt that the evaluations of data taken from patients and experts decisions are most important factors in diagnosis. However, artificial intelligence techniques and expert systems are gaining popularity in this field by dint of their high diagnosis capability and effective classification. In this context, various articles have been published in the aim of classifying breast cancer databases using artificial intelligence techniques as Neural Networks (Marcano-Cedeno et al.,2011)(Timmy Manning and Paul Walsh, 2013)(Zadehand et al., 2012)(Aboul Ella Hassanien et al., 2014), SVM(Mahnaz and Broumandnia, 2013)(Aboul Ella Hassanien et al., 2013); Genetic Algorithms(Jain, R. and J. Mazumdar, 2003)(Mazurowski, M.A., et al., 2007) Expert Systems (Wan Noor et al., 2013) and Artificial Immune Systems(Sharma and Sharma, 2011)(Daoudi et al., 2013)(Daoudi et al., 2013).

The natural immune system is composed of diverse sets of cells and molecules that work together with other systems (like neural and endocrine) for maintaining homeostatic state. It primary function is to protect the body from foreign substances called antigens by recognizing and eliminating them. This process is known as the immune response. It makes use of a huge variety of antibodies to neutralize these antigens (Leung, K. et al., 2007).

The Artificial Immune Systems (AIS) are adaptive systems which are inspired by human immune system and offer similar features of biological immune system such as self-organization, noise tolerance and memory mechanism, while having the ability to learn(J. H. Ang and al., 2010).

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There are many models of Artificial Immune Systems including negative selection, clonal selection and immune networks.

The immune network theory was first proposed by Jerne in 1947 (Jerne, N.K, 1974), the hypothesis was that the immune system maintains an idiotypic network of interconnected antibodies to recognize an antigen (Aickelin et al., 2014). The negative selection is a mechanism that protects the body from self-reactive lymphocytes. It deals with the immune system's ability to detect unknown antigens while not reacting self-cells (Daoudi et al., 2013). The Clonal Selection algorithms are derives from the clonal selection principle, which is based on initiation of candidate solution, affinity maturation, selection, cloning, mutation and reselection.

In the last decade, AIS have proven their effectiveness in different areas and especially in the medical field, they were applied to the detection of lung disease, diagnosis of diabetes, tuberculosis, heart disease and the detection of several types of cancers... etc..

This paper proposes enhancements of a popular clonal selection algorithm named CLONALG, for classification of breast cancer cells into benign/malignant classes taking into account three new descriptors of the Digital Database for Screening Mammography (DDSM). The results obtained are compared to different AIS algorithms and SVM.

2 DDSM CLASSIFICATION METHOD

In This Section, we first present CLONALG algorithm and it limitations, and then we give detailed descriptions of the enhancements made on this algorithm for breast cancer classification.

2.1 CLONALG Limitations

From proposed works respectively in (Daoudi et al., 2013a) and (Daoudi et al., 2013b), we try to enhance CLONALG algorithm. The first approach named Cells Clonal Selection (CCS-AIS), the principle is to select the best cells to be cloned by calculating the averages of groups of the most competent cells. The second one Medial Filter Artificial Immune System (MF-AIS), the algorithm introduces median filter principle to create the cell to be cloned.

Both algorithms propose improvements of CLONALG algorithm (De Castro et al., 2002) which is one of the most popular algorithms in the field of the Artificial Immune systems using the principle of the clonal selection.

We can distinguish two main limitations in CLONALG algorithm. Indeed, the first limitation we can observe is in the initialization step, CLONALG algorithm takes a random population of antibodies before launching the learning step. These cells are selected randomly from the set of training examples, which means that the initial cells do not represent necessarily all of the cells to learn. Learning will then depend on this set of randomly initialized cells.

The second limitation of CLONALG is in the training step, CLONALG select for each example to learn a set of memory cells, clone and mutate these cells; a reselection of the best mutated clones is made thereafter to be added to the memory cells set. Next, CLONALG replace P worst cells by randomly created ones, even if the randomly generated cells are worse than the rejected ones or if the rejected cells can be more representatives of other training examples in next generations, no check is made. Figure 1 provides a simple flowchart of the CLONALG algorithm.

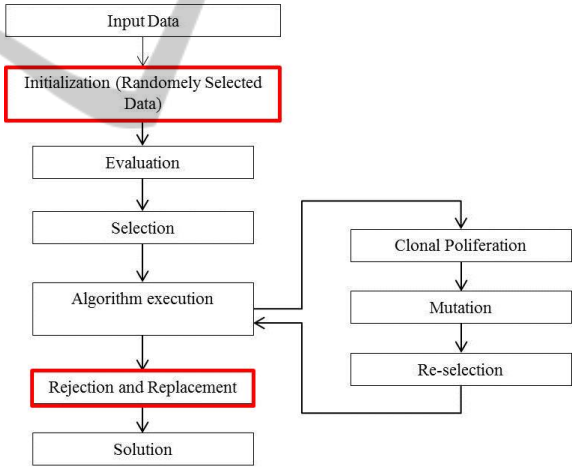

Figure 1: Flowchart of CLONALG.

2.2 Cloned Cell Creation in CLONALG System by CCS-AIS and MF-AIS

The first improvement proposed in both proposed techniques treats the problem of initialization of antibodies before launching the learning, instead of picking randomly some examples of training database, the initialization step consists in dividing every class of learning into subgroups, the average cell of every local subgroup is considered as initial antibody created to launch the learning algorithm.

This process will allow the initial antibodies to represent all the examples to be learnt and not some only. Other various improvements brought to CLONALG in both approaches are during the learning phase, in the choice of the cell to be cloned.

In CCS-AIS, for each example to learn, the selection of the closest cells is made and an average cell of these cells is created, if the average cell has better affinity than the nearest memory cell, it will be added to the set of memory cells, and a set of the best mutated clones of this average cell maximizing the affinity with the learning example is selected to join the set of memory cells, otherwise the best antibody will undergo to the operators of cloning and mutation. Figure 2 presents the flowchart of the CCS-AIS algorithm.

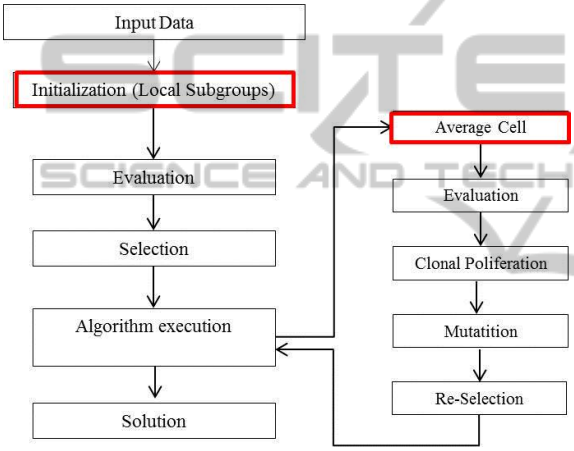

Figure 2: Flowchart of CCS-AIS.

In MF-AIS, the learning phase consists in creating a cell that will be cloned and mutated named median cell. Knowing that the learning base is composed of N attributes, the process of creating the median cell is done by selecting N closest cells to the learning example by measuring affinity, and taking the median value of each attribute from these cells. The median cell created is subsequently evaluated and if it has a higher affinity than the nearest antibody, it will be added to all memory cells as well as all its best mutated clones. The diagram of MF-AIS is given in Figure3.

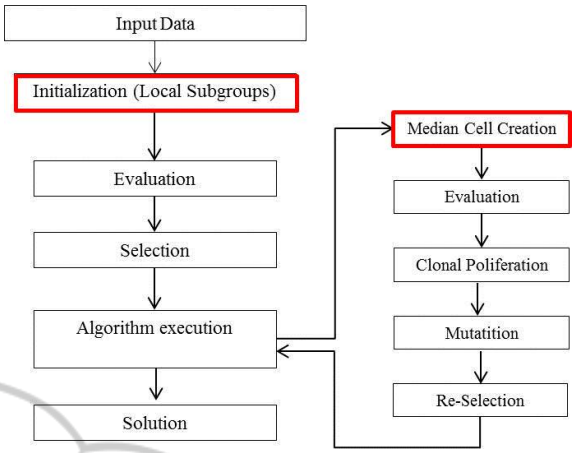

Figure 3: Flowchart of MF-AIS.

The classification step consists of comparing each example to classify to all memory cells obtained at the end of learning, and the example is assigned to the class of the memory cell that maximizes the affinity.

Both detailed above approaches have been applied for the diagnosis of breast cancer on the Wisconsin Breast Cancer Database (WBCD), and the results were promising, to validate the approaches, we propose in this article apply them on another database widely used in the field of detection of breast cancer using new descriptors, and to compare the results obtained with other AIS methods.

2.3 Improvements on DDSM

In order to compare the results obtained in our previous work and validate our approaches, we chose a database constructed from digitized films named Digital Database for Screening Mammography (DDSM). It was assembled by a group of researchers from the University South Florida and was completed in 1991 (M. Heath et al., 2000). DDSM contains 2620 cases collected from Massachusetts General Hospital, Wake Forest University School of Medicine, Sacred Heart Hospital and Washington University of St. Louis School of Medicine.

Digital Database for Screening Mammography was widely used by the scientific community in the field of breast cancer; it has the advantage of using the same lexicon standardized by the American College of Radiology in BI-RADS. The different patient records were made in the context of screening and were classified into three cases: normal case (no lesions), benign case and malignant

case, each file is composed of four views containing the mediolateral-oblique incidence (MLO) and the Cranio-Caudal incidence (CC) of each breast. These files are also provided with annotations provided by expert radiologists. Fig 4 shows samples DDSM used in the evaluation.

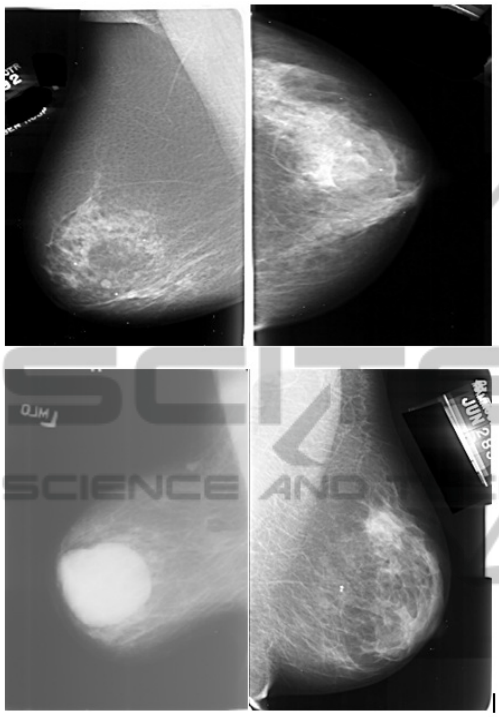

Figure 4: Samples of DDSM database used in evaluation.

Sub-base of DDSM was created consisting of 242 masses: 128 benign and 114 malignant. These examples will be partitioned into training examples and test examples.

Part description of breast masses is a very important part , in (Cheikhrouhou, 2012), the author proposed three new descriptors: the skeleton endpoint (SEP), Protuberance selection (PS) and the spiculated mass Descriptor (SMD), which were compared to 19 other descriptors proposed in the literature including:

- Area;
- Perimeter;
- Circularity;
- Squareness;
- Modified squareness;
- Compactness;
- Curvature;
- Elliptic normalized skeleton;
- Number of large protuberances and depressions;
- Average of the normalized radial length;
- Standard deviation of the normalized radial length;
- Entropy;
- Ratio of surface;
- Roughness;
- Rate of zero crossing;
- Difference of the standard deviations;
- Modified entropy;
- Report of surface modified;
- Rate of modified crossing in zero.

In this work, all of the 22 descriptors are used in the stage of classification by both approaches detailed in the section 2.1; the results obtained as well as a comparison of the results are presented in the following part.

3 RESULTS AND DISCUSSION

3.1 DDSM Classification Results

The performances of the approaches are studied using DDSM, the training data are antigens represented by feature vectors, also, the antibodies have the same shape as the antigenic vectors, and the Euclidean distance is used as a measure of similarity; the 5-CV (Cross validation) is used. Specifically, each dataset is split into five equal subsets. In every run of each algorithm, one of the subsets was used as test set, and the remaining four comprised the training set. The average of 5 times of successive runs is taken as classification result. After 1, 2, 5, 8 and 10 iterations, memory cells generated at the end of learning are used in classification, by comparing each cell to classify to all of the created memory cells, and assigning it to the class containing the memory cell with the highest measure of similarity, simulation and implementation are done using MATLAB 7.11.0. Tables 1 and 2 summarize the results obtained:

Table 1: Classification accuracies of Cells Clonal Selection AIS on DDSM.

Iteration N°	Classification Accuracies (%)	
	Train	Test
1	72,85	71,21
2	93,24	96,48
5	93,56	96,81
8	93,74	96,69
10	97,70	98,13

Table 2: Classification accuracies of Median Filter AIS on DDSM.

Iteration N°	Classification Accuracies (%)	
	Train	Test
1	95,89	92,89
2	96.76	94.23
5	95,18	93,87
8	95,31	96,96
10	96,33	97.74

So as to compare the results obtained, we have implemented different AIS algorithms and applied them on DDSM using the same parameters; Table 3 shows the test results of five successive runs, the average accuracy and supported by the standard deviation value of each AIS classification algorithm:

$$\sigma = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(Xi - \overline{X})^2} \quad (1)$$

Calculating the standard deviation (1) of successive runs of each algorithm allows us to know how the results of different executions are far from the average accuracy. Indeed, for CCS-AIS de standard deviation is 0.82 while it is 1.85 for CLONALG algorithm.

Table 3: Classification accuracies of different AIS algorithms on DDSM.

AIS Algorithm	Classification Accuracies (%)						σ (Standard Deviation)
	1st run	2nd run	3rd run	4th run	5th run	Average	
CSA	90.15	92.21	88.34	93.67	89.33	**91.17**	**2.21**
CLONALG	96.35	92.67	97.26	94.83	96.75	**95.57**	**1.85**
CLONAX	95.77	93.84	91.96	94.51	95.18	**94.25**	**1.47**
AIRS	81.27	83.54	80.12	84.67	81.16	**82.15**	**1.88**
CCS-AIS	98.33	99.09	97.92	96.87	98.46	**98.13**	**0.82**
MF-AIS	98.94	96.87	97.75	96.66	98.49	**97.74**	**0.99**

To validate the new proposed descriptors, author in (Cheikhrouhou, 2012) classified each one separately using SVM classifier, on order to compare our approaches, we applied CCS-AIS AND MF-AIS on the three new descriptors, the results obtained are given in Table 4, and ROC curves representing the results of the two proposed approaches are presented un Figure 5 and Figure 6 .

Table 4: Classification accuracies of different AIS algorithms on DDSM.

Descriptors	Classification Accuracies		
	SVM (Cheikhrouhou,2012)	CCS-AIS	MF-AIS
SEP	92%	95.43	93.12
PS	93%	97.69	96.52
SMD	97%	98.95	98.57

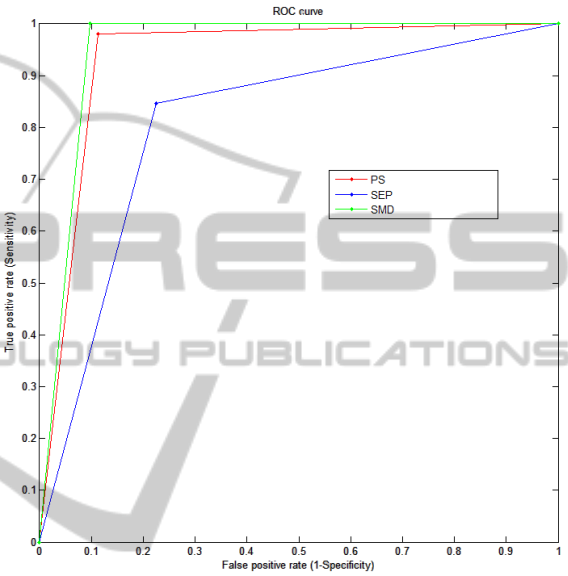

Figure 5: Roc Curves of test results Cells Clonal Selection-AIS on the three new descriptors proposed.

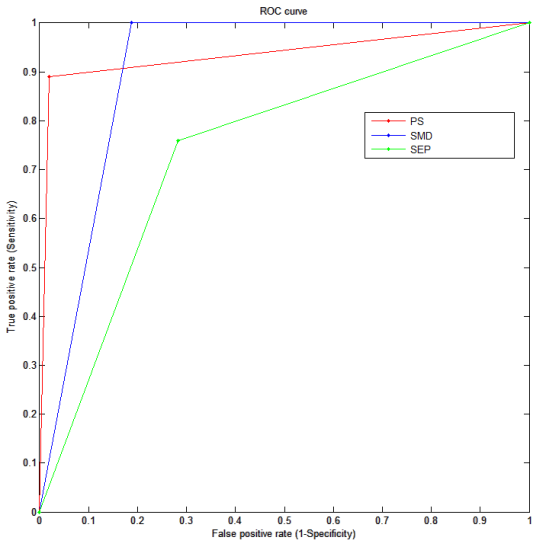

Figure 6: Roc Curves of test results of Median Filter-AIS on the three new descriptors proposed.

3.2 Discussion

From the tables above, we can see that the improvements brought to CLONALG show effective. The choice of the initial antibodies to launch an AIS algorithm directly affects the results, it is necessary that these antibodies represent all learning classes and not just some examples only, it will allow to find the cell which represents most exactly the example to learn. The creation of local subgroups from learning classes has treated this problem in each of the both proposed approaches.

The creation of the cloning cell also played an important role in the learning phase, in Cells Clonal Selection AIS, the creation of this cell was done by calculating an average cell of the best memory cells, while in median Filter AIS, the median cell was created from the median values of each attribute of the matrix of the nearest memory cells, and to maximize the affinity of each cell created, they are compared to the best antibodies and they are added to the set of memory cells only if they are better. No cell can be representative in next generation was rejected.

Classification results after 20 iterations on DDSM taking into account three new descriptors proposed in (Cheikhrouhou, 2012) are 98.71% for cells clonal selection AIS and 98.21% for Median Filter for AIS, efficient results compared to other approaches AIS.

The classification results of each one of the new descriptors separately prove that the proposed approaches prove the effectiveness of the proposed techniques comparing to the SVM classifier.

4 CONCLUSION

In this work, the classification of DDSM by Clonal Selection-Based AIS was presented. Each of the two techniques deals with the problem of initialization of the antibodies before the launching of the training Phase for the representation of the entirety of the data to learn and proposes a new method for the choice of the cell to clone in order to maximize affinity with the training example. Cells Clonal Selection AIS proposes the creation of an average cell from the closest memory cells, and Median Filter AIS introduces the principle of the median filter to create a median cell for the cloning. The obtained results indicate that the improvements brought to CLONALG are effective and can be of a precious help to the experts for a second opinion in their diagnosis of breast cancer.

Note that we have made is that the two approaches in particular and AIS algorithms generally require heavy computation time , our next work will focus on the treatment of this problem.

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