An experimental comparison of supervised classification algorithms for breast cancer detection

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Abstract. Breast cancer is considered as one of the most common cancers worldwide. It affects millions of women, of all ages. The automatic or semi-automatic detection of breast cancer lesions is still a challenge for the scientific community, and several methods have been proposed to perform this task. In this paper, we evaluate the performance of several supervised classification algorithms, for breast cancer detection. We also explore the impact of rough Set based feature selection technique in breast cancer data obtained from mammography images. The experimental results show that bio-inspired techniques based on Artificial Immune Systems obtain promising results.

Keywords: breast cancer · supervised classification · experimental comparison.

1 Introduction

The most common cancers among the world are breast, colon, lung and prostate cancer [1]. Breast cancer is a serious problem in women's health around the entire world. According to the paper presented by Felicia Marie Knaul and collaborators [2], since 2006, breast cancer is the worldwide second cause of death among women between 30 and 54 years. In Mexico, an increase of 16,500 annual cases is estimated by 2020, due to population growth and aging. Breast cancer causes many more deaths compared to cervical cancer [2], and affects adult women of all ages and all economic levels. Aging is a factor in the development of cancer; however, age is not a main factor given that breast cancer does not depend directly on it but certain types of cancer occur more frequently at older ages. Therefore, it is highly recommended to perform an annual examination for breast lesions for women aged between 40 and 49.

There is a necessity in all countries to promote the use of techniques to detect breast cancer in early phases. The data presented [1] shows that only between 5% and 10% cases of breast cancer in Mexico are detected in early phases compared to 50% of the cases detected in the United States of America. The automatic or semi-

automatic detection of breast cancer lesions is still a challenge for the scientific community [3-5]. Several works have been proposed for breast image segmentation and classification [6-8], and international repositories of breast cancer data are now available [9-11]. However, there is a lack of recent comparative studies in the performance of supervised classification algorithms for detecting breast cancer. In this paper we address this issue, by performing an experimental comparison of several classification algorithms over mammographic image data. Our comparison includes classic algorithms and bio-inspired algorithms, which presented competitive performance compared to classic algorithms. We also explore the influence of feature selection methods in breast cancer classification.

The paper is organized as follows. Section 2 addresses some previous works in the field of automatic or semi-automatic breast cancer diagnosis. Section 3 explains the classification algorithms under comparison, while section 4 presents the experimental results. The paper finalizes with conclusions and future work.

2 Previous Works

Breast cancer is a serious problem in women's health around the entire world. There are several techniques used for the accurate diagnosis of breast cancer, such as mammography studies [12], Magnetic Resonance Image (MRI) [13], ultrasounds [14] and biopsy [15], among others. The automatic and semi-automatic detection of breast cancer lesions have been addressed since 1987 [16]. Later in 1993 [17] a method was proposed for cancer diagnosis based on image analysis. In 1999, Pena-Reyes and Sipper proposed an automatic diagnosis of breast cancer combining two methodologies: fuzzy systems and evolutionary algorithms [18]. In 2015 a work was presented [19] using Krill Herd optimization algorithm to classify breast cancer datasets. This work obtained a simple classification rule in order to classify breast cancer lesions. This rule can be used in the decision making process for the breast cancer diagnosis. In 2016 Magna et al. proposed an ensemble of classification models based on artificial immune systems to identify mammography anomalies for breast cancer detection [20]. This resulted in promising results using it for classification tasks, which represents an important advance in artificial immune systems.

Nevertheless, there is no a comparison of algorithms used for classification task including bio-inspired algorithms. In this paper, we addressed this issue, by performing a wide-range comparison of several supervised classifications algorithms, for detecting the presence or absence of breast-cancer in mammography images data.

3 Classification algorithms used in the experiments

Supervised classifiers aim at predicting the class of a new, unlabeled instance, by considering the information of previously labeled instances; that is, the instances in

the training set. In the following section, we will explain the main aspects of the supervised classification algorithms under comparison.

The Nearest Neighbor (NN) classifier was proposed by Cover and Hart in 1967 [21] as an algorithm to classify patterns according to the k nearest neighbors in the previously learnt patterns. This algorithm is one of the most fundamental and simpler classification methods, positioning it as one of the first choices for a classification task.

It has been used to solve a wide range of problems, such as on-chip template reduction [22], study of unfolded state of peptides and proteins [23], traffic flow forecasting [24] and breast cancer classification [25].

Naïve Bayes classifier is based on the Bayes Theorem and is useful to deal with issues of uncertainty and noise [26].

Naïve Bayes assumes that all the attributes are not related and even with that assumption the Naïve Bayes classifier has showed a nice performance for estimations and feature selection for text classification [27]. This classifier has also been used for risk classification [28], fault diagnosis [29] and recently for breast cancer detection [30].

Support Vector Machines (SVM) have been gaining popularity within pattern recognition [31-33]. SVM has been used for recognizing human actions [31], protein classification [32], and also for breast tumor classification [33].

Decision trees are a family of supervised classifiers. A decision tree produces a model with rules for both continuous and categorical variables [34]. Among decision trees, the C4.5 algorithm is highly relevant [35]. This method is used for predicting categorical outcomes and it has been used for imbalanced data sets and redundant features in text categorization [36]. It has also been used for breast cancer prediction in ultrasound images [37], heart disease prediction [38] and satellite network fault prediction [39].

RIPPER is a rule-based classifier [40]. This classifier is one of the most popular algorithms because of the set of rules generated using incremental reduced error. This algorithm is based on finding a set of rules that cover all the patterns for each class in the dataset [40].

Among bio-inspired classification techniques, the ones based on the Immune System have acquired a high relevance for several disease classifications, such as chest diseases [41] breast cancer [20] and Parkinson [41].

The Immune system is a complex system which allows processing information using pattern recognition, learning skills and pattern memory. This system is decentralized, which implies that this system is fault tolerant. The Artificial Immune System tries to mimic the behavior of the Biological Immune System [42].

The Biological Immune System is composed of cells, molecules and organs whose function is to keep a healthy organism, protecting it from harmful agents (Antigens).

The innate Immune System has, since we were born, the ability to recognize and destroy antigens. This system is the responsible for activating the adaptive immune system response.

There are many algorithms based on Artificial Immune Systems which try to mimic some process or characteristic of the Biological Immune System [42]. The most common are:

Immune network: It is based on creating a network that has connected nodes that recognizes; also it has nodes that interact with external antigens [43].

Negative Selection: It is based on discriminating cells which belong and not belong to the system. Also it detects changes in the system behavior using detectors that do not necessarily have communication with other detectors [44].

Clonal Selection: It is based on the idea that only the best lymphocytes responding to the presence of antigens will be reproduced using cloning algorithms [45].

Dendrite cells: It is based on a network that represents the behavior of cells in a population. It is used in multi-scale approach [46].

In this paper we explore two immune-based algorithms and their variations: the Clonal Selection based algorithms [45], and the Artificial Immune Recognition System (ARIS) algorithms [47].

Clonal Selection algorithm is very similar to genetic algorithms but the population is dynamic. Also, only the best antibodies of the population are taken using an affinity function. These antibodies are cloned and mutated using an inverse affinity function (The higher the affinity, the lower the probability of mutation). Antigens are chosen with the highest affinity and the process is repeated.

On the other hand, ARIS algorithm was proposed by Watkins [48] in 2001 as an unsupervised learning algorithm inspired by the biological theory of clonal selection proposed by Burnet in 1957 [49]. The AIRS algorithm was designed later for classification problems [47]. Typically the Euclidean distance is used as affinity function. For this algorithm, all the cells are initialized with small random quantities. All the algorithms were tested in the WEKA software [50] using the implementations of Jason Brownlee in 2015.

4 Experiments

The dataset used in this paper was from the Breast Cancer Digital Repository [10] by the Faculty of medicine in the University of Porto, in Portugal.

This dataset is composed of 200 biopsy-tested lesions of 190 women, rendering 362 segmentations including clinical data and descriptors based on the segmented images.

This is a binary class dataset (Benign class and malignant class) due to the classification made by the radiologist. The dataset has missing values wich are represented as NaN (Not a number). The lesion outlines were identified by a group of expert radiologists.

Using the AIRS classifiers implementation for WEKA software [50], we obtained the performances for the algorithms implemented as showed in Table 3. There are three fundamental models implemented in AIRS classifiers: Based on AIRS algorithm, Based on Clonal Selection algorithm and Based on Immune Systems.

According to Table 3, only the algorithms that had the best performances were used for later tests. The validation algorithm used for all algorithms was 10-fold cross-validation [51].

Table 3. Performances of the bio-inspired algorithms in WEKA using default configurations.

Algorithm	Performance
AIRS 1	70.442%
AIRS 2	67.6796%
AIRS 2 Parallel	71.2707%
CLONALG	56.3536%
CSCA	56.0773%
Immunos 1	56.0773%
Immunos 2	59.3923%
Immunos 99	55.8011%

The algorithms used in the comparisons were AIRS 1 [48], CLONALG [52] and Immunos2 [53] because they showed to be the algorithms with the best performances for each fundamental model. The default parameters and their descriptions of AIRS 1 and CLONALG are presented in Table 4 and Table 5. Immunos2 does not have modifiable parameters.

The parameters in bold letters of Table 4 and Table 5 are very sensitive to modifications in order to obtain a better performance. Each parameter was changed by the values of Table 6. When changing the previous parameters, we obtained the performances shown in Table 7.

The classical supervised classifiers were used with their default parameters. Gathering all the information, we can definitely analyze the performances of the classifications made by all the algorithms tested in this paper. The results are shown in Table 8.

We can observe that AIRS algorithm is the second best algorithm according to the performances shown.

Feature selection has been used for classification tasks as presented in 2016 [54]. However, feature selection was performed using the LEX algorithm [55] for the dataset presented in this paper, although it shown that for this dataset, the performance was lower in all proven cases.

Some of the tests for the reducts [56] are shown in Table 9, the first column shows the index attribute used in the Reduct, and the following columns represent the performances of each bio-inspired algorithm.

As we can deduct from Table 9, using a reduct for the dataset does not result in a better performance. All the results showed that the use of reducts decrease the performance in both bio-inspired algorithms.

Table 4. Parameter descriptions for AIRS algorithm.

Parameter	Description	Default value
Affinity threshold scalar	Used to determine whether or not a candidate memory cell can replace the previous best matching memory cell	0.2
Initial ARB cell pool size	Number of randomly selected training data instances used to seed the ARB cell pool	1
Clonal rate	Determine the number of mutated clones	10
Hypermutation rate	Determine the number of clones a memory cell can create using the clonal rate	2
k-Nearest Neighbor	**The number of best matching memory cells used during the classification stage to majority vote the classification of unknown data patterns**	**3**
Initial memory cell pool size	Specifies the number of randomly selected training data instances used to seed the memory cell pool	1
Mutation rate cloned ARBs	Determine the degree of mutation of cloned ARB	0.1
Total training instances to calculate affinity threshold	Specifies the number of training data instances used to calculate the affinity threshold (mean affinity between data instances)	-1
Stimulation threshold	**Determine when to stop refining the pool of ARBs for an antigen**	**0.9**
Total allocable resources	Specifies the maximum number of resources (B-cells) that can be allocated to ARBs in the ARB pool	150

Table 5. Parameter descriptions for CLONALG algorithm.

Parameter	Description	Default value
Antibody pool size	**Antibodies maintained in the memory pool and remainder pool**	**30**
Clonal factor	**Used to scale the number of clones created by the selected best antibodies**	**0.1**
Total generations	**Total number of times that all antigens are exposed to the system**	**10**
Remainder pool percentage	Percentage of the total antibody pool size allocated for the remainder pool	0.1
Selection pool size	Total number of best antibodies selected for cloning and mutation each iteration	20
Total replacements	**The total number of antibodies in the remainder pool that are replaced each iteration**	**0**

Table 6. Modified parameters descriptions for immune-based algorithms.

AIRS	CLONALG
k-Nearest Neighbor = 1	Antibody pool size = 28
Stimulation threshold = 0.99	Antibody pool size = 28
	Total generations = 15
	Total replacements = 3

Table 7. Performances of the different AIRS algorithms in WEKA using modified configurations in the parameters.

Algorithm	Performance
AIRS	77.9006 %
CLONALG	59.3923 %

Table 8. Performances of all the classification algorithms tested in WEKA ordered by descendant performance.

Algorithm	Performance
SVM (SMO)	80.1105 %
AIRS	**77.9006 %**
JRip	75.1381%
J48 (C4.5)	75.1381 %
3NN	74.8619 %
1NN	73.4807 %
Naïve Bayes	72.3757 %
Immunos	**59.3923%**
CLONALG	**59.3923 %**

Table 9. Performances of the different reducts found by LEX algorithm using modified configurations in the parameters for the bio-inspired algorithms in WEKA.

Reduct	Performance AIRS	Performance CLONALG
{20;2;3;4;8;9;13;15;18;19;0;21;22;23;28;32}	69.6133%	48.3425%
{20;2;3;4;8;9;10;11;12;13;15;18;19;0;21;22;23}	69.6133%	54.6961%
{20;2;3;4;8;9;10;11;13;15;18;19;0;21;22;23;24;27}	71.8232%	53.8674%
{20;2;3;4;8;9;10;11;13;15;18;19;0;21;22;23;25}	70.7182%	53.0387%

5 Conclusions

According to the tests performed in this paper, the bio-inspired algorithms for pre-diagnosis of breast cancer are as competitive as classic algorithms. The use of this kind of algorithms is very useful in the dataset presented as the performances of the bio-inspired algorithms were nearly at the top, just after Support Vector Machines. Adjusting the parameters of the bio-inspired algorithms can result in having a better performance according to the tests made in this paper. The use of Rough Set based feature selection did not show any improvement in classifier performance.

Acknowledgments

The authors would like to thank the Instituto Politécnico Nacional (Secretaría Académica, Comisión de Operación y Fomento de Actividades Académicas, Secretaría de Investigación y Posgrado, Centro de Investigación en Computación, and Centro de Innovación y Desarrollo Tecnológico en Cómputo), the Consejo Nacional de Ciencia y Tecnología (Conacyt), and Sistema Nacional de Investigadores for their economic support to develop this work

6 References

1. Borja-Aburto, V. H., Dávila-Torres, J., Rascón-Pacheco, R. A., González-León, M., Fernández-Gárate, J. E., Mejía-Rodríguez, I., ...& Escudero-de los Ríos, P. M. (2016). Cancer mortality in the Mexican Social Security Institute, 1989-2013. salud pública de méxico, 58(2), 153-161. (2016)
2. Knaul, F.M., Nigenda, G., Lozano, R., Arreola-Ornelas, H., Langer, A., Frenk, J.: Breast cancer in Mexico: an urgent priority. Salud publica de Mexico 51, s335-s344 (2009)
3. Cecchini, R.S., Swain, S.M., Costantino, J.P., Rastogi, P., Jeong, J.-H., Anderson, S.J., Tang, G., Geyer, C.E., Lembersky, B.C., Romond, E.H.: Body mass index at diagnosis and breast cancer survival prognosis in clinical trial populations from NRG Oncology/NSABP B-30, B-31, B-34, and B-38. Cancer Epidemiology Biomarkers & Prevention 25, 51-59 (2016)

4. Gubern-Mérida, A., Vreemann, S., Martí, R., Melendez, J., Lardenoije, S., Mann, R.M., Karssemeijer, N., Platel, B.: Automated detection of breast cancer in false-negative screening MRI studies from women at increased risk. European journal of radiology 85, 472- 479 (2016)
5. Krawczyk, B., Galar, M., Jeleń, Ł., & Herrera, F. (2016). Evolutionary undersampling boosting for imbalanced classification of breast cancer malignancy. Applied Soft Computing, 38, 714-726. (2016)
6. Kowal, M.: Computer-aided diagnosis for breast tumor classification using microscopic images of fine needle biopsy. Intelligent Systems in Technical and Medical Diagnostics, pp. 213-224. Springer (2014)
7. Su, H., Shen, Y., Xing, F., Qi, X., Hirshfield, K.M., Yang, L., Foran, D.J.: Robust automatic breast cancer staging using a combination of functional genomics and image-omics. In: Engineering in Medicine and Biology Society (EMBC), 2015 37th Annual International Conference of the IEEE, pp. 7226-7229. IEEE, (2015)
8. Gu, P., Lee, W.-M., Roubidoux, M.A., Yuan, J., Wang, X., Carson, P.L.: Automated 3D ultrasound image segmentation to aid breast cancer image interpretation. Ultrasonics 65, 51-58 (2016)
9. Lichman, M.: UCI machine learning repository. University of California, Irvine, School of Information and Computer Sciences (2013)
10. Moura, D.C., López, M.A.G.: An evaluation of image descriptors combined with clinical data for breast cancer diagnosis. International journal of computer assisted radiology and surgery 8, 561-574 (2013)
11. Van't Veer, L.J., Dai, H., Van De Vijver, M.J., He, Y.D., Hart, A.A., Mao, M., Peterse, H.L., van der Kooy, K., Marton, M.J., Witteveen, A.T.: Gene expression profiling predicts clinical outcome of breast cancer. nature 415, 530-536 (2002)
12. Wu, Y., Giger, M.L., Doi, K., Vyborny, C.J., Schmidt, R.A., Metz, C.E.: Artificial neural networks in mammography: application to decision making in the diagnosis of breast cancer. Radiology 187, 81-87 (1993)
13. Kriege, M., Brekelmans, C.T., Boetes, C., Besnard, P.E., Zonderland, H.M., Obdeijn, I.M., Manoliu, R.A., Kok, T., Peterse, H., Tilanus-Linthorst, M.M.: Efficacy of MRI and mammography for breast-cancer screening in women with a familial or genetic predisposition. New England Journal of Medicine 351, 427-437 (2004)
14. Warner, E., Plewes, D.B., Hill, K.A., Causer, P.A., Zubovits, J.T., Jong, R.A., Cutrara, M.R., DeBoer, G., Yaffe, M.J., Messner, S.J.: Surveillance of BRCA1 and BRCA2 mutation carriers with magnetic resonance imaging, ultrasound, mammography, and clinical breast examination. Jama 292, 1317-1325 (2004)
15. Kuhl, C.K., Elevelt, A., Leutner, C.C., Gieseke, J., Pakos, E., Schild, H.H.: Interventional breast MR imaging: clinical use of a stereotactic localization and biopsy device. Radiology 204, 667-675 (1997)
16. Wittekind, C., Schulte, E.: Computerized morphometric image analysis of cytologic nuclear parameters in breast cancer. Analytical and quantitative cytology and histology/the International Academy of Cytology [and] American Society of Cytology 9, 480-484 (1987)
17. Wolberg, W.H., Street, W.N., Mangasarian, O.L.: Breast cytology diagnosis via digital image analysis. Analytical and Quantitative Cytology and Histology 15, 396-404 (1993)
18. Pena-Reyes, C.A.s., Sipper, M.: A fuzzy-genetic approach to breast cancer diagnosis. Artificial intelligence in medicine 17, 131-155 (1999)
19. Arumugam, M.M., Kumari, S.: Application of bio-inspired krill herd algorithm for breast cancer classification and diagnosis. Indian Journal of Science and Technology 8, (2015)
20. Magna, G., Casti, P., Jayaraman, S.V., Salmeri, M., Mencattini, A., Martinelli, E., Di Natale, C.: Identification of mammography anomalies for breast cancer detection by an ensemble of classification models based on artificial immune system. Knowledge-Based Systems 101, 60-70 (2016)
21. Cover, T.M., Hart, P.E.: Nearest neighbor pattern classification. Information Theory, IEEE Transactions on 13, 21-27 (1967)

22. Xia, W., Mita, Y., Shibata, T.: A Nearest Neighbor Classifier Employing Critical Boundary Vectors for Efficient On-Chip Template Reduction. (2015)
23. Toal, S.E., Kubatova, N., Richter, C., Linhard, V., Schwalbe, H., Schweitzer-Stenner, R.: Randomizing the Unfolded State of Peptides (and Proteins) by Nearest Neighbor Interactions between Unlike Residues. Chemistry–A European Journal 21, 5173-5192 (2015)
24. Zou, T., He, Y., Zhang, N., Du, R., Gao, X.: Short-Time Traffic Flow Forecasting Based on the K-Nearest Neighbor Model. traffic 1, 36 (2015)
25. Bagui, S.C., Bagui, S., Pal, K., Pal, N.R.: Breast cancer detection using rank nearest neighbor classification rules. Pattern recognition 36, 25-34 (2003)
26. John, G.H., Langley, P.: Estimating continuous distributions in Bayesian classifiers. In: Proceedings of the Eleventh conference on Uncertainty in artificial intelligence, pp. 338-345. Morgan Kaufmann Publishers Inc., (1995)
27. Chen, J., Huang, H., Tian, S., Qu, Y.: Feature selection for text classification with Naïve Bayes. Expert Systems with Applications 36, 5432-5435 (2009)
28. Minnier, J., Yuan, M., Liu, J.S., Cai, T.: Risk classification with an adaptive naive bayes kernel machine model. Journal of the American Statistical Association 110, 393-404 (2015)
29. Sharma, R.K., Sugumaran, V., Kumar, H., Amarnath, M.: A comparative study of naïve Bayes classifier and Bayes net classifier for fault diagnosis of roller bearing using sound signal. International Journal of Decision Support Systems 1, 115-129 (2015)
30. Kharya, S., Soni, S.: Weighted Naive Bayes Classifier: A Predictive Model for Breast Cancer Detection. International Journal of Computer Applications 133, 32-37 (2016)
31. Schüldt, C., Laptev, I., Caputo, B.: Recognizing human actions: a local SVM approach. In: Pattern Recognition, 2004. ICPR 2004. Proceedings of the 17th International Conference on, pp. 32-36. IEEE, (2004)
32. Leslie, C.S., Eskin, E., Noble, W.S.: The spectrum kernel: A string kernel for SVM protein classification. In: Pacific symposium on biocomputing, pp. 566-575. (2002)
33. Wu, W.-J., Lin, S.-W., Moon, W.K.: An Artificial Immune System-Based Support Vector Machine Approach for Classifying Ultrasound Breast Tumor Images. Journal of digital imaging 28, 576-585 (2015)
34. Duda, R., Hart, P., Stork, D.: Pattern Classification, Jon Wiley & Sons Inc. New York 630-633 (2001)
35. Quinlan, J.R.: C4. 5: programs for machine learning. Elsevier (2014)
36. Gabrilovich, E., Markovitch, S.: Text categorization with many redundant features: using aggressive feature selection to make SVMs competitive with C4. 5. In: Proceedings of the twenty-first international conference on Machine learning, pp. 41. ACM, (2004)
37. Kuo, W.-J., Chang, R.-F., Chen, D.-R., Lee, C.C.: Data mining with decision trees for diagnosis of breast tumor in medical ultrasonic images. Breast cancer research and treatment 66, 51-57 (2001)
38. Sharma, P., Saxena, K., Sharma, R.: Heart Disease Prediction System Evaluation Using C4. 5 Rules and Partial Tree. Computational Intelligence in Data Mining—Volume 2, pp. 285-294. Springer (2016)
39. Lin, Y., Ding, S., Wang, Y., Geng, J.: A method of satellite network fault synthetic diagnosis based on C4. 5 algorithm and expert knowledge database. In: Wireless Communications & Signal Processing (WCSP), 2015 International Conference on, pp. 1-5. IEEE, (2015)
40. Cohen, W.W.: Fast effective rule induction. In: Proceedings of the twelfth international conference on machine learning, pp. 115-123. (1995)
41. Er, O., Cetin, O., Bascil, M.S., Temurtas, F.: A Comparative Study on Parkinson's Disease Diagnosis Using Neural Networks and Artificial Immune System. Journal of Medical Imaging and Health Informatics 6, 264-268 (2016)
42. Nasaroui, O., Gonzalez, F., Dasgupta, D.: The fuzzy artificial immune system: Motivations, basic concepts, and application to clustering and web profiling. In: Fuzzy Systems, 2002. FUZZ-IEEE'02. Proceedings of the 2002 IEEE International Conference on, pp. 711-716. IEEE, (2002)

43. de Castro, L.N., Timmis, J.: An artificial immune network for multimodal function optimization. In: Evolutionary Computation, 2002. CEC'02. Proceedings of the 2002 Congress on, pp. 699-704. IEEE, (2002)
44. Ji, Z., Dasgupta, D.: Real-valued negative selection algorithm with variable-sized detectors. In: Genetic and Evolutionary Computation–GECCO 2004, pp. 287-298. Springer, (2004)
45. De Castro, L.N., Von Zuben, F.J.: The clonal selection algorithm with engineering applications. In: Proceedings of GECCO, pp. 36-39. (2000)
46. Greensmith, J., Aickelin, U., Cayzer, S.: Introducing dendritic cells as a novel immune-inspired algorithm for anomaly detection. Artificial Immune Systems, pp. 153-167. Springer (2005)
47. McEwan, C., Hart, E.: On AIRS and clonal selection for machine learning. Artificial Immune Systems, pp. 67-79. Springer (2009)
48. Watkins, A.B.: AIRS: A resource limited artificial immune classifier. Mississippi State University (2001)
49. Burnet, F.M.: A modification of Jerne's theory of antibody production using the concept of clonal selection. Australian J. Sci. 20, 67-69 (1957)
50. Hall, M., Frank, E., Holmes, G., Pfahringer, B., Reutemann, P., Witten, I.H.: The WEKA data mining software: an update. ACM SIGKDD explorations newsletter 11, 10-18 (2009)
51. Stone, M.: Cross-validatory choice and assessment of statistical predictions. Journal of the royal statistical society. Series B (Methodological) 111-147 (1974)
52. De Castro, L.N., Von Zuben, F.J.: Learning and optimization using the clonal selection principle. Evolutionary Computation, IEEE Transactions on 6, 239-251 (2002)
53. Brownlee, J.: Immunos-81, the misunderstood artificial immune system. Faculty of Information & Communication Technologies (ICT) (2005)
54. Sudha, M., Selvarajan, S.: Feature Selection Based on Enhanced Cuckoo Search for Breast Cancer Classification in Mammogram Image. Circuits and Systems 7, 327 (2016)
55. Santiesteban, Y., Pons-Porrata, A.: LEX: a new algorithm for the calculus of typical testors. Mathematics Sciences Journal 21, 85-95 (2003)
56. Velayutham, C., Thangavel, K.: Unsupervised quick reduct algorithm using rough set theory. Journal of Electronic Science and Technology 9, 193-201 (2011)