

Original Research Paper

Boosting-BoW Algorithm for Finding Kidney Diseases from Medical Test Reports

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Abstract: This paper introduces an approach to increase the accuracy rate of classification by employing Bag-of-Words (BoW) as a feature selection method along with machine learning algorithms to obtain a more accurate output. Because of its capability in quickly processing large sets of data and getting accurate results, this approach can be used in medical areas. Different ensemble approaches are generated by different researchers to obtain good results as mentioned in the literature review. In this study a novel algorithm is proposed to analyze medical kidney test reports, using BoW for selecting the features and analyzing them via Boosting four different machine learning classification algorithms like Sequential Minimum Optimization (SMO), k-Nearest Neighbors (k-NN), Random Forests (RF) and Naïve Bayes (NB). With the help of specialists in urology, the proposed algorithm is tested against multiple datasets of different kidney tests. The accuracy of the proposed Boosting algorithms outperforms its counterpart algorithms like SMO, k-NN, RF and NB when they had shown their performances alone.

Keywords: Bag-of-Words, Sequential Minimum Optimization, k-Nearest Neighbors, Random Forests, Naïve Bayes, Boosting Algorithms

Introduction

It has been many years that technological advancements play important role in developing human healthcare systems. Developing electronic medical systems to automatically process clinical diagnosis reports is a significant success. This is because the manual process is slow performing and makes the diagnosis hard for the physicians.

About a half-century ago, health care scientists launched the first so-called “Hospital Automation System” that used classification algorithms (Khachidze *et al.*, 2016). But after several years of development, still there is no such algorithm with 100% accuracy rate, for this reason, scientists are continuously conducting research to develop and find new algorithms that outperform the current ones. The accuracy of the output is affected by different characteristics, such as data size, feature selection technique, classification algorithm, etc.

There are two types of classification; the first one is manual, using hand or classifying texts based on rules and

vocabularies. The second one is automated, which uses different methods to perform this kind of classifications, like Machine Learning algorithms, Information Retrieval (IR) methods and Boosting algorithms technique which can be formed through combining two or more different classification algorithms (Khachidze *et al.*, 2016; Lakshmi and Ponnaivaikko, 2009).

There are various forms of medical records, which differs from different institutions, that is why they are not analyzed and understood by machines easily. Information Retrieval can be used in medical fields. Systems can be developed for this purpose, to help the physicians and the patients, in a way to predict diseases from medical records to support the physicians while they decide on diagnosis of the diseases. The key idea for that type of systems is the reuse of knowledge retrieval (Chou *et al.*, 2008).

Developing an algorithm with a high accuracy rate allows guaranteeing the system that works well for the specified domain (Zhou, 2012). For this purpose, a new algorithm is proposed that finds the disease name from

medical test reports containing tests, such as; blood pressure, calcium rate, albumin rate, etc.

This paper is organized as follows. Section 2 mentions the works previously done that are related to the proposed work. Section 3 explains the materials and methods used in this work. Results and discussion are discussed in section 4. Finally, the conclusion and feature works are presented in section 5.

Literature Review

Clinical test classification is considered as a case of information retrieval, it can also be applied in text classification and electronic medical records (Kotfila and Uzuner, 2015; Gao *et al.*, 2015). Classification in medical diagnosis also needs to cover feature selection, because combining feature selection techniques with machine learning algorithms as classifiers produce an output with a higher accuracy rate (Opitz and Maclin, 1999).

The diagnosis of diseases is a complicated work which needs to be performed accurately. That is why the automation of health-care systems are very needed to help the physicians to diagnose diseases. Computer aided diagnosis systems are discussed as classification problems, the goal is to raise the rate of true decisions and reduce the false ones (Elsayad and Fakhr, 2015).

Nowadays it is a fact that, automated tools are taking less time to classify documents than the manual way. Different researches show that the machine learning algorithms varies depending on the type of the classification task of the diseases. For example, SVM produces quite good results for the classification of diseases like diabetes and cancer (Revathy and Amalraj, 2011; Guyon *et al.*, 2002). The accuracy of the algorithms is also changing due to the type and complexity of the diseases (Nadkarni *et al.*, 2011).

Brazilian Pediatric Healthcare Institution has successfully used a combination of feature selection technique as information retrieval with machine learning algorithms for classification of medical databases (Korde and Mahender, 2012). Khachidze *et al.* (2016) have done a research on the classification of 24,855 medical records using well-known algorithms like KNN and SVM, according to the results obtained, both machine learning algorithms were capable for completing the task successfully with a high accuracy rate, but SVM showed a little more excellence.

Sorich *et al.* (2003) reported that the SVM algorithm produces a good prediction for the medical datasets and also reported that the Naïve Bayesian algorithm produces better performance than SVM. Harper (2005) reported that there is no only a single classification algorithm to classify medical data with the best accuracy.

Fida *et al.* (2011) proposed an ensemble algorithm to enhance the decision of the classification algorithms in diagnosis of heart diseases and they could produce an algorithm with an optimal result. Ahmad *et al.* (2012)

presented a novel ensemble approach based on seeking an optimal combination of multiple algorithms to raise the rate of correct decisions in solving regression problems. Peng (2006) also proposed an ensemble algorithm which began to generate a pool of candidate base classifiers according to the gene sub-samplings, then the process of selection of a subset of appropriate base classification algorithms starts to construct the classification committee based on classifier clustering. Experimental results showed that the proposed approach outperforms the baseline classification algorithms.

In this work Boosting technique is used, where a set of individual classifiers are combined for classifying novel instances. As a result, Boosting technique is often shows great accuracies, since it comes from the voting of decisions of multiple classifiers (Bauer and Kohavi, 1999).

Materials and Methods

The material under process is caught into the medical domain, which is for classifying the medical test reports that contain test names and their results, such as; blood pressure is 80, calcium rate is 10.8, anemia rate is abnormal, ...etc. This work is done with the aim of diagnosing diseases with a high accuracy rate.

There are various machine learning algorithms for feature selection, among all BoW has been chosen to select the features with the aim of simplifying the sets of data. And there are also various classifiers for data classification, in this work, four different algorithms have been selected from four different classification families. The algorithms have good capabilities for medical purposes, so they can be used in the selected domain. SMO has been chosen from the Functions family, k-NN from the Lazy, RF from the Trees and NB from the Bayes family. All the four algorithms have been tested twice, firstly, without employing any feature selection algorithms and then, after employing the BoW algorithm. Rising in results have been noticed after employment of the BoW.

Then all the four algorithms, SMO, k-NN, RF and NB are combined to produce a single Boosting algorithms. In Boosting algorithms, the result is selected using the majority of voting of the results from the four algorithms. As an example, if three of the four algorithms selected a disease and the other one selected a different disease, then the majority will be for the disease that was selected by the three algorithms. In some cases, there is a 50% by 50% equality, which means that there is no any majority and each of two algorithms selected a disease, for that reason, a cost function is applied for the algorithms in a way that priority will be set for each of the four algorithms. In This occasion, the highest priority is set for SMO, then k-NN, RF and NB in sequence. So, there will be no conflict of majority such as a 50% by 50% for any two diseases.

The four algorithms used in this study were tested twice against three different datasets called UCI, MDC and ARYO datasets. Once before using BoW and once after employing the BoW as feature selection algorithm. After employing BoW, rising in the number of correctly classified instances can be noticed very clearly when a comparison is done with the algorithms that showed their performances before employing BoW.

Finally, after employing BoW, the Boosting algorithms also showed a higher rate of correctly classified instances when compared to the classifiers when they showed their performances alone. The study showed that the proposed algorithm can be used as a new classification algorithm in medical and related areas. So, the Boosting algorithms is selected to be trained against the three datasets, then to be used as a trained algorithm for the testing phase to diagnose the kidney diseases from medical test reports. The methodology of the proposed algorithm is shown in Fig. 1.

The materials and the methods used in this work are the followings:

Performance Datasets

Three different medical test datasets for patients with kidney diseases were collected from three different sources, each contains different medical tests with their results. The first dataset is from the University of California, Irvine (UCI) database (Rubini, 2015), which is one of the world's greatest databases for scientific datasets. The dataset contains clinical records; each record contains 24 different attributes for 400 different patients which have taken from the Apollo Hospital in India. The second dataset is from Medya Diagnostic Center (MDC) in Erbil, Iraq; which is a high qualified diagnostic center in the Middle East. The MDC dataset contains 10 different tests for 576 patients. And the last dataset is from ARYO center which supervises more than 70 medical test laboratories in Erbil, the dataset contains 10 different tests for 383 patients. Finally, 70% of all the three datasets were selected as the training set and 30% as the testing set. The number of samples, training and testing set instances of each dataset are shown in Table 1.

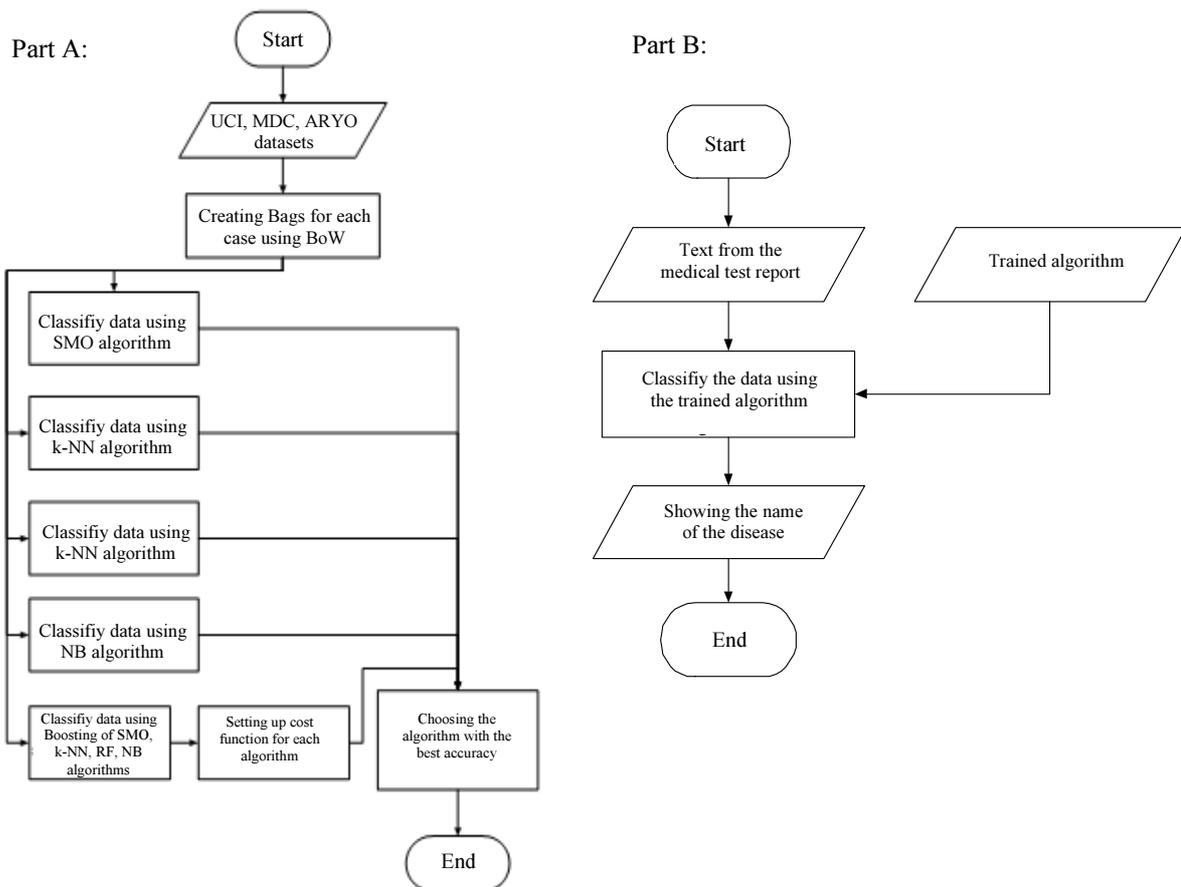


Fig. 1: Flowchart showing the methodology of the proposed algorithm. Part A shows the methodology of the training phase and part B shows the methodology of the testing phase

Feature Selection

In machine learning, feature selection is the process of selecting a subset of relevant variables or features to be used in model construction. It is also known as variable subset selection and attribute selection (Saeys and Larrañaga, 2007). There are four main advantages of using feature selection techniques (Bermingham *et al.*, 2015):

- Simplifying the model to make it easier to be interpreted by tools or users
- Time-saving for training
- Decreasing the number of attributes or features
- Reducing variance

Feature selection methods work to decrease and remove irrelevant features which have no impact on the output. It enhances the data for the next step, thus the classification of new instances will be more accurate.

In the proposed algorithm, the authors selected BoW as feature selection algorithm, since it has a great capability for selecting features. The algorithm creates bags for each instance types, in this work bags are created for each disease types for all the three datasets used.

Bag-of-Words (BoW)

Also called Vector Space Model (Polpinij and Ghose, 2008) and Bag of Features (BoF). In this technique, a sentence or a text in a document is represented as the multiset (bag) of its words. The order of the word and the grammar does not affect the output, but the number of the occurrences affects. The BoW model is also used widely in natural language processing, information retrieval and computer vision areas. This model is commonly used in document classification algorithms, where the occurrence of each word is used as a feature for its document type (Russell and Norvig, 2016).

Classification of the Data

The classifiers used in this work are the followings:

Sequential Minimum Optimization (SMO)

The SMO algorithm is proposed in 1998, as a solution for a common problem in SVM where arising in the problem of Quadratic Programming (QP) occurred during the training process of SVM. It breaks down a large QP problem into a series of smaller QP problems and those smaller QP problems are solved analytically and saves time. SMO can process very large training set sizes because the amount of memory needed is linear in SMO (Platt, 1998).

k-Nearest Neighbors (k-NN)

k-NN is a non-parametric and instance-based learning algorithm and is commonly used for classification and regression (Altman, 1992). In the feature space, the input consists of k closest training examples for both the classification and regression. It flows into lazy learning or instance-based learning. The k-NN algorithm is one of the simplest and common machine learning algorithms. It is a very useful technique and it can be used to assign weight to each object with the help of its neighbor objects as shown in Fig. 2. This way the nearer neighbors have more impact on the average than the others which are more distant. For example, the weighting scheme of each point is done by giving each neighbor a weight which is equal to $1/d$, where d is the distance to each neighbor from that object.

Random Forests (RF)

The RF was discovered in 2001, which is a successful algorithm for classification and regression, it can be used for biological and chemical purposes. It shows excellent performance in cases where the number of variables is so larger than the number of observations, it combines several randomized decision trees and outputs the result by aggregating predictions via averaging as shown in Fig. 3. It has great capability to be used for large-scale problems (Breiman, 2001). RF can be used for applications in many fields, such as; decision support systems in healthcare, risk management, to find clusters of patients based on tissue marker data and tailored health communications (Khalilia *et al.*, 2011).

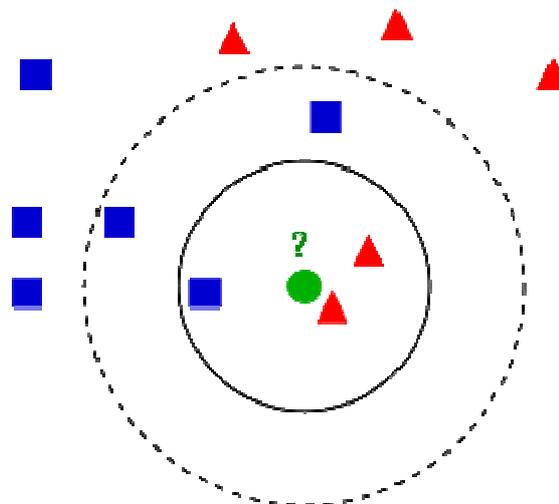


Fig. 2: An example of k-Nearest Neighbors (Ajanki, 2018)

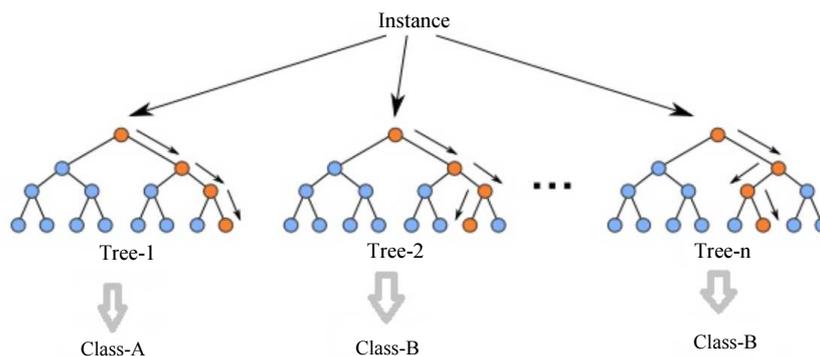


Fig. 3: An example of random forests (Breiman, 2001)

Table 1: Shows the number of the samples, training and testing set instances of each dataset

Dataset name	Total number of samples	Number of samples for the Training phase	Number of samples for the Testing phase
UCI	400	285	115
MDC	576	410	166
ARYO	383	274	109

Naïve Bayes (NB)

It was discovered and fall into the community of text retrieval in 1960 (Russell and Norvig, 2016). It could remain as a baseline technique in the domain of text categorization. In machine learning, NB classifiers are a group or family of "probabilistic classifiers" that are simple and based on applying the theory of Bayes with assumptions between the features that are strong and independent. It is popular to be used as a solution to the problem of documents to decide that to which category it belongs, by using word frequencies as features for the categories. NB classifiers are scalable as high level, in learning problems it requires a number of parameters linear with the number of features (variables). One of the common fields that it finds is automatic medical diagnosis applications (Rish, 2001).

Boosting Algorithms

The Boosting algorithms was discovered in 1998, based on the question "can a set of weak learners create a single strong learner?" which is posed by Kearns (Freund *et al.*, 1999). It is an ensemble algorithm of the machine learning algorithms, is primarily used for reducing the bias and discrepancy in supervised learning. It is also a machine learning algorithm, which produces a strong algorithm from weaker algorithms (Zhou, 2012). A strong learner is a classifier that many instances of the algorithm are being grouped together and is well-correlated with the true classification. While a weak learner is a classifier which is only relatively poorly correlated with the true classification, its accuracy is above chance and just better than random guessing.

Results and Discussion

Classification is done for the UCI, MDC and ARYO datasets after splitting them into 70% as training set and 30% as testing set, then using four different machine learning classification algorithms; SMO, k-NN, RF and NB to classify the data.

Firstly, SMO, k-NN, RF and NB algorithms separately tested against the UCI, MDC and ARYO datasets without employing the BoW as feature selection algorithm. Table 2 shows the complete accuracy rate for each algorithm.

Then, SMO, k-NN, RF and NB algorithms separately tested against the UCI, MDC and ARYO datasets after employing the BoW as feature selection algorithm. Table 3 shows the complete accuracy rate for each classifier after selecting the features using the BoW algorithm.

As seen in Table 2 and 3, the accuracy rates of classification for UCI dataset after selecting the features using BoW for SMO is raising from 0.860 to 0.930, k-NN from 0.834 to 0.943, RF from 0.857 to 0.944 and NB from 0.860 to 0.965. The accuracy rates of MDC dataset for SMO is raising from 0.952 to 0.983, k-NN from 0.950 to 0.982, RF from 0.962 to 0.982 and NB from 0.964 to 0.982. The accuracy rates of ARYO dataset are also raising; SMO from 0.908 to 0.977, k-NN from 0.899 to 0.995, RF from 0.929 to 0.978 and NB from 0.963 to 0.990.

In this research Boosting Algorithms is used to obtain better results from the combination of all the four classifiers. The goal behind doing this was to select the algorithm that has the best result on each of the specified records. Table 4 shows the results of the boosting of all the four classifiers without using any feature selection algorithms.

Table 2: Accuracy of classification results before employing BoW

Dataset name	SMO algorithm	k-NN algorithm	RF algorithm	NB algorithm
UCI	0.860	0.834	0.857	0.860
MDC	0.952	0.950	0.962	0.964
ARYO	0.9082	0.899	0.929	0.963

Table 3: Accuracy of classification results after employing BoW

Dataset name	SMO algorithm	k-NN algorithm	RF algorithm	NB algorithm
UCI	0.930	0.943	0.944	0.965
MDC	0.983	0.982	0.982	0.982
ARYO	0.977	0.995	0.978	0.990

Table 4: Accuracy of results using Boosting algorithms before using BoW

Dataset name	Boosting algorithms
UCI	0.913
MDC	0.970
ARYO	0.981

Table 5: Accuracy of results using Boosting algorithms after applying BoW

Dataset name	Boosting algorithms
UCI	0.973
MDC	0.982
ARYO	1.000

Finally, Boosting the four classifiers used to classify the data after using BoW for selecting the features, Table 5 shows the results of the boosting of all the four classifiers after using BoW as feature selection algorithm.

As seen in Table 4 and 5, the accuracy rates of classification using Boosting of the four classifiers for UCI dataset after selecting the features using BoW is raising from 0.913 to 0.973, for MDC dataset is raising from 0.970 to 0.982 and for ARYO dataset is raising from 0.981 to 1 (which is the highest rate).

Tu *et al.* (2009) proposed an algorithm to diagnose heart diseases from medical records of 920 patients, in which they made a comparison between three algorithms, the best was Bagging with Naïve Bayes algorithm with the accuracy rate 0.940. As a comparison made between the mentioned algorithm with the one proposed in this research, we can reach a decision, in which the proposed algorithm in this research with the worst accuracy rate which is 0.973 when it is tested against UCI dataset, outperforms its counterpart one with the accuracy rate 0.940.

Conclusion and Future Works

Medical data classification is a sensitive field of study. It is related to human's life. Therefore, the studies done in this field need to be specific and should have very good accuracy rates. It is obvious that further studies and developments are required to be performed in this domain. The proposed algorithm in this study

performs feature selection using the BoW algorithm and performs classification using Boosting of four machine learning classification algorithms; SMO, k-NN, RF and NB. The algorithm is tested against three different datasets; UCI, MDC and ARYO. These datasets contain different medical test results for patients with kidney disease.

Experimental results showed that using BoW with Boosting algorithms improves the results and increases the accuracy rate as mentioned previously in the results and discussion section. The result is obtained when it is trained and tested against three different datasets that contained medical tests related to kidney diseases. So, finally, this paper concludes to develop an algorithm by using BoW as the feature selection algorithm and Boosting algorithms as the classification algorithm to obtain accurate results for diagnosing kidney diseases from medical test reports.

Another perspective of future work has been introduced during the development of the proposed algorithm. As we observed that the accuracy rate of the proposed algorithm exceeded 97.3% and could show 100% in some cases for diagnosing kidney diseases, which is a very high rate. We believe that the proposed algorithm can be used in identifying other diseases related to different organs rather than using that technique for kidney diseases only.

While working on that case, we observed that there are no limitations to generate algorithms with better accuracy rates. So, different algorithms with high accuracy rates can be introduced for the future works.

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Author's Contributions

Wisam A. Qader: Implementing the proposed algorithm, analyzing the results and writing the manuscript.

Abbas M. Ali: Finding the resources, designing the methodology and reviewing the manuscript.

Ethics

This study is self-contained and the authors confirm that they have read and approved this document and there is no any ethical issues involved.

References

- Ahmad, A., S.M. Halawani and I.A. Albidewi, 2012. Novel ensemble methods for regression via classification problems. *Expert Syst. Applic.*, 39: 6396-6401. DOI: 10.1016/j.eswa.2011.12.029
- Ajanki, A., 2018. K-Nearest Neighbors algorithm. https://en.wikipedia.org/wiki/K-nearest_neighbors_algorithm
- Altman, N.S., 1992. An introduction to kernel and nearest-neighbor nonparametric regression. *Am. Stat.*, 46: 175-185.
- Bauer, E. and R. Kohavi, 1999. An empirical comparison of voting classification algorithms: Bagging, boosting and variants. *Machine Learn.*, 36: 105-139. DOI: 10.1023/A:1007515423169
- Birmingham, M.L., R. Pong-Wong, A. Spiliopoulou, C. Hayward and I. Rudan *et al.*, 2015. Application of high-dimensional feature selection: evaluation for genomic prediction in man. *Scientific Rep.*, 5: 10312. DOI: 10.1038/srep10312
- Breiman, L., 2001. Random forests. *Machine Learn.*, 45: 5-32. DOI: 10.1023/A:1010933404324
- Chou, S., W. Chang, C.Y. Cheng, J.C. Jehng and C. Chang, 2008. An information retrieval system for medical records and documents. *Proceedings of the 30th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, Aug. 20-25, IEEE Xplore Press, Vancouver, BC, Canada, pp: 1474-1477. DOI: 10.1109/IEMBS.2008.4649446.
- Elsayad, A. and M. Fakhr, 2015. Diagnosis of cardiovascular diseases with Bayesian classifiers. *J. Comput. Sci.*, 11: 274-282. DOI: 10.3844/jcssp.2015.274.282
- Fida, B., M. Nazir, N. Naveed and S. Akram, 2011. Heart disease classification ensemble optimization using Genetic algorithm. *Proceedings of the IEEE 14th International Multitopic Conference*, Dec. 22-24, IEEE Xplore Press, Karachi, Pakistan, pp: 19-24. DOI: 10.1109/INMIC.2011.6151471
- Freund, Y., R. Schapire and N. Abe, 1999. A short introduction to boosting. *J. Japanese Society Artificial Intell.*, 14: 771-780.
- Gao, H., E.J.A. Bowles, D. Carrell and D.S. Buist, 2015. Using natural language processing to extract mammographic findings. *J. Biomed. Inform.*, 54: 77-84. DOI: 10.1016/j.jbi.2015.01.010
- Guyon, I., J. Weston, S. Barnhill and V. Vapnik, 2002. Gene selection for cancer classification using support vector machines. *Mach. Learn.*, 46: 389-422. DOI: 10.1023/A:1012487302797
- Harper, P.R., 2005. A review and comparison of classification algorithms for medical decision making. *Health Policy*, 71: 315-331. DOI: 10.1016/j.healthpol.2004.05.002
- Khachidze, M., M. Tsintsadze and M. Archuadze, 2016. Natural language processing based instrument for classification of free text medical records. *BioMed. Res. Int.* DOI: 10.1155/2016/8313454
- Khalilia, M., S. Chakraborty and M. Popescu, 2011. Predicting disease risks from highly imbalanced data using random forest. *BMC Med. Inform. Decis. Mak.*, 11: 51-51. DOI: 10.1186/1472-6947-11-51
- Korde, V. and C.N. Mahender, 2012. Text classification and classifiers: A survey. *Int. J. Artificial Intell. Applic.*, 3: 85-99.
- Kotfila, C. and Ö. Uzuner, 2015. A systematic comparison of feature space effects on disease classifier performance for phenotype identification of five diseases. *J. Biomed. Inform.*, 58: S92-S102. DOI: 10.1016/j.jbi.2015.07.016
- Lakshmi, C. and M. Ponnaivaikko, 2009. Boosting kernel discriminative common vectors for face recognition. *J. Comput. Sci.*, 5: 801-810. DOI: 10.3844/jcssp.2009.801.810
- Nadkarni, P.M., L. Ohno-Machado and W.W. Chapman, 2011. Natural language processing: An introduction. *J. Am. Med. Inform. Assoc.*, 18: 544-551. DOI: 10.1136/amiajnl-2011-000464
- Opitz, D. and R. Maclin, 1999. Popular ensemble methods: An empirical study. *J. Artificial Intell. Res.*, 11: 169-198. DOI: 10.1613/jair.614
- Peng, Y., 2006. A novel ensemble machine learning for robust microarray data classification. *Comput. Biol. Med.*, 36: 553-573. DOI: 10.1016/j.combiomed.2005.04.001
- Platt, J., 1998. Sequential minimal optimization: A fast algorithm for training support vector machines.
- Polpinij, J. and A.K. Ghose, 2008. An ontology-based sentiment classification methodology for online consumer reviews. *Proceedings of the 2008 IEEE/WIC/ACM International Conference on Web Intelligence and Intelligent Agent Technology*, Dec. 9-12, IEEE Xplore Press, Sydney, NSW, Australia, pp: 518-524. DOI: 10.1109/WIAT.2008.68
- Revathy, N. and R. Amalraj, 2011. Accurate cancer classification using expressions of very few genes. *Int. J. Comput. Applic.*, 14: 19-22.

- Rish, I., 2001. An empirical study of the naive Bayes classifier. Proceedings of the Workshop on Empirical Methods in Artificial Intelligence, (MAI' 01), IBM, New York, pp: 41-46.
- Rubini, L.J., 2015. UCI machine learning repository. Alagappa University, Karaikudi, TamilNadu.
- Russell, S.J. and P. Norvig, 2016. Artificial Intelligence: A Modern Approach. 3rd Edn., Pearson Education Limited, Malaysia, ISBN-10: 1292153962, pp: 1132.
- Saeyns, Y., I. Inza and P. Larrañaga, 2007. A review of feature selection techniques in bioinformatics. *Bioinformatics*, 23: 2507-2517.
DOI: 10.1093/bioinformatics/btm344
- Sorich, M.J., J.O. Miners, R.A. McKinnon, D.A. Winkler and F.R. Burden *et al.*, 2003. Comparison of linear and nonlinear classification algorithms for the prediction of drug and chemical metabolism by human UDP-glucuronosyltransferase isoforms. *J. Chem. Inform. Comput. Sci.*, 43: 2019-2024.
DOI: 10.1021/ci034108k
- Tu, M.C., D. Shin and D. Shin, 2009. A comparative study of medical data classification methods based on decision tree and bagging algorithms. Proceedings of the 8th IEEE International Conference on Dependable, Autonomic and Secure Computing, Dec. 12-14, IEEE Xplore Press, Chengdu, China, pp: 183-187. DOI: 10.1109/DASC.2009.40
- Zhou, Z.H., 2012. Ensemble Methods: Foundations and Algorithms. 1st Edn., Chapman and Hall/CRC, ISBN-10: 1439830037, pp: 236.