CHRONIC KIDNEY DISEASE (CKD) PREDICTION USING SHUFFLED FROG LEAPING ALGORITHM AND METABOLIC PROFILING

Veni Devi Gopal[1], Angelina Geetha[2]
iNurture Education Solutions, B.S.A. Crescent University, Chennai

Abstract

The world of biomedicine is overflowing with massive volume of high dimensional data, which if probed as it should be, will facilitate in predicting many disease. Chronic Kidney Disease is an illness which will not reveal any indications in the early stages. Nuclear Magnetic Resonance (NMR) is a practice which is commonly used in the medical field to explore the metabolites. The key crisis with this practice is the weak correlation among high dimensional data. This insists on the need for a potential method for processing the data along with the machine learning techniques to speed up the task. In this paper, the shuffled frog leap algorithm is proposed for investigating the metabolites. The approach is to select only certain key features from NMR and recognize the patients who tend to have renal kidney disease and who are not affected by it.

Index Terms: Biomedical, Chronic Kidney Disease, Nuclear Magnetic Resonance (NMR), Prediction.

I. INTRODUCTION

Chronic Kidney Disease affects millions of people throughout the world. While dealing with this disease, the primary concern is that it does not demonstrate any signs in the primary phases. Only when the disease goes to the advanced stage the body starts exhibiting symptoms. By then the treatment becomes more complicated. A preset predicting technique that is capable of realizing and assimilating the assorted biological practices combined with path physiology will be of immense help to realize the rigorousness of the disease.

Every living organism survives only because the metabolic action. It is the bio-chemical process that occurs within a living organism to be alive. The metabolic profiling is the process of analyzing this metabolic process. Biofluids are the most common inputs to metabolic profiling. Nuclear Magnetic Resonance is a well established technique for metabolic profiling. The NMR technology investigates the magnetic properties of the atomic nuclei and verifies if sufficient metabolites are available in the biological sample. The more the number of metabolites, less is the probability of CKD and vice-versa.

As the biological data is massive and heterogeneous, spotting out the appropriate data and analyzing that alone is a very big mission. For this purpose, shuffled frog leap algorithm is used. The shuffled frog leap algorithm mainly works on localization and information sharing with the neighboring memeplexes. This algorithm is used in this work to identify the relevant features in the high dimensional data and for further analysis.

This work is organized as follows: related research is presented in II. Shuffled Frog Leap Algorithm, metabolic profiling and Chronic Kidney Disease (CKD) is introduced in Section III and IV. Section V is detailed with the proposed method. The paper closes with a conclusion in Section VI.

II. RELATED STUDY

Jente Boelaert, in his work has discussed about the CKD and NMR based metabolic profiling [1]. They have come with the idea that the NMR spectra data and the metabolites can help in identifying the CKD in the early stages.

Suresh et al have analyzed that the huge volume of data can be categorized either using supervised or unsupervised data clustering [2]. It has been proved that the shuffled frog leaping algorithm (SFLA) performs better for unsupervised data clustering. When huge data set are used for analyzing and optimizing high dimensional data available in medical field, selecting the needed features alone helps in better performance of Shuffled Frog Leap Algorithm [3]. It has been proved that this algorithm improves the capability to select features in the high dimensional data and also improves the predictability in them. In the works of Murat Kand Ahmet the SFLA algorithm has been used for clustering the data [4]. It has been proved that the performance of SFLA algorithm is much better than the other meta-heuristic algorithms like particle swarm optimization and artificial bee colony optimization algorithm.

There are problems with multiple objectives and when optimization is needed to be done it becomes multiple objective optimizations [5]. Though the other meta-heuristic algorithms can be used, when there is too much difference between each group and data set is massive, then the shuffled frog leap algorithm has been proved to give better results. Luck et al have proposed Metabolic Profiling of 1H NMR Spectra in Chronic Kidney Disease with Local Predictive Modeling [6]. Anu et al have presented a review paper on various predictive methodologies and approaches to diagonise chronic kidney diseases. This work helps in analyzing the pros and cons of various approaches adapted so far.

III. SHUFFLED FROG LEAP ALGORITHM

In the evolution of living organisms, the information patterns of the organisms can be passed with the help of gene. The issue with this is that it can be transferred only from one generation to another. There exists a unique way in frogs for transferring the information patterns, memes. The Shuffled Frog Leap (SFL) Algorithm is one of the most widely used bio-inspired algorithms in the recent days. It combines the working of Memetic Algorithms and Swarming Optimization algorithms. It is based on the working nature of the frogs. The working principle: The frogs are divided in subgroups (memeplexes) and each subgroup is searched locally to find the optimal value. Once the optimal value is found, it is shuffled to the other sub-groups. This way, the information about all the subgroups will be known to everyone. This will help the frog to move to an optimal position in search of food. The algorithm steps are listed below and the figure 1 depicts the same.

Steps in SFL Algorithm:
1. Randomly select the initial population of frogs, from all the available frogs.
2. Each frog will have a given set of characteristics.
3. Calculate the fitness of the frogs according to their characteristics.
4. Sort the frogs based on the characteristics.
5. Now the complete population of frogs is divided into 'n' memeplexes.
6. The frogs based on their fitness value will be distributed to the memeplexes i.e. first frog to first memeplex group, second to second memeplex group and so on.
7. Within each memeplex, the frogs with best fitness and worst fitness are identified.
8. Based on these values from all the memeplexes, a global best fitness is

determined.

9. Within each subgroup, adjustments are done to change the position of the worst fit frog.
10. If after the adjustments the, calculate the fitness value of the worst fit frog.
11. If the fitness improves then repeat the above steps.
12. Else, a new solution set is selected and the same process is repeated.
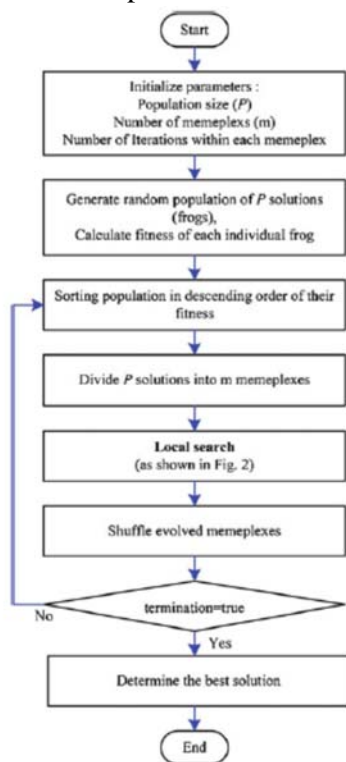

Figure 1 : Shuffled Frog Leap Algorithm

IV. METABOLIC PROFILING AND CHRONIC KIDNEY DISEASE

The Chronic Kidney Disease (CKD) is characterized by the gradual decrease in the functioning of kidney due to the hoarding of uremic retention solutes thereby leading to complete failure of kidney. This also increases the risk of cardiovascular diseases. Serum creatinine or urinary albumins are the commonly used bio-markers to find the CKD. But these bio-markers seldom allow the early detection of the CKD. The Nuclear Magnetic Resonance(NMR) based metabolic profiling is one of the most widely used methods for identifying the different stages in identifying CKD. NMR utilizes the magnetic properties of the atomic nuclei and finds the abundance of the metabolites in the given sample. The combination of the NMR spectra data and complex metabolites in the biofluids can be the correct input for the prediction of CKD in the early stages. Currently there is no proper technique for identifying the bio-markers and using it in the diagnosis. Proper search of the metabolites can definitely lead to proper diagnosis. NMR metabolic make use of Chemometric methods classify the high dimensional bio-fluids. This method sets a target value for each of the metabolite and utilizes this for the classification and analysis of the bio-fluids.

V. PROPOSED METHOD

The proper analysis of the bio fluids by determining the bio markers will help in predicting the Chronic Kidney Diseases. Applying local search on the metabolites to identify the suitable features and then performing necessary operations to identify diseases will definitely help in detecting the CKD in the initial stages. Shuffled Frog Leaping Algorithm has been identified as one of the best algorithms for feature selection and finding the best fit from the various features. The proposed work is influenced by the general functioning of the SFL algorithm. Initially, the bio-fluids are collected. Random local samples are selected and the value of the metabolites is compared with the threshold. If the metabolite value of the current sample is greater than the threshold value then the global variable is set as minimum. After analyzing the entire local sample, calculate the global metabolite value. If the global metabolite value is greater than the threshold, then the chances of CKD will be less and vice-versa. This is depicted in Figure 2.

Steps in the Proposed Work:

Step 1: Collect the initial biofluids data set.
Step 2: Decide the metabolic threshold needed for the nuclei atoms.
Step 3: Apply shuffled frog leap algorithm and select the atomic nuclei with high magnetic properties.

Step 4: Once the hybrid of all data is found, analyze the metabolic threshold.

Step 5: If the metabolic threshold is more, then there is less probability of Chronic Kidney Disease.

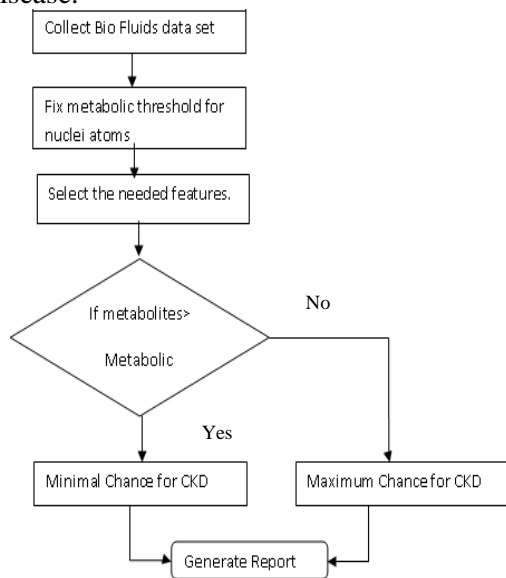Step 6: Else the metabolic threshold is less, and then there is more probability of Chronic Kidney Disease.

Figure 2 : Flow Chart of the Proposed Work

VI. EXPERIMENTAL ANALYSIS

The test data for the proposed has been collected from medical repositories. The proposed system is under implementation.

VII. CONCLUSION AND FUTURE WORK

Predicting the chronic kidney disease in the early stages itself will help people take precautionary measures to avoid it. The magnetic properties of the atomic nuclei can be analyzed using the NMR technology. In the proposed work, the high dimensional biofluids are collected and the necessary features alone are selected using the shuffled frog leap algorithm. The metabolites are checked and if it is found in more amount, it can be predicted that the chances of CKD is less and if it is less, then the chances are more. In future, the proposed work can be implemented and the results can be analyzed.

REFERENCES

[1] Jente Boelaert,rederic Lynen,Griet Glorieux, Eva Schepers, Nathalie Neirynck, Raymond Vanholder, "Metabolic profiling of human plasma and urine in chronic kidney disease by hydrophilic interaction liquid chromatography coupled with time-of-flight mass spectrometry: a pilot study", Analytical and Bioanalytical Chemistry, March 2017, Volume 409, Issue 8, pp 2201–2211.

[2] Suresh Chittineni, Dinesh Godavarthi, A. N. S. Pradeep,Suresh Chandra Satapathy, P. V. G. D. Prasad Reddy, "A Modified and Efficient Shuffled Frog Leaping Algorithm (MSFLA) for Unsupervised Data Clustering", International Conference on Advances in Computing and Communications, ACC 2011: Advances in Computing and Communications pp 543-551.

[3] Bin Hu, Yongqiang Dai, Yun Su, Philip Moore, Xiaowei Zhang, Chengsheng Mao, Jing Chen, Lixin Xu, "Feature Selection For Optimized Highdimensional Biomedical Data Using An Improved Shuffled Frog Leaping Algorithm", IEEE/ACM Transactions On Computational Biology And Bioinformatics, Doi 10.1109/Tcbb.2016.2602263, IEEE/ACM.

[4] Murat Karakoyun, And Ahmet Babalik, "Data Clustering with Shuffled Leaping Frog Algorithm (SFLA) for Classification", 2015 Int'l Conference on Intelligent Computing, Electronics Systems and Information Technology (ICESIT-15) Aug 25-26, 2015 Kuala Lumpur (Malaysia).

[5] Junwan Liu,Zhoujun Li, Xiaohua Hu,Yiming Chen,Feifei Liu, "Multi-objective dynamic population shuffled frog-leaping biclustering of microarray data", BMC Genomics. 2012; 13(Suppl 3): S6, Published online 2012 Jun 11. doi: 10.1186/1471-2164-13-S3-S6.

[6] M. M. Luck; A. Yartseva; G. Bertho; E. Thervet; P. Beaune; N. Pallet; C. Damon, "Metabolic Profiling of 1H NMR Spectra in Chronic Kidney Disease with Local Predictive Modeling", 2015 IEEE 14th International Conference on Machine Learning and Applications (ICMLA), Pages: 176 - 181, DOI: 10.1109/ICMLA.2015.155.

[7] Anu Batra; Usha Batra; Vijendra Singh, "A review to predictive methodology to diagnose chronic kidney disease", 2016 3rd International Conference on Computing for Sustainable Global Development (INDIACom), Pages: 2760 – 2763.