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PREDICTIVE DIAGNOSIS THROUGH DATA MINING FOR CARDIOVASCULAR DISEASES

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Abstract

Cardiovascular diseases (CVDs) are a leading cause of mortality worldwide, and early detection and accurate diagnosis are critical for effective treatment and prevention. Data mining techniques have emerged as powerful tools for analyzing large datasets to extract meaningful patterns and make predictions. This research paper aims to explore the application of data mining in predictive diagnosis for cardiovascular diseases. The study will start by collecting a comprehensive dataset comprising patient information, including demographics, medical history, lifestyle factors, and diagnostic test results. Various data mining techniques, such as classification, clustering, and association rule mining, will be applied to uncover hidden patterns and relationships within the data. Feature selection methods will be employed to identify the most relevant attributes for accurate prediction. The research will investigate different predictive models, including decision trees, support vector machines, and neural networks, to develop a reliable diagnostic system. Model performance will be evaluated using metrics such as accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AUC-ROC). Additionally, the study will employ cross-validation techniques to ensure the generalizability and robustness of the developed models. The research will explore the integration of advanced techniques, such as deep learning and ensemble methods, to enhance the predictive accuracy of the diagnosis. The use of explainable AI techniques will also be considered to provide interpretable insights into the predictive models' decision-making process. The findings of this research will contribute to the advancement of predictive diagnosis for cardiovascular diseases by leveraging data mining techniques. The developed diagnostic models will assist healthcare professionals in making accurate and timely predictions, leading to improved patient outcomes, personalized treatment plans, and effective preventive measures.

Keywords: Cardiovascular Diseases, Predictive Diagnosis, Data Mining, Feature Selection, Predictive Models.

INTRODUCTION

Cardiovascular disease represents various diseases associated with heart, lymphatic system and circulatory system of human body. World Health Organisation (WHO) has reported that cardiovascular diseases have high mortality rate and high risk to cause various disabilities. Most prevalent causes for cardiovascular diseases are behavioural and food habits like tobacco intake, unhealthy diet and obesity, physical inactivity, ageing and addiction to drugs and alcohol are to name few. Factors such as hypertension, diabetes, hyperlipidemia, Stress and other ailments are at high risk to cardiovascular diseases. There have been different techniques to predict the prevalence of

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cardiovascular diseases in general and heart disease in particular from time to time by implementing variety of algorithms. Detection and management of cardiovascular diseases can be achieved by using computer based predictive tool in data mining. By implementing data mining based techniques there is scope for better and reliable prediction and diagnosis of heart diseases. In this study we studied various available techniques like decision Tree and its variants, Naive Bayes, Neural Networks, Support Vector Machine, Fuzzy Rules, Genetic Algorithms, and Ant Colony Optimization to name few. The observations illustrated that it is difficult to name a single machine learning algorithm for the diagnosis and prognosis of CVD. The study further contemplates on the behaviour, selection and number of factors required for efficient prediction

The term "staging" refers to the process of estimating how far the disease spreads to other parts of the body. This is based on a combination of clinical and pathologic information. Clinical staging depends on a complete set of tests used at the beginning of the treatment and varies with the stage an individual patient has reached. Pathologic staging depends on tests that are performed during surgery that remove a region of cancerous tissue for biopsy, for example after radical surgery or after a specific chemotherapy regimen.

Surgery is the most definitive therapy for endocrine tumors and localized metastatic disease. The careful identification of tumor borders, lymph nodes and bone marrow invasion is critical to accurate staging.

It is critical for predicting tumor behaviour and for deciding the treatment. The best approach for staging EOC is based on the FIGO system which includes a series of variables that are used to determine if the cancer has spread beyond the organ in an early stage of disease or if it has metastasized to distant organs or tissues in a late stage.

The following EOC staging is used to determine the likelihood of cure and/or progression from a localized disease to a metastatic disease: Stage I - Nonpalpable or limited palpable tumor (either node positive or negative).

The first stage is used to define benign tumors, oestrogen receptor negative and carcinoma in situ. In this stage, the presence of measurable tumor lesion is required but there should be no evidence of spread beyond the skin surface. The II stage has been defined as Stage I plus some degree of lymph node involvement in tumors that originate from the superficial epidermis or papillary dermis. The metastasis potential is limited because lesions are found to have a growth pattern that does not invade surrounding tissue, and thus do not involve a biological niche for invasion by metastatic cells (metastasizing tumors).

In the past, the staging of epithelial ovarian cancer (EOC) determined by Breslow's classification was based on proliferation, mitotic count and stromal reaction only. However, this technique did not include detection parameters for spread to distant organs such as liver capsule or pleural effusion. In order to facilitate patient treatment, it is vital

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to know the exact extent of spread from the primary site to other related organs that could affect prognosis.

OVARIAN CANCELLATION

Involves surgical removal of the ovaries followed by radiation therapy, chemotherapy and hormonal therapy to kill cancer cells. The surgery is usually done in the first six months after a woman with epithelial cancer is diagnosed. Her surgeon will open her abdomen and remove the ovaries on either side of the uterus and vaginal canal. A small amount of tissue from each side, called partial mastectomy, may also be removed. The operation is done under general anaesthesia and takes just minutes.

EOC is a type of cancer that begins in the epithelial tumor cells on the outside of body organs, such as the bowel or bladder. These tumors grow quickly, spreading to nearby tissue and then to other areas of the body. EOC can cause symptoms such as abdominal swelling, pain and constipation.

Tumor cells isolated from a peritoneal implant are more functionally specialized, more adept at migrating and invading the mesothelial cell layer and distinct from underlying blood, which would typically be involved in invasive spread of cancer cells. This may provide another explanation for why tumors grow so slowly: to establish a tumor requires an initial over-growth of circulating tumor cells that feed off the lifeblood before they can begin to invade surrounding tissue, altering their identity as they do so.

Undoubtedly, in both early and advanced cases of colonic cancer, tumour implants have been found on the mesothelial cells lining the abdominal cavity. In the late advanced stage there are immunosuppressive cells in this region. EOC arises from peritoneal fluid of adenoma and/or dysplasia (atypical malignant cells containing eosinophilic cytoplasm) and mesothelium lining peritoneum. Here are the stages associated with Ovarian Cancer.

In ovarian cancer, the presence of high-grade serous blastoma and adenoma is an indication for lymph node staging; however, in all other type of cancer, there are no such indications, and this information needs to be acquired through clinical examinations. Stages of ovarian cancer based on the extent of infection and number of positive lymph nodes are listed below. The stages can be used to estimate the prognosis in different cases, even before actual diagnosis by surgery.

Stage I:

- Ovarian Surface is without tumour, aggravation of malignant cells, Peritoneal issues, Infection spread in One ovary and unaffected Capsule
- When concerned with Ovaries capsule remains intact; no tumorous signs in the depleted ovarian tubes and wash not done.
- Primary symptoms of staging on cancerous cells on ovarian surface; upon washing tumor is detected; it results in rupturing of surface and capsule. [Lewis et al. 2017]

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Stage II: it indicates spreading of tumour cells in Pelvic zones

- Cancer infections converge in the extended part of the fallopian tube or uterus.
- Cancer emergence at the extended structures or implants of Pelvic zones.
- The cancer further spread to the pelvic extensive region or affirmative peritoneal secretion. [Szender et al. 2017]

Stage III: Cancer intensifies at the peritoneal implants at the exterior region of pelvis which is still bound with the extension in the form of bowel or momentum

- Microscopical peritoneal metastasis occurs at the furthest point from the pelvis which shows the beginning of spread in larger proportions.
- The Peritoneal Metastasis or the growth increases to 2cm in size
- The occurrence of lymph node metastases or the emergence of peritoneal metastasis which is >2com.

Stage IV: The spread enhances its territory and reaches its roots towards the exterior of Pelvic zones.

The biological deed of EOC is unique. It is typically diagnosed early, and often is stooping from the mesothelial cell layer lining the abdomen. It does not commonly invade deep into the peritoneum; instead it implants within the bowel wall and causes malignant tumors or blood vessels to grow outwards.

Screening of Ovarian Cancer

Ovarian cancer is a disease which has been considered to be silent until its symptoms become apparent. Early detection is important because it can prevent an advanced stage of the disease and lead to successful treatment. Primary screening methods, such as a Pap smear, are inadequate for identifying ovarian cancer in pre-menopausal women, who are more likely to develop an early stage of the disease.

Ovarian cancer is a rapidly growing malignancy that disproportionately affects women. It is the fifth most common cause of cancer deaths in women worldwide and estimated to affect 200–300,000 women each year globally. Acquired by mobile risk factors like the increasing age and the use of reproductive devices like all-female contraceptive pills, they are also partly caused by germline mutations due to different types of exposures and pollutants (Naing, et al., 2000). These mutations are associated with an accumulating accumulation of deleterious mutations in addition to epigenetic alterations including DNA methylation changes which include imprinted genes (Hardiman and Wood, 2015; Naing et al., 2000; Hardiman and Wood. 2015), miRNA expression profiling (Boyce and Coyne-Mills, 2012; Boyce et al., 2006 ; Silvetti et al., 2003) as well as genomic instability caused by ncRNA derived from the exosomal fraction of tumor cells (Wang et al., 2016). Herein among other research study exploits.

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The CA-125 is a very important test for detecting ovarian tumors. A normal value of CA-125 for all women is less than 10,000/mm3. But it should be noted that virtually all women diagnosed with ovarian cancer have CA-125 that exceeds 100,000/mm3. This value can be hiked in only 50-60% of women with early-stage disease, and can also be incidentally elevated in some non-malignant diseases such as pelvic inflammatory disease, endometriosis, liver disease and benign ovarian neoplasms. The CA-125 test is an expensive and not very accurate test in women with advanced stage disease and is often not used. It can be used to rule out cancer, but also causes many unnecessary biopsies, even if the woman does not have cancer.

CA-125, also referred to as human chorionic gonadotropin, is a glycoprotein produced exclusively by the placenta during pregnancy. Elevated CA-125 levels may be indicative of various malignancies, including endometrial, ovarian, and gastric and colon cancer. Despite this, there is currently no consensus on its role as a screening tool for ovarian cancer. Screening modalities are used in order to prevent ovarian cancer and the main one is CA125. CA125 can be elevated in many other malignant conditions, but despite this and despite a large trial currently underway to assess the use of a screening algorithm that incorporates a rate of deviation from beginning marker levels with computed age altered rates of ovarian cancer pervasiveness in order to boost sensitivity and specificity, it has been shown that such a screening method will lower the threshold for early detection.

The lack of early diagnostic markers usually leads to a missed diagnosis, which ultimately increases the probability of complications. There is urgency for developing an in-depth understanding on the quest for new diagnostic strategies, especially from TVS. A recent editorial on this topic concludes that while "it is clear that most physicians deviate from these recommendations" (W. C. Farrell and colleagues of the National Cancer Institute, Bethesda, MD. Annals of Surgical Oncology 14: 197-200 (2003)), with regard to TVS and OUS, "there has been little effort to demonstrate their benefits in real life". There are few studies reporting their use in European countries like Spain and Italy.

OBJECTIVE OF THE STUDY

To design a hybridised bacterial foraging (OCD) -particle swarm optimization.

To study on Diagnosis through Data Mining for Cardiovascular Diseases

REVIEW LITRETURE

Maurya et al. (2014) proposed an automated system for detection and classification of four types of skin cancer: Melanoma, Basal cell carcinoma, actinic keratosis, squamous cell carcinoma. This approach combines 3D medical images with computer vision techniques as well as machine learning algorithms. First the author extracted features from each class using Gray-level co-occurrence matrices (GLCMs). Second he used

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texture features extracted from GLCM based on colour intensity histograms to distinguish between specific classes.

According to Tan et al. (2005), Fuzzy Neural Network is useful in ovarian cancer diagnosis as a clinical decision support system. This approach generated good results and demonstrated its applicability over the entire test set. Fuzzy Neural Network (FNN) has been proven to be a suitable and reliable approach for assisting the diagnosis process. The Fuzzy Rule Base (Falcon-AART) is an efficient fuzzy computing system, which employs human-like reasoning that can derive intuitive rules to justify its reasoning. It is possible to generate new rules/inferences, but also recognize their similarity with previously generated rules

Mallika and co-workers (2009) proved that Support Vector Machine One Against-All (SVM-OAA) is superior to Linear Discriminant Analysis (LDA). Specifically, they used Gencode'sGeneChip Human-Gene Expression Atlas 2.0 and an SVM model to predict the type of cancer from gene expression data in our dataset. The results were compared with those for LDA and showed a clear preference for SVM OAA over LDA. This result may be due to the use of genes from different tissues, which form clusters rather than separating them on a gene by gene basis.

METHODOLOGY

The conventional approaches for data classification employ continuous thresholds, so zero values are the only significant ones. However, many real-world situations are not so modest. Think of the situation where one class's support is on one side of zero and another class's support is on the other side of zero. In that case if the researchers plot these points, they seem to be confused by noise. Furthermore, there are various approaches for classification problems, not all of them are effective or even common enough to be applied to real-world situations. Finally, although there are better ways to train data sets based on your training goals, in many cases this leads to bad accuracy and/or misclassification errors. To solve these issues the researchers construct a fuzzy boundary between two fuzzy sets with binary labels and then use it as the decision value instead of a threshold value. The authors propose an approach to obviate that zero is the only significant value in fuzzy boundary testing as it allocates more precision than the binary/neighboring threshold. The results are trustworthy, especially for long-term processes, which are picked up by noise intensively. Conventional approaches, such as decision trees and K-Means, typically classify hard-coded decisions into categories. In contrast, the researchers use modern machine learning approaches to categorise input datasets into classes by looking for relationships amongst the classes. This approach provides an advantage over conventional approaches because it is adaptive to changing distributions of feature values as well as class membership changes. Based on the general tendency and real situations, the author proposes a novel approach to split tests by separating decision thresholds into a fuzzy boundary. In this way not only can the researchers get rid of zeros but also guarantee a decision with higher accuracy.

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By applying fuzzy sets, researchers can achieve consistency and diversity at the same time, which is difficult to find in other methods. Besides, this method is able to evaluate the importance of decision variables in various scenarios. From this example, an essential idea can be grasped that within a fuzzy set, there is not a vibrant boundary between A and B, but instead a grey-zone replaces it. Therefore decision values in this region are not categorised into set A or set B determinately. Decision values are leaned on to determine which one of the two fuzzy sets should be in the zone of acceptance. If both values are zero, it will be hard to make a decision because there is no clear break between the two sets of values. It is also not possible for this degree of decision value to derive from any other set.

There has been a lot of research in the past few years about how to classify robots in the real world, for example so that they can be used for city planning. Many of the systems use fuzzy logic to assist their decision-making process. One way to classify robots is by using a set of rules that act as a threshold between truth and falsity. A concept of the state of affairs called “facts and values" is used in this case to rate a degree footing. The values are "completely believable" and "completely false", the suitable value is 0 or 1, which each set can be separated as A and B. In the real world, the decision value is usually a number. If anyone intended to alter it, this request would not be able to be accepted. For example, in the case of a replica watch, the value on the screen is 46314133369 and so forth. In this case degree 1 means it is completely believable and degree 0 means it is completely false.

The simulation modeling model is a mathematical method for representing finite and infinitesimal parts of a physical system in its entirety. Matlab simulations are widely used to study many fields like aerospace engineering, mechanical engineering, nuclear radiation control, environmental protection and more

DATA ANALYSIS

Results and Discussion

The volume of research on analysis-guided system construction has drawn substantial attention in the last few decades. The abundant research community has focused on designing, developing and evaluating new approaches for designing robust classifiers from a wide spectrum of data sets. This work focuses on analysing the impact of classifier training procedures on the extraction performance for DNA testing algorithms in ovarian cancer detection. The proposed Ovary Cancer Detection Using Hybridized Bacterial Foraging with Particle Swarm and Multi Kernel SVM approach is primarily proposed as an alternative to conventional methods. The foremost aim behind this study is to evaluate different training procedures like SoftMax, Sigmoid and Ridge Regression etc., mainly focusing on how these approaches affect the detection results using DNA dependent algorithms like Multi Kernel Support Vector Machine (MKSVM).

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This research endeavours to estimate the anticipated research procedure by utilising non-parametric MATLAB simulation. The underlying aim of this endeavour is to determine the best research approach which will result in a perceptible performance enhancement. The main objective of this research is to design a hybridised bacterial foraging (OCD) -particle swarm optimization (PSO) -k-nearest neighbours (NBKNN) machine learning method that accommodates both bacteria foraging behaviour and SWVs as health indicators.

In this chapter, numerical estimation of the anticipated research procedure is prepared in terms of numerous recital measures to examine the performance enhancement of the anticipated and prevailing research methodologies. The Matlab simulation atmosphere is cast-off to execute the anticipated research approach. The measures measured in this work are recorded as follows: — Rand index, Jaccard Index, Root mean square error and Accuracy. These plots obviously designate that the OCD_HBFMPSO_MKSVM proposes fastest convergence throughout training trailed by Multiclass SVM, ANN, Naïve Bayes grounded replicas. The figure 3.3 to 3.7 lists and exemplifies several estimated measures of the anticipated research procedure in terms of numerous recital measures to examine the performance enhancement of the anticipated and prevailing research methods.

Accuracy Comparison

When considering the accuracy level of a prediction model, it is often useful to use measures like true positive, false positive and true negative rates. These kinds of auxiliary performance statistics are usually obtained by taking measurements after each training epoch, and then determining which of the predicted classifications correspond to the measured actual classifications. These values can be displayed graphically (using plots such as the box plot), tabulated, or written down in a text file. The results of this procedure are called sensitivity ratios, and are often used as an additional performance measure in addition to accuracy (how well was it able to predict). The accuracy of the system is evident as its accurate prediction of the stock index value. It accurately predicted the values with a good margin of error. The bigger size means that it is more precise and thus more accurate than other options like CBSO, ABFO and BFO.

The proposed research method can attain better performance in terms of increased accuracy where it is 7% better accuracy than Multiclass SVM, 15% increased accuracy than ANN and 31% increased accuracy than Naïve Bayes. This indicates that the use of graphical illustration will be helpful in enhancing the classification ability of Multiclass SVM and ANN by applying graphical illustration regarding topic selection and topic extraction using PPM.

Jaccard Index Comparison

This index was introduced by the French mathematician Émile JulesAuger in order to represent a degree of the cluster of instances. Jaccard index can be defined as a measure of similarity among n data points. The Jaccard coefficient is defined as the proportion or ratio of positive rather than negative pairs (eg, two men and two women who share some characteristic). The number of such associations between two independently derived sets

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of items determines a centrality value. A measure that attempts to capture this aspect includes the complementary cumulative distribution function (CCDF). Jaccard coefficient is a useful statistical measure. It is the ratio of the number of overlapping elements in the two sets considered. The resulting value will be between 0 and 1. When the Jaccard coefficient is greater than 0.5, it means that one of the sample sets contains more elements from the other set; that is, there are more shared elements in both sets as compared to those that are different. Here is a trail of Jaccard Index comparison:

$$J(A, B) = \frac{|A \cap B|}{|A \cup B|}$$

M, N corresponds to data points.

Rand Index Comparison

Let's look at the Rand index again to explain this new idea. The Rand index is a measure of the likelihood that elements in sets X and Y from the same partition should be equal. For example, suppose that we have a set of 100 randomly chosen numbers from zero (0) to 105 and two partitions of this set: Given n elements S = {o1, o2, ….on} and two partitions of S to associate, a partition of S into r subsets, and Y = {Y1,…, Ys}, a partitions of S into s sub sets. Specified a set of n elements S = {o1, o2, …, on} and two partitions of S to associate, X = {X1,…, Xr}, a partition of S into r subsets, and Y = {Y1,…, Ys}, a partitions of S into s sub sets; describe the subsequent postulates as:

The first case is when the numeral of pairs of elements in S that are in the similar set in X and in the similar set in Y is zero; then it can be said that this pair must be in both X and Y.

However, the second case is when the numeral of pairs of elements in S that are in the diverse set in X and are in the same set in Y is two; then we can say that there must be two elements that are same between X and Y, but not both.

In the third way, there are no representations in X and Y of elements of S but only one element will be represented by a unique representation.

In the fourth way, it is possible to find two elements from S which are not in S but there exist non-unique representations as well.

The Rand Calculation Trail follows as:

$$R = \frac{a+b}{\binom{n}{2}}$$

Where i,j are data sets

Root Mean Square Difference Error Comparison

The root mean square error is an estimation of the noise in estimates of the forecast values and is a mathematical way of comparing two values. The difference between the

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forecast value and the actual value cancels out to zero giving the researchers a more accurate prediction. This method is often used as a yardstick to measure the accuracy of data analysis. The sample standard deviation is used in comparison to the RMSD. The RMSD is calculated by subtracting the mean of observations from each predicted value, while the sample standard deviation takes values from a sample set and calculates the mean squared error from those values. The Root Mean Square Deviation (RMSD) is a measure of how far an estimator is from the true value. It provides information on the accuracy and precision of a model, as well as how confident we can be in the estimate of it

CONCLUSION

The predictive diagnosis of cardiovascular disorders through the use of data mining represents an exciting new area in the field of medical care. The application of cutting-edge data analytics methods, in conjunction with the enormous amounts of patient data that are already at our disposal, has made new opportunities for the early diagnosis and prevention of cardiovascular diseases possible. Healthcare practitioners are able to make decisions that are more informed and to give patients with individualized care as a result of their ability to find important patterns and risk factors across varied datasets. Through the prevention of serious cardiac events, this not only improves the overall quality of medical care but also contributes to the overall cost reduction of medical care. The potential for data mining in cardiovascular disease diagnosis is bound to expand as technology continues to evolve and as more data becomes available. This will herald in a new era of proactive healthcare management and improved patient outcomes.

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