

# Early Detection of Cancer Disease using classifiers of Data Mining

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**Abstract:** Classification has been utilized in the area of Bio-medical research in scientific and experimental trail, prediction of weather, target customer segmentation, detection of fraud, diagnosis and detection of various diseases on biomedical domain. Using classification methods, various types of cancer diseases can be predicted and diagnosed for early treatment based on the toxicity of patients. Various types of mining techniques has been proposed in early prediction and diagnosis of cancer diseases. Our paper proposes technique of classification in classifying cancer disease based on demerits and merits. The aim and objective of the paper is to analyze various techniques of data mining in classifying the disease of cancer and for improving in prediction of accuracy in detection at the early stages and can reduce the death rate

**Keywords:** Data Mining, Classification, Cancer Classification, Prediction.

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## I. Introduction

Data mining (Reena, G. 2011) is the iterative process of discovering the interesting knowledge from the large amounts of data stored in the data base. It is relatively young and interdisciplinary field of computer science, and it is the process of extracting the patterns form the large data sets by combining the various data mining techniques. The recent technical advances in the processing power, storage capacity, and inter connectivity of computer technology the data mining is the important tool.

The data mining algorithms (Ismaeel, A. G., et.al.2016) are extensively utilized to classify the cancer disease in the early stage. Recent days the several recent techniques are used to classify the cancer disease such as supervised one unsupervised classification methods. The supervised methods used are Naïve Bayes classifier, J48 Decision Trees and Support Vector Machines, whereas the unsupervised method is an adaptation of the K-means clustering method.

### 1.1 Classification of cancer

Cancers are classified in two ways: by the type of tissue in which the cancer originates (histological type) and by primary site, or the location in the body where the cancer first developed. The international standard for the classification and nomenclature of histologies is the International Classification of Diseases for Oncology, Third Edition (ICD-O-3).

From a histological standpoint there are hundreds of different cancers, which are grouped into six major categories:

- Carcinoma
- Sarcoma
- Myeloma
- Leukemia
- Lymphoma
- Mixed Types

#### 1.1.1 Carcinoma

Carcinoma refers to a malignant neoplasm of epithelial origin or cancer of the internal or external lining of the body. Carcinomas, malignancies of epithelial tissue, account for 80 to 90 percent of all cancer cases. Epithelial

tissue is found throughout the body. It is present in the skin, as well as the covering and lining of organs and internal passageways, such as the gastrointestinal tract. Carcinomas are divided into two major subtypes: adenocarcinoma, which develops in an organ or gland, and squamous cell carcinoma, which originates in the squamous epithelium.

Adenocarcinomas generally occur in mucus membranes and are first seen as a thickened plaque-like white mucosa. They often spread easily through the soft tissue where they occur. Squamous cell carcinomas occur in many areas of the body. Most carcinomas affect organs or glands capable of secretion, such as the breasts, which produce milk, or the lungs, which secrete mucus, or colon or prostate or bladder.

### **1.1.2 Sarcoma**

Sarcoma refers to cancer that originates in supportive and connective tissues such as bones, tendons, cartilage, muscle, and fat. Generally occurring in young adults, the most common sarcoma often develops as a painful mass on the bone. Sarcoma tumors usually resemble the tissue in which they grow.

Examples of sarcomas are:

- Osteosarcoma or osteogenic sarcoma (bone)
- Chondrosarcoma (cartilage)
- Leiomyosarcoma (smooth muscle)
- Rhabdomyosarcoma (skeletal muscle)
- Mesothelial sarcoma or mesothelioma (membranous lining of body cavities)
- Fibrosarcoma (fibrous tissue)
- Angiosarcoma or hemangioendothelioma (blood vessels)
- Liposarcoma (adipose tissue)
- Glioma or astrocytoma (neurogenic connective tissue found in the brain)
- Myxosarcoma (primitive embryonic connective tissue)
- Mesenchymous or mixed mesodermal tumor (mixed connective tissue types)

Leukemias ("liquid cancers" or "blood cancers") are-patient. In order to achieve the various feature reductioncancers of the bone marrow (the site of blood cell-schemes the set of simple classifier utilized in this paper.production). The word leukemia means "white blood" in-Initially the Principal component analysis (PCA), FactorGreek. The disease is often associated with the-Analysis (FA) and Discrete Fourier Transform (DFT)overproduction of immature white blood cells. These-utilized to reducing the dimension, after that theseimmature white blood cells do not perform as well as they-reduction dimensions are used to build the intelligentshould, therefore the patient is often prone to infection.-classifiers by using the various functional link ArtificialLeukemia also affects red blood cells and can cause poor-Neural Network (FLANN).----- blood clotting and fatigue due to anemia. Examples of-Elyasigomari, V., et.al. [5] proposed hybridleukemia include:-----approach MRMR-COA-HS (Minimum Redundancy and

- Myelogenous-or-granulocytic-leukemia-Maximum Relevance-Cuckoo Optimization Algorithm-
- (malignancy of the myeloid and granulocytic-Harmony Search) to overcome the gene selection issue to
- white blood cell series)-----classification of cancer. Initially the MRMR utilized in the
- Lymphatic, lymphocytic,-or-lymphoblastic-pre processing stage to select the top 100 genes, then the
- selected-genes-are-fed-in-to-the wrapper-set up which
- leukemia-(malignancy of-the-lymphoid-and-----
- contains-the-COA-HS-algorithm-and-the--SVM
- lymphocytic blood cell series)-----
- classification technique used in present technique it
- Polycythemiavera or erythremia (malignancy of-
- provides the high accuracy then finally classification
- various blood cell products, but with red cells-performance of the selected genes are measured in terms of
- predominating)-----accuracy.-----

### 1.1.5 Lymphoma-Liu, H., et.al. [6] proposed the Ensemble Gene

Lymphomas develop in the glands or nodes of the-selection method (EGS) to chosen the multiple gene

lymphatic system, a network of vessels, nodes, and organs-subsets for classification purpose. In this technique the(specifically the spleen, tonsils, and thymus) that purify-genes are chosen based on the conditional mutualbodily fluids and produce infection-fighting white blood-information. The result shows that the present gene subsetcells, or lymphocytes. Unlike the leukemias which are-has good discriminative capability for data classification.sometimes called "liquid cancers," lymphomas are "solid-Additionally the number of selected genes of the presentcancers". Lymphomas may also occur in specific organs-techniques also finds out self adaptively. In order tosuch as the stomach, breast or brain. These lymphomas are-increase the diversity of the present technique the initialreferred to as extranodal lymphomas. The lymphomas are-points are allocate to various genes with highest

subclassified into two categories: Hodgkin lymphoma and-information. If the multiple gene subsets have beenNon-Hodgkin lymphoma. The presence of Reed-Sternberg-obtained the present technique provides the train basecells in Hodgkin lymphoma diagnostically distinguishes-classifiers and then the result is integrated by the majorityHodgkin lymphoma from Non-Hodgkin lymphoma.--voting strategy. The result shows that the present technique is outperform than the traditional techniques.--

**1.1.6 Mixed Types**-----Jeleń, Ł., et.al. [7]presents the application ofThe type components may be within one category or from-pattern recognition and image processing techniques todifferent categories. Some examples are:---examine the significance of the feature extraction from the

- adenosquamous carcinoma-----fine needle aspiration biopsy images and the cause of the
- mixed mesodermal tumor-----reducing-large-number-features-by-utilizing the-various
- feature-selection-methods-with-small-loss-of-the
- carcinosarcoma-----
- classification accuracy.-The-present-technique-used to
- teratocarcinoma-----
- reduce the size of the feature vector size then perform the-----

## II. Literature Survey-

classification with less information and deliver the satisfiedresults. The reduction of the feature vector leads to reduce

Nilashi,-M., et.al.-[3]-presented the knowledge-based-the complexity-of-classification. The-best-classificationsystem-to classification-of-breast-cancer-by-using the feed forward to the neural network when the

correlation clustering, noise removal and classification techniques. In-measures-are-utilized.-The-present technique-with

present-techniques-the-expectation-maximization-(EM)-----correlation feature vector reach good performance and able used as the clustering method for clustering the data in the-classify the breast cancer data with high accuracy while the related groups. Then the classification and Regression trees-feature vector size reduced iteratively.are utilized to generate the fuzzy rules for classification of-----Nguyen, T., et.al. [8]proposed the novel approach the breast cancer disease in the present knowledge based-for classification for predicting-the-cancer-through-genesystem of fuzzy rule techniques. In order to overcome the-----expression profiles which is build with supervised learning multi collinearity issue-we-include-Principal-component-hidden markov models (HMMs). The gene expression of Analysts (PCA) in the present technique. The present-

each tumour is designed by HMM and the prominent discriminant genes are chosen by the present techniques depends on the modification of the analytic hierarchy process (AHP). The modified AHP allows quantitative factors which are used to rank the outcomes of the individual gene selection methods such as t-test, entropy, receiver operating characteristic curve, Wilcoxon test and signal to noise ratio.The result shows that the HMM is the powerful tool for cancer classification better than the classical classification techniques. The combinations of AHP-HMM provide the better stability and robustness to selection of gene and improve early detection, ease of use to the treatment of cancers in effective and efficient manner.

Xie, H., et.al. [9] presents random projection (RP) technique utilized to reduce the high dimensional features in to low dimensional space with the short duration to predicting the classification of cancer disease. In order to improve the accuracy of the random projection technique it's combining with other techniques such as Principle Component Analysis (PCA), Linear Discriminant Analysis (LDA), and Feature Selection (FS). The different combination of the methods tested with the microarray dataset. The result shows that the feature selection with random projection improves the classification accuracy better than the PCA and LDA.

Piao, Y., et.al. [10] presents the feature subset based ensemble method to classifying the multiple cancers by utilizing the miRNA expression data in order to generate the multiple subsets the feature relevance and redundancy considers. The present techniques utilize the C4.5 decision tree algorithm and SVM algorithm for classification. The present techniques tested with the sequence based miRNA expression datasets and validated with the 10 fold and leave one out cross validations. The result shows that the present technique reaches higher prediction accuracy than the traditional ensemble techniques.

Bharathi, A., & Natarajan, A. M. et al. [11] proposed a simple yet very effective method which is used to cancer classification using the very few gene expression. The aim of the present technique is the finding the smallest gene subsets for accurate cancer classification from micro array data by using supervised machine learning algorithms (SVM). The present techniques involves in two phase such as chosen some important genes by using the 2 way Analysis of Variance (ANOVA) ranking scheme, then test with the SVM classifier it provides the good accuracy.

Thein, H. T. T., & Tun, K. M. M. et al [12] presents the analysis of feed forward neural network and the island differential evolution propagation algorithm utilized to train this network. The aim of the present technique is a creating the effective tool for construct the neural models which helps to proper classification of different classes of breast cancer. The present techniques proposed two different migration topologies such as random topology and torus topology. The performances are tested with Wisconsin Breast Cancer Diagnosis problem and the result shows that the random topology provides good classification accuracy compare to torus topology.

Dora, L., et.al. [13] proposed the novel Gauss Newton Representation based Algorithm (GNRBA) for classification of breast cancer. It uses the sparse representation with feature selection and evaluates the sparsity in a computationally efficient way. Then the present technique proposed new gauss Newton based classifier to find optimal weights for training samples for classification. The present techniques are tested with Wisconsin breast cancer database and Wisconsin Diagnosis breast cancer database from the UCI machine learning repository. The result shows that the present technique provides better accuracy, sensitivity, specificity, confusion matrices compare to traditional approaches.

Reis, S., et.al. [14] presents the analysis of categorize and automated classification of breast cancer by using the multi scale basic image features (BIF) and local Binary Patterns (LBP) combined with the random decision trees classifier used for the classification of breast cancer. The present techniques demonstrate the text based classification of Hematoxylin and Eosin (H&E) images from IBC. The result shows that the multi scale approach provides the good accuracy.

Kourou, K., et.al. [15]presents the recent Machine Learning (ML) approaches to predicting the cancer. The various predictive models are discussed based on ML techniques as well as various input features and data samples. The ML is the branch of artificial intelligence which is used to relate the problem of learning from the data samples in the concept of inference. The each learning process contains two phases. (i) Estimation of unknown dependencies in a system from the given dataset. (ii) Then the usage of the estimated dependencies to

prediction the new outputs of the system. In this work the two main methods used such as supervised learning and unsupervised learning.

Krishnaiah, V., et.al. [16]presents the various data mining techniques in the several types of lung cancer datasets to enhance the lung cancer diagnosis. In this technique the most effective model to predict patients with lung cancer appears to be the Naive bayes which is used to follow the IF-THEN rules, decision trees and neural networks. The decision tree result is easier to read and interpret. The present techniques of predicting lung cancer can be further enhanced and expanded.

Kharya, S., et.al. [17]presents the several data mining techniques to diagnosis and prediction of breast cancer. The prediction of outcome of the disease is the one of the complex task to enhance the data mining applications. The usage of the computers with automated tools, the large volumes of the medical data are gathered and available within the medical research groups. The data mining techniques are popular research tool for medical researcher to predictions of the exploit patterns and related with large number of variables which is used to improve the prediction of disease using the historical datasets. The several data mining techniques are such as Decision trees, Digital Mammography classification using association rule mining and ANN, Association rule based classifier, neural

S. N	Author Name	Methods Used	Dataset Used	Merits	Demerits	Performance
1	Jayanya, D., & Rami, D. K. U. [18]	Decision tree classifier (CART)	Breast Cancer Dataset	Easy to generate rules	Need large amounts of memory to store the entire tree for deriving the rules	Accuracy=94.72%
2	Romani, R. G., A. Jamb, S. G. [19]	Hybrid feature selection	Gene Set Enrichment Analysis database (GSEA.db)	Easy to use and improve accuracy	Complexity issue occur	Accuracy= 87 %

network based classifier system, Naive bayes classifier, support vector machine, logistic regression and Bayesian network. The result shows that the Bayesian network is perform well to predict out Breast Cancer and diagnosis. However the Bayesian networks requires large amount of probability data.

Chaurasia, V., & Pal, S., et.al.[20]presents to analysis the performances of several data mining techniques. The classification of Breast cancer data can be utilized to find out the result of some disease or discover the common nature of cancer disease. The several data mining techniques are used to analyse the cancer disease, the present novel approach used to find out the compare performances of decision tree classifier such as Sequential Minimal Optimization (SMO), K-Nearest Neighbor Classifier, andBest First Tree. The result shows that the performance of SMO provides good result compare to other classifier in terms of accuracy, low error rate and performance.

Agrawal, A., et.al. [23]presents to improve the prediction models for lung cancer using data mining techniques. In present techniques utilizes the ensemble voting of five decision tree based classifiers and Meta classifiers used to find out the lung cancer prediction in terms of accuracy and according to the ROC curve. Additionally the lung cancer outcome calculator was developed by using this present technique. The prediction quality of the technique is calculated by this calculator is very efficient to find out the lung cancer prediction.

### III. Discussion

The above survey provides the detailed description of classification of cancer using various data mining techniques as depicted in Table 1.

7	Silanga, G. I., Abdelhalim, M., & Zaid, M. A. E. [26]	Multi Classifiers	Wisconsin Breast Cancer (WBC), Wisconsin Diagnose Breast Cancer (WDBC)	Work well on both numeric and textual data	Computation time complexity occur	Accuracy =97.28%
6	Zheng, B., Yoon, S. W., & Lam, S. S. [25]	Hybrid of K-means and support vector machine algorithm	Breast Cancer Wisconsin (Original) Dataset	Reduce computational time	Not easy to interpret	Accuracy =97.38%
5	Shajiquran, S. S., Shanithi, S., & ManojChitra, V. [24]	Decision Tree	Breast cancer dataset	Classification accuracy improved and reduce problem complexity	Training time is relatively expensive	Accuracy = 100%
4	Mishra, D., & Sahu, B. [22]	Multiple filter multiple wrapper approach (MFMW)	Leukemia Data set	Easy to implement	Slow Execution and Lack of generality	Accuracy = 100%
4	Mishra, D., & Sahu, B. [22]	Multiple filter multiple wrapper approach (MFMW)	Leukemia Data set	Easy to implement	Slow Execution and Lack of generality	Accuracy = 100%
3	Jacob, S. G., & Ganauhi, R. G. [21]	Random tree and Quinlan's C4.5 algorithm	Wisconsin Prognostic Breast Cancer (WPBC)	Classification accuracy improve	Limited utility for future enhancement	Accuracy = 100%

8	Glaab, E., Bagardi, J., Garibaldi, J. M., & Kratoch, N. [27]	Evolutionary machine learning technique	Microarray cancer datasets	Efficiently work with large scale dataset.	Time consuming for training.	Accuracy = 96.6%
11	Salim, H., Alya, G., & El-Elsbawy, N. [30]	New Novel Approach based on gene expression profiles	Microarray gene expressions datasets	Improve the classification accuracy	Time complexity	Accuracy = 100% Specificity = 97.3% Sensitivity = 99.78%

#### IV. Conclusion

In this survey the several data mining techniques have been discussed in classification of cancer disease prediction. The several data mining techniques such as Artificial Neural Network (ANN), Ensemble gene selection methods, pattern recognition, Learning Hidden Markov Models, random projection (RP), Ensemble Method, SVM classifier, Random Topology, Novel Gauss Newton Representation, Machine Learning, Decision tree, Sequential Minimal Optimization, Multiple filter multiple wrapper approach and Skewed gene selection algorithm etc used in the literatures and these methods have both merits and demerits. According to the biomedical domain the information gain and genetic algorithm methodology have efficiently used for classification of cancer by using gene expression data. Initially the information gain is used for selects the significant features from the input patterns. Then the selected features are reduced by using the genetic algorithm (GA). The genetic algorithm has several major advantages such as does not need any mathematical requirements, the ergodicity of evolution operators makes GA very effective at performing the global search and the GA provides the great flexibility to hybridize with domain depend heuristics to make the efficient implementation for the specific problems. Then the information gain also has several advantages like it is used to reduce a bias towards multi valued attributes by taking the number of attributes with a large number of distinct values. Finally the gene expression profiles are utilizing to classify the human cancer disease chosen to improve the prediction of cancer classification. Further the research work can be extended to implement the hybrid or new classification algorithm to classify gene expression dataset for better accuracy and prediction.

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