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Enhanced Multimode DBN for Optimal Classification of Heterogeneous Cancer Images for HealthCare System

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ABSTRACT

Medical data has grown tremendously in recent years. Health and medical science are advancing through big data and deep learning techniques to predict outcomes. Existing interventions focus on Brain, Breast and Bone cancer separately. In this study, we proposed an e-MDBN (enhanced Multimode Deep Belief Network) model, which is primarily based on an optimized parallel CRBM (Clipped Restricted Boltzmann Machine) Algorithm that trains the layer, then fine-tunes the e-MDBN model and classifies the image into Brain, Breast and Bone cancer. This deep learning-based image classification workflow delivers efficient results. Pyspark's distribution platform, which has an improved e-MDBN network structure, has the fastest and highest accuracy rate. Accuracy, precision, mean squared error, and recall of the recommended methodological configurations are superior to the state-of-the-art alternatives

1. INTRODUCTION

Sustainability aims to promote well-being and health for all individuals of all ages. Every day, thousands of images are produced in medical imaging facilities. Despite the increasing volume of data, the situation remains uncontrolled. Modern machine learning (ML) techniques allow for a new generation of image analysis using big data. Big data in healthcare has materialized and aided healthcare practitioners and scientists worldwide in detecting hidden patterns for future clinical decision-making [1]. The volume of Electronic Health Records (EHR) that has accumulated owing to high-end IT-based technology that has increased in the last century for the early identification of illnesses is the key challenge encountered in the real-world application arena. Because of computing requirements, old technological techniques could not discover hidden patterns [2]. In healthcare, big data has a generous requirement due to its different forms and the increased pace at which it must be processed to improve diagnostic interventions. In their evaluation process, contributors should take into account the discussed needs to develop a sustainable solution to deliver a predictive universal digital healthcare ecosystem.

The current annual rate of new cancer diagnoses is 1.8 million, and it is not uncommon for cancer to be discovered in more than one organ at a time. Tumours are abnormal growths of potentially malignant tissue that can exhibit themselves in any body organ [3], [4]. Malignant growths, or tumours, can manifest in various forms inside the human body. Replacement of dead tissues with new cells is necessary for maintaining good health. From time to time, issues may arise during this process. Because of this, new cells thrive when we might not need them, and old cells do not die when they should. Eventually, a mass of these extra cells can form a tumour. Among female malignant tumours, breast cancer (BC) has been studied the most frequently. It is a malignancy that begins in the breast and progresses when normal breast cells begin multiplying at an abnormal and uncontrollable rate. One out of every three women diagnosed with this form of cancer will ultimately succumb to it [5].

The development of breast cancer (BC) can start in a variety of breast tissues. The majority of BC diseases (ductal malignancies) begin in the ducts that transport milk to the areola or areola, while others begin in the milk-producing glands themselves (lobular cancers). It is crucial to understand that the vast majority of breast abnormalities are benign tumours and not cancerous. Non-cancerous tumors are rare, but they are usually not life-threatening because they do not spread externally [4]. However, malignant breast tumours are extremely dangerous because they invade neighbouring tissues and harm them. Multiple vital organs can be affected by metastatic cancer when cells of a harmful tumour spread to them. It spreads through the body's circulatory and lymphatic systems and initiates a secondary tumour formation [6]. Examination methods currently used for detecting BC include MRI, mammography (x-rays), Sonography, and other Medical (pathological) tests [7]. For patients who have undergone other tests, like mammograms, but still have concerns about the accuracy of the diagnosis, histopathology images are widely regarded as the gold standard. Cancer and its effect on surrounding tissues can be studied more thoroughly and accurately using histopathology.

In addition to breast cancer, brain tumours are among the worst cancers. Brain tumour patients frequently experience a variety of symptoms, including seizures, confusion, odd behaviour, and memory loss. The complex anatomy of the brain makes it difficult to locate a tumour with any degree of accuracy. Cancer and brain tumours both involve the abnormal and uncontrolled multiplication of cells. Any abnormal cell growth inside the human skull has the potential to disrupt crucial organ function and spread throughout the body. Primary tumours (originating in the brain) are usually benign, while secondary tumours (those that spread from other parts of the body) are malignant. A glioma is a common malignant tumour that, if it has progressed to the final stage, can cut life expectancy drastically. This disease rapidly progresses from patient to patient by embedding itself in various brain structures [8].

In the field of medical imaging, magnetic resonance imaging (MRI) has assumed a pivotal role due to its increased spatial resolution and wealth of data useful for the detection and assessment of brain tumors. Computerized imaging technology is employed to spot brain disorders with pinpoint precision. Bone cancer also is a rare form of cancer that develops when cells in the bone begin to grow uncontrollably. The human skeletal system encompasses many hard tissues, including bones, cartilage, tendons, and ligaments. The human skeleton accounts for about 20% of the total body mass. The human skeleton is made up of 206 bones. Children's skeletons are more complex than those of adults because some bones, including those of the skull, fuse as the child develops. Differentials exist between male and female skeletons as well. The average male skeleton is significantly longer and more robust in bone mass than the average female skeleton.

On the other hand, the female skeleton features a more spacious pelvis, which is ideal for carrying a baby and giving birth. There are five main types of bones: long, short, flat, irregular, sesamoid, and structural. Different kinds of bone develop in different places and carry out various tasks. It is common for bones to contain both compact and cancellous tissue. The chemical makeup of bones demonstrates this. Bone comprises collagen fibres, an inorganic mineral, and tiny crystals. Depending on the type of bone, water can make up anywhere from 10 to 20 percent of a living organism's skeleton. The mineral bone accounts for roughly 60–70% of its dry weight [9], [10].

Along with ailments and diseases that resemble them, bone tumours appear in various shapes and sizes. Even though these conditions are not bone tumours, they typically require the same treatment. While the cancerous bone fragment is removed, the associated muscles, nerves, tendons, and blood arteries are kept as much as possible. The surgeon will remove the tumour and a portion of the surrounding healthy tissue. Since its discoveries can be used to prevent health issues, medical image processing is an important field of study. It is a reliable method for tumour detection that is also faster and more accurate. Medical imaging is changing quickly due to improvements in image processing methods. Our research work contributes to Big Data and Deep Learning (DL). In an environment of big data, CRBM-based DBN can more concisely distinguish tumour mammograms from healthy ones.

A brief introduction to cancer image classification is presented in the first section of the paper. A theoretical background is presented in section 2 of the paper. In section 3, we discuss the proposed system in detail, and in section 4, we discuss the results and discussions. Section 5 presents the conclusion.

2. RELATED WORK

This section included three subsections that reflect the relevant work for the Brain, Breast and Bone separately. Each of these subsections will detail the process of the papers, which will be stated below.

2.1 Survey on Breast Tumour

The author proposed two different SVM (Support Vector Machine) models, the C-SVM and the V-SVM, [9] for detecting breast cancer using SVM. Hybridization is performed using the WAUCE method, which calculates the weighted area under the receiver operating characteristics curve. The model in question performed more favourably compared to other studies that only employed a single SVM structure. The high time and financial investment needed to complete this study is a major drawback. This strategy is very excessive. Grading of the tumour [11] has occasionally been linked to the occurrence, advancement, and invasive carcinoma (such as breast DCIS). These links, however, are heavily influenced by the heterogeneity of tumours and mixed grading (i.e., multiple gradings). Approximately 50% of cases appear to exhibit mixed grading, which presents considerable challenges for investigators.
In a recent paper, researchers proposed a hybrid method of SVM and two-step clustering to diagnose breast cancer (HBSVM-C) [12]. They used a hybrid strategy to improve

the prediction system's ability to diagnose breast cancer. Using the WBC dataset as a test subject, the suggested system's estimated precision was 99.1%, respectively.

[13] Mammograms can be classified according to their CAD-based properties. Features are selected, and dimensions are reduced using genetic algorithms, while classification is performed using support vector machines.

A dual purpose was proposed by [14]. The primary goal is to investigate the various learning models for describing histopathology images of bosom malignant development. This review identifies the most precise models for the two, fourth, and eighth orders of the histopathological image information bases for bosom disease. Based on the supplied data, DL models achieved higher accuracy scores when pre-handling, transfer learning and augmented information approaches were considered. The final synthesis can also be inspired by the latest models that have been scrutinized little or no in previous research. The most current ImageNet informative index findings have been connected to Dual-Path Net, ResNeXt SENet, and NASNet models. A two-overlap and an eight-overlap model was examined.

2.2 Survey on Brain Tumour:

The author [15] suggested an algorithm for identifying and separating tumours. After the MRI image has undergone standard preprocessing measures like brightness, threshold, and Filtering, it is sent to the skull masking stage, where the region of interest (ROI) is determined. As well as splitting the shaved skull in half down the middle, morphological procedures are performed. In terms of classification, SVM classifiers come in last.

A technique for detecting and labelling tumours of the brain in MRI scans was first presented by [16]. The author paid special attention to noise cancellation methods, GLCM feature extraction, and wavelet DWT coefficient extraction. PNNs (probabilistic neural networks) were used for classification. This method can distinguish between healthy and diseased tissues with near-perfect precision.

It has been shown that using Discrete Wavelet Transform (DWT) to extract features, Principal Component Analysis (PCA) to reduce features, and ANN and KNN to classify images, the author [17] has been able to classify 80 images of brain tumours into normal and abnormal with 97% accuracy and 98% accuracy, respectively.

It was proposed by [18] that CNN be used to classify pathological images of gliomas into grades II, III, and IV. In both cases, they were successful 71% of the time and 96% of the time. In this research [19], neural networks were used to transfer perceptual information from MRI images to predict the arrangement of cortical tumours. With a focus on Res.Net, Xception, and Mobil-Net-V2, the deployed study examines different CNN architectures. DL simulations are constructed, supported, and examined in three sections in this study. It contains 80% of the sample and was modified to fit the simulation. The surplus is distributed appropriately to certify and test the construction. The findings from this framework were the most effective, with evaluations of 98.25% precision and 98.43% F1-score, respectively.

2.3 Survey on Bone Tumour:

The author [20] proposed a research study that specifies a bone cancer recognition and classification approach utilizing fuzzy clustering and classifier. Researchers use fuzzy C-mean clustering to detect bone cancer. MRI pictures of the bone were used to evaluate the proposed method's precision. ANFIS was used to distinguish benign from malignant bone cancers.

From MR images, GLCM was extracted to train and test the ANFIS network. Bone pictures that were taken to be divided into training and test images underwent an accurate cross-validation. The classification result's accuracy, sensitivity, and specificity were assessed using three output matrices- accuracy, sensitivity, and specificity.

By employing a region-growing algorithm, [21] suggested a unique method for determining the tumour size with the point of bone cancer. A region-growing procedure was used to segment the study area. Tumor size is computed based on pixels in the retrieved tumour portion. Pixel values are used to determine the cancer stage. Choosing the right seed point is challenging because it relies on the image.

Feature extraction is essential in many applications, including image processing, data mining, and computer vision [22]. According to [23], bone malignancies can be diagnosed using a textural characteristic called the Grey Level Co-occurrence Matrix (GLCM). Two trials were conducted, one with hog feature sets and another without using two ML models. Based on hog feature sets, SVM models achieved an accuracy of 92.5%. To extract features, however, a CNN appears preferable [24]. The development of a DNN model to differentiate between healthy and damaged bones was emphasized by the authors of [25]. The dataset was expanded, and overfitting was avoided by using data augmentation techniques. Five-fold cross-validation demonstrated 92.4% accuracy for the DNN model using Softmax and Adam. This study identifies whether patients with prostate cancer metastases by categorizing their bone scintigraphy images [26]. The three classifications used by the suggested technique are malignant, healthy, and degenerative.

3. PROPOSED SYSTEM

MRI, CT, and X-ray clinical data will be used to develop a model that predicts malignancy in brain, breast, and bone tumours. There are two components to this challenge.

1. Preprocessing: This stage ensures the cancer dataset is well prepared for classification. This stage ensures the dataset's quality in noise and duplicate removal, outlier detection and processing, and encoding for a numerical representation of categorical and nominal variables. The output of this stage is a ready dataset for further analyses and model pre-training.

2. Pre-training and Fine-tuning the Model: This step involves stacking Restricted Boltzmann Machines (RBMs) to form a deep net and training. DBN is a generative-graph multi-layered model. The process in which the model is used to predict either in a supervised or unsupervised manner is known as pre-training. RBMs are trained for each deep hidden layer. As a first step in training DBN, layers are trained sequentially, starting from the bottom visible layer (observed) features.

Apache Framework: Apache Spark is a large data-focused distributed computing platform that has evolved into one of the most powerful frameworks. One of the most widely used frameworks is Apache Spark, which effectively conserves enormous amounts of data and processes it over several systems in conjunction with other disseminated computing technologies. Kafka, HDFS, and Flume are all sources of data that Spark streaming can consume. GraphX, Spark SQL, and Spark MLlib are some of the other components of Apache Spark: the Spark core and high-level libraries. Adapting the hybrid architecture, Apache Spark is a powerful platform for big data processing. In a hybrid architecture, batch processing and stream processing are supported. Hadoop's MapReduce engine shares many of Spark's guiding principles, but Spark is more performant.

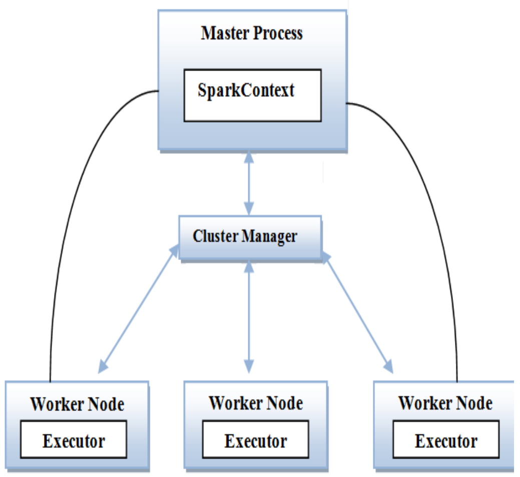

Fig. 1: Overview of Apache Spark Architecture Diagram.

Fig.1 depicts the Apache Spark architecture, which includes a driver program that aids in carrying out the system's primary task and creating Spark Context objects. Spark Context ties in with many kinds of cluster managers to run on a cluster. It locates the executor on the cluster nodes, moves our system code to the executor, and then delivers it to the job for execution using Spark Context. The cluster manager's job is to distribute the resource across the systems. The Standalone scheduler, Hadoop YARN, and Apache Mesos are just a few examples of the several kinds of available cluster administrators. The cluster's location is supported by the worker node or secondary node [27].

Our approach creates an end-to-end deep learning pipeline built on the Spark platform using the Python packages Tensorflow, PySpark, and Elephas. The Apache Spark's potential may be increased using the Python API in Spark, which is made possible via PySpark.

DBN Architecture: A DBN consists of many layers of hidden cells. Alternatively, it can be viewed as a graphical model consisting of many Restricted Boltzmann Machines (RBMs). As long as there is a concealment layer of RBM, that layer will always be considered the visible layer of subsequent RBM. $v = (v_1, \dots\dots, v_p)$ is the visible parameter, while $h = (h_1, \dots\dots, h_q)$ is the hidden parameter. To show twofold information, the existing RBM [Fig.2] uses two irregular factors $(v, h) \in \{0,1\}^{p+q}$ as the irregular factors. In equation (1), EBM's Energy function is derived:

$$E(v, h) = -\sum_{i=1}^{p} b_i v_i - \sum_{j=1}^{q} c_j h_j - \sum_{i=1}^{p}\sum_{j=1}^{q} v_i W_{ij} h_j \qquad (1)$$

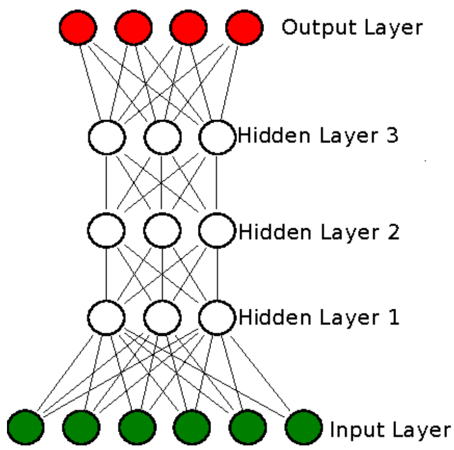

Fig. 2: DBN Architecture

Deep neural networks frequently encounter the problem of disappearing and increasing gradients (exploding). Due to the deep nature of the networks, weights are modified over a long period. Gradients can either vanish or explode due to weights spreading with time. It is primarily concerned with establishing a guideline to avoid gradient bursts. Clipped ReLU [28] layers adhere to the clipping boundary, and data is worth more than it is assigned to the clipping value. It reduces the problem of gradient bursting by using the Clipping approach when training RBM hidden layers.

However, time-consuming training remains a problem that cannot be ignored. Using Spark, we propose a parallel comparison divergence algorithm. As a result, it trains the CRBM with the nCD [29] model so that the training speed can be improved. The method outperforms traditional sequential algorithms in the experiments. MRI, CT, and X-ray image classification are performed using CRBM-trained layers. Compared with traditional algorithms, it shows improved precision and speed of training. Parallel iteration has been adopted into the CRBM training process. This algorithm considers normalizing parameter unknowns. As a result, the likelihood function has two subfunctions. Two parameters are involved in the model distribution: the normalizing parameter and the model distribution parameter. It is possible to determine the parameter that needs to be evaluated in a highly efficient way when the normalizing parameter and the model distribution parameter are combined. It is not a complex process to train. The algorithm is capable of improving RBM [30] when training data is available.

A diagram illustrating the proposed methodology is shown in Fig 3. All three datasets are first preprocessed and fine-tuned with an optimized parallel CRBM algorithm, which trains the layer and then fine-tunes the e-MDBN model and classifies the image into Brain, Breast and Bone cancer.

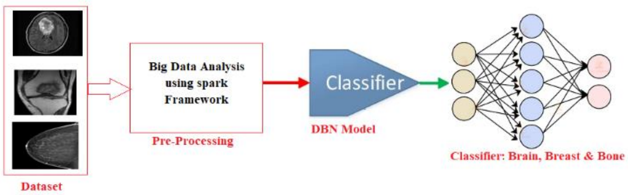

Fig. 3: Proposed Architecture of Heterogeneous e-MDBN

The proposed e-MDBN (enhanced Multimode Deep Belief Network) model uses weight initialization to produce classification results for Brain, Breast, and Bone cancer images. The e-MDBN was first constructed as three-layer DBNs, one for each modality (Brain, Breast, Bone). There are separate RBM structures for the brain, breasts, and bones. An explanation of the features of RBM can be found in probability distribution functions and energy functions. In Eqn. (2) homogeneous cancer images are defined as having a probability distribution.

$$P = (n, S^1, \ldots \ldots . S^w) = \left(\prod_{x=1}^{w} P\left(S^w / S^{w+1}\right) \right) X \, P\left(S^{w-1} / S^w\right) + \sigma(W_{vh+} S_w) \qquad (2)$$

where, $n = S_{o,}$ $P\left(S^w / S^{w+1}\right)$ indicates the condition-based distribution of improved optimized CRBM and $P\left(S^{w-1} / S^w\right)$ denotes the alternate top phase of the trained layer.

The algorithm for the proposed e-MDBN:

Step 1: Initialization of a DBN with n layers of CRBM.

Step 2: Biased vector and weight vector are included in layer-based unsupervised learning. The first CRBM is given the original input along with preset parameters. Additionally, the second CRBM's input stage receives the first CRBM's output before moving on to the final CRBM. In the end, e-MDBN is created.

Step 3: The network adjusting procedure using fine-tuning.

Step 4: A classifier is added to the e-MDBN at this point. The layout is derived from backpropagation, and the weight matrix of the network is revised.

Step 5: Make use of the Softmax Classifier. The Softmax classifier's input stage receives the output of e-MDBN at the conclusion.

4. RESULT AND EXPERIMENT

A description of the experimental setup, a description of the dataset, an analysis of the results, and a description of the time complexity of the experiment are presented in this section.

4.1 Datasets: The dataset includes many CT, MRI and X-ray pictures of normal, Brain, Breast and Bone cancer patients. We used the breast cancer Wisconsin (original) dataset to predict breast cancer. The dataset includes 699 instances and 11 attributes, along with the class label. Eight benchmark datasets were used to assess the effectiveness of brain cancer treatments, including BRATS 2012, 2013, 2014, 2015, and ISLES 2016 and 2017. This study utilizes X-ray images from the Indian Institute of Engineering Science and Technology, Shibpur (IIEST), to diagnose bone cancer.

4.2 Image preprocessing: As part of the preprocessing, images were enhanced, transformed, cropped randomly, resized, rescaled, flipped, and rotated to increase detection accuracy. It is used to improve the image's contrast prior to further processing. It improves the robustness and accuracy of the image. A grayscale, thresholding, and median filter are used as preprocessing stages. The use of grayscale reduces the noise in RGB images. As a result, the grayscale image will be more intense in terms of light. It is used to sharpen images that are too dark or too bright by flattening the light intensity. Gaussian filters are used during the preprocessing process to remove noise and unwanted signals from the input image prior to enhancement. It improves image quality by reducing image contrast and blurring image edges. The Gaussian filter reveals hidden properties. The provided image is subsequently subjected to thresholding.

The simplest way of image segmentation is thresholding. The segmentation process is demanding because of the variety and difficulty of images. It divides an image into many sections or parts. Thresholding replaces each pixel in an input image with a black or white pixel to make it easier to analyze the data for disease classification. The process is carried out on a picture using the Region of Interest (ROI). Using the Region of Interest (ROI) method, disease sizes can be evaluated based on imagery boundaries. It filters out unnecessary pixels and focuses on a specific picture area to classify the condition.

4.3 Performance metrics:

A performance metric is the Mean Squared Error (MSE), which is used to rate the efficiency of the proposed method. [31]. Eqn. (3, 4, 5 and 6) determines the performance metrics as follows:

Accuracy (A): Correctly predicted events as a percentage of total events. The mathematical explanation is presented in Eqn. (3)

$$Accuracy(A) = \frac{(TP + TN)}{(TP + TN + FP + FN)} \quad (3)$$

A positive event confirms the prediction of the system, where TP represents the true positive value. TN represent the true negative value. The system correctly predicts these negative events. FP represents false positives. The system predicts negative events as positive events. FN represents the false negative value. The system predicts negative outcomes for these positive events.

Precision (P): An accurate prediction occurs by Eqn. (4).

$$Precision\ (P) = \frac{TP}{(FP + TP)} \quad (4)$$

Recall (R): All positive events divided by correctly predicted events as mentioned in Eqn. (5).

$$Recall\ (R) = \frac{TP}{(FN + TP)} \quad (5)$$

Mean Squared Error (MSE): In Eqns. (6) average square values are calculated as the difference between predictions and observations.

$$MSE = \frac{1}{D}\sum_{j=1}^{D}(y_{j-}\, y_k)2 \quad (6)$$

An observation is indicated by D, a predicted result is indicated by y_k, and an observation is indicated by y_j.

4.4 Performance Comparison

DT, K-Nearest Neighbours, SVM, Traditional Neural Networks, and Linear Discriminant Analysis were compared with this method [32]. The result representations are shown below:

Fig. 4 shows how the proposed method compares with existing classifiers. It performs better than other existing classifiers (97.5%). Aside from KNN, SVM, DT, TNN, and LDA, other existing classifiers provide similar accuracy values, including 93%, 92%, 96%, and 96%.

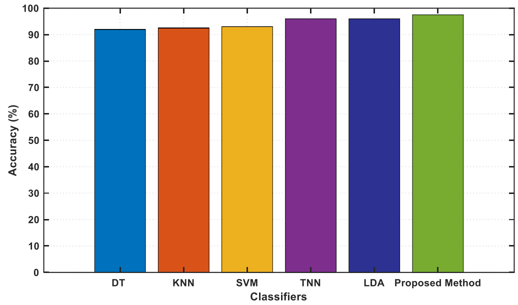

Fig. 4: Accuracy performance analysis based on the number of classifiers.

Based on the performance of various existing classifiers, Figure 5 illustrates the precision of the proposed method. The e-MDBN can achieve a precision of 96.5%, while precisions of 93%, 93.5%, 94.5%, 94%, and 95% are achieved by KNN, SVM, DT, TNN and LDA, respectively. It is more precise than other approaches.

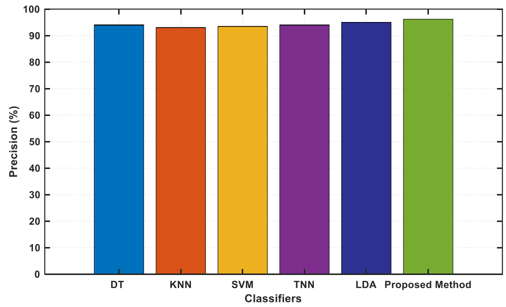

Fig. 5: Precision performance analysis based on the number of classifiers.

The proposed method is illustrated in Fig. 6 with a recall analysis. An accuracy rate of 97.5% was obtained using the proposed method. The KNN, SVM, and DT recall performance is very low. There is a higher recall rate with this approach than with others.

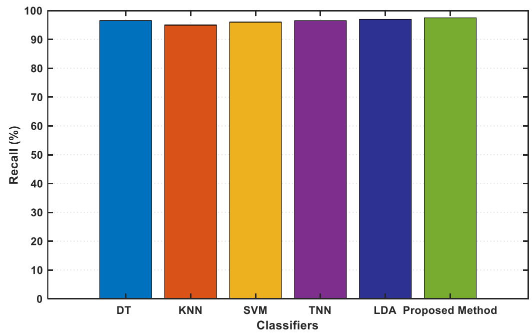

Fig. 6: Recall performance analysis based on the number of classifiers.

Figure 7 compares the e-MDBN with other classifiers based on their MSE. There is a reduction in MSE (11.5%) using the proposed method.

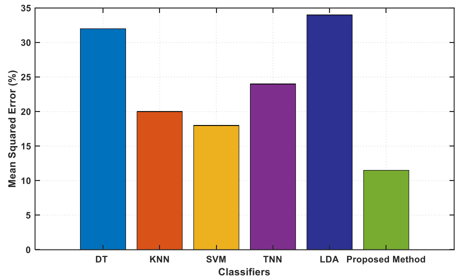

Fig. 7: MSE performance analysis based on the number of classifiers.

The simulation analysis indicates that the proposed e-MDBN is more accurate, precise, and recallable and has a smaller MSE than the existing approaches. The proposed e-MDBN system has a lower time complexity from the analysis and a faster performance speed. It proved that the proposed e-MDBN system improved brain, breast, and bone cancer classification.

5. CONCLUSION

In this paper, we propose a heterogeneous cancer classification model using e-MDBN. Experimental results demonstrate the effectiveness. However, time-consuming training remains a problem that cannot be ignored. This study offers a parallel comparison divergence technique that utilizes Spark. It utilizes it to train the parallel CRBM model to increase the training pace to overcome this problem. It also employs optimized parallel CRBM with nCD based on Spark. The simulation results indicate that the approach is quicker than a conventional sequential algorithm. For technology solutions to be sustainable, data capture, storage, and analytics need to be efficient and effective. New feature section techniques are used with this number of classifiers in the future.

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