Detection Of Tumor Affected Part From Histopathological Bone Images Using Morphological Classification And Recurrent Convoluted Neural Networks

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Abstract

The bone tumor (BT) remains a sickness type that is marked by unlimited cell growth and results in numerous early demises worldwide. Hence, diagnosing BT in the earlier phases and classifying them turned into a vital job for healing the sick person. Springing out of the bone, BT disseminates throughout the body swiftly impacting sick persons. By assessing histopathological images (HPIs), BT’s swift and early prognosis could be started. Centered upon this, a survey has been performed on BT identification employing diverse approaches to image processing and observed that there remain several issues, and the adversities did by BT enhance while it is unidentified at the right time. The abnormalities in the bone image are identified from the region of interest. For these problems, many research works were carried out to develop several Computer-aided diagnosis systems, having as a major challenge to define the features that better represent the images to classify. To overcome the problem this paper aims to develop Recurrent CONVuluted neural networks (Rec-CONVnet) based classification for the assessment of tumor type based on analyzing MRI images. For the smoothing process wiener filter is used to reduce the mean square error (MSE) and hence image enhancement is done by using a convoluted Gabor filter. The performance analysis is done by comparing with three traditional methods such as Dense Convolutional neural network (DCNN), Random Forest (RF), and Decision Tree (DT) in terms of accuracy, sensitivity specificity, f1 score, recall, and is found that the proposed Rec-CONVnet achieves 98.34% of accuracy, 97.96% of precision, 98.72% of recall, 98.33% of specificity and 98.32% of f1-score.

Keywords- bone tumor, classification, neural networks, preprocessing, MRI image

1. Introduction

The bone contains the organs of the body termed femur or tibia and bone tissue (BTS) or osseous, which is the main cause of all confusion and complexity. The BTS is segregated as cancellous or trabecular or spongy bones and the other is cortical or compact bones [1]. The cancellous bones cover more surface area as less dense with softer, flexible, and weaker characteristics. This type of bone is generally present on top of the femur, end of long bones, tibia, and interior vertebrae. Besides, these are extremely vascular and normally comprise red bone marrow where the blood cells are produced. Trabecula is the functional element of this cancellous bone [2]. Bone tumors have a broad variation in biological activities and need various management techniques based on benign, intermediate, or malignant categories [3]. For local recurrence, benign types namely osteochondroma, osteoid osteoma, and have only restricted ability and are readily cured always. Intermediate tumors like giant cells,
chondroblastoma, and so on rarely can be locally aggressive or metastasize. Thus, this group of bone tumors frequently requires broad excision margins and/or uses adjuvant therapy to confirm local control [4]. The other type called Malignant class such as chondrosarcoma, osteosarcoma, and so on potentially have local destructive growth and recurrence and also carries substantial risk for distant metastases.

Mostly, primary bone tumor diagnoses rely on conventional radiographs and the patient’s age. To differentiate these cases, the plain radiograph is most useful, while for some selected special cases, CT and MRI are used. Moreover, demographic information like the age of the patient and radiographic tumor appearances such as size, margin, location, matrix type, periosteal reaction, and cortical destruction are clues that assist the radiologist in differentiating indolent bone tumors from the aggressive ones [5]. As the appearance of bone tumors varies and is comparatively unusual, radiologists require appropriate experts for diagnosis. Low accuracy in interpreting bone tumors is very dangerous and causes severe harm to the patient. Numerous benign tumor patients, referred to as bone biopsy, have issues of more injury and cost.

Because of the increase in cancer occurrence and sick person-specific treatment choices, cancer prognosis and medicament are turning very intricate [6]. Pathologists should expend an exceedingly lengthy duration [7]. Mis-prognosis frequently happen because of the broad tasks, which lessen the prognosis’ accuracy. The osteoblasts’ morphology possesses a small disparity in distinguished cells that turns the image hardly differentiable. Additionally, the biopsy remains an important and long-drawn phase for discerning the malignant tissue’s existence. Meantime, Computer-Aided Detection (CAD) approach provides a solution for radiotherapists to automatically identify malignancies [8]. For handling these constraints, the microscopic image-based assessment remains the basis for cancer prognosis over the past few years [5]. Nevertheless, this remains impractical prior to the 2000s owing to reasonably less identification precision. The CAD’s worst execution turned medical applications unrealistic till the latest progressions in computerized image identification [9]. Latest progressions facilitated the feasibility of changing histological slides into digital image databases wherein ML could interfere with computerized images for dealing with a few constraints. Because of the emergence of whole slide imaging (WSI), digital pathology gives novel opportunities for establishing novel algorithms and software. A histological image could be computed in a system for enhancing the pathological operations. The system digitalizes glass slides with stained tissue portions at more HD images that turn computerized image assessment feasible [6]. The phases include images’ registry, identification, and classification [7].

MRI scanned images play a significant role in diagnosing the tumor, providing treatment, and, moreover, improving the classification accuracy. Long Short-term memory Networks (LSTM), Auto-Encoders, Recurrent Neural Network (RNN), Convolutional Neural Network (CNN), and Generative Adversarial Networks (GAN) are examples of deep learning (DL) approaches [8]. The standard approach among these is CNN which produces better results than that of the knee bones [9]. Moreover, DL approaches perform feature engineering automatically. The limitation is that, in medical and health science domains, computational time is the main issue, particularly with radiology images. Thus, there has aroused a need to diagnose these images by providing high accuracy and consuming less time than GPU and not CPU.

The objectives of this work are as follows: to detect the presence of tumors in the bone of the affected part in histopathological images using morphological operations. Then, the detected tumor has been classified using recurrent convoluted neural networks. The contribution of this work are as follows,

- Pre-processing for image enhancement and smoothing process, wiener filter with the addition of convoluted Gabor filter is used to reduce the mean square error (MSE)
- Introduction of fuzzy c- means contrast enhancement for segmentation and Feature extraction using convoluted Gabor filter
- We examined Recurrent CONVolved neural networks to combine temporal and spatial information from ReLU data to detect high-risk cancer.
The organization of this paper is as follows: Section 1 portrays the outline of bone tumors, the function of histopathology in tumor detection, and the application of neural networks in tumor detection. Section 2 depicts the current strategies for tumor prediction with its limitation. Section 3 gives classification process. Section 4 gives productive experimental analysis, and, finally, Section 5 sums up with a conclusion and future work.

2. Related works
In [10], Kishore et al. introduced an approach to detect the size of the bone tumor and its stage. For classifying the bone MRI images, the seed region growing algorithm was involved. It produced better results based on the seed point selection and similarity criteria. Once the tumor region is segmented, the tumor area is estimated by which stage of the tumor was detected. In [11], Krupali et al., integrated k-means and fuzzy c-means clustering algorithms to detect bone tumors from MRI scan images. To detect enchondroma bone tumor, mean pixel intensity was involved. In [12], Zheng et al. stated the use of conditional random fields as recurrent neural networks (CRF-RNN). In CRFs, the interpretation step is considered as a series of recursions, which are back-propagated as RNNs. In [13], Zhao et al. used CRFs as RNN for the classification of the map during post-processing. In [14], Le et al. integrated a recurrent fully convolutional network (RFCN) with variational level sets (VLS) for classifying the tumor. Rather than the previous approaches, in this RFCN, the deconvolutional layer considers the output of the prior convolutional layer as input for processing. In [15], Wang et al. developed a cascaded convolutional neural network (CCNN) using the hierarchical information of the sub-regions for decomposing a multi-class classification problem as binary classification one. In [16], Brosch et al. used FCNs with skip connections to separate several sclerosis lesions. In [17], Isensee et al. modified the U-Net approach for classifying bone tumors using dice loss function and extensive data augmentation to successfully avoid over-fitting. In [18], Dong et. al., to maintain the output dimension, employed zero padding at every convolutional layer while up-sampling as well as down-sampling paths. In [19], Dolz et al. modified U-Net using multi-input channels and dense concatenation to detect lesions. In [20], Jesson et al. improved FCN in which multiple-scale loss function was used with the limitation, and it does not model the settings explicitly in the label domain. By using this type of function, different resolutions are produced and minimize the function by integrating lower and higher resolutions for modeling the settings both in the label domain as well as images. In [21], a 3 pathways CNN was employed for segmenting bone MRI scanned images. The kernel size of the local pathways is 5 × 5 and 7 × 7 while that of the global one is 9 × 9 each containing three convolutional layers where features were simultaneously exploited. In [22], Havaei et al. designed a novel two-pathway architecture that examined the local information of the bone and environmental settings. The kernel size for the local pathway was 7 × 7 while that of the global one was 13 × 13. In [23], Jesson and Arbel developed a boundary-aware FCNN which used two up-sampling. The first, which identified the borders, intended in learning the boundary data of the whole tumor by regarding this as the binary classification issue. The next, which identified the area, divided them into sub-areas to classify. The study [24] as well employs a DL paradigm for identifying and classifying Osteosarcoma cells. The study [25] proffers a CNN-related paradigm for enhancing the efficacy and precision of Osteosarcoma tumor classification. The study [26] proposes a methodology that amalgamates pel-related and object-related approaches employed in the tumor features such as nuclei cluster, density, and the tumor area’s circulatory for the classification as possible and impossible. The study [27] presents several DL-related paradigms for classifying and identifying Osteosarcoma histopathology images (OHI). This study as well introduces a CNN-related paradigm to classify OHI by employing balanced and imbalanced image databases.

The above survey leads the work on bone cancer detection in a manner that if the feature extraction is done to get the right segmentation and finding the core part of the bone because the cancerous bone identification requires to identify all those features which are responsible for the bone cancer like bone density, bone color, and bone texture. To get the right feature, there is a need to apply the machine learning technique that can find the features and classify the healthy bone and cancerous bone.

3. System model
This segment illustrates the employment of fuzzy c-means (FCM) contrast optimization for identifying the tumor’s existence within the bone of the infected section in the HpIs by employing morphological procedures. Especially, in pre-processing for image enhancement and smoothing process, wiener filter with the addition of convoluted
Gabor filter is used to reduce the mean square error (MSE). Then the detected tumor has been classified using recurrent convoluted neural networks.

![Overall system architecture of bone tumor classification process](image)

**Figure 1** Overall system architecture of bone tumor classification process

### 3.1 Dataset description
This database will be publicly accessible upon the TCIA webpage for study intentions. It consists of 1144 Osteosarcoma’s Hematoxylin and Eosin stained histology images (HIs) with the image dimension of 1024 × 1024 pels. This database comprises 3 HIs’ classes: (i) Non-Tumor (NT), (ii) Non-Viable Tumor (NVT), and (iii) Viable Tumor (VT). The database’s preponderance class remains NT, which comprises 536 images of bone’s ordinary tissues, blood vessels, and cartilage. NVT and VT remain the database’s minority classes having 263 and 345 images accordingly. The NVT class comprises images of dead or recovering phase tissues possessing a somewhat pale color. The VT remains an area in HIs in which the nuclei will be compactly assembled intact in dark color [29].

### 3.2 Data preprocessing
Preprocessing helps to enhance the quality of the bone image by eliminating the noisy and unwanted parts in the background. This enhancement helps to minimize the complication while interpreting. This pre-processed image is the input for feature extraction and classification. The weights are computed by estimating the cross-correlation as well as covariance matrices of noisy signals thereby providing an accurate estimation of the undistorted deterministic signal under Gaussian noise. The estimated noise statistics are utilized to find the weights of the set of optimal filters. When a new input noise signal with optimal filter weights is processed, the signal deterministic component is determined. For Gaussian noise distribution, this method is optimal. Further, only very few computational steps are required which is also very fast.

In the Fourier Domain, Wiener Filter is given as:

\[
G(u,v) = \frac{H'(u,v)p_n(u,v)}{H(u,v)p_n(u,v) + pn(u,v)}
\]  \( \text{(1)} \)

\[
G(u,v) = \frac{H(u,v)}{H(u,v) + p_n(u,v)}
\]  \( \text{(2)} \)
here, H(u,v) and H'(u,v) represents degradation function and its complex conjugate respectively. Ps(u,v) and Ps(u,v) represents Power Spectral Density of Noise and un-degraded image respectively.

The noise from the degraded image is removed based on statistics determined from a local neighborhood of every pixel. This filter is based on the variations of the noise of a degraded image. With larger variance, the filter performs little smoothing while that of the smaller one the smoothing is more.

3.3 Classification using fuzzy c- means contrast enhancement
Consider that there are N image pixels, xi where i ranges from 1 to N which are clustered into K groups. For every group, cj represents its center where j ranges from 1 to K. uij provides the existence of pixel i for cluster j. For K -Means clustering, uij is either 0 or 1 representing the absence and presence of pixel respectively. Fuzzy C-Means (FCM) utilized here provides uij as a real number ranging from [0 , 1]. The equation below is always precise:

\[ \sum_{j=1}^{K} u_{ij} = 1 \]  

(3)

Total in-group variation function is given as

\[ J = \sum_{j=1}^{K} \sum_{i=1}^{N} u_{ij} (x_{i} - c_{j}) \]  

(4)

For optimum image pixel classification, j has to be minimized as in-group variation when less leads to more between-group variances. Then, Lagrangian is defined as

\[ L = \sum_{j=1}^{K} \sum_{i=1}^{N} u_{ij} (x_{i} - c_{j}) + \beta u_{ij} - \sum \beta j \]  

(5)

\( \lambda \)i representing the Lagrangian multiplier is obtained after the L-minimization problem is solved.

\[ \frac{\partial y}{\partial x} = \mu(ij). (x_{i} - c_{j}) + \beta i j = 0 \]  

(6)

Based on the existence of the pixels, the above equation estimates the center of cluster j. uij is then determined using the below equation based on the given center of the cluster.

\[ \frac{\partial y}{\partial x} = \sum_{j=1}^{K} (2 u_{ij} (x_{i} - x_{ij}) = 0 \]  

(7)

This process is recursive and is performed till the L value converges.

3.4 Feature extraction using convoluted Gabor filter
Once the classification is done using the fuzzy c-means method, the feature is extracted using a convoluted Gabor filter where the image is represented as a Gabor wavelet is the convolution of the image that is formulated as in Eq.8. For an image, assume that I(x,y) is the gray level distribution, then convolution and Gabor kernel \( \psi_{\mu, v} \) is described as

\[ O_{x,y}(z) = I(z) * \psi_{x,y}(z) \]  

(8)

Here, the convolution operator is \( z = (x,y) \) and \( * \), and convolution result at scale \( v \) and orientation \( \mu \) with respect to the Gabor kernel is \( O_{x,y}(z) \). Thus, for \( v \in \{0,\ldots,4\} \) and \( \mu \in \{0,\ldots,7\} \), set \( S = \{O_{x,y}(z)\} \) forms the Gabor wavelet of the image I(z). 

By convolution, every \( O_{\mu, v}(z) \) is derived using Eq. 9 by applying Fast Fourier Transform (FFT):

\[ F\{O_{x,y}(z)\} = F\{I(z)\} \{ \beta_{x,y}(z) \} \]  

(9)

\[ O_{x,y} = F^{-1}(F(I(z)))F(\beta_{x,y}(z)) \]  

(10)

where \( F \) and \( F^{-1} \) indicates Fourier transform and its inverse respectively.

Sensitive filters are constructed with edges at 90° and 270° orientations. For every kernel, the weight values are selected by changing the kernel values that are based on the sum of weight values.

3.5 Classification using Recurrent CONVoluted neural networks (Re-CONVnet)
As motivated by deep residual, RCNN, and UNet models, a model for classification named Rec-CONVnet is proposed. The functions of Recurrent Convolutional Layers (RCL) are carried out according to the discrete-time steps as stated by RCNN. The training target of the network maximizes the log-likelihood of a given class. With the uniform distribution, the weights of the network are initialized as depicted in figure- 2. In the architecture of
Rec-CONVnet, components like RCLs, inception units, and residual layer are considered to be more important. The input that is given to the input layer passes through inception units where, after applying RCLs, the final outputs are provided as the inputs to Rec-CONVnet. In the inception unit, the recurrent convolution operations are carried out based on kernels of various sizes. As the recurrent structure is present in the convolution layer, the outputs of the current and previous time steps are summed up. Then, the current time step outputs are provided as the input for the time step following the current time step.

![Figure 2 Architecture of Rec-CONVnet](image)

Table 1 Details about layers of Rec-CONVnet

<table>
<thead>
<tr>
<th>Layer name</th>
<th>Frequency</th>
<th>Number of units</th>
<th>Activation function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input layer</td>
<td>5</td>
<td>45</td>
<td>softmax</td>
</tr>
<tr>
<td>Max-pooling</td>
<td>4</td>
<td>436</td>
<td>sigmoid</td>
</tr>
<tr>
<td>Fully Connected Layer</td>
<td>6</td>
<td>423</td>
<td>softmax</td>
</tr>
<tr>
<td>Recurrent Convolutional Layers</td>
<td>2</td>
<td>462</td>
<td>softmax</td>
</tr>
<tr>
<td>Conv+ReLU</td>
<td>2</td>
<td>413</td>
<td>sigmoid</td>
</tr>
<tr>
<td>Output layer</td>
<td>5</td>
<td>45</td>
<td>sigmoid</td>
</tr>
</tbody>
</table>

Assume that $x_l$ and pixel at I are the input samples in the $l^{th}$ layer of Rec-CONVnet block and $k^{th}$ feature map in the RCL respectively. Moreover, consider $Oijkl(t)$ as the output of the network at the time step $t$ and is defined as,

$$X_{ijkl}(t) = wk(t).x^{ijkl}(t) + (wk(t).x^{ijkl}(t-1) + bk$$

(11)

where $x^{ijkl}(t)$ and $x^{ijkl}(t-1)$ represent the inputs of convolution layers and $l^{th}$ Rec-CONVnet accordingly. The values of $wkf$ and $wkr$ are the weights of the convolutional layer and $k^{th}$ Rec-CONVnet feature map accordingly where $bk$ stands for bias. The outputs of Rec-CONVnet are provided as input to the activation function $f$ of the standard FC layer that is formulated as:

$$(xl , wl ) = f(Oijkl(t)) = \max(0,Oijkl(t))$$

(12)

$(xl , wl )$ is the $l^{th}$ layer output of Rec-CONVnet. The output of $(xl , wl )$ is involved in down-sampling and up-sampling layers in the encoding and decoding units of the convolutional layers. Assume $x_{l+1}$ as the output of the Rec-CONVnet -block that is computed as:

$$x_{l+1} = xl + (xl , wl )$$

(13)
The final outputs of the Rec-CONVnet unit are defined as \((xl, wl)\), which is defined as,
\[
(xl, wl) = y_{1x1}(x) \bigotimes y(x) \bigotimes y_{1x1} p(x)
\]  
(14)

where \(\bigotimes\) is the concatenation operator performing operations concerning the channel or feature map axis. The outputs of the Conv+ReLU unit and the inputs of the Inception Recurrent Residual Convolutional Neural Network (IRRCNN) block are added up. For the Conv+ReLU block, the residual operation is defined by.
\[
x_{l+1} = x_l + (xl, wl)
\]
(15)

Here, \(x_{l+1}\) is input for the subsequent transition block, \(xls\) is the input sample of the Rec-CONVnet block, \(wl\) and \((xl, wl)\) are the kernel weights and output of \(l^{th}\) Conv+ReLU block respectively. Convolution filters used were only of size \(1 \times 1\) and \(3 \times 3\), as used in NiN and Squeeze Net models. This helps in maintaining a minimum number of parameters in the network. As the \(1 \times 1\) filter is used, the non-linearity of the decision function is increased, which produces no impact on the convolution layer. In the Conv+ReLU units, there is no change in the size of input and output features. Thus, the result is just a linear projection on the same dimension, and non-linearity is added to the activation functions of the RELU and ELU layers. In the transition block, after every convolution layer, there occurs a 0.5 dropout. At last, a softmax or normalized exponential function layer is used in the architecture. The softmax operation for the \(i^{th}\) class can be defined as
\[
P(y = i|x) = \frac{e^{x(wi)}}{\sum_{k=1}^{K} e^{x(wk)}}
\]
(16)

where \(x, w, \) and \(k\) are the input sample, weight vector, and distinct linear functions. With this proposed architecture, several advantages exist to using U-Net. Few of them are efficient in the number of parameters that are not increased due to the recurrent and residual operations. But, they significantly impact the performance of training as well as testing.

3.6 Algorithm

Input: Testing data (Tes_data), training data (train_data), predicted label (pred_lab), neighbors (n), distance (d), nodes (N), leaf (l).
Output: malignant or benign

Initialize the parameters Tes_data, train_data
For

Compute Euclidian distance (Ed)
\[
X(I,j) \leftarrow ED
\]
Rank (N,l) \(\leftarrow y\)
ED \(\leftarrow y\) (I,j)
Avg (ED) \(\leftarrow X(I,j)\)
if
P<0
Activate randomforest
Else
Avg1 (ED)⇔X(I1,j1)
Compute error
Wi = max(M) − Mi
Wi<0
Normalize Wi = Mi
End for
Mi= 0⇔indicates begin
Mi= 1⇔indicates malignant

Start
Initialize the training and testing data
Find the Euclidian distance
Compute the Euclidian distance (ED) for training data
Check the rank and denote it as ‘v’. If ED<v (I,i)
Find the average Euclidian distance
Activate random forest
Find the error and normalize it
Stop
4 Comparative analysis
Contradicting of this algorithm is done with the existing algorithms using various parametric measures like accuracy, precision, specificity, f1 score, and recall. To confirm that the suggested Recurrent CONVoluted neural network (Rec-CONVnet) is more efficient than the existing methods such as Dense Convolutional neural network (DCNN), Random Forest (RF), and Decision Tree (DT), the graphs are given here. For simulation here, PYTHON is chosen.

4.1 Evaluation metrics
- Accuracy is the count of correct predictions divided by predictions made totally. Mathematically it is given as follows,

\[
\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \tag{17}
\]

- The rate of precision is the ratio of the positive sample number. Rather, precision represents the proportion of the prediction models of cancer where cancer is actually present. The rate of precision\( (P) \) is defined as:

\[
\text{Precision} = \frac{TP}{TP+FP} \tag{18}
\]

- If recall refers to the detectability to accurately detect cancer in the dataset, the sensitivity calculation does not take indeterminate test results into account since the test cannot be repeated, and indeterminate samples should all be excluded from the analysis.

\[
\text{recall} = \frac{TP}{TP+FN} \tag{19}
\]

- Specificity refers to the detection ability to correctly reject non-cancer parts in the dataset. Mathematically, this can also be given as follows,

\[
\text{Specificity} = \frac{TN}{TN+FP} \tag{20}
\]
Figure 4 shows the confusion matrix for Rec-CONVnet in which the rows represent the predicted output class and columns denote the actual target class of data pertaining to tumor detection. The diagonal dark blue and light blue denotes that are correctly and incorrectly classified. The column on the right side indicates every predicted class while the row at the bottom represents the performance of every actual class.

Figure 5 ROC curve of Rec-CONVnet

Figure 5 shows the ROC curve of Rec-CONVnet. As stated in the above figure, the ROC curve for train data is increasing steadily from epoch 0 to epoch 6, and the TP is equal to 83.17%. The ROC curve is then constant until epoch 300, with TP equal to 86.28%. For train data, the loss curve declines steadily from epoch 0 to 6, where the loss is 43.77%, and then becomes constant until the completion of the training process (epoch 300) where the loss is 36.56%. With the test data, the loss curve is 37.85% for epoch 300. According to the confusion matrix, for the first image class (normal type), the model was able to correctly recognize 1634 images in the normal class, and 95 were identified as images of breast cancer. Similarly, for the second image class (images with breast cancer) the model correctly recognized 1277 images while 252 images were classified as normal.

Table 2 Comparison of accuracy

<table>
<thead>
<tr>
<th>Number of epochs</th>
<th>DCNN</th>
<th>RF</th>
<th>DT</th>
<th>Rec-CONVnet</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>97</td>
<td>95</td>
<td>96.3</td>
<td>98.5</td>
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<td>20</td>
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<td>100</td>
<td>97.1</td>
<td>96</td>
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<td>98.3</td>
</tr>
</tbody>
</table>
Figure 6 shows the accuracy comparison of the existing and proposed algorithms. The X-axis and Y-axis show the number of epochs and accuracy in percentage respectively. Accuracy of suggested Rec-CONVnet achieves better performance than the existing methods.

Table 3 Comparison of Precision

<table>
<thead>
<tr>
<th>Number of epochs</th>
<th>DCNN</th>
<th>RF</th>
<th>DT</th>
<th>Rec-CONVnet</th>
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<tbody>
<tr>
<td>10</td>
<td>94.5</td>
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<td>95.2</td>
<td>96.3</td>
<td>98.6</td>
</tr>
</tbody>
</table>
Figure 7: Comparison of precision

Figure 7 shows the precision comparison of the existing and proposed algorithms. The X-axis and Y-axis show the number of epochs and precision in percentage respectively. The precision of the suggested Rec-CONVnet algorithm achieves better performance than the existing methods.

Table 4 Comparison of recall

<table>
<thead>
<tr>
<th>Number of epochs</th>
<th>DCNN</th>
<th>RF</th>
<th>DT</th>
<th>Rec-CONVnet</th>
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<td>10</td>
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<td>98.7</td>
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<td>96.3</td>
<td>96.3</td>
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<tr>
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<td>96.3</td>
<td>96.4</td>
<td>97.4</td>
<td>98.5</td>
</tr>
</tbody>
</table>
Figure 8: Comparison of recall

Figure 8 shows the recall comparison of the existing and proposed algorithms. The X-axis and Y-axis show the number of epochs and recall in percentage respectively. Recall of suggested Rec-CONVnet achieves better performance than the existing methods.

Table 5 Comparison of specificity

<table>
<thead>
<tr>
<th>Number of epochs</th>
<th>DCNN</th>
<th>RF</th>
<th>DT</th>
<th>Rec-CONVnet</th>
</tr>
</thead>
<tbody>
<tr>
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<td>93.5</td>
<td>93.4</td>
<td>98.5</td>
<td><strong>98.4</strong></td>
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<tr>
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<td>96.5</td>
<td><strong>98.4</strong></td>
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<td>97.1</td>
<td>95.5</td>
<td>96.5</td>
<td><strong>98.4</strong></td>
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<td><strong>98.7</strong></td>
</tr>
<tr>
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<td>96.3</td>
<td><strong>98.3</strong></td>
</tr>
<tr>
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<td>96.3</td>
<td>96.4</td>
<td>100</td>
<td><strong>98.5</strong></td>
</tr>
</tbody>
</table>
Figure 9: Comparison of specificity

Figure 8 shows the specificity comparison of the existing and proposed algorithms. The X-axis and Y-axis show the number of epochs and specificity in percentage respectively. Specificity of suggested Rec-CONVnet achieves better performance than the existing methods.

Table 6 Comparison of F1-score

<table>
<thead>
<tr>
<th>Number of epochs</th>
<th>DCNN</th>
<th>RF</th>
<th>DT</th>
<th>Rec-CONVnet</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
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<td>98.5</td>
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<tr>
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<td>96.3</td>
<td>96.4</td>
<td>96.3</td>
<td>98.5</td>
</tr>
</tbody>
</table>
Figure 9 shows the F1-Score comparison of the existing and proposed algorithms. The X-axis and Y-axis show the number of epochs and F1-Score in percentage respectively. F1-score of suggested Rec-CONVnet achieves better performance than the existing methods.

Table-7 shows the overall comparative analysis between the existing Dense Convolutional neural network (DCNN), Random Forest (RF), and Decision Tree (DT) with the proposed Recurrent CONVolutional neural networks (Rec-CONVnet).

**Table 7 Overall Comparative Analysis**

<table>
<thead>
<tr>
<th>Parameters</th>
<th>DCNN</th>
<th>RF</th>
<th>DT</th>
<th>Rec-CONVnet (proposed)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accuracy (%)</td>
<td>97.25</td>
<td>96.83</td>
<td>96.77</td>
<td><strong>98.34</strong></td>
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<td>Precision (%)</td>
<td>100</td>
<td>100</td>
<td>94.11</td>
<td>97.96</td>
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<tr>
<td>Recall (%)</td>
<td>93.97</td>
<td>93.75</td>
<td>100</td>
<td>98.72</td>
</tr>
<tr>
<td>Specificity (%)</td>
<td>95.19</td>
<td>93.93</td>
<td>100</td>
<td>98.33</td>
</tr>
<tr>
<td>F1-Score (%)</td>
<td>96.89</td>
<td>96.77</td>
<td>96.96</td>
<td><strong>98.32</strong></td>
</tr>
</tbody>
</table>

**Conclusion**

Bone cancer results in abnormal cell growth rampantly in the bone wherein the growth instead damages the typical BTS and begins spreading to the rest of the parts. Identifying cancer tissue remains a chief problem for pathologists in discerning and detecting potential lesion tissue. This study details Rec-CONVnet-based classification for predicting knee bone’s cancer state out of HPIs and establishes an appropriate paradigm execution by employing training and testing images. As a result, the proposed Rec-CONVnet achieves 98.34% of accuracy, 97.96% of precision, 98.72% of recall, 98.33% specificity, and 98.32 of f1-score. For future work, there is a plan to construct new three-dimensional neural network architectures to improve the accuracy and classification rate.


