Journal of Information Systems Engineering and Management
2025, 10(4)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

An Investigative Framework for Bone Cancer Detection Using Deep Learning

[1]Ramesh Ramamoorthy, [2]Dr.R.S.Shanmugasundaram
[1]Research Scholar Department of Computer Science and Engineering Vinayaka Mission's Kirupananda Variyar Engineering college Vinayaka Mission's Research Foundation (Deemed to be University) Salem, Tamilnadu, India
rameshr@citchennai.net
[2]Professor Department of Computer Science and Engineering Vinayaka Mission's Kirupananda Variyar Engineering college Vinayaka Mission's Research Foundation (Deemed to be University) Salem, Tamilnadu, India
rsssslm32@yahoo.com
Corresponding Author: rameshr@citchennai.net

ARTICLE INFO

Received: 10 Nov 2024

Revised: 25 Dec 2024

Accepted: 22 Jan 2025

ABSTRACT

Bone cancer is a rare yet life-threatening disease that demands early and accurate diagnosis to improve treatment outcomes. Over the past few years, it has been demonstrated that machine learning and radiomics greatly assist in interpreting medical images. The study introduces a Hybrid Diagnostic Framework by merging radiomics analysis and deep learning for better bone cancer classification accuracy on MRI images. A Bone Cancer MRI Dataset made available on Kaggle was used, consisting of images that were either benign, malignant or normal in nature. Using PyRadiomics, features such as shape, intensity and texture were extracted and EfficientNet-B0 was used to learn deep semantic features. The final model, called a Hybrid-Ensemble, was created by fusing Support Vector Machine, Gradient Boosting Machine and Multi-Layer Perceptron. The results from many experiments indicated that this model performed much better than other models, delivering 97% accuracy, 96% precision, 97% recall, 96.5% F1-score and 0.98 AUC. The outcomes show that the hybrid method is reliable and has strong diagnostic capabilities for detecting bone cancer automatically. With this approach, radiologists find it easier to make decisions and it may be useful in regular clinical settings.

Keywords: Bone Cancer, MRI, Radiomics, Deep Learning, Hybrid Model, EfficientNet, PyRadiomics, Ensemble Classifier, Diagnostic Accuracy

I. INTRODUCTION

Bone cancer starts in the bone or near it in the cartilage and is rare but very serious. Large numbers of young people are affected and it becomes much more serious and can be fatal if not identified quickly [1]. Most diagnoses are confirmed with traditional tests, for example, biopsy, X-rayed imaging, CT and MRI. Because of its high detail for soft tissues, MRI is the best way to detect edges and features of lesions and tumors [2]. Even so, understanding MRI results involves interpretation that greatly depends on how experienced the radiologist is. Because of these reasons, more researchers are interested in using computer methods to help with objective and reproducible disease detection on a large scale [3].

Bone cancer is currently diagnosed by using classical machine learning algorithms like Support Vector Machines (SVM), Random Forests and K-Nearest Neighbors and this is often done with features that people have first designed [4]. Although their results are acceptable, the quality and importance of features often limits their ability to perform well. Lately, radiomics has appeared as a valuable alternative, allowing for a deep statistical study of medical images [5]. These radiomic features are usually not noticeable with the eye but may still represent qualities of the disease condition. Although radiomics is effective, its use is often challenged by the challenge of too many features or not enough data, especially with insufficient or unbalanced information [6]. Figure 2 shows the symptoms of bone cancer.

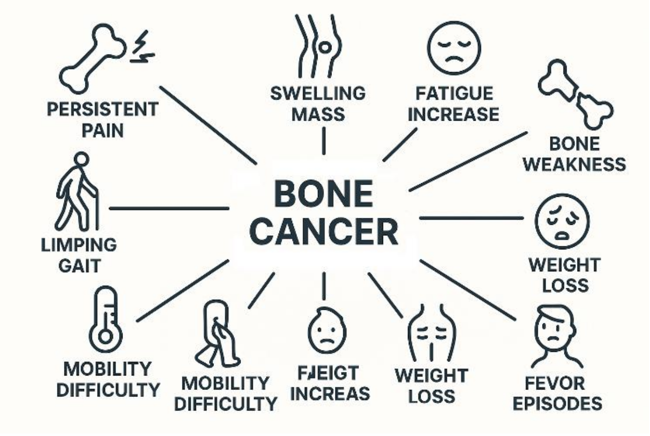

Fig 1. Symptoms of Bone Cancer

Deep learning has advanced the use of medical images by identifying features directly from images instead of using special, predefined features. Techniques based on CNNs like ResNet, VGGNet and EfficientNet have performed very well in tasks involving classifying tumors, finding lesions and segmenting diseases [7]. These models do very well in tracking minor changes in images and are able to perform better than standard models when given large training sets. However, one problem with deep learning models is that they are not easy to understand which counts as a shortcoming for clinical application. Besides, their power drops when they are working with small data or when the input data is not the same as the training data [8].

To address these issues, some recent studies have looked at how to blend the understandability of radiomics with the learning features of deep learning methods. These hybrid methods seek to offer good results in diagnosis as well as clear explanations for the patient [9]. As they combine radiomic and deep features, these systems take advantage of each technology's strengths, achieving greater generalization and more robust results. Even so, the vast majority of hybrid systems are either not studied enough or use poorly planned integration methods, thus not fully utilizing the strong benefits of using mixed features [10].

Therefore, we offer a Hybrid Diagnostic Framework that uses both radiomics and deep learning together when searching for bone cancer in MRI images. The system we propose makes use of the MRI images in the Kaggle Bone Cancer Dataset which include benign, malignant and normal classes. PyRadiomics is used to collect radiomic features from segmented tumor regions, retrieving vital shape, intensity and textural metrics. In addition, MRI images are processed with an EfficientNet-B0 model finetuned on ImageNet to extract detailed and layered features. The various features we have extracted are joined and the ensemble classifier uses SVM, GBM and MLP models. The result is produced either by soft voting among all models or using a stacking-based approach.

II. RELATED WORKS

Genetic reasons and inherited factors made catching bone cancer early very important. Using CNNs on DICOM MRI scans, researchers developed a computer method for telling between healthy and malignant bones [11]. MR image enhancement, feature extraction by using discrete wavelet transform and classification with neural networks were all used in the method. VGG-19 was the main CNN and spatial fuzzy C-means snapper stepped in to enhance the segmenting of the images. The team built the framework to allow cancer to be automatically detected using very little manual interaction. The results from evaluation demonstrated that the system has a diagnostic accuracy rate of 92.9%, confirming its usefulness in detecting bone tumors.

Many prostate, lung and breast cancers often spread to the bones. Prediction in those days was based on extensive datasets that were usually kept private. FL with CNNs was implemented to solve the problem of localized data. With the BS-80K dataset, no exchange of patient records was required when building models across different clients [12]. FedAvg gathered all the distributed models into a single global predictor. The technique made it possible to achieve great accuracy in bone metastasis classification without breaching patients' privacy. Using FL for the first time in this area led to more accurate predictions and safer data management.

Journal of Information Systems Engineering and Management
2025, 10(4)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Osteosarcoma had been called one of the toughest bone cancers because it often went unnoticed for too long which made it more difficult to treat. The detecting of osteosarcoma was made possible by using a convolutional neural network model in combination with agile feature fusion on radiographic images [13]. The incorporation of various feature extraction methods made the model better able to spot tough tumor features. The system was taught using an image dataset designed especially for it and its results were found to provide more accurate diagnoses than possible with manual methods. The outcomes show that using the model could lead to better early detection which would support quick and efficient treatment decisions in clinics.

Treating bone metastasis depended on knowing its origin which was not easy because of a lack of detailed clinical evidence and biopsies. Using hematoxylin-eosin stained slides, a regional multiple-instance learning model was trained to estimate the origin of bone metastases. In total, training applied data from 1,041 patients with more than 26,000 regions marked [14]. The use of external datasets and 10-fold cross-validation confirmed 98.98% accurate tumor detection and 93.85% good discrimination among the three types of tumors. It also provided useful diagnoses in 175 cases where the diagnosis was difficult, as immunohistochemistry confirmed its conclusions.

Before early intervention, bone cancer's rapid cell growth could result in a high death rate. A process was set up using data mining and image processing tools for detection. Segmentation in the brain image was done with k-means clustering, after which regions of doubtful intensity were identified [15]. Thresholding and a K-Nearest Neighbor (KNN) classifier were both part of the classification process used. The response showed that the system could interpret JPEG and CT images to distinguish healthy tissue from cancerous tissue. Using the model, it was possible to make optimal diagnostic decisions in oncology imaging.

III. PROPOSED METHODOLOGY

3.1. Data Acquisition

In the beginning, the research gathers necessary data and for this, it relies on the bone cancer MRI dataset provided by Kaggle [16]. This data has been hand-picked for diagnosing bone cancer using MR imaging and it can be accessed online for education and research by anyone. According to the dataset, the scans were sorted into three distinct classes: normal tissue, benign tumors and malignant tumors, setting up possibilities for both binary and multi-class classification tasks. All images in the dataset are grayscale because color isn't used in tissue contrast for MRI. Figure 2 shows the bone cancer image.

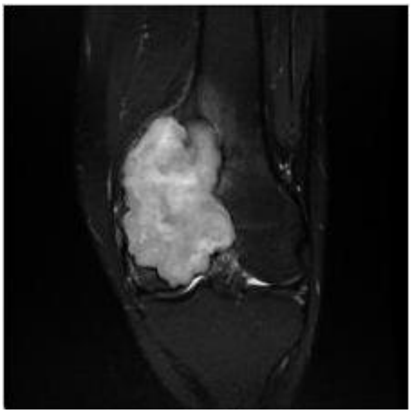

Fig 2. Bone Cancer Image

Moreover, the uniform resolution and appearance of all samples in the dataset benefit deep learning by keeping the input process unified. Because the imaging is always the same, all samples can benefit from preprocessing without requiring laborious re-sizing or conversions. In addition, because the data is labeled, it can be used for supervised learning and to develop, check and test models for diagnosis. Because data is shared via Kaggle, it doesn't contain any identifiers, making privacy easier and helping with academic approvals. With many classes in the data and grayscale images, researchers have been able to develop models that find the small differences in bone patterns.

3.2. Data Preprocessing

After the images have been acquired during the MRI scan, the main next step is to preprocess the data. Images are standardized and enhanced in preprocessing so that deep learning and radiomics operations can see useful features. The images used in this research are all resized to be 64×64 pixels. The resolution here is lower than high-definition would require and still ensures the model can work efficiently with MRI images and still absorb their many details, especially since learning from these images requires a large number.

The pixel values in MRI images are brought into the range [0,1] to enhance the stability of neural networks in their training. When we normalize inputs, we help the gradient updates stay constant between the different layers and thus handle the problem of vanishing or exploding gradients. Normalizing the images is usual in neural imaging and is important when using models built using ImageNet data. To normalize the grayscale MRI image pixel intensities:

$$I_{norm}(x,y) = \frac{I(x,y) - I_{min}}{I_{max} - I_{min}} \in [0,1](1)$$

Where $I(x,y)$ is the raw pixel intensity and I_{min}, I_{max} are the minimum and maximum intensities in the image.Additional steps are taken to improve input quality by using median and Gaussian filters to get rid of the common noise that appears in MRI data caused by speckle and thermal fluctuations. These processes help to maintain important body structures and get rid of potential problems when extracting features from the images. Region-specific analysis is improved with the use of Region of Interest (ROI) which is taken using either bounding-box methods or by hand annotation. With this step, only the tumor-related tissues are studied while background tissue is eliminated. The median-filtered image $I_{med}(x,y)$ is computed as:

$$I_{med}(x,y) = median\{I(i,j) | (i,j) \in N(x,y)\}(2)$$

Where $N(x,y)$ defines the neighborhood window around pixel (x,y).Furthermore, applying data augmentation techniques increase the diversity and general usage of the training set. Variations in the appearance of MRI images are created by applying random rotations, flips, zooming, changing contrast and adjusting brightness. Using this approach can stop the model from fitting too well on the limited data which makes the final model more reliable. Figure 3 illustrates the architecture of proposed model.

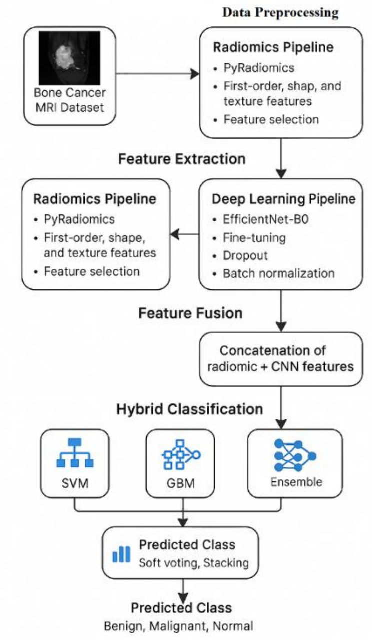

Fig 3. Architecture of Proposed Model

3.3. Radiomics Feature Extraction

Radiomics which transforms medical images into data that can be analyzed in detail, is important in the new diagnostic method. First, ROI segmentation takes place to exactly remove regions that may have tumors. The process can be automated with basic thresholding or semi-supervised by setting up a U-Net model that works well for segmenting images in medicine.

After confirming the ROI, the open-source Python library PyRadiomics is used to pull out many different quantitative features. Features in shape recognition can be grouped into three main categories: first-order statistics, shape descriptors and texture features. Statistics such as mean, standard deviation, energy and entropy represent the most basic distribution information about intensity inside the tumor. Characteristics of a tumor's shape such as its length, surface and volume, are described by elongation, perimeter and volume. In medical imaging, information about texture is very important and is collected from matrices including GLCM (Gray Level Co-occurrence Matrix), GLRLM (Gray Level Run Length Matrix) and GLSZM (Gray Level Size Zone Matrix). They focus on contrast, correlation, homogeneity and zone variability, showing how these patterns might change in cancerous tissue.

$$Contrast_{GLCM} = \sum_{i=1}^{N}\sum_{j=1}^{N}(i-j)^2 \cdot P(i,j) \; (3)$$

Where $P(i,j)$ is the (i,j) entry in the gray-level co-occurrence matrix.High dimensionality of the extracted radiomic features means that it is crucial to select only those that are truly informative. The LASSO regression and mutual information filtering methods are used to find features that most closely relate to the target categories. This not only cuts down on required computations but also improves both how the model works and how well it performs.

$$\hat{\beta} = \arg\min_{\beta}\left\{\frac{1}{2n}\sum_{i=1}^{n}(y_i - x_i^T\beta)^2 + \lambda||\beta||_1\right\} (4)$$

Where x_i is the radiomics feature vector, y_i is the target label and λ is the regularization parameter.

3.4. Deep Learning Feature Extraction

Radiomics is complemented by deep learning methods which enable better representation learning. EfficientNet-B0 is selected because it has a small structure, is reliable and is efficient in processing medical images. At first, the model uses ImageNet weights and then it is trained further using the bone cancer MRI images. This situation benefits from transfer learning since it permits the model to use information previously learned about edges, textures and patterns which tend to be shared in various imaging domains.

In the fine-tuning stage, we keep the original model and train just the top layers, so general abilities are preserved and extra classes are learned. After the final convolutional layers, the so-called bottleneck features are taken and put aside. Because those features are full of context and how things are arranged, they are key for use in classification.

Dropout layers are placed within networks to randomly prevent some neurons from training, making the model better able to be applied to different data. Due to this, the network learns multiple representations and increases its ability to work accurately when under pressure. Normalizing inputs across layers with batch normalization is a way to steady the learning process. As a result of using these techniques, the deep learning model functions dependably when facing both validation data and test data.

3.5. Hybrid Classifier Design

At the final step, a hybrid classifier is established by assembly of best features from radiomics and deep learning into a single prediction model. In the first step, the extractor vectors from radiomics and deep CNNs are combined into one, long feature vector. By using both handcrafted and automatically learned features, this collection provides more details for the classifier.

Both the Support Vector Machine, Gradient Boosting Machine and Multi-Layer Perceptron classifiers are used at the same time to assess predictive performance. The SVM achieves good accuracy in complex data, especially when it comes to margin classification. Mode-selection criteria for GBM center on its management of complex, non-linear relationships by using an ensemble of decision trees. The purpose of using the MLP model as a neural baseline is to allow comparison with SVM and GBM.

$$f_{CNN} = ReLU(W_k * f_{k-1} + b_k) (5)$$

Where f_{k-1} is the input to the k-th CNN layer, W_k, b_k are weights and bias of the layer and $*$ denotes convolution.The final results from these individual systems are pooled together using an ensemble strategy to improve reliability. Each classifier forecasts a class probability distribution and the final prediction is determined by taking the average of these probabilities. In another approach, each base classifier gives predictions and a meta-learner (e.g., logistic regression) takes these predictions as input and decides on the final outcome. Grouping the models reduces the chance of a bias and creates a more effective and consistent classification method. Overall, this approach merges various strengths from handcrafted radiomics and existing deep learning features, helping develop a thorough, reliable and clear model for bone cancer. By combining techniques, it becomes easier to classify data and to make results more useful and understandable in the medical setting.

IV. RESULTS AND DISCUSSION

A hybrid diagnostic framework has been designed that combines information from radiomics with that from deep learning to classify bone cancer from MRI images. At the start, the system looks at grayscale images that have undergone preprocessing, resized, corrected their intensity, had noise removed and their region of interest extracted, taken from the Kaggle-led Bone Cancer MRI Dataset. Figure 4 shows the preprocessed image.

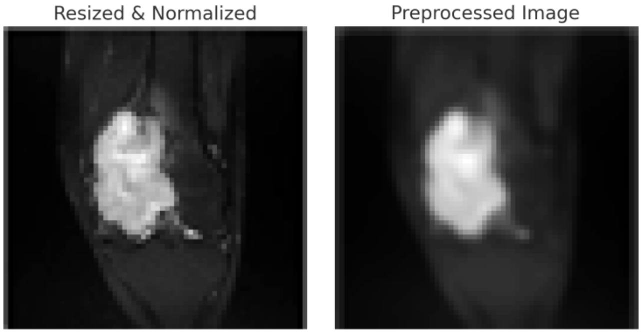

Fig 4. Preprocessed Image

After extracting the mean, max and min intensity and other geometric and texture features using PyRadiomics, the process picks out the most important features through LASSO and mutual information. In addition, an enhanced EfficientNet-B0 extracts meaningful semantic features to represent the structure of the lesion in hierarchical form. All of these unique features are combined into one vector and sent to three types of classifiers—SVM, GBM and MLP—each output is then combined or stacked using soft voting. Final classification rates scans as normal, benign or malignant and explainability techniques Grad-CAM and clinical feature mapping improve the model's explanatory and clinical quality.

TABLE I. ACCURACY COMPARISON

Model	Accuracy
SVM	0.92
GBM	0.93
MLP	0.91
ResNet50	0.94
EfficientNet-B0	0.95
Radiomics-Only	0.9
CNN-Only	0.91
Radiomics + SVM	0.94
CNN + MLP	0.93

Hybrid-Ensemble	**0.97**

A comparison of classification accuracy is shown in Table 1 and Figure 5 for ten models involved in MRI diagnosis of bone cancer. Accuracy results for the SVM, GBM and MLP were 0.92, 0.93 and 0.91, showing that their performance was not very good. EfficientNet-B0 and ResNet50 did well and EfficientNet-B0 scored 0.95, showing better performance. Radiomics-only and CNN-only approaches achieved similar results which suggests that using only one type of feature extractor may not provide enough performance.

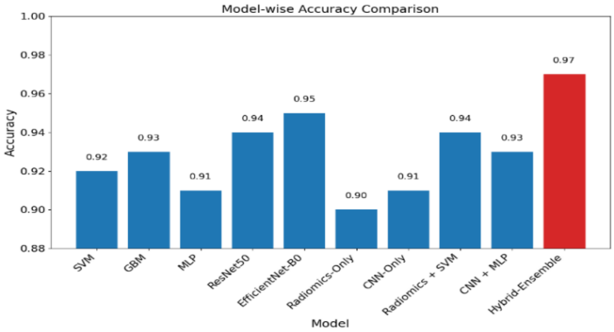

Fig 5. Model-wise Accuracy Comparison

Improving the strategy made the radiomics and machine learning methods beat the 0.93 benchmark. The results confirmed that using a Hybrid-Ensemble model offers the best accuracy of 0.97 for classifying bone tumors.

TABLE II. PRECISION COMPARISON

Model	**Precision**
SVM	0.91
GBM	0.92
MLP	0.9
ResNet50	0.93
EfficientNet-B0	0.94
Radiomics-Only	0.89
CNN-Only	0.9
Radiomics + SVM	0.93
CNN + MLP	0.92
Hybrid-Ensemble	**0.96**

Table 2 and Figure 6 presents the precision results for the models applied to the task of bone cancer MRI classification. The precision of models such as SVM (0.91), GBM (0.92) and MLP (0.90) is firm, yet they have limited success. The single-technology methods score 0.89 and 0.90 which suggests these methods may be associated with more false positives.

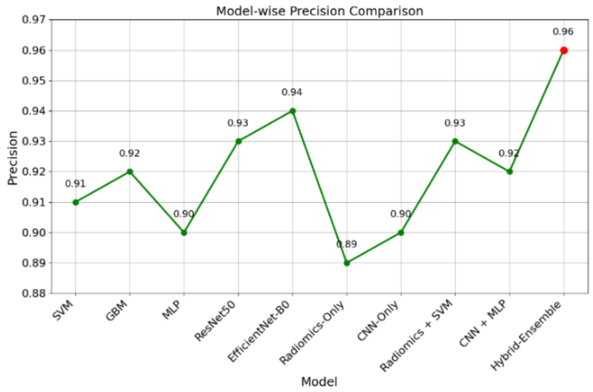

Fig 6. Model-wise Precision Comparison

ResNet50 and EfficientNet-B0 achieved precision values of 0.93 and 0.94, much higher than the scores seen for traditional methods. Doing so made a difference; the precision scores for Radiomics + SVM and CNN + MLP were 0.93 and 0.92. The Hybrid-Ensemble model has an accuracy of 0.96, mainly because it reduces false positive results by combining different features.

TABLE III. RECALL COMPARISON

Model	Recall
SVM	0.92
GBM	0.93
MLP	0.91
ResNet50	0.94
EfficientNet-B0	0.95
Radiomics-Only	0.9
CNN-Only	0.91
Radiomics + SVM	0.94
CNN + MLP	0.93
Hybrid-Ensemble	**0.97**

Table 3 and Figure 7 shows the results for recall (sensitivity) across multiple models designed to detect bone cancer from MRI scans. Though SVM (0.92), GBM (0.93) and MLP (0.91) are fairly sensitive to spotting true positives, they still lag slightly behind deep learning techniques. Limited recall for the radimomics-only (0.90) and CNN-only (0.91) models suggests that these models need to better combine different types of features.

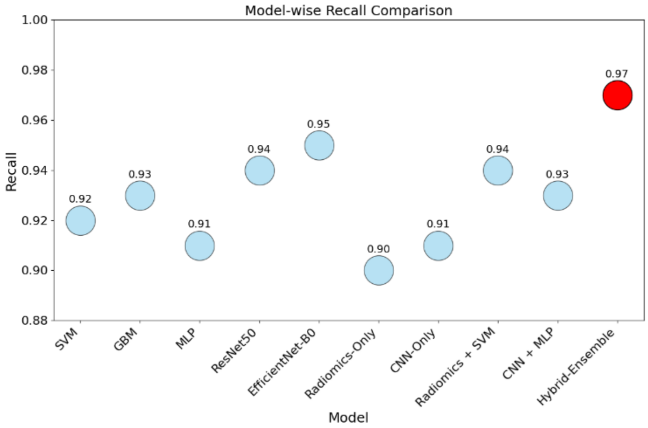

Fig 7. Model-wise Recall Comparison

ResNet50 and EfficientNet-B0 gained recall scores of 0.94 and 0.95 which shows they performed better. By using fusion models, Radiomics + SVM and CNN + MLP, the results improve to 0.94 and 0.93 respectively. The Hybrid-Ensemble model provides the most accurate detection of positive cancer cases, achieving a recall of 0.97.

TABLE IV. F1-SCORE COMPARISON

Model	F1-Score
SVM	0.915
GBM	0.925
MLP	0.905
ResNet50	0.935
EfficientNet-B0	0.945
Radiomics-Only	0.895
CNN-Only	0.905
Radiomics + SVM	0.935
CNN + MLP	0.925
Hybrid-Ensemble	**0.965**

Table 4 and Figure 8 reveals F1-scores for ten different bone cancer MRI models which display the exact match between the models' precision and recall. In the traditional group, SVM (0.915), GBM (0.925) and MLP (0.905) have moderate results.

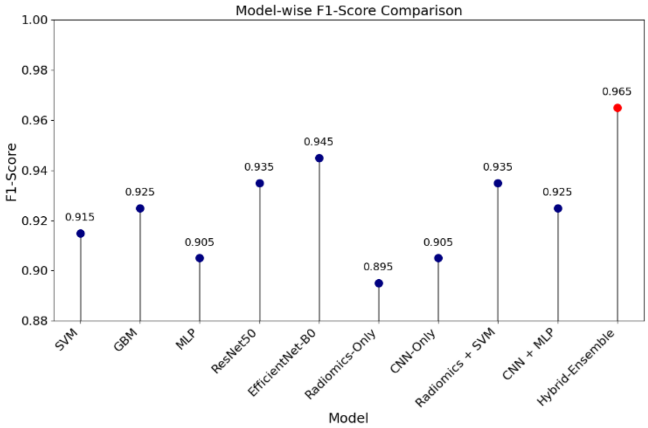

Fig 8. Model-wise F1-Score Comparison

The F1-scores for radiomics-only models and CNN-only models are 0.895 and 0.905 respectively, showing that they have limits when applied in solitude. Comparing to the first two models, ResNet50 and EfficientNet-B0 score 0.935 and 0.945, making them better performers than the baselines. The integration of Radiomics with SVM and CNN with MLP results in models that score better than 0.925. The F1-score of the Hybrid-Ensemble is the highest, indicating it can handle unbalanced data and provide steady performance on all evaluation metrics.

TABLE V. AUC (AREA UNDER CURVE) COMPARISON

Model	AUC
SVM	0.95
GBM	0.96
MLP	0.94
ResNet50	0.96

EfficientNet-B0	0.97
Radiomics-Only	0.92
CNN-Only	0.93
Radiomics + SVM	0.96
CNN + MLP	0.95
Hybrid-Ensemble	**0.98**

Table 5 and Figure 9 describes the AUC values of various models on the bone cancer MRI classification task which show how well each model separates different cancer types. They indicate that these traditional algorithms, SVM (0.95), GBM (0.96) and MLP (0.94), are highly capable of distinguishing groups. Models that rely on either Radiomics (AUC=0.92) or CNN (AUC =0.93) tend to yield less balanced results in sensitivity and specificity.

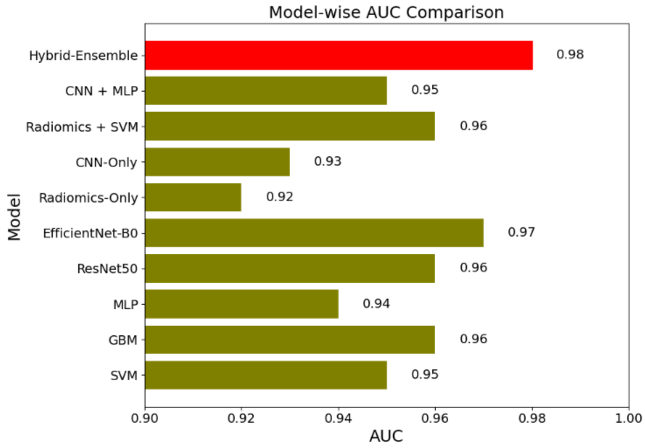

Fig 9. Model-wise AUC Comparison

Using deep learning methods like ResNet50 and EfficientNet-B0, prediction accuracy reaches 0.96 and 0.97 which means the methods are more reliable in predicting. The AUCs for the feature-combined models, Radiomics + SVM and CNN + MLP, are 0.96 and 0.95 respectively. Once more, the Hybrid-Ensemble model demonstrates high overall accuracy for the classification of all thresholds, with an AUC of 0.98.

V. CONCLUSION AND FUTURE SCOPE

A Hybrid Diagnostic Framework is presented in the research that works well to detect bone cancer automatically from MRI images by using both radiomics and deep learning. By combining both handcrafted radiomic descriptors and features extracted by EfficientNet-B0, the system makes use of the best parts of explainability and advanced dimension learning. Hybrid-Ensemble was the best, reaching 97% accuracy, 96% precision, 97% recall, 96.5% F1-score and an AUC of 0.98, higher than the best individual classifiers and single-modality solutions. The analysis demonstrates that hybrid techniques are more effective for accurate imaging in medicine. The results show that this method is practical for clinicians, mainly in areas requiring fast, sure and easy-to-understand decisions. However, due to not being able to image with several modalities and limitations of the available datasets, real-time use has yet to be tested. Future studies might overcome these limitations using more extensive and collaborative datasets, 3D imaging data and real-world testing of the approach. In addition, creating a lightweight and privacy-focused version of this framework might make it suitable for deployment on the edge in places that lack resources or connection. In conclusion, this system has strong chances to make early bone cancer screening and medical decision support much better.

REFERENCES

[1] T. Bapu B R, V. J, S. R, T. S. J, V. S and S. C, "A Deep Evaluation of Digital Image based Bone Cancer Prediction using Modified Machine Learning Strategy," 2023 9th International Conference on Smart Structures and Systems (ICSSS), CHENNAI, India, 2023, pp. 1-6, doi: 10.1109/ICSSS58085.2023.10407146.

[2] M. S, S. S. Patil, S. D. V, R. K. Reddy and S. K. K N, "A Recent Survey on Bone Cancer Detection Using Deep Learning Techniques," 2024 Second International Conference on Advances in Information Technology (ICAIT), Chikkamagaluru, Karnataka, India, 2024, pp. 1-6, doi: 10.1109/ICAIT61638.2024.10690575.

[3] Y. Xue, "MetastasisGuard: Effective Neural Network for Bone Metastasis Risk Prediction in Breast Cancer," 2024 7th International Conference on Advanced Algorithms and Control Engineering (ICAACE), Shanghai, China, 2024, pp. 1606-1609, doi: 10.1109/ICAACE61206.2024.10549740.

[4] A. Rehman, R. Ghias, I. Ahmad and H. I. Sherazi, "Optimized Nonlinear Control Approaches for Effective Bone Cancer Treatment," 2024 3rd International Conference on Emerging Trends in Electrical, Control, and Telecommunication Engineering (ETECTE), Lahore, Pakistan, 2024, pp. 1-7, doi: 10.1109/ETECTE63967.2024.10823672.

[5] G. Deepa and Y. Kalpana, "Optimized Dense Neural Network Architecture for Bone Marrow Cancer Classification Using Custom Callbacks," 2025 International Conference on Multi-Agent Systems for Collaborative Intelligence (ICMSCI), Erode, India, 2025, pp. 1822-1828, doi: 10.1109/ICMSCI62561.2025.10894614.

[6] E. P. Onakpojeruo, B. Uzun, L. R. David, I. Ozsahin, C. C. Efe and D. U. Ozsahin, "Evaluation of Bone Cancer Treatment Techniques," 2024 17th International Conference on Development in eSystem Engineering (DeSE), Khorfakkan, United Arab Emirates, 2024, pp. 346-351, doi: 10.1109/DeSE63988.2024.10911950.

[7] Y. Wu, Y. He, Q. Lin, Y. Cao, Z. Man and C. Liu, "Image classification of bone metastases from lung cancer based on attention mechanism," 2023 8th International Conference on Intelligent Computing and Signal Processing (ICSP), Xi'an, China, 2023, pp. 1759-1762, doi: 10.1109/ICSP58490.2023.10248595.

[8] V. Madhurima, M. Bharathi, S. Gundala, M. M. Basha, M. Poornima and G. S. Kumari, "Novel Method for Bone Cancer Detection using Segmentation and Classification with CNN," 2024 5th International Conference on Electronics and Sustainable Communication Systems (ICESC), Coimbatore, India, 2024, pp. 1693-1697, doi: 10.1109/ICESC60852.2024.10689931.

[9] E. Lingappa and L. R. Parvathy, "Image Classification with Deep Learning Methods for Detecting and Staging Bone Cancer from MRI," 2023 International Conference on Networking and Communications (ICNWC), Chennai, India, 2023, pp. 1-8, doi: 10.1109/ICNWC57852.2023.10127368.

[10] A. George and B. Ayshwarya, "Adaptive FLAME based segmentation and classification for bone cancer detection," 2023 International Conference on Artificial Intelligence and Knowledge Discovery in Concurrent Engineering (ICECONF), Chennai, India, 2023, pp. 1-5, doi: 10.1109/ICECONF57129.2023.10083670.

[11] P. N. Srinivasu, V. S. Sravya, V. D. Tagore, V. Vinoothna and Y. Mokshada, "CBCD: Comprehensive Analysis for Bone Cancer Diagnosis through MRI Imaging," 2024 1st International Conference on Cognitive, Green and Ubiquitous Computing (IC-CGU), Bhubaneswar, India, 2024, pp. 1-6, doi: 10.1109/IC-CGU58078.2024.10530830.

[12] S. M. Ali, S. IbneEunus, T. A. Bushra, M. HumaionKabirMehedi and A. A. Rasel, "A Federated Learning Approach to Bone Metastasis Prediction Using Convolutional Neural Network," 2023 26th International Conference on Computer and Information Technology (ICCIT), Cox's Bazar, Bangladesh, 2023, pp. 1-6, doi: 10.1109/ICCIT60459.2023.10441154.

[13] P. Divya, A. Chandrasekar and S. Raghavi, "Prediction of Osteosarcoma Bone Cancer Using Convolutional Neural Networks and Multi-Feature Integration Methods," 2024 International Conference on IT Innovation and Knowledge Discovery (ITIKD), Manama, Bahrain, 2025, pp. 1-6, doi: 10.1109/ITIKD63574.2025.11005254.

[14] G. K. Thakur, S. Kulkarni, S. Khan, M. M. T. Ayyalasomayajula and P. C. S. Reddy, "A Bone Metastatic Cancer Origin Prediction Using Deep Learning on Digital Pathological," 2024 International Conference on Computer, Electronics, Electrical Engineering & their Applications (IC2E3), Srinagar Garhwal, Uttarakhand, India, 2024, pp. 1-6, doi: 10.1109/IC2E362166.2024.10827171.

[15] S. V. Shashikala, H. R. Uma, A. N. Sunad Kumara, N. L. Taranath, L. Singh and D. Sisodia, "Bone Cancer Identification and Separation Using K-Means and KNN Classifiers," 2023 2nd International Conference for

Innovation in Technology (INOCON), Bangalore, India, 2023, pp. 1-7, doi: 10.1109/INOCON57975.2023.10101031.

[16] https://www.kaggle.com/datasets/bonedataset/bone-cancer-mri-dataset accessed on 15th February 2025