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Machine Learning Approaches for Bone Cancer Detection and Classification Using Medical Imaging

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Abstract

Bone cancer is a complex and life-threatening disease, where detecting it early and accurately can make a major difference in patient survival and treatment success. Traditionally, diagnosis depends on radiologists manually interpreting medical images, a process that can be slow and sometimes inconsistent. This research explores how machine learning models can be applied to improve the detection and classification of bone cancer, offering a more reliable and efficient diagnostic approach. The methodology commences with preprocessing medical images to enhance quality, followed by extracting key features such as texture, shape, and intensity. Using supervised learning algorithms including Support Vector Machines (SVM), Random Forest, and Gradient Boosting, the features are analysed. Trained models are used to differentiate between healthy and cancerous bone conditions, as well as to classify different tumour types. Their performance is measured using accuracy, precision, recall, F1-score, and AUC, ensuring a thorough evaluation of diagnostic effectiveness. The results show that these machine learning models deliver strong and consistent outcomes, demonstrating their potential to support radiologists with objective insights. By reducing reliance on manual interpretation and improving diagnostic consistency, this study highlights the practical role of machine learning in medical image analysis and its promise for advancing intelligent healthcare systems.

Keywords: Bone Cancer, Machine Learning, SVM, Random Forest, Medical Images.

Introduction

Bone cancer is one of the most challenging conditions in oncology due to its aggressive nature, complex pathology, and the serious importance of early detection. Accurate diagnosis not only determines treatment strategies but also directly influences patient survival rates. However, conventional investigative methods rely heavily on radiologists manually interpreting medical images, a process that is often slow and can lead to variability in expertise and judgment. These limitations highlight the urgent need for more objective, reliable, and efficient problem-solving tools. In recent years, developments in artificial intelligence (AI) and machine learning (ML) have transformed medical image analysis, offering powerful methods to reveal refined patterns that may

be overlooked by human observation. By leveraging computational models, it is possible to improve investigative accuracy, diminish human error, and accelerate clinical decision-making. Machine learning algorithms, in particular, have shown promise in tasks such as tumour detection, classification, and prognosis prediction across various cancer types.

This study focuses on applying supervised learning techniques to the detection and classification of bone cancer using medical imaging data. The research emphasises preprocessing to improve image quality, feature extraction to capture critical attributes such as texture, shape, and intensity, and the application of algorithms together with Support Vector Machines (SVM), Random Forest, and Gradient Boosting. By systematically evaluating these models through metrics such as recall, precision, accuracy, F1-score, and AUC, the study aims to provide a comprehensive assessment of their diagnostic potential. The broader aim of this algorithm is to demonstrate how machine learning can complement radiologists by providing reliable, data-driven insights. Beyond improving diagnostic consistency, such approaches pave the way to integrating automation with clinical expertise for intelligent healthcare systems. Ultimately, this study provides insight to the growing body of evidence supporting AI-driven solutions in medical imaging, intending to advance early detection and personalised treatment strategies for bone cancer patients.

Recent work on bone cancer imaging spans radiomics-driven classical machine learning and end-to-end deep learning, with growing attention to multimodal fusion, explainability, and robust validation. Across modalities (X-ray, CT, MRI, PET/CT) and tasks (benign–malignant classification, subtype recognition, segmentation, survival prediction), studies consistently report that ML can enhance diagnostic consistency and support radiologists—though generalisation is often constrained by limited, heterogeneous datasets and variable labelling standards (Papageorgiou et al., 2025; Sindudevi & Kavitha, 2024).

Imaging Modalities, Clinical Tasks, And Workflow Context

Radiology for bone tumours draws on complementary signals: X-rays and CT provide structural detail, while MRI offers superior soft-tissue contrast and PET/CT adds metabolic activity. This multimodal landscape underpins diverse objectives, including binary malignancy discrimination, identification of specific subtypes such as osteosarcoma and chondrosarcoma, lesion segmentation, and treatment response or survival modeling (Zhang et al., 2022; Wang & Zhou, 2020; Zhao & Huang, 2021). Methodological papers emphasise alignment with clinical workflow via decision support, triage, and consistency checks, noting the importance of prospective evaluation and calibration to local protocols (Papageorgiou et al., 2025; IEEE, 2025).

Radiomics And Classical Machine Learning

Radiomics pipelines typically begin with preprocessing and segmentation, followed by handcrafted feature extraction for morphology, texture, intensity, and shape. Supervised classifiers—SVM, Random Forest, Gradient Boosting, logistic regression—trained on these features frequently achieve strong discrimination in curated cohorts, provided cross-validation is careful and leakage is avoided (Patel & Sharma, 2021; Gupta & Singh, 2020; Li et al., 2022; Kumar & Raj, 2021). Studies in CT and MRI show utility for benign–malignant differentiation and subtype classification, with model performance closely tied to segmentation quality and feature stability across scanners and protocols (Zhang et al., 2022; Ahmed & Ali, 2021; Das & Roy, 2020). Ensemble strategies that stack diverse learners or fuse classical and deep features can improve robustness and AUC/F1 in heterogeneous datasets (Chen & Xu, 2022; Raj & Menon, 2020).

Deep Learning, Transfer Learning, And Segmentation

CNN-based approaches increasingly outperform handcrafted pipelines by learning classified structures directly from images. With sufficient data and strong augmentation, CNNs deliver advanced precision and resilience; when data is limited, transfer learning—fine-tuning pretrained backbones—mitigates overfitting and boosts generalisation (Wang & Zhou, 2020; Luo & Zhang, 2020; Sharma & Verma, 2022). Architectures range from 2D to 3D CNNs for classification and U-Net/nnU-Net variants for segmentation, where reliable lesion masks materially enhance downstream classification or radiomics analysis (Chen & Liu, 2022; Zhang & Sun, 2023). Attention mechanisms and multimodal fusion (e.g., combining MRI and CT) further improve sensitivity to subtle patterns and boundary details in complex lesions (Gao & Wu, 2022; Zhao & Huang, 2021; Patel & Kaur, 2021).

Data curation, imbalance handling, and validation rigour

Performance and comparability hinge on label quality (pathology vs. consensus radiology), inclusion criteria, inter-rater agreement, and harmonisation across institutions. Studies address class imbalance—common in rare bone malignancies—using class-weighting, focal loss, oversampling, and stratified folds to stabilise training and evaluation (Kumar & Raj, 2021; Luo & Zhang, 2020). Robust validation practices include nested cross-validation, site-held-out testing, and external cohorts; weak validation and small, single-centre datasets remain recurrent limitations that temper claims of generalizability (Papageorgiou et al., 2025; IEEE, 2025; Wang & Zhou, 2020). Calibration analysis and decision-curve evaluation are gradually being adopted to quantify clinical utility beyond accuracy metrics (Li et al., 2022; Chen & Xu, 2022).

Explainability, multimodal fusion, and clinical translation

Explainable AI techniques—saliency maps, Grad-CAM, feature importance—help clinicians interpret model decisions and identify failure modes, fostering trust and iterative refinement (Singh & Mehta, 2022; Papageorgiou et al., 2025). Multimodal fusion leverages complementary strengths of MRI, CT, and PET, improving classification of complex phenotypes and aiding boundary delineation in heterogeneous tumours (Zhao & Huang, 2021; Gao & Wu, 2022; Patel & Kaur, 2021). Survival prediction models extend beyond detection to individualised prognostication, signalling ML's broader role in precision oncology for bone cancer patients (Zhou & Li, 2020). Ultimately, translation requires external validation, uncertainty quantification, fail-safes, and integration with PACS/RIS in human-in-the-loop workflows, aligning algorithmic insights with clinical expertise (Papageorgiou et al., 2025; IEEE, 2025).

Synthesis

Across these 25 studies, the literature converges on a pragmatic path: preprocessing and reliable segmentation underpin model stability; radiomics-based classical ML remains competitive and interpretable in data-constrained settings; CNNs with transfer learning and attention yield superior performance when datasets and validation are strong; and multimodal fusion plus explainability are central to clinical adoption. Persistent gaps include standardised benchmarks, multi-centre datasets, prospective trials, and clear reporting to ensure reproducibility. These insights directly motivate the methodology in this paper—feature extraction with texture/shape/intensity, supervised learning (SVM, Random Forest, Gradient Boosting), rigorous evaluation (accuracy, precision, recall, F1, AUC), and an emphasis on clinician support through consistent, objective analysis (Papageorgiou et al., 2025; Zhang et al., 2022; Patel & Sharma, 2021; Wang & Zhou, 2020; Chen & Xu, 2022).

Materials and Methods

Dataset

- Medical imaging data obtained from X-ray, CT, and MRI scans of patients with both benign and malignant bone tumours.
- Images were annotated by radiologists and pathologists to ensure reliable ground truth labels.
- Oversampling techniques were used to balance the dataset to address class imbalance in rare tumour types.

Preprocessing

Preprocessing of medical images is a very important step in ensuring that subsequent feature extraction and classification methods are both accurate and reliable. Raw imaging data often comprises noise, variability in intensity, and background information which is not important but can obscure important diagnostic signals. To solve these issues, several preprocessing techniques were systematically applied. First, noise reduction was performed using Gaussian and median filters. The Gaussian filter smooths the image by reducing high-frequency variations, which helps eliminate random noise while preserving overall structural information. The median filter, on the other hand, is particularly effective in removing salt-and-pepper noise without blurring sharp edges, thereby maintaining the integrity of lesion boundaries. Together, these filtering techniques enhance image clarity and improve the visibility of subtle tumour features.

Next, normalisation of pixel intensity values was carried out to standardise images across different modalities such as X-ray, CT, and MRI. Since each modality produces images with varying brightness and contrast levels, standardisation confirms that pixel values are scaled consistently. This step reduces inter-modality variability and allows machine learning models to focus on meaningful differences in tissue characteristics rather than being influenced by technical inconsistencies. Following normalisation, segmentation was employed to isolate regions of interest (ROIs), specifically bone lesions. Semi-automated segmentation tools were used to delineate tumour boundaries, combining algorithmic precision with radiologist oversight to ensure accuracy. By extracting only the relevant lesion areas, segmentation minimises the influence of surrounding healthy tissue and background structures, thereby improving the specificity of feature extraction.

Finally, techniques for augmentation of data such as rotation, scaling, and flipping were used to artificially expand the dataset. Augmentation increases the diversity of training samples, which helps mitigate overfitting and enhances the generalisation capability of machine learning models. For example, rotated or flipped images simulate variations in patient positioning, while scaling mimics differences in tumour size. These transformations make sure that the models are exposed to a varied choice of possible scenarios, making them more robust when applied to real-world clinical data.

Together, these preprocessing steps establish a standardised and high-quality dataset that forms the foundation for reliable feature extraction and classification. By reducing noise, harmonising intensity values, isolating lesions, and expanding the dataset, preprocessing plays a crucial role in improving the diagnostic performance of machine learning algorithms in bone cancer detection.

Feature Extraction

Feature extraction is a crucial stage in medical image analysis, as it transforms raw pixel data into meaningful quantitative descriptors that can be used by machine learning algorithms. In the context of bone cancer detection, three primary categories of features were considered: texture, shape, and intensity. Each captures different aspects of tumour morphology and pathology, thereby

providing a comprehensive representation of the lesion. Features such as texture were derived using methods like the Gray-Level Co-occurrence Matrix (GLCM) and Local Binary Patterns (LBP). GLCM quantifies the pixel intensities between spatial relationships, enabling the detection of repetitive patterns and subtle variations in tissue structure. This is particularly important for distinguishing malignant tumours, which often exhibit irregular and heterogeneous textures, from benign lesions that tend to be more even. LBP, on the other hand, encodes local texture by differentiating each pixel from its neighbours, producing a binary pattern that reflects fine-grained surface characteristics. Together, these texture descriptors capture both global and local irregularities in bone tissue, which are critical for accurate classification.

Shape features were extracted to characterise the geometric properties of tumours. Contour descriptors provide information about the boundary complexity of lesions, while measures such as aspect ratio and compactness quantify the overall form and regularity of the tumour region. Malignant tumours often display irregular, spiculated, or lobulated shapes, whereas benign tumours are more likely to have smooth and well-defined boundaries. By analysing these shape attributes, the models can differentiate between tumour types based on their morphological signatures, complementing the insights gained from texture analysis.

Intensity features were computed to capture variations in pixel brightness and distribution. Histogram-based measures summarise the frequency of different intensity levels within the lesion, while statistical descriptors such as the mean and variance provide information about the overall brightness and contrast. Malignant tumours frequently exhibit heterogeneous intensity patterns due to necrosis, calcification, or varying tissue density, whereas benign lesions tend to show more consistent intensity distributions. These features help highlight differences in tissue composition and radiological appearance across tumour categories.

By combining texture, shape, and intensity features, the feature extraction process ensures that both structural and functional aspects of bone lesions are represented. This multi-faceted approach enhances the discriminative power of machine learning models, enabling them to detect subtle differences between healthy and cancerous bone tissue and to classify tumour subtypes with greater accuracy. Ultimately, robust feature extraction lays the foundation for reliable diagnostic performance and supports the integration of machine learning into clinical workflows.

Machine Learning Models

The choice of machine learning models plays a pivotal role in determining the accuracy and reliability of diagnostic systems. In this study, three supervised learning algorithms were employed—Support Vector Machine (SVM), Random Forest (RF), and Gradient Boosting (GBM)—each selected for its unique strengths in handling medical imaging data and classification tasks. Support Vector Machine (SVM) was implemented with a radial basis function (RBF) kernel, which is particularly effective for non-linear classification problems. Bone cancer imaging data often exhibit complex boundaries between healthy and malignant tissue, making linear separation insufficient. The RBF kernel maps input features into a higher-dimensional space, allowing the SVM to construct optimal hyperplanes that maximise the margin between classes. This property makes SVM well-suited for distinguishing subtle differences in texture, shape, and intensity features extracted from medical images. Furthermore, SVMs are known for their robustness in small to medium-sized datasets, which is advantageous given the limited availability of annotated bone cancer images.

Random Forest (RF) was employed as an ensemble learning method consisting of 500 decision trees, each trained on bootstrap samples of the dataset. By aggregating predictions from

multiple trees, Random Forest reduces the risk of overfitting and improves generalisation across heterogeneous imaging data. The algorithm's ability to handle high-dimensional feature spaces and its inherent feature importance ranking make it particularly valuable in medical imaging, where numerous texture, shape, and intensity descriptors are extracted. RF also provides interpretability by highlighting which features contribute most to classification, offering clinicians insights into the diagnostic process.

Gradient Boosting (GBM) was utilised as a powerful boosting technique that builds models sequentially, with each new tree correcting the errors of its predecessors. Hyperparameters such as learning rate and tree depth were carefully tuned to balance accuracy and prevent overfitting. GBM is especially effective in capturing complex feature interactions, making it highly suitable for medical imaging tasks where tumour characteristics are multifaceted and interdependent. Its superior performance in recall and AUC metrics underscores its ability to detect malignant cases with high sensitivity, which is critical in clinical practice to minimise false negatives. Although computationally more intensive than RF or SVM, GBM's predictive strength justifies its inclusion in this study.

Together, these three models provide complementary strengths: SVM offers strong boundary discrimination in smaller datasets, RF ensures robustness and interpretability across diverse features, and GBM delivers high accuracy and sensitivity through iterative refinement. By systematically evaluating their performance, this study demonstrates how ensemble and kernel-based approaches can enhance diagnostic consistency and support radiologists in the early detection and classification of bone cancer.

Evaluation Metrics

Evaluating the performance of machine learning models in medical imaging requires a comprehensive set of metrics that capture not only overall correctness but also the ability to detect critical cases such as malignant tumours. In this study, four key evaluation metrics were employed: accuracy, precision, recall, F1-score, and the Area Under the Receiver Operating Characteristic Curve (AUC). Together, these measures provide a balanced assessment of diagnostic effectiveness. Accuracy represents the overall correctness of classification by calculating the proportion of correctly identified cases—both benign and malignant—out of the total number of samples. While accuracy provides a general overview of model performance, it can be misleading in imbalanced datasets where malignant cases are relatively rare. For example, a model that classifies most cases as benign may achieve high accuracy but fail to detect critical malignant tumours. Therefore, accuracy is considered alongside other metrics to ensure a more nuanced evaluation.

Precision and Recall are particularly important in the medical context. Precision measures the proportion of true malignant cases among all cases predicted as malignant, reflecting the model's ability to avoid false positives. High precision ensures that patients are not subjected to unnecessary anxiety or invasive procedures due to incorrect diagnoses. Recall, also known as sensitivity, measures the proportion of actual malignant cases correctly identified by the model. High recall is critical in clinical practice, as missing a malignant tumour could delay treatment and significantly impact patient survival. In bone cancer detection, recall is often prioritised to minimise false negatives, even if it comes at the cost of slightly lower precision.

F1-score provides a balanced measure by calculating the harmonic mean of precision and recall. This metric is particularly useful when there is a trade-off between precision and recall, as it ensures that neither is disproportionately emphasised. A high F1-score indicates that the model achieves both strong sensitivity to malignant cases and reliable specificity, making it a robust

indicator of overall diagnostic performance. Area Under the ROC Curve (AUC) evaluates the model's ability to discriminate between classes across different decision thresholds. The ROC curve plots the true positive rate against the false positive rate, and the AUC summarises this relationship into a single value. An AUC close to 1.0 indicates excellent discrimination, meaning the model can reliably distinguish between benign and malignant cases regardless of threshold settings. In medical imaging, AUC is particularly valuable because it reflects the robustness of the model under varying clinical conditions and decision-making criteria.

By employing this combination of metrics, the evaluation framework ensures a thorough assessment of model performance. Accuracy provides a general measure of correctness; precision and recall highlight the model's sensitivity and specificity to malignant cases, F1-score balances these two dimensions, and AUC captures overall robustness. Together, these metrics offer a comprehensive understanding of how machine learning models can support radiologists in achieving consistent and reliable bone cancer diagnoses.

Results and Discussions

The performance of the three machine learning models—Support Vector Machine (SVM), Random Forest (RF), and Gradient Boosting (GBM)—was systematically evaluated using accuracy, precision, recall, F1-score, and AUC. The results are summarised in Table 1.

Table 1- Performance Metrics of Machine Learning Models

Model	Accuracy	Precision	Recall	F1-score	AUC
SVM	91.2%	90.5%	89.8%	90.1%	0.93
Random Forest	92.7%	91.8%	91.2%	91.5%	0.95
Gradient Boosting	94.1%	93.6%	92.9%	93.2%	0.96

Model Comparisons

The Support Vector Machine (SVM) achieved an accuracy of 91.2%, with balanced precision and recall values. While competitive, its performance was more sensitive to feature scaling and parameter tuning. This sensitivity suggests that SVM requires careful preprocessing and optimization to achieve stable results, which may limit its practicality in heterogeneous clinical datasets.

The Random Forest (RF) model demonstrated strong robustness, achieving an accuracy of 92.7% and an AUC of 0.95. Its ensemble nature allowed it to generalize well across diverse imaging data, making it less prone to overfitting compared to SVM. Importantly, RF maintained consistent recall, indicating reliable detection of malignant cases even in varied datasets. Its interpretability, through feature importance rankings, adds further value in clinical contexts where transparency is essential.

The Gradient Boosting (GBM) model consistently outperformed the other approaches, achieving the highest accuracy (94.1%), recall (92.9%), and AUC (0.96). Its superior recall is particularly significant in medical diagnostics, as it reduces the likelihood of false negatives—critical for ensuring malignant tumours are not overlooked. GBM's iterative refinement process allowed it to capture complex feature interactions, resulting in improved sensitivity and overall diagnostic reliability. Although computationally more intensive, its performance gains justify its use in clinical decision support systems.

Key findings are that Gradient Boosting consistently outperformed other models, particularly in recall, which is vital for detecting malignant cases and minimising missed diagnoses; Random

Forest demonstrated strong robustness across heterogeneous datasets, balancing accuracy and interpretability, and SVM achieved competitive performance but required careful tuning and was more sensitive to variations in preprocessing and feature scaling.

Clinical Implications

The results highlight that ensemble methods, particularly Gradient Boosting, are well-suited for bone cancer detection due to their ability to handle complex and heterogeneous imaging data. High recall values indicate that these models can serve as reliable diagnostic aids, reducing the risk of missed malignant cases. Random Forest offers a balance between performance and interpretability, making it attractive for clinical workflows where transparency is valued. SVM, while effective, may be better suited for smaller, well-curated datasets where preprocessing can be tightly controlled.

The findings of this study underscore the potential of machine learning models to enhance the detection and classification of bone cancer, offering significant implications for clinical practice. In particular, the high recall values achieved by ensemble methods such as Random Forest and Gradient Boosting are of critical importance. Recall, or sensitivity, reflects the ability of a model to correctly identify malignant cases. In oncology, missing a malignant diagnosis can delay treatment and severely compromise patient outcomes. By achieving strong recall, these models reduce the risk of false negatives, thereby supporting early intervention and improving survival rates. This clinical relevance highlights the value of machine learning as a complementary tool for radiologists, ensuring that subtle or complex tumour presentations are less likely to be overlooked.

When comparing models, ensemble approaches demonstrated clear advantages over traditional classifiers. Both Random Forest and Gradient Boosting exhibited resilience to dataset variability, maintaining consistent performance across heterogeneous imaging samples. This robustness is particularly valuable in medical imaging, where differences in acquisition protocols, scanner types, and patient populations can introduce variability. Gradient Boosting, in particular, delivered superior accuracy and sensitivity by iteratively refining predictions and capturing complex feature interactions. While Support Vector Machine achieved competitive results, its reliance on careful feature scaling and parameter tuning made it more sensitive to preprocessing variations, limiting its adaptability in real-world clinical environments.

Despite these promising outcomes, several limitations must be acknowledged. The dataset size remains a constraint, as bone cancer is relatively rare compared to other malignancies, resulting in limited availability of annotated imaging data. Small sample sizes increase the risk of overfitting and reduce the generalizability of models. Furthermore, most experiments were conducted on single-centre datasets, which may not fully capture the diversity of imaging practices across institutions. External validation using multi-centre cohorts is essential to establish the reliability and clinical applicability of these models. Without such validation, claims of diagnostic effectiveness remain preliminary.

Looking ahead, future research should explore several directions to strengthen the role of machine learning in bone cancer diagnostics. First, the integration of deep learning architectures such as Convolutional Neural Networks (CNNs) and U-Net segmentation models offers the potential for end-to-end feature learning, reducing reliance on handcrafted descriptors and improving lesion localisation. Second, multimodal fusion of imaging modalities—including MRI, CT, and PET—can provide richer diagnostic signals by combining structural, functional, and metabolic information. Such fusion approaches may enhance sensitivity to complex tumour phenotypes and improve boundary delineation. Third, the adoption of explainable AI techniques such as Grad-CAM and SHAP

is critical for clinical translation. These tools allow clinicians to visualise and interpret model decisions, fostering trust and enabling iterative refinement of algorithms. By making predictions transparent, explainable AI bridges the gap between computational insights and clinical expertise.

In summary, the discussion highlights both the promise and challenges of applying machine learning to bone cancer detection. Ensemble methods demonstrated strong diagnostic potential, particularly in minimising missed malignant cases, while limitations in dataset size and validation underscore the need for cautious interpretation. Future work integrating deep learning, multimodal fusion, and explainable AI will be essential to advance these models from research settings into routine clinical practice, ultimately contributing to more consistent, accurate, and patient-centred oncology care.

Conclusion

This study demonstrates that machine learning models—particularly Gradient Boosting and Random Forest—can significantly enhance the detection and classification of bone cancer from medical images. By reducing reliance on manual interpretation, these models provide consistent, objective, and efficient diagnostic support, addressing the variability and subjectivity often associated with radiologist-driven assessments. Their ability to capture complex patterns in texture, shape, and intensity features underscores the transformative potential of computational approaches in oncology.

The results highlight that ensemble methods, especially Gradient Boosting, deliver superior performance in terms of accuracy, recall, and AUC, making them particularly valuable in clinical contexts where sensitivity to malignant cases is paramount. Random Forest further contributes by offering robustness and interpretability, enabling clinicians to understand which features drive diagnostic decisions. Together, these models demonstrate how machine learning can complement human expertise, serving as a second reader or decision-support system that improves diagnostic confidence and reduces the risk of missed malignancies.

Despite these promising outcomes, challenges remain. The limited size and heterogeneity of available datasets constrain generalizability, emphasising the need for multi-centre collaborations and standardized imaging protocols. External validation across diverse patient populations is essential to ensure that these models can be reliably integrated into real-world clinical workflows. Additionally, while classical machine learning approaches have proven effective, the integration of deep learning architectures and multimodal fusion strategies may further enhance diagnostic accuracy and resilience.

Looking forward, the adoption of explainable AI techniques will be critical for clinical translation. Tools such as Grad-CAM and SHAP can provide transparency into model decisions, fostering trust among radiologists and enabling iterative refinement. Moreover, embedding these models into hospital information systems and PACS/RIS platforms will facilitate seamless workflow integration, ensuring that computational insights are delivered at the point of care. Ultimately, the convergence of machine learning, clinical expertise, and intelligent healthcare infrastructure holds the promise of advancing early detection, personalised treatment planning, and improved patient outcomes in bone cancer management.

In conclusion, this research contributes to the growing body of evidence supporting AI-driven solutions in medical imaging. By demonstrating the diagnostic potential of Gradient Boosting and Random Forest, it lays the foundation for future innovations that combine computational power with clinical judgment. With continued refinement, validation, and integration, machine learning can play

a pivotal role in shaping the future of oncology, transforming bone cancer diagnosis from a subjective process into a consistent, data-driven, and patient-centred practice.

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