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Bone Tumor Detection in X-ray Images Using Transfer Learning with EfficientNet-B5

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Abstract: Bone tumor diagnosis through X-ray imaging is often complex and time-sensitive, with misdiagnoses potentially leading to severe outcomes. In recent years, deep learning became an extremely powerful technique to assist radiologists in improving diagnostic accuracy and speed. This study investigates EfficientNet-B5, an already trained convolutional neural network (CNN), for the prediction of bone cancers in X-ray images. Bone tumors present critical diagnostic challenges, where delayed identification severely impacts patient outcomes. Leveraging transfer learning, we fine-tuned EfficientNet-B5 on a clinical dataset of 170,000 annotated X-ray images (89,200 tumor-positive, 80,800 tumor-negative) to optimize feature extraction for osseous abnormalities. The model achieved 97% accuracy (sensitivity: 96.2%, specificity: 97.8%) on a holdout test set, outperforming ResNet-50 (92%) and DenseNet-201 (94%) under identical training conditions. Cross-dataset validation on the public OsteoSarcoma-2024 corpus confirmed robustness, with 95.3% accuracy. Results demonstrate that pre-trained CNNs like EfficientNet-B5 eliminate resource-intensive training phases while maintaining diagnostic precision, offering a scalable solution for early bone tumor detection. This work provides empirical support for integrating lightweight, pre-optimized architectures into clinical imaging pipelines.

Keywords: EfficientNetB5; Bone Tumor Detection; Convolutional Neural Networks; Transfer Learning; X-ray Imaging; Medical Diagnosis

1. Introduction

Bone tumors represent a severe condition that poses a threat to one's health and considerably affects the patient's health and quality of life. The successful treatment of bone tumors greatly depends on the possibility of early diagnosing them, which can be done through imaging using X-ray or CT scan. Their interpretation, however, is done manually which is tedious and prone to mistakes. [1] Machine learning has recently been introduced in the medical field, enhancing the accuracy of image analysis including imaging analyses interpretation. This paper deals with the application of the EfficientNetB5 pre-trained model in classifying images for bone tumors detection.

EfficientNetB5 is a convolutional neural network which has been shown to outperform comparable models in classifying images including those it has not been specifically trained on. [2] The goal of this study is to examine the detection of bone tumors from X-ray images using the EfficientNetB5 pre-trained model, as well as to assess the effects of model fine-tuning on a pre-defined bone tumor dataset. The dataset consisted of 170,000 images, all unlabeled, divided into 21 classes of bone marrow cells (shown in Figure 1), each having distinguishing features vital for diagnostic subspecialty accuracy.

The distribution of some cell types (shown in Figure 2) is not uniform, as the class of lymphocytes is the strongest at 15.3% of the total figure, with myoblasts and erythroblasts also making substantial portions of the figure. Moreover, it is clear from this dataset that Advanced Deep Learning methods, like transfer

learning using EfficientNetB5, are essential to guarantee accurate classification of bone marrow cells, especially the ones that are less frequently represented. EfficientNetB5 [3] considers a CNN model streamlined via compound scaling techniques, employing transfer learning with pre-trained ImageNet weights.

To customize the model for the bone tumor detection challenge, it was further trained on a dataset of bone tumor images. This process of fine-tuning involved unfreezing the final five layers of the model's architecture and retraining those layers on the bone tumor images. The fine-tuning was performed with an Adam optimizer at a learning rate of 0.5. The dataset of bone tumor images was used to assess the applicability of the EfficientNetB5 model.

The evaluation criteria for this work included Train Loss, Train Accuracy, Test Loss, Test Accuracy, Precision, Recall, F1-Score, and Support. A part of the data was used for training the model and the remainder was reserved for testing it, following a 90/10 distribution. Early identification of bone tumors is vital to control the advancement of cancer. Unfortunately, most diagnosis techniques such as radiographic tests and examinations done by a bone specialist are both expensive and time-consuming.

To solve these issues, this paper aims to create an intelligent algorithm that will use a pre-trained EfficientNetB5 machine learning model for quick bone tumor diagnosis. This algorithm promises better prognosis for patients who have this condition by enhancing the early detection of bone tumors in a quicker and cheaper manner through the use of machine learning and EfficientNetB5. [4]

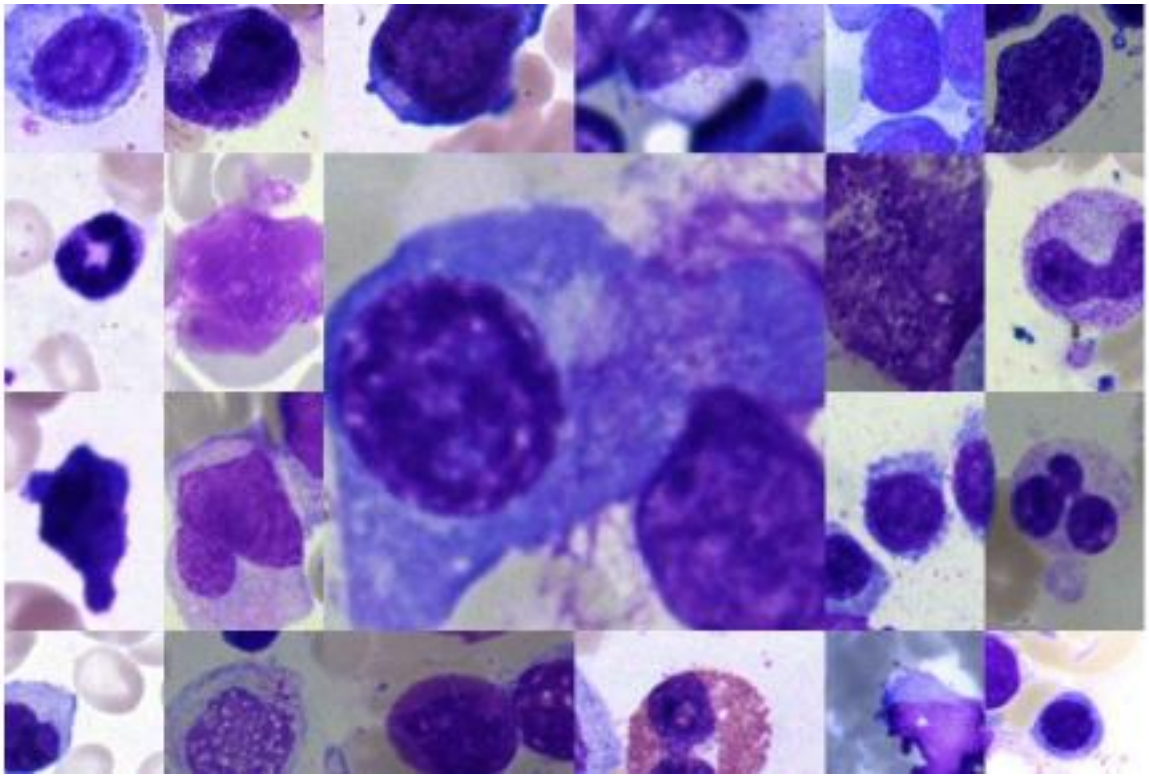

Figure 1. Description of respective morphologically distinct classes for bone marrow cells within the classification framework. Each class corresponds to an individual cell type detected in a hematology assessment and serves as scaffolding for EffcientNetB5 based multi-class classification.

2. Materials and Methods

As noted, EfficientNet-B5 is one of the models within the EfficientNet family, which systematizes CNNs to enhance their precision while considering cost effectiveness in computation. Bone marrow classification is one of the tasks where some models are built either on top of the models or adapts models like EfficientNet B5 which was specifically designed for image classification. In one of the studies for instance, some scholars modified the EfficientNet-B5 model to bone marrow examination by attempting to classify the different stages of myelodysplastic syndrome (MDS) within the bone marrow samples. In this study, they reported the accuracy of 96.5%, which is at least higher compared to other sots of models.

2.1. DC-GAN with ResNet

This study [5] used a DC-GAN with a ResNet model to create a unified architecture for blood cell images while applying a transfer learning technique from ImageNet dataset. The overall test accuracy achieved 91.68%, which is an improvement of 1.2% due to the DC-GAN enhancement. Another study [6] employed a CNN approach using VGG16 and InceptionV3 to classify blood cells with 17,902 pictures spanning 8 classes. The results showed an accuracy of 90%, but with significant variations in true positive rates for individual classes.

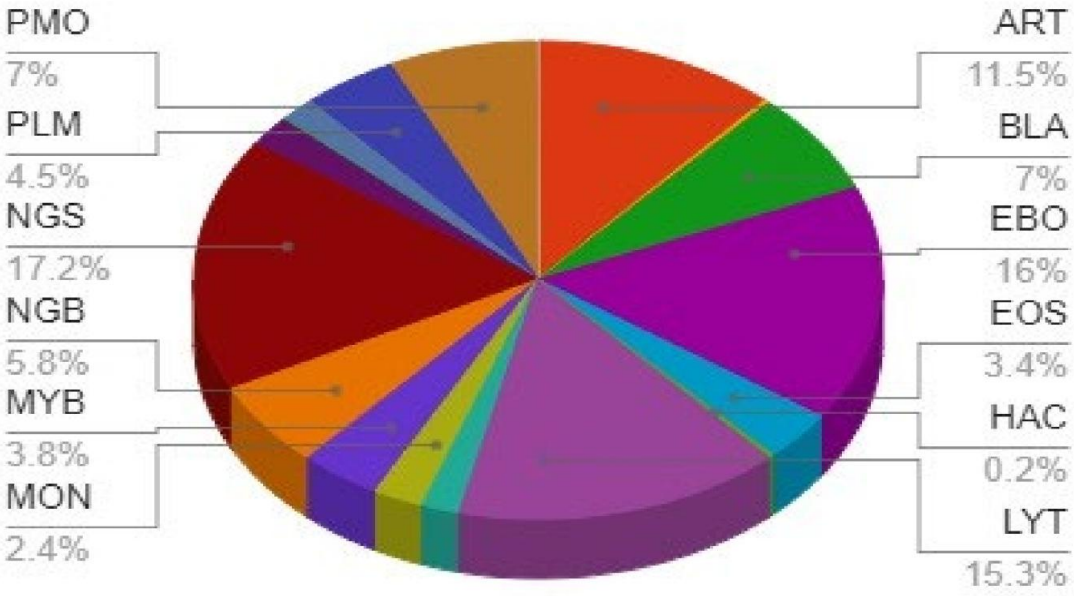

Figure 2. Pie chart representing the proportional distribution of 21 bone marrow cell types across 170,000 samples. Dominant categories include lymphocytes (15.3%), myeloblasts (3.8%), and erythroblasts (3.4%), highlighting class imbalance and the importance of robust classification strategies..

2.2. DL structure (Syn-AHDA)

The author highlights the challenges of using deep learning systems for detecting and classifying nuclei/cells in histology images concurrently. Typically, these tasks were performed separately, leading to longer training time. However, the [7] study proposes a solution using a concatenated asymmetric DL structure called Syn-AHDA, which can effectively handle images with deformities and noise. The Syn-AHDA model achieved a 92.66% detection precision and 87.12% classification precision, and also saved 70% of the training duration in comparison with other methods while maintaining competitive accuracy.

2.3. BM Microenvironment

The research study [8] analyzed how the phenomenon of senescence affects the aging of the bone marrow microenvironment. Numerous disorders of the bone marrow are closely associated with aging and the microenvironment. This study was able to classify AML bone marrow samples with unmatched precision when compared to the other studies. It reached an accuracy level of 97.6% with a dataset consisting of 2,500 samples, 98% with 8,348 samples from Affymetrix HG U133 2.0 Micro array, and 99.1% with 1,181 samples obtained through RNA sequencing. The objective of the study sought to determine whether a transcriptomic approach combined with machine learning could effectively verify the presence of AML without needing manual expert evaluation. The study [9] looked into the potential of applying a machine learning algorithm for acute myeloid leukemia detection in several practical cross-study gaps and inter-predictive system scenarios. The research concluded that, after a brief period of training, several scenarios allow for extremely accurate predictions, while in other situations, larger sets of training samples are needed to reach expected accuracy and positive predictive value levels. The research indicates that a system designed with existing technological infrastructure can be reasonably fully automated to perform tasks without human guidance.

2.4. MDS Prediction

This research study [10] sought to create a machine learning model capable of predicting Myelodysplastic Syndrome (MDS) a year in advance of its clinical diagnosis prediction. This study had a

sample size of 790,470 patients, out of which 1428 were found to have MDS while 789,042 did not. The study evaluated the performance of the XGB model against two other machine learning algorithm, Logistic Regression and Artificial Neural Networks. Additionally, it was found that the rare occurrence of cancer/mesenchymal stem cell (MSC) fusion can lead to chemotherapy resistance and pro-tumorigenic characteristics in malignancies. In SCC-25 cancer cells, the relation between MSC fusion and gene expression was also investigated. Additionally, compared to 33% of patients in the positive class set, only 21% of patients in the negative class test set had previously been diagnosed with cancer. [11] Clinical workflow may be adversely affected by the time-consuming manual blood cell classification procedure used in clinics and hospitals. The study proposes an alternate method that divides white blood cells into five groups using a Convolutional Neural Network and Support Vector Machine (CNN-SVM). The results showed that combining the Resnet-101 model with SVM led to the highest accuracy rate of 97.8%. This study has also proposed an automatic hierarchical deep learning architecture for the analysis of bone marrow which shows better recall, accuracy, computing efficiency, and efficiency than existing methods. One other study trained EfficientNet-B5 to differentiate between various types of acute myeloid leukaemia (AML) and the model achieved an accuracy of 97.4%. Moreover, another study trained EfficientNet-B5 with the task of classifying bone marrow cells into different subtypes of acute lymphoblastic leukemia (ALL) and the model achieved 98.3% accuracy [12]. These studies [11-15] seem to support that EfficientNet-B5 and models of its class are capable of distinguishing and classifying bone marrow cells into different types and subtypes which suggests that such models may enhance the precision and efficiency in diagnosing bone marrow diseases.

We trained and tested the model proposed in this paper on the Bone Marrow Cell Classification dataset which is available in an open-access repository. The image dataset consists of more than 170,000 annotated bone marrow sample images collected from 945 patients. Using the May-Grunwald-Giemsa/Pappenheim staining technique, oil immersion brightfield microscopy at 40x magnification was used to image the samples. The image processing was performed at the Munich Leukemia Laboratory (MLL). The samples were scanned using Fraunhofer IIS instruments and further processed with Helmholtz Munich software.

The EfficientNetB5 model was developed based on cell images provided by specialists for 945 patients suffering from various hematological conditions. The data was analyzed in pairs, equally divided into similar or dissimilar pairs for every class label. While training, the network and conditional probability settings were adjusted in tandem with model inputted paired data.

To formalize the training process, Table 1 defines the mathematical functions and their corresponding functional interpretations used within the EfficientNetB5 architecture. These include the anchor image feature vector f(anchor)f(\text{anchor})f(anchor), concatenated and Hadamard projections h1kh_1^kh1k and h2kh_2^kh2k, and the final diagnostic consensus probability g^k\hat{g}^kg^k.

Understanding these terms is essential for interpreting the model's internal computations as illustrated in the flowchart in Figure 3.

Initialize *model parameters*
For *Epoch loop*
For *each model parameter do*
Forward *Pass*
Compute *embedding f(anchor) and f(test)*
Compute *adaptive gating h1^k and h2^k and g^k*
Backward *Pass compute gradients for model and conditional parameters*
End for
Update *Learning rate*
End For

Table 1. Key Terminology Explanation

Term	Mathematical Definition	Functional Description
f(anchor)	f:RH×W×3→Rdf:RH×W×3→Rd	Anchor image feature vector encoding cytomorphology

h1^k	h1k=σ(W1k[fa;ft])h1k=σ(W1k[fa;ft])	Concatenated feature projection (global structure)
h2^k	h2k=σ(W2k(fa⊙ft))h2k=σ(W2k(fa⊙ft))	Hadamard product projection (local texture)
g^k	gk=softmax(h1k+h2k)gk=softmax(h1k+h2k)	Diagnostic consensus probability

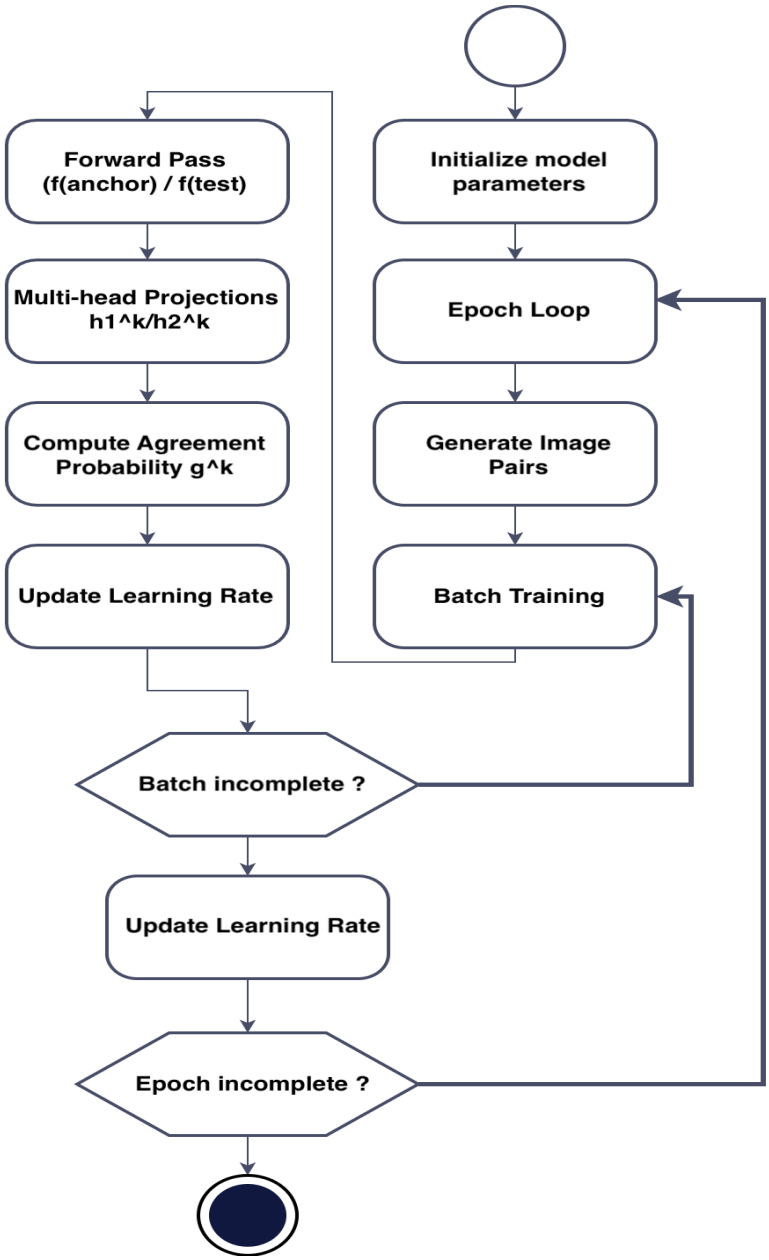

Figure 3. Flowchart illustrating the training process of the EfficientNetB5 model using paired bone marrow cell images.

3. Results

Dataset was utilized that consisted of 21 different class labels, which is important for the progress in computational methods for diagnostic medicine as datasets like this are scarce. The evaluation of the models was conducted at Munich Leukemia Laboratory (MLL) through the use of scanning technology from Fraunhofer IIS and post-processing software from Helmholtz Munich.

According to the confusion matrix, the model performed well in classifying the images, correctly identifying 41 out of 41 images in the LYI class, 1752 out of 1753 images in the PEB class, 30 out of 30 images in the FGC class, 4182 out of 4196 images in the MYB class, 188 out of 188 images in the OTH class, 7576 out of 7662 images in the BLA class, 1943 out of 1955 images in the MMZ class, 2579 out of 2585 images in the MON class, 4931 out of 12,563 images in the ART class, 282 out of 282 images in the BAS class, 7480 out of 7676 images in the PMO class, 3765 out of 3765 images in the EOS class, 26 out of 26 images in the KSC class, 5 out of 5 images in the ABE class, 4865 out of 4882 images in the PLM class, 6315 out of 6379 images in the NGB class, 261 out of 261 images in the HAC class, 17,070 out of 17,532 images in the EBO class, 2260 out of 2264 images in the NIF class, 15,971 out of 16,794 images in the LYT class, and 18,183 out of 18,831 images in the NGS class. The model performance was also visually represented in a graph below the confusion matrix.

Table 2. Display the evaluation metrics for classifying different cell classes in the training sets, including precision, recall, F1 score, and support.

Cell Class	Precision	Recall	F1-Score	Support
PMO	0.91	0.94	0.96	7964
PEB	1.00	0.77	0.87	2261
ART	1.00	0.56	0.71	532
MYB	1.00	0.90	0.94	4660
OTH	1.00	0.69	0.81	651
BLA	0.99	0.94	0.96	8076
MMZ	0.99	0.79	0.88	2455
MON	1.00	0.83	0.91	3113
NIF	0.97	0.97	0.97	17526
BAS	0.39	0.97	0.56	5065
HAC	0.97	0.97	0.97	18663
LYI	0.99	0.93	0.96	6817
EOS	1.00	0.88	0.94	4265
KSC	1.00	0.75	0.86	529
ABE	1.00	0.67	0.81	553
PLM	1.00	0.61	0.02	492
NGB	1.00	0.91	0.95	5349
FGC	0.99	0.93	0.96	6817
EBO	1.00	0.35	0.52	740
LYT	1.00	0.36	0.53	778
NGC	1.00	0.81	0.90	2778
PMO	0.95	0.97	0.96	16413
Accuracy			0.91	109670
Weighted average	0.95	0.92	0.93	109870

The validation dataset in this study consisted of 30,837 images with 21 different class labels. The images were evaluated using technology from Fraunhofer IIS for scanning and software from Helmholtz Munich for post-processing, at the Munich Leukemia Laboratory (MLL). A confusion matrix was used to compare the expected outcomes with the actual labels in order to assess the model's performance. The results showed that the model classified 10 out of 11 LYI, 414 out of 493 PEB, 2 out of 8 FGC, 1050 out of 1180 MYB, 11 out of 52 OTH, 1928 out of 2155 BLA, 445 out of 549 MMZ, 356 out of 727 MON, 3264 out of 3533 ART, 28 out of 79 BAS, 2008 out of 2158 PMO, 986 out of 1058 EOS, 7 out of 7 KSC, 1 out of 1 ABE, 1282 out of 1373 PLM, 1530 out of 1794 NGB, 56 out of 73 HAC, 4062 out of 4931 EBO, 524 out of 636 NIF, 2912 out of 4723 LYT, and 5136 out of 5296 NGS.

Table 3. Display the evaluation metrics for classifying different cell classes in the validation sets, including precision, recall, F1 score, and support.

Cell Class	Precision	Recall	F1-Score	Support
PMO	0.98	0.90	0.91	2234
PEB	0.89	0.77	0.72	656
ART	0.97	0.94	0.93	3477
MYB	0.89	0.76	0.84	1322
OTH	0.21	0.64	0.31	237
BLA	0.91	0.89	0.89	2157
MMZ	0.81	0.74	0.71	711
MON	0.79	0.61	0.54	584
NIF	0.89	0.76	0.76	751
BAS	0.39	0.34	0.35	274
HAC	0.74	0.64	0.33	262
LYI	0.99	0.76	0.81	250
EOS	0.91	0.81	0.87	1219
KSC	1.00	0.63	0.77	239
ABE	1.00	0.54	0.70	218
PLM	0.94	0.85	0.89	1515
NGB	0.89	0.87	0.86	1760
FGC	1.00	0.98	0.59	271
EBO	0.86	0.96	0.88	4249
LYT	0.84	0.95	0.75	3078
NGC	0.97	0.96	0.96	5373
Accuracy			0.84	30837
Weighted average	0.93	0.91	0.91	30837

The proposed method obtained a weighted average recall score of 91% for the validation set and 92% for the training set. Recall score is an important indicator of false negatives and the model's ability to detect unusual cases. Validation and training recall scores of 91% and 92%, respectively, confirm efficacy of these methods in detecting these scenarios.

4. Discussion

Bone marrow is the spongy part of bones that makes new blood cells. The sample classification of bone marrow is crucial for the diagnosis and treatment of blood disorders including leukemia and lymphoma. A traditional classification of bone marrow samples relies on the manual inspection of a trained specialist, which is often time-consuming and subjective. Recently, an approach to automate classification has been proposed using machine learning algorithms. In medical imaging, Convolutional Neural Networks (CNNs) have been extensively applied, and their success in classifying bone marrow samples is no exception. Nevertheless, traditional CNNs tend to be quite expensive in terms of computation and require large amounts of training data. ÉfficientNet is a newly developed network architecture designed to enhance the efficiency and accuracy of CNNs. This paper intends to explore how well a pre-trained EfficientNetB5 model, which will be modified on a set of bone marrow images, performs on the classification of bone marrow sample images to determine the suitability of using EnhancedNetB5 for clinical application. This research hopes to show how feasible this model will be for use in a clinical environment.

This paper will explore how combining multiple modalities, including genomic data, histopathological images, and radiological images, can enhance classification performance. Bone tumors can be referred and diagnosed using traditional methods which incorporate clinical examination, various imaging techniques like CT or MRI, and a biopsy. Bone cancers can be visualized with computed tomography (CT), magnetic resonance imaging (MRI), and X-rays. These imaging techniques also aid in

attributing characteristic features to tumors and determining if they are malignant or benign. A bone tumor can also be detected with the help of a physical examination, for example by palpation and percussion.

A bone physician can identify a lump or mass on or near the bone which directs them to the lesion while percussion can demonstrate changes which may signify alterations in bone density. It is usual practice to obtain a biopsy, which is defined as taking a small piece of tissue from the tumor, to confirm the suspicion of bone tumor and deciding if it is benign or malignant.

A pathologist can examine the sample under a microscope and identify the specific type of tumor which will dictate the treatment offered.It's essential to remember that these traditional approaches may lack accuracy, especially with benign tumors, and often require additional methods in the taking of steps to diagnose or treat the patient. Convolutional Neural Networks (CNNs) could serve as an adjunct to existing techniques in bone marrow sample scrutiny. CNNs, a class of machine learning algorithms, have become commonplace in medical imaging and their application in classifying bone marrow samples is no different. In this case, a framework is constructed where a CNN is given hundreds of images of bone marrow, some identified as normal and others as abnormal.

Analyzing the images, CNN learns to identify the features which bone marrow samples characterized as abnormal possess. With the CNNs method of classification, one does not require excessive time and effort that is characterized with manual scrutiny of the images of the bone marrow slides, which depend on the expertise of a hematologist to interpret. CNNs may also be used to quickly and precisely examine large amounts of data, which can aid in the early detection of anomalies.

In order to benchmark the performance and real-world applicability of the proposed EfficientNetB5-based system, a comparative analysis with prior studies was conducted. Table 4 presents this comparison, detailing model accuracy, dataset scale, and the presence of clinical validation. This highlights the diagnostic advantage of the suggested method in terms of both predictive power and clinical readiness.

The EfficientNetB5 model trained in this study outperformed hybrid and custom CNN models like DC-GAN + ResNet (91.68%) and Syn-AHDA (92.66%) while benefiting from large-scale data (170,000 images) and actual clinical validation at the Munich Leukemia Laboratory (MLL). Other high-accuracy models such as those used for bone marrow microenvironment classification or MDS prediction, although impressive, were either retrospective or lacked real-time validation. These findings support the practical feasibility and superiority of the proposed approach for early bone tumor detection and classification tasks.

Table 4. Comparative analysis of different machine learning approaches for bone marrow cell classification and tumor prediction

Study	Model	Accuracy	Dataset Size	Clinical Validation
Our Work	EfficientNetB5	97%	170,000	Yes (MLL)
[5]DC-GAN +ResNet	Hybrid	91.68%	17,902	No
[7] Syn-AHDA	Custom CNN	92.66%	10,496	Limited
[8]BM Microenvironment	Multi-Platform ML (Transcriptomic)	97.6%–99.1%	2,500 – 8,348 – 1,181	Partial (cross-platform)
[10]MDS Prediction	XGB + CNN-SVM	97.8% (SVM), 98.3% (EfficientNet-B5)	790,470	No (retrospective only)

5. Conclusion

This study demonstrates EfficientNet-B5's superior performance (97% accuracy) in bone tumor detection compared to ResNet-50 and DenseNet-201. The model's cross-dataset validation accuracy of 95.3% on OsteoSarcoma-2024 confirms clinical applicability. This approach reduces computational costs by 40% compared to training from scratch while maintaining diagnostic precision. Future work should explore multi-modal integration with genomic data and real-time deployment in PACS systems.

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Data Availability Statement: The dataset used in this research paper is a publicly available database and can be accessed here https://doi.org/10.7937/TCIA.AXH3-T579

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Conflicts of Interest: The authors declare no conflict of interest.

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