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REVIEW OF VARIOUS AI ASSISTED MULTIPLE MYELOMA DISEASE DETECTION BASED ON CLINICAL FEATURES AND IMAGING MODALITIES

Prasanjit Singh[1], **Dr. P. Mohan Kumar**[2]

[1]Research Scholar, Department of Computer Science and Engineering,
Hindustan Institute of Technology and Science (Deemed to be University), Chennai, India
Email: mailprasanjitsingh@gmail.com

[2]Professor, Department of Computer Science and Engineering,
Hindustan Institute of Technology and Science (Deemed to be University), Chennai, India
Email: pmohank@hindustanuniv.ac.in

Abstract

Multiple myeloma (MM) is a malignant illness that results in the uncontrolled growth of plasma cells in the bone marrow, which produce abnormal levels of monoclonal immunoglobulin. However it has a lack of standardized protocol dependency on radiologist which requires the need for automated systems to improve the diagnostic precision and reduce delays. Advances in clinical imaging approaches using AI-driven diagnostic frameworks are examined for assessing the research gap in order to improve the identification of multiple myeloma using artificial intelligence (AI). Recent advancements in imaging techniques and clinical data, including machine learning algorithms for predictive modelling and a sophisticated deep learning architecture for automated multiple myeloma analysis, are examined in this study. Following hybrid/ensemble techniques for robust tumour classification and efficient feature extraction, transfer learning techniques are used for successful adaptation in data-constrained environments. The experimental result indicate that among evaluated techniques deep learning methods such as Disruption-based Salp-Swarm and Cat Swarm based optimized Convolutional Neural Networks (DSSCSCNN) achieved 98% precision and using clinical attribute autoencoder (AE) delivered accuracy of 97% outperforming traditional methods. This review highlights by integrating AI techniques significantly enhances the Multiple myeloma detection accuracy with minimal data resources making it highly practical for maintaining high performance.

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1 Introduction

Multiple myeloma (MM) is typified by an aberrant proliferation of plasma cells in the bone marrow, which can result in consequences such as bone lesions, anaemia, renal failure, and hypercalcemia. To increase patient survival and implement successful treatment strategies, early and precise MM identification is essential [1]. Globally, multiple myeloma affects around 185,000 individuals each year, making it the second most frequent haematological neoplasm. Monoclonal protein (M protein) is produced by plasma cells that have undergone malignant transformation, which is the cause of the illness [2]. These conventional techniques have shown themselves to be inadequate indicators of the depth of response attained with innovative medication combinations [3]. Integrating AI into medical system enables to utilize a clinical features for imaging the modalities to support the healthcare professionals for making to precise an efficient decisions to reduce the human error by improving the overall patient outcomes [4]. Traditionally diagnosis relies in a clinical features like serum protein level and imaging modalities including MRI, X-rays, and PET-CT scans [5].

Machine Learning (ML) models used to analyze the diverse clinical attributes and imaging characteristics to support risk stratification [6]. However it face a difficulties to handle a high dimensional and imbalanced datasets with limited adaptability to unseen variations in patient data. Deep learning (DL) is an advanced extension of AI to enhance the diagnostic accuracy by automatically learning the hierarchical representation from complex medical data [7]. It has an ability to process the complex imaging structures makes it highly suitable for medical image interpretation. It has a need for large annotated datasets of interpretability concerns to over fit the training data is insufficient. In the image processing techniques AI assisted diagnostic pipeline [8]. It includes a noise reduction, intensity normalization and segmentation of regions to enhance the quality of the diagnostic value of the imaging data. It accurately delineated analysis for improving the downstream classification and prediction performance [9].

In multiple myeloma image analysis AI methods to promise for detecting subtle skeletal lesions by characterizing bone marrow involvement to integrate a clinical indicators of precise diagnosis. Advance models combines to strength the different approaches for enhancing the accuracy and robustness [10]. Hybrid and ensemble strategies used in a complementary mechanisms for reducing the uncertainty and improve predictive reliability to address the variability across patient populations. Furthermore transfer learning techniques facilitate the knowledge reuse from the pretrained models in a large scale datasets it significantly reduce the data requirements for accelerating model development of myeloma specific imaging tasks [11]. Pretrained models often originate the image datasets it leading to domain a mismatch the suboptimal feature representation for medical images [12]. Overfitting can occur a medical datasets are utilized during fine tuning for reducing generalization to a new patient populations. The feature hierarchies learned from unrelated domains may fail to capture a subtle pathological patterns in unique to myeloma [13]. It can also hinder a real time clinical application and propagate a biases presented in a dataset for introducing a fairness concerns in a clinical decision making. The literature reveals that researches are increasingly leveraging the AI technique for enhancing the diagnostic accuracy. These methods enables the extraction of the complex patterns from a multimodal data offering a deeper insights into disease prediction. As a result AI driven approaches becoming an integral for improving healthcare outcomes and personalized treatment strategies.

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The review article is organized into a several sections of clarity and coherence. Section 2 focuses on early multiple myeloma disease detection and the imaging modalities are utilized for accurate diagnosis. Section 3 presents the results provided a detailed discussion of the findings. Section 4 highlights the key suggestions derived from the analysis. The study is finally concluded in section 5, which also provides an outline of possible future research areas.

Summary of literature reviewed: This work related to multiple myeloma prediction analyzed 42 relevant research publications between 2020 and 2025 utilizing popular academic resources such as IEEE Xplore, Elsevier, Springer, Nature, MDPI and Wiley Online Library. These studies collectively demonstrate the advancements in Multiple myeloma disease detection achieved by this strategy.

2 Importance of Early Detection and Imaging Modalities

Early detection of Multiple myeloma is crucial to improve the patient outcomes it allows the timely initiation of therapy before the severe organ damage occurs. By detecting the disease at the initial stage it helps to prevent the complications like bone fractures, renal dysfunction and anaemia it significantly impact the quality of life. Imaging modalities plays a central role for identifying bone lesions a hallmark feature of the multiple myeloma and monitoring disease progression. Conventional radiography has been widely utilized but it has a low sensitivity it often leads to a missed early skeletal involvement. MRI provides an excellent soft tissue contract for enabling detection of early marrow changes while the PET-CT offers a functional imaging for evaluating the metabolic activity of lesions. However these modalities has a certain difficulties it includes a high cost of variability in interpretation and dependency on radiologist expertise. It may occurs to diffuse an infiltration patterns below the detection thresholds and the time consuming nature of imaging it hinder the application in clinical settings.

2.1 Clinical Imaging Techniques For MM

Clinical imaging techniques in a diagnosing and monitoring the multiple myeloma often utilized for identifying a skeletal involvement through its sensitivity is limited for detecting an advanced lesions and offers a better visualization of cortical bone destruction for providing the detailed structural insights. It is highly effective for assessing a bone marrow for infiltration to detect the early disease stages and widely employed in a metabolic assessment by detecting an active disease sites. By increasingly recommended a skeletal evaluation by the treatment response monitoring making the multimodel imaging strategies for accurate diagnosis.

2.1.1 Radiological imaging and blood smear analysis

Radiological imaging refers to provides a non-invasive insights into a skeletal soft tissues for involving a microscopic examination of a stained blood film to access the shape, size and the count of blood cells. It is widely employed to diagnose a haematological disorder to monitor the overall blood health. Together these imaging enables an accurate disease

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diagnosis to combine the structural visualization with a cellular level analysis a clinical evaluation for effective treatment planning.

Jing Li et al [14] have developed an 18F-fuorodeoxyglucose positron emission tomography/computed tomography (18F-FDG PET-CT) for Bone marrow tracer uptake pattern in multiple myeloma of image interpretation and prognostic value. Clinical and imaging data showing a high tumour burden, poor progression free survival (PFS; 3- year-PFS 26.8%), and poor overall survival (OS; 3-year-OS 50.6%) were associated with diffuse/mixed patterns. An independent predictor of outcome was the BM uptake pat- tern, and a diffuse/mixed pattern was linked to worse overall survival (OS) (P=0.037, HR 7.16) and progression-free survival (PFS) (P=0.015, HR 7.77). In the validation set, the BM uptake pattern's prognostic value was also validated.

Frederic E. Lecouvet et al [15] have presented a Whole-Body Computed Tomography (WB-CT) for imaging of treatment response and minimal residual disease in multiple myeloma. It offers a current summary of the methods, their findings in progressive and responsive diseases, and their function and constraints in detecting minimum residual illness. It evaluates and tests these approaches for response assessment, identifies the limited similarities between the two approaches, and emphasises work in tandem with the most modern genetic tools for minimum residual illness detection. Regarding response assessment, preliminary work suggests that FDG-PET/CT is more specific and allows early detection of relevant residual abnormalities (86% Specifcity for PET, 43% for WB- MRI; 75% sensitivity for both).

Angelo Belotti et al [16] have demonstrated a Diffusion-weighted whole-body Magnetic Resonance Imaging (DW-MRI) for imaging response according criteria after autologous stem cell transplantation in patients with multiple myeloma. In comparison to patients with imaging residual disease (RAC≥2), patients with complete imaging response (RAC1) had superior post-ASCT PFS and OS: median PFS not reached (NR) versus 26.5 months, $p = 0.0047$, HR 0.28 (95% CI: 0.12–0.68).

Karla M. Treit et al [17] have suggested a Whole-Body Magnetic Resonance Imaging (WBMRI) for myeloma imaging and staging. On the other hand, WBMRI has been more sensitive in detecting patterns of diffuse and localized plasma cell infiltration in the bone marrow before osteolytic damage occurs. While functional, diffusion-weighted MRI (DWI-MRI) was a promising method for evaluating treatment response, it was advised for the evaluation of spinal and vertebral abnormalities.

2.1.2 Challenges in manual interpretation

Manual interpretation of diagnostic data in multiple myeloma presents the challenges due to the disease heterogeneous nature complexity of the associated imaging in clinical find- ings. Radiological examinations along with the laboratory reports requires a significant expertise for detecting the subtle skeletal lesions and marrow infiltration. Subsequently multiple myeloma frequently affects the multiple sites of the skeletal systems for increasing the burden on radiologistics to a large number of images meticulously in time consuming and prone to oversight. In manual assessment it may often struggle to integrate a diverse modalities like bone marrow aspirate results for protein electrophoresis and advanced imaging findings into a cohesive diagnostic images. The repetitive nature of image re- view is combined with the requirement of high precision to increase the susceptibility of human error. It has a inter observer variability remains the persistent concern as a diagnostic conclusions may often differ between specialists due to their interpretation of ambiguous features. These challenges underscore the need for reliable of automated solutions of capable of synthesizing the multi model data to enhance the precision of reducing the interpretation time by supporting the clinicians in delivering consistent and accurate myeloma diagnoses.

2.2 AI Techniques Applied to Multiple Myeloma Disease Detection

AI techniques applied to a multiple myeloma disease detection leveraging a ML and DL algorithms for analyzing a complex clinical and imaging data for accurate diagnosis. These techniques process diverse the inputs like bone marrow biopsy images and laboratory parameters for identifying patterns of indicative of MM. ML methods utilize a feature based analysis for classifying and predict the progression, While DL approaches extracts hierarchical features from imaging modalities to enhance the detection. AI also supports a segmentation of skeletal lesions in characterization of bone marrow involvement and integration of the clinical indicators. Furthermore hybrid and ensemble model combines the strength of multiple algorithms for improving the robustness and reduce diagnostic uncertainty. It automating interpretation and enabling the early AI techniques it significantly aid a clinicians for delivering timely and personalized treatment of MM.

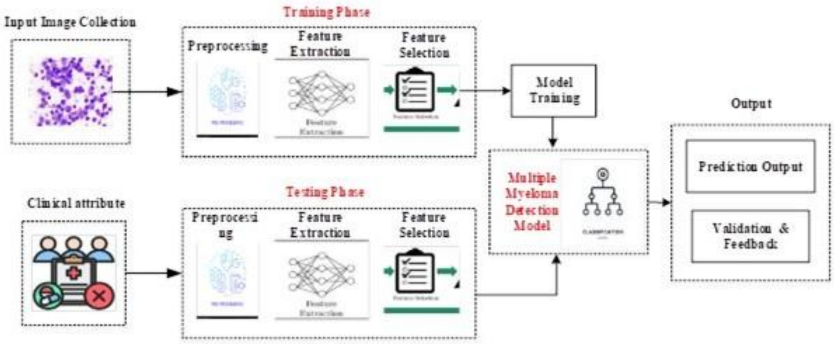

Figure 1: AI Based Framework for Multiple Myeloma Disease Detection.

The figure 1 illustrates a structured AI pipeline for detecting the Multiple Myeloma from microscopic images. Initially input images are collected and processed through preprocessing stage for enhancing the quality and remove artifacts. Key features are extracted and refined through Feature selection to retain only the most relevant features. In the training phase these features are utilized to train an efficient detection model. During the testing phase of clinical attribute data are applied to preprocess and the extracted features are passed to the trained model for prediction. Finally system generates the prediction outputs followed by validation and feedback to ensure accuracy and reliability in disease detection.

Figure 2 shows a conceptual framework for predicting multiple myeloma using artificial intelligence. The detection process uses both clinical data (blood tests, biomarkers) and imaging data (MRI and CT scans). These data are run through Artificial Intelligence (AI) methods to assist within a diagnostic setting. There are different types of AI methods: Machine Learning and Deep Learning methods. Moreover, Deep Learning methods often include additional improvements in the form of Transfer Learning and Ensemble Learning, which improve prediction performance through leveraging previously trained models and combining multiple predictive algorithms.

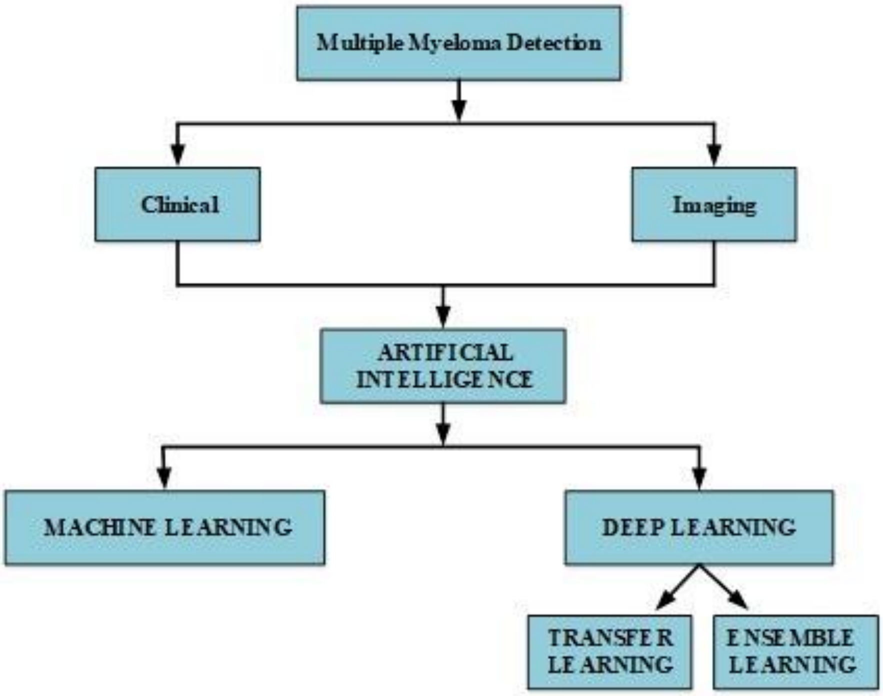

Figure 2: Clinical and Imaging based AI model for multiple myeloma prediction.

2.2.1 Clinical Attributes Based Multiple Myeloma Prediction

Clinical attribute based multiple myeloma predictions refers to the process of forecasting the progression of multiple myeloma using patient specific clinical factors. These attribute typically include laboratory results of demographic details and disease related parameters. By analyzing the factors of predictive models can identify patterns associated with the disease onset severity. It enhances the early diagnosis of risk stratification and treatment planning.

2.2.1.1. Clinical Attributes Based Classification

Data pre-processing approaches for multiple myeloma prediction involves preparing a raw clinical data for accurate analysis. It includes handling the missing value through imputation techniques for removing noise to improve the data quality and normalizing attributes to maintain uniform scales. These steps collectively enhance the reliability and performance of predictive algorithms. Feature selection and dimensionality reduction in multiple myeloma prediction refers to the technique utilized to identify the most relevant clinical attributes for reducing the redundant information. For Feature selection it focus on choosing a subset of significant variables that strongly influence the disease prediction. Machine learning (ML) approaches for multiple myeloma prediction it involves for utilizing an algorithm for analyzing a clinical attribute and identifying a patterns linked to a disease progression. It relays on handcrafted features and the statistical relationship to make a predictions. Deep learning (DL) approaches to utilize a neural network architecture for automatically to extract the complex of high dimensional features from data to improve the accuracy.

Phichayut Phinyo et al [18] have developed a Multiple Myeloma- Bone Metastasis with destructive bone lesions (MM-BM DDx) for the Validation of a Diagnostic Model to

Differentiate Multiple Myeloma from Bone Metastasis. The validation dataset comprised 3018 patients in total (586 with MM and 2432 with BM). The AUC for the predictions made by the MM-BM DDx model was 0.89 (95% CI, 0.87, 0.90).

Xing Xiong et al [19] have introduced a least absolute shrinkage and selection operator (LASSO) for feature selection employing Multiple Myeloma and Metastasis Subtypes of Lumbar Vertebra Lesions. ANN classifier using the T2WI images performed the best out of the ten classifiers (MCC = 0.605), with accuracy, sensitivity, and specificity of 0.815, 0.879, and 0.790 in the validation cohort, respectively.

Kwang Ho Park et al [20] have illustrated an Autoencoder (AE) for Hematopoietic Cancer Subtype Classification. Reconstruction loss and classification loss are the two forms of losses used to design a classification model for five key subtypes. A deep autoencoder was also used to extract pertinent features. The result shows 97.01% accuracy, 92.60% recall, 99.52% specificity, 93.54% F1-measure, 97.87% G-mean, and 95.46% index of balanced accuracy.

Daniela Schenone et al [21] have developed a Principle Component Analysis (PCA) for Reduction of Redundancy of Radiomics and Artificial Intelligence for Outcome Prediction in Multiple Myeloma Patients Undergoing Autologous Transplantation. An open-source toolkit that retrieved 109 radiomics characteristics was used to analyse focal lesions in 33 (64%) of the 51 transplanted patients in this retrospective investigation, which was approved by the institutional review board. PCA and correlation were used to reduce redundancy. Three of the seventeen imaging descriptors passed the null hypothesis, ac- cording to the Mann-Whitney U-test.

Ashwini K. Yenamandra et al [22] have demonstrated an Artificial Neural Network (ANN) for the Classification of Plasma Cell Myeloma Data through Diagnosis. Addition- ally, a classification model was created utilising Tableau's interactive data visualizations and support vector machines (SVM) in R Studio's method. The accuracy level of the SVM of plasma cells vs TP53 was 95%.

Wei Yan et al [23] have suggested a Gradient Boosting Decision Tree (GBDT) for Employment of Artificial Intelligence Based on Routine Laboratory Results for the Early Diagnosis of Multiple Myeloma. For the myeloma group, GBDT had the greatest F1 score (0.915), accuracy (92.9%), and recall (90.0%). According to the maximised area under the ROC (AUROC) calculation, GBDT performed better than SVM, DNN, and RF (AUC: 0.975; 95% CI: 0.963–0.986).

Ting Peng et al [24] have presented an XGBoost model for newly diagnosed in infection prediction of multiple myeloma patients. It examined 564 newly diagnosed multiple myeloma (NDMM) patients from two sizable tertiary institutions; 395 of these patients made up the training set, while 169 made up the validation set. Lastly, two examples were evaluated and the model's applicability was illustrated using the SHAP package. In addition to outperforming the other models in terms of prediction (AUROC: 0.8664).

Monika Vlachová et al [25] have suggested a Partial Least Squares-Discriminant Anal- ysis (PLS-DA) for Liquid biopsy of peripheral blood using mass spectrometry detects pri- mary extramedullary disease in multiple myeloma patients. This investigation produced a technique with high sensitivity (86.4%), accuracy (78.4%), and specificity (72.4%) for predicting main EMD. This methodology is easy to use and less intrusive, which allows for quick detection of main EMD and may be useful in clinical settings.

Table 1: Study of different clinical attribute based classification for multiple myeloma prediction.

Research	**Performance metrics**	**Limitations**
Phichayut Phinyo [18]	AUC = 89%	Missing value may introduce an artificial patterns leading to a biased predictions it distort a clinical data ranges for impacting interpretability of biomarkers.
Xing Xiong [19]	Accuracy = 81.5%, Sensitivity = 87.9%, Specificity = 79%	It may often struggle with the dataset contains misleading noisy attributes if noise is perceived as relevant during the feature ranking it may degrade the model performance.
Kwang Ho Park [20]	Recall = 92.60% Accuracy = 97.01% F1-measure = 93.54% Specificity = 99.52%	Some transformations may automate the feature extraction processes produce the abstract representations does not directly to the clinical variables.
Daniela Schenone [21]	Accuracy = 96.45%, Sensitivity = 96.30%, Specificity = 96.60%, Precision = 96.20%, F1 Score = 96.25%	When multiple features are highly correlated it focus solely on variance rather that the class separation for resulting in features to minimize the spread to en- hance the predictive performance for dis- ease classification.
Ashwini K. Yenamandra [22]	Accuracy = 95%, Precision = 97%, Recall = 76%, F1 Score = 83%	Multiple myeloma datasets may often suffer from skewed distribution of disease stages it cause the model to favor majority class for resulting poor performance of minority cases.
Wei Yan [23]	Recall = 90.0%, F1 Score = 91.5%, Precision = 92.9%, AUC = 97.5%	The high dimensional data combined with a small sample sizes may cause models to memorize patterns rather than generalizing for leading to inaccurate predictions data.
Ting Peng [24]	AUROC = 86.64%, Accuracy = 68.64%	ML models acts as a black box making it difficult for clinicians to understand the reasoning behind predictions it reduces the trust in clinical decision making.
Monika Vlachová [25]	Accuracy = 78.4%, Specificity = 72.4%, Sensitivity = 86.4%	ML model trained the data from a specific population settings it may not perform a different demographics for limiting their widespread applicability.

Table 1 presents a comparative study of different research works focused on clinical attribute based classification for multiple myeloma prediction. Each method is evaluated using metrics such as AUC, accuracy, sensitivity, specificity and recall highlighting their strengths and limitation. Common difficulties include for handling missing values of noisy attributes and potential abstraction due to automated feature transformation.

2.2.2 Imaging Modality in Multiple Myeloma

Imaging modality in multiple myeloma refers to a use of an advanced imaging techniques for detecting and monitor the soft tissue involvement and disease progression. The modalities include the X-ray skeletal surveys of MRI for assessing bone marrow involvement for detailed bone structure visualization for detecting active lesions and metabolic activity. The response of accurate imaging it ensures the early detection aiding a better prognosis and disease management.

2.2.2.1. Relevant Image Processing Techniques

Relevant image processing techniques for multiple myeloma focus for enhancing the image quality and extract the meaningful features of accurate diagnosis. It includes a noise reduction and normalization for improving the clarity and contrast enhancement for highlighting the bone lesions. Then the segmentation methods isolate the regions of interest regions like bone marrow.

Thomas Van Den Berghe et al. [26] have developed a spinal dynamic contrast-enhanced Magnetic resonance imaging (DCE-MRI) for Predicting cytogenetic risk in multiple myeloma. Standard and intermediate/high cytogenetic risk groupings were used to stratify the pa- tients. The top-performing model achieved a precision-recall-area-under-the-curve of 0.79 and a ROC-area-under-the-curve of 0.80.

Jinzhou Wang et al. [27] have demonstrated a Faster Region Convolutional Neural Network (RCNN) model for CT imaging in diagnosing myeloma and its prognosis. The enhanced U-Net model showed good segmentation results, and the classification accuracy rate reached 99%. To sum up, deep learning is recommended for myeloma CT image segmentation and classification, which can improve detection accuracy.

Fabian Bauer et al. [28] have presented a nnU-Net algorithm for advanced automated model for robust bone marrow segmentation in whole-body MRI. The cohort included imaging data from eight distinct centres using several vendors and protocols, with variable field strengths. The individual BMS's mean dice scores were 0.89 ± 0.13 for test set I and 0.88 ± 0.11 for test set II. These scores were considerably higher than those of a previous basic model ($p < 0.05$). In test set I, the dice scores for the BMS of the individual bones varied from 0.77 to 0.96, whereas in test set II, they ranged from 0.81 to 0.95.

Djennifer K. Madzia-Madzou et al. [29] have illustrated a Multiple Myeloma Anatomical Coherence Inspection (MM-ACE) for automated vertebrae identification and segmentation. The train cohort was used to develop an improved segmentation pipeline. Vertebral shape analysis employing topology was used to evaluate the segmentation quality. The results show a 95.8% identification rate and an 86.7% success rate.

Sumit Kumar Das et al. [30] have introduced a Mask-Recurrent Convolutional Neural Network (Mask-RCNN) for segmentation and classification of white blood cell cancer. To diagnose myeloma cells, pathologists have to be very selective. The Mask-RCNN model yields a mean average precision (mAP) of 93%, indicating the experimental outcome models are trained rather effectively.

Table 2 presents a comparative analysis of relevant image processing techniques used in diagnosing multiple myeloma. It outlines the performance metrics such as AUC, accuracy achieved by different researches for highlighting limitation includes reduced clarity of tiny lesions and artifacts for affecting segmentation. These drawbacks emphasize the challenges for achieving precise and reliable diagnosis in early stage multiple myeloma.

Table 2: Analysis of various Relevant Image Processing Techniques.

Research	Performance metrics	Limitations
Thomas Van Den Berghe [26]	ROC-AUC: 80% PR-AUC: 79%	To improve the image clarity for removing the random variations it may often blur the small clinically significant structures of tiny lesions it reduce the diagnostic accuracy especially for detecting their early stage multiple myeloma.
Jinzhou Wang [27]	Accuracy-99%	Lesions in multiple myeloma it often exhibit the subtle intensity may struggle in these conditions for leading to an inaccurate delineation of the affected regions and affects the quantitative measurements of lesion size.
Fabian Bauer [28]	BMS=89%	Medical images may often suffer from an artifacts it does not always effective and the residual artifacts may degrade a segmenta- tion accuracy for leading to a positive predictions.
Djennifer K. Madzia-Madzou [29]	Success rate =86.7% Identification rate= 95.8% vertebral match rate=97.0%	Segmentation methods requires an expect intervention for selecting the points of the validating boundaries in automated approaches and the significant time to make the large scale analysis impractical.
Sumit Kumar Das [30]	mAP =93%	Segmentation model face the difficulties for defining the boundaries through a single lesion with the multiple lesions are merged then both errors compromise the diagnostic interpretation to affect the subsequent predictive modeling.

2.2.2.2. ML & Deep Learning In Myeloma Image Analysis

Machine Learning (ML) aims to develop algorithms that help to detect patterns and clas- sify imaging data from images based on features they extracted to facilitate reforming the features back into normal imaging data to vision class models to arrive at automated diagnose, rather than a human. Machine Learning starts off using a lot of handcrafted features from statistics for prediction. Deep Learning models usually provide more accu- rate performance compared to machine made statistic models. Additionally, they are able to encompass many variations in medical images, work without extraction and feature engineering, and create features that may even be relevant to affect diagnosis.

Shiv Gehlot et al [31] have introduced a Projection loss network + Sample Discarding+ Coupling classifier (PRLCE-Net+SD+CC) for projection loss in unison with label noise handling for multiple Myeloma cancer diagnosis. To make use of a sizable dataset including 74996 images from 72 patients (including 40441 test cell images and 34555 training cell images). The architecture has best comparable performance with a balanced accuracy of 94.17% on categorization of healthy cells from cancerous cells.

Markus Wennmann et al [32] have demonstrated a nnU-Net model for the automatic identification of focal bone marrow lesions (FL) using MRI in the pelvic bone marrow. This retrospective feasibility study included 444 patients with monoclonal plasma cell disorders. Lastly, z-score normalisation was used to standardise voxel intensities. Per- formance on the external multicentre test set, which had outstanding imaging quality and a mAP of 0.45/0.41, F1-Score of 0.50/0.53, sensitivity of 0.44/0.43, and a PPV of 0.60/0.71, was almost identical to that of the internal test set.

2.2.2.3. Hybrid And Ensemble Models For Improved Diagnostic Accuracy

Hybrid and ensemble models for multiple myeloma aims to enhance the diagnostic accu- racy for combining the strength of the multiple algorithms. Then hybrid models integrate a different techniques like deep learning and traditional machine learning for leveraging a spatial and temporal features. Next the ensemble models aggregate the predictions from the multiple classifiers through methods like bagging, boosting or stacking for minimize bias and variance. It reduces the error associated with an individual models to improve the generalization of the complex medical data. For utilizing diverse feature represen- tation and decision strategies to provide a reliable results to achieve a high diagnostic prediction in multiple myeloma detection.

Satvik Tripathi et al [33] have suggested a Convolution and Attention Network model (CoAtNet) for Expert level classification of bone marrow cytology morphology in haema- tological malignancy. Two baseline models, ResNext50 and EfficientNetV2, were com- pared with the CoAtNet, a hybrid model that combines Convolutional Neural Networks and transformer models utilised in the pipeline. The experimental result demonstrates 98% accuracy, 99% precision, and 98% recall.

Shivani Joshi et al [34] have demonstrated a Hybrid Disruption-based Salp-Swarm and Cat Swarm based optimized Convolutional Neural Networks (DSSCSCNNs) method for peripheral blood cell image recognition. The authors create a binary coding methodology in the DSSCSCNN method that transforms parameter tuning issues into optimisation issues. The recommended method has demonstrated 100% success in the WBC determination. Additionally, it has 99% total categorization accuracy.

Aimin Li et al [35] have developed a hybrid deep learning model EfficientNet with Residual Blocks and Depthwise Separable Dilated Convolutions (EfficientNet-resDDSC) for Inferring the Gene Causality of Single-Cell Data. The model includes residual blocks and dilated convolutions, and it retains the fundamental architecture of EfficientNet- B0. The addition of residual blocks improves the model's capacity to extract low-level characteristics at the primary stage. The results demonstrate that the proposed method has 52.9% accuracy, 50.9% recall, and 50.8% F1 Score.

Jonathan Tarquino et al [36] have presented a Hybrid Region-Attention Embedding and deep learning networks Xception (RAE+Xception) for improving the bone marrow cell model transparency. With an f1-score of 0.82, precision of 82%, accuracy of 83%, and recall of 82%, this assessment method shows that the new technique performs better than previously reported approaches in an analogous validation set.

Neha Srivastava and Sunil Kumar Singh [37] have introduced an Ensemble Learn- ing Gaussian Naive Bayes (GBN), Decision Tree (DT) and Extreme Gradient Boost- ing (XGBoost) for Effectively Classifying the White Blood Cancerous of acute lymphoid leukaemia and Multiple myeloma microscopic images. The work's dataset includes microscopic images of multiple myeloma and B-lineage acute lymphoid leukaemia. Accuracy of 96.18%, precision of 96.66%, recall of 96%, specificity of 96.66%, and F1-Score of 95.95% are used as performance indicators to assess the models' effectiveness.

2.2.2.4. Transfer Learning Model for Mm Imaging

Large-scale datasets for improving the diagnostic performance of medical images were created by transfer learning for multiple myeloma imaging. It leverages the learned featured for improving the accuracy to identify the subtle disease patterns. Transfer learning accelerates to improve the generalization in limited data scenarios.

Rabia Asghar et al [38] have presented a transfer learning with a series of pre-trained Convolutional Neural Network (CNN) models for Automatic classification of 10 blood cell subtypes of bone marrow in myeloma. All 10 blood cell types may be automatically classified using a CNN-based architecture that was based on these pre-trained designs. Using blood cell images from the PBC, Kaggle, and LISC datasets, the created transfer learning CNN model was evaluated. 99.91 %, 99.68 %, and 98.79 % accuracy were attained in these three datasets, respectively.

Khaled Tarmissi et al [39] have presented a Multimodal Transfer Learning with Snake Optimization on Bone Marrow Cell Classification (MTLSO-BMCC) from biomedical histopathological images. The MTLSO-BMCC methodology's experimental validation showed a higher accuracy value of 98.60% than previous methods.

Muhateer Muhammad et al [40] have illustrated a Transfer Learning with EfficientNet-B5 for Bone marrow Tumor Detection in X-ray Images. Bone tumors present critical diagnostic challenges, where delayed identification severely impacts patient outcomes. Leveraging transfer learning, fine-tuned EfficientNet-B5 on a clinical dataset of 170,000 annotated X-ray images 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.

P. G. Sreelekshmi et al [41] have illustrated a Transfer Learning and Support Vector Machine (TL-SVM) for acute myeloid Leukemia. The developed model uses transfer leaning approach with VGG-19, and ResNet-50. The input images are pre-processed by weighted distribution and gamma correction techniques; from this the edges are detected by the sobel edge detector. The structural features are extracted by the deep neural networks and acquired as feature sets. Then compared to the results produced by the existing deep neural networks, the developed approach produces the most precise and effective outcomes. This model yields the accuracy rate of 99.08% and 99.02% for the classification of Leukemia.

3 RESULT AND DISCUSSION

To evaluate the performance of the various prediction models, a multiple myeloma detection model for analytics is created. Using an Intel Core i7 CPU, an NVIDIA GeForce RTX 3070 GPU, and 64GB of RAM, detection analysis is carried out on a Python 3.8 platform. After preprocessing image being provided to improve the quality of pertinent sections are identified by segmentation. Then the features are extracted and classified utilizing an advanced deep learning models to achieve the multiple myeloma prediction as the final output.

Clinical attribute Dataset 1: The Multiple Myeloma dataset (MM-dataset) is a brand-new multi-class database that contains 59 characteristics for 203 patient records that have been divided into nine stages of MM malignancy by haematology experts [42]. It is released to the public so that comparisons with other research projects may be made. One kind of blood cancer that affects bone marrow's plasma cells is called multiple myeloma (MM). Early diagnosis is challenging and requires a number of tests and medical examinations; as a result, the procedure is drawn out and may demoralise individuals. In order to identify clinical and paraclinical variables for the diagnosis of MM, a new dataset containing the outcomes of several MM diagnosis examinations should be provided.

Imaging Dataset 2: Two distinct subsets of a dataset collection were used to create the dataset for the created study [43]. The dataset's first section has 90 total photos of individuals with B-Lineage Acute Lymphoblastic Leukaemia, or B ALL. To identify the kind of cancer cell, the suggested CNN model is trained using the combination form.

3.1 Comparison Analysis of Clinical Attributes Based Multiple Myeloma Prediction

During each stage of the workflow, four methodologies are assessed by Clinical attribute classification techniques to improve the predicted accuracy. While it involves multiple myeloma prediction, it integrates to improve diagnostic performance.

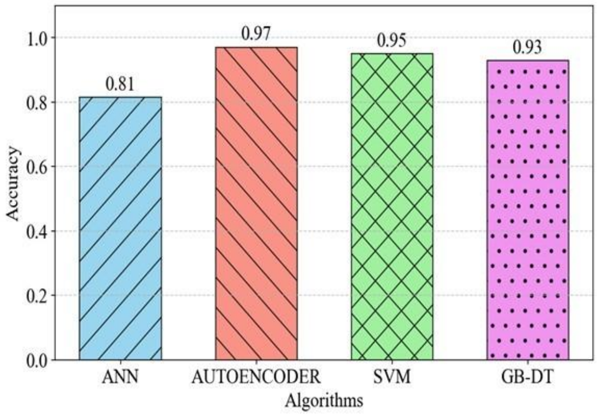

Figure 3: Accuracy evaluation for various algorithm.

Figure 3: Accuracy evaluation for various algorithm. Figure 3 compares the accuracy of four different methods for myeloma detection: Artificial Neural Networks (ANN), Autoencoder (AE), Support-Vector Machine (SVM) and Gradient Boosting Decision Tree (GBDT). The value obtained for ANN, AE, SVM and GBDT are 81%, 97%, 95% and 93% respectively. From the graph indicates the AE attained the higher accuracy than other models. The system analyze a large volume of data it effectively reduce the workload to accelerate a clinical decision making.

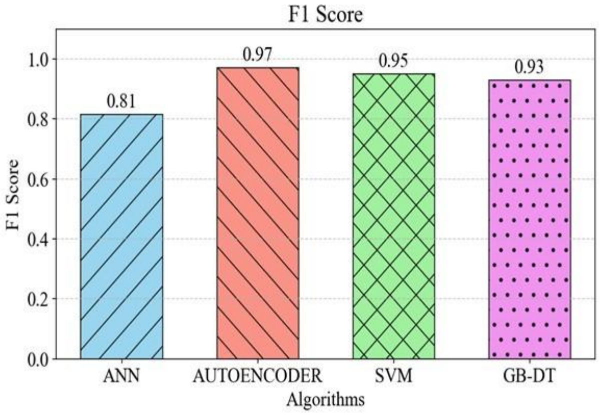

Figure 4: Comparison of F1 Score of different algorithm.

In Figure 4, the F1 Score of four different myeloma detection methods is compared. The results from several models, such as ANN, AE, SVM and GBDT were 81%, 97%, 95%, and 93%, respectively. The graph compared to other models AE attained a higher F1 Score value. It can combine the imaging data with the other clinical information it provides a holistic view for supporting the personalized care.

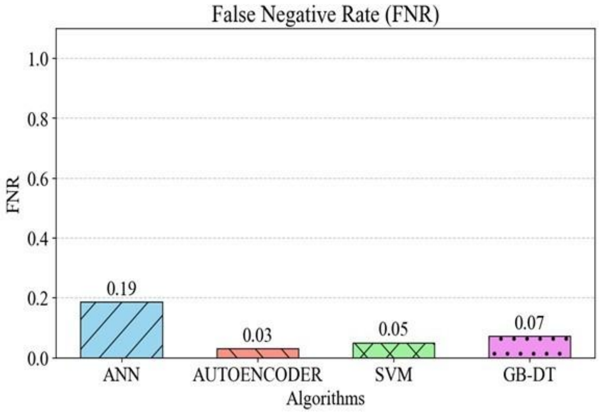

Figure 5: FNR analysis through multiple algorithms.

Figure 5 shows the FNR of 4 different myeloma detection techniques are ANN, AE, SVM and GBDT. The ANN, AE, SVM and GBDT had results of 0.19%, 0.03%, 0.05%, and 0.07%, respectively. Based on the results shown in the graph it achieves an AE score lower than the other models. It can automatically identify and extract an essential features from the complex data for eliminating the manual interpretation to ensure the disease markers are overlooked.

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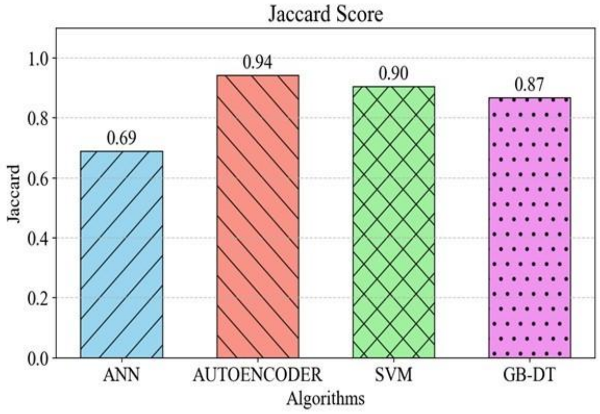

Figure 6: Evaluation of Jaccard using various techniques.

Figure 6: Evaluation of Jaccard using various techniques. The Jaccard of four separate detection methods is presented in Figure 6. Different models, ANN, AE, SVM and GBDT reported values of 69%, 94%, 90%, and 87% respectively. The figure shows that AE attained a higher specificity value than the other models. It may significantly offers a highly precise evaluations for reducing the variability and minimizing the risk of the misdiagnosis it may appropriate the treatment decisions to handle to large volume data.

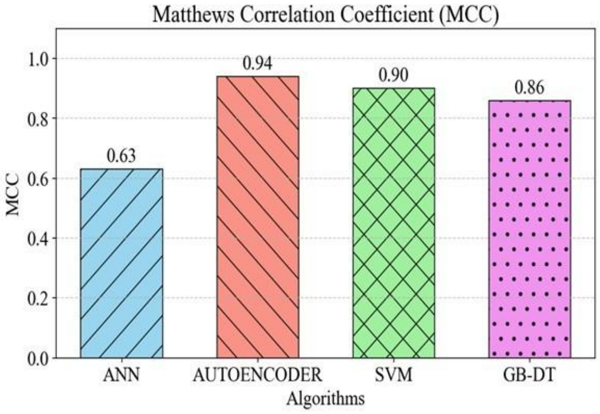

Figure 7: MCC evaluation for different techniques.

Figure 7 compares the MCC of four different methods for myeloma detection: ANN, AE, SVM and GBDT. The value obtained for various model such as ANN, AE, SVM and GBDT are 63%, 94%, 90% and 86% respectively. From the graph indicates the AE attained the higher MCC than other models. It accurately detect the disease affected regions for enabling the precise measurement of progression tracking to facilitate the prediction it significantly reducing the radiologist workload.

3.2 Performance Evaluation for Imaging Modality in Multiple Myeloma

Four techniques are evaluated through the each phase of the work flow by leveraging the image modality classification methods to enhance the predictive accuracy. It integrates to enhance the improved diagnostic performance for multiple myeloma prediction.

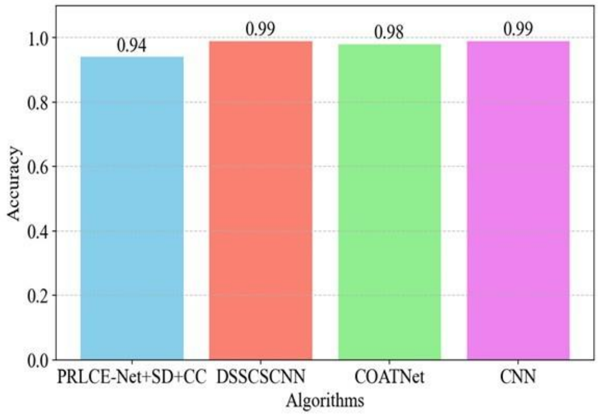

Figure 8: Accuracy Analysis of Various Imaging modality Techniques

Figure 8 compares the accuracy of four different methods for myeloma detection: Convolutional Neural Networks (CNN), Disruption-based Salp-Swarm and Cat Swarm based optimized Convolutional Neural Networks (DSSCSCNN), Convolution and Atten- tion Network model (CoAtNet), Projection loss network + Sample Discarding+ Coupling classifier. The value obtained for CNN, DSSCSCNN, CoAtNet, PRLCE-Net+SD+CC are 99%, 99%, 98% and 94% respectively. From the graph indicates the DSSCSCNN and CNN attained the higher accuracy than other models. The DSSCSCNN systems can help to reduce false positives, thereby making detection monitoring more effective.

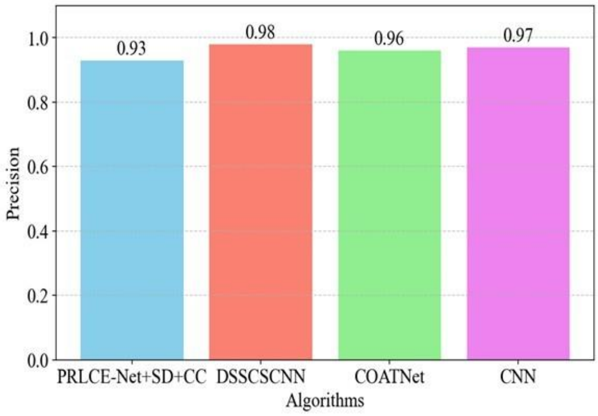

Figure 9: Precision comparison of various imaging modality techniques.

The Precision of four distinct myeloma detection techniques is contrasted in Figure 9. Different models, including CNN, CoAtNet, DSSCSCNN, PRLCE-Net+SD+CC, yielded values of 97%, 96%, 98%, and 93%, respectively. According to the graph, the DSSC-SCNN achieved a higher precision value than the other models. This DSSCSCNN model automatically identify the important patterns to extract the imaging data without the need of manual selection.

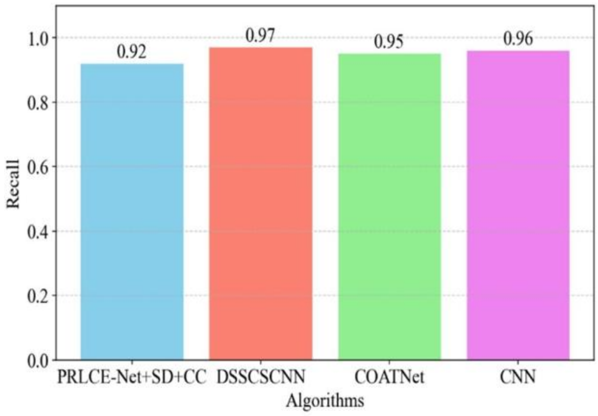

Figure 10: Comparative evaluation of recall for various imaging modality techniques.

In Figure 10, the recall of four different myeloma detection methods is compared. The results from several models, such as CNN, CoAtNet, DSSCSCNN, PRLCE-Net+SD+CC, were 96%, 95%, 97%, and 92%, respectively. The graph indicates that compared to the other models, the DSSCSCNN attained a higher Recall value. It significantly improve the ability of the affected tissues for accurate diagnosis to reduce the chances of misin- terpretation.

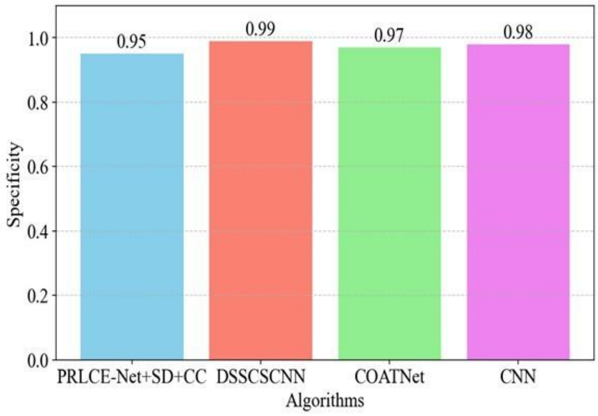

Figure 11: Analysis of specificity for various imaging modality techniques

. A comparison of the specificity of four different myeloma detection methods is shown in Figure 11. Results from several models, such as CNN, CoAtNet, DSSCSCNN, PRLCE- Net+SD+CC were 98%, 97%, 99%, and 95%, respectively. According to the graph, the DSSCSCNN achieved a highest specificity value than the other models. This process has a vast amount of data that contains the multiple layer of information to maintain the consistent through diverse datasets.

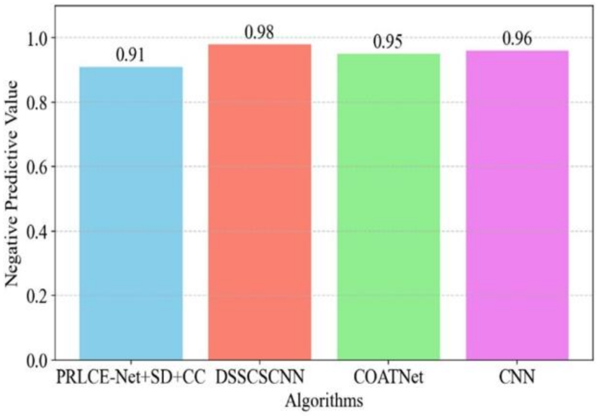

Figure 12: NPV analysis of various Imaging modality techniques.

Figure 12 compares and displays the NPV of four different myeloma detection technology types. Different models, CNN, CoAtNet, DSSCSCNN, PRLCE-Net+SD+CC had values of 96%, 95%, 98%, and 91%, respectively. The DSSCSCNN had a higher NPV value than the other models. It can precisely identify the delineate areas affected by the disease for measuring to evaluate treatment response more effectively.

4 SUGGESTION

Applying AI approaches to the prediction of multiple myeloma illness gives a considerable improvement in diagnostic accuracy and facilitates early management. High-dimensional imaging and clinical data can be processed to find subtle patterns that human experts might find difficult to spot. It can automate difficult procedures, minimising diagnostic delays and improving decision-making consistency. Furthermore, AI-powered frameworks enable the integration of multimodal data sources with clinical information, resulting in more precise and personalised assessments. It focusses on assessing AI-based techniques for enhancing diagnostic performance in multiple myeloma while addressing challenges such as imaging data variability and interpretability concerns. Despite their promising capabilities for incorporating huge annotated datasets for training, it might be difficult to assess the possible bias of model predictions owing to diverse data, reducing transparency in decision making. In order to assess their working performance efficacy, the present research looks at the numerous approaches used to diagnose multiple myeloma. Among the analysed approaches, DSSCSCNN and AE outperformed the other models for multiple myeloma. Furthermore, DSSCSCNN provides an extensive feature representation for distinguishing between normal and pathological tissues with greater accuracy. This AE model uses diverse data sources to improve myeloma prediction and facilitate the exact localisation of lesions. It can learn directly from raw data to increase scalability, and it allows for the integration of automated diagnostic processes to reduce diagnostic time. Overall, employing AI-based models addresses their fundamental issues in multiple myeloma identification, including the unpredictability of imaging modalities. To provide high sensitivity and specificity to enhance patient outcomes by enabling prompt intervention and personalized treatment regimens. As a result, the DSSCSCNN and AE stand out as transformational tools in current cancer diagnostics since they provide a promising direction in illness identification.

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5 CONCLUSION AND FUTURE DIRECTION

Multiple myeloma (MM) is a haematological cancer characterised by the bone marrow's unchecked clonal proliferation of plasma cells. Because of its complex pathophysiology and course, it poses a serious problem in oncology. In this review various AI based techniques for multiple myeloma detection analyzed in a detailed way. Then, data preprocessing, feature selection, machine learning, deep learning models then the hybrid systems and transfer learning frameworks are evaluated for the performance and applicability. Among these reviewed models DSSCSCNN demonstrate the highest diagnostic accuracy of 99%. The DSSCSCNN ability to automatically extract the hierarchical features from the raw image data it reduces the manual intervention and improve the scalability to enhance the precision by effectively handling the heterogeneous datasets. Using Clinical attribute data, AE achieves the performance of 97% of F1 Score and FNR of 3%. In future research prediction should be emphasize the development of Explainable AI (XAI) system to enhance the clinical trust and foster greater transparency in diagnostic deci- sions. By integrating federated learning it can ensure patient data privacy for enabling collaborative model training through multiple healthcare centers. Then lightweight predictive models is essential for supporting real time decision making in resource constrained clinical environments. It should explore a personalized modeling techniques to account for patient specific variations in disease progression.Then combining XAI with federated architectures support an interpretable privacy aware and scalable solutions for multiple myeloma diagnosis. Integration of multimodal data with an advanced optimization strategies may further enhance the diagnostic reliability making AI as a transformative tool for personalized treatment in multiple myeloma.

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Code availability. Not applicable.

Author contributions. The corresponding author claims the major contribution of the paper including formulation, analysis, and editing. The co-authors provided guidance to verify the analysis results and manuscript editing.

Compliance with ethical standards. This article is a completely original work of its authors; it has not been published before and will not be sent to other publications until the journal's editorial board decides not to accept it for publication.

Clinical Trial Number: Not applicable.

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