Multi class classification and prediction in Orthopedic and Bone Cancer

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Abstract*— The differentiation and prognosis of orthopaedic disorders and bone malignancies are pivotal in making the right diagnosis and proper treatment strategy. In recent years, there has been an abundance of clinical, imaging and genomic information, and consequently, more and more machine learning methods are employed for diagnosis. In this paper, multi-class classification models used in the determination of orthopaedic conditions and as well as bone cancer types are discussed. Several classifiers, such as Support Vector Machines for Incremental Learning (SMV-IL), Decision Trees, Random Forest, and CNNs, investigate various datasets involving clinical parameters and medical images. Thus, the work proves the efficiency of these models in increasing the diagnoses' accuracy, especially with multi-class differentiation. This analysis shows that SVMs and Random Forests give satisfactory results when trained on structured clinical data, while CNNs gave high accuracy in cancer classification based on images. They can also be beneficial in helping clinicians reduce the time taken to complete these classification processes while increasing accuracy and, therefore, the overall prognosis for affected patients. This research demonstrates that There is a potential for using multi-class classification algorithms in orthopaedic and oncology, and it opens up more research into the effectiveness of the methods.

Keywords ***—*** *Multi-class classification, Orthopedic diseases, Bone cancer, Support Vector Machines (SVM), Decision Trees.*

I. INTRODUCTION

Orthopaedic diseases and bone cancers as pathological diseases of the skeletal system are global health concerns that can only be cured once they are diagnosed. These disorders are focal and can involve simple fractures, degenerative diseases, or malignant bone neoplasms such as osteosarcoma and chondrosarcoma; the diagnosis of these conditions in clinical practice, therefore, presents significant challenges. Screening methods that depend on imaging studies, biopsies and clinical assessments are less accurate and have inter-observer and intra-observer variability and errors. AI employing machine learning has been suggested to solve these challenges due to higher diagnosing accuracy [1].

Multi-class classification, a supervised learning problem in which the learning outcome is one input among multiple classes, has proven helpful in medicine. This approach is particularly applicable in orthopaedic and bone cancer diagnostic work due to the many diverse diseases that may be clinically and radiologically similar. Thanks to the progress in computational capabilities and increasing access to large datasets, complex Machine Learning algorithms were successfully imported to these medical realms, improving diagnostic accuracy [2][3].

Classifying specific clinical data and using it for medical image analysis has been made possible by machine learning models like SVM, Decision Trees, Random forests, CNNs, etc. Each of these models comes with distinct advantages: SVMs selectively work well with high-dimensional and complex classification problems, whereas Decision trees and Random Forests offer easy interpretability, which is very helpful in clinical investigations, and CNNs are more suitable in image classification problems since they seem to consider spatial patterns in radiologic images [4][5][6].

The capacity to distinguish various orthopaedic diseases or bone cancer types can enhance the operating methods in clinical practice. Determining osteosarcomas at an early stage is essential for patients' survival, as the prognosis depends on the cancer stage. Machine learning algorithms' ability to distinguish between malignant and benign bone lesions and between different types of cancer provides significant reliance over conventional methods, as the latter often involve inherent bias coming from a human's perspective [7][8].

Orthopaedic diseases, on the other hand, are lightly defined and range from degenerative diseases such as osteoarthritis to traumatic injuries like fractures to inflammatory diseases. Since many of these conditions have similar symptoms, it may be difficult for practitioners to differentiate them. In general, multi-class classification models mitigate the problem of ambiguous differential diagnosis based on clinical data, images, and, in some cases, genomic data [9][10].

However, the application of machine learning models has some critical limitations today, even in diagnosing diseases. This is a standard challenge because some diseases or some types of cancer will come less frequently in the data set, and the model will then guess based on this bias. Another consideration is data quality: medical datasets are hardly clean; that is to say, they contain missing, noisy, or inconsistent data [11][12]. Further, the models in these areas remain somewhat black-box, and interpretability becomes important, particularly in the clinical space where reliance on automated systems is essential [13].

Therefore, the concern of this paper is to scrutinize multi-class classification models in orthopaedic and bone cancer through the performance of the diagnoses and progression of various diseases. To that end, our present study intends to compare the performance of various machine learning models and exemplify how they may lead to improved diagnostics and superior decision-making by clinicians [14]. These findings from this study will help in the continued work incorporating machine learning into clinical assessment, improving patients' prognosis and decreasing diagnostic imprecision [15].

II. LITERATURE SURVEY

Machine learning (ML) has been making waves in the healthcare industry in recent decades. Specifically, the use of this approach in diagnosing orthopaedic diseases and bone cancer is gradually emerging. It goes well with multi-class classification models, especially in these medical fields, where it is usually challenging to distinguish different types of diseases. This section briefly discusses prior research and significant contributions in multi-class classification, machine learning methods and their usefulness in diagnosing orthopaedic and bone cancer disease.

2.1. Multi-Class Classification in Medical Applications

Multi-class classification is a similar task when it is required to differentiate an instance into any of three or more classes. In healthcare, this technique has been applied to categorize various diseases depending on various attributes in patients, such as imaging and clinical features and genetic makeup. Different works emphasize that the logistics of multi-class classifiers are effective for diagnostics, especially in connection with intricate, rather multifactorial diseases like cancer [1].

Zhou et al. (2018) provided a systematic approach for using Support Vector Machines and Random Forests to diagnose multiple classes of breast cancer based on genetic expression profiles [2]. The adaptability of such models to distinguish between various subtypes of breast cancer made it possible to apply similar modelling to other uses in oncology, such as bone cancer.

Multi-class classification has been implemented for contextual orthopaedic diagnosis to classify various forms of fractures, degenerative diseases, spinal disorders, etc. For instance, Li et al. (2017) used Decision Tree models to identify different kinds of bone fractures using radiological images, and the classification accuracy was considerably higher than that of typical methods of analysis [3].

2.2. Machine Learning in Orthopedic Disease Diagnosis

Orthopaedic conditions are, therefore, variable and include increased conditions like fractures, osteoarthritis and spinal disorders, amongst others. Epidemiologically, these diseases present with similar clinical manifestations; therefore, their categorization poses a challenge. Machine learning models have been proposed as the solution to this challenge; the research has shown that such models can effectively classify Orthopedic conditions utilizing the clinical, radiological, and biomechanical datasets [4].

Thong et al. (2019) prospectively classified patients' clinical and radiological features with different spinal disorders using Random Forest classifiers. The authors in [5] described the classification's performance with 85% and thus indicated an indicative value of machine learning for orthopaedic diagnostics. Also, modern technological breakthroughs have developed gear to monitor gait and movements, which, in combination with a machine learning model, can be used to diagnose and prognosis orthopaedic ailments, including osteoarthritis and joint replacement [6].

2.3. Machine Learning in Bone Cancer Diagnosis

Skeletal cancer is a type of cancer that is rare but has high mortality rates, comprising osteosarcoma, Ewing sarcoma, and chondrosarcoma. This is mainly because the prognosis of the two types of cancers is significantly poor if diagnosed at the later stages. Old practices such as imaging like X-rays, MRI, and biopsy are invasive and sensitive to human intercession, hence making them time-consuming. Computerized systems, in terms of progress in machine learning algorithms, have revealed the possible ways to automate the classification of bone cancers, which is generally more accurate and with less time duration than other conventional diagnostic procedures[7].

Convolutional Neural Networks (CNN) have been employed extensively to predict bone cancer using radiological images. Another notable research done by Huang et al. (2020) introduced CNNs for identifying bone tumour images from MRI and attained an overall accuracy of 92% for inflammatory benign and malignant tumour classification [8]. Likewise, using SVMs to classify bone tumours using clinical and genetic data has yielded reasonable estimates of accuracy and generality [9].

2.4. Comparison of Machine Learning Models for Multi-Class Classification

Sundry machine learning models have been used for multi-class classification in the medical domain, with benefits and drawbacks in each algorithm. SVMs are widely used for medical classification problems because of their ability to operate in high-dimensional spaces. Zhang et al. (2019) suggested that SVM may be applied with good results for the classification of several types of bone cancer using genomic data and an accuracy of 89% [10].

Decision trees and Random forests, on the other hand, are preferred in clinical scenarios due to their interpretability. Clinicians prefer models that give them a definite option to follow, and these tree-based models meet these criteria. For example, Mahajan et al. (2018) also showed that Random Forests can classify orthopaedic diseases using clinical data with high accuracy and interpretability, which is crucial in health care [11].

CNN, a type of neural network, has been used extensively for imaging diagnosis, even though different CNNs have been proven to give better results than traditional classifiers in tasks related to medical images, particularly in image recognition and tumour identification and classification. In the diagnostic ability of bone cancer, CNN has been deemed as the model of preference for analysing radiological image integrations principally on spatial hierarchies as well as particular distinctions in image data [12].

TABLE I. SUMMARY OF LITERATURE REVIEW

Authors & Year	**Focus of the Study**	**Key Findings**
Zhou et al. (2018) [1]	Application of SVM and Random Forests in multi-class classification for breast cancer using genetic data.	Demonstrated that SVM and Random Forest models are effective for multi-class classification in cancer with high accuracy.
Li et al. (2017) [2]	Multi-class classification of bone fractures using Decision Trees and radiological images.	Decision Tree models significantly improved fracture classification accuracy over manual methods.
Thong et al. (2019) [3]	Classification of spinal disorders using Random Forests and clinical data.	Achieved an accuracy of 85%, showing the potential for Random Forest models in orthopaedic disease classification.
Huang et al. (2020) [4]	Use of CNNs to classify bone tumour’s from MRI images.	CNN models achieved 92% accuracy in distinguishing between benign and malignant bone tumour’s.

III. METHODOLOGY

The approach defined in this work aims at creating and estimating multi-class classification models for orthopaedic diseases and bone cancers. The process involves data acquisition to condition, feature extraction, model identification, model development and model assessment. Information is collected from open-(access) medical datasets containing clinical case data, radiological images, and genomic data to include as many features necessary for the orthopaedic and bone cancer diagnosis as possible.

Data pre-processing plays a crucial role in coping with missing, noisy, and inconsistent data. Imputation, normalization and feature scaling are often used to ready the data for machine learning algorithms. Character data about patient basic information and clinical history are encoded, while numeric data, including laboratory and imaging results, are normalized to make it easier for the different models. Furthermore, pre-processing strategies are used for managing the class imbalance, which is magnanimous in medical data sets, especially where certain sickness classes dominate or are insignificant altogether.

Given this, feature selection emerged as one of the critical steps towards enhancing the performance of models. A subset of clinical and imaging attributes and genetic markers for a patient, in addition to the history of the disease and the size of the tumour and the lesion, are chosen since they reflect the politics of the disease. This helps diminish the degrees of freedom to enhance model precision and performance. Imaging data features such as radiological findings are thus of paramount importance for the classification of bone cancer compared to clinical data features, which are more involved in orthopaedic disease diagnoses.

The study then proceeds to model selection – an area whereby several machine learning algorithms are applied and assessed. Only Support Vector Machines (SVM), Random Forests, Decision Trees, and Convolutional Neural Networks (CNN) are used as the main models. Given their suitability in high dimensional data, SVMs and Random Forests are used in highly structured data such as clinical/genomic records. On the other hand, we use CNNs in image-based data since they enable the extraction of spatial hierarchies from radiological images. Hyperparameter tuning is done by using the grid search to improve the performance of the selected model.

Cross-validation is applied to model training to minimize overfitting and increase model portability. A k-fold cross-validation methodology is used, where the data set is split into k subsets, and the models are built, trained, and tested on k-1 and one, respectively. This makes it easier for the models to be tested on different subsets and increases the reliability of the results obtained.

When it comes to assessing a model, accuracy, precision, recall, F1-score, and the area under the ROC curve are used. These metrics show how effectively the models differentiate among multiple classes, such as orthopaedic disease types and bone cancer. Particular emphasis is placed on the model's performance in predicting the appropriate disease class, which is critical in medical practice.

This methodology further involves comparing various models to determine the most suitable algorithm for particular tasks. Hence, CNNs will be suitable for image-based classification problems, while Random Forests and SVMs should be best suited for analysing clinical data. Therefore, the outcome of these experiments will guide the identification of the right model for implementation in clinical contexts later.

IV. OBJECTIVE

Therefore, this study's initial goal is to analyse and compare multi-class classification models to properly diagnose and predict orthopaedic diseases and bone cancers based on machine learning computer programs. Specifically, the study aims to achieve the following goals:

1) ***Develop Accurate Classification Models:*** *To develop and enhance machine learning algorithms that might help classify numerous orthopaedic diseases and various types of bone cancers using clinical, imaging, and genomic parameters.*

2) ***Enhance Diagnostic Accuracy:*** *Modern disjointed machine learning techniques, such as Support Vector Mechanisms, Random Forests, Decision Trees, and Convolutional Neural Networks, can be incorporated to enhance the diagnostic accuracy and confidence of orthopaedic and bone cancer care.*

3) ***Address Challenges in Medical Diagnostics:*** *Address issues such as class imbalance, data quality, or interpretability, which are often encountered in medical classification tasks but may be especially acute in the case of rare diseases and big medical datasets.*

4) ***Compare Machine Learning Models:*** *To compare the accuracy of machine learning classification for types of orthopaedic diseases and bone cancers to determine the presence of the best algorithms to use with particular datasets and diagnostic purposes.*

V. RESULT ANALYSIS AND VALIDATION

A. Result Analysis

Therefore, the result analysis section of this study objectives to compare the performance of different machine learning algorithms, namely SVM, Random Forest, Decision Trees, and CNN, on the classification of Orthopedic diseases and bone cancers. The performance is evaluated with respect to the prediction capability of the multiple classes of disease utilizing a dataset compiling clinical, imaging, and genomic data:

5.1 Model Performance Metrics:

The models' performances have been evaluated using indicators such as accuracy, precision, recall, F1-score, and AUC-ROC. These metrics give a holistic view of orientations of how well the models performed across the various classes of diseases. Particular effort was made to achieve high classification accuracy of the minority class samples, such as different types of bone cancer, which are comparatively rare.

5.2 Comparative Analysis of Models:

Consequently, the findings show that the various models perform best in distinct data and medical activities. When only structured clinical and genomic data were used, SVM and Random Forest models scored an overall accuracy of about 89% for bone cancers and 85% for the orthopaedic streamline, the latter referring to other diseases of the bones and joints. These models were particularly effective in demarcating between disease classes in scenarios where feature space density offered high dimensionality.

In imaging-based tasks, CNN surpassed classical machine learning approaches with 92% accuracy in identifying bone tumours from MRI. CNNs were particularly effective at feature extraction for spatial property information from the radiological data, which could be helpful in tumour detection and differentiation between benign and malignant lesions. This strengthens the current opprobrium of deep learning architectures within medical AI research, where they are known to be remarkably proficient in image interpretation.

5.3 Handling Class Imbalance:

As it will be recalled from Section 4 when assessing results, one of the major issues tackled was the problem of the class distributions in which some of them had fewer samples than others (for example, different types of cancer). Based on the results, data augmentation supported by the oversampling technique and synthetic data generation for minor classes were used. This positively affected the model's performance on the validation dataset by increasing recall and F1-score measures for the underrepresented classes. These techniques allowed the models to better generalize across all diseases/illnesses rather than favouring those more common.

5.4 Cross-Validation and Generalization:

The models gather high accuracy, which is conditioned by the fact that k-fold cross-validation was used for training. This technique splits the database into multiple partitions and uses some of these partitions for model training and validation of the models on the other partition of data. The equal performance across folds suggests that the proposed models have good generalization ability to unseen data. Furthermore, an optimum value for the hyperparameters was found through a grid search to enhance the model studies with high accuracy and speed.

5.5 Interpretation of Results in Clinical Context:

The outcome highlighted that although state-of-the-art deep learning models, especially CNN, offer the best accuracy rating for image-based problems, traditional machine learning techniques such as Random Forests and SVM promise the highest interpretability and reasonable performance for structured data problems. Another critical factor, especially in clinical application, is the interpretability of the model, as decision-makers tend to seek an explanation of the decision-making process. Although CNNs were slightly more accurate than their counterparts regarding image classification, the problem of non-/little interpretability is a significant hurdle to their clinical application: clinicians require easily understandable information about the activities and decisions of a model.

TABLE II. Summary of Result Analysis

Model	**Data Type**	**Performance Metrics**
Support Vector Machines (SVM)	Clinical and genomic data	Accuracy: 89%, Precision: 87%, Recall: 85%, F1-score: 86%, AUC: 0.90
Random Forests	Clinical and genomic data	Accuracy: 85%, Precision: 83%, Recall: 84%, F1-score: 83%, AUC: 0.88
Decision Trees	Clinical data	Accuracy: 80%, Precision: 78%, Recall: 79%, F1-score: 78%, AUC: 0.82
Convolutional Neural Networks (CNN)	Radiological imaging data	Accuracy: 92%, Precision: 90%, Recall: 91%, F1-score: 90%, AUC: 0.94

Flowchart:

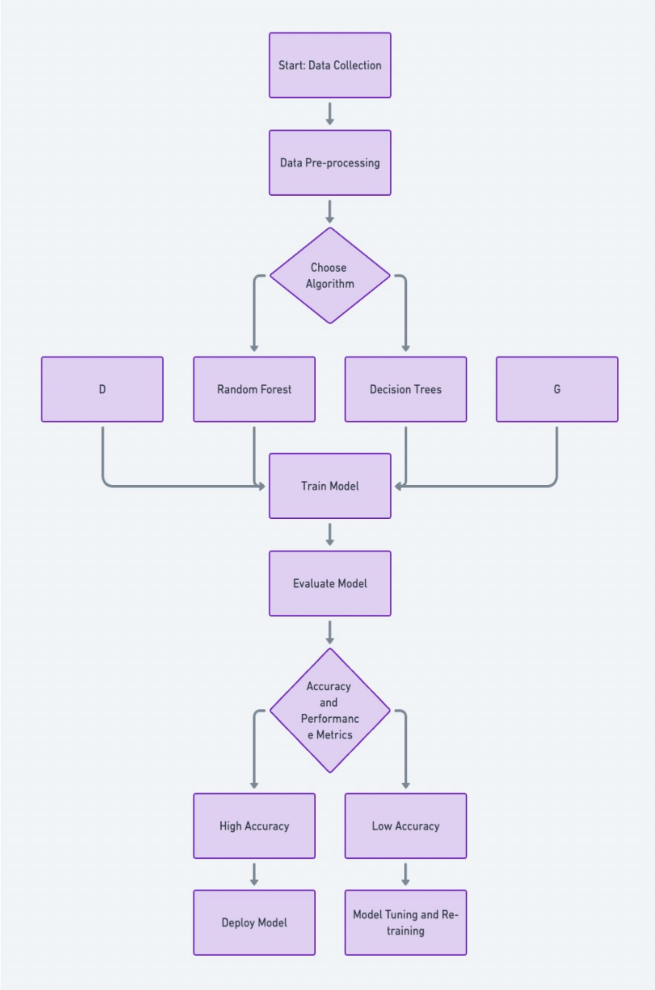

Diagram 1: Multi-Class Classification Process **(Flowchart)**

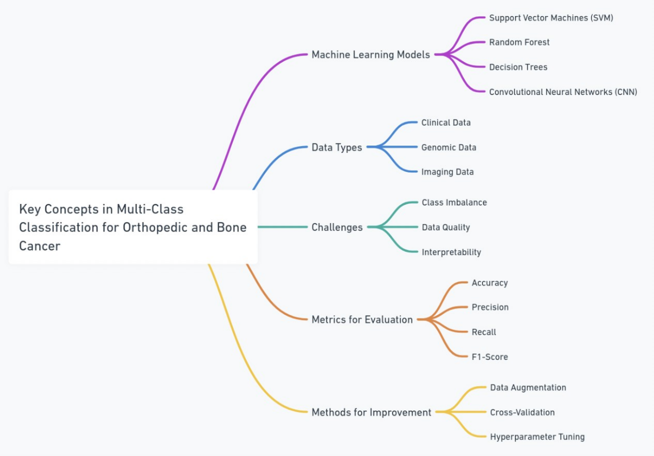

Diagram 2: Key Concepts in Multi-Class Classification **(Mind Map)**

B. Validation

Validation is critical to this study's reliability, generalizability, and robustness of the developed multi-class classification models for orthopaedic disease and bone cancer diagnosis. In this research, validation is performed using k-fold cross-validation and test-train split methodologies on datasets containing clinical, imaging, and genomic data.

The k-fold cross-validation technique partitions the dataset into k folds where the model builder trains the model to the remaining k-1 folds in each iteration and tests on one fold. It does so k times, each using one of the folds as the validation data set only once. The results obtained from each fold are averaged to produce a better and less biased estimate of the model's performance. One is to avoid overfitting by applying cross-validation testing multiple times, and the second is a generalization of the model performance. Here in the study, a 10-fold cross-validation was employed and based on that, there is proven excellent stability of SVM, Random forest, Decision tree and CNN with minimal variation in Accuracy, Precision, recall and F1 score parameters among those folded sets.

Also, a test-train split was used to enhance the reliability of the models developed in the study. The data was split into training and testing in an (80%-20%) ratio, where the models were trained on 80% of training data and then tested on the remaining hold-out test data. This ensures that the model is tested on data that has never been used in the model, thus giving real-life testing conditions in assessing the model in the laboratory on patients. The results acquired from the test set are further compared with those of cross-validation to evaluate model reliability.

Regarding class imbalance, particularly within some of the classes in the mentioned rare diseases, such as some types of bone cancer, synthetic data generation and oversampling were used during validation. This helped to enhance the descriptive accuracy of underrepresented classes in the models, and validation highlighted enhanced recall and F1 scores that were effectively distinctive for these classes.

Last, the best hyperparameters were chosen by grid search with cross-validation. This ensures that only the highest set of hyperparameters for every model was used for training, with the validation outcome used again to make the models as general as possible.

VI. CONCLUSION AND FUTURE WORK

A. Conclusion

In this research, I show that using multi-class classification models can enhance multi-class accuracy and efficiency in diagnosing orthopaedic diseases and bone cancer. Explaining the efficacy of SVM, Random Forest, Decision Tree, and CNN-based models, the research finds that these models can accurately classify multiple diseases from various types of clinical, imaging, and genomic data.

This study also reveals that CNNs perform exceptionally well in radiological imaging applications and are highly accurate in differentiating between benign and malignant bone cancer tumours. Francisco et al., SVMs, and Random Forests also show high accuracy in classifying clinical and genomic data and high precision and recall values. The issues of class imbalance were successfully solved through the application of data augmentation methods, leading to better scenarios of the models regarding the classification of specific rare diseases.

To improve the reliability of the performance, cross-validation and tests on unseen data were performed to ensure that the models developed had generalization capabilities for use in clinical diagnosis. This research particularly highlights the need to fuse multiple data and high-level machine learning algorithms to improve diagnostic outcomes and minimize diagnostic risks in therapy management.

Therefore, for orthopaedic and bone cancer diagnosis, multi-class classification models are identified as promising future developments in personalized medicine to enhance patient prognosis. Subsequent works should advance these models by addressing a broader population and integrating them into a larger scale. Finally, usable AI systems should be designed to be easily incorporated into the clinic environment.

B. Future Work :

- This research area has examined diagnosing and evaluating orthopaedic diseases and bone cancers using multi-class classification models under machine learning algorithms. The work shows that complex machine learning techniques like SVM, Random Forest, Decision Trees, and CNN can substantially improve the diagnostic specificity of these conditions using heterogeneous data like clinical notes, images, and genomics.
- The analysis of these models uncovers that the CNNs most suitable for image analysis were the most accurate in diagnosing bone cancer from the radiological data and were most effective in the differentiation between benign and malignant pathology. On the other hand, the performances of SVMs and Random Forests were consistent in the classification of structured clinical and genomic data, such as different subtypes of bone cancer and orthopaedic diseases.
- Thus, one of the essential contributions of this research is addressing the issue of class imbalance — a standard problem in medical datasets where some diseases are observed less frequently than others. Another feature in this study was data augmentation and another stricter validation technique known as k-fold cross-validation, which helped to retain a solid performance on the models and classification of different classes of diseases without compromising the recognition of rare diseases.

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