Classification of Osteoarthritis from Rheumatoid Arthritis based on Stacked Ensemble Machine Learning

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Abstract. There are two primary types of arthritis: osteoarthritis and rheumatoid arthritis, respectively. Pain and stiffness are symptoms of osteoarthritis when the cartilage and underlying bone deteriorate. Osteoarthritis seems to affect adults in their middle years more frequently. As an autoimmune disease, rheumatoid arthritis involves joint inflammation caused by an infection; our resistant system often assists in protecting our body from disease and infection. Using clinical data analysis, rheumatoid arthritis patients were predicted in this study. To identify rheumatic illness, clinical data were examined, and threshold values were periodically examined using the k-means approach for the RA factor, anti-CCP, SJC, and ESR factors. This data analysis suggested that rheumatoid disease might develop if either the RF or AC were positive. In this study, we used four criteria for rheumatic disease diagnosis to predict rheumatic disorders using machine learning.

Keywords: Machine Learning, Rheumatoid arthritis, Osteoarthritis, Autoimmune disease, deep learning

1 Introduction

In chronic rheumatoid arthritis, our own immune system targets healthy joint tissue, causing health issues with the heart, skin, nerves, and lungs. An inflammatory condition that affects more than just our joints. Rheumatoid arthritis-related inflammation can harm not just the affected joint but also surrounding tissues. Joint cartilage disintegration is the primary cause of arthritis in the majority of cases. Cartilage is a sturdy, supple connective tissue that protects joints and bones. Your bones' ends reduce friction and prevent them from slamming into one another, acting as the body's primary shock absorber.If the bone is cracked or ripped, which may cause friction in the joint, the rough bone surfaces may be visible. KOA is an enduring condition that will affect how well your knee functions, can be brought on by damaged cartilage. The

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bones and tendons that move in joints can do so without running the danger of getting hurt or irritated because synovium is present. For these reasons, there is a critical unmet need for an automated scoring algorithm that can effectively and reliably anticipate the narrowing and degradation of SvH values. First, radiological reports often list mild, moderate, or severe damage, which is very arbitrary, indicating that RA-related joint damage is not quantifiable in clinical practice. Patient symptoms and the degree of damage shown on radiographs appear to frequently conflict. There is no doubt that CNNs have demonstrated exceptional performance in resolving issues in the field of medical imaging when it comes to resolving problems.

2 Literature Survey

Numerous antibody systems have been discovered in forward-looking RA. They consist of antibodies against carbamylated (anti-CarP) and citrullinated (ACPA) proteins, both of which have been used as diagnostic indicators (Fig. 1). Synovial fluid (SF) and serum are the main locations of these auto-antibodies in RA patients [1]. (The classification is based on 2010 ACR/EULAR criteria[2]. Joint involvement, provocative indicators such as ESR and CRP, illness duration, and serology (RF and ACPA autoantibodies) scores are all included in this classification scheme. In those with undifferentiated arthritis, the development of RA [3] and a poorer clinical course with greater joint erosions are both associated with the existence of autoantibodies. By means of an enzyme reaction with PAD(A), citrullination is the process by which an arginine is changed into a citrulline. Image modified from references [4,5].Autoantibodies can recognize these PTMs. Anti-CarP, anti-carbamylated protein, and RF were some of the most prevalent antibodies in the identification of RA.

The conventional disparities between ACPA-positive and negative have vanished as a result of improvements in disease progression and cartilage damage, as well as in disease outcomes that tend to be most significant among patients (e.g., pain, fatigue, work ability) [6]. Only disease progression can be monitored by measurements of bone and cartilage, such as by calculating the evolution of bone lesions [7]. Recently, CNNs were trained with visual scores as the basis for reality based on deep learning techniques to quantify synovitis directly from the full image [8]. In MRI with contrast, the surrounding synovium was characterized and inflammation was quantified. The measurement of tenosynovitis also requires automated segmentation of tendons. BME could also be automatically determined using static post-contrast wrist MRI imaging, especially in early RA [9]. Numerous traditional AI techniques have been used to estimate cartilage thickness and volume in MRI scans [10]. Knee cartilage has been identified using deep learning [11], which has recently been improved to classify cartilage lesions. [12] Similar methods for locating cartilage in wrist joints have also been applied using CNNs [13].AI may be able to find patterns that are hidden from human sight and the human brain, or it may be able to minimize the number of dimensions. ML-based decision-making outperformed physician-only decision-making in its initial prospective clinical trials when it came to treating intensive care patients [14].

The random forest algorithm [15], in which samples are categorized by the majority vote of all decision trees, is an enhancement over decision trees. SVMs are trained to adjust the weights of polynomial functions to catch the predominant feasible departure of several classifications. Simulators can be used to expose machine learning approaches to an extensive variety of novel circumstances [16, 17]. RNN exists in a division of ANN that can evaluate the patterns of inputs

like handwriting, voice, or numerical time series, thanks to their internal memory. In the field of medicine, one type of recurrent neural network LSTMs is used to forecast outcomes in intensive units [18], failure in heart functions [19], or trajectories in health care using medical records [20]. Recently, it was possible to distinguish between OA and RA using synovial tissue transcriptome data obtained from microarrays [21].By calculating the significance of traits, the most distinctive genes was found using random forests. They were able to get a very high accuracy of 96% with random forests, k-nearest neighbors, and SVMs, as well as 100% sensitivity and 90% specificity. On radiographs of the knee or hip, OA has been found using a variety of techniques. Tibia texture analysis was performed by Brahim et al. [22] 83% accuracy, 81% specificity, and 87% precision was achieved in identifying OA. 93% accuracy, 95% sensitivity, and 91% specificity were achieved in this study. Xue et al.'s [23] pelvic radiographs, which are on par with a senior radiologist's performance [24], used two-dimensional convolutional neural network models to diagnose femorotibial lesions and automatically detected cartilage lesions with an 81% sensitivity and 88% specificity. In accordance with clinical expertise, menisci and patella femoral cartilage lesions were detected using three-dimensional convolutional neural networks from MRI datasets [25]. The use of compositional approaches, particularly T2 mapping, is made possible by MRI coupled with morphological datasets, enabling the quantitative assessment of tissue structure in three dimensions [26, 27]. The ARAC-AOL [28] technique for precise RA classification aids in the discovery of orthopedic and RA-related health issues. The MF approach is used as the primary pre-processing step in the ARAC-AADL technique. AOA is then combined with the ECN model in the ARAC-AOADL approach to create feature vectors. The MKELM model was used by the ARAC-AOADL approach to classify RA.

Convolutional neural networks (CNNs) were fine-tuned by LinluBai et al. [29] after clinical data from patients was converted into two-dimensional images in order to determine whether or not they had RA. To determine whether their training method was beneficial, they used five-fold cross-validation with an artificial neural network (ANN). Six features—patient's age, gender, RF, ACCP, anti-14-3-3, and anti-carbamylated protein—are included in the model. Among others, Iain S. Forrest [30] In spite of the fact that systemic autoimmune rheumatic disorders (SARDs) patients frequently go through protracted diagnostic processes before receiving a diagnosis and treatment, SARDs can have catastrophic consequences if left untreated.Knitza and others [31] Rheport is an online referral tool for rheumatology that permits automatic appointment triage of new referrals for rheumatology patients based on the possibility that they might develop an inflammatory rheumatic disease (IRD). Koo et al proposed machine learning approach successfully identified clinical traits related to remission in each of the bDMARDs. ESR measurements are made prior to and after follow-up to calculate the severity of the disease in 28 joints. [32] When the follow-up was conducted, the DAS28-ESR was less than 2.6, which was deemed to indicate "remission" by the prediction model's evaluation of the effects of bDMARDs. Examining how deep learning techniques might be used to diagnose RA was the aim of Jun Fukae's [33] research. There are no clear diagnostic standards or objective indicators for RA. The proposed simple method is advantageous for RA screening and helps in the diagnosis of RA. While SMOTE was utilized in the second experiment to balance the training dataset, the first experiment used original data to train the algorithms. With a score of 94.03%, 96.00%, and 93.51% for accuracy, recall, and precision, respectively, it outperformed other traditional classifiers.

3 Methodology

The major goals of this research are to examine stacked ensemble learning methods referred in Fig 1, to enhance the efficiency and accuracy of machine learning algorithms in differentiating between rheumatoid arthritis and other types of arthritis. To prevent the data from becoming overfit, tree-based techniques include classification and regression models using bagging. Boosting is used to reduce the processing errors in algorithms, which are used in machine learning. SVM, Naive Bayes, KNN, and Random Forest are well-known diversified classifiers with extreme gradient boosting (XGBoost) classifiers to enrich accuracy in classification. Each of these classifiers has a unique architecture and initial learning characteristics. Healthy tissues could be harmed by the immune system protein rheumatoid factor.

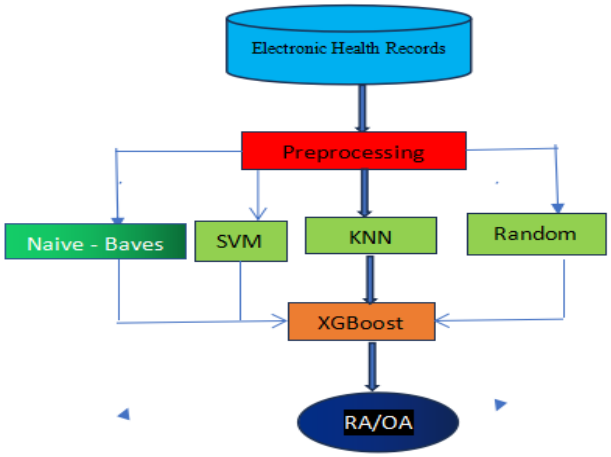

Fig.1 Proposed stacked ensemble model

RA or any autoimmune disease may be indicated by the existence of ANAs.Human leukocyte antigen (HLA), a genetic marker, is checked for during this test. According to certain research, almost 60% of RA cases may be hereditary. When a person carries specific antigens, their risk of developing RA may increase. Smoking, however, is not the only factor that might cause sickness. Blood HLA markers can aid in predicting the likelihood of developing immune-related diseases like RA. Support vector machine algorithms can resolve multi-class problems with the help of other kernels, including polynomials. SVM is trained to use a variety of function weights, such as polynomials, to determine the most likely separation of several categories. An advantage of decision trees over other machine learning techniques is that they combine the classification functions and features into a single model. In order to reduce predictors and associated variables, the Random Forest can be used to handle correlation coefficients and action between features effectively. KNN is applied to forecast a new example by employing the nearest samples from the preparation set [36]. Naive Bayes Classifier algorithm allows models to predict outcomes with high accuracy. Each object's likelihood is taken into consideration when forecasts are made. The output of first layer is given as an input to the second layer in a stacked ensemble learning algorithm. XGBoost classifier offers a parallel tree

boosting procedure to successfully complete a variety of data science jobs, which is otherwise called "Extreme Gradient Boosting". A series of weak classifiers are combined using the ensemble learning approach called "boosting" to produce a strong classifier. The bias-variance trade-off is significantly controlled by boosting algorithms. The loss function's value ought to fall with each iteration. When a specific number of trees have been created, an external validation dataset is no longer improved upon, or training is stopped when the loss falls below a predefined level. There is a danger of overfitting with the greedy gradient boosting method when it comes to training data. Regularization techniques like subsampling, shrinkage, early halting, or tree trimming are used to improve algorithm performance by reducing overfitting.

4 Results and Discussion

This classification is done through various tests like ESR, CRP, RF, ACCP, ANA, and HLA-DRB1. The correlation between each and every feature referred in fig 2, calculated to identify the key features needed to diagnose RA. After finding the key features, various models were trained using training clinical samples and tested using testing samples. Models performances were evaluated using various performance metrics, like accuracy, precision, and recall. The stacked ensemble machine learning algorithm includes two layered approaches. In the first layer, various anticipated nodes and machine learning methods are applied, and the calculation of first-layer models is given as an input to the second-layer algorithm to enhance model performance.

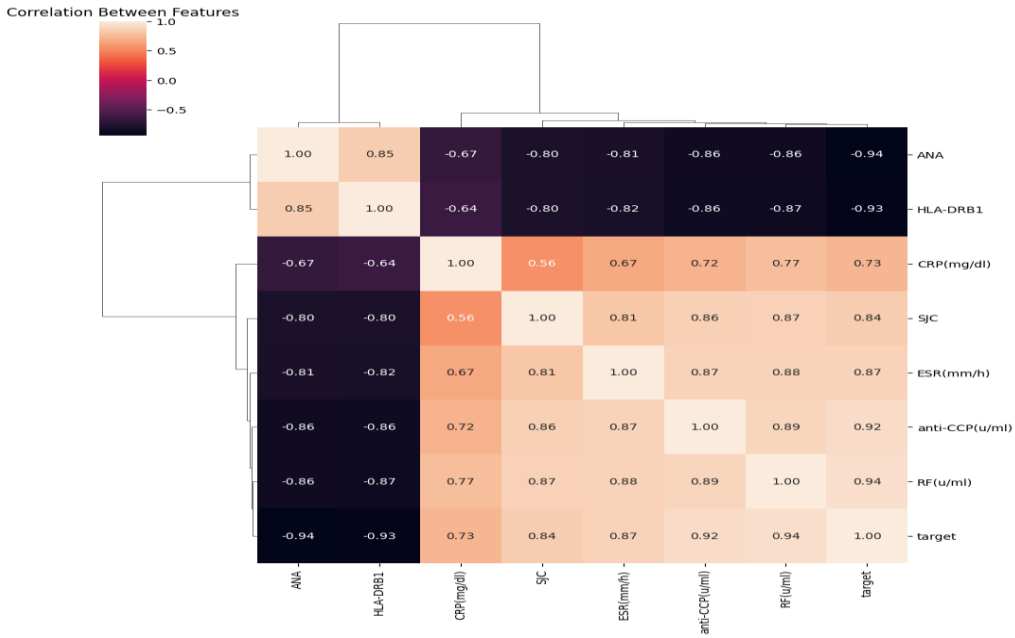

Fig 2: Correlation between features

Table 2 compares the stacking strategy with other machine learning algorithms, we can train many models to address related problems and then build a new, more effective model using the

results of all the trained models. Finally, the stacked ensemble learning model using the XGBoost algorithm provides greater accuracy, precision, and recall.

Table 2.Performance Evaluation

Classifier	Performance Evaluation Methods		
	Accuracy %	Precision%	Recall %
KNN	93.3	92.8	93.3
SVM	94.63	94.21	94.51
Random Forest	94.33	94.21	94.33
Naive Bayes	95.61	94.89	95.62
Proposed stacked ensemble XGBoost	97.13	97.01	97.13

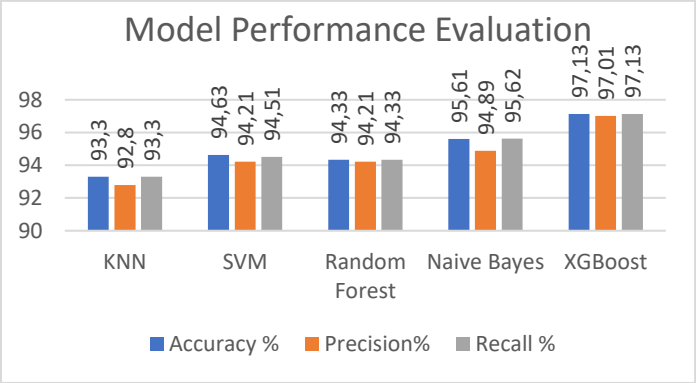

Fig 3: Model performance comparison Graph

5 Conclusion

Rheumatology has greatly benefited from the study of autoantibodies. Rheumatology is only just beginning to use AI. According to preliminary research, rheumatologists may be able to classify patients based on the likelihood that their diseases will advance by using clinical, radiological, and biologic parameters. Similar to prospective biomarkers, several have been discovered but have not yet been proven to be accurate predictors of therapy response. The capacity to trace the development of the disease and make an early identification of arthritis, either OA or RA, is difficult. To make quick and effective decisions for medical professionals and researchers, progressive machine learning models are required. Accurate predictive modelling for the course of arthritis may be challenging to create in the absence of machine learning models. By using our proposed stacked ensemble prediction models, we can quickly

and accurately identify individuals with early arthritis and those whose condition will worsen quickly. The amount of data samples in the training set is insufficient to fully reflect the range of possible input data values due to its limited size.

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