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A Deep Learning Approach to Detect Rheumatoid Arthritis Using Medical Images and Blood Samples

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Abstract: Rheumatoid arthritis (RA) is a long-term autoimmune disease that mainly affects the joints. It happens when the immune system, which should aid in defending the body against illness and infection, unintentionally targets healthy tissues. This may result in joint pain, edema, stiffness, and loss of function. RA postures are a noteworthy clinical challenge due to their inveterate nature and potential for joint deformation and systemic complications. Conventional demonstrative strategies frequently drop briefly in giving exact and opportune discovery, requiring imaginative approaches. In this way of thinking, the developed novel system coordinates profound learning strategies with multi-modal information, counting blood biomarkers and restorative pictures of influenced joints of the hand, to revolutionize RA discovery and seriousness assessment. By leveraging a comprehensive dataset and considering indication length, the proposed approach outperforms the confinements of existing strategies, advertising prevalent symptomatic precision and early discovery capabilities. Through fastidious assessment, the system illustrates the diminishment of wrong positives and untrue negatives, hence progressing persistent results and diminishing long-term joint damage. Furthermore, this novel system contributes to progressing the understanding of RA pathophysiology and treatment viability by cultivating logical advances through the development of a comprehensive dataset. As part of the multi-modal framework integration process, the American College of Rheumatology/European League Against Rheumatism (ACR/EULAR) 2010 criteria are taken into account, and the system is improved by drawing on existing systems or discovered techniques. Specifically, the investigation was done on automating RA seriousness assessment using Profound Learning computations associated with hand X-ray pictures. Notwithstanding these advances, difficulties persist in accurately identifying early indications of RA from common variations or other joint disorders, as well as in identifying subtle joint deviations from the norm. To improve demonstration accuracy and advance in the comprehension of care outcomes in Rheumatoid Joint pain determination and severity evaluation, machine learning methodologies and multi-modal information integration were used.

Keywords: Rheumatoid Arthritis, ACR/EULAR 2010 criteria, Deep Learning, Ensemble, Healthcare.

I. INTRODUCTION

Rheumatoid Arthritis is a persistent autoimmune condition marked by synovial inflammation, a global health concern affecting countless individuals and placing considerable strain on healthcare infrastructures. The RA load in India is further intensified by the country's urbanization and the scarcity of healthcare availability, especially in rural regions. Traditional diagnostic procedures are often marred by issues of precision and promptness, thereby necessitating the introduction of sophisticated Artificial Intelligence (AI) powered solutions.

In the domain of hand anatomy, precise identification and characterization of joints play a pivotal role in the accurate interpretation of medical images for RA detection. The human hand comprises a complex arrangement of joints, each serving distinct functional roles. Among these, the prominent joints include the distal interphalangeal (DIP) joints, proximal interphalangeal (PIP) joints, metacarpophalangeal (MCP) joints, and carpal joints. The carpals are a group of eight small bones located in the wrist region. These bones form the foundation of the hand's skeletal structure and provide essential support and flexibility for hand movements. While RA can affect joints throughout the body, it predominantly targets the small joints, particularly those in the hands and feet. Anti-Cyclic Citrullinated Peptide (anti-CCP) antibodies exhibit high specificity for RA diagnosis, with a significant positive predictive value, making them valuable indicators for effective treatment initiation. Rheumatoid Factor (RF), although less specific than anti-CCP, is more related tothe age and gender of the patient and, hence is a sensitive marker for RA diagnosis. C - Reactive protein (CRP) and Erythrocyte Sedimentation Rate (ESR) are nonspecific markers but serve as essential auxiliary indicators in confirming RA diagnosis. Due to the autoimmune etiology of RA, exclusive dependence on X-ray imaging for early detection lacks requisite precision, necessitating the integration of serological markers including Anti-CCP antibodies, RF, acute phase reactants CRP and ESR, and symptom duration as outlined in the ACR/EULAR 2010 criteria, thereby augmenting diagnostic accuracy through comprehensive assessment of diverse disease manifestations. Evaluating both serological profiles and X-ray images is imperative for comprehensive RA diagnosis, as these parameters collectively reflect disease activity and severity, guiding timely therapeutic interventions.

The proposed system seeks to transform RA diagnosis by amalgamating AI and Deep Learning methodologies. By employing multi-modal data amalgamation, encompassing medical imagery and biomarkers such as anti-CCP and RF, this work aims to bolster early detection and management. Central objectives encompass the development of enhanced Deep Learning models for the identification of joint anomalies, with the model for accurate anomaly detection in the serology and demographic information of the patient, hence establishing a clinical decision aid system that aligns with the ACR/EULAR guidelines. Hand X-ray images are exclusively utilized to train the deep learning model, mirroring clinical practice where RA diagnosis primarily relies on hand X-rays due to heightened joint movement and symptom manifestation. Notably, the emphasis on hand imaging is justified by the increased mobility and symptom prevalence in these joints compared to the feet. The project's reach encompasses broad-scale implementation in healthcare, providing a more efficient diagnostic procedure and resource utilization. Furthermore, it promises to accelerate the process of clinical trials and propel the progression of RA treatment development. This document details the extensive strategy followed, placing a spotlight on the innovative application of technology in RA detection.

II. RELATED WORK

To improve the diagnosis of RA, Bai et al. suggest using an artificial neural network (ANN), to solve problems with conventional diagnostic techniques. The work shows enhanced accuracy in RA diagnosis using machine learning models, namely an ANN, by carefully following diagnostic criteria and selecting pertinent biomarkers. Their methodology performs better than earlier approaches, underscoring the importance of sophisticated computational tools in the diagnosis of RA [1].

Using statistical features, Mrs. Swati A. Bhisikar and Dr. Sujata N. Kale conducted an automatic analysis of rheumatoid arthritis. With an emphasis on joint space narrowing in hand radiographs, Bhisikar and Kale offer a thorough examination of computer-aided analysis techniques for diagnosing RA. The authors suggest an automated solution that uses MATLAB and involves painstaking methodological stages such as image segmentation and statistical feature extraction. Their method has the potential to improve diagnostic precision in clinical practice because it produces accurate results in RA severity assessment [2].

Using machine learning approaches and explainable AI, Sakaria et al. present a novel approach to RA prediction. Their technique, which combines blood samples and medical imaging, shows great accuracy in diagnosing RA; the Convolutional Neural Network (CNN) algorithm performs better than other algorithms. The work shows how machine learning can transform RA diagnosis and individualized treatment plans, despite some constraints like dataset size and a deficiency of X-ray pictures [3].

Using deep learning techniques on hand X-ray pictures, Wang et al. develop a comprehensive computer-aided diagnosis system for RA severity assessment respecting the Modified Total Sharp/van der Heijde Score. Their method shows remarkable effectiveness in combined detection and severity classification by utilizing the You Only Look Once (YOLO) model and classification algorithms. The research highlights the revolutionary potential of deep learning in augmenting RA diagnostic and treatment approaches, even despite constraints associated with dataset size and dependence on X-ray images [4].

III. WORKING METHODOLOGY

The methodology of the developed system encompasses a structured approach toward RA detection, integrating user input, deep learning models, and comprehensive scoring mechanisms. It orchestrates a seamless workflow from data input to diagnostic conclusion, leveraging advanced techniques for enhanced accuracy and efficiency. In the initial step, users will interact with the system through a web-based interface, where they will input relevant data about RA. This data can include medical images, such as hand X-rays, as well as serology data and demographic information. Upon submission of the form in the web interface, an API call is triggered, transmitting the input data to the backend system. This API call serves as the bridge between the frontend and backend components of the application, facilitating seamless data transfer. Within the backend system, rigorous checks are performed to validate the format of the data provided by the user.

Techniques such as resizing may be applied to standardize the dimensions of hand X-ray images for consistency. Subsequently, the pre-processed data, including the resized images and accompanying serology and demographic data, are routed to separate modules for analysis. The pre-processed image data is fed into a deep-learning model tailored for joint abnormality detection. Leveraging the power of artificial intelligence, the model will make predictions based on learned features extracted from the input data. Also, the anomaly detection model is fed with the serology and demographic information to detect abnormalities. Following the predictions made by the deep learning model and abnormalities detected, a scoring mechanism is employed to quantify the likelihood of RA presence and the severity of detected abnormalities. This scoring process aids in prioritizing cases based on the perceived risk levels, thereby facilitating targeted intervention strategies.

The outcome scores of the anomaly detection and joint abnormality detection are synthesized to generate comprehensive summary messages. These messages are categorized according to the detected abnormalities, serology data, and demographic attributes. Such categorization enables tailored insights relevant to each aspect of the RA diagnosis. Scores provided based on each category, are aggregated to derive a holistic assessment of the RA likelihood and severity. A conclusion summary is constructed based on the collective insights garnered from the scoring process, providing a concise overview of the diagnosis outcome. The backend system formulates a response encapsulating the generated summary and diagnostic conclusions. This response is transmitted back to the front end via the API, enabling seamless communication between the user interface and the underlying analytical engine. Finally, visualization of the RA severity in the detected joints of the provided hand X-ray image is presented to the user through an interactive interface, followed by a summary containing diagnostic conclusions and insights. This intuitive display interface facilitates user comprehension and decision-making, empowering stakeholders with actionable information for further clinical assessment and intervention. Figure 1 depicts the overall pipeline of the proposed RA detection system, illustrates a systematic process for automated joint abnormality detection.

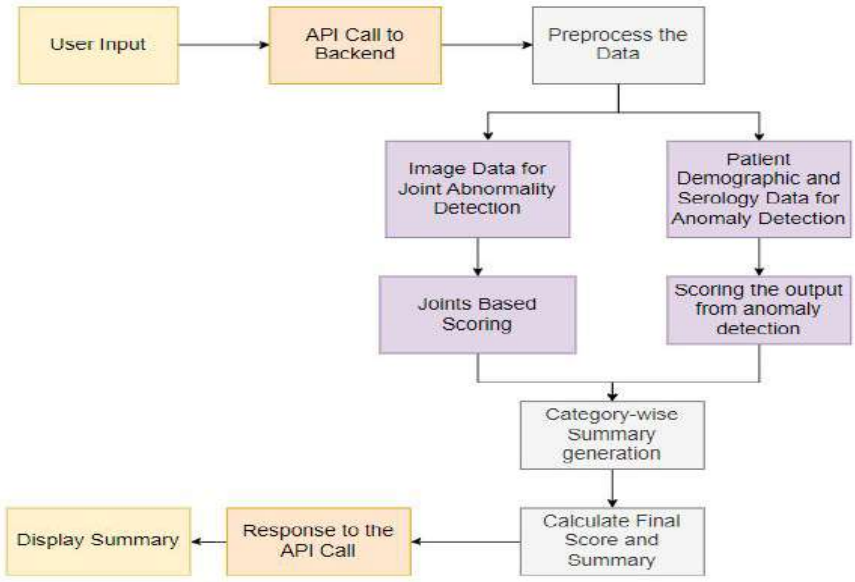


Figure 1: Overall pipeline of the proposed RA Detection System

Figure 2 presents scores corresponding to distinct categories encompassing joint detection, serology classification, acute phase reactants, and symptom duration, integral components of the diagnostic framework. The cumulative score, derived by aggregating individual category scores, serves as a pivotal parameter, with a predefined threshold of 6 delineating the boundary between negative and positive outcomes, aligning with the refined scoring system delineated in the ACR/EULAR criteria, thus facilitating nuanced diagnostic assessments for RA.

Category 1: Joint-Detection

Count_Type	Score
0_Small	0
1-3_Small	2
4-10_Small	3
>10_Small	5
0_CrpIs	0
1_CrpIs	1
2_CrpIs	2

Category 2: Serology Classification

Anti-CCP

Type	Score
Negative	0
Low-Positive	2
Medium-Positive	3
High-Positive	4

Rhematoid Factor (RF)

Type	Score
Negative	0
Positive	3

Category 3: Acute-Phase Reactants

C-Reactive Protein (CRP)

Type	Score
Normal	0
Abnormal	1

Erythrocyte Sedimentation Rate (ESR)

Type	Score
Normal	0
Abnormal	1

Category 4: Duration of Symtoms

Duration	Score
<6 Weeks	0
>=6 Weeks	1

Final Sum-Score

Score	Output
<6	Low Chance Of RA Positive
>=6	High Chance Of RA Positive

Figure 2: Scoring mechanism adopted in the system for detecting RA based on the ACR/EULAR 2010 criteria

IV. TECHNICAL SPECIFICATION, CONFIGURATION AND PROCESS

In the paradigm of joint detection within hand X-ray images for rheumatoid arthritis, employing YOLO within a novel system offers distinct advantages. YOLO's single-stage detection architecture provides superior efficiency and real-time performance compared to traditional two-stage methods, owing to its ability to simultaneously predict object bounding boxes and class probabilities. Moreover, YOLO's unified framework optimizes localization and classification tasks, enabling seamless integration of contextual information for precise joint identification. This versatility, coupled with YOLO's streamlined architecture and ease of implementation, renders it a leading choice for RA detection, facilitating enhanced diagnostic accuracy and clinical decision-making.

In this research, YOLO versions v5, v8, and v9 are compared to assess their performance in joint detection within hand X-ray images for RA diagnosis. This comparative analysis enables the evaluation of advancements and optimizations introduced in successive versions, aiding researchers in selecting the most suitable model for their specific application and computational constraints. Additionally, it is noteworthy that the latest version, YOLOv9, has demonstrated better efficiency and efficacy compared to its predecessors, solidifying its status as a more advanced and capable iteration in the realm of joint detection for RA diagnosis. The YOLO models come in various sizes, offering a trade-off between speed and accuracy. The smaller models (YOLOv5s, YOLOv8s, YOLOv9s) are designed for rapid inference, making them suitable for real-time applications, albeit at the cost of some accuracy. The medium models (YOLOv5m, YOLOv8m, YOLOv9m) provide a balance between speed and precision, making them versatile across a range of computational constraints. The larger models (YOLOv5l, YOLOv8l, YOLOv9l) focus on achieving the highest accuracy possible, with more extensive network architectures that require greater computational resources.YOLOv9 introduces the 'c' and 'e' variants, with 'c' denoting 'compact' and 'e' signifying 'enhanced'. The compact variant is optimized for environments where model size and speed are critically constrained. In contrast, the enhanced variant is engineered to push the boundaries of accuracy, integrating advanced techniques for improved performance in complex diagnostic tasks.

Further in RA detection, the decision trees have been utilized on a set of biomarkers to classify the likelihood of the disease. Decision trees are employed to effectively analyze and interpret complex interactions between various serological markers such as anti-CCP antibodies, RF, CRP, and ESR, providing a systematic framework for identifying patterns indicative of RA diagnosis with high accuracy and interpretability. For anti-CCP levels considered in EU/mL, values below 20 are considered negative, indicating a low probability of the disease. Levels between 20 to 39 suggest a weak positive, 40 to 59 are moderately positive, and values above 59 denote a highly positive result, each reflecting an increasing likelihood of RA.For the RF in IU/mL, gender and age play a crucial role. In males aged under 30, an RF level below 20 is negative, while a level of 20 or above is positive. In males over 30, the threshold increases to 25. For females under 30, an RF level below 18 is negative, and for those over 30, the negative threshold is below 22.For CRP in mg/L, values less than 10 are considered normal, or else as abnormal. Lastly, for ESR in mm/hr, levels below 20 are considered normal, while levels 20 or above are abnormal, indicating potential inflammation associated with RA. The respective decision trees are visualized below in Figure 3.

Configuration: In the quest for the optimal joint detection model in X-rays, a comprehensive training and validation process is conducted. The research work was done by experimenting with different model sizes for three distinct architectures to find the best fit based on the needs. The chosen model underwent further fine-tuning on a larger dataset to enhance its overall detection accuracy.

This training leveraged the powerful capabilities of an Nvidia T4 GPU with 16GB of VRAM. For development, Python was used as the programming language, utilizing PyTorch and the Ultralytics packages. For Labelling the X-ray images, the LabelImg tool has been utilized. To create a user-friendly interface, the Angular framework on the web user interface and the Flask package for constructing the back-end services have been utilized.

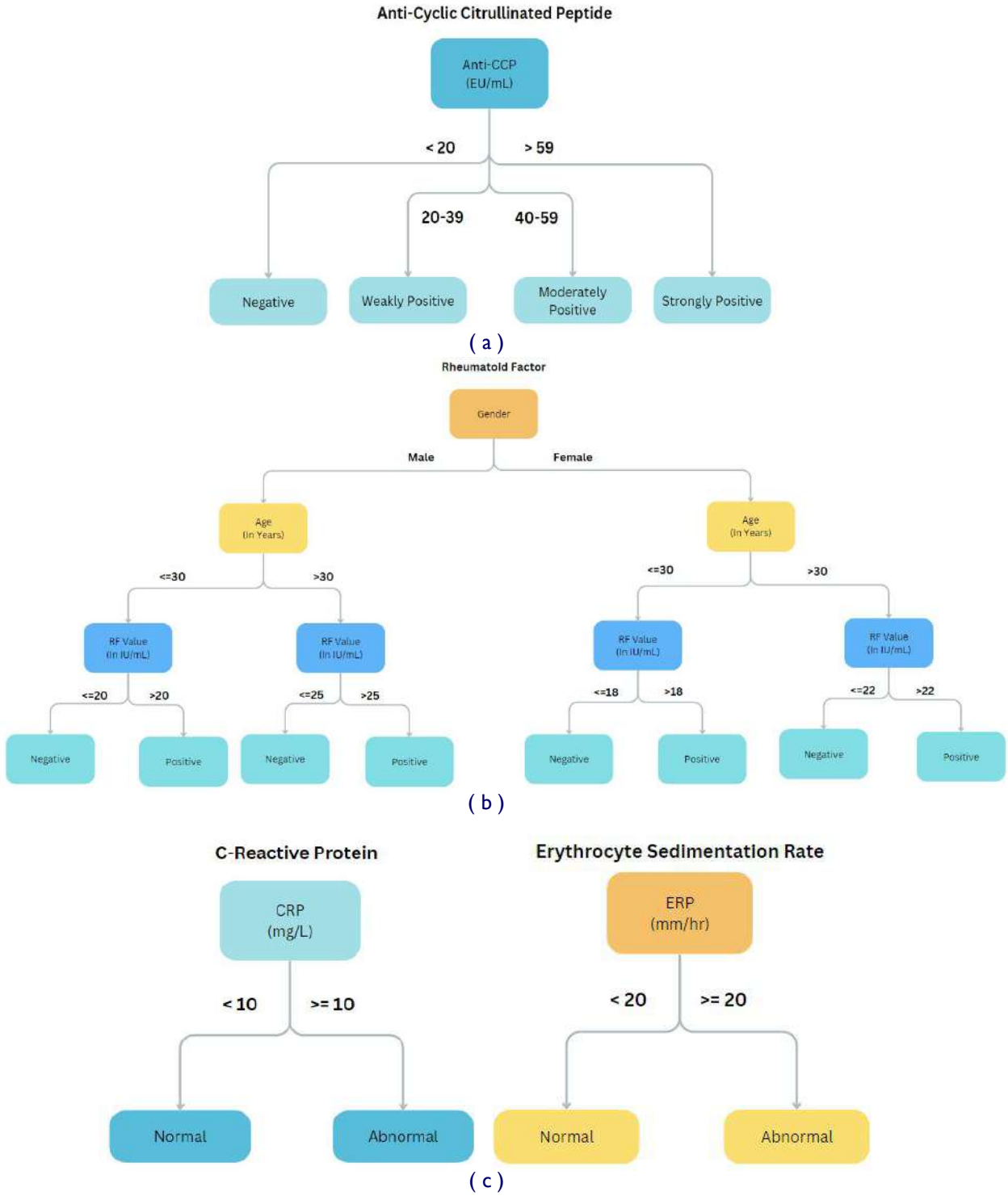


Figure 3: Decision tree criteria for a) Anti-CCP, b) RF, c) CRP and ESR values

Process: The initial phase of this research work involved the meticulous collection of X-ray images depicting hands affected by RA. The dataset is curated to represent a wide spectrum of severity levels, thus enhancing the robustness of subsequent models. Coupled with the acquisition of relevant demographic and clinical data, construct decision trees accordingly. Data preprocessing ensures cleaning and standardizing the dataset to eliminate inconsistencies and potential biases, followed by a comprehensive annotation of the X-ray images. In the comparative research conducted on RA detection in the hand x-ray images, the training dataset consisted of 1904 images with corresponding annotations, while the testing set comprised 476 images, both sets of images in JPG format. Predictions were made on a subset of 100 images for evaluation purposes.

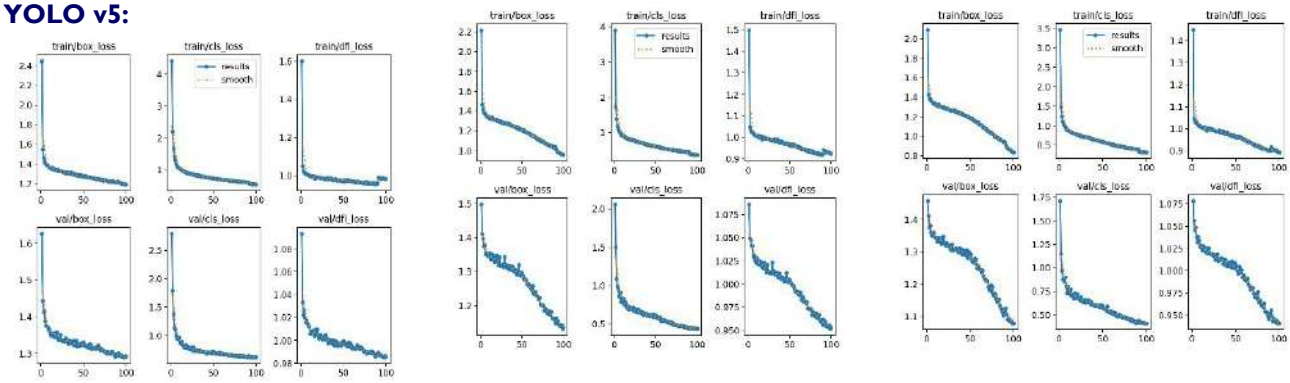
The sample set, originally containing 595 images, was augmented fourfold through rotation techniques. However, the prediction set, consisting of 100 images, remained unaltered and was not utilized during training to ensure an unbiased evaluation of model performance. The evaluation metrics used to assess model performance included precision, recall, mean Average Precision at an Intersection over Union (IoU) threshold of 0.5 (mAP50), and mean Average Precision at an IoU threshold of 0.5-0.95 (mAP50-95). These metrics provide insights into the model's ability to accurately detect and classify instances of rheumatoid arthritis in medical images. Additionally, loss diagrams and graphs were generated for each training iteration to visualize the training process and model convergence. The training outcomes demonstrated strong performance across all three models, with their accuracy assessed and presented in Table 1. It is essential to acknowledge that the effectiveness of these models can differ based on the particular dataset and evaluation criteria employed.

YOLO Versions	Version Type	Precision	Recall	mAP50	mAP50-95
YOLO v5	v5s	0.768	0.83	0.846	0.66
	v5m	0.789	0.798	0.842	0.656
	v5l	0.744	0.847	0.819	0.63
YOLO v8	v8s	0.749	0.825	0.84	0.659
	v8m	0.775	0.84	0.844	0.653
	v8l	0.772	0.87	0.838	0.65
YOLO v9	v9c	0.765	0.868	0.85	0.661
	v9e	0.784	0.835	0.843	0.659

Table 1: Three models evaluation on different metrics

The graphs in Figure 4, depict the training and validation losses of various YOLO versions across 100 iterations over the entire dataset (epochs), illustrating the convergence and performance of each model in terms of bounding box loss, classification loss, and depth-wise convolutional layer loss, providing insight into their training dynamics and optimization trajectories.

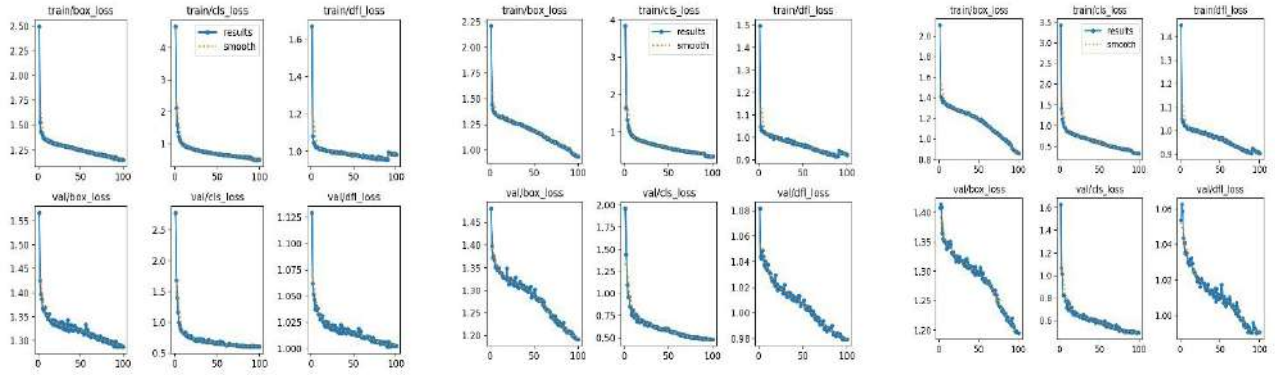
YOLO v5:



v5s v5m v5l

(a)

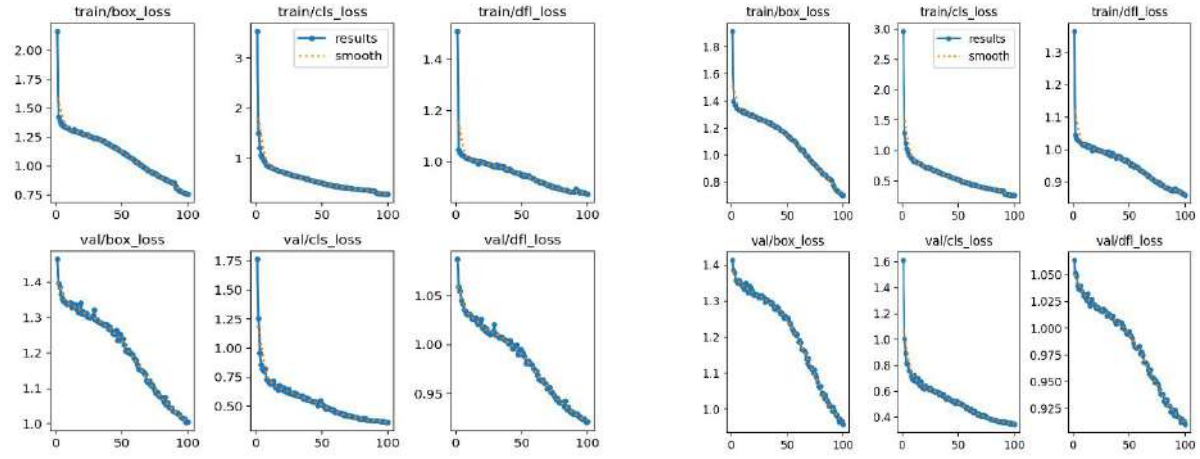
YOLO v8:



v8s v8m v8l

(b)

YOLO v9:



(c)

Figure 4: Results generated from training and validation on YOLO a) v5, b) v8, and c) v9 versions respectively

Upon the culmination of the initial research, which entailed rigorous comparative analysis of various YOLO models for the detection of RA in X-ray images, YOLOv9c emerged as the most suitable model for the objectives. This compact variant of the YOLOv9 family was specifically chosen for its balance between speed, model size, and diagnostic performance. The selected model was trained on a dataset of 3,717 X-ray images, which were subsequently augmented through four-fold rotation to generate a total of approximately 14,490 images for a more robust training process. The final model exhibited a precision of 0.85, a recall of 0.893, a mAP@0.50 of 0.912, and a mAP@0.50:0.95 of 0.83, signifying a high degree of accuracy in localizing RA-affected joints. Simultaneously, a custom anomaly detection model is developed to process the serological biomarker data. This model is developed to detect deviations from established normal ranges that are indicative of RA, taking into consideration overlapping symptoms to enhance diagnostic accuracy. An ensemble approach is then employed to synthesize the outputs from both image and text data analysis models. This technique leverages the strengths of multiple models, thereby improving the accuracy and reliability of the diagnostic output. The final product is a comprehensive report summarizing the observations made by the hybrid model, offering interpretable results to assist healthcare professionals in decision-making processes related to the presence and severity of RA. Validation of the models is conducted using an independent dataset, ensuring the generalizability of the models to unseen cases. Metrics such as sensitivity, specificity, and accuracy are employed to rigorously evaluate the performance of the individual models and the ensemble system as a whole. Throughout the project, ethical considerations are paramount. The research adheres to stringent guidelines regarding patient data privacy and consent. Mechanisms are also put in place to mitigate bias within the models, acknowledging the profound impact such biases could have on patient outcomes. The methodology thus reflects a commitment to both scientific rigor and ethical responsibility, aiming to advance the field of medical diagnostics through the application of deep learning techniques.

Figure 5, illustrates a structured workflow that encompasses data preprocessing, ensuring the proper provision of hand X-ray images and blood values, followed by the utilization of deep learning models for detecting RA in hand X-ray images, and anomaly detection using serology and demographic data. Ensemble techniques are then incorporated to synthesize scores, culminating in a succinct summary.

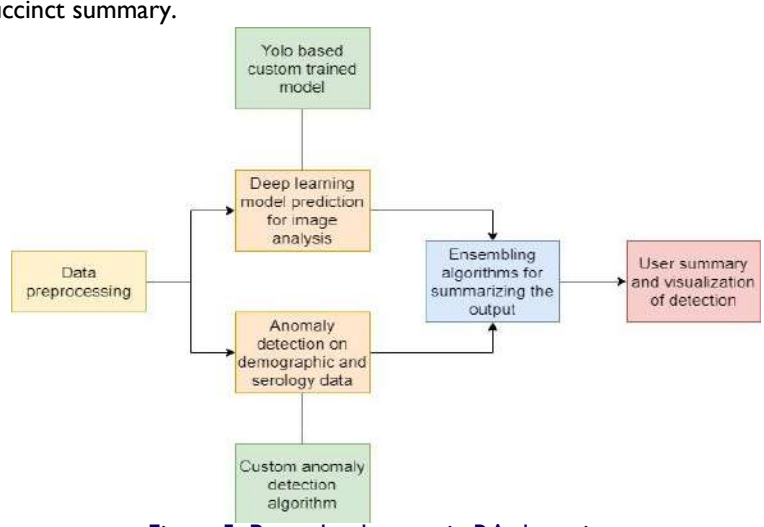
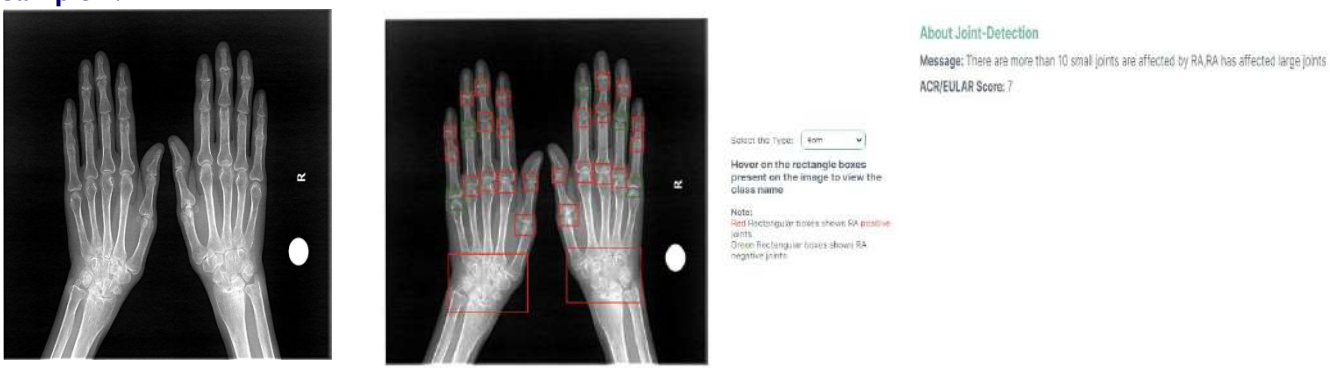


Figure 5: Procedural stages in RA detection

V. RESULTS

The results section encapsulates the outcomes of the comprehensive system, encompassing joint detection, anomaly detection, and the synthesis of final diagnostic summaries.

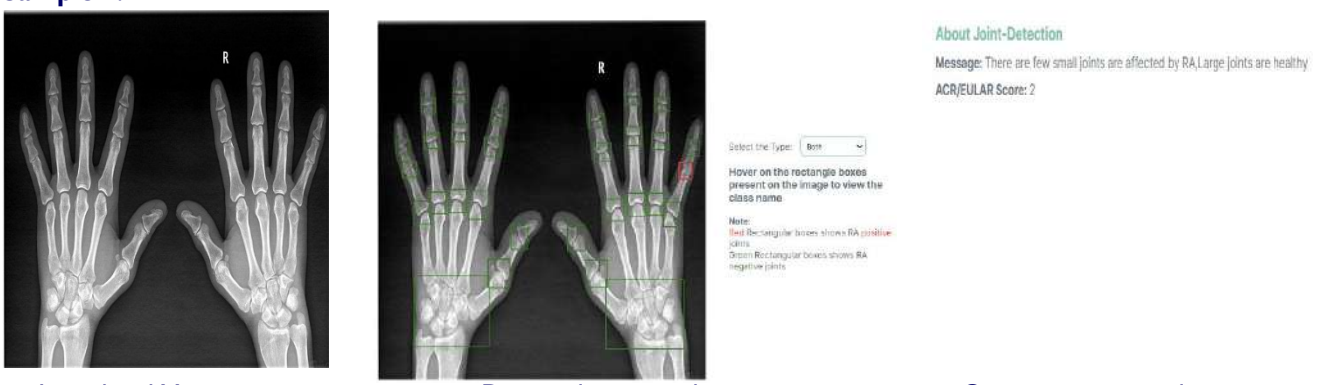
Sample 1:



Input hand X-ray image | Detected joints in the image | Output message and score

(a)

Sample 2:



Input hand X-ray image | Detected joints in the image | Output message and score

(b)

Figure 6: Hand X-ray image input, output visualization, and respective message and score produced by the system on a) Sample 1 and b) Sample 2

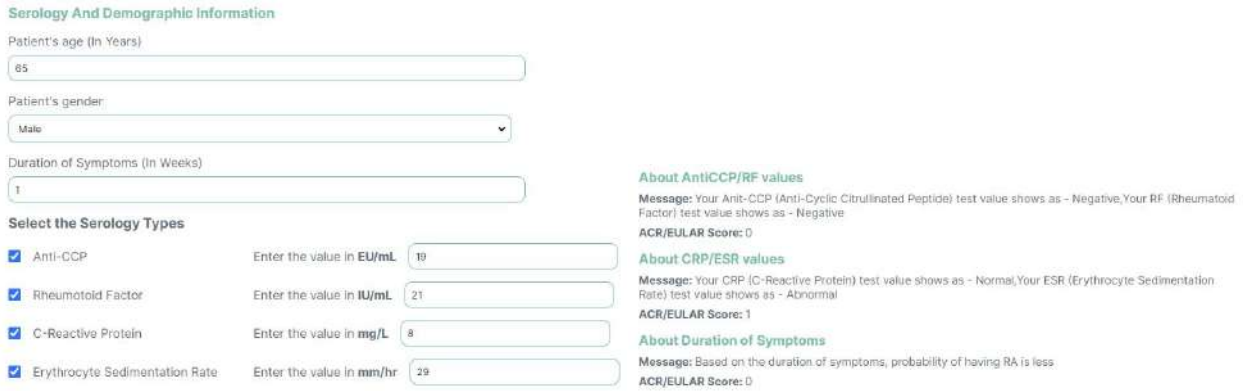
Figure 6, comprises the original input hand X-ray image alongside visual representations of the deep learning model's output for joint detection. Within these visualizations, distinct bounding boxes delineate unaffected joints, depicted in green, and joints afflicted by RA, highlighted in red. Additionally, each identified joint is accompanied by an associated score, reflective of the system's assessment of RA likelihood. Corresponding diagnostic messages contextualize the severity and implications of the detected abnormalities. Two distinct samples, labelled Sample 1 and Sample 2, elucidate the variability and efficacy of the system's predictive capabilities across different cases. Two sample sets of serology and demographic data are considered, each analyzed for anomalies. The system assigns scores and generates corresponding diagnostic messages, elucidating the detected anomalies and their severity and implications within the context of RA diagnosis are shown in Figure 7.

Sample 1:

Input serology and demographic data | Output message and score

(a)

Sample 2:

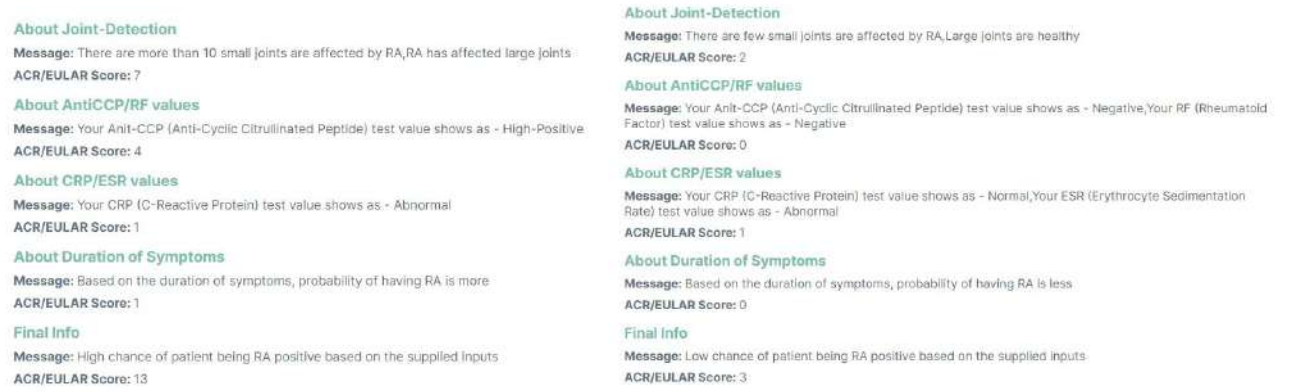


Input serology and demographic data Output message and score

(b)

Figure 7: Serology and demographic data input and respective message and scores produced by the system on a) Sample 1 and b) Sample 2

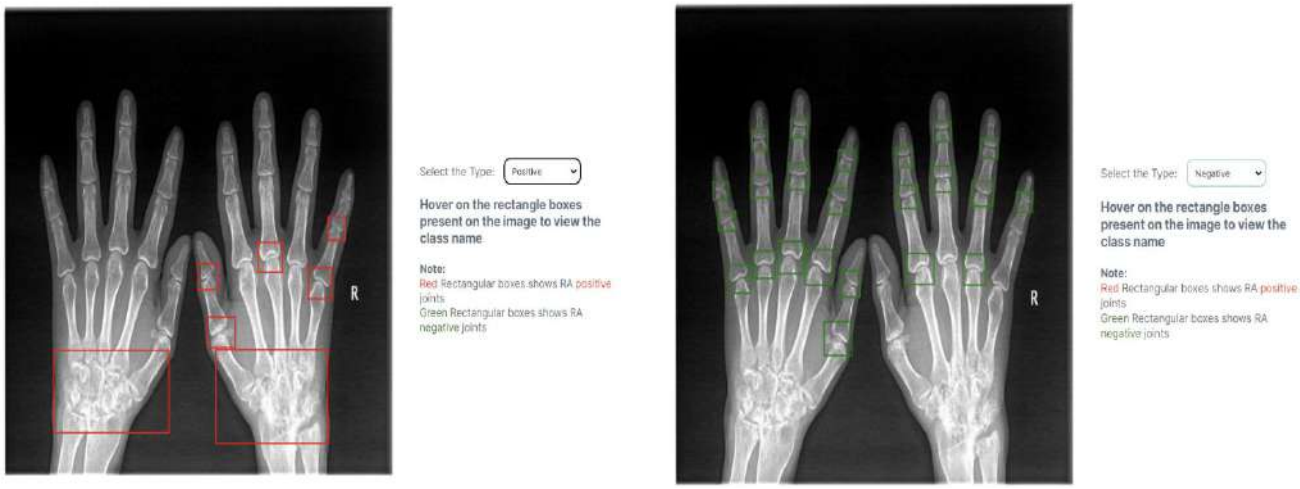
Upon input of the two sample sets comprising X-ray images, serology, and demographic data into the system, the final evaluation yields a conclusive score representing the likelihood of RA occurrence. Users are presented with diagnostic messages indicating whether the chance of RA occurrence is categorized as low or high, facilitating informed clinical decision-making are presented in Figure 8.



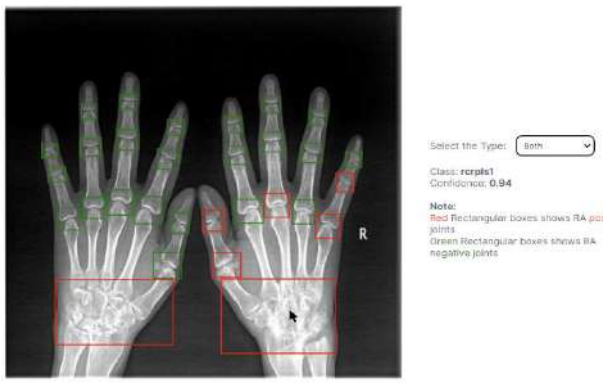
Sample 1 final output summary Sample 2 final output summary

Figure 8: Final summary provided on the inputs of Sample 1 and Sample 2, including all four categories and the final message and score

The visualization shown in Figure 9, demonstrates interactive features enabling users to discern affected and unaffected joints efficiently. The first part of Figure 9 (a), showcases the selective display of RA-affected joints, highlighted in red bounding boxes, facilitating focused analysis. In the second part of Figure 9 (a), users can isolate unaffected joints, distinguished by green bounding boxes, streamlining comparative assessments. Moreover, the Figure 9 (b), illustrates a user-friendly interface allowing users to hover over bounding boxes to access class and confidence information, enhancing interpretability and usability.



Visualization with RA-affected joints by red boxes Visualization with RA-unaffected joints by green boxes (a)



Class and confidence of RA-affected and unaffected joints on interaction (b)

Figure 9: Visualization of a) identified affected and unaffected joints and b) class and confidence of particular joint upon interaction

VI. CONCLUSION

The value of this initiative lies in its potential to meet a critical requirement in the medical realm by employing deep learning methodologies for the diagnosis of Rheumatoid Arthritis. By integrating medical imagery with the haematological examination, the accuracy of RA identification is heightened, facilitating timely intervention and improving patient prognosis. The ramifications for healthcare are immense, as a successful deployment of this initiative could transform RA diagnosis and therapy. Through the earlier detection enabled by the diagnostic instrument, health practitioners can intervene more effectively, potentially curbing the progression of RA and augmenting the quality of existence for impacted individuals. Ethical aspects, especially those concerning data privacy, are integral to the project. The commitment to upholding exemplary ethical standards and ensuring responsible management of patient data has been thoroughly integrated across all stages of development and execution. Adherence to applicable regulations and guidelines is invariable as patient confidentiality and privacy are prioritized. In conclusion, this initiative not only signifies a notable progression in the domain of rheumatology but also highlights the commitment to enhancing healthcare results while adhering to ethical principles and data privacy norms. Through collaborative efforts and a steadfast commitment to excellence, the goal is to make a meaningful difference in the lives of individuals affected by Rheumatoid Arthritis.

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