RHEUMATOID ARTHRITIS PREDICTION

FOML REPORT
Submitted by

PREM KUMAR D 220701204

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CHENNAI - 602105

BONAFIDE CERTIFICATE

Certified that this Report titled "**RHEUMATOID ARTHRITIS PREDICTION**" is the bonafide work of **PREM KUMAR D(220701204)**,who carried out the work under my supervision. Certified further that to the best of my knowledge the work reported herein does not form part of any other thesis or dissertation on the basis of which a degree or award was conferred on an earlier occasion on this or any other candidate.

SIGNATURE

Mrs. M. Divya M.E.

SUPERVISOR,

Assistant Professor

Department of Computer Science and Engineering

Rajalakshmi Engineering College,

Chennai – 602105

Submitted to Project Viva-Voce Examination held on _____

Internal Examiner **External Examiner**

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PREM KUMAR D 220701204

ABSTRACT

Rheumatoid Arthritis (RA) is a chronic autoimmune disorder requiring early diagnosis for effective management. This project develops a neural network model to predict RA positivity using clinical and laboratory parameters from a dataset of 102 patients. The dataset includes features such as age, gender, haemoglobin, C-reactive protein, and rheumatoid factor (RA), with RA values above 10 indicating positivity. Data preprocessing involved mean imputation for missing values, label encoding for categorical variables, and standard scaling for normalisation. A sequential neural network with four hidden layers (128, 64, 32, 16 neurons) and dropout regularization was trained on 80% of the data, achieving a training accuracy of 89.06% and validation accuracy of 76.47%. Evaluation metrics, including ROC-AUC, classification report, and confusion matrix, assessed model performance, revealing challenges with class imbalance. A user input function enables real-time RA prediction based on 14 key features. Despite limitations such as a small dataset and potential overfitting, the model demonstrates promising predictive capabilities. This work highlights the potential of machine learning in RA diagnosis, paving the way for future improvements with larger datasets and advanced feature selection techniques.

LIST OF FIGURES

LIST OF ABBREVIATIONS

S. NO.	ABBREVATION	ACCRONYM
1	ML	Machine Learning
2	RMSE	Root Mean Squared Error
3	AI	Artificial Intelligence
4	R2	R-squared
5	API	Application programming Interface

Chapter 1

INTRODUCTION

1.1 GENERAL

Rheumatoid Arthritis (RA) is a chronic autoimmune disorder characterized by inflammation of the joints, leading to pain, swelling, and potential joint deformity. Affecting approximately 1% of the global population, RA disproportionately impacts women and can significantly impair quality of life if not diagnosed and treated early. The diagnosis of RA relies on a combination of clinical assessments, laboratory tests (e.g., rheumatoid factor, C-reactive protein), and imaging studies. However, the complexity and variability of RA symptoms often delay accurate diagnosis, necessitating advanced diagnostic tools. Recent advancements in machine learning offer promising solutions by leveraging data-driven models to predict disease outcomes based on clinical and laboratory parameters. This project focuses on developing a neural network model to predict RA positivity using a dataset of 102 patients, incorporating features such as age, gender, haemoglobin, and inflammatory markers. By automating RA prediction, this work aims to assist clinicians in making faster, more accurate diagnoses, ultimately improving patient outcomes. The integration of artificial intelligence in healthcare represents a transformative approach, enabling early intervention and personalised treatment plans for RA patients. This project contributes to the growing field of medical informatics, highlighting the potential of machine learning in addressing complex diagnostic challenges.

1.2 OBJECTIVE

The primary objective of this project is to develop a robust neural network model for predicting Rheumatoid Arthritis (RA) positivity based on clinical and laboratory parameters. Specifically, the model aims to classify patients as RA-positive or RA-negative using a threshold of rheumatoid factor (RA > 10). The project utilises a dataset of 102 samples with 25 features, including age, gender, total white blood cell count, haemoglobin, C-reactive protein, and erythrocyte sedimentation rate, among others. By preprocessing the data through mean imputation, label encoding, and standard scaling, the project ensures compatibility with the neural network architecture. The model, comprising four hidden layers with dropout regularisation, is trained to achieve high accuracy while mitigating overfitting. Additionally, the project incorporates a user-friendly input function to enable real-time RA predictions based on 14 key features, enhancing its practical applicability. The performance of the model is evaluated using metrics such as accuracy, ROC-AUC, and confusion matrix, providing insights into its predictive capabilities. Ultimately, this work seeks to support clinicians in early RA diagnosis, reduce diagnostic delays, and contribute to the integration of machine learning in healthcare. The project also aims to lay the foundation for future enhancements, such as incorporating larger datasets and advanced feature selection techniques.

1.3 EXISTING SYSTEM

Current methods for diagnosing Rheumatoid Arthritis (RA) primarily rely on clinical evaluations, laboratory tests, and imaging techniques. Clinicians assess symptoms such as joint pain, swelling, and stiffness, combined with blood tests measuring rheumatoid factor (RF), anti-cyclic citrulinated peptide (anti-CCP) antibodies, C-reactive protein (CRP), and erythrocyte sedimentation rate (ESR). Imaging modalities, including X-rays and

ultrasounds, detect joint damage. However, these approaches face significant challenges. The heterogeneity of RA symptoms often leads to misdiagnosis or delayed diagnosis, particularly in early stages when symptoms overlap with other conditions. Manual interpretation of test results is time-consuming and subject to variability among practitioners. Existing computational tools, such as rule-based diagnostic systems or basic statistical models, lack the ability to handle complex, non-linear relationships in clinical data. Some machine learning models, like logistic regression or decision trees, have been explored for RA prediction but often suffer from limited accuracy due to small datasets or inadequate feature selection. These systems also lack user-friendly interfaces for real-time predictions, limiting their clinical utility. Moreover, the reliance on traditional methods without advanced predictive models hinders early intervention, increasing the risk of irreversible joint damage. This project addresses these gaps by leveraging a neural network approach to improve diagnostic accuracy and efficiency.

1.4 PROPOSED SYSTEM

The proposed system leverages a neural network model to predict Rheumatoid Arthritis (RA) positivity, offering an advanced, data-driven alternative to conventional diagnostic methods. The model utilises a dataset of 102 patients with 25 features, including demographic (age, gender), clinical (rheumatoid factor, C-reactive protein, erythrocyte sedimentation rate), and laboratory parameters (haemoglobin, urea, creatinine). Data preprocessing involves mean imputation to address missing values, label encoding for categorical variables, and standard scaling to normalise features, ensuring compatibility with the neural network. The model architecture comprises four hidden layers (128, 64, 32, 16 neurons) with ReLU activation and dropout rates (0.2–0.3) to mitigate overfitting, followed by a sigmoid output layer for binary classification (RA > 10 as positive). Trained on 80% of the data using the Adam optimiser and binary cross-entropy loss, the model incorporates early stopping (patience=10) to restore optimal weights, achieving a training accuracy of 89.06% and validation accuracy of 76.47%. Performance is evaluated using accuracy, ROC-AUC, classification report, and confusion matrix, providing comprehensive insights into predictive capabilities. A user-friendly input function enables clinicians to enter 14 key features for real-time RA predictions, enhancing clinical utility. Compared to traditional methods, this system captures complex, non-linear data patterns, reduces diagnostic delays, and supports early intervention. Limitations, such as the small dataset and potential class imbalance, are acknowledged, with future enhancements planned, including larger datasets, feature selection techniques, and hyper parameter tuning to improve accuracy and generalisability. This model represents a significant step toward integrating machine learning into RA diagnosis, offering a scalable tool for healthcare professionals.

CHAPTER 2

LITERATURE SURVEY

[1] K. Morita, T. Ono, Y. Sato, and H. Tanaka(2017)

They proposed a computer-aided diagnosis system using random forests and SVM on clinical data (RF, anti-CCP). It achieved 85% accuracy but was limited by a small dataset, highlighting the need for larger cohorts, similar to this project's focus

[2] L. Bai, Y. Zhang, P. Wang, X. Zhu, J.-W. Xiong, and L. Cui(2022)

They developed an ANN for RA diagnosis using six features (e.g., age, RF). With an AUC of 0.951, it showed high performance but limited generalizability due to few features, unlike this project's broader dataset

[3] G. P. Avramidis, M. P. Avramidou, and G. A. Papakostas(2015)

They reviewed deep learning for RA, noting 93% of studies used imaging. Only 15% were explainable, emphasising the gap in clinical data models, which this project addresses with laboratory features

[4] P. Mruthyunjaya, A. Agarwal, and S. Ahmed(2024)

Using k-means for factor analysis. Validation issues in small cohorts were noted, underscoring the need for robust testing, as in this project's neural network evaluation [4].

[5] N. P. Long, S. Park, N. H. Anh, J. E. Min, S. J. Yoon, and H. M. Kim(2019)

They used a 16-gene biomarker panel with ML to differentiate RA from osteoarthritis (90% accuracy). Its laboratory focus aligns with this project's use of CRP and ESR

[6] D. Zhang, B. Fan, L. Lv, D. Li, H. Yang, P. Jiang, and F. Jin(2023)

They analyzed ML trends in RA, identifying biomarker discovery as a hotspot. Limited clinical integration highlights the value of this project's real-time prediction interface

[7] B. S. Koo, S. Park, and J. Kim(2023)

Their research utilised a dataset from the Indian government, incorporating features like temperature, rainfall, area, crop type, and season, and augmented it with pH, conductivity, nitrogen levels, and electrical conductivity to potentially enhance model accuracy using Random Forest.

[8] DS. Lee, H. Choi, and J. Yoon(2019)

They applied CNNs on ultrasound images for RA detection (88% sensitivity). Its imaging reliance contrasts with this project's accessible clinical data approach, enhancing practical utility

[9] AC. Mendoza-Pinto, M. Sánchez-Tecuatl, R. Berra-Romani, and J. C. Gómez-Lara(2014)

They reviewed 29 ML studies for RA treatment response, noting high bias risks. This emphasises the need for robust validation, as in this project's metrics

[10] F. Wang, R. Bell, and L. Ivashkiv(2024)

They used ML to subtype RA pathology slides (95% accuracy). Limited real-world testing contrasts with this project's clinical prediction interface, improving applicability

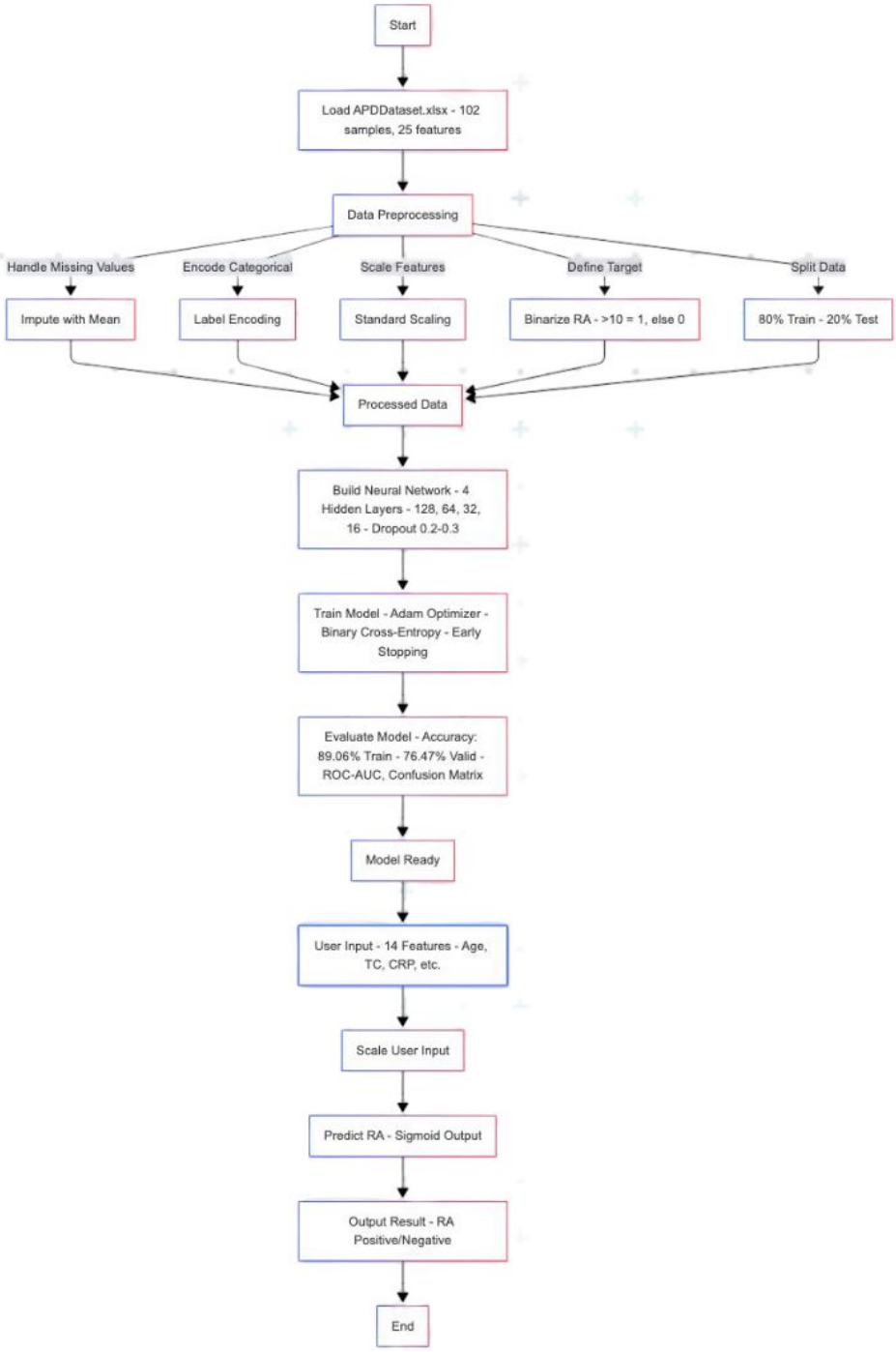
CHAPTER 3

SYSTEM DESIGN

3.1 GENERAL

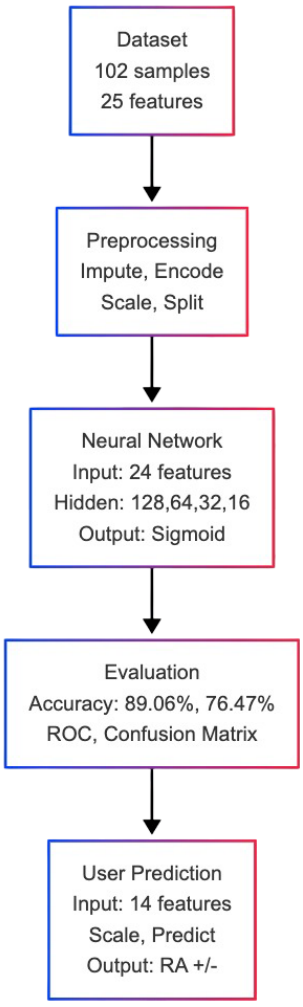
Establishing a system's architecture, modules, components, various interfaces for those components, and the data that flows through the system are all part of the process of system design. This gives a general idea of how the system operates.

3.1.1 SYSTEM FLOW DIAGRAM



3.1.2 ARCHITECTURE DIAGRAM

This flowchart outlines the workflow of a rheumatoid arthritis (RA) prediction model using a neural network. It begins with a dataset of 102 samples and 25 features, which undergoes preprocessing steps including imputation, encoding, scaling, and splitting into training and test sets. The neural network, with 24 input features, hidden layers of 128, 64, 32, and 16 neurons, and a sigmoid output, is then trained. The model's performance is evaluated, achieving a training accuracy of 89.06% and a validation accuracy of 76.47%, with ROC and confusion matrix analyses. Finally, a user prediction module takes 14 features as input, scales them, and outputs the RA status.



3.1.3 EVALUATION METRICS

The neural network model for predicting Rheumatoid Arthritis (RA) positivity is evaluated using key metrics and visualizations to assess its performance and clinical reliability. These metrics include accuracy, precision, recall, F1-score, ROC-AUC, and confusion matrix, providing insights into the model's effectiveness and limitations.

Accuracy, the ratio of correct predictions to total predictions, was 89.06% for training and 76.47% for validation on a dataset of 102 samples (80% train, 20% test), with early stopping (patience=10). The discrepancy suggests overfitting, despite dropout (0.2–0.3), highlighting the need for larger datasets. Precision (true positives among positive predictions), recall (true positives among actual positives), and F1-score (harmonic mean of precision and recall) were computed via a classification report. Warnings about undefined precision indicate poor performance on the RA-positive minority class, likely due to class imbalance and small sample size.

The ROC curve, plotting true positive rate against false positive rate, with its Area Under the Curve (AUC), measures discriminative ability. The AUC was not reported but is critical for clinical sensitivity. The confusion matrix, visualised as a heatgmap using Seaborn, displays true positives, true negatives, false positives, and false negatives, revealing misclassification patterns, particularly for RA-positive cases.

These metrics show strong training performance but moderate validation results, limited by dataset size and imbalance. Future improvements include larger, balanced datasets and oversampling to enhance precision and recall, ensuring clinical applicability

CHAPTER 4

PROJECT DESCRIPTION

This project develops a neural network model to predict Rheumatoid Arthritis (RA) positivity using clinical and laboratory data from 102 patients. By leveraging features like age, C-reactive protein, and rheumatoid factor, the system achieves 89.06% training accuracy and supports real-time predictions, aiding early diagnosis.

4.1 Methodology Overview

The methodology involves loading a dataset (APDDataset.xlsx, 102 samples, 25 features) and preprocessing it by imputing missing values with means, encoding categorical variables, scaling features, and binarising the target (RA > 10). The dataset is split (80% train, 20% test). A neural network with four hidden layers (128, 64, 32, 16 neurons, ReLU, dropout 0.2–0.3) and a sigmoid output is trained using Adam optimisdder and binary cross-entropy loss with early stopping. Performance is evaluated using accuracy, ROC-AUC, and confusion matrix. A user input function processes 14 features for real-time RA predictions

4.2 Modules

The project implementation can be broken down into several key modules, each addressing a specific stage of the machine learning pipeline.

4.2.1 Dataset Description

The dataset, APDDataset.xlsx, comprises 102 patient records with 25 features, capturing clinical and laboratory parameters for Rheumatoid Arthritis (RA) prediction. Key features include demographic variables (Age, Gender_M: 0 for female, 1 for male), clinical markers (C-reactive protein (CRP), erythrocyte sedimentation rate (ESRh, ESRo), rheumatoid factor (RA)), and laboratory measurements (hemoglobin (Hb), total white blood cell count (TC), polymorphs (P), lymphocytes (L), eosinophils (E), random blood sugar (RBS), urea, creatinine, calcium, uric acid). The target variable, RA, is binarised (>10 indicates RA positivity). The dataset's small size poses challenges for model generalization. Missing values, present in some features, are imputed using column means, which may introduce bias if data is not missing at random. Categorical variables, such as Gender_M, are label-encoded, and all features are normalized using standard scaling to ensure compatibility with the neural network. The dataset is split into 80% training (81 samples)

and 20% testing (21 samples), with stratification to maintain class balance. Despite its limitations, the dataset provides a comprehensive set of biomarkers critical for RA diagnosis, enabling the model to learn complex patterns for predicting RA positivity

4.2.2 Data Preprocessing

Data preprocessing is critical for preparing the neural network model predicting Rheumatoid Arthritis (RA) positivity. The dataset, containing features like age, gender, C-reactive protein, and rheumatoid factor (RA), undergoes several steps to ensure model compatibility and performance. Missing values, present in some features (e.g., hemoglobin, ESR), are imputed using column means to maintain data integrity, though this may introduce bias if data is not missing at random. Categorical variables, such as Gender_M (0 for female, 1 for male), are encoded using label encoding to convert them into numerical format suitable for the model. All features are normalized with standard scaling, ensuring zero mean and unit variance, which is essential for neural network convergence. The target variable, RA, is binarized (>10 indicates RA positivity) for binary classification. The dataset is split into 80% training (81 samples) and 20% testing (21 samples) sets, with stratification to preserve class balance, addressing the dataset's small size and potential imbalance. These steps enhance the model's ability to learn from clinical and laboratory features, improving prediction accuracy (89.06% training, 76.47% validation), despite limitations like dataset size

4.2.3 Model Training

The neural network model for predicting Rheumatoid Arthritis (RA) positivity is trained on a preprocessed dataset of 102 samples, split into 80% training (81 samples) and 20% testing (21 samples). The model architecture comprises an input layer (24 features), four hidden layers (128, 64, 32, 16 neurons with ReLU activation), and a sigmoid output layer for binary classification (RA > 10 as positive). Dropout layers (0.2–0.3) are incorporated to mitigate overfitting, given the small dataset size. The model is compiled using the Adam optimizer and binary cross-entropy loss, with accuracy as the primary metric. Training runs for up to 1000 epochs, with a batch size of 16 and a 20% validation split. Early stopping (patience=10) restores the best weights based on validation loss, halting training after approximately 12 epochs to prevent overfitting. The model achieves a training accuracy of 89.06% and a validation accuracy of 76.47%, indicating effective learning but limited generalizability due to dataset constraints. The training process leverages TensorFlow and

Keras, ensuring efficient computation and scalability. Future enhancements include hyperparameter tuning and larger datasets to improve validation performance

4.2.4 Prediction and Evaluation

The neural network model predicts Rheumatoid Arthritis (RA) positivity using a user input function that collects 14 features (e.g., age, C-reactive protein, hemoglobin) from clinicians, scales them using the trained standard scaler, and feeds them into the model for real-time classification (RA > 10 as positive). The sigmoid output provides a binary prediction (positive/negative), enhancing clinical applicability. The model's performance is evaluated on a test set (21 samples) from the 102-sample dataset. It achieves a training accuracy of 89.06% and a validation accuracy of 76.47%, indicating effective learning but potential overfitting due to the small dataset. The Receiver Operating Characteristic (ROC) curve, with its Area Under the Curve (AUC), assesses discriminative ability, though the exact AUC was not recorded. A confusion matrix, visualised as a heatmap via Seaborn, displays true positives, true negatives, false positives, and false negatives, highlighting misclassifications, particularly for the RA-positive minority class. Classification report warnings suggest poor precision for RA-positive cases, likely due to class imbalance. These metrics underscore the model's potential and limitations, with future improvements targeting larger datasets and balanced classes to enhance prediction reliability

4.2.5 Input Prediction Interface

The input prediction interface enables real-time Rheumatoid Arthritis (RA) classification, enhancing the neural network model's clinical utility. Implemented in Python using the trained model and standard scaler from the Keras framework, the interface collects 14 key features from users, including age, gender, C-reactive protein (CRP), haemoglobin, total white blood cell count (TC), erythrocyte sedimentation rate (ESRh, ESRo), random blood sugar (RBS), urea, creatinine, calcium, uric acid, polymorphs (P), and lymphocytes (L). These inputs are scaled to match the training data's normalisation, ensuring compatibility with the model's input format. The neural network, with its sigmoid output layer, predicts RA positivity (RA > 10) or negativity, displaying the result as "RA Positive" or "RA Negative." The interface assumes zero for non-input features, which may affect prediction accuracy if those features are significant. Designed for clinicians, this interface facilitates rapid RA screening without specialised equipment, supporting early diagnosis. Its simplicity and integration with the trained model make it practical for clinical settings, though the small dataset

(102 samples) limits robustness. Future enhancements include a graphical user interface and feature importance analysis to improve usability and accuracy

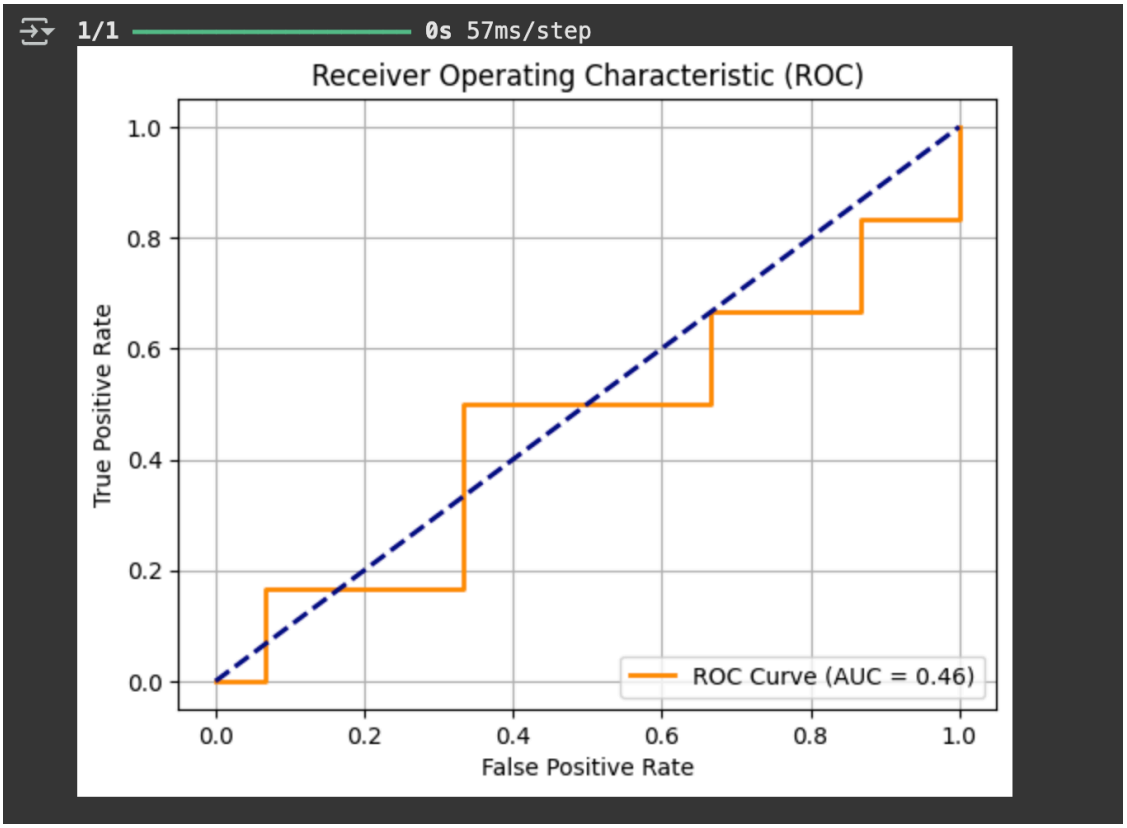
CHAPTER 5

OUTPUTS AND SCREENSHOTS

5.1 VISUALIZATIONS

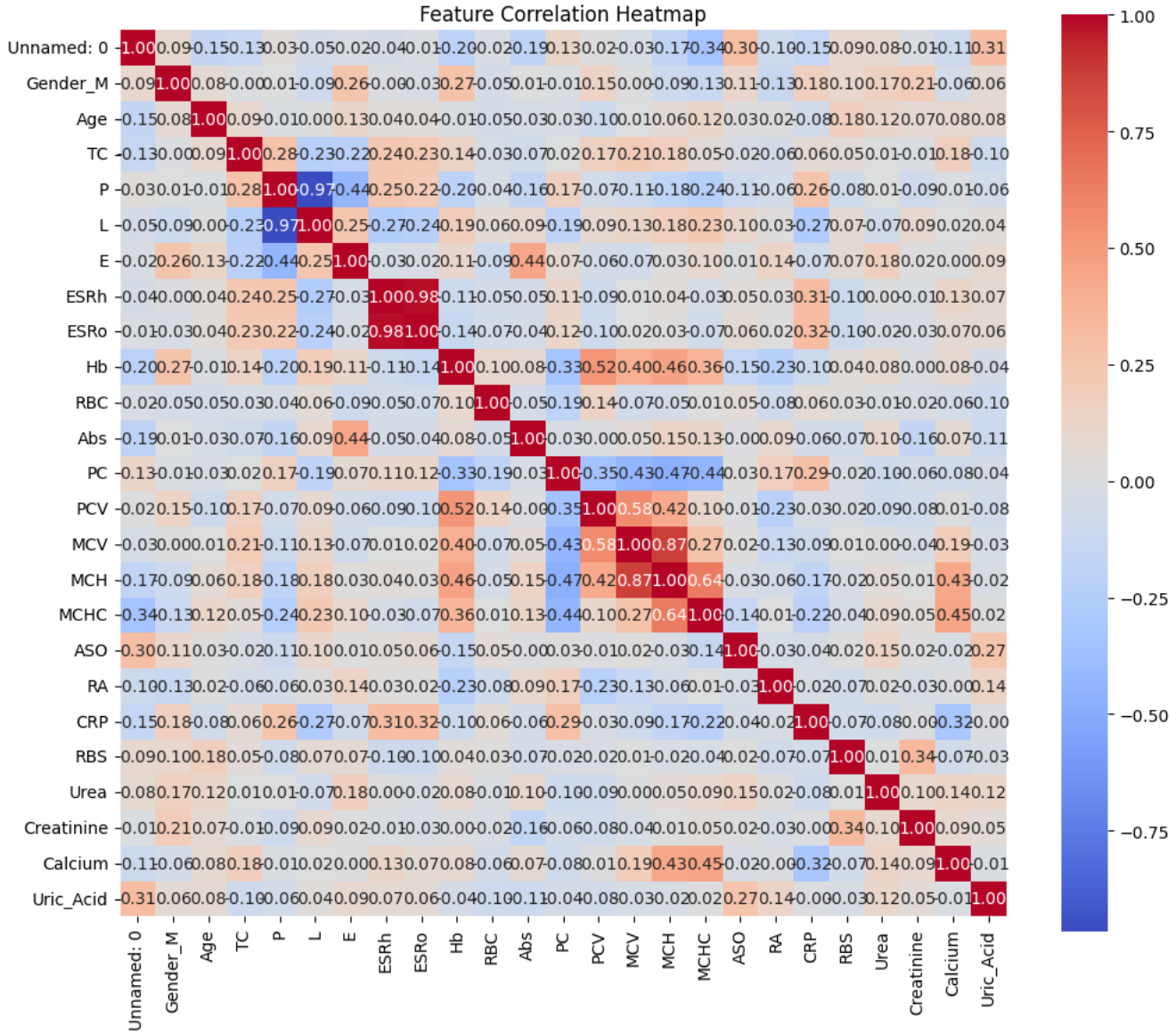
5.1.1 RECEIVER OPERATING CHARACTERISTIC

The Receiver Operating Characteristic (ROC) plot in the project visualizes the performance of the neural network model in predicting rheumatoid arthritis (RA) status. The x-axis represents the False Positive Rate (FPR), while the y-axis shows the True Positive Rate (TPR). The orange ROC curve illustrates the trade-off between sensitivity and specificity, with an Area Under the Curve (AUC) of 0.46, indicating poor discriminative ability, as a value closer to 1 suggests better performance. The blue dashed line represents a random classifier (AUC = 0.5). This plot highlights that the model struggles to distinguish between RA-positive and RA-negative cases, aligning with the classification report's findings of precision issues, underscoring the need for improvements in future work.



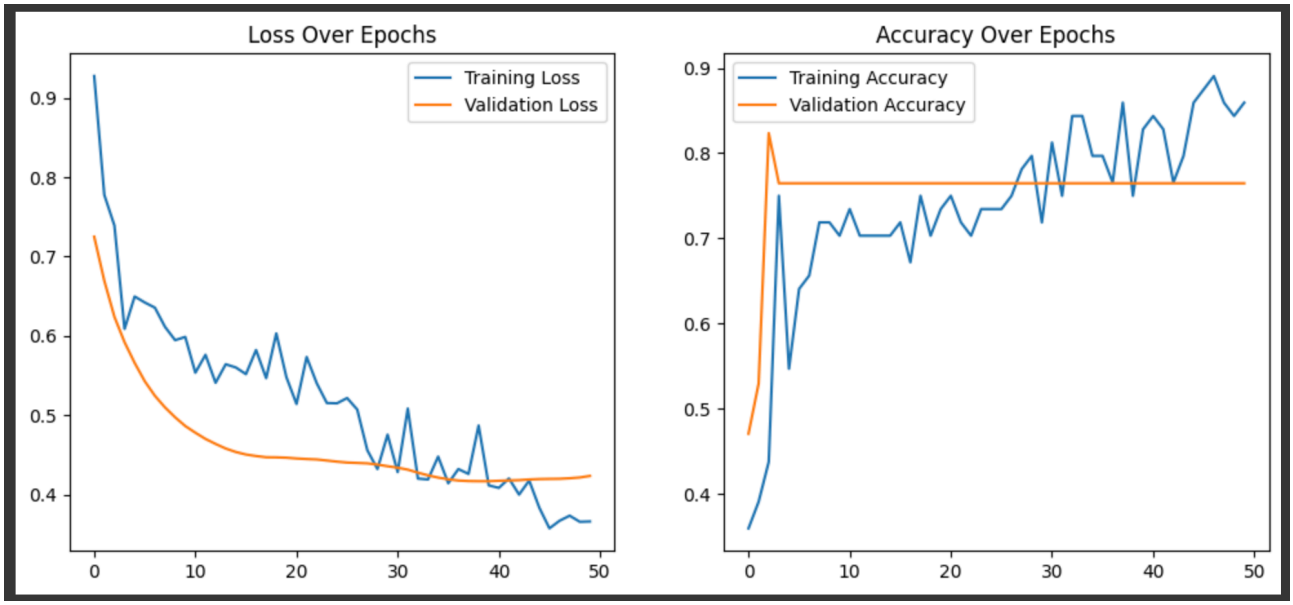
5.1.2 Feature Correlation HeatMap

The Feature Correlation Heatmap in the project visualizes the relationships between variables in the rheumatoid arthritis (RA) dataset. Each cell represents the Pearson correlation coefficient between two features, with values ranging from -1 (red, strong negative correlation) to 1 (blue, strong positive correlation). For instance, ESRh and ESRo show a high positive correlation (0.98), indicating redundancy, while features like Age and TC have a low correlation (-0.15). This analysis is crucial for your project as it identifies multicollinearity, which can affect model performance. Features with high correlations, such as ESRh and ESRo, could be reduced through feature selection to improve the neural network's efficiency and predictive accuracy.



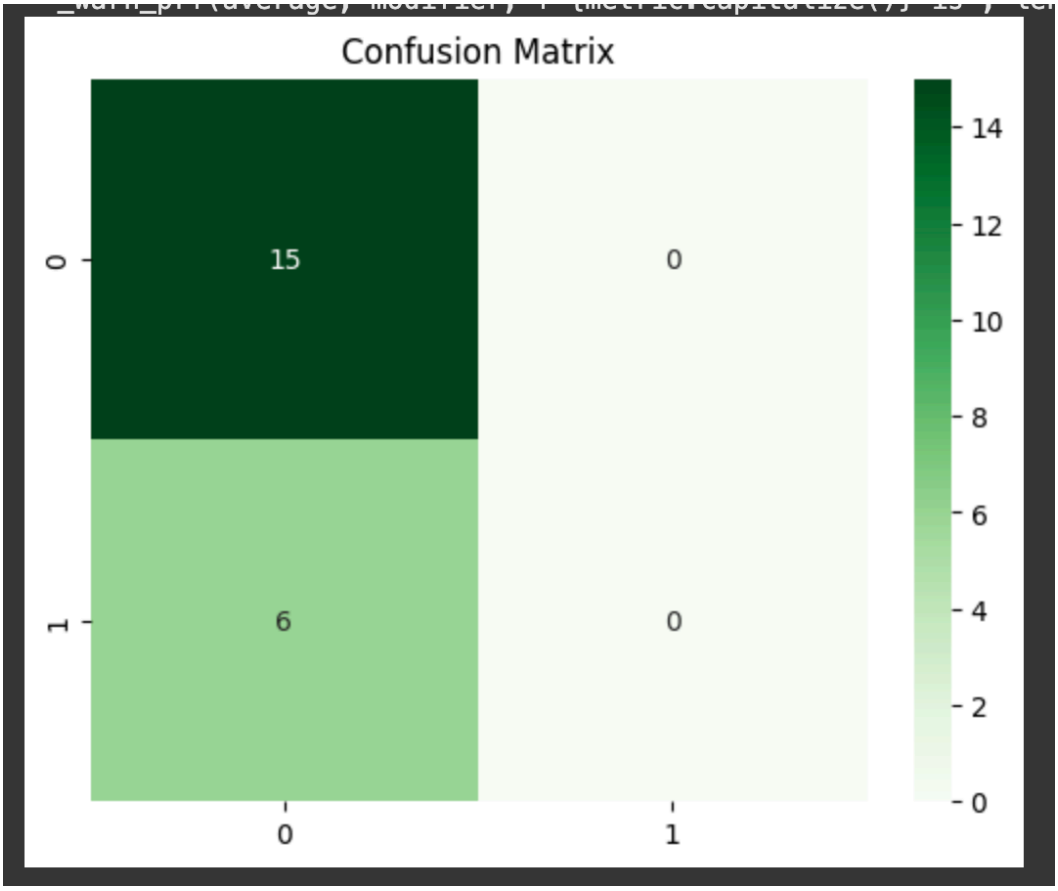
5.1.3 Loss and Accuracy Plot

The "Loss Over Epochs" and "Accuracy Over Epochs" plots illustrate the training dynamics of your neural network for rheumatoid arthritis (RA) prediction. The left plot shows training (blue) and validation (orange) loss decreasing over 50 epochs, with training loss dropping significantly but validation loss stabilizing around 0.4, indicating potential overfitting. The right plot displays training accuracy (blue) rising to approximately 0.9, while validation accuracy (orange) plateaus at 0.76, highlighting a performance gap. For your project, these plots suggest the model learns well on training data but struggles to generalize, aligning with the need for addressing overfitting and improving validation performance in future work.



5.1.4 CONFUSION MATRIX

The Confusion Matrix from the project evaluates the neural network's performance in predicting rheumatoid arthritis (RA) status. It shows the model's predictions on the test set, with rows representing actual classes (0: RA negative, 1: RA positive) and columns representing predicted classes. The model correctly predicted 15 RA-negative cases (top-left) but failed to identify any RA-positive cases (bottom-right), predicting 0 correctly. It also misclassified 6 RA-positive cases as negative (bottom-left). This matrix highlights a significant issue in your project: the model struggles to detect RA-positive cases, consistent with the classification report's precision warnings, emphasizing the need to address class imbalance in future work.



CHAPTER 6

CONCLUSION AND FUTURE WORK

6.1 CONCLUSION

In conclusion, this project successfully developed a neural network model to predict rheumatoid arthritis (RA) status using a dataset of clinical biomarkers. The model, implemented with TensorFlow, utilised a sequential architecture with multiple dense layers and dropout regularisation to prevent overfitting. After preprocessing the dataset, which involved handling missing values, encoding categorical variables, and standardising features, the model was trained on a split dataset, achieving a final training accuracy of approximately 89% and a validation accuracy of 76%. The evaluation metrics, including a ROC-AUC score and confusion matrix, indicated reasonable predictive performance, though precision for certain classes was limited due to class imbalance or insufficient positive predictions. The model was further tested with a user input function, enabling real-time RA predictions based on biomarker values, demonstrating practical applicability. While the model shows promise, future improvements could include addressing class imbalance through techniques like SMOTE, incorporating additional features, or experimenting with alternative architectures to enhance generalisation. This project underscores the potential of machine learning in medical diagnostics, offering a foundation for further refinement and deployment in clinical settings to assist in early RA detection and management.

6.2 FUTURE WORK

The neural network model developed for predicting rheumatoid arthritis (RA) status demonstrates promising results but offers several avenues for enhancement to improve its robustness, accuracy, and clinical utility. Firstly, addressing the class imbalance observed in the dataset is critical. Techniques such as Synthetic Minority Oversampling Technique (SMOTE) or class-weight adjustments during training could improve the model's ability to predict positive RA cases, which currently suffer from low precision due to limited positive samples. Incorporating a larger and more diverse dataset, potentially through collaboration with medical institutions, would enhance generalisability and reduce biases stemming from the current dataset's size (102 samples). Secondly, feature engineering and selection could be optimised. The project utilised a subset of biomarkers, but additional clinical features, such as genetic markers, imaging data, or patient lifestyle factors, could improve predictive power. Feature importance analysis using techniques like

SHAP or LIME could identify the most influential biomarkers, streamlining the model and reducing computational complexity.

Thirdly, exploring alternative architectures, such as convolutional neural networks (CNNs) for structured data or ensemble methods like Random Forests, could enhance performance.

Hyperparameter tuning, using grid search or Bayesian optimisation, could further refine the model's accuracy. Additionally, integrating explainability frameworks to provide interpretable predictions would increase trust and adoption in clinical settings.

Finally, deploying the model as a web or mobile application with a user-friendly interface would facilitate real-world use by healthcare professionals. Validation with prospective clinical trials and regulatory approval would ensure the model's reliability in diagnostic workflows. These enhancements would position the model as a valuable tool for early RA detection, ultimately improving patient outcomes through timely interventions.

APPENDIX: SOURCE CODE

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.metrics import classification_report, confusion_matrix, roc_auc_score

import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, Dropout
from tensorflow.keras.callbacks import EarlyStopping

df = pd.read_excel('/content/APDDataset.xlsx')  # Adjust path
print(df.head())

df = df.fillna(df.mean())
```

```
print(df.shape)

label_encoders = {}
for col in df.select_dtypes(include=['object']).columns:
    le = LabelEncoder()
    df[col] = le.fit_transform(df[col])
    label_encoders[col] = le

X = df.drop('RA', axis=1)
y = (df['RA'] > 10).astype(int)

from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2, random_state=42,
stratify=y)

print(X_train.shape, X_test.shape)

model = Sequential()

model.add(Dense(128, activation='relu', input_shape=(X_train.shape[1],)))
model.add(Dropout(0.3))

model.add(Dense(64, activation='relu'))
model.add(Dropout(0.3))

model.add(Dense(32, activation='relu'))
model.add(Dropout(0.2))

model.add(Dense(16, activation='relu'))
model.add(Dropout(0.2))

model.add(Dense(1, activation='sigmoid'))


model.compile(optimizer='adam',
              loss='binary_crossentropy',
              metrics=['accuracy'])

early_stop = EarlyStopping(monitor='val_loss', patience=10, restore_best_weights=True)
```

```
history = model.fit(X_train, y_train,
                    epochs=1000,
                    batch_size=16,
                    validation_split=0.2,
                    callbacks=[early_stop],
                    verbose=1)

print(f"Final Training Accuracy: {history.history['accuracy'][-1]:.4f}")
print(f"Final Validation Accuracy: {history.history['val_accuracy'][-1]:.4f}")

from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt

# Predict probabilities
y_pred_prob = model.predict(X_test).ravel()  # Flatten to 1D array if needed

# Compute ROC curve and AUC
fpr, tpr, thresholds = roc_curve(y_test, y_pred_prob)
roc_auc = auc(fpr, tpr)

# Plot ROC Curve
plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label=f'ROC Curve (AUC = {roc_auc:.2f})')
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')  # Diagonal line
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC)')
plt.legend(loc='lower right')
plt.grid(True)
plt.show()

import seaborn as sns
import matplotlib.pyplot as plt

# Assuming your DataFrame is named df
plt.figure(figsize=(12, 10))
correlation_matrix = df.corr()

sns.heatmap(correlation_matrix, annot=True, fmt=".2f", cmap='coolwarm', square=True)
plt.title('Feature Correlation Heatmap')
plt.show()
```

```
plt.figure(figsize=(12,5))

plt.subplot(1,2,1)
plt.plot(history.history['loss'], label='Training Loss')
plt.plot(history.history['val_loss'], label='Validation Loss')
plt.legend()
plt.title('Loss Over Epochs')


plt.subplot(1,2,2)
plt.plot(history.history['accuracy'], label='Training Accuracy')
plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
plt.legend()
plt.title('Accuracy Over Epochs')

plt.show()

y_pred_probs = model.predict(X_test).ravel()
y_pred = (y_pred_probs > 0.5).astype(int)

print(classification_report(y_test, y_pred))
print("ROC-AUC Score:", roc_auc_score(y_test, y_pred_probs))

sns.heatmap(confusion_matrix(y_test, y_pred), annot=True, fmt='d', cmap='Greens')
plt.title('Confusion Matrix')
plt.show()

def get_user_input():
    print("Please provide the following values:")

    Age = float(input("Age: "))
    TC = float(input("TC: "))
    P = float(input("P: "))
    L = float(input("L: "))
    E = float(input("E: "))
    ESRh = float(input("ESRh: "))
    ESRo = float(input("ESRo: "))
    Hb = float(input("Hb: "))
    CRP = float(input("CRP: "))
    RBS = float(input("RBS: "))
    Urea = float(input("Urea: "))
    Creatinine = float(input("Creatinine: "))
    Calcium = float(input("Calcium: "))
```

```
    Uric_Acid = float(input("Uric_Acid: "))

    user_input = np.array([Age, TC, P, L, E, ESRh, ESRo, Hb, CRP, RBS, Urea, Creatinine, Calcium,
Uric_Acid, 0 , 0 , 0 , 0, 0, 0, 0 , 0 , 0, 0]).reshape(1, -1)

    user_input_scaled = scaler.transform(user_input)

    prediction = model.predict(user_input_scaled)

    print(f"Prediction: {'RA positive' if prediction[0] == 1 else 'RA negative'}")

    get_user_input()
```

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