|  |
| --- |
| **IPL Score Prediction using Machine Learning Algorithms** |
| **By: -** |
| **Akash Rao (4NM19CS013)** |
| **Amogha Mayya K S (4NM19CS019)** |
| **Bachelor of Engineering** |
| **in** |
| **COMPUTER SCIENCE AND ENGINEERING** |
| **Under the guidance of** |
| **Dr. Aravinda C. V** |
| **Associate Professor** |
| ***Mini Project – Report Submitted to NMAM Institute of Technology, Nitte an Autonomous Institution affiliated to VTU Belagavi*** |
| **DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING** |



ISO 9001:2015 Certified; Accredited with ‘A’ Grade by NAAC

June 2022



ISO 9001:2015 Certified

Accredited with ‘A’ Grade by NAAC

*Department of* ***Computer Science & Engineering***

CERTIFICATE

*Certified that the Part I of the project work entitled* ***IPL Score Prediction using Machine Learning Algorithms*** *carried out by* ***Akash Rao & Amogha Mayya,*** *USN* ***4NM19SCS013 & 4NM19CS019*** *a bonafide student of* ***NMAM Institute of Technology****,* ***Nitte*** *has been carried out satisfactorily. The Mini Project –the report has been prepared as per the prescribed format.*

**Name & Signature of Guide(s) Name & Signature of HOD**

### Project – Part I Evaluation

**Name of the Examiners Signature with Date**

*1.*

*2.*

# ACKNOWLEDGEMENT

The success and final outcome of this project required a lot of guidance and assistance from many people, and I am extremely fortunate to have got their support all along with the completion of our project.

I take this opportunity to express my profound gratitude and deep regards to my Project Guide **Dr. Aravinda C V.,** Associate Professor, Department of Computer Science and Engineering, for his exemplary guidance, monitoring, and constant encouragement throughout the course of this project.

I also express a deep sense of gratitude to **Dr. Jyothi Shetty.,** Head of the Department, of Computer Science and Engineering, for her cordial support, valuable information, and guidance, which helped me in completing this project through various stages.

Lastly, I thank almighty, my parents and friends for their constant encouragement.

- XXX

# ABSTRACT

**Motivation:** Malaria is a serious disease which affects hundreds of people around the world, each year. If not treated in time, it can be fatal. According to WHO’s latest *World malaria report*, there were an estimated 241 million malaria cases and 627 000 malaria deaths worldwide in 2020. Despite recent developments in malaria diagnostics, the microscopy method to detect malaria remains the most common. Unfortunately, the accuracy of microscopic diagnostics is dependent on the skill of the microscopist and limits the throughput of malaria. Distinguishing the multiple growth stages of parasites remains an especially challenging task.

**Goal:** To develop a system to identify malaria stages in blood smear

**Results:** To prevent number of people getting affected by malaria, the diagnosis should be in early stage and accurate. Therefore, it takes a rapid identification system with a high percentage of accuracy to reduce the risk of death. This research aims to build an identification system of malaria parasite stages in thin blood film using machine learning models.

**TABLE OF CONTENTS**

|  |  |  |
| --- | --- | --- |
| **Chapter No. Title** | | **Page**  **No.** |
|  | **ABSTRACT** |  |
| **1** | **INTRODUCTION** | **1-4** |
| **2** | **LITERATURE SURVEY** | **5-10** |
| **3** | **METHODOLOGY** | **11-17** |
| 3.1 | Proposed method | **11** |
| 3.2 | Dataset collection | **12** |
| 3.3 | Image Segmentation | **13** |
| 3.4 | Feature Extraction | **13** |
| 3.4.1 | Working of LBP | **14** |
| 3.5 | Machine Learning Algorithm | **16** |
| 3.6 | Hardware and software used | **16** |
| **4** | **RESULTS AND DISCUSSION** | **18-20** |
| 4.1 | Segmentation | **18** |
| 4.2 | Classification Report | **19** |
|  | **REFERENCES** |  |

**LIST OF FIGURES**

|  |  |  |
| --- | --- | --- |
| **FIGURE NO.** | **FIGURE NAME** | **PAGE NO.** |
| 1.1 | Five different human malaria Plasmodium species and their life stages in thin blood films | 2 |
| 1.2 | Stages of malaria in blood smears | 4 |
| 3.1 | Block diagram of proposed method | 11 |
| 3.2 | Sample images from dataset | 12 |
| 3.3 | Preprocessed image divided in to several small regions | 14 |
| 3.4 | Example of LBP Operator | 14 |
| 3.4.1 | Circularly neighbor-sets for three different values of p and r | 16 |

**LIST OF TABLES**

|  |  |  |
| --- | --- | --- |
| **TABLE NO.** | **TABLE NAME** | **PAGE NO.** |
| 4.1 | Comparison of segmented images | 18-19 |
| 4.2 | Classification Report of Random Forest Model | 20 |

**INTRODUCTION**

**IPL stands for Indian Premier League, a T20 cricket tournament which was originally established in 2008. It is traditionally played from April through to June each year and, from 2022, the competition will be expanded to include a total of ten teams.**The Indian Premier League **starts with a round robin tournament where each franchise will play each other twice –** home and away. Sides will earn two points for a win while the teams will earn one point each if there is an abandoned game.At the end of this sequence, the top four sides in the table will progress to the playoffs while the remaining franchises will be eliminated.

**The playoffs start with the first qualifier** where the top two sides in the table play each other and the winner goes straight through to the final.**Next up is the eliminator** where the third and fourth placed sides face off. The winner goes through to the second qualifier while the loser is eliminated.In the second qualifier, the winner of the eliminator takes on the loser of the first playoff match. The winner of that game progresses to the final.It sounds a little complicated on paper but it’s actually easy to follow and it’s a fairer system than having straight semi finals.

In particular, here we will be looking at how you can train a model from scratch and embed it in the web app using simple and powerful libraries like **sklearn, pandas, and flask**. Also, some **web**development is involved.

The Beneath segment gives an outline and a few rules and you are prescribed to go through it previously.

### Overview

* 1 – Data Gathering
* 2 – EDA – Exploratory Data Analysis
* 3 – Data Cleaning
* 4- Data Preparation
* 5 – Model Development
* 7 – Conclusion
* 8 – References
* 6 – Model Deployment – Optional
* Open Sources –  This data is readily available in the form of structured data (rows and columns) and can be downloaded from sites like [Kaggle](https://www.kaggle.com/), [UCI-ML-Repository](https://archive.ics.uci.edu/ml/index.php), and [Open Government Data](https://data.gov.in/).
* Collection by Individuals – Often it happens that in some cases, data is not available so the team gathers data using tools like we scrapper or go out and gather data for themselves.
* CrowdSourcing – In this technique, people like ours help in annotating data for eg. Captcha services.

For our use case, we are going to use the IPL Scores Dataset (link in reference) which has 76104 observations and 15 features  :

## EDA – Exploratory Data Analysis for IPL Score Predictor

Having looked at the data quickly, let’s dive deeper into the dataset and explore some of the insights. This procedure is very important and will allow us to understand the data and plan our next steps. Luckily pandas provide easy-to-use functions to perform our analysis. So let’s begin.

# CHAPTER 2

**LITERATURE SURVEY**

Sen Li, Zeyu Du, Xiangjie Meng, Yang Zhang[1] developed a novel deep learning approach for the recognition of malaria parasites of various stages in blood smear images using deep transfer graph convolutional network. The proposed model is based on unsupervised learning by knowledge transfer obtained from source images containing the distinguishing morphological features of the malaria parasite at several stages. This transferred information ensures efficient identification of the target parasite. This approach first learns the source identical representations to establish topological correlations between groups of source classes and unlabelled target patterns. At this point, GCN was performed to extract graphical feature representations for multistage malaria parasite identification. The proposed method has shown superior accuracy and efficiency in publicly available multistage malaria micrographs compared with a variety of modern methods.

Due to the high number of cases and lack of sufficient diagnostic facilities and experienced medical personnel, there is a need for advanced diagnostic procedures to complement existing methods. For this reason, Abubakar, Aliyu, Mohammed Ajuji, and Ibrahim Usman Yahya [2] in their study proposed the use of machine-learning models to detect the malaria parasite in blood-smear images. Six different features— VGG16, VGG19, ResNet50, ResNet101, DenseNet121, and DenseNet201 models were extracted. Then Decision Tree, Support Vector Machine, Naïve Bayes, and K- Nearest Neighbour classifiers were trained using these six features. Extensive performance analysis is presented in terms of precision, recall, f-1score, accuracy, and computational time. The results showed that automating the process can effectively detect the malaria parasite in blood samples with an accuracy of over 94% with less complexity than the previous approaches.

Malaria, a fatal but curable disease claims hundreds of thousands of lives every year. Early and correct diagnosis is vital to avoid health complexities, however, it depends upon the availability of costly microscopes and trained experts to analyze blood-

smear slides[3]. Deep learning-based methods have the potential to not only decrease the burden of experts but also improve diagnostic accuracy on low-cost microscopes. However, this is hampered by the absence of a reasonable size dataset. One of the most challenging aspects is the reluctance of the experts to annotate the dataset at low magnification on low-cost microscopes.They presented a dataset to further research on malaria microscopy over the low-cost microscopes at low magnification. The large-scale dataset consists of images of blood-smear slides from several malaria-infected patients, collected through microscopes at two different cost spectrums and multiple magnifications. Malarial cells are annotated for the localization and life-stage classification task on the images collected through the high-cost microscope at high magnification. A design mechanism was proposed to transfer these annotations from the high-cost microscope at high magnification to the low-cost microscope, at multiple magnifications. Multiple object detectors and domain adaptation methods are presented as the baselines. Furthermore, a partially supervised domain adaptation method is introduced to adapt the object-detector to work on the images collected from the low-cost microscope.

Malaria, caused by the parasite plasmodium, infects the cells of the host and multiplies using their resources. One of the best ways to test malaria involves forming blood smears and examining the slides [4]. Malarial cell count detection is a crucial process in classifying the extent of malarial infection. We have devised and tested an algorithm that automates the process of malarial cell count detection and classifies the images according to stage of malaria present. Images from various patients were obtained and tested.They used morphological operations to demarcate malaria infected cells, and hyper-parameter tuning was employed to optimize the algorithm for better accuracy. The proposed algorithm for malarial cell count detection is capable of automating the cell count process and produces accuracy levels greater than 90% in finding the correct count of parasite infected cells in the sample and greater than 90% accuracy in correctly classifying the stage of malaria.

Mehedi Masud, Hesham Alhumyani, Sultan S. Alshamrani, Omar Cheikhrouhou, Saleh Ibrahim, Ghulam Muhammad, M. Shamim Hossain and Mohammad Shorfuzzaman, [5] proposed a work which investigates the use of deep learning algorithms for detecting a deadly disease, malaria, for mobile healthcare solutions for patients, with the aim of developing an efficient mobile device. The main idea is to demonstrate how deep learning architectures, such as convolutional neural networks (CNN), can be used in real-time malaria detection from input images in an efficient and accurate manner. According to the conclusions, the output of a custom CNN model using a cyclical stochastic gradient descent (SGD) optimizer with an automated learning rate finder is evaluated, and an accuracy of 97.30 percent is obtained in classifying safe and contaminated cell images with high precision and sensitivity.

Malarial fever disease mainly caused by Plasmodium parasite that is infectious to red blood cells. Manual mode of blood cell counting is a tedious process, this leads to distressing method for diagnosis. This processes mainly impacted on larger screening process. Aravinda C V,Meng Lin ,Udaya Kumar Reddy K R ,Amar Prabhu G[6] proposed a method on analysis of this malarial disease, based on Gabor Filters followed by the comparison of XG-Boost classifier, Support Vector Machine and Neural Network Classifier algorithms chosen as architecture of choice for recognition and classification of these malarial blood cells. From the experiments the models such as S.V.M achieved 94% and XG-Boost achieved 90% neural network classifier achieved 80%, out of these S.V.M performed good results in classifying and recognizing the parasitized and uninfected blood cells to increase the accuracy in decision making.

Malaria is a female anopheles’ mosquito-bite inflicted life-threatening disease which is considered endemic in many parts of the world. This article [7] focuses on improving malaria detection from patches segmented from microscopic images of red blood cell smears by introducing a deep convolutional neural network. Compared to the traditional methods that use tedious hand engineering feature extraction, the proposed method uses deep learning in an end-to-end arrangement that performs

both feature extraction and classification directly from the raw segmented patches of the red blood smears. The dataset used in this study was taken from National Institute of Health named NIH Malaria Dataset. The evaluation metric accuracy and loss along with 5-fold cross validation was used to compare and select the best performing architecture. To maximize the performance, existing standard pre- processing techniques from the literature has also been experimented. In addition, several other complex architectures have been implemented and tested to pick the best performing model. A holdout test has also been conducted to verify how well the proposed model generalizes on unseen data. The propsed best model achieves an accuracy of almost 97.77%.

Md. Khayrul Bashar[8] proposed a supervised approach for identifying malaria parasite stages from microscope pictures in the paper. This approach combines colour and texture characteristics with a support vector machine (SVM) classifier to achieve the goal. Three texture characteristics, including the histogram of oriented pattern (HOG), local binary pattern (LBP), and Grey-level Co-occurrence Matrix (GLCM), as well as four colour features, including local colour moments (StatMom) and colour histograms (HSV, LAB, and YCrCb), were evaluated. An imbalanced dataset of 46,978 single-cell thin blood smear pictures was used in an experiment, and the colour characteristics outperformed the texture features. The proposed colortexture feature (YCrCb HOG) seems to have the best accuracy rate (96.9%) on average using the SVM classifier, exceeding a previously published approach utilising the HOG LBP feature with the SVM classifier (87.1 percent ).

Image recognition algorithms and machine learning techniques were used to measure parasitaemia in microscopic blood slides to improve diagnosis[9]. This article provides a summary of these methods as well as a discussion of recent advances in image processing and machine learning for microscopic malaria diagnosis. Different methods are explored based on imaging techniques, image pre- processing, parasite identification and cell segmentation, attribute computation, and automated cell classification. The most recent advancements in deep learning and mobile technologies for future malaria diagnosis are also addressed.

Park, Han Sang, et[10] al presented an automated analysis method for detection and staging of red blood cells infected by the malaria parasite *Plasmodium falciparum* at trophozoite or schizont stage. this study uses quantitative phase images of unstained cells. To improve the diagnostic capacity, various machine learning techniques like linear discriminant classification (LDC), logistic regression (LR), and *k*-nearest neighbor classification (NNC) have been applied. Results showed that LDC provides the highest accuracy of up to 99.7% in detecting schizont stage infected cells compared to uninfected RBCs. NNC showed slightly better accuracy (99.5%) than either LDC (99.0%) or LR (99.1%) for discriminating late trophozoites from uninfected RBCs. However, for early trophozoites, LDC produced the best accuracy of 98%. Discrimination of infection stage was less accurate, producing high specificity (99.8%) but only 45.0%-66.8% sensitivity with early trophozoites most often mistaken for late trophozoite or schizont stage and late trophozoite and schizont stage most often confused for each other.

Vinayak K. Bairagi and Kshipra C. Charpe[11] presented an automatic method for diagnosis of malaria parasite in the blood images. Image processing techniques are used for diagnosis of malaria parasite and to detect their stages. The diagnosis of parasite stages is done using features like statistical features and textural features of malaria parasite in blood images. This paper gives a comparison of the textural based features individually used and used in group together. The comparison is made by considering the accuracy, sensitivity, and specificity of the features for the same images in database.

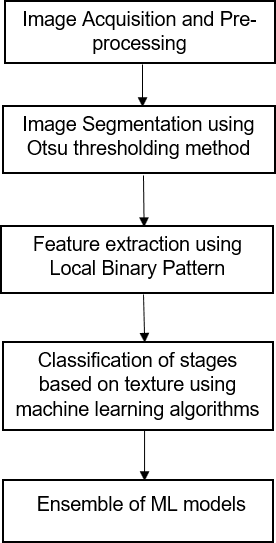
The method proposed by Akshay,Sparsh.et.al [12]involves acquisition of the thin blood smear microscopic image at 100x magnification, pre-processing by partial contrast stretching, separation of infected cell from the image by applying k-means clustering on the a\*b component of L\*a\*b color space, feature extraction (shape and textural) of the infected cell, feature reduction using one way ANOVA and finally training the K-nearest neighbor classifier to test the images. Instead of extracting features for the entire group of erythrocytes present in the image, the algorithm only processes the infected cells increasing the speed, effectiveness and efficiency of

testing. The KNN classifier is trained with 300 images to detect three lifecycle stages (trophozoite, schizont and gametocyte) for each of the four species of malarial parasites (Falciparum, P.vivax, P.malariae, and P.ovale) with an accuracy of 90.17% and sensitivity of 90.23%.

# CHAPTER 3

**METHODOLOGY**

## Proposed method



**Fig 3.1**. Block diagram of Proposed method

Figure 3.1 shows the flow of proposed method.It involves the following steps

* + 1. The input image is a giesma stained blood samples of multi stage malaria cells.
    2. Image is then segmented using Otsu segmentation process
    3. Feature extraction of an image is done using LBP technique. These characteristics can help the classification unit to decide which human host if effected by malaria and in what stage it is in.
    4. Following that suitable machine learning classifiers are used to classify them to different classes.
    5. Finally, based on the feature classes discovered by the classifier, a decision is made about the information conveyed by the image
    6. Ensemble of different machine learning models

## Dataset Collection

The multi-stage malaria infected cell images were captured from blood smear samples stained with Giemsa reagent. This image set consists in total of 1,364 images at 1,000× magnification and is publicly available at the Broad Bioimage Benchmark Collection (BBBC) website [1]. All of the images were manually captured from Plasmodium vivax–infected patients in Manaus, Brazil, and Thailand under 1,000× magnification, annotated by 3 different experts globally[1]. This dataset contains images 2 classes of uninfected cells (RBCs and leukocytes) and 4 classes of parasitized cells (gametocytes, rings, trophozoites, and schizonts) with Giemsa stain as seen in the figure 3.2. In this study totally 7,456 microscopic images are used out of which 6,856 images are used for training and 600 images for testing. This dataset is released on April 21,2021.



a) b) c)



d) e) f)

**Fig 3.2**. Sample images from dataset a) gametocyte b) leukocyte c) red blood cell d) Ring e) schizont f) trophozoite

## Image Segmentation

Image segmentation is an important part in image processing. In this work Otsu thresholding method is used for image segmentation. OTSU method is a global adaptive binarization threshold image segmentation algorithm. In computer vision and image processing, Otsu's method, named after Nobuyuki Otsu is used to perform automatic image thresholding. It is the process of detecting an image from background and then breaking that image in to different segments. It will be easier to do processing on those segmented images.

Segmentation is necessary because -

* It changes representation of an image into something that is more meaningful and easier to analyze.
* After segmentation it is easy to locate the objects and boundaries of the image more precisely.
* It is a process of assigning label to every pixel in an image such that pixel with same label share certain characteristics.

Otsu segmentation is based on histogram of images.Image contains 2 classes of pixels such as foreground and background pixels. The aim is to find the threshold value where sum of foreground and background pixel is at its minimum.

## Feature Extraction

Feature extraction is the method for creating a new and smaller set of features that captures most of the useful information of raw data. It is related to dimensionality reduction. When the input data to an algorithm is too large to be processed and it is suspected to be redundant, then it can be transformed in to reduces set of features. This process is called feature extraction. The extracted features are expected to contain relevant information from the input data so that the desired task can be performed by using this reduced representation instead of complete initial data.

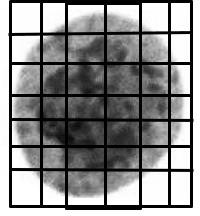
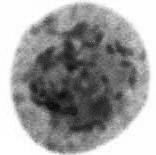
In this work Local Binary Pattern (LBP) is used for extracting features. It is a popular technique used for image representation and classification. The original LBP operator was introduced by Ojala et al. [18]. Local Binary Pattern (LBP) is a simple yet very

efficient texture operator which labels the pixels of an image by thresholding the neighbourhood of each pixel and considers the result as a binary number[16].LBP is used to automatically classify and identify textures and patterns in images.

It have been used for wide range of applications like face detection, texture classification, object detection system etc.LBP when applied on the acquired image of blood sample it can determine the texture characteristics.

* + 1. **Working of LBP**

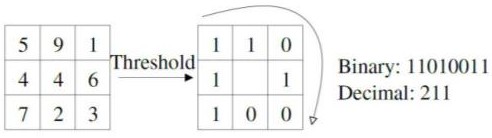
With LBP it is possible to describe the texture and shape of a digital image. This is done by dividing an image into several small regions from which the features are extracted (figure 3.3)



**Fig 3.3.** Preprocessed Image divided in to several small regions

LBP has four parameters like radius, neighbors, grid x(number of cells in horizontal direction),grid y(number of cells in vertical direction).This algorithm uses sliding window concept based on parameters like radius, neighbors

The most common approach however dictates that each 3x3 window in the image is processed to extract an LBP code. Figure 3.4 shows the example of LBP operator. The processing involves thresholding the center pixel of that window with its surrounding pixels using window mean, window median or the actual center pixel, as thresholds. It uses histogram of the patterns for texture classification.



**Fig 3.4.** Example of LBP Operator

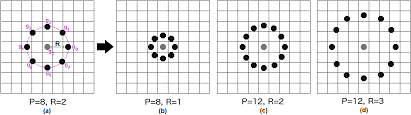
LBP steps[16]:

* we have a multi stage malaria infected cell image converted in to grayscale.
* Since this algorithm uses sliding window concept it dictates that each 3x3 window in the image is processed to extract LBP code.
* It can also be represented as a 3x3 matrix containing the intensity of each pixel (0~255).
* Then, take the central value of the matrix to be used as the threshold.
* This value will be used to define the new values from the 8 neighbors.
* For each neighbour of the central value (threshold), set a new binary value. Set 1 for values equal or higher than the threshold value and 0 for values lower than the threshold.
* Now, the matrix will contain only binary values (ignoring the central value). Concatenate each binary value from each position from the matrix line by line into a new binary value (e.g., 11010011).
* Then, we convert this binary value to a decimal value and set it to the central value of the matrix, which is actually a pixel from the original image.
* At the end of this procedure (LBP procedure), we have a new image which represents better the characteristics of the original image

Primary benefit of this LBP implementation is that we can capture extremely fine- grained details in the image. Being able to capture details at such small scale is also biggest drawback to the algorithm. So, to handle this two parameters have been introduced by Ojala et.al[17][18].

* + - 1. number of points p in circularly symmetric neighbourhood to consider
      2. radius of circle r,which allows us to account for different scales.

Given number of points p in LBP there are p+1 uniform patterns. Figure 3.4.1 shows the circularly neighbour-sets for three different values of P and R.



**Fig 3.4.1**. Circularly neighbor-sets for three different values of P and R [17].

The advantage of LBP is that monatomic grayscale changes do not change, computational complexity is low, slight rotation invariant, illumination invariant and easy multiscale extensions.

## Machine Learning Algorithms

* + 1. **Random Forest:** Random Forest is a comprehensive machine learning (ML) classification approach. An ensemble of decision trees enables RF. Each tree separately anticipates a classification and “votes” for the necessary parameters, with the majority of the votes determining the entire RF predictions. Use of multiple trees reduce the risk of overfitting.

## Hardware and Software used

All the ML models were trained and tested on Windows 10 operating system with an 8th generation Intel i5 processor and 1TB of RAM. The models were developed on Spyder version 5 using Python 3.7.9 including other libraries like Numpy Pandas Scikit-learn, Matplotlib etc.

### Libraries used:

**NumPy,** which stands for Numerical Python, is a library consisting of multidimensional array objects and a collection of routines for processing those

arrays. Using NumPy, mathematical and logical operations on arrays can be performed

**pandas** is a software library written for the Python programming language for data manipulation and analysis.

**Seaborn** is a library mostly used for statistical plotting in Python. It is built on top of Matplotlib and provides beautiful default styles and color palettes to make statistical plots more attractive.

**Plotly** is python graphing library makes interactive, publication-quality graphs.

**Scikit-learn (Sklearn)** is the most useful and robust library for machine learning in Python. It provides a selection of efficient tools for machine learning and statistical modeling including classification, regression, clustering and dimensionality reduction via a consistence interface in Python

**CHAPTER 4**

# RESULTS AND DISCUSSION

## Segmentation

Table 4.1: Comparison of segmented images

|  |  |  |
| --- | --- | --- |
| Stages | Original Image | Segmented Image by  Otsu |
| Gametocyte |  |  |
| Leukocyte |  |  |
| Red blood cell |  |  |
| Ring |  |  |
| Schizont |  |  |

|  |  |  |
| --- | --- | --- |
| Trophozoite |  |  |

The results in Table 1 shows the visual performance of otsu segmentation technique.

## Classification Report:

Classification report provides comprehensive summary of precision, recall, F1score and support for each class. It provides a better understanding of the overall performance of our trained model.

* Precision is defined as the ratio of true positives to sum of true and false positives. It indicates the proportion of positive identifications which were actually correct. A model which produces no false positives has a precision of 1.0
* Recall is defined as the ratio of true positives to the sum of true positives and false negatives. It indicates the proportion of actual positives which were correctly classified. A model which produces no false negatives has a recall of 1.0.
* F1 is the weighted harmonic mean of precision and recall. Closer the value of the F1 score is to 1.0, the better the expected performance of the model is.
* Support is the number of actual occurrences of samples in each class in the dataset
* Accuracy is the proportion of correct classifications from overall number of cases.
* Macro Avg is the average precision, recall and F1 score between classes
* Weighted avg is the weighted average precision, recall and F1 score between classes. Weighted means each metric is calculated with respect to how many samples there are in each class.

ification report of different models:

Table 4.2: Classification Report of Random Forest Model

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Precision | Recall | F1-Score | Support |
| gametocyte | 0.00 | 0.00 | 0.00 | 6 |
| leukocyte | 0.00 | 0.00 | 0.00 | 7 |
| Red\_blood\_cell | 0.86 | 0.95 | 0.90 | 508 |
| ring | 0.50 | 0.05 | 0.09 | 21 |
| Schizont | 0.00 | 0.00 | 0.00 | 5 |
| trophozoite | 0.70 | 0.59 | 0.64 | 139 |
| accuracy |  |  | 0.83 | 686 |
| Macro avg | 0.34 | 0.27 | 0.27 | 686 |
| Weighted avg | 0.79 | 0.83 | 0.80 | 686 |

# REFERENCES

[1]. [https://www.analyticsvidhya.com/blog/2021/10/building-an-ipl-score-predictor- end-to-end-ml-project/](https://www.analyticsvidhya.com/blog/2021/10/building-an-ipl-score-predictor-%20%20%20%20%20%20%20%20%20%20%20end-to-end-ml-project/)

[2]. <https://www.geeksforgeeks.org/ipl-score-prediction-using-deep-learning/>

[3]. <http://ictactjournals.in/paper/IJSC_Vol_11_Iss_1_Paper_2_2199_2204.pdf>

[4].<https://www.irjmets.com/uploadedfiles/paper/volume3/issue_5_may_2021/10362/1628083416.pdf>

[5].<https://github.com/thatfreakcoder/IPL-Score-Prediction-with-Machine-Learning>

[6]. <https://papers.ssrn.com/sol3/papers.cfm?abstract_id=4062937>

[7]. <https://arxiv.org/abs/1809.09813>