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Deep Learning Techniques to Detect Malaria

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ABSTRACT: Medicine is one of the most technologically advanced areas, and there is a growing desire for quicker and more accurate detection of a wide range of disorders. Complex issues requiring the discovery of hidden patterns in data and their precise prediction and diagnosis may be solved using deep learning methods. Detecting the presence of malaria parasites in blood cell images is the primary goal of this endeavour. The presence of the malaria parasite may be recognised in a microscopic picture of blood cells using Deep Learning algorithms and can forecast whether or not the blood cell is infected.

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KEYWORDS: Deep learning, Diagnosis, Microscopic Image, Malaria Parasite, Blood Cells.

I. INTRODUCTION

This parasitic disease, caused by five species of single-celled germs from the genus protozoa that may infect humans, is considered infectious. Primary vectors of the disease are female Anopheles mosquitoes that have been infected with anopheles. According to the most recent statistics, almost 240 million cases of malaria are reported annually in Africa, mostly in Sub-Saharan Africa, putting 40 percent of the world's population at risk. New malaria cases per 1,000 individuals worldwide are shown in Figure 1. More than 90% of the world's malaria infections and deaths occur in Africa, with the majority occurring in children under the age of five. The most frequent symptoms of malaria are fever, nausea, and a headache. – CDC Yellow skin, seizures, and coma are all possible symptoms in certain cases. Every year, hospitals throughout the world review millions of blood films in an attempt to detect malaria cases. When counting parasites and infected red blood cells, manual methods are typically used, which are both time-consuming and error-prone[3, 4].

II. LITERATURE REVIEW

Diagnosing malaria in people is most often done using thin blood cell microscopy and an antigen diagnostic test. Rapid diagnostic tests based on antigens are less successful than the earlier procedure's laborious identification of 5000 cells. The malaria parasite is often found in low-income and politically unstable countries. A lack of timely admissions or funding for antigen-based quick treatment diagnostic investigations is a factor of poor mental health outcomes. Patients in these areas are unable to get medical care. By studying a book [1, 3, 4], a person may readily detect malaria. A lower level of diagnostic quality and, eventually, inaccurate diagnoses will be the result of working in an environment where resources are sparse and no mechanisms are in place to assist microscopists develop their talents or CAD tools to help them make better diagnostic judgments. Such techniques may help microscopists improve the accuracy of blood film classification and ultimately inaccurate diagnoses. Malaria-infected cells in medical imaging have been exposed to a number of categorization research in recent years, including those employing machine learning and morphology. A knowledgeable and skilled surgeon is required to perform these procedures [5]. Recent advances in AI-based technologies, such as computer-aided diagnosis or decision support systems, have enhanced the identification of malaria in blood films. An emerging AI technique known as deep learning (DL) might be used to better discern between different types of cell images and minimise

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erroneous diagnoses. A form of machine learning (ML) known as deep learning shines in the realm of medicine for its variety and strength. This is the case because of the way DL deals with raw and multidimensional data (1D or2D). In addition to medical applications, deep learning, which has lately gained the interest of academia and has witnessed an increase in its use cases, may aid other industries. In recent years, several artificial intelligence algorithms [5- 7] have been used to identify malaria on blood film images. Examples of these techniques include artificial neural networks, support vector machines, and convolutional neural networks.

III. SYSTEM DESIGN

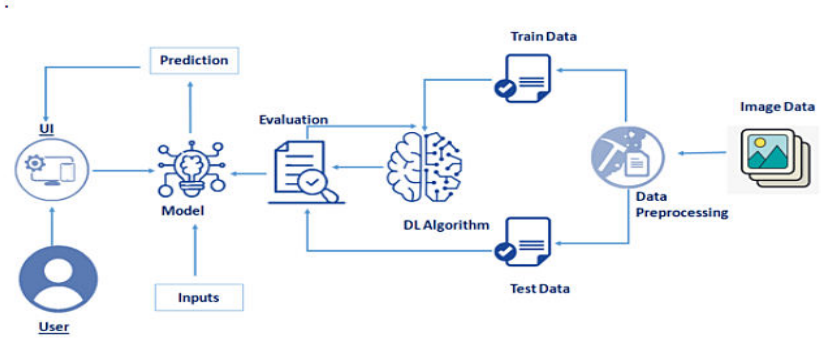

Fig: System Architecture of the project

In this part, a technique for automated Malaria detection is created and explained, taking limitations from prior research into consideration. We've used the Waterfall approach to get things done. An SDLC approach known as the Waterfall Model is one of the oldest. The Cascade approach divides the software development process into a number of distinct steps, each of which is characterised by a downward flow of progress (as in a waterfall). The "linear sequential life cycle model" refers to the software design process.

DATA ACQUISITION:

The dataset for this study is made up of images taken from the "KAGGLE" website. A computer may then alter the numerical representations of the dataset's optimal images using the computer's own algorithms. When designing a system to distinguish parasitic from non-parasitic or infected RBC cells, a significant number of records is required. Datasets 1 and 2 are provided here. However, both of them are in good health.

PRE- PROCESSING DATA:

Image The first stage in transferring a photograph to digital form is pre-processing. Prior to any image enhancement or enhancements, one must first do any essential image pre-processing steps such as adjusting the contrast, sharpness, and saturation. There have been many ways used in this work to pre-process, refine, compress and reconstruct Malaria cell pictures. These include image improvement, feature extraction and classification. Image retouching.

FEATURE EXTRACTION AND MODEL:

In Feature Extraction, a range of attributes are collected using different methodologies in order to discriminate between infected and non-infected pictures. TensorFlow, the foundation for the Keras sequential model, on which the convolutional neural network was built, only has two input tenses and two output tenses. In order to generate the sequential model using the Keras API in less time, we used the Keras API, resulting in computationally lighter

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models. The number of layers and factors like node count and batch size were fine-tuned in an iterative process to arrive at our final model. Model overfitting and underfitting were balanced by evaluating a variety of alternative models on the identical training and test datasets (the training and test datasets are independent of each other).

IV. RESULTS AND DISCUSSION

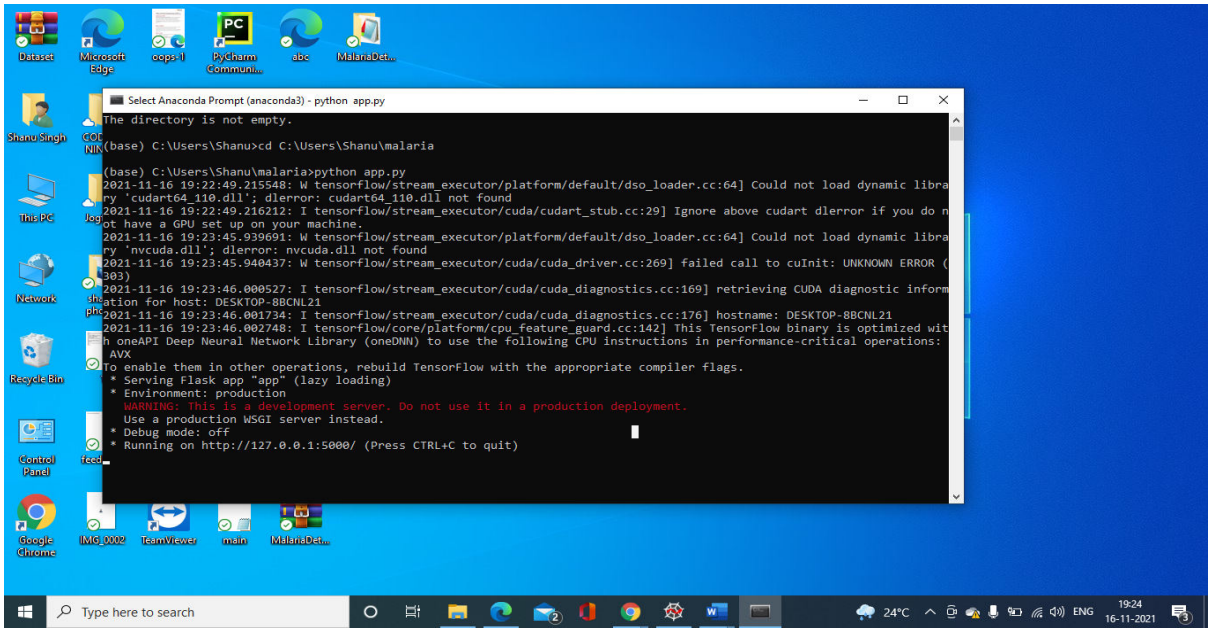

Fig: Running the code.

Fig: Home page of the website.

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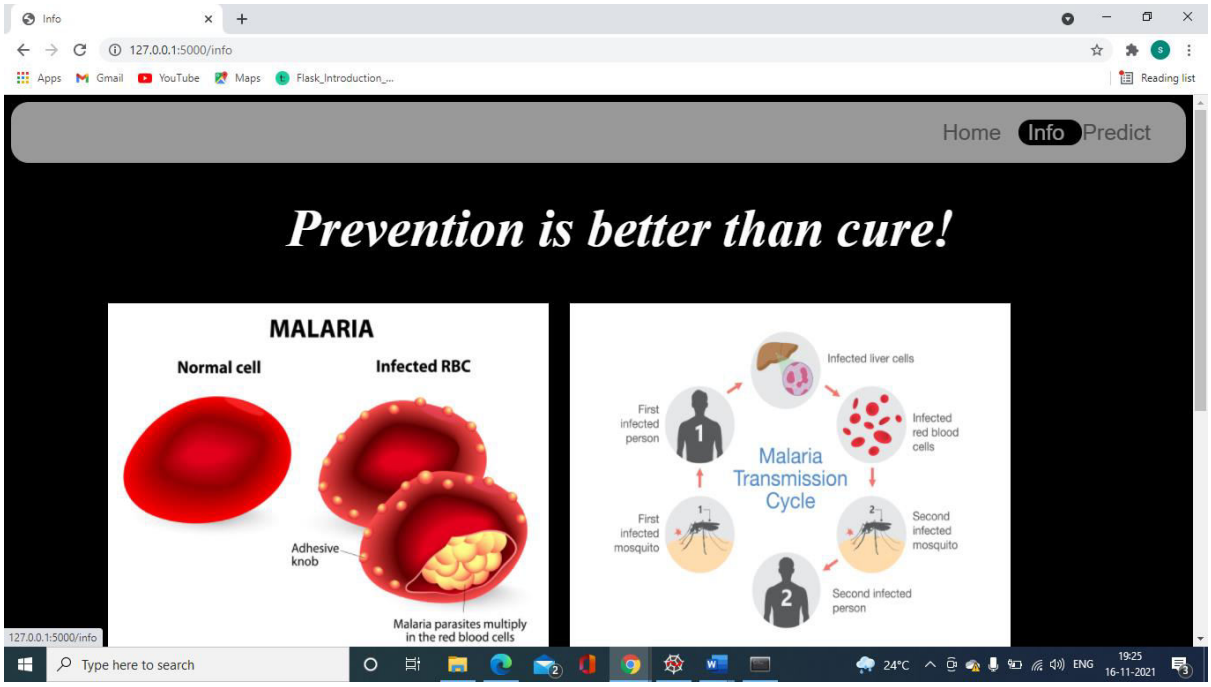
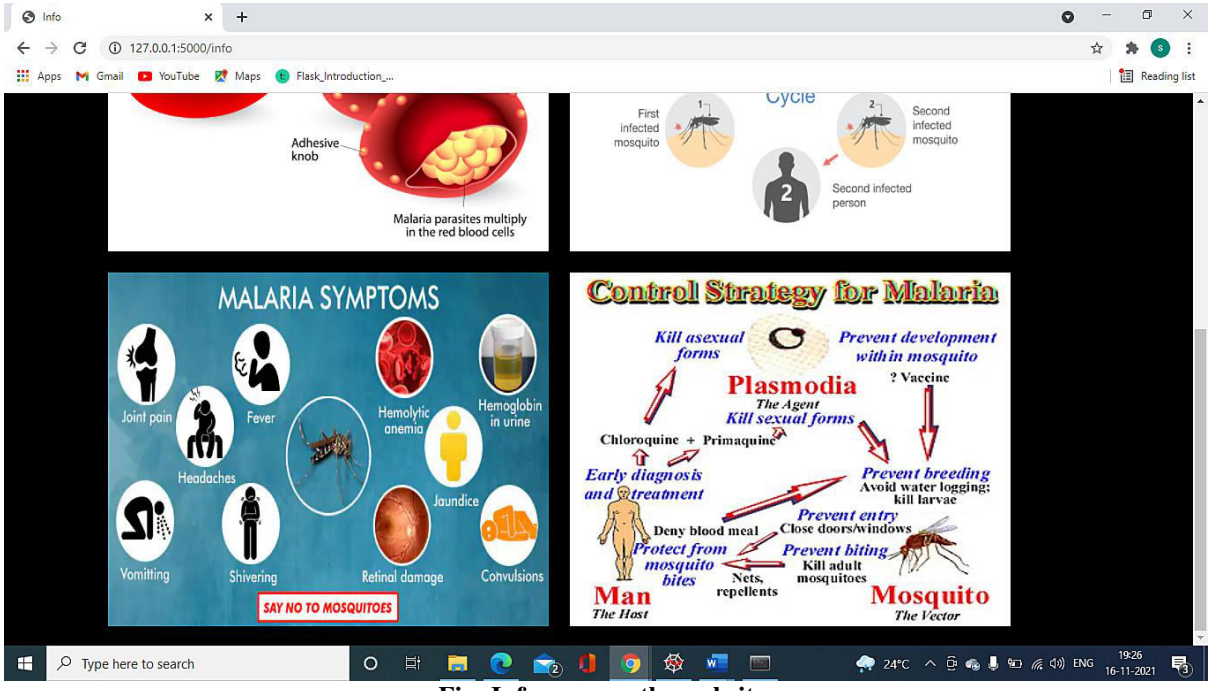


Fig: Info page on the website.



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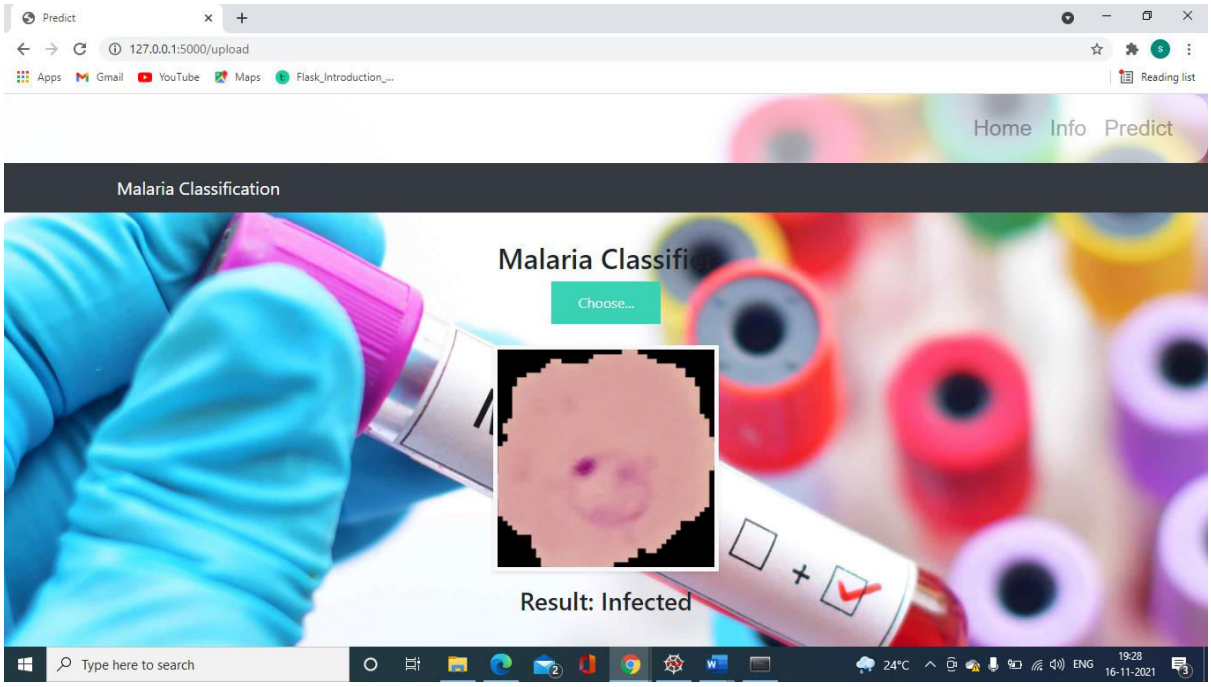

Fig: Output shown after inserting an infected RBC image.

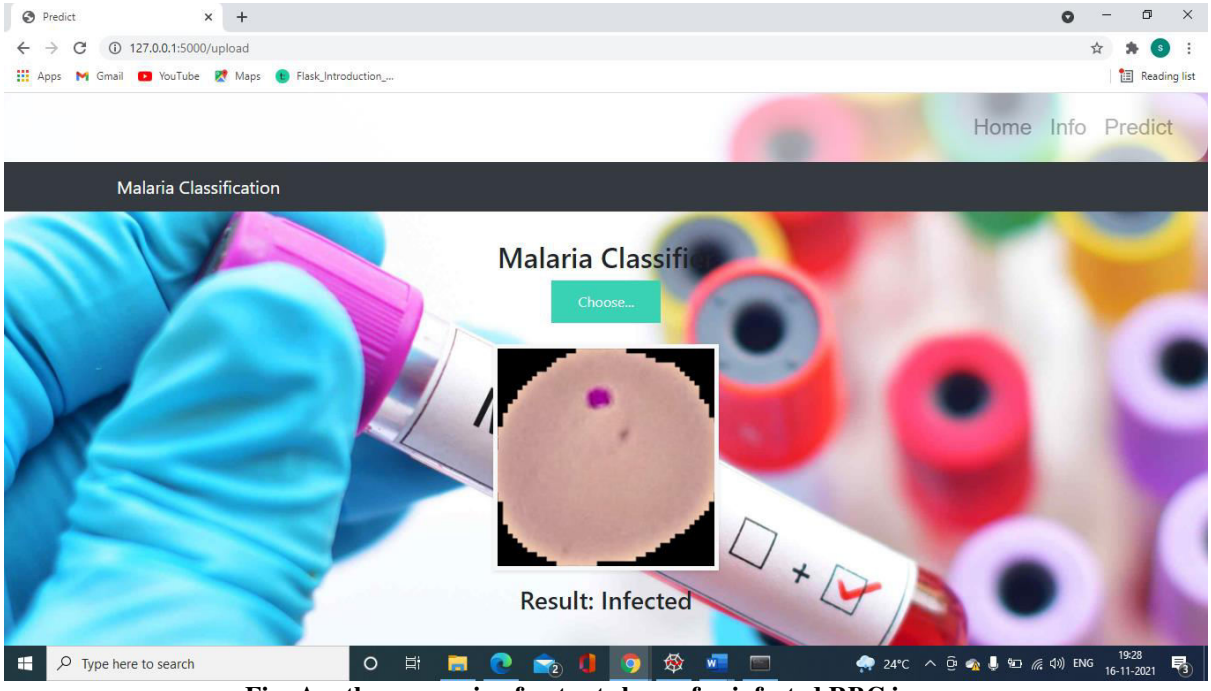

Fig: Another scenario of output shown for infected RBC image.

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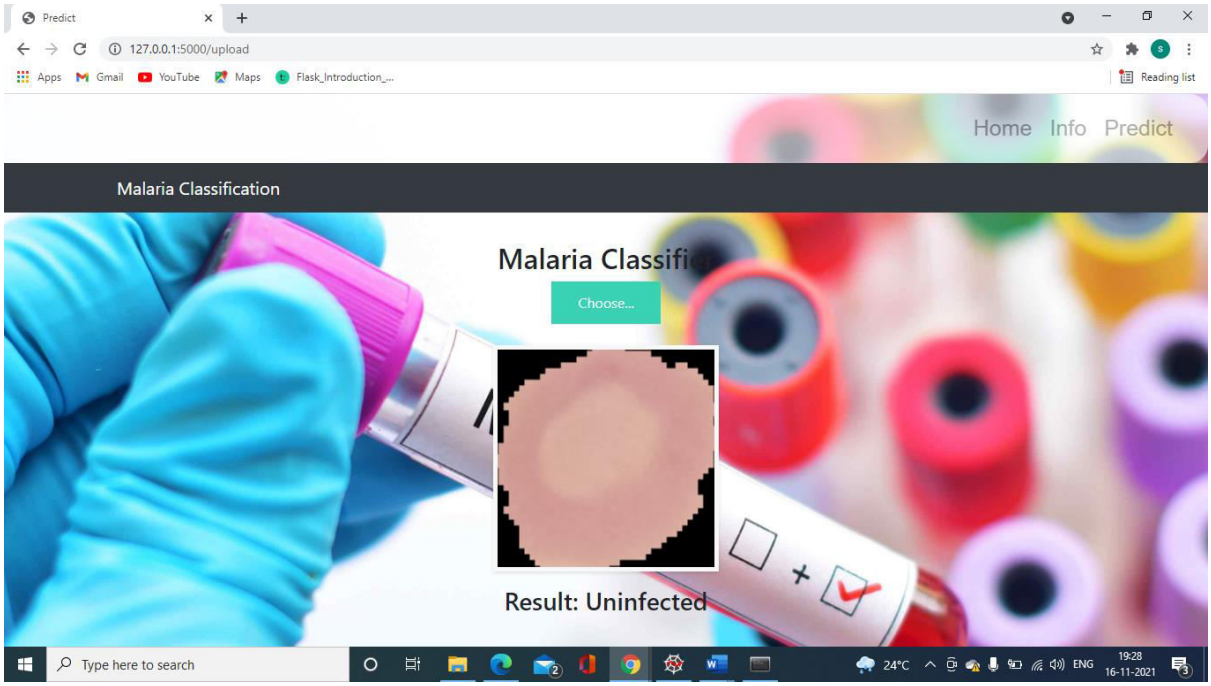

Fig: Result shown after inserting uninfected image of an RBC.

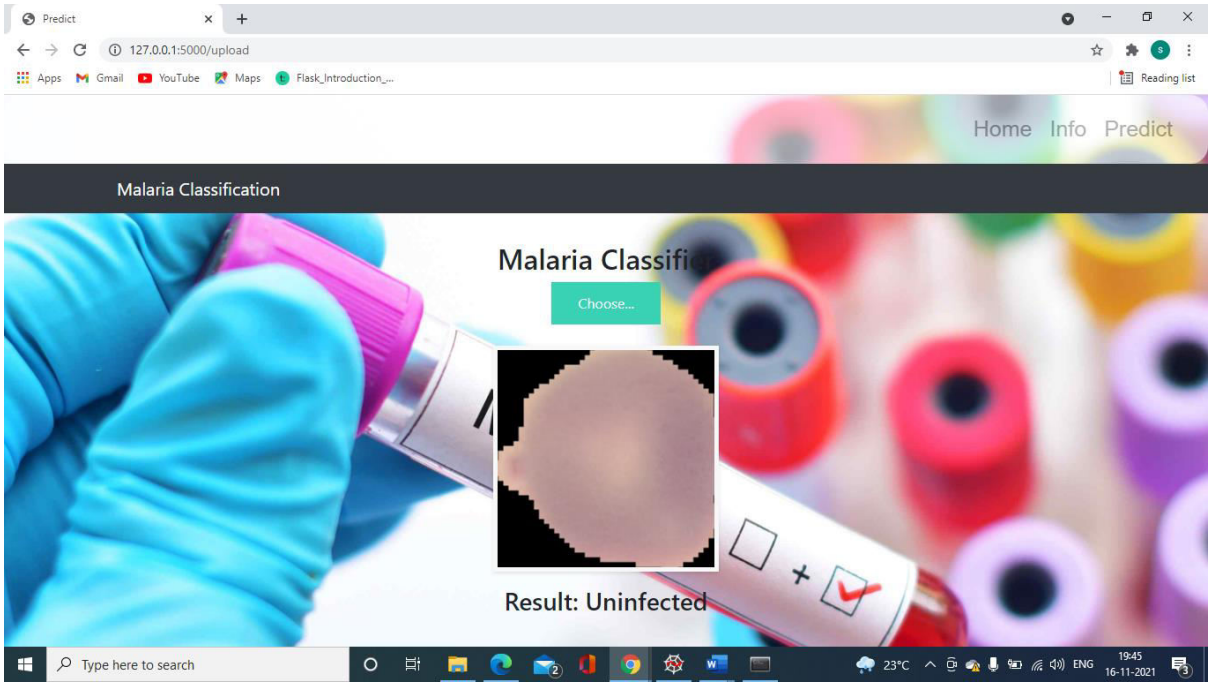

Fig: Another scenario of result shown after inserting uninfected RBC image.

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V. CONCLUSION

From the observation that has been made, we concluded the Malaria cell, infected and uninfected and processing is precise, accurate, and the proposed work is user-friendly to use. Moreover, our technique provides better display results using these techniques. Machine learning, which is becoming a desirable approach for solving most of the complex real-world problems, is being chosen for detecting Malaria disease as well. We deployed our best performing model into an application to facilitate simpler and faster malaria detection. Thus, we believe that the results obtained from this work will benefit towards developing valuable web-based solutions so that reliability of the treatment and lack of medical expertise can be solved. In the future, we also plan to achieve better prediction by using ensemble methods through model stacking

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