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Infection detection:

Bridging the gap from pixels to malaria diagnosis

Publicly defended, on **19/ 06 / 2023**, before the jury composed of:

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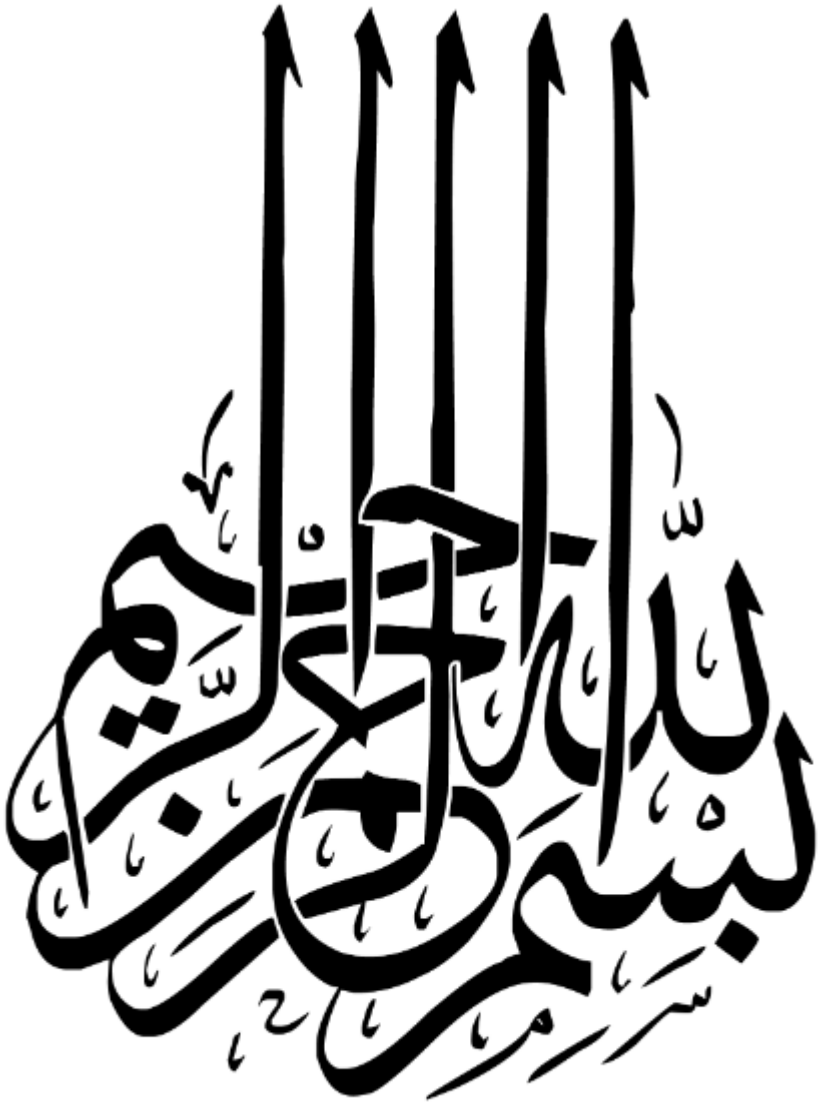
بسم الله الرحمن الرحيم

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DEDICATION:

Praise be to Allah, and prayers be upon the beloved Mohammed, his family, and those who fulfilled his faith.

Praise be to Allah, who has enabled us to value this step in our journey. This is the fruit of effort and success, thanks to Him Almighty.

Presented to my honorable ***parents****, may God protect them*

And keep them as à light for my path.

To all the honorable family that supported me and still does, from brothers and sisters to companions of the journey who shared its moments with me, may Allah bless them and grant them success:
chahd, Ghoufran, Ziad, Oumaima, Rabiha

To all those who had an impact on my life, and to all those whom my heart loved and whom my pen forgot.

Maghboune fadeau

DEDICATION:

Praise be to Allah and prayers and peace be upon the beloved Muhammad and his family and companions.

Thank Allah for helping us appreciate this step in our journey. This is the fruit of effort and hard work, thanks to Allah Almighty.

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To all those who have had an impact on my life, and to all those whom my heart has loved and whom my pen has forgotten.

Mahdi Oumaima

Abstract:

Malaria, a serious disease that affects millions of people worldwide, continues to pose a significant global health challenge. remains a major global health challenge. In this context, we present a new method for detecting malaria in images of blood cells using long-term memory (LSTM) networks. Our primary goal is to develop an automated diagnostic system that can assist specialists in accurately identifying infected and uninfected blood cells. We have successfully captured complex sequence relationships within these images, which leads to high-resolution detection results. The achieved performance of our model reached an impressive accuracy of 98%, confirming its effectiveness in detecting malaria.

key words: malaria, cell images, detection, LSTM.

Résumé :

Le paludisme, une maladie grave qui touche des millions de personnes dans le monde, continue de poser un problème de santé mondial important, demeure un enjeu sanitaire mondial majeur. Dans ce contexte, nous présentons une nouvelle méthode de détection du paludisme dans des images de cellules sanguines à l'aide de réseaux de mémoire à long terme (LSTM). Notre objectif principal est de développer un système de diagnostic automatisé qui peut aider les spécialistes à identifier avec précision les cellules sanguines infectées et non infectées. Nous avons réussi à capturer des relations de séquences complexes dans ces images, ce qui conduit à des résultats de détection à haute résolution. Les performances obtenues de notre modèle ont atteint une précision impressionnante de 98%, confirmant son efficacité dans la détection du paludisme.

mots cles: paludisme, images des cellules, detection, LSTM.

الملخص:

لا تزال الملاريا، وهي مرض خطير يصيب ملايين الأشخاص في جميع أنحاء العالم، تشكل تحديًا صحيًا عالميًا كبيرًا. لا يزال يمثل تحديا صحيا عالميا كبيرا. في هذا السياق، نقدم طريقة جديدة للكشف عن الملاريا في صور خلايا الدم باستخدام شبكات الذاكرة طويلة المدى (LSTM) هدفنا الأساسي هو تطوير نظام تشخيص آلي يمكنه مساعدة المتخصصين في تحديد خلايا الدم المصابة وغير المصابة بدقة. لقد نجحنا في التقاط علاقات تسلسل معقدة داخل هذه الصور، مما يؤدي إلى نتائج اكتشاف عالية الدقة. وصل الأداء المحقق لنموذجنا إلى دقة مذهلة بلغت 98٪، مما يؤكد فعاليته في الكشف عن الملاريا.

الكلمات المفتاحية : الملاريا, صوة الخلايا ,الكشف,LSTM.

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General Introduction

Malaria, a serious disease, has a profound impact on millions of people worldwide, representing a substantial danger to their well-being, particularly in tropical and subtropical regions. The accurate and timely diagnosis of malaria is crucial for effective treatment and disease control. However, traditional methods of diagnosis, such as manual microscopic examination of blood smears, are time-consuming, labor-intensive, and require expertise.

Our aim is to contribute to the field of medical image analysis by proposing a solution that can help addressing the challenges associated with malaria diagnosis. By combining medical knowledge with image classification and segmentation techniques, it seeks to develop a reliable and efficient automated system for malaria cell image classification. This work presents a comprehensive study on the classification of malaria-infected cell images using advanced image analysis techniques. Our research delves into three main chapters, each addressing crucial aspects of the subject matter.

Chapter I: Medical Introduction of paludism

In this chapter, we provide a thorough medical introduction of malaria. Starting from an overview of the disease, its epidemiology, etiology, to its impact on global health. we explore the various types of malaria parasites, their life cycle, and the mechanisms through which they infect human red blood cells. Furthermore, it sheds light on the obstacles related to the diagnosis and treatment of malaria, underscoring the crucial significance of precise and timely detection.

Chapter II: Image Segmentation and Classification Techniques and Applications

This chapter serves as an introduction to image classification and segmentation techniques. It covers the fundamental concepts and methodologies employed in these areas. The chapter also presents an overview of popular image classification and segmentation algorithms, such as LSTM and threshold segmentation.

Chapter III: The Methodical Journey: Procedural Implementation and Exemplary Outcomes

In the final chapter we focuse on the implementation aspect of our thesis. we detail the experimental setup, including the dataset used, data preprocessing techniques, and the choice

of algorithms for malaria cell image classification. The chapter presents the development and training of the classification model, explaining the model architecture, and the evaluation metrics used to assess its performance. It also discusses any enhancements made to improve the accuracy and efficiency of the classification system in the future.

Chapter I:

Medical Introduction of paludism

I.1. Introduction:

Malaria, a dangerous infectious disease that poses a significant global health burden, particularly in regions with limited resources. According to the World Health Organization (WHO) in 2021, there were more than 247 million cases of malaria worldwide. However, advances in scientific research have allowed scientists to gain a better understanding of malaria and unravel its mysteries, enabling the development of treatments and diagnostic strategies. This chapter provides a comprehensive medical introduction to malaria; we will explore the key aspects of malaria, including its symptoms, types, and transmission, which will lay the foundation for understanding the complex nature of this disease. [1].

I.2. Definition:

Malaria is a highly contagious disease caused by parasites of the genus Plasmodium, which are transmitted to humans through the bites of previously infected Anopheles mosquitoes. These parasites invade red blood cells to burst them, causing great harm to the body and potentially fatal result [2].

Figure 1: The Anopheles Mosquito [3].

I.3. History:

Malaria, also known as malaria, originates from the Italian language and literally means "bad air". Every year this disease causes the death of almost a million people in the world, 90% of which are registered in Africa, mainly in the tropics.

Dating back to 2700 BC, the symptoms of malaria were first described in the Chinese book called "Ni Ching", which means "Canon of Medicine".

On November 6, 1880, the French physician Alphonse Laveran made a pioneering discovery in the Algerian city of Constantine. He identified the Plasmodium parasite as the cause of the disease.

Then, on August 20, 1897, Ronald Ross, a British officer working for the Indian Medical Services, became the first to discover that malaria was transmitted from an infected person to a mosquito. This discovery brought a definitive answer to the question of transmission of the disease from one individual to another [4].

I.4. Plasmodium types:

There are five types of malaria parasites that humans can get infected with:

I.4.1 Plasmodium falciparum:

This type of malaria is highly perilous and prevalent, with a significant mortality rate. It is distinguished by rapid multiplication of the parasite and manifests symptoms including recurring infections, severe anemia, and the blockage of blood vessels. When examined under a microscope, infected cells undergo a distinct transformation, taking on a crescent shape [5] [6].

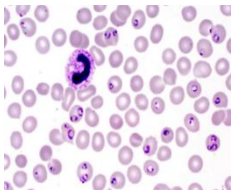


Figure 2: Infected Cell with P Falciparum under Microscope [7].

I.4.2 Plasmodium vivax:

It is the second most prevalent type of malaria, and its danger lies in the challenge of early detection. In its initial stages, it remains asymptomatic and dormant within the liver for a prolonged period, which can extend to several years. However, it can activate abruptly and rapidly spread throughout the body, leading to severe relapses. An indicator of this type is the significant enlargement of the affected blood cells [5] [6].

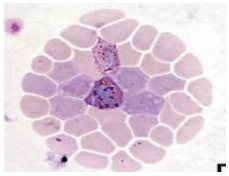


Figure 3: Infected Cell with P vivax Under Microscope [8].

I.4.3 Oval Plasmodium:

Its initial emergence occurred in West Africa, and it accounts for a small portion of malaria infections. Infected cells exhibit enlargement, have a rounded shape, and display a granular appearance [5] [6].

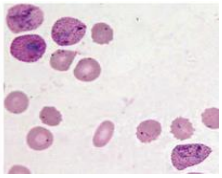


Figure 4: Infected Cell with P oval Under Microscope [8].

I.4.4 Plasmodium malaria:

It is generally non-fatal, although it can become chronic if left untreated. It typically induces a fever that can persist for multiple days, and the affected cells exhibit a rounded shape with a coarse granular appearance [5] [6].

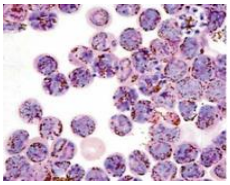


Figure 5: Infected Cell with P malaria Under Microscope [8].

I.4.5 Plasmodium Knowles:

It is predominantly found in Southeast Asia and poses a significant risk due to its rapid progression, transforming from a mild case to a life-threatening condition. The transmission of this type of malaria from monkeys to humans remains somewhat enigmatic [5] [6].

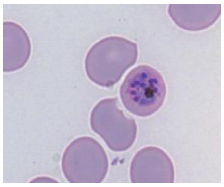


Figure 6 : Infected Cell with P Knowles under Microscope [8].

It is mostly found in Southeast Asia and poses a significant risk due to its rapid progression, going from a mild case to a life-threatening condition. The transmission of this type of malaria from monkeys to humans is still somewhat of a mystery

We can summarize the distinction between the five types of malaria by noting the characteristics of trophozoites, annelids, and schizonts, as shown in the accompanying figure.

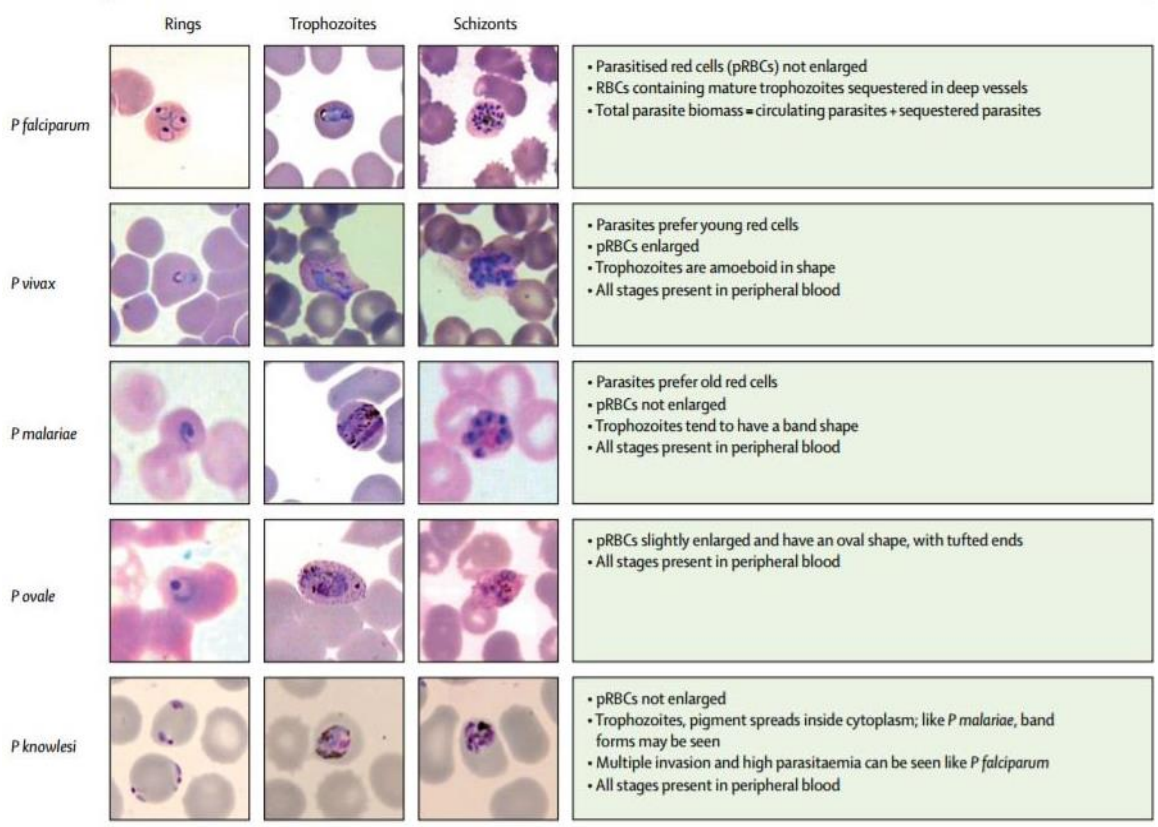


Figure 7 : The difference between the five types of malaria [9].

I.5.Disease Transmission:

The extent of disease transmission is influenced by various factors associated with the parasite, the vector, the human host, and the environment.

I.5.1 The parasite:

It is a living organism that makes its host an essential source of its survival, so it depends entirely on it for its food. It lives either outside or inside the host's body according to where its needs are met and the characteristics that help its survival. Scientists divided it into three major families depending on the type of host and its characteristics: protozoa, helminths, and ectoparasites [10] [11]:

- **Helminths:** They are organisms that can coexist inside and outside the body, such as flatworms, tapeworms, and others.
- **Ectoparasites:** They are multicellular organisms such as insects and spiders that have the ability to coexist on the skin or feed on it.
- **Protozoa:** Protozoa are single-celled organisms such as infections called Giardia that can coexist and reproduce inside the body.

Among them, we find the parasite Plasmodium, which is the main cause of all types of malaria, as depicted in the following table [12]:

Protozoa	
Plasmodium falciparum	Paludism
Plasmodium vivax	
Plasmodium oval	
Plasmodium malaria	
Plasmodium Knowles	
Toxoplasma gondii	Toxoplasmosis
Sarcocystis hominins	Coccidioses intestinalis
Cystoisospora belli	
Cryptosporidium spp	
Cyclospora cayetanensis	

Table 1 : Some types of parasites of the Protozoa type and the most important diseases that they cause [13].

I.5.2 The vector:

Vectors are living organisms capable of transmitting infectious micro diseases between humans, or from animals to humans, as defined by the World Health Organization (WHO).Vector-borne diseases are human illnesses caused by parasites that are transmitted by vectors [14].

I.5.3 The human host:

Human immunity plays a crucial role in the transmission of malaria. In Africa, we observe that most malaria-related deaths occur among children and pregnant women due to their relatively weaker immune systems during those stages. The stronger the immune system, the lower the risk of infection, and the milder the symptoms and impact of the disease on the body [15].

I.5.4 The environment:

This type of mosquito depends on water for its life, survival and reproduction, so we find it abundantly in places with a humid climate and available on water complexes we also notice that it increases its activity after every rainy season, and this is what makes the environment the most important factor for its spread [15].

I.6. Life Cycle of Malaria Parasite:

The life cycle of the malaria parasite is highly intricate. Similar to other parasites, it relies entirely on its host for survival. During the early stages of the parasite's life, the mosquito serves as its host, while in the later stages, the human becomes the primary host [16].

I.6.1 Life Cycle in Mosquito:

When a mosquito bites an infected person, the blood containing the parasites is taken to the mosquito's stomach for 10 days or more. The parasites undergo a complex development, in which the mature parasite moves to reside in the mosquito's salivary glands [17]:

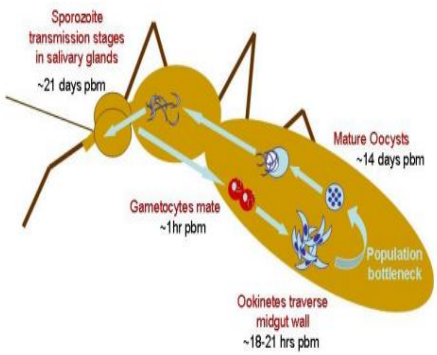


Figure 8 : Schematic Diagram of The Life Cycle of Plasmodium in Mosquitoes (pbm: before blood meal) [18].

I.6.2 Life cycle of plasmodium in the human body:

When a healthy person is bitten by an infected mosquito, the virus is transmitted in the form of sporozoites. These sporozoites travel to the liver and undergo rapid replication for a period of at least five days, transforming into schizonts. Eventually, the infected liver cells rupture, releasing numerous parasites called merozoites. These merozoites invade red blood cells, multiply within them, and cause the infected cells to burst, releasing more parasites. This cycle of replication continues, and the parasites spread throughout the body, causing damage to various organs. The parasites include both male and female gametocytes, which can be picked up by healthy mosquitoes when they feed on an infected individual [19].

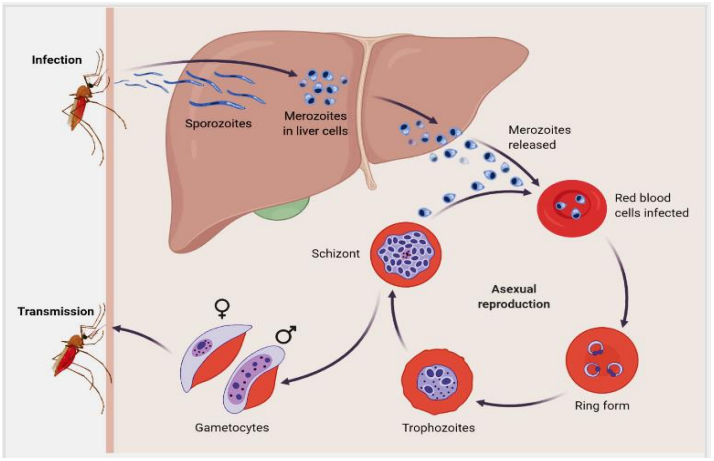


Figure 9 : Schematic Diagram of The Life Cycle of Plasmodium in Human host [20].

I.7. The transmission of the disease between humans:

There are several factors that contribute to the transmission of malaria, which can be summarized as follows [21] [19]:

A. **Blood transfusion:** In some cases, blood donors' medical history is not thoroughly reviewed before the transfusion takes place, potentially leading to the transfer of infected blood to the recipient.

B. **Organ transplantation:** Malaria parasites may remain dormant in an organ for several months before becoming active, posing a risk of infection to the recipient.

C. **Sharing personal items:** Sharing personal items, such as needles or razors that have come into contact with infected blood can result in the transmission of malaria.

D. **Contaminated syringes:** The use of syringes and needles contaminated with infected blood can introduce the malaria parasite into a person's bloodstream.

E. **Vertical transmission:** Malaria can be transmitted from an infected mother to her fetus during spregnancy, leading to congenital malaria.

I.8.Incubation:

The incubation period is the time it takes for the parasite from initial infection to develop symptoms. It differs from one type to another [22], as we note:

- P. falciparum - 9 to 14 days.
- P. vivax - 12 to 18 days.
- P. oval - from 12 to 18 days.
- P. Malaria: 18-40 days.

It can take to several months for P. vivax and P. oval. Rapid intervention also affects this period.

I.9. Symptoms of paludism:

The most prominent symptom of malaria is the cyclical occurrence of sudden chills, followed by high fever and sweating, typically appearing between 8 to 25 days after the initial signs of infection. These symptoms include [23] [6]:

- Lack of awareness.
- Severe weakness.
- Inability to feed.
- Seizures.
- Reduction of blood pressure.
- Breathing problems.

I.10. Precautions:

To tackle malaria globally, we must prioritize some key prevention measures, employing diverse strategies and interventions to control the disease's impact. By adopting

these preventive measures, we can effectively reduce the burden of malaria and improve public health outcomes [6]:

a. Realizing the risk of infection:

A person must be aware of the risk of infection and try to avoid all areas in which there is even a small possibility of infection.

b. Prevention of stings:

Individuals and communities can significantly reduce their susceptibility to malaria and contribute to the global efforts of malaria control by implementing a comprehensive set of preventive measures. The most important points are:

- Trying to cover the whole body.
- Spraying pesticides on overexposed areas of the body and over clothes after wearing them.
- Close doors and windows when staying inside.
- Before sleeping, the bedroom should be sprayed with pesticides and a special net should be used.

c. Taking pills to prevent malaria:

These are pills that are taken to prevent malaria, but before taking them, several points must be considered including travel period, pregnancy, or breastfeeding. Of these pills, we mention chloroquine and proguanil.

d. Obtaining a proper diagnosis:

Getting an accurate diagnosis as soon as symptoms of malaria complications appear is critical in preventing the disease from progressing. By identifying and confirming the presence of malaria early on, appropriate treatment and preventive measures can be implemented to mitigate the impact of the disease.

I.11. Diagnostic:

Malaria diagnosis methods can be divided into three main approaches: clinical examination, biological examination and automated diagnosis.

I.11.1 Clinical examination:

When patients experience symptoms, seeking medical diagnosis is often their first step to confirm the presence of a disease. Doctors then utilize various tests to identify the specific type and underlying cause of the illness [6].

I.11.2 Biological examinations:

Biological examination is an important method for diagnosing malaria. This technique involves laboratory testing to detect the presence of malaria parasites or their components in blood samples. Multiple techniques areused in this field [6] :

a) Blood film and thick membranes:

The gold standard for malaria diagnosis is the microscopic examination of a blood sample. Initially, a thick blood smear is used to detect the presence of the parasite and confirm the infection. Subsequently, a thin smear is performed to identify the specific types of parasites causing the disease. However, due to the challenge of detecting parasites, especially in the early stages, this examination needs to be repeated with samples taken every 6 to 8 hours during the first 72 hours. This is because infected cells may reside in deep areas and may not be easily detected in peripheral blood samples.

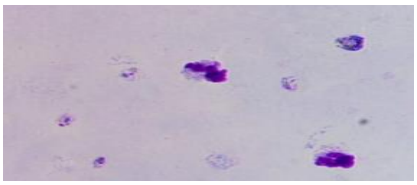


Figure 10 : Thick blood film Plasmodium vivax [24].

b) Immunological serological test:

The presence of the parasite's antibodies in the patient's blood indicates the existence of immunity against the parasite.

c) Sophisticated serological tests:

The immune fluorescent antibodies technique (IFAT) is utilized to detect specific antibodies against the studied parasites in the blood. Additional tests, such as elevated levels of blood pigment (Hb) and white blood cells (WBC), can serve as indicators of the body's immune response. However, it is important to note that these auxiliary tests may not provide accurate results for diagnosing malaria.

d) **A rapid diagnostic test:**

The Rapid Diagnostic Test (RDT), also known as an antigen test, provides a quick means of diagnosing malaria. By placing a small blood sample from a finger prick onto a test strip, the color change indicates whether the person is infected or not.

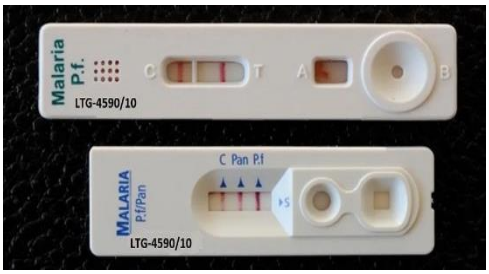


Figure 11 : malaria antigen test [25].

e) Polymerase Chain réaction (PCR) :

The polymerase chain reaction (PCR) is a well-established method for extracting the DNA of the malaria parasite. This technique, facilitated by readily available kits, involves a thermal cycling process that amplifies the parasite's DNA. The presence of a gelatinous substance specific to the parasite's DNA confirms the diagnosis.

I.11.3 Automatic diagnosis:

Diagnosing malaria has relied primarily on labor-intensive laboratory procedures, which rely heavily on human expertise. To address this challenge, Researchers have explored the implementation of artificial intelligence systems utilizing classification techniques and advanced algorithms, which have introduced automated diagnostics

- In a study by the authors in [26], an approach combining Support Vector Machine (SVM) and Inception v3 was developed for malaria detection. The research utilized a comprehensive database consisting of 27,560 cell images. The proposed model successfully distinguished between infected and uninfected cell images, achieving an impressive accuracy of 94.8%. This study demonstrates the potential of integrating SVM with Inception v3 in malaria detection, showcasing promising results and advancements in diagnostic applications using machine learning techniques.

- Furthermore, in [27], the authors proposed a lightweight CNN model that can accurately identify malaria parasitic red blood cells and distinguishing them from healthy red blood cells. they trained their model in three different configurations, varying the proportion of data used for training. Across all three configurations, the proposed model achieves an impressive accuracy of approximately 96%.

I.12. Conclusion:

In this chapter, we have provided a comprehensive medical introduction to malaria, emphasizing its profound impact on global health. Where we discussed various aspects of the disease, including transmission, symptoms, complications, and treatment options. In addition, we have highlighted important advances in automatic diagnosis of malaria.

In the next chapter, we will delve more into the technical aspects of image segmentation and classification techniques, and explore their potential to further enhance the diagnosis of malaria. By leveraging these technologies, we will gain a more sufficient understanding to contribute to ongoing efforts in combating this global health challenge.

Chapter II:

Image segmentation and classification techniques and applications

II.1. Introduction:

In recent years, there has been remarkable progress in harnessing segmentation and classification techniques for the development and enhancement of disease detection and diagnosis, including within the field of malaria. In this chapter, we will delve deeper into these techniques, exploring their application and impact on medical imaging. The chapter will be divided into three sections.

- The first section is an introduction where we define the image and discuss its types and characteristics. This foundation will pave the way for understanding segmentation and classification.
- Moving on to the second section, we delve deeper into image segmentation, exploring its importance and discussing different image segmentation techniques. By gaining insight into these techniques, we understand their contributions to identifying and separating objects or areas of interest within images.
- Finally, our focus turns to image classification and the use of LSTM (Long Term Memory). We explore classification algorithms that assign labels or categories to images, enabling machines to recognize patterns and make predictions.

II.2. Definition of an image:

An image can be defined as a visual representation of a person or object, created using mediums such as sculpture, painting or photography. Also, it can be thought of as an organized collection of information that makes sense to the human eye when displayed on a screen [28].

II.3. Digitization:

An image is essentially a projection of a scene described by a continuous symmetric fluorescence function I (x, y), defined in a finite field where x and y are the spatial coordinates of a point in the image, and I is a function of light intensity and color. However, such a representation of the image cannot be used by a device that needs to be digitized. With an array of points or scalar values f (x, y), called a pixel, where [29]:

- x, y are the Cartesian coordinates of a point in the image.
- f (x, y) is the gray level or color value at that point .

II.4. Digital image definition:

A digital image is composed of pixels, which are elementary units representing a portion of the image. These pixels are organized in a two-dimensional array that forms the image. Digital images can be classified into two main types [29]:

- **Vector images:** data is represented using mathematical descriptions of simple geometric shapes.
- **Raster images:** raster images are represented using an array of points or pixels.

The raster image is defined by the number of pixels that constitute the image in length and height, as well as the range of colors or shades of gray that each pixel can take. This range is referred to as the image's dynamics.

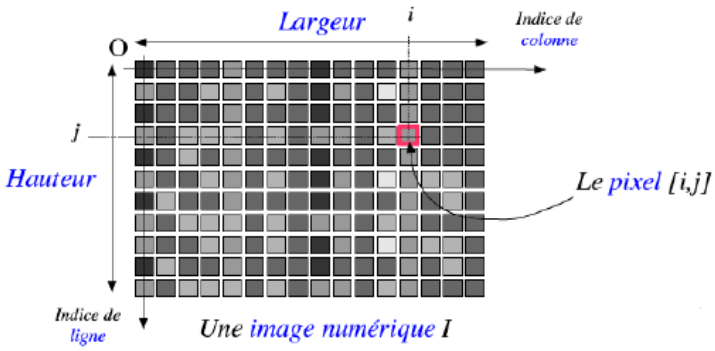


Figure 12 : Pixels and gray level of a raster image [30].

II.5. Image point operations:

An image consists of an organized set of information, which is characterized by the following parameters:

A. Image size:

The size of the image corresponds to its dimension. The total number of pixels is calculated by multiplying the number of rows by the number of columns [31].

B. The pixel:

The pixel is the fundamental element of a digital image, representing the smallest visual unit. These pixels are arranged in a two-dimensional array to form the complete image.

Given that the screen is scanned from left to right and top to bottom, the coordinates [0, 0] are generally used to denote the pixel located at the top left of the image [31].

C. Pixel coding:

Almost always, a pixel is expressed by a binary word composed of K bits, which allows it to take a value from the interval [0...2K-1]. This is called the depth of the image. These pixels are organized in a two-dimensional matrix to form the final image obtained [32].

D. Picture Resolution:

In digital photography, resolution refers to the level of detail in displaying or capturing an image, usually expressed as the number of pixels per unit area, or "pixel density". As the resolution of the image increases, so does its quality [32].

E. Luminance:

Image luminance refers to the level of brightness at each point and is expressed by dividing the luminance intensity by the surface [33].

F. Image contrast:

The contrast of an image refers to the perceptible dissimilarity between two regions, specifically between dark and light regions. Its definition is contingent upon the luminance values of two zones within the image [33].

G. The image histogram:

A histogram is a tool used to provide a simplified representation of the content of an image. There are three types of histograms [34]:

- **Monomodal Histogram:** Characterized by a single peak representing either the object or the background.
- **Bimodal histogram:** Consists of two separate peaks indicating the presence of both the object and background.

- **Multimodal histogram:** It has multiple discrete modes (peaks separated by valleys) that reveal the presence of multiple objects in the image [34].

H. The Noise:

When an image recording system is used, the restitution of the image is never perfect. Indeed, unwanted elements are randomly superimposed on the details of the original scene, this phenomenon is commonly called "noise" [35].

II.6. Images types:

Here are three types of digital images:

II.6.1 Binary images (in black and white):

Binary images are the simplest. Whose pixels can only have the values 0 and 1. 0 corresponds to a black pixel and 1 to a white pixel. The gray level is therefore coded on a single bit [28].

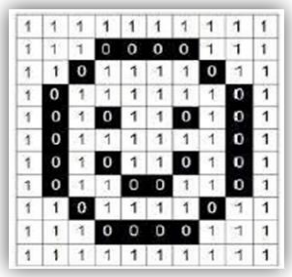


Figure 13 : example of a binary image [36].

II.6.2 Grayscale images:

At a given point in a digital image, the level of gray corresponds to the brightness intensity. The pixel's color can range from black to white, with a limited number of intermediary levels.

Grayscale images typically consist 6 gray shades. As per convention, the value 0 represents pure black, and 255 pure represents white. This convention is due to the fact that each integer that represents a gray level is encoded using 1 byte [28].

Figure 14 : example of a grayscale image and its quantization [29].

II.6.3 Coloured images:

There are several methods for representing colors, but the RGB (red, green, blue) model is the most widely used in digital images. In this model, each color is encoded in 1 byte, which means that each pixel is represented by 3 bytes, equivalent to 24 bits in total. The value of red can vary from 0 to 255, just like that of blue and green [29].

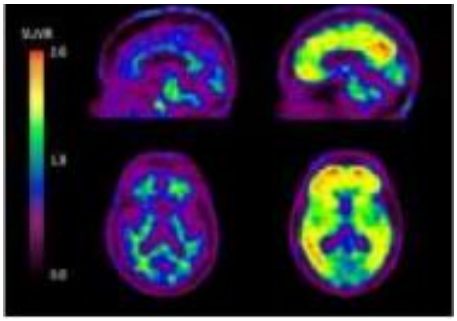


Figure 15 : colored MRI [37].

II.7. Some classic treatment:

There are a multitude of image processing that we can explore. Here are some examples among them:

II.7.1 Thresholding :

The threshold is called by this name because it divides the pixels of the image into two parts "object" and "background" (by finding the gray level value s) [38]. **(Will be explained later on)**

II.7.2 Filtering:

The concept of filtering comes from the principles of physics and signal processing techniques. Whether for electrical, radio, photographic, or other signals, image filtering is a local processing method widely used to perform spatial analysis of images. Its purpose is to enhance the intensity contrasts of the image, detect edges and reduce unwanted noise present in it [32].

II.8. Image processing lens:

The main goal of image processing is to extract valuable information that may be hidden by noise or affected by optical defects in imaging devices. Recently, advanced techniques have been developed to improve the visual quality of images, including correcting brightness differences caused by vignetting. Thus, it becomes necessary to improve the overall image quality before extracting the object [32].

II.9. Segmentation definition:

The purpose of segmentation is to divide the image into zones grouping together pixels having similar characteristics in terms of color, shape or texture. Each zone can represent an object or part of an object. This step is of great importance and is very delicate, since the quality of the segmentation plays a fundamental role in most image processing techniques, such as pattern recognition [39].

Here is an example of image segmentation that illustrates the concept of homogeneous regions:

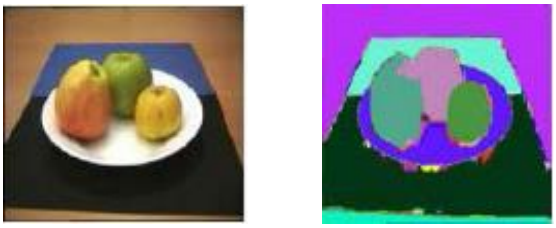


Figure 16 : Color image segmentation [31].

II.10. Segmentation objectives:

Image segmentation helps [33]:

- Provides uniform regions (according to a certain criterion).
- Noise reduction.
- The study and interpretation of anatomical structures.
- Accurately define the contours of regions.

II.11. Segmentation approachs:

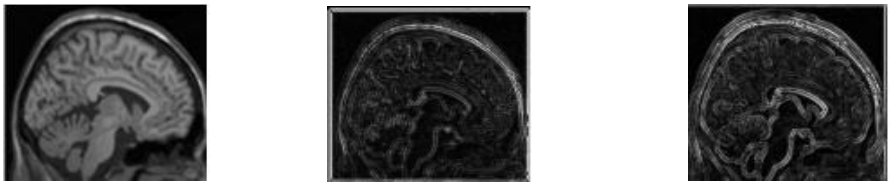
Several techniques are utilized for image segmentation due to the complexity and diversity of this open problem. Some of these techniques include [29]:

- Edge based segmentation.
- Region based segmentation.
- Segmentation using thresholding.
- Segmentation using classification.

II.11.1 Edge based segmentation:

Edge-approach approaches are distinguished by their exclusive focus on information about the edges of objects. Early segmentation models use methods for detecting rapid changes in light intensity or color, which correspond to image edges. By using contour detectors based on derived filters, it is possible to extract the contours of objects present in the scene.

Among the frequently used approaches, we can mention those based on finite differences, such as the gradient operator, the Laplacian operator, the filters of Sobel, Prewitt and Roberts, as well as methods based on optimality criteria, such as Canny-Deriche filters. However, these methods frequently encounter limitations due to the existence of unclosed edges, noise or undetected edges [30].



(a) (b) (c)

Figure 17 : Original image (a), edge detection by Laplacian (b), edge detection by Sobel (c) [31].

II.11.2 Region based approach:

Its goal is to distinguish between regions of an image based on their properties such as texture, shape, etc. Resolution standards are mainly used to divide an image into distinct regions that differ from each other based on pixel similarity. There are many techniques in this approach, and one of them is the split and merge method. This method involves dividing the image into multiple regions and then merging them to improve the results, grouping together similar regions, and finally achieving accurate segmentation of the image [40].

II.11.3 Segmentation using thresholding:

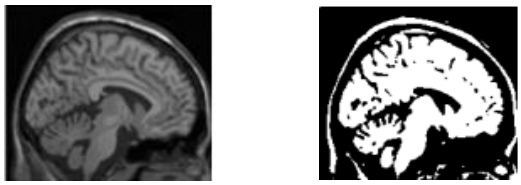
It is a tool that is widely used to segment an image into multiple categories using a histogram. Several methods are available for determining the threshold of a graph, but they are not properly applied unless the peaks of the graph are separated from each other. Thresholding methods Can be global or local [28] [30].

A. Global Threshold (threshold for the whole image):

It is based on comparing the gray level of each pixel denoted by xi of the image with a fixed global boundary denoted by T [30].

B. Local or adaptive thresholding (thresholding of part of the image):

It is based on taking into account the value of neighboring pixels and you need to calculate the thresholds. [30].



(a) **(b)**

Figure 18 : Original image (a), segmentation by thresholding (threshold=80) [31].

According to the graph, segmentation is a special case of segmentation according to classification. It allows us to divide pixels into categories according to their gray levels. After that, the categories are defined by thresholds [28].

II.12. Classification definition:

Image classification is an essential type of computer vision task that uses machine learning techniques such as deep learning to categorize an image into a specific class, taken from an existing database obtained through a model previously trained on a large image dataset with appropriate labels. Once successfully trained, it can be used to classify new images by predicting the probability that they will fall into each of the predefined classes [41].

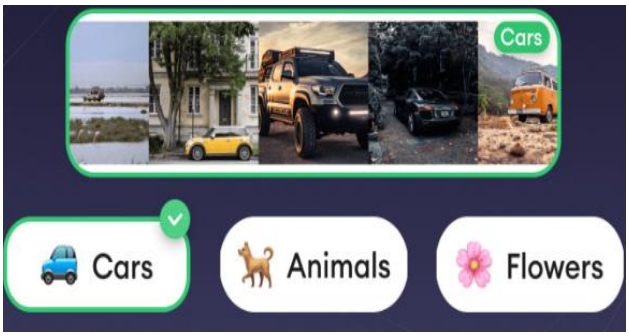


Figure 19 : Classification of Car Images into a Single Category [41].

II.13. Classification principle:

Images are composed of numerous small pixels. The computer needs to analyze its components to classify the image as a whole. The process involves considering the image as a collection of matrices, each with dimensions determined by the image resolution. Pixels in the

digital image that share similar attributes are organized into distinct groups known as “classes” [42] [43].

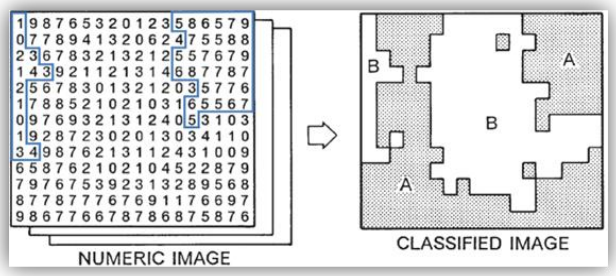


Figure 20 : Pixel Classification in a Digital Image Based [42].

The process then varies depending on the chosen algorithm, which extracts the connected components and labels pixels belonging to the same class. This assists the classifier in determining the image's class [41] [43] [44].

II.14. Stages in Classification:

There are two main stages in images classification:

a) The training stage:

During this stage, a dataset is used to train a classification model. This stage involves a learning process that identifies a representation space for objects, discovers distinctive parameters, and produces a spectral characteristic called a signature for each class. These signatures serve to differentiate between different object classes [43] [44].

b) The testing stage:

In this stage, the trained and validated model is used to classify new, unseen data and assess the accuracy of its predictions and its overall performance in allocating undefined objects to specific classes based on its predictions in the representation space defined during the learning phase [44].

II.15. Classification types:

Image classification is not a simple task that can be accomplished using a single straightforward approach, and the two most prominent methods are supervised and unsupervised classification.

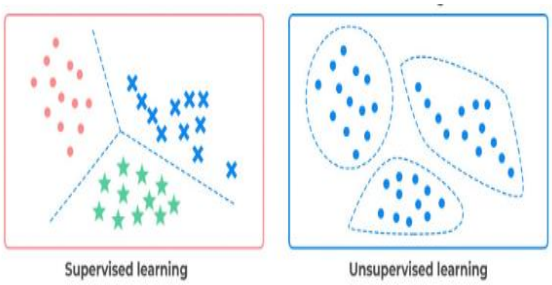


Figure 21 : supervised vs unsupervised classification [45].

II.15.1 unsupervised approaches (Software Classification):

Unsupervised classification is an image classification technique that automatically analyzes and groups unlabeled datasets using machine-learning algorithms. The process of grouping data based on their similarities or differences is called clusterization, meaning that it does not require any prior knowledge of the correct output or labeled training data [42] [46] [44].

A. Unsupervised classification techniques:

There are various techniques for unsupervised classification, and the best one for a particular dataset depends on the nature and characteristics of the data and the most common one is k-means.

- **K-means Cluster:**

K-means clustering is an approach that partitions a dataset into distinct clusters based on the characteristics of its cases or variables, ensuring that there is no overlap between the clusters. The process involves repeatedly transferring data points from one cluster to another to create clusters with high similarity among their members and low similarity with members of other clusters. This is achieved by using one vector to represent the mean of each cluster, forming a centroid model [48] [47].

I.15.2 Supervised approach (Human-guided):

Supervised classification is a process of categorizing pixels of unknown identity in an image into specific classes using samples of known identity.

An analyst chooses representative training sites in the image that represent specific classes and guides the algorithm to use these sites as references for the classification. The selection of training data is a crucial step in supervised classification that determines the accuracy of the classification results. Additionally, the analyst determines the number of classes into which the image is divided and can detect and rectify errors [42].

A. Advantages of supervised Classification:

Supervised classification is a method of classifying data that offers certain advantages in comparison to other approaches. Through the analysis of training data, it helps identify mistakes and determine whether samples have been accurately classified. This allows for improved accuracy when performing classification tasks. Furthermore, supervised learning also gives operators greater control over performance as they are able to easily spot errors throughout the process [42] [49].

B. Supervised classification techniques:

Supervised classification techniques are utilized in numerous fields, and there is a wide range of methods available, each with its own set of strengths and limitations. The selection of a specific method depends on the unique characteristics of the data being classified and the particular problem being addressed. One of the most commonly used methods is neural networks.

1) Neural Networks:

A neural network (NN) is a type of computational learning system that employs a network of functions to analyze and transform input data into a desired output format. This concept is inspired by the structure and function of the human brain, which is composed of a vast network of interconnected neurons that transmit electrical signals to convey information. As we learn and accumulate experience, our brains adapt by strengthening neural pathways that are frequently used, which is analogous to the process of training in neural networks. Thus, neural networks can be seen as a simplified model of how the brain functions [50] [51].

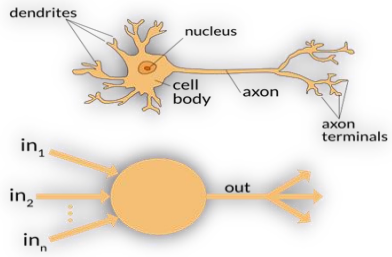


Figure 22 : Nerve cell and perceptron [52].

a) Neural network functionality:

An NN model typically consists of an input layer, followed by hidden layers, and ends with an output layer [51].

- **The input layer:** is the initial layer of neurons that receives input data or information from the external environment. Its primary task is to transmit the processed input data to the hidden layers.
- **Hidden layers:** in a neural network are composed of interconnected neurons that carry out computations on the input data obtained from the input layer. The computations conducted aim to extract significant features and patterns from the input data.
- **The output layer:** is the last layer of neurons in a neural network, responsible for generating the final output or conclusions of the model. This output is derived based on the computations and analysis performed in the previous layers of the network.
- **Important definitions:**
  - **Nodes**: Also, called neurons are a neural network's basic components that perform computations on the input data.
  - **Bias:** which is an additional parameter added to each neuron that affects the neuron's output and represents its tendency to adjust regardless of input [53].
  - **Weights:** In a neural network, each layer is connected to the next layer through a group of interconnections that connect every node in the first layer to every node in the second layer, also known as weights, connecting the nodes in adjacent layers. This

weights are adjusted based on the error to enhance the performance of the network during the training process [54] [53].

- **The activation function:** it aims to introduce non-linearity to the output of a neuron, enabling the network to recognize complex patterns and relationships in the input data. Without non-linear activation functions, a neural network would be limited to linear relationships and unable to learn complex patterns.

To illustrate the general equation of a neural network, let's consider a small network consisting of four layers: the input layer, two hidden layers, and the output layer.

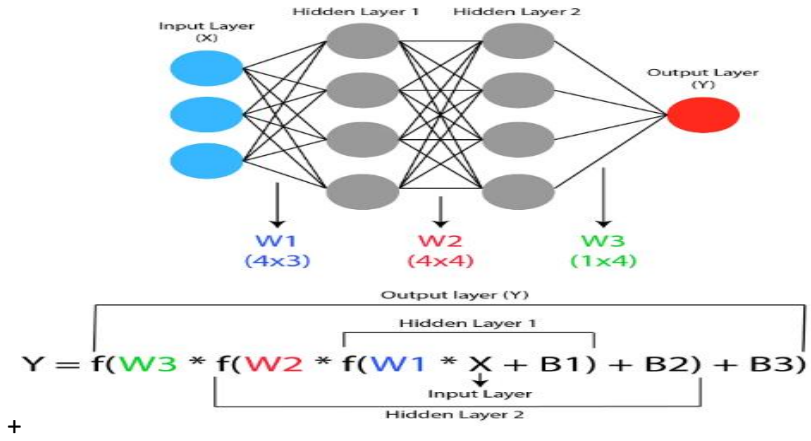


Figure 23 : illustrate the general equation of a neural network [54].

Where :

- **Y:** is the output value.
- **X:** denotes the input vector.
- **W:** represents The weight matrix in each layer
- **B:** represents bias in each layer
- **f:** The activation function

Once a vector of input data is provided, the nodes in each layer multiply the values with a sequence of weight matrices and apply activation functions, layer by layer until the final output is obtained at the output layer. This is the process by which a neural network produces an output: its classification or prediction [54].

b) How Neural Networks Works:

➢ Backpropagation:

It is a widely used algorithm in artificial neural networks (ANNs) for training deep learning models. It is a supervised learning technique that adjusts the weights of neurons in the network to minimize the error between the predicted and actual outputs [55] [56].

➢ The Backpropagation Algorithm process:

1) Random Initialization of the network weights [55].
2) The Forward Propagation of the input through the network to get the predicted output.
3) Error Computation by comparing the predicted output with the actual output.
4) Propagate the error backwards through the network to compute the gradient of the loss function with respect to each weight.
5) Weight Update by adjusting the weights in the opposite direction of the gradient using an optimization algorithm (a set of procedures used to minimize the loss function, which measures the difference between the predicted output and the actual output) like Stochastic Gradient Descent (SGD).
6) Iterative Process: Repeat steps 2 to 5 for multiple iterations until the weights converge and the network achieves the desired level of accuracy.

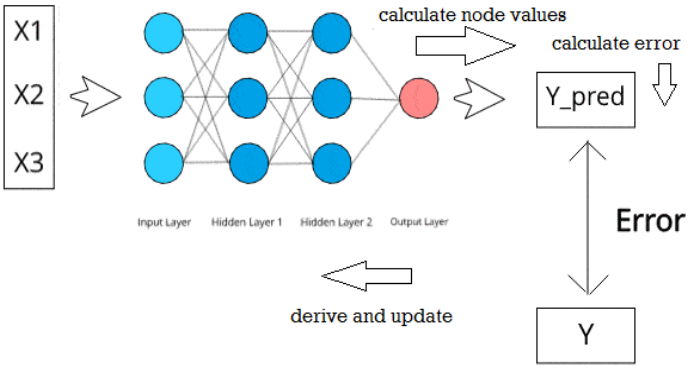


Figure 24 : Illustration of The Backpropagation process [54].

2) Recurrent Neural Network (RNN):

Definition:

Recurrent Neural Networks or **RNN**s are a type of neural network that utilize information from previous observations to influence future decisions. They are especially useful in tasks that involve processing sequences of data. RNNs are named "recurrent" because they perform the same operation for each element in a sequence, with the output depending on previous calculations. They have a "memory" that captures information about previous calculations and decisions. The "hidden state" is a vector of information that circulates through each time step and provides context based on past decisions [57] [58].

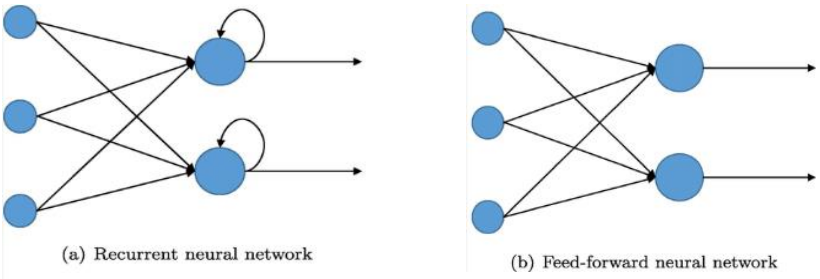


Figure 25 : The deference between the feed forward and RNN architectures [56].

a) Recurrent neural networks structure:

RNNs process the information of each element in a sequence (which is set of data points that are presented to the network one after another [60]) and the information of all the elements before it. In other words, RNNs have two input layers: one for the current element and one for the previous accumulated information, there are also two outputs: one primary output for the relevant prediction that the RNN is being trained for, which is usually ignored until all elements have been processed. The other output represents all the accumulated information of the input elements so far [54].

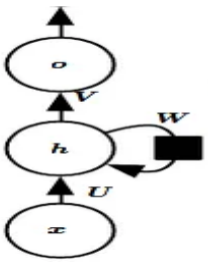


Figure 26 : The fundamental structure of an RNN [59].

To comprehend the functioning of RNNs, let's consider a sequence consisting of three words, which can be fed into a neural network with three layers, one for each word. If we unfold the RNN into a full network (which means expanding it into a complete network by representing it for the entire sequence) [61] we get:

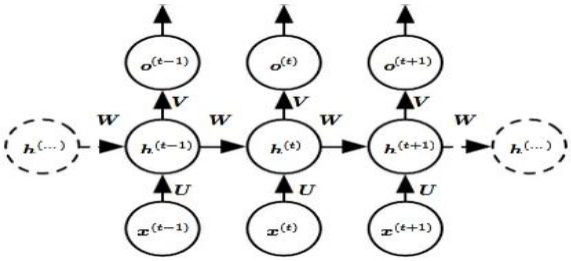


Figure 27 : Representation of the RNN unfolded into a full network [61].

- **Input:** x (t) represents the input provided to the network at a specific time step t, in the given example it could be x1 which correspond to a victor of one word from the sequence [61].
- **Hidden state**: h (t) it is a hidden state at time t and has the role of a "memory" provided for the network [62].

Can be computed using the current input and the previous time step's hidden state resulting in: [61]

$$h(t) = f(U x(t) + W h(t-1)). \text{ [61]} \qquad (1)$$

Where :

- **h (t)** is the hidden state at time t.

- **x (t)** is the input at time t.
- **f ()** is an activation function like sigmoid.
- **U** a weight matrix that define the input to hidden networks.
- **W** a weight matrix that define the hidden-to-hidden networks.
- **V** a weight matrix that define the hidden-to-output networks.

- A point to note is that the weights are utilized consistently across different time steps [61].
- **Output:** o (t) represents the network's output at time step t. defined by:

$$O(t) = f(v\,h(t)). \text{ [61]} \qquad (2)$$

b) RNN Architectures :

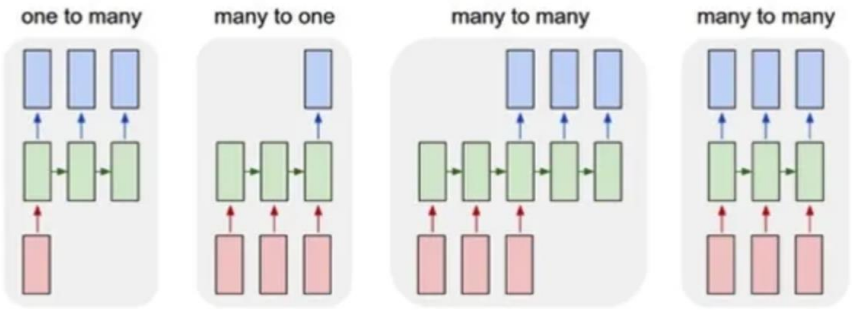


Figure 28 : RNN Architectures [61].

1. **One to many:** one input leads to a sequence in the output [62].
2. **Many to one:** a sequence in the input leads to one output [62].
3. **Many to many:** it has two types:

- The length of the input sequence does not match the length of the output sequence [62].
- The input and output length are equals [62].

c) Challenges:

Recurrent Neural Networks (RNNs) are a powerful concept in theory, but training them properly can be a challenging task. This model comes with a significant obstacle which is the vanishing gradient problem.

- **Gradient descent:** is a commonly used optimization algorithm which enables us to identify the optimal combination of weights and biases for our model to achieve optimal performance on a given task.

As previously mentioned, information in neural networks flows through time, and errors are back propagated through the network to update the weights. However, there are some differences with RNNs.

1. RNNs use the information from previous time steps as input for the current time step, adding a temporal aspect to the network.
2. The error is calculated at each time step, and the model's output is compared to the desired output.

During training, there is an error value for each time step in the sequence, which enables tracking of the model's performance over time.

The problem arises when updating Wrec, which represents the connection from the hidden to the hidden layer in the unfolded network. By multiplying the same weight many times by a tiny value, the weight's value decreases rapidly, resulting in a decrease in gradient with each multiplication [64].

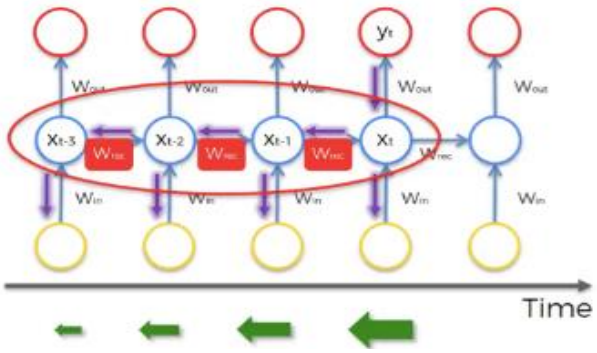


Figure 29 : The vanishing gradient problem [62].

- **Solutions:**

The vanishing gradient [64]:

- Weight initialization
- Long Term Memory Networks (LSTMs).

3) Long Term Memory Networks:

a) Definition:

Sepp Hochreiter and Juergen Schmidhuber proposed the Long Short-Term Memory (LSTM) as an approach to overcome the vanishing gradient problem in RNNs. LSTM works by altering the hidden layer in the RNN to enable the retention of information from past inputs over extended periods. To achieve this, LSTM employs three gating mechanisms: the input gate, forget gate, and output gate, which play a critical role in controlling the transmission of information within the LSTM network. By selectively choosing to remember or forget specific details from the input sequence, LSTM demonstrates a high level of proficiency in handling long-term dependencies. Consequently, LSTM proves to be a valuable tool for surpassing the limitations associated with traditional RNNs [62] [65].

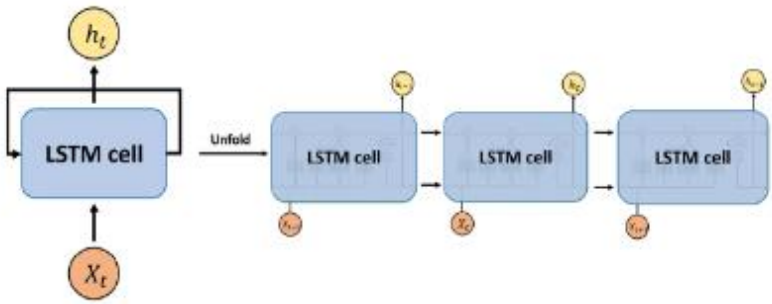


Figure 30 : Demonstration of an unfolded LSTM network [66].

- **The forget gate:** responsible for discarding or removing information from the cell state that is deemed irrelevant or no longer useful [62].
- **The input gate:** allows for the incorporation of valuable information into the cell state. [62].
- **Output gate**: It contributes additional valuable information to the state of the cell [62].

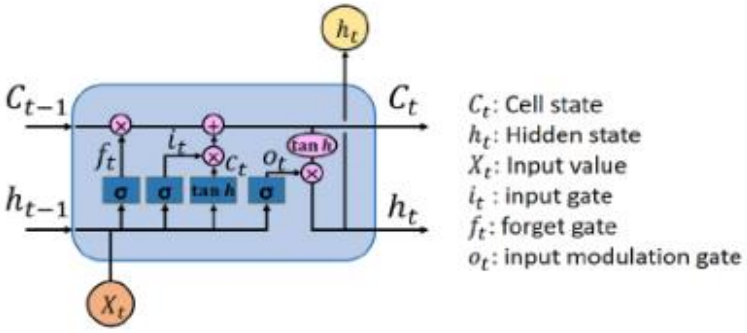


Figure 31 : The architecture of an LSTM cell [66].

b) The mechanism of LSTMs in RNN:

LSTMs operate through a three-step process:

- **Step 1: Determine the Optimal Amount of Historical Data for Retention:**

The initial stage of the LSTM involves determining which information should be excluded from the cell during a specific time step. This decision is made using the sigmoid function, which considers both the previous state (h (t-1)) and the current input (x (t)) to calculate the function. [62] [65].

$$\boldsymbol{f_t = \sigma\left(W_f * [\, h_{t-1} * x_t \,] + b_f\right)}\ \textbf{[65]} \qquad (3)$$

The forget gate (f_t) analyzes the input sequence, evaluating the significance of each piece of information by considering contextual cues like punctuation and word patterns. This helps identify potential shifts or changes in context. Comparing this information with the current input sentence, it determines whether the previous information should be retained or discarded. When a subsequent sentence introduces a new subject or topic, the LSTM network recognizes the irrelevance of the previous information and discards it accordingly. Consequently, the network reallocates its resources, creating space for accommodating new and more pertinent information [65].

- **Step 2: Determine the Contribution of This Unit to the Current State:**

There are two components in the second layer: the sigmoid function and the tanh function:

- **The sigmoid function**: determines the extent to which values are allowed to pass through, resulting in binary outputs of 0 or 1 [65].
- **The hyperbolic tangent (tanh):** function assigns weights to the passed values, determining their significance on a scale from -1 to 1 [65].

$$\boldsymbol{i_t = \sigma(W_i * [h_{t-1} * x_t] + b_i)[65]} \quad (4)$$

$$\boldsymbol{\widetilde{C}_t = tanh(W_C * [h_{t-1} * x_t] + b_C \quad [65]} \quad (5)$$

The input gate (i_t) assesses the importance of information from the current input (x (t)). It determines the relevance of essential details while disregarding or forgetting less significant information. By doing so, the input gate enables the system to incorporate new relevant information effectively [65] [66].

- **Step 3: Determine the Portion of the Current Cell State Included in the Output:**

The third step involves determining the output. This is achieved by utilizing a sigmoid layer to determine the portions of the cell state that contribute to the output. The cell state is then processed through the tanh function to restrict the values within the range of -1 to 1. Finally, the output of the sigmoid gate is multiplied by the transformed cell state to obtain the final output [65] [66].

$$\boldsymbol{o_t = \sigma(W_o[\, h_{t-1} * x_t] + \, b_0)} \quad \textbf{[65]} \quad (6)$$

$$\boldsymbol{h_t = \, o_t * tanh(C_t)} \quad \textbf{[65]} \quad (7)$$

II.16. Conclusion:

In this chapter, we have provided a comprehensive exploration of the various techniques and algorithms used for image segmentation. We have discussed the importance of segmentation in identifying and separating objects within images, and examined common

methods such as thresholding, area growth, and edge detection. Moreover, we investigated the functions and workings of neural networks, specifically (LSTM). Where we explored the unique properties and their effectiveness in processing sequencing data. By combining segmentation techniques with the power of LSTM, we aim to demonstrate the improved ability of our model to accurately identify and classify objects in images.

In the forthcoming chapter, we will transition from theory to practical implementation, demonstrating the true potential of these cutting-edge technologies in action.

Chapter III:

The Methodical Journey: Procedural Implementation and Exemplary Outcomes

III.1.Introduction:

In this chapter, and in light of what we discussed in the previous chapter about the techniques of accurate classification and segmentation of medical images, specifically in the context of images of malaria cells, we will discuss the development of our proposed program for the classification of images of malaria cells through which we seek to establish an accurate and reliable classification system that helps in early detection on malaria, and its role in improving classification accuracy. In the following sections, we provide step-by-step insights into the implementation process, highlighting the selected techniques, libraries and software used in its implementation as well as evaluating its performance.

III.2.The proposed approach:

The model proposed for automated malaria diagnosis is visualized in Figure 32. Its primary objective is to accurately classify blood smear images into either the healthy or infected category. This classification process, discussed in the following sections, offers comprehensive insights into the methodology employed in the proposed program and involves three crucial steps. Firstly, the input data comprises a collection of blood smear images captured using a smartphone under a microscope. The images undergo a preprocessing phase, including thresholding and resizing processes, to give them a standard form to facilitate subsequent processing. Finally, a pre-trained model, utilizing an LSTM network, detects the presence of malaria infection in the blood smear and outputs a '1' if infected or '0' if not.

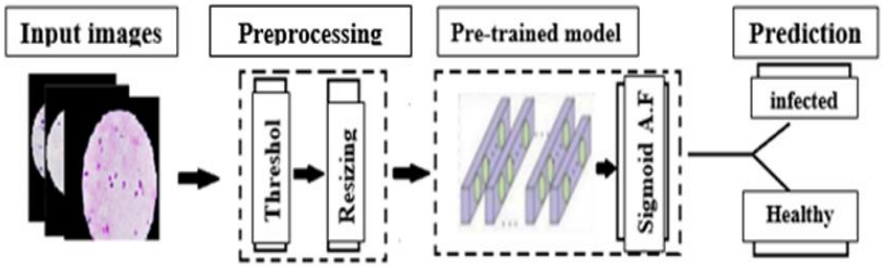


Figure 32: A suggested automated approach for diagnosing malaria.

III.3.Data collection:

In this study, we used a pre-existing dataset retrievable from the National Library of Medicine's website. The dataset exhibits a balanced distribution, with an equal number of 300

infected and 300 uninfected images. This balance ensures that the model receives sufficient exposure to both classes during the training process, these images were captured using a smartphone camera and represent blood derived from real-world malaria cases samples obtained from patients suspected with malaria.

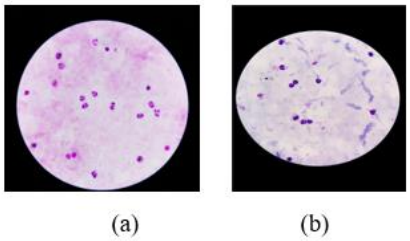


Figure 33: Sample from the NLM dataset: (a) representative of an uninfected cell, and (b) representative of a Vivax-infected cell.

III.4.Programming Environment:

To build the model architecture and perform data processing we employed a range of tools that varied from hardware provided in the computing resources to the software that included programming language and a variety of computing libraries which allowed us to handle data manipulation.

a. Equipment used:

	PC 01	PC 02
CPU Model Name	Intel(R)Core(TM)	AMD A4-9120RADEON 3
RAM	8 GB	4 GB
Disk Space	154 GO	462

Table 2 : Hardware resources.

b. Programming platform (Google Colab):

Google Colab, also known as "Colaboratory", is a free cloud service offered by Google to promote research in Deep Learning and Artificial Intelligence. These fields often face the challenge of the need for high computing power for model training and success.

This platform overcomes this obstacle by allowing the direct training of Deep Learning models in the cloud, without the need to install additional software on your computer. All you need is a web browser to access the Google Colab development environment.

By using Google Colab, you can leverage the computing power of the cloud to perform intensive tasks, such as training deep neural networks, without worrying about the hardware limitations of your own machine. This facilitates experimentation, iteration, and access to scalable compute resources for your Deep Learning and Artificial Intelligence projects [67].

Why google colab:

When utilizing Google Colab, programmers have a range of capabilities available to them [67]:

- They can write and execute Python code.
- Notebooks can be created, downloaded, and shared.
- Notebooks can be imported and saved directly to Google Drive.
- External datasets can be incorporated into their work.
- They can seamlessly integrate with PyTorch, TensorFlow, Keras, and OpenCV.
- Access to a complimentary GPU is provided through the free cloud service.

Figure 34:google colab logo [68].

c) Programming language (Python):

Python stands out as an exceptional programming language renowned for its impressive power and user-friendliness. It excels in facilitating seamless interactions between Raspberry Pi and the physical world. Python's clean syntax places a strong emphasis on readability, using familiar English keywords such as print, input, and if. As an interpreted language, Python embraces a multi-paradigm approach and is compatible across different platforms. It supports imperative, functional, and object-oriented structured programming styles. With its robust dynamic typing, automatic memory management via garbage collection, and efficient exception handling system, Python proves to be a terrific choice for software development [69].

Figure 35: python-logo [70].

- In addition to these advantages, it is worth noting the advantages of Python over other languages [71]:
- Less coding required and you don't need extensive knowledge to start programming in Python. This makes it more user friendly for beginners.
- Python is very affordable and can be accessed by the entire community because it is free. Due to its increasing popularity, it also has better technical support.
- Python is an ideal choice for XML processing. It provides built-in features that make it easy to manipulate XML data, making it a valuable tool in this field.
- Python is the most widely used and popular language in the field of artificial intelligence. Its syntactic simplicity, wealth of dedicated AI libraries and frameworks, such as TensorFlow, as well as its large developer community make it the preferred choice for AI projects.

Figure 36: Python libraries [72].

- **Keras:**

Keras, an open source neural network library written in Python, was chosen because of its many advantages. Compatible with other frameworks, it is specifically designed to enable rapid experimentation with deep neural networks.

Its user-friendliness, its modularity and its scalability are key characteristics that have won over. Keras was developed under the supervision of François Chollet, engineer at Google and main author of this library [73].

- **Matplotlib:**

It is a plotting library for the Python programming language. This library provides an object-oriented API for integrating graphics into applications using general-purpose GUI toolkits such as Tkinter, Python, Qt, or GTK+ [74].

- **Pandas:**

The Pandas library is indispensable when it comes to organizing and making our data more accessible and understandable. It provides the ability to structure, which facilitate the clear representation and customization. Pandas specifically offers data structures and operations specifically designed for manipulating numeric arrays and time series. This library, distributed under the name Pandas, is free software distributed under the BSD license [74].

- **Tensorflow:**

  Tensorflow is a free and open source machine learning library created by Google. It enables the development and implementation of machine learning and deep learning applications, offering a wide range of models and algorithms for different applications. We used this library to learn about human activities based on real-time sensor data collected from smartphones [62].

- **Numpy:**

  Numpy is a Python library that extends the functionality of the language by providing support for manipulating large arrays and multidimensional arrays.

Furthermore, Numpy offers a wide range of high-level mathematical functions that make it easy to perform advanced operations on these arrays [73].

- **Scikit-Learn:**

Previously known as scikits.learn and sklearn, is a free machine learning library for the Python programming language. It offers a variety of classification, regression, and clustering algorithms, such as gradient boost, k-means, and others. Scikit-Learn is specifically designed to integrate with Python's numerical and scientific libraries, including Numpy and SciPy [73].

III.5.model architecture:

The architecture of our classification model utilizes the LSTM framework, which consists of multiple layers designed to effectively process sequential data.

The following diagram illustrates the processing steps we followed in order to achieve the resulted model:

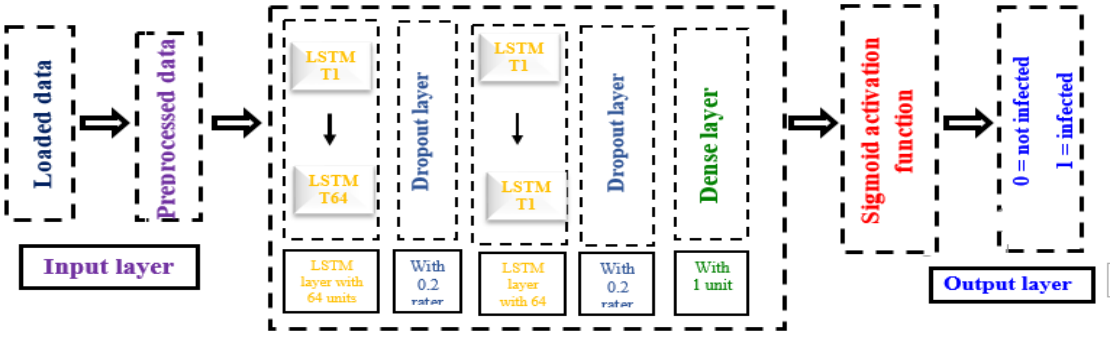


Figure 37: The functional block diagram illustrating the proposed model.

a) Loading data:

We performed the entire process of loading the dataset in our programas following:

Firstly, we imported the necessary libraries and modules. Then, we mounted the Google Drive using the **drive.mount ()** function, which granted us access to the essential files and folders stored there. The approach we used ensured that we successfully loaded the dataset into our program for further analysis and processing.

b) Image Preprocessing:

After loading each image using Image. Open (img_path), the program proceeds to preprocess the images following the next steps:

1. The image is converted the original image to grayscale level image.
2. Threshold segmentation is applied to the grayscale image resulted.
3. To ensure a consistent size for further analysis, the image is resized to a fixed dimension of 100x100 pixels.

These preprocessing steps are applied to each loaded image, both for infected and uninfected images, before they are appended to the respective lists (infected_images and uninfected_images) for further processing. This images then are combined under '**images**' variable. Similarly, their labels are combined and assigned to the '**labels**' variable. Then both Lists are converted to NumPy Arrays to facilitate further processing and compatibility with machine learning libraries.

c) Building the model:

The model consists of 5 layers:

The first LSTM layer: consists of 64 LSTM units and is set to return sequences it plays a crucial role in capturing and comprehending the sequential information inherent in the dataset, enabling the model to learn intricate patterns

The first Dropout layer: it is added after the first LSTM layer with a dropout rate of 0.2. It helps prevent overfitting (which arises when a model becomes excessively intricate and begins to memorize the training data rather than acquiring general patterns that can be extrapolated to unseen data.) by randomly dropping 20% of the connections serving as a regularization technique to enhance generalization.

The second LSTM layer: same as the previous one it consists of 64 LSTM units but doesn't return sequences.

The second dropout layer: it is added after the second LSTM layer with similar characteristics to the first one.

The dense layer: consists of a single neuron with a sigmoid activation function. It produces a single output value indicating the probability of the input image being infected or uninfected.

d) Model Training:

- **Data splitting:** The preprocessed data was split using the **train_test_split** function with **20%** of the total dataset being allocated to testing, and the remaining **80%** being used for training.

- **Model compilation phase:** The LSTM model is configured with a binary crossentropy loss function (which measures the dissimilarity between the predicted probabilities and the true binary labels, guiding the model to minimize the difference between them) and the Adam optimizer that enhance the training process by adapting the learning rate.

- **Training parameters:**

Epochs: which represents how many times the model goes through all the dataset provided for training. To ensure that the model had sufficient iterations with it, we used 100 epochs this give the model the chance to analyze the data repeatedly, and extract intricate patterns, relationships, and variations present in the dataset to learn from it.

Batch Size: The batch size determines the number of samples that will be fed into the model at each iteration which allow it to compute the loss and updating its weights accordingly.in our case the dataset was divided into 32 batches.

III.6.Results and Evaluation:

a) Results:

During the training process, our model was trained for 100 epochs. In the initial 20 epochs, the model achieved a training accuracy of 0.97. We recorded the accuracy and loss at each epoch and plotted the curves to visualize the training and test results. These curves provided valuable insights into the evolution of accuracy and loss over the epochs.

The training accuracy and test accuracy demonstrated a varying increase with each epoch, but they eventually reached a plateau during the later epochs. This suggests that the model's performance stabilized and did not improve significantly beyond a certain point. The graphs bellow represent the training and test results:

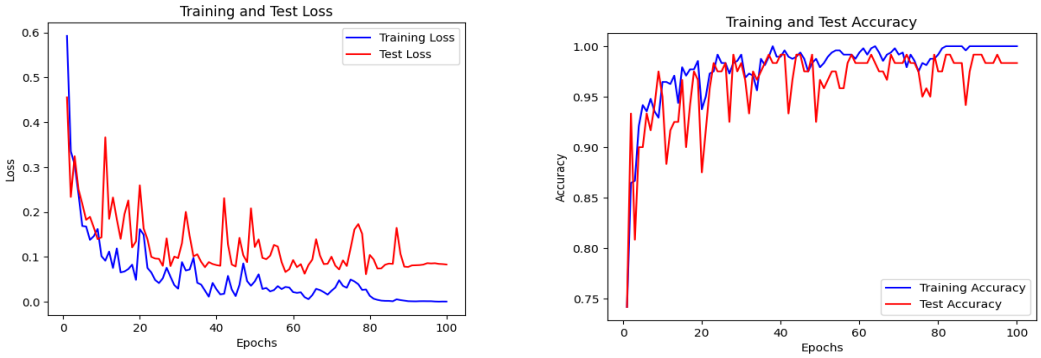


Figure 38: The training and test results.

It's worth noting that the test loss was slightly higher than the training loss, which is a common occurrence in machine learning models. As the model generalizes to unseen test data, it may encounter patterns or examples that differ from what it learned during training, resulting in a slightly higher loss.Throughout the training process, both the training loss and validation loss consistently decreased with each epoch. This indicates that the model gradually improved its predictions and became more accurate over time.

The table below represents the overall accuracy and loss obtained during the training and evaluation phases of the model:

	Accuracy	**Loss**
Training	**0.9700**	**0.0831**
Test	**0.9833**	**0.0831**

Table 3: The overall training and test accuracy and loss.

b) Evaluation:

We evaluated the performance of our trained model on the test data that indicates how well the model can generalize to unseen data and make accurate predictions. In our case, we used the F1 score, which is a commonly used evaluation metric in binary classification tasks, so it was a preferred tool for detection of malaria-infected and uninfected cells. It combines the precision and recall of a model to provide a single measure of its overall performance.

Here are the formulas for precision, recall, and F1 score:

Precision = TP / (TP + FP)

Recall = TP / (TP + FN)

F1 Score = 2 * (Precision * Recall) / (Precision + Recall). [75] **(8)**

Where:

- TP (True Positive) represents the number of correctly predicted positive instances.
- FP (False Positive) represents the number of incorrectly predicted positive instances.
- FN (False Negative) represents the number of incorrectly predicted negative instances.

As a result, we got an F1 score of 0.9838709677419355 and this signifies the strong performance and reliability of our model in accurately classifying malaria-infected and uninfected cells, which reinforces the model's effectiveness in contributing to the detection and diagnosis of malaria.

III.7. Practical example:

For further evaluation, we utilized a pre-trained model and provided it with an unseen image. This image was obtained from the same source as the dataset and depicts a blood smear infected with Plasmodium falciparum. The process yielded the following results :

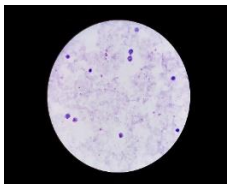


Figure 39: Blood smear image infected with Plasmodium falciparum.

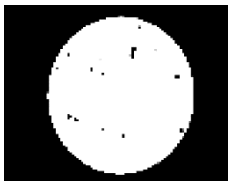


Figure 40: The resulted preprocessed image.

Classification Result :

```
1/1 [==============================] - 0s 40ms/step
New image classification: Infected
```

Figure 41: A captured image of the resulted classification

The new image was classified sucssefully, and the result obtained indicates that it is classified as "infected", which is actually the case. This further confirms the effectiveness of the model in identifying infected cells.

III.8. Conclusion:

In this chapter, we presented the implementation of an LSTM-based model for malaria blood cell classification. We discussed the dataset used in our study, described the architecture of our model then proceeded to evaluate its performance.

Our LSTM-based model for malaria blood cell classification has yielded encouraging results, Attaining high accuracy in distinguishing between infected and non-infected blood cells. Although certain limitations were presented, such as the need for additional data, this study contributes to the field by providing an automated and reliable approach for blood cell classification, achieving the objective of our study by aiding healthcare professionals in malaria diagnosis and treatment decisions.

General Conclusion:

In this thesis, our primary objective was to develop an effective approach for the classification of malaria cell images using a Long Short-Term Memory (LSTM) model. The study consisted of three main chapters, each contributing to the overall goal of accurate malaria diagnosis through advanced image classification techniques.

The first chapter provided a comprehensive introduction to malaria, its prevalence, and the challenges associated with its diagnosis. We highlighted the importance of timely and accurate identification of malaria-infected cells to ensure appropriate treatment and prevent the spread of the disease. By understanding the unique characteristics of malaria parasites, we established a solid foundation for our subsequent research.

In the second chapter, we delved into the topic of image classification and segmentation, focusing on the applications of deep learning models in medical image analysis. We discussed the significance of LSTM, a type of recurrent neural network (RNN), for handling sequential data such as time series or sequential image data. The LSTM model's ability to capture long-term dependencies makes it suitable for analyzing the complex patterns present in malaria cell images.

Building upon the knowledge gained from the previous chapters, the final chapter presented the implementation of our proposed LSTM model for the classification of malaria cell images. By leveraging the temporal dependencies within the sequential image data, our approach aimed to improve the accuracy and reliability of malaria diagnosis. We trained the LSTM model using a large dataset of annotated malaria cell images, optimizing its performance through appropriate hyperparameter tuning and training techniques.

Through extensive experimentation and evaluation, we demonstrated the effectiveness of our LSTM-based approach. The model showcased impressive results in accurately classifying malaria-infected and uninfected cells, surpassing traditional methods in terms of both accuracy and efficiency. Our findings highlight the potential of LSTM models in aiding medical professionals by providing reliable and automated malaria diagnosis.

In conclusion, this thesis bridges the gap between malaria diagnosis and advanced image classification techniques, specifically leveraging the LSTM model. By combining medical knowledge, deep learning expertise, and sequential analysis, we have developed an effective approach for the classification of malaria cell images. Our research opens new avenues for future studies in the field of automated malaria diagnosis, ultimately aiding in the fight against this global health issue.

Perspectives in future works:

The results demonstrated by our model highlight the potential value of the LSTM network as a valuable tool for the classification of malaria blood cell images. Proven effective in detection. This field is broad and could be strengthened in future research, here are some points:

- **Classification of Malaria Types**: based on what we achieved our model can extend to identify specific malaria type or effect degree on the human body.

- **Development of a Mobile Application**: using the advanced image-capturing capabilities of smartphones, our model can be further developed into a mobile application. Which will be of a great help especially in remote areas with limited access to medical facilities.

Expansion to Other Diseases: the model's capabilities can be expanded to include various infectious diseases

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Références bibliographiques

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