Pathogen Of Malaria Detection from Thick Smears of Blood Using Dl Algorithms Over Smart Mobile Devices

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Abstract:
The focus of this investigation lies in the realm of automated malaria parasite detection within thick blood smears, with a particular emphasis on the integration of smartphones as the primary platform for its deployment. In our pioneering endeavor, we introduce a novel deep learning methodology, a groundbreaking innovation engineered for the purpose of malaria parasite detection in thick blood smear images, meticulously designed to operate seamlessly on smartphone devices. The methodology that underpins our approach consists of a two-tiered processing paradigm. Initially, we embrace the utilization of an intensity-based Iterative Global Minimum Screening (IGMS), a rapid and meticulous mechanism that screens thick smear images, sifting through the visual landscape to identify prospective parasite candidates. Following this initial screening, we enlist the expertise of a customized Convolutional Neural Network (CNN), purpose-built for the classification of each candidate, deftly categorizing them as either parasites or belonging to the background. As a hallmark of our commitment to the advancement of scientific knowledge and research, we accompany this paper with the gracious offering of a dataset, containing 1819 thick smear images culled from the lives of 150 patients. This repository, made freely accessible to the global research community, stands as a testament to our dedication to fostering collaboration and innovation in the realm of malaria parasite detection. Our rigorous scientific inquiry leverages this dataset for both the training and testing of our deep learning methodology, as meticulously documented within the pages of this paper. The results of our comprehensive endeavor are artfully summarized through a patient-level five-fold cross-evaluation. This evaluation bears witness to the efficacy of our customized CNN model, as it adeptly discriminates between positive (parasitic) and negative image patches. The litmus test is exemplified through a suite of performance indicators, each revealing a facet of the model's prowess in capturing the nuances of the data landscape.

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1. Introduction

The 2018 malaria report from the World Health Organization (WHO) [1] revealed that in 2017, approximately 219 million cases of malaria were identified globally, resulting in roughly 435,000 fatalities. Malaria diagnosis traditionally relies on the examination of stained thick and thin blood smears through microscopy, regarded as the gold standard [2], [3]. This method is cost-effective and widely accessible but time-intensive. Furthermore, the accuracy of microscopy-based diagnosis hinges significantly upon the expertise of parasitologists [4], who often operate in resource-constrained settings without established mechanisms for maintaining their skills and diagnostic precision. This scenario frequently leads to erroneous diagnoses, consequently prompting inappropriate treatments [4]. False-positive results necessitate unnecessary administration of anti-malaria drugs, leading to side effects like abdominal discomfort and nausea, while false negatives trigger unwarranted antibiotic usage, secondary consultations, and potentially exacerbate more severe malaria cases [5]. Therefore, a compelling research objective is the creation of an automated system for malaria diagnosis, aiming to enhance individualized patient care and management. Automatic parasite detection offers two significant advantages: firstly, it promises more dependable diagnoses, especially in regions with limited resources, and secondly, it curtails diagnostic expenses. Accurate parasite counts play a pivotal role in malaria diagnosis and the assessment of disease severity. They also serve as a key parameter for monitoring patients to gauge the efficacy of treatments and the emergence of potential drug resistance. This study is dedicated to investigating the automatic detection and quantification of malaria parasites in digital images of thick blood smears, obtained using smartphones.

The thick blood smear, an invaluable diagnostic modality, is meticulously employed in the pursuit of uncovering the presence of elusive malaria parasites residing within a minute droplet of crimson vitality. It distinguishes itself by its remarkable proficiency in parasite detection, boasting an elevated sensitivity of nearly elevenfold in comparison to its daintier counterpart, the thin blood smear [5]. As the thin blood smear unfolds, its essence lies in the art of diffusing a solitary sanguine droplet across a pristine glass canvas, a tapestry finely woven to delineate the intricacies of parasite taxonomy and ontogeny. In the realm of both thick and thin blood smears, delineated succinctly within the visage of Figure 1, the unique morphology of the parasitic inhabitants necessitates the orchestration of distinct methodologies to discern their presence. Gazing upon the ethereal landscape of the thin blood smear, an enthralling tapestry unfurls where the sentinel guardians, the white blood cells (WBCs), and the lifeblood itself, the red blood cells (RBCs), lay bare before the observer. An orchestration of automatic parasite detection in the ethereal domain of thin smears commences with the intricate ballet of red blood cell segmentation, culminating in the solemn decree of infection or unblemished innocence [5]–[7]. However, the thick blood smear, as if enshrouded in an arcane mist, discloses only the sovereignty of the white blood cells and the phantasmal nuclei residing within the red blood cells' sanctuaries (as is illustrated in Figure 1(a)). Herein lies the enigma: the parasites of malevolent mien must be apprehended directly, and thus, a customary prelude is enacted whereby prospective parasitic candidates are tenderly selected and later inducted into the tribunal of authenticity, or conversely, cast into the abyss of background noise. The challenge, a Sisyphean endeavor of sorts, resides in the labyrinthine folds of this domain, for the nuclei of white blood cells and an array of non-parasitic constituents, akin to chameleons, assume the nefarious hues of stain absorption, casting forth artful specters that may beguile and mislead the discerning eye towards erroneous proclamations of parasitic dominion.

2. Related Works

Of late, within the annals of time, a cornucopia of methodologies and stratagems have sprouted forth like spring blooms, diligently dedicated to the intricate domain of image manipulation and scrutiny, with a resolute focus directed towards the realm of both dainty and robust blood smears. The raison d'être of this myriad of cerebral endeavors lies in the pursuit of the elusive dream, the dream of a future wherein the automated unmasking of the parasitic specters becomes the new reality, and scholars, in their erudition, have thoughtfully inscribed comprehensive reviews upon this scroll of knowledge, which may be perused within the pages of [5], [8], and [9]. In the forthcoming passage, we shall unfurl the tapestry, though briefly, of the manifold approaches conceived for the discernment of the malevolent malaria entities, concealed amidst the thick coagulation of life's vital fluid.

Conventional techniques employed in the quest for parasitic entities frequently unfurl a choreography of segmentation strategies [10]–[13], a complex dance interwoven with the threads of thresholding and the thespian artistry of morphological operations. Among these thespian visionaries, Kaewkamnerd et al. [10] have bestowed upon the world an innovative tableau, an ode to the adaptive threshold etched within the very fabric of the HSV image's V-value histogram. With this muse, they artfully conjure forth candidates for parasitic communion and the spectral guardians known as white blood cells, culminating in an exquisite discourse wherein parasites and white blood cells are delineated by the metric of their girth. Within this sonnet, their magnum opus, a mosaic of 20 images, comes alive, revealing the proposed technique's applause-worthy accuracy, ensconced at a modest 60%. Another virtuoso of this hallowed domain, Hanif et al. [11], masterfully conduct an overture in the form of an intensity-stretching symphony, augmenting the contrasts within the tapestries of 255 thick blood smears, to bestow upon them the breath of life. With an empirical wand, they conjure forth a threshold, separating malaria parasites from the woven fabric of existence. In their opus, qualitative results manifest across an array of images, each graced by diverse empirical thresholds, each unfurling before the eyes the beguiling dance of satisfying segmentation. In the annals of exploration, Chakrabortya et al. [12], a triumvirate of visionaries, artfully interweave the dance of morphology with the vibrant tapestry of color intelligence, a waltz amidst the thick blood smears. Their experiments, a testament to their dedication, unfurl before a captive audience of 75 images, a patchwork of evaluation that reveals a triumphant detection rate of 95%, yet bespeaks of a siren's call, a false positive ratio of 10%. Finally, the magicians of the ages, Dave et al. [13], armed with the spells of histogram-based adaptive thresholding, weave incantations within the folds of denoised images. With masterful precision, they beckon forth the spectral residents, the red blood cells, ensnared in the malevolent web of malaria parasites, dwelling within both thin and robust blood smears. A tale spun with the elegance of artistry, this chronicle of diagnostic achievement remains a testament to their enigmatic prowess.

At the microcosmic scale of patch-level scrutiny, the hallowed ritual unfolds, as 87 images are subjected to the probing gaze of methodical inquiry. Here, the method, like a vigilant sentinel, unveils its prowess, discerning 533 parasitic apparitions, in stark juxtaposition to the 484 parasites enshrined in the annals of ground truth. Tradition, in its undying simplicity and expeditious stride, is a distinguished muse. Yet, therein lies its Achilles' heel, for when traversing the treacherous terrain of extensive datasets, its limitations become evident. Traditional methodologies, steeped in their time-honored principles, succumb to the capricious winds of image variance. They are bound by the whims of empiricism, their parameters delicately calibrated by the hands of tradition. A minstrel's ballad, the performance evaluation on the patch level, dances upon the stage of modest datasets, spanning from a mere score to three centuries of images. Yet, when the opus extends its tendrils into the vast expanse of grandiose datasets or scales its sonorous notes to the level of the image or the very threshold of patient scrutiny, a symphony of transformation ensues. The transmutation is a marvel, where the delicate melodies of small datasets become an intricate mosaic, each tessellated piece of the performance echoing a different truth, a symphony where the notes of evaluation resonate with a diverse resonance of understanding.

In the realm of feature-based methodologies, the intricate symphony begins with a meticulous ballet of feature extraction and classification, wherein machine learning techniques reign supreme [14]–[18]. The magnum opus of Elter et al. [14] unveils an orchestration of 174 features, culled with precision from the pre-detected plasmodia candidates. These fragments of data are tenderly laid before the altar of a Support Vector Machine (SVM) classifier, their presence serving as an offering to the pursuit of parasite identification. A sensitivity of 97% adorns their accomplishments, as 256 images grace the stage at the patch level. Meanwhile, Purnama et al. [15] embark on a journey of color spectra, casting their nets into the vast sea of RGB and HSV spaces, each an ocean of data. Genetic Programming, their guide, whispers the secrets of identifying parasite type and stage, culminating in an opus of classification. With 180 patches in their mosaic, an average accuracy of 95.58% for parasite identification and 95.49% for the non-parasitic ilk adorns their magnum opus. The minstrels, Yunda et al. [16], summon forth a tapestry woven with the hues of color, the intricate textures revealed through co-occurrence, and the delicate strokes of wavelet-based intricacies, all extracted from the pre-segmented canvas. Principal Component Analysis (PCA), the maestro, undertakes a symphony of reduction, rendering redundant features silent, while a neural network, the virtuoso, unveils the final classification. In a gallery of 110 images, the melody played resonates at 76.45% sensitivity for the elusive parasite. Quinn et al. [17], the architects of meticulous division, split each image into 475 serendipitous, overlapping patches, in a waltz of downsampling and sliding window screening. From these fragments, the notes of connected components and moment features emerge, forming a song that finds its crescendo in the embrace of a randomized tree classifier. The grandeur of their endeavor finds fulfillment in the vast auditorium of 2903 images, gracing 133 patients with a precision of 90% at a recall of 20% on the patch level. Lastly, Rosado et al. [18], with a palette of adaptive thresholding, paint the canvas of parasite detection, their brush strokes accentuated by geometry, color, and texture features. A kernel of Radial Basis Function (RBF) SVM lends resonance to the composition, while an audience of 94 images from 6 patients bears witness to their automatic prognostications. An astonishing patch-level accuracy of 91.8%, adorned with a sensitivity of 80.5% and a specificity of 93.5%, celebrates their prophecy, while the WBC detection echoes at 98.2% sensitivity and 72.1% specificity. In this grand symphony, the feature-based approaches adorn themselves with laurels at the patch level, where each image fragment becomes a note in their composition. Yet, it is with caution that we tread, for the ultimate crescendo, the melody of malaria patient diagnosis, yearns for the harmonious detection and classification of all patches, both those graced by parasites and those marred by false positives. The virtuosity displayed at the patch level may, at times, be a deceptive prelude, for the image-level and patient-level cadenzas demand a unique resonance, a chorus that the realm of feature-based approaches must aspire to attain.

3. Novelties In This Work

In comparison to the preexisting body of work dedicated to the intricate realm of processing thick blood smears, we bespeak the manifestation of several noteworthy contributions. First and foremost, we unveil the culmination of our endeavors in the form of a novel smartphone system, meticulously devised for the purpose of automated parasite detection within the labyrinthine depths of thick blood smears. This technological marvel finds its genesis in the conceptualization of our innovative intensity-based Iterative Global Minimum Screening (IGMS) method, a paragon of swift and automatic preselection of prospective parasite candidates. Moreover, our ensemble is enriched by the presence of a bespoke Convolutional Neural Network (CNN) model, adorning our arsenal with its prowess [19]–[21], [26]–[28]. To the best of our knowledge, this pioneering work stands as the maiden voyage of its kind, a monumental quest for parasite detection in the realm of smartphones, wherein the paradigms of deep learning cast their enchanting spell. Secondly, our creation prides itself on the celerity of its operation. An orchestration of detection, graceful and agile, unfurls its symphony in a mere 10 seconds, caressing the contours of a 3024 × 4032 image, nestled within the warm embrace of an unassuming Android smartphone. Lastly, our intrepid voyage of exploration unfolds upon the vast canvas of a much larger image compendium, drawn from the collections of 138 patients. This extensive collection includes a veritable trove of 1819 thick smear images, each meticulously annotated, and a bountiful repository of 84,961 meticulously documented parasites, ready to grace the public sphere. As a grand gesture of transparency, we bestow upon the world this vast and invaluable resource, to be shared in unison with the chronicles contained within these very pages.

We have meticulously structured the subsequent sections of this composition as a testament to our systematic approach: in the realm of Section II, a detailed exposition awaits, meticulously unfurling the intricate tapestry of our proposed methodology for the automated detection of elusive parasites. Section III ushers forth the advent of comprehensive knowledge, where the troves of dataset intricacies are unveiled, along with the ethereal stage set for experimentation, and the pearls of results awaiting their moment to shine. Venturing into the chambers of Section IV, we transcend the mere examination of results and delve into the profundities of discourse, an intellectual dialogue wherein our findings find resonance, pondered and analyzed. With the graceful closing of the penultimate chapter in Section V, a resonant denouement emerges, the conclusion befitting our journey, as the symphony of our narrative concludes with a flourish, leaving an indelible mark on the annals of this scholarly expedition.

4. Methodologies Adopted

The initial phase of our process, known as the screening stage, serves as the vanguard in our quest to narrow the expansive expanse of the search area, refining it to a more discernible realm that beckons us to uncover the most plausible candidates among the parasites. The selection of these would-be parasite candidates is meticulously orchestrated through a symphony of grayscale intensity analysis, wherein the solemnity of their selection is ordained. This method exploits the inherent darkness of the nuclei belonging to both parasites and white blood cells (WBCs), a stark contrast to the luminosity of the background (as depicted in Fig.2). In our pursuit of precision, we embark upon the endeavor of eliminating any distractions caused by the presence of white blood cells. This meticulous effort unfolds as the WBC detection phase, an artful curation that banishes the presence of these cellular entities from the canvas. With this verdant field cleared, the method for preselecting parasite candidates based on intensity is revealed as a two-part ballet. Firstly, the WBC detection ritual purges the image of their presence, akin to the vanishing of mist under the morning sun. Following this, the parasite candidate generation commences, gracefully sketching regions of interest that captivate our attention. These regions are identified by the localization of the most muted intensities strewn across the expansive landscape of a thick blood smear image, much like a cartographer mapping the intricacies of a mysterious realm.

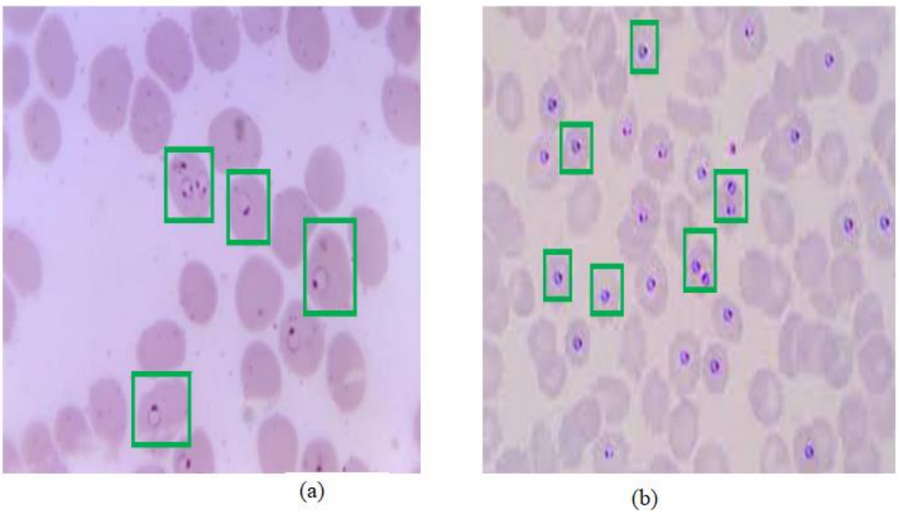

Figure 1 Depictions of smears of bloods – both smears of blood that are (a) thick and (b) thin smears.

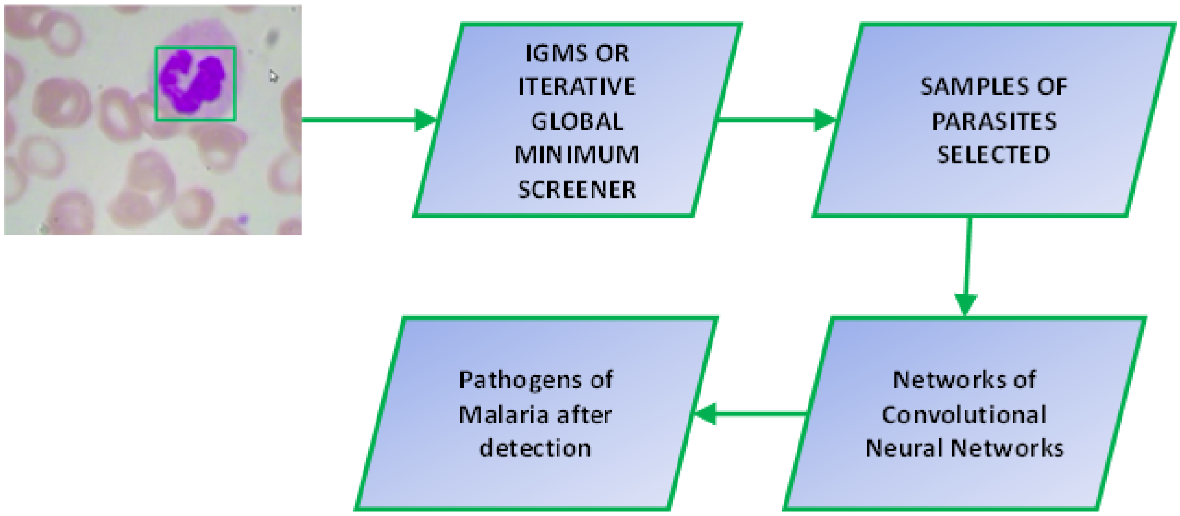

Figure 2 Procedures for detecting of pathogens of Malaria from blood smears.

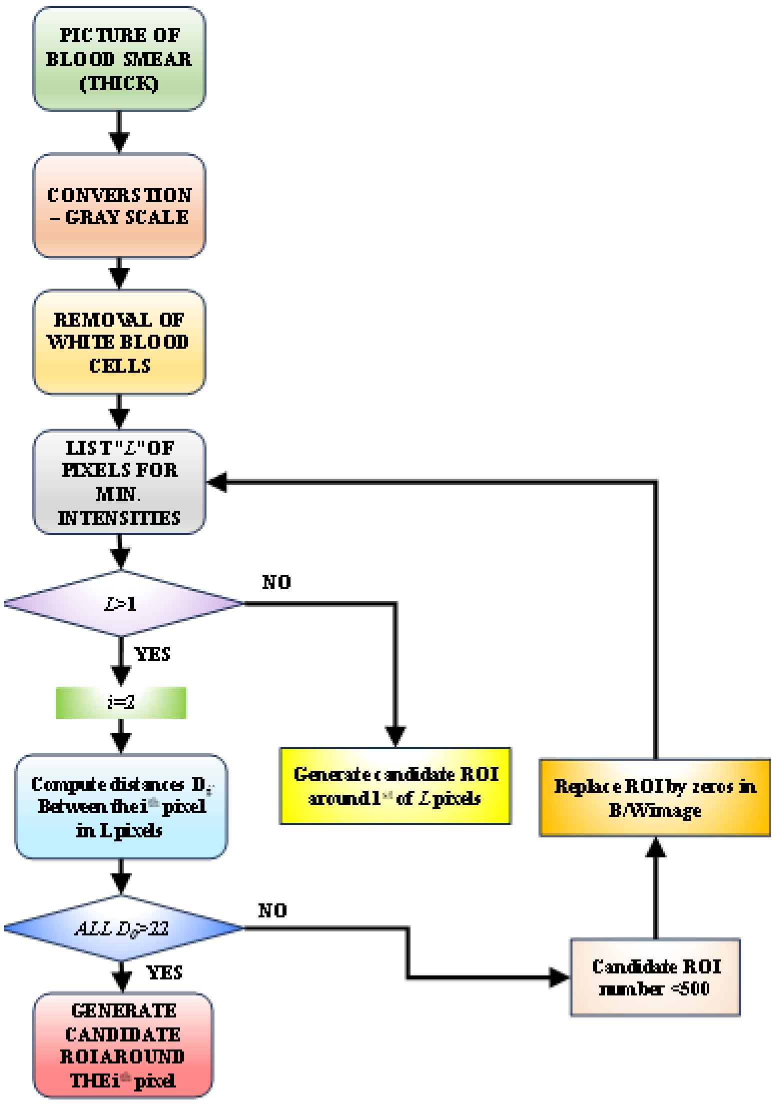

Figure 3. Flowchart to screen pathogens (IGMS methodology)

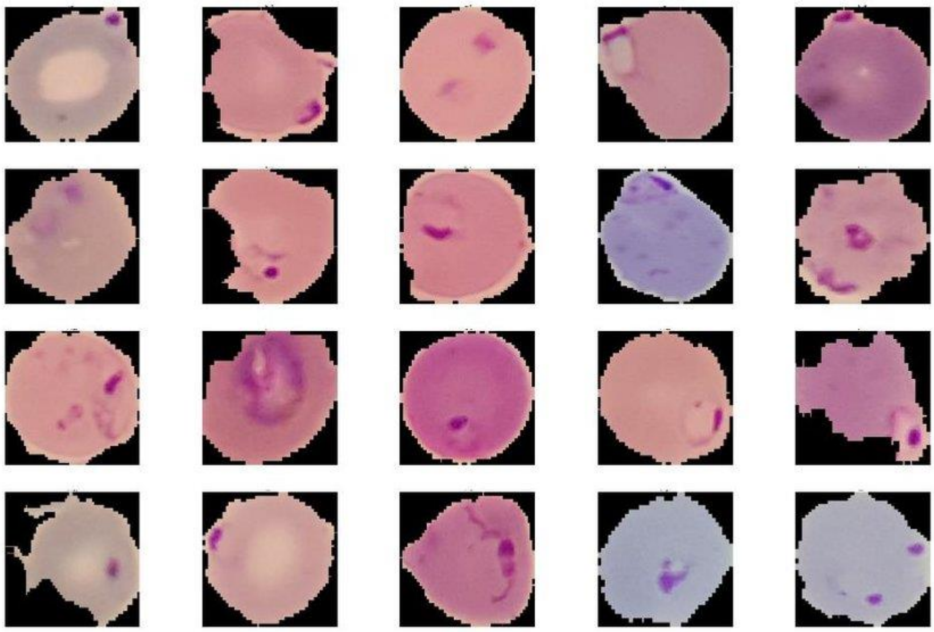

Figure 4. 20 number of patches of blood smears for pathogens of malaria by IGMS methodology.

Detecting White Blood Cells: In the intricate tableau depicted in Figure 3(a), we encounter a glimpse of a representative smear image, a vibrant canvas of visual data, captured in all its RGB richness. Our initial endeavor, akin to an alchemical transformation, commences with the metamorphosis of this RGB image into the realm of grayscale, where colors fade into the monochromatic tapestry of luminance, a vital transmutation that forms the very foundation of our analytical journey. In the tapestry of binary representation, a veil is cast upon the grayscale image through Otsu's method [29], which conjures forth a binary mask, denoted as M1. Within this binary mask, a transformation unfolds, where the expansive region corresponding to the field of view is enshrouded in luminescence, a stark portrayal of foreground, while the entities of white blood cells (WBCs) retreat into the background, their silhouette rendered in a darker hue. This cryptic binary mask, represented in Fig. 2, becomes the harbinger of distinctions, a visual demarcation of the field of view. A refined perspective emerges as we embark on the quest to obtain the field of view mask, known as M2, gracefully captured in Fig. 2. This mask, born from the enlargement of the field of view ROI area, augments the clarity of our purpose, serving as a refined instrument to further discern our entities of interest. In the delicate choreography of separation, the WBCs are gently extricated, shedding the cloak of the field of view. By subtracting the binary mask M1 from the ROI mask M2, as observed in Fig. 2, these elusive figures stand apart from the realm of our focus, their distinct presence affirmed. With meticulous artistry, we partake in the final purification of this entity. The unruly specters of noisy artifacts, akin to errant brushstrokes on a masterpiece, are selectively brushed aside, leaving behind the pristine form of clean white blood cells, as elegantly portrayed in Fig. 2. With this delicate operation, the canvas is prepared, as the pixels of the white blood cells are tenderly rendered void, poised for the forthcoming overture in the saga of parasite detection.

Preselecting of pathogens utilizing IGMS: The innovative methodology christened as Iterative Global Minimum Screening (IGMS) unfurls a vivid canvas within the landscape of its operations, generating prospective RGB parasite candidates through a meticulous process of intensity localization within a grayscale image. In the elegant choreography of this undertaking, when the ephemeral presence of a solitary pixel stands as the only sentinel, a circular expanse blooms forth, centered at the very heart of this pixel's abode. With a predefined radius of 22 pixels, akin to the average radius of a parasite, this circle is discreetly cropped from the original RGB image and is anointed as a chosen parasite candidate, as elegantly depicted in Fig. 5(a). However, when a congregation of pixels convenes, the tapestry unfolds further, weaving a new candidate into the fold. This burgeoning candidate emerges as the fulcrum, encircled by the stipulation that all distances between it and its predecessors exceed the sacred threshold of 22 pixels. As this delicate waltz ensues, the selection of a parasite candidate carries an unspoken decree, for within its chosen realm, the intensity values encased in the grayscale image are gently erased, replaced with the pristine countenance of zeros. This artful transformation ensures the convergence of the IGMS method. The symphony of the screening stage orchestrates a cessation, marked by the numerical threshold that signifies the attainment of a predetermined number of parasite candidates. In our extensive forays, we have elected to select 500 such candidates for each image, an orchestra crafted to encompass the authentic parasites to the utmost extent. In the labyrinthine landscape of experimentation, a dataset culled from 138 patients unveils our triumph, where the sensitivity, akin to a golden chalice, gleams resplendently, soaring above 97% on the patch level, the image level, and the noble realm of patient scrutiny. Each of these illustrious candidates, a $44 \times 44 \times 3$ RGB patch image, is imbued with a sense of purpose, for those pixels residing beyond the distance of 22 from the regal center are relegated to the realm of nullity, their presence elegantly muted. A visual symphony of transformation, Fig. 3, donned in its processing regalia, elegantly outlines the flowchart that befits IGMS, while Fig. 5, resplendent with its portrayal of positive and negative patches, captures the poetic essence of this wondrous endeavour.

5. Data Analysis And Results Of Experiments

Our journey begins with a comprehensive statistical examination, extending its gaze across the extensive dataset encompassing a total of 138 patients. Within this expansive realm, a grand tally of 84,961 parasites stands as the subjects of meticulous annotation. These parasites, with their varying radii, span a spectrum that ranges from two to 96 pixels, although the collective mean rests at a harmonious 22 pixels, as gracefully depicted in Fig. 7. Within the confines of each image, a diverse congregation of parasites resides, their number spanning from a solitary entity to a grand assembly of 341. The tapestry of this collective endeavor unfurls an average count of 47 parasites per image, as elegantly illustrated in Fig. 7. The enigmatic realm of each patient set, contained within this dataset, unfolds in a kaleidoscope of diversity. The gamut of images within each patient's realm ranges from a trifling three to a bountiful 22, with an average standing at the poised number of 12 images, a phenomenon artfully exemplified in Fig. 7. Intriguingly, the inhabitants of the parasite kingdom within these patient sets exhibit their own unique tapestry. Here, the population of parasites within each patient's dominion ranges from a mere eight to a staggering 3,130, attaining an equilibrium at an average number of 522 parasites. This captivating narrative unfolds in the visual tableau presented in Fig. 7.

In our meticulous assessment of the automated parasite detection method, we embark on a comprehensive journey that involves the strategic application of both the Iterative Global Minimum Screening (IGMS) technique and the CNN classifier. This analytical quest unfolds within the ambit of 30 patients, encapsulated in Set B, which collectively contributes 375 images and a rich tapestry of 12,777 parasites. Our initial phase, guided by IGMS, unfurls as we generate an impressive ensemble of 187,500 patches. Within this expansive assembly, the discerning eye singles out 13,066 patches, deemed positive due to their intimate overlap, surpassing the 50% threshold of accordance with the ground truth annotations. The subsequent act within our narrative features the application of our customized CNN model to the grand ensemble of 187,500 patches. Under its scrutinizing gaze, 13,687 patches are anointed as parasites, as guided by a threshold of 0.6 for the classifier score. This threshold, notably derived from the highest accuracy attained during the five-fold cross-validation on Set A, as elegantly expressed through the ROC curve. In the realm of granular analysis, the ensuing tableau of performance metrics, at the patch level, manifests a realm of distinctions. The accuracy, AUC, sensitivity, specificity, precision, and F-score unfurl as 97.26%, 97.34%, 82.73%, 98.39%, 78.98%, and 80.81%, respectively. These metrics, akin to celestial constellations, delineate the model's prowess in discerning the nuances and exhibiting a judicious balance between comprehensive identification and precision. Within the visual realm of Fig. 5, the ROC curve paints a compelling narrative. It reveals the potential to achieve a sensitivity of 93%, even while maintaining a lofty specificity of 90%. This revelation, born from the adjustment of the classifier score threshold, stands as a testament to the dynamic adaptability of our methodology.

TABLE 2

CLASSIFYING OF WORKING ON 5-FOLD FOR DATASET A

	F-SCORE	SPECIFICITY	PRECISION	NEGATIVE PREDICTION	SENSITIVITY
92.34%	92.59%	92.41%	93.11%	93.21%	91.53%
± 0.45%	± 0.37%	± 1.46%	± 1.05%	± 1.24%	± 0.95%

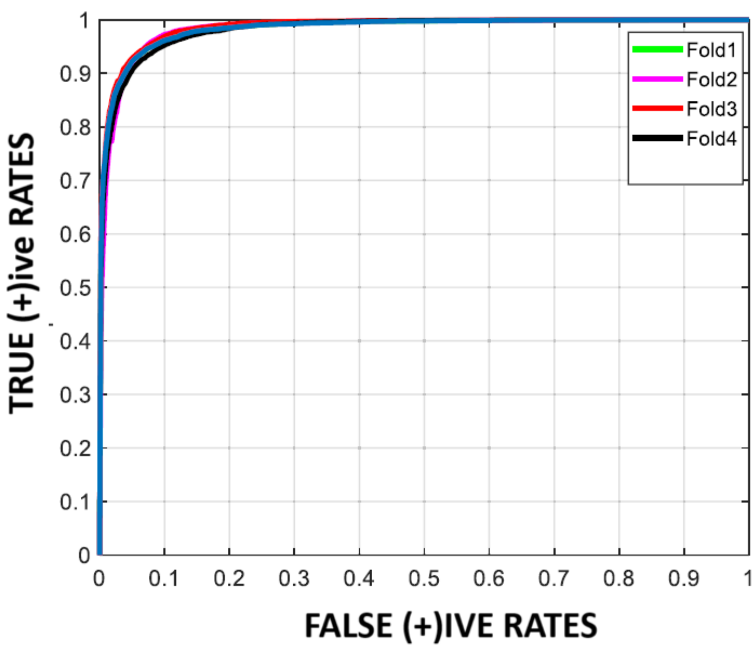

Figure 5. ROC curves of the customized Convolutional Neural Networks frameworks with four-fold crosses

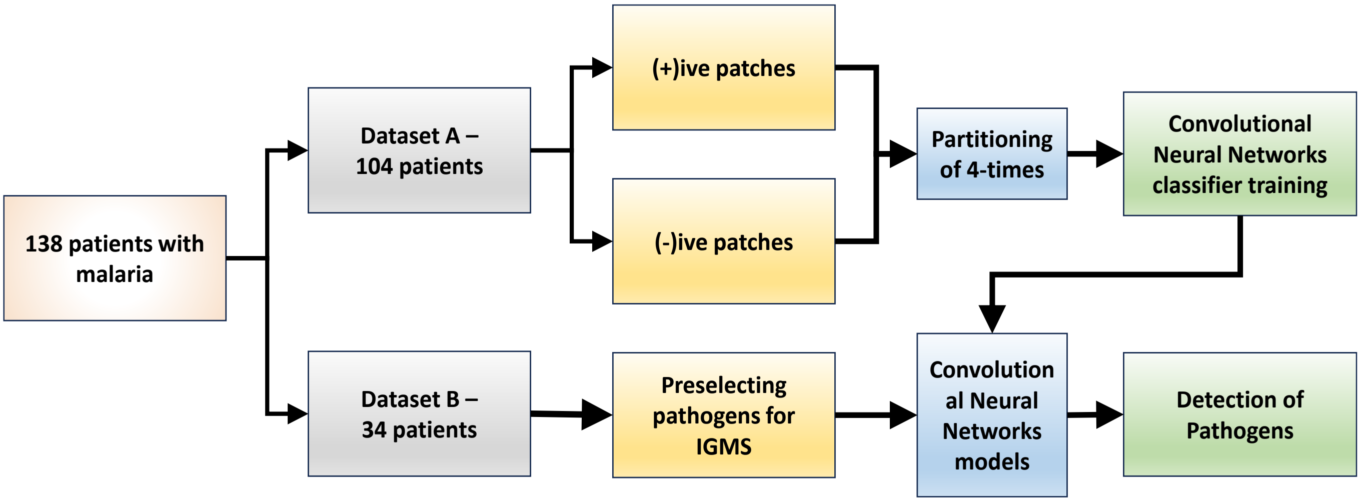

Figure 6. Data division strategy of dividing information for experiments

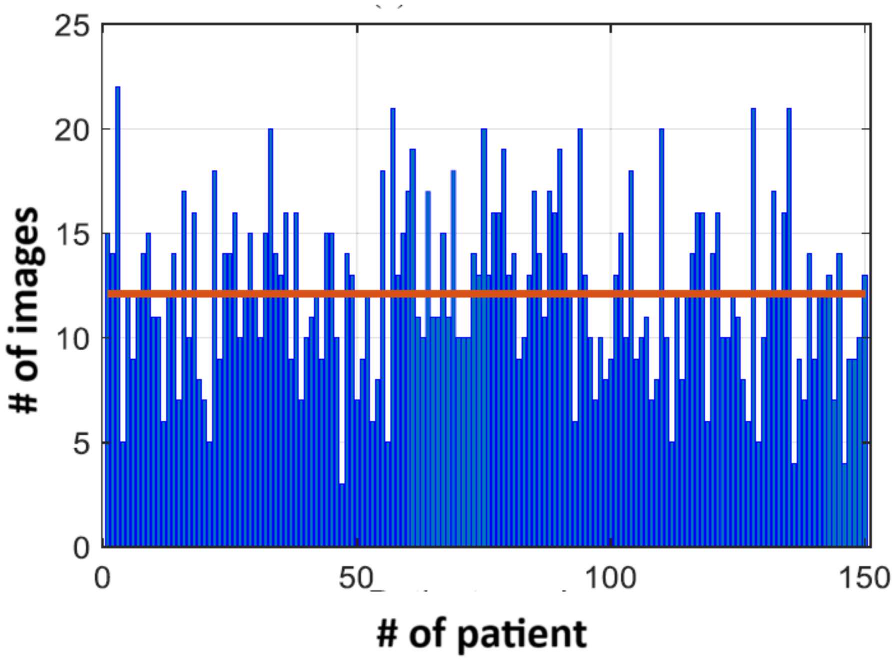

Figure 7. numbers of pictures and pathogens in each patient is illustrated in the diagram

TABLE 3

MATRIX OF CONFUSION FOR SET B ON THE LEVEL OF PATCH

	POAITIVE PREDICTION	NEGATIVE PREDICTION
NON-PATHOGENS	0.9%	92.04%
PATHOGENS	6.1%	0.9%

TABLE 4

RESULTS OF VARIOUS NETWORK ON DATASET -B

NETWORKS	SENSITIVITY	ACCURACY	PRECISION	F-SCORES	AUC	SPECIFICITY
ResNet-50 IGMS	91.77%	82.12%	56.07%	66.12%	96.91%	95.32%
VGG19 IGMS	92.89%	88.56%	53.41%	64.97%	97.05%	95.11%
ALEX-NETWORK IGMS	97.11%	83.45%	69.87%	77.13%	97.31%	98.21%
PROPOSED CNN-IGMS	98.23%	83.13%	77.98%	81.26%	96.41%	99.01%

TABLE 5

COMPARING OF PERFORMANCES FROM CNN MODELS AND DEEP-LEARNING MODELS ON DATASET-A

NETWORKS	CENTRAL PROCESSING UNIT /GRAPHICS PROCESSING UNIT	LEARNING RATE	TIME TO TRAIN	ACCURATENESS
PROPOSED CNN	GPU	0.001	1387	93.88%
VGG19	GPU	0.001	14521	92.09%
ALEX-NET	GPU	0.001	1591	93.75%
RESNET-50	CPU	0.001	48123	93.01%

6. Conclusion

Within this scholarly manuscript, we present our endeavor in crafting a deep learning application, purpose-built for the discerning realm of smartphones, with the lofty ambition of malaria parasite detection in the intricate domain of thick smear images. Our methodological orchestration, designed for the automated identification of these elusive parasites, elegantly unfolds in a duet of two distinct stages: the initial parasitic screening, followed by the subsequent classification. The initial act, performed with precision, unveils an intensity-driven Iterative Global Minimum Screening (IGMS), a swift sentinel that sweeps through the expanse of a thick smear image. It deftly produces the candidates for potential parasites, their forms sculpted by the discriminating eye of intensity-based analysis. The second chapter of our odyssey is painted by a customized Convolutional Neural Network (CNN) model, as it undertakes the delicate task of classifying each candidate, distinguishing between the rightful parasites and the unassuming background. The empirical fruits of our labor, delineated through a collection of experimental results, gracefully exemplify the pragmatic utility of our methodology in the realm of automated malaria parasite detection. In the annals of scholarship, our contribution stands as the second document of its kind to manifest a smartphone application, conceived to scrutinize the intricate world of thick blood smear screening [18]. Furthermore, it proudly hoists the banner as the inaugural endeavor to fuse the capabilities of deep learning techniques with the realm of parasite detection in the thick smears of smartphones. The validation of our efforts transcends mere patches or images, as we undertake an evaluation that ascends to the very level of patient scrutiny. As an offering to the collective wellspring of research, we unshackle our dataset, a treasury holding 1819 images sourced from 138 patients. This gesture of sharing, performed with noble intent, seeks to ameliorate the prevailing dilemma of scarce training data in the domain of automated malaria diagnosis for thick blood smears. In the vistas of the future, our pledge remains steadfast. We are committed to the quest of enhancing the efficacy of our automated parasite detection method, with a deliberate focus on the utilization of network ensemble techniques. Simultaneously, we ardently aspire to refine the operational efficiency of our application on the confined yet formidable platforms of smartphones, as we continue our unending journey of exploration and innovation.

References

1. World malaria report," WHO, Geneva, Switzerland, 2018.
2. [2] WHO, *Guidelines for the Treatment of Malaria*, 3rd ed. Geneva, Switzerland:World Health Organization, 2015.
3. [3] K. S.Makhija, S. Maloney, and R. Norton, "The utility of serial blood film testing for the diagnosis of malaria," *Pathology*, vol. 47, no. 1, pp. 68–70, 2015.
4. [4] WHO, *Malaria Microscopy Quality Assurance Manual*. Geneva, Switzerland:World Health Organization, 2016.
5. [5] M. Poostchi, K. Silamut, R. J. Maude, S. Jaeger, and G. Thoma, "Image analysis and machine learning for detecting malaria," *Transl. Res.*,vol. 194, pp. 36–55, Apr. 2018.
6. [6] Z. Liang *et al.*, "CNN-based image analysis for malaria diagnosis," in *Proc.IEEE Int. Conf. Bioinf. Biomed.*, Shenzhen, China, 2017, pp. 493–496.
7. [7] S. Rajaraman *et al.*, "Understanding the learned behavior of customized convolutional neural networks toward malaria parasite detection in thin blood smear images," *J. Med. Imag.*, vol. 5, no. 3, Jul. 2018, Art.no. 034501.

8. [8] L. Rosado, J. M. Correia da Costa, D. Elias, and J. S. Cardoso, "A review of automatic malaria parasites detection and segmentation in microscopic images," *Anti-Infective Agents*, vol. 14, no. 1, pp. 11–22, Mar. 2016.
9. [9] P. A. Pattanaik and T. Swarnkar, "Comparative analysis of morphological techniques for malaria detection," *Int. J. Healthcare Inf. Syst. Inform.*, vol. 13, no. 4, pp. 49–65, Oct. 2018.
10. [10] S. Kaewkamnerd, A. Intarapanich,M. Pannarat, S. Chaotheing, C. Uthaipibull, and S. Tongsima, "Detection and classification device for malaria parasites in thick-blood films," in *Proc. IEEE Int. Conf. Intell. Data Acquisition Adv. Comput. Syst.*, Prague, Czech Republic, 2011, pp. 435–438.
11. [11] N. S. M. M. Hanif, M. Y. Mashor, and Z. Mohamed, "Image enhancement and segmentation using dark stretching technique for Plasmodium Falciparum for thick blood smear," in *Proc. Int. Colloq. Signal Process Its Appl.*, Penang, Malaysia, 2011, pp. 257–260.
12. [12] K. Chakrabortya, "A combined algorithm for malaria detection from thick smear blood slides," *J. Health Med. Inform.*, vol. 6, no. 1, pp. 179–186, Jan. 2015.
13. [13] I. R. Dave and K. P. Upla, "Computer aided diagnosis of malaria disease for thin and thick blood smear microscopic images," in *Proc. Int. Conf. Signal Process. Integr. Netw.*, Noida, India, 2017, pp. 4–8.
14. [14] M. Elter, E. Hasslmeyer, and T. Zerfass, "Detection of malaria parasites in thick blood films," in *Proc. IEEE Eng. Med. Biol. Soc.*, Boston, MA, USA, 2011, pp. 5140–5144.
15. [15] I. K. E. Purnama, F. Z. Rahmanti, and M. H. Purnomo, "Malaria parasite identification on thick blood film using genetic programming," in *Proc. Int. Conf. Instrum., Commun., Inf. Technol., Biomed. Eng.*, Bandung, Indonesia, 2013, pp. 194–198.
16. [16] L. Yunda, "Automated image analysis method for p-vivax malaria parasite detection in thick film blood images," *Rev. S&T*, vol. 10, no. 20, pp. 9–25, Mar. 2011.
17. [17] J. A. Quinn, A. Andama, I. Munabi, and F. N. Kiwanuka, "Automated blood smear analysis for mobile malaria diagnosis," in *Mobile Point-of-Care Monitors and Diagnostic Device Design*,W. Karlen and K. Iniewski, Eds., Boca Raton, FL, USA: CRC Press, 2014, pp. 1–20.
18. [18] L. Rosado, J. M. C. Da Costa, D. Elias, and J. S. Cardoso, "Automated detection of malaria parasites on thick blood smears via mobile devices," *Procedia Comput. Sci.*, vol. 90, pp. 138–144, Dec. 2016.

19. [19] A. Krizhevsky, I. Sutskever, and G. E. Hinton, “ImageNet classification with deep convolutional neural networks,” in *Proc. Advances Neural Inf. Process. Syst.*, Dec. 2012, pp. 1–9.
20. [20] Y. Sun, X. Wang, and X. Tang, “Deep learning face representation from predicting 10,000 classes,” in *Proc. IEEE Conf. Comput. Vision Pattern Recognit.*, Columbus, OH, USA, 2014, pp. 1891–1898.