

Review

Recent advances of malaria parasites detection systems based on mathematical morphology

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Abstract: This paper investigates existing mathematical morphology based techniques applied for performing malaria parasites detection and identification in both Giemsa and Leishman stained blood smears images. Malaria is an epidemic health disease and a rapid, accurate diagnosis is necessary for proper intervention. Generally, pathologists visually examine blood stained slides for malaria diagnosis; this kind of visual inspection is subjective, error-prone and time consuming. In order to cope with such issues, computer-aided methods have been increasingly evolved for abnormal erythrocyte and/or parasites detection, segmentation and semi/fully automated classification. The aim of this paper is to present a review of mathematical morphology based methods for malaria parasite detection.

Keywords: malaria, red blood cells segmentation, mathematical morphology, medical image analysis

1. Introduction

Haematology is the branch of medicine concerned with the study, diagnosis, monitoring, treatment, and prevention of diseases related to the blood and blood-forming organs. Haematology studies the blood in health and pathological conditions, firstly to identify the patient's health condition and, secondly, to predict how the bone marrow may have contributed to reach that condition.

Thus, haematology studies the relationship between the bone marrow and the systemic circulation. In fact, there are many diseases, disorders, and deficiencies that can affect the number and type of blood cells produced, their function and their lifespan. Usually, only normal, mature or nearly mature cells are released into the bloodstream but certain circumstances can induce the bone marrow to release immature and/or abnormal cells into the circulation. One of the most frequently ordered test to monitor the proportion of the cell components into the blood stream is the Complete Blood Count (CBC), that offers various hematologic data represented by the numbers and types of cells in the peripheral circulation. The cells percentage is compared with the reference ranges in order to determine if the cells are present in their expected percentage, if one cell type is increased, decreased or if immature cells exist. Reference ranges for blood tests are sets of values used to interpret a set of diagnostic test results from blood samples. Since it is difficult to prove that healthy-considered subjects may not have infections, parasitic infection and nutritional deficiency, it is more feasible to talk about reference ranges rather than normal ranges. A reference range is usually defined as the set of values in which 95% of the normal population falls within. It is determined by collecting data from vast numbers of laboratory tests result from a large number of subjects who are assumed to be representative of the population. With automatic counters or the flow cytometry an automated CBC can be performed

32 quickly. However, if the results from an automated cell count indicate the presence of abnormal cells
33 or if there is a reason to suspect that abnormal cells are present, then a blood smear will be collected
34 [1]. A blood smear is often used to categorize and/or identify conditions that affect one or more types
35 of blood cells and to monitor individuals undergoing treatment for these conditions. The results of
36 a blood smear typically include a description of the cells appearance, as well as any abnormalities
37 that may be seen on the slide. The manual analysis of blood smears is tedious, lengthy, repetitive and
38 it suffers from the presence of a non-standard precision because it depends on the operator's skill.
39 The use of image processing techniques can help to analyse, count the cells in human blood and, at
40 the same time, to provide useful and precise information about cells morphology. Peripheral blood
41 smears analysis is a common and economical diagnosis technique by which expert pathologists may
42 obtain health information about the patients. Although this procedure requires highly trained experts,
43 it is error-prone and could be affected by inter-observer variations. Moreover, blood cells images
44 taken from microscope could vary in their illumination and colouration conditions, as shown in fig. 1.
45 Typical blood cells images contain three main components of interest: the platelets (or thrombocytes),
46 the red blood cells (or erythrocytes) and the white blood cells (or leukocytes). It is worth considering
47 that blood cells exist with different shapes, characteristics and colourations, according to their types.
48 Many tests are designed to determine the number of erythrocytes and leukocytes in the blood, together
49 with the volume, sedimentation rate, and haemoglobin concentration of the red blood cells (blood
50 count). In addition, certain tests are used to classify blood according to specific red blood cell antigens,
51 or blood groups. Other tests elucidate the shape and structural details of blood cells and haemoglobin
52 and other blood proteins. Blood can be analysed to determine the activity of various enzymes, or
53 protein catalysts, that either are associated with the blood cells or are found free in the blood plasma.
54 Blood also may be analysed on the basis of properties such as total volume, circulation time, viscosity,
55 clotting time and clotting abnormalities, acidity (pH), levels of oxygen and carbon dioxide, and the
56 clearance rate of various substances. There are special tests based on the presence in the blood of
57 substances characteristic of specific infections, such as the serological tests for syphilis, hepatitis, and
58 human immunodeficiency virus (HIV, the AIDS virus)¹. Among the several available blood tests,
59 the most common are certainly the blood cells counts, e.g., a CBC is a measure of the hematologic
60 parameters of the blood. Included in the CBC is the calculation of the number of red blood cells
61 (red blood cell count) or white blood cells (white blood cell count) in a cubic millimetre (mm^3) of
62 blood, a differential white blood cell count, a haemoglobin assay, a hematocrit, calculations of red
63 cell volume, and a platelet count. The differential white blood cell count includes measurements
64 of the different types of white blood cells that constitute the total white blood cell count: the band
65 neutrophils, segmented neutrophils, lymphocytes, monocytes, eosinophils, and basophils. A specific
66 infection can be suspected on the basis of the type of leukocyte that has an abnormal value [2].

67 Human malaria infection is not strongly related to cells count but it needs different tests in order
68 to be identified. It can only be caused by parasitic protozoans belonging to the Plasmodium type.
69 The parasites are spread to people through the bites of infected female Anopheles mosquitoes, called
70 "malaria vectors". There are five parasite species that cause malaria in humans and two of these
71 species, *Plasmodium falciparum* and *Plasmodium vivax*, constitute the greatest threat. *Plasmodium*
72 *ovale*, *Plasmodium malariae* and *Plasmodium knowlesi* are the three remaining species which are
73 less dangerous in human [3], as shown in fig.2. All five species may appear in four different life-cycle
74 stages during the infection phase in peripheral blood: ring, trophozoite, schizont and gametocyte.
75 Some examples are shown in fig.3. The life-cycle-stage of the parasite is defined by its morphology,
76 size and the presence or absence of malarial pigment. The species differ in the changes of infected
77 cell's shape, presence of some characteristic dots and the morphology of the parasite in some of the
78 life-cycle-stages [4].

¹ <https://www.britannica.com/topic/blood-analysis>

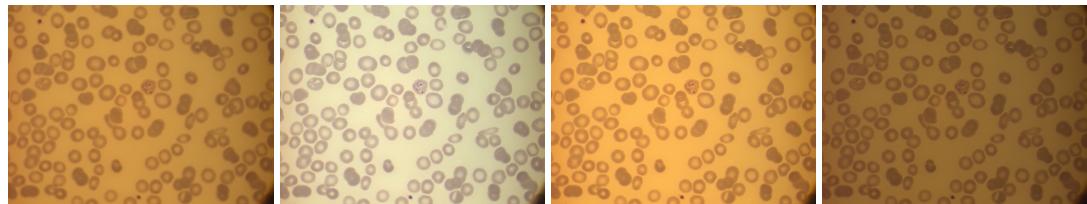


Figure 1. Different illumination conditions generate different images, because of the absence of a standardized acquisition procedure. From left to right: acquisition of the same smear with four microscope's brightness levels.

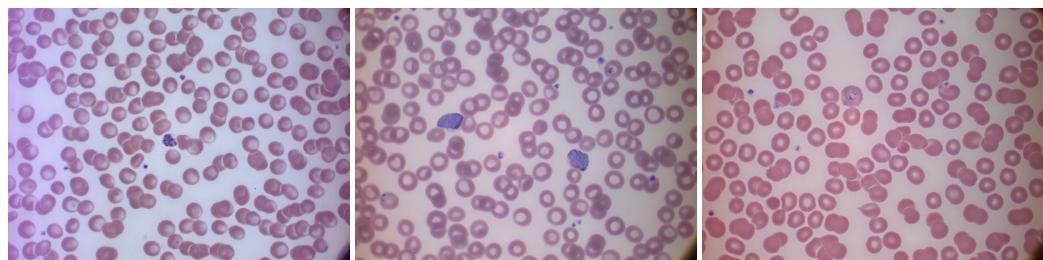


Figure 2. Types of human malaria: from left to right, *P. Falciparum* in its schizont stage, *P. Vivax* in two gametocytes specimens and one ring stage, *P. Ovale* in its ring stage.

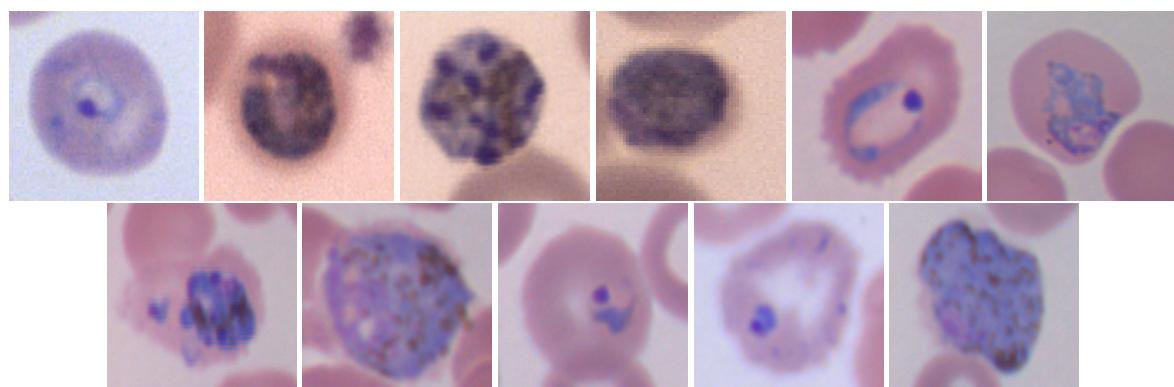


Figure 3. Examples of malaria parasite stages. From top left: *P.falciparum* ring, trophozoite, schizont, gametocyte; *P.ovale* ring, trophozoite, schizont, gametocyte; *P.vivax* ring, developed trophozoite, gametocyte. [5]

79 Computer vision techniques for malaria diagnosis and recognition represent a relatively new
 80 area for early malaria detection and, in general, for medical imaging, able to overcome the problems
 81 related to manual analysis, that is performed by human visual examination of blood smears. The
 82 whole process requires an ability to differentiate between non-parasitic stained components/bodies
 83 (e.g. red blood cells, white blood cells, platelets, and artefacts) and the malarial parasites using
 84 visual information. If the blood sample is diagnosed as positive (i.e. parasites present) an additional
 85 capability of differentiating species and life-stages (i.e. identification) is required to specify the infection.
 86 Numerous methods of automatic malaria diagnosis have been proposed so far, in order to overcome
 87 the issues before mentioned. The aim of this paper is to review and analyse the works of different
 88 researchers who in particular have used mathematical morphology as a powerful tool for computer
 89 aided malaria detection and classification.

90 1.1. Mathematical morphology

91 Mathematical morphology (MM) can be defined as a theory for the analysis of spatial structures.
92 It is called morphology because it aims at analysing the shape and form of objects. It is mathematical
93 in the sense that the analysis is based on set theory, integral geometry, and lattice algebra. MM
94 is not only a theory, but also a very powerful image analysis technique [6]. It was introduced by
95 Matheron as a technique for analysing geometric structure of metallic and geologic samples. It refers
96 to a branch of non-linear image processing and analysis that concentrates on the geometric structure
97 within an image. The morphological filter, which can be constructed on the basis of the underlying
98 morphological operations, are more suitable for shape analysis than the standard linear filters since
99 the latter sometimes distort the underlying geometric form of the image. Some of the salient points
100 regarding the morphological approach are as follows [7]:

- 101 • Morphological operations provide for the systematic alteration of the geometric content of an
102 image while maintaining the stability of the important geometric characteristics.
- 103 • There exists a well-developed morphological algebra that can be employed for representation
104 and optimization.
- 105 • It is possible to express digital algorithms in terms of a very small class of primitive morphological
106 operations.
- 107 • There exist rigorous representations theorems by means of which one can obtain the expression
108 of morphological filters in terms of the primitive morphological operations.

109 Dilation and erosion are the basic morphological processing operations. They are defined in terms of
110 more elementary set operations, but are employed as the basic elements of many algorithms. Both
111 dilation and erosion are produced by the interaction of a set called structuring element (SE) with a set of
112 pixels of interest in the image. The structuring element has both a shape and an origin. From these two
113 basic operators, others have been derived (opening, closing, hit-or-miss). They can be applied to extract
114 image components useful in the representation and descriptions of region shapes, such as boundaries,
115 skeleton, or convex hull. Also morphological operators can be used for image preprocessing and
116 postprocessing, such as morphological filtering, thinning, and especially for segmentation.

117 2. Scope of this review

118 In this paper we present a review of computer-aided methods oriented to malaria parasites
119 detection and segmentation by mathematical morphology based techniques. Most of the studies were
120 followed Di Ruberto's work [8], which first proposed a system to evaluate parasitaemia in the blood.
121 The system was able to detect the parasites by using an automatic thresholding and morphological
122 operators. A morphological approach to cell segmentation which is more efficient than watershed
123 algorithm was proposed. Finally, the parasites classification was still based on morphological operators.
124 Since then many systems for computer aided diagnosis of malaria have been proposed. Most of them
125 make use of mathematical morphology to process and analyse malaria-infected peripheral blood cells
126 images. The scope of this paper is to review and analyze the recent works of different researchers
127 in the area of malaria parasite recognition using computer vision which benefit from mathematical
128 morphology.

129 The rest of the paper is organised as follows. Section 2 presents a review of the considered
130 works, according to a typical pipeline of a computer-aided image analysis process: preprocessing,
131 segmentation, feature extraction.

132 All the considered works make use of morphological operators in at least one of the phases of
133 image analysis. Section 3 contains an overall discussion about the methods and the conclusions are
134 expressed in section 4.

135 3. Computer aided diagnosis of malaria by using mathematical morphology

136 This section presents a review of some of the main recent studies existing in literature regarding
137 the analysis of malaria infected blood smears using mathematical morphology. A typical approach
138 usually comprises four different image processing and analysis tasks, as follows:

- 139 1. Pre-processing.
140 2. Segmentation.
141 3. Feature extraction.
142 4. Classification.

143 Since morphological techniques have been used in the first three phases, the reviewed works have
144 been divided into the following sub-sections: pre-processing, segmentation and feature extraction.
145 Each sub-section contains description about methods that cope with malaria parasites (MP) stained
146 components analysis, both on thin and thick blood smears, without distinction.

147 Extensive search of articles has been made in PubMed and Google Scholar search engines based
148 on the keywords: "malaria, mathematical morphology, automated malaria diagnosis" up to October
149 2017. The search includes papers published in English and titles and abstracts of potentially relevant
150 studies were selected and presented from the most recent ones. Thereafter, the full texts of these studies
151 were evaluated as per the exclusion criteria.

152 Two main factors are generally considered if we refer to staining techniques: the type of
153 colouration, in which Giemsa and Leishman are the most common, and the thickness of blood slide,
154 which may be thick or thin. The majority of studies have been employed on thin blood smear images
155 (over two-third of the total count) while only a few have used thick blood smear images. Typically,
156 thin smears permit the identification of specific parasitic stage and quantification of malaria parasite;
157 on the other hand, thick smears are better if the target is to perform an initial identification of malaria
158 infection using blood pathology. Some examples are shown in fig. 4. Giemsa stained blood smear is
159 considered in most of the analysed literatures whereas Leishman stain is considered in few studies.

160 It is reported that Leishman stain has bigger sensitivity for parasite detection than Giemsa [9] and
161 is superior for visualization of red and white blood cell morphology [10]. On the contrary, Giemsa
162 stain highlights both malaria parasites and white blood cells and, therefore, it is an additional issue
163 to deal with. Giemsa stain is much costly and also time-taking procedure than Leishman. Moreover,
164 magnification of 100X by using an oil immersion objective is used for capturing microscopic images of
165 thin blood smear for identification of specific parasites and their infected stage.

166 3.1. Preprocessing

167 In image analysis field, especially when we refer to complex computer-aided pipelines,
168 pre-processing methods are particularly used in order to improve the image data by suppressing
169 unwanted noise or enhancing some image features for further processing. It is worth to mention
170 pre-processing methods because they are an important step regarding image analysis field but, for
171 what concerns the malaria-affected blood image analysis, in our review we particularly found methods
172 which operate for illumination correction and noise filtering purposes. Generally speaking, digital
173 microscopy images can be acquired in different lighting conditions, with several types of acquisition
174 devices or from blood smears stained with various staining protocols and, consequently, the features
175 of similar images could differ a lot. Different techniques for illumination correction have been
176 suggested to reduce such variation, e.g., a lot of authors work with grayscale-converted images
177 as an illumination correction method. On the other hand, noise filtering aims to remove the noise
178 introduced by mishandling the slides and/or the camera settings. Morphological operators have
179 been extensively used as preprocessing for image enhancement in major studies. Erosion and dilation
180 operations on raw smear images allow discarding undesired patterns and help in the selection of
181 required cells or regions of interest. Morphological operators are useful for removal of unwanted
182 objects, holes filling, splitting, thinning and thickening. Different researchers during automated

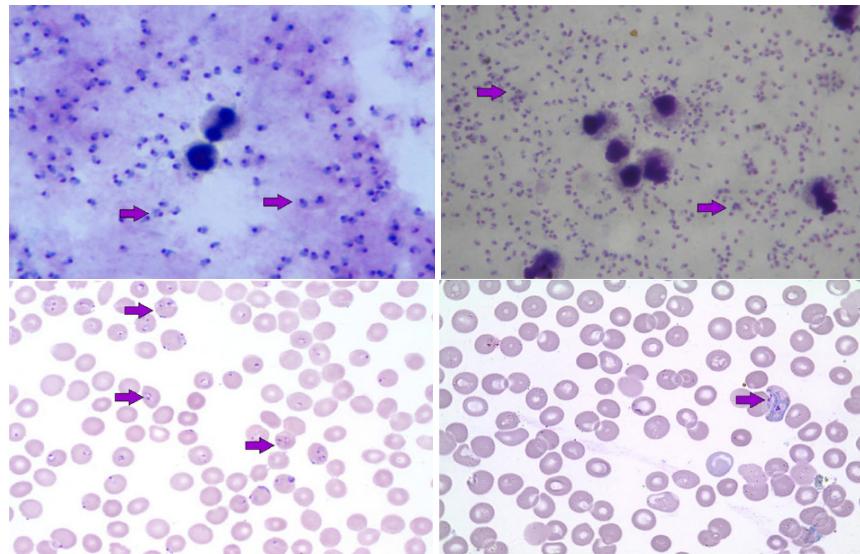


Figure 4. Malaria infected blood smear images. From top left, clockwise: thick smear with Giemsa stain, thick smear with Leishman stain, thin smear with Leishman stain, thick smear with Giemsa stain [11]. Arrows in top images indicate chromatin dots while, in the bottom ones, they show the infected erythrocytes.

183 diagnosis of malaria used morphological operations in preprocessing phase and the most recent are
184 listed below.

185 In [12] Gonzalez-Betancourt *et al.* proposed a system to determine markers for watershed
186 segmentation based on the Radon transform and mathematical operators. In the first step of the
187 process small irrelevant structures and part of the noise are eliminated by a morphological filter, in
188 order to ensure the preservation of the cells edges. Image smoothing is performed by a morphological
189 erosion-reconstruction and dilation-reconstruction filter with a disk structuring element of radius
190 equal to 20 pixels, which is 0.274 times smaller than the average radius of the RBCs. In this way the
191 influences of the size and the shape of the structures can be separated in the smoothing process. At the
192 same time the objects which are not eliminated remain unchanged. Also, a morphological closing is
193 performed with a disc structuring element having radius smaller than half the average of the RBCs'
194 radii, in order to connect the possible (more than one) markers that can appear on a single cell.

195 In [13] Karen *et al.* illustrated a morphological approach for blood cell identification and use the
196 image features such as intensity, histogram, relative size and geometry for further analysis. Before
197 the identification of blood cells, the authors propose a novel morphological filtering based on the
198 size of RBC for platelets and/or artifacts elimination. A dilation is performed by a concentric ring
199 structuring element and erosion by disk shaped structuring element. The radius of the structuring
200 element depends on the radius of the RBC, so that all the components smaller than the RBCs can be
201 removed.

202 The system proposed in [14] by Oliveira *et al.* is based on image processing, artificial intelligence
203 techniques and an adapted face detection algorithm to identify Plasmodium parasites. The latter
204 uses the integral image and haar-like features concepts, and weak classifiers with adaptive boosting
205 learning. The search scope of the learning algorithm is reduced in the preprocessing step by removing
206 the background around blood cells by means of morphological erosions both for training and for
207 testing.

208 Romero *et al.* in [15] presented an algorithm that uses morphological operations, the watershed
209 method, the Hough transform and the clustering method of k-means to detect overlapped RBCs. In
210 the pre-processing stage white blood cells and platelets are removed before the segmentation task.
211 During this step, some noise, the WBC cytoplasm and platelets still remain on the image. Therefore,

212 the small objects are removed using a morphological opening and then the image is dilated with a
213 disk-shaped structuring element.

214 Reni *et al.* in [16] described a new algorithm for morphological filtering of the blood images
215 as a pre-processing tool for segmentation. Conventional morphological closing on blood images
216 removes the unwanted components but also useful information. On the opposite the proposed method
217 preserves the necessary information of foreground components while removing noise and artefacts.

218 In the method proposed in [17] by Sheikhhosseini *et al.* the first phase is the stained object
219 extraction which detects candidates objects that can be infected by malaria parasites using intensity
220 and colour. Before detecting the stained objects the method firstly extracts the foreground. Foreground
221 image is a binary image which is produced after applying morphological hole filling on such pixels
222 which have lower intensity value than average intensity value of green layer. After the stained objects
223 extraction process, a series of morphological operations is also employed in order to eliminate small
224 components and complete the final stained objects.

225 An edge-based segmentation of erythrocytes infected with malaria parasites using microscopic
226 images is proposed by Somasekar *et al.* in [18]. A fuzzy C-means clustering is applied to extract
227 infected erythrocytes, which is further processed for the final segmentation. A morphological erosion
228 is used to erase some small noises and spots before the segmentation and holes inside the infected
229 erythrocytes are filled using a morphological hole filling operation for the final segmentation.

230 In [5] Tek *et al.* presented a complete framework to detect and identify malaria parasites in images
231 of Giemsa stained thin blood film specimens. Also, the system is able to identify the infecting species
232 and life-cycle stages. The preprocessing step of the proposed method is applied to reduce the variations
233 in the observed size, intensity, and colour of the cells and stained objects before the detection and
234 classification steps. The aim is to correct the non-uniform illumination in the images. The estimation
235 is based on a morphological closing operation using a sufficiently large structuring element. The
236 sufficiently large size for an input image is determined automatically with respect to its average cell
237 size computed from the area granulometry distribution.

238 3.2. Segmentation of RBCs and parasites

239 Segmentation is a key step in image analysis because it permits the identification and separation
240 of the regions that compose an image, according to certain criteria of homogeneity and separation. Its
241 main target is to divide the image into parts that have a strong correlation with objects or areas of the
242 real world contained in the image. The commonly used segmentation methods essentially operate
243 considering characteristics such as the brightness value, colour and reflection of the individual pixels,
244 identifying groups of pixels that correspond to spatially connected regions. As for many problems of
245 image processing, there is no standard solution valid in general, so different segmentation techniques
246 can be applied, according to the characteristics of the images to process and of the objects to segment.
247 Medical images segmentation is typically performed using two main strategies: the first level aims to
248 separate whole cells or tissues from the background and the second one aims to separate the tissue
249 structure in different regions or the cell in their components as the nucleus from the cytoplasm or
250 intracellular parasites. The latter case is commonly used in applications in which the cell class depends
251 on the morphological characteristics of its components.

252 Several other authors attempted to use thresholding combined with morphological operation as
253 segmentation method in their computer-aided systems and they are described as follows.

254 Arco *et al.* in [19] worked on thick blood films and proposed a method that uses an adaptive
255 thresholding based scheme, which also allows an effective classification of pixels. This means that the
256 election of whether a pixel belongs to the background or to the signal (parasites and white blood cells)
257 is only established by the pixels around it, that is its neighbourhood. Then, morphological methods
258 are applied to evaluate the area of connected components, labelling those belonging to parasites and
259 counting their number.

260 Anggraini *et al.* [20] proposed a method for separating blood cells, parasites and other components
261 from background in a microscopic field of a thin blood smear. They applied several global thresholding
262 methods and visually compared the results to qualitatively determine which technique yields the best
263 result. The binary image was then subjected to hole filling morphological operator and applied as
264 marker to label blood cells. From each identified cell (RBC and WBC), constituents of the parasite
265 (nucleus and cytoplasm) were extracted using multiple threshold.

266 Dave *et al.* in [21] performed image segmentation using histogram based adaptive thresholding
267 followed by mathematical morphological operations (erosion and dilation). The detection of infected
268 RBCs is based on a unsupervised learning technique.

269 The proposed automated method in [22] by Elter *et al.* for parasite detection and identification
270 worked on thin blood film acquired with Giemsa stain. The authors found that the G and B channels of
271 the RGB colour are very good features to identify objects containing chromatin in Giemsa stained blood
272 films, being not only considered highly discriminative but also almost independent of differences in
273 illumination and staining intensity. They transformed the colour input image into a monochrome
274 image $I(x,y)$, that highlights objects containing chromatin: $I(x,y) = \arctan \frac{I_{green}(x,y)}{I_{blue}(x,y)}$. In this work,
275 mathematical morphology has been used with a black top-hat operator to separate MP from both
276 leukocytes and platelets, with a non-flat paraboloid structuring element of radius of 9 and a slope of 1
277 pixel. It should be taken into account that these fixed parameters might not be suitable for images with
278 different pixel resolutions. The black top-hat operator is followed by a thresholding operation with
279 a fixed threshold, which according to the authors is reliable given the independence of the G and B
280 channels with regard to illumination and staining intensity. However, the authors do not define the
281 value of this fixed threshold on the publication.

282 In [23] Ghosh *et al.* used divergence based threshold selection in order to segment P.vivax parasites
283 from Leishman-stained thin blood films. This method is based on Cauchy membership function [24]
284 and is applied to the C channel of CMYK colour space. Morphological operators of opening and
285 closing have been used for artefacts removal.

286 Kareem *et al.* in [25] used the Annular Ring Ratio transform method. Before applying it, a pre
287 processing phase for removing platelets, parasites and other artefacts in the image has been performed.
288 In the proposed method, the image after being converted to grayscale undergoes a morphological
289 opening similar to closing. Unlike conventional closing (dilation followed by erosion) which uses the
290 same structuring element, two different structuring elements are used, a concentric ring for dilation
291 and a disk for erosion. The inner and outer diameter of the dilation ring is set to 35% and 70% of
292 RBCs size, respectively and the erosion disk has the same diameter. Therefore, considering that fixed
293 manually defined parameters are used for this strategy, the results may substantially differ depending
294 on the image resolution. This approach results in locating only the stained components in the image
295 instead of all the cells and hence will not only speed up the operation but reduces the complexity.

296 Mushabe *et al.* [26] used morphological and statistical classification to detect malaria in blood
297 smears by identifying and counting red blood cells and Plasmodium parasites. Morphological
298 operations and histogram-based thresholding are used to extract RBCs and boundary curvature
299 calculations and Delaunay triangulation are used for splitting clumped RBCs. They worked on
300 Giemsa-stained thin blood smears.

301 In [27] Ross *et al.* proposed a method which provides a positive or negative diagnosis of malaria
302 and differentiates parasites by species. The segmentation step relies on a thresholding strategy which
303 aims to identify and segment potential parasites and erythrocytes from the image background after a
304 six steps threshold selection. Mathematical morphology has been used for parasite size estimation,
305 erythrocytes reconstruction and cells bigger than erythrocytes removal.

306 Savkare *et al.* [28] worked on thin blood films with Giemsa staining and used global threshold
307 and Otsu threshold [29] on grayscale enhanced image (green channel) for separating foreground from
308 background. Hole filling has been performed on identified cells and morphological operators have

been used to identify overlapping cells. Then, watershed transform has been applied for separating overlapped cells.

Also in the method proposed in [30] by Somasekar *et al.* the segmentation of the infected parasites is based on thresholding. The segmentation is achieved in two stages by maximizing between-class variance of an original image and consequently by an iterative threshold selection from a stage-one threshold image with suitable stopping criteria. The segmented results are post processed to improve the accuracy of the detection of malaria parasites by morphological operators (erosion and closing).

On the other hand, a lot of works have been realized by means of mathematical morphology and/or granulometry in the segmentation stages, even in combination with thresholding strategies. They are briefly analysed underneath.

Airwhar *et al.* [31] based their approach on thresholding and granulometry. The histogram of the complemented, green component has been used and it is said to be a bimodal distribution in all the considered images. Then, both local and global thresholds are used, and the union of the two binary images is chosen as the parasite marker image. A morphological opening filter, using a disk-shaped SE with radius equal to the mean erythrocyte radius less the standard deviation, is applied to the grayscale morphologically filtered green component of the image to remove any objects smaller than an erythrocyte. The morphological gradient is then calculated using a diamond-shaped SE with unity length. The segmentation method is applied to each object in the reconstructed binary image of erythrocytes individually. Those objects that do not exceed the area of a circle with radius equal to the mean erythrocyte radius plus the standard deviation are regarded as being single cells, and are unmodified. On the other hand, the clumped cells are segmented as follows. First, the intersection of the morphological gradient image and the dilated cell cluster is taken. This image is then transformed to a binary image by thresholding any value greater than zero. A series of morphological operations, namely a closing operation, thinning, and spur removal are then applied to generate a contour of the segmented erythrocytes. The contours are filled, and the segmented mask is again reconstructed with the valid parasite marker image to result in a segmented mask of infected cells.

Di Ruberto *et al.* [8] aimed to detect the parasites by means of an automatic thresholding based on a morphological approach applied to cell image segmentation, that is more accurate than the classical watershed-based algorithm. They have applied grey scale granulometries based on opening with disk-shaped elements, flat and hemispherical. They have used a hemispherical disk-shaped structuring element to enhance the roundness and the compactness of the red cells improving the accuracy of the classical watershed algorithm, while they have used a disk-shaped flat structuring element to separate overlapping cells. These methods make use of the red blood cell structure knowledge, that is not used in existing watershed-based algorithms.

Khan *et al.* in [32] presented a novel threshold selection technique used to identify erythrocytes and possible parasites present on microscopic slides that greatly takes benefit of morphological operations, such as granulometry and morphological reconstruction.

In [33] Rosado *et al.* proposed a system using supervised classification to assess the presence of malaria parasites and determine the species and life cycle stage in Giemsa-stained thin blood smears. For the RBCs segmentation, they used an adaptive thresholding approach followed by a closing morphological operation with an elliptical structuring element.

Soni *et al.* [34] performed segmentation of erythrocytes by using granulometry as well. The size and eccentricity of the erythrocytes are also required for the calculation of some feature values (as these can be indicative of infection). The shape of the objects (circular erythrocytes) is known a priori, but the image must be analysed to determine the size distribution of objects in the image and to find the average eccentricity of erythrocytes present. Gray-scale granulometries based on opening with disk shape elements are then used. Non flat disk shaped structural element are applied to enhance the roundness and compactness of the red blood cells and flat disk shaped structural element applied to segment overlapping cells. The object to be segmented differs greatly in contrast from the background image. Changes in contrast can be detected by operators that calculate the gradient of an image. The

359 gradient image can be computed and a threshold can be applied to create a binary mask containing the
360 segmented cell. The binary gradient mask is dilated using the vertical structuring element followed by
361 the horizontal structuring element. The cell of interest has been successfully segmented, but it is not
362 the only object that has been found. Any objects that are connected to the border of the image can be
363 removed.

364 In [5] Tek *et al.* the localisation of the parasites is achieved after a foreground and background
365 segmentation step. Firstly, a rough foreground image using morphological area top-hats (using the
366 average cell area value) is extracted. Then, from these rough foreground and background regions two
367 different threshold values are determined and used in morphological double thresholding of the input
368 grey level image to produce a refined binary foreground mask. From the foreground image the stained
369 pixels are detected using again a thresholding approach and finally used as markers to extract the
370 stained objects by morphological area top-hats based on the estimated average area value.

371 In [35] Yunda *et al.* proposed a method for P.vivax parasites detection. The segmentation phase
372 is a combination of border and region detection that allows rejection of the image background and
373 permits identifying each of the objects. Initially, the morphological gradient method is used to enhance
374 the borders of previously found objects. This is followed by a threshold detection stage using the
375 K-Median method. Furthermore, Laplacian operator was used to discriminate the pixels that are
376 interior or exterior in relation to the regions of the images and then erosion operation followed by two
377 dilations were applied to delete the pixels which did not make part of any object. In the end, Absence
378 of Gradients and Nernstian Equilibrium Stripping (AGNES) and K-Median techniques were applied
379 to assign the remaining number of pixels to each region, using the image regions previously identified
380 as objects and background as the starting point.

381 Several authors used marker controlled watershed with morphological approach, as following
382 described.

383 Das *et al.* in [36], [37], [38], [11] segmented erythrocytes as aforesaid and then morphological
384 operators are used to eliminate unwanted cells like leukocytes and platelets. To conclude, overlapping
385 erythrocytes are segmented by using marker controlled watershed segmentation technique.

386 In the paper [39] Devi *et al.* proposed a computer assisted system for quantification of erythrocytes
387 in microscopic images of thin blood smears. The performance of the system in classifying the isolated
388 and clump erythrocytes by geometric features is evaluated for the different classifiers. The clump
389 erythrocytes are segmented using marker controlled watershed with h-minima as internal marker.

390 In [40] Dey *et al.* presented an automatic system for segmenting platelets, useful for identifying
391 disease as malaria, using a color based segmentation and mathematical morphology (opening
392 operations with a disk element of radius 2).

393 In the study presented in [41] by Diaz *et al.* for quantification and classification of erythrocytes
394 in stained thin blood films infected with Plasmodium falciparum, the authors used connected
395 morphological operators in the segmentation step. The RBCs are detected as follows: firstly, a pixel
396 classification allowed to label each image pixel as either background or foreground, based on its color
397 features. Afterward, an inclusion-tree structure represented the hierarchical object relations between
398 background and foreground so that a filtering process allows to remove irrelevant structures such as
399 artifacts generated at the staining or digitization processes.

400 Khan *et al.* [32], among other experimentations, used it in order to try to separate overlapping
401 cells because, according to their statements, watershed transform can separate touching cells but it is
402 not sufficient for overlapping cells.

403 In the algorithm described by Romero-Rondon *et al.* in [15] the detection of overlapped RBCs is
404 still based on marker-controlled watershed transform. To define the suitable markers in watershed
405 transform they used three different approaches, based on a morphological erosion operation, on Hough
406 transform and on clustering method of k-means.

407 Savkare *et al.* in [42] segmented cells using k-mean clustering and global threshold. Overlapping
408 cells are separated using Sobel edge detector and watershed transform. Watershed transform is applied

409 on each cluster separately. Over-segmentation is minimized by series of morphological operations,
410 like erosion and dilation utilizing disk shaped structuring element.

411 In [43] an approach to detect red blood cells with consecutive classification into parasite infected
412 and normal cells for further estimation of parasitemia is proposed. For separation of overlapping cells
413 watershed transform is applied on distance transform of binary mask of cells having larger area.

414 In [44] Špringl performed red blood cell segmentation by using marker-controlled watershed
415 transformation based on the image gradient. Markers are computed as a combination of the binary
416 mask of the red blood cells and centres of the cells which are computed using a similar algorithm that
417 was utilized for the evaluation of the average cell radius. The binary mask is obtained by thresholding
418 the grey-scale image with an automatically estimated threshold using Otsu method[29].

419 In [45] Sulistyawati *et al.* combined morphological operations (erosion, dilation, opening and
420 closing) and blob analysis to segment and identify malaria parasites with a high degree of accuracy.

421
422 Tek *et al.* in [46] proposed a classifier-based method, for the segmentation stage, which relies
423 on a Bayesian pixel classifier to distinguish among stained and non-stained pixels. In particular,
424 they used a non-parametric method based on histograms in order to produce the probability density
425 functions of stained and non-stained classes. Stained pixels can belong to other components such
426 as WBCs, platelets or artefacts, in addition to the parasites and so the detection procedure requires
427 a further classification to distinguish among parasite and non-parasite pixels. However, the stained
428 pixels have to be represented as connected sets, representing stained objects, to extract features for the
429 classifier. Furthermore, top-hat extraction and infinite reconstruction were applied to find the regions
430 that include the objects.

431 To conclude many systems for computer aided diagnosis of malaria disease made use of
432 mathematical operations in order to smoothen the boundary of the regions obtained from the
433 segmentation process.

434 3.3. Feature extraction

435 Feature extraction has the target of reducing the computational complexity of the subsequent
436 process and facilitating a reliable and accurate recognition for unknown novel data, considering
437 that the input data to an algorithm could be too large to be processed and it could be redundant
438 (e.g. repetitiveness of pixels patterns in an image). Moreover, the in-depth understanding of the
439 domain-specific knowledge gained by human experts on the problem being addressed can be of
440 extreme importance for the design of a reliable and effective feature extraction engine [47]. It starts
441 from determining a subset of the initial features and this procedure is called feature selection. The
442 selected features are expected to contain the relevant information from the input data, so that the
443 desired task can be performed by using this reduced representation instead of the complete initial
444 data. Malaria parasite infection causes micro structural changes in erythrocytes. The microscopic
445 features of the RBCs are usually specific to morphology, intensity and texture. They may also represent
446 the differences that occur among healthy and unhealthy cells. Most of the studies have reported
447 both textural and geometric features for describing malaria infection stages [11]. Generally speaking,
448 features may be distinguished according to the following characteristics: morphological features and
449 textural and intensity features.

450 It is a well known mathematical morphology approach to compute a size distribution of grains in binary
451 images, using a series of morphological opening operations. It is the basis for the characterization
452 of the concept of size. Some authors used area granulometry for pre-processing purposes in malaria
453 characterization [5] even though it is certainly effective for extracting cells size features information
454 [46],[48],[44]. In [5] local area granulometry combined with colour histogram are used as features. The
455 area granulometry feature is calculated locally on the binary mask of the stained objects, for the RGB
456 channels and then concatenated. Morphological features are also used in [36] (opening, closing) and in
457 [8] (skeleton) to classify parasites.

458 4. Discussions

459 In the review we have only considered the methods which employed mathematical morphology
460 in at least one step of the pipelines and it has been structured by considering the following information:
461 preprocessing, segmentation, features extraction. Most of the studies are based on *P. vivax* and/or
462 *P. falciparum* characterization. With regards to the showed approaches and related results, it is clear
463 that malaria parasites detection and segmentation techniques in microscopic images needs further
464 experiments and improvements. In general, the analysed works have been tested with a limited
465 number of images and the datasets are not publicly available; therefore, a comparison between
466 different approaches is very difficult. Despite promising results reported during the past years,
467 the great majority of the computer-aided methods found on the literature for malaria diagnosis are
468 based on images acquired under well controlled conditions and with proper microscopic equipment.
469 However, one should take into account that 80% of malaria cases occur in Africa, where this type of
470 equipment is scarce or even nonexistent in common healthcare facilities [33]. Moreover, this review
471 showed that *P. falciparum* is the most analysed if we refer to segmentation and detection, considering
472 that it is the most widespread among malaria parasite types. The majority of the works used thin
473 blood smear. It is typically used for identification of malaria infected stages, types of parasitic infection
474 and percentage of parasitemia, while thick blood smear is used for identification and quantification of
475 malaria parasite count against leukocyte count per microliter blood.

476 Preprocessing phase is typically taken on with filters and the most used in the analysed works is
477 certainly the median filter which permits to preserve sharp edges. Apart from the classic histogram
478 equalization and contrast stretching techniques, other filters have been employed, e.g., geometric mean
479 filter to remove Gaussian noise preserving edges, Laplacian filter, in order to find edges, and so on.
480 Median filter has been found to be effective for reducing impulse noises from the microscopic images,
481 even though recent studies have shown that geometric mean filter provides better performance than
482 the median filter [37], [11]. However, morphological operators have been greatly used with successful
483 performances, imposing themselves as powerful alternatives to more common and used techniques
484 for image enhancement and noise filtering ([8], [12], [25], [13], [48], [26], [14], [16], [15], [27] [17], [18],
485 [44], [5]).

486 Malaria parasites may be discriminated according to two different strategies: by segmenting the
487 whole erythrocyte from the blood smear image on the basis of which malaria infection is detected,
488 otherwise by segmenting chromatin dot or parasite infection region for characterizing parasite infection
489 stages based on some extracted target features. In general, thresholding-based approach is still widely
490 used for segmentation purposes. In particular, a lot of authors affirm that Otsu thresholding suffers
491 from limitations when textural variation is high, while histogram thresholding can not deal sufficiently
492 good in identifying valley regions in case of unimodal histograms. However, such a simple and fast
493 approach can greatly benefit from mathematical morphology as recent studies demonstrate ([31], [20],
494 [19], [8], [22], [23], [25], [26], [33], [27], [28], [42], [30], [5]).

495 Another greatly used segmentation approach is clearly the watershed transform. The classic
496 watershed approach is reported to produce over segmentation results [28], whereas the marker
497 controlled approach does not suffer from this issue and it is reported to be very effective for overlapping
498 cells segmentation even though some authors affirm that it may fail to segment highly overlapped
499 cells ([36], [37], [38], [11], [39], [32], [15], [42], [43], [44]).

500 Other authors ([31], [8], [32], [26], [27], [34], [5]) employed granulometry and stated that it is very
501 effective to segment cells with regular size.

502 The analysed works performed classification phase for different purposes. The majority of them
503 aimed to distinguish among two classes only, malaria infected and noninfected RBCs, or to detect and
504 count parasites in a malaria blood image ([20], [19], [36], [21], [11], [8], [22], [23], [13], [9], [48], [26],
505 [14], [28], [43], [4], [18], [30], [34], [45], [46]).

506 More complex classification strategies aimed to classify parasites into different classes, i.e. different
507 human parasites species ([31], [37], [38], [32], [5]), and/or different parasites life stages ([20], [37], [38],
508 [8], [41], [5]).

509 5. Conclusions

510 This work reviewed several computational microscopic imaging techniques oriented to
511 mathematical morphology approach, proposed in literature for malaria parasites detection and
512 segmentation in blood smear microscopic images.

513 The computer vision methodologies reported in the literature are based on light microscopic
514 images of human peripheral blood smears for computer-aided detection of malaria parasites and their
515 different life stages. Image preprocessing, segmentation of erythrocytes and parasites, malaria parasite
516 feature extraction, malaria detection techniques have been discussed here.

517 It is worth noticing that cells colours and the colour contrast between cells and background can
518 vary so often according to the different, existing staining techniques, thickness of smear, microscope
519 illumination and microscope's image acquisition procedure, as shown in fig. 1. A standardization
520 of the procedure should be really useful to avoid superfluous differences in similar images' features
521 and to have fair comparisons among the several proposed methods. The main efforts towards the
522 realization of a fully automatic blood cells segmentation and classification system cannot leave this
523 aspect out.

524 Mathematical morphology techniques have been widely used for image processing purposes.
525 Among the application fields, it has been applied for fingerprint feature extraction, recognition of
526 handwritten digits, license plate detection, border extraction, denoising using morphological filters,
527 text extraction and detection of imperfection in printed circuit boards [49]. Apart from this kind
528 of fields, mathematical morphology has been employed successfully in biomedical image analysis,
529 especially in preprocessing and segmentation techniques.

530 Morphological cell analysis is used to face off abnormality identification and classification, early
531 cancer detection. It has been integrated in new methods for biomedical applications, such as automatic
532 segmentation and analysis of histological tumour sections, boundary detection of cervical cell nuclei
533 considering overlapping and clustering, the granules segmentation and spatial distribution analysis,
534 morphological characteristics analysis of specific biomedical cells, understanding the chemotactic
535 response and drug influences, or identifying cell morphogenesis in different cell cycle progression.
536 Morphological feature quantification for grading cancerous or precancerous cells is especially widely
537 researched in the literature, such as nuclei segmentation based on marker-controlled watershed
538 transform and snake model for hepatocellular carcinoma feature extraction and classification, which
539 is important for prognosis and treatment planning, nuclei feature quantification for cancer cell cycle
540 analysis, and using feature extraction including image morphological analysis, wavelet analysis, and
541 texture analysis for automated classification of renal cell [50].

542 Moreover, non-linear filtering has become increasingly important in many image processing
543 applications. Initially, the attraction to non-linear filters was mostly limited to the impulse-removing
544 and edge-preserving qualities of the median filter. However, as the number and sophistication of
545 non-linear filters have increased, so has the variety of applications for these filters. The shape-based
546 methods of mathematical morphology, in particular, are now used in a wide variety of medical
547 applications, including electrocardiography, ultrasound imaging, radiology, and histological image
548 analysis [51].

549 Furthermore, microscopic image analysis and, in particular, malaria detection and classification
550 can greatly benefit from the use of mathematical morphology. The interest in this approach to image
551 processing ad analysis is proved by the increasing number of works proposing methods for malaria
552 image analysis based on mathematical morphology techniques.

553 In the end, it is worth considering that the development of new mobility-aware microscopic
554 devices (and ideally low cost) is an area that can greatly improve the chances of the successful

555 deployment of computer vision CAD solutions for malaria diagnosis in the field. The mobile phone is
556 currently Africa's most important digital technology, and is boosting African health as it emerges as a
557 platform for diagnosis and treatment. Considering the recent significant improvements of the new
558 generation of mobile devices in terms of image acquisition and processing power, if a reliable automatic
559 diagnostic performance is ensured through the usage of those devices, one would dramatically reduce
560 the effort in the exhaustive and time consuming activity of microscopic examination. Moreover, the
561 lack of highly trained microscopists on malaria diagnosis in rural areas could then be complemented
562 by a significantly less specialized technician that knows how to operate the system and prepare blood
563 smears. The usage of mobile devices in the system architecture can also bring significant improvements
564 in terms of portability and data transmission, like the systems proposed by [14] and [33]. Finally,
565 malaria diagnosis might be just one element of a suite of diagnostic software tests running on this type
566 of system. Several other tests could simultaneously be carried out using the same images, for instance
567 cell counting or detection of other hemoparasites like microfilaria or trypanosoma [52].

Authors	Preprocessing	Segmentation	Features	Classification	Performance
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Ahirwar <i>et al.</i> , 2012	-	thresholding + granulometry, opening, morphological gradient, dilation, closing, thinning, spur removal	-	five (<i>P.falciparum</i> , <i>P.vivax</i> , <i>P.ovale</i> , <i>P.malariae</i> infected, and noninfected)	-
Anggraini <i>et al.</i> , 2011	-	thresholding + hole filling	-	two (<i>P.falciparum</i> infected and noninfected) + two life-cycle-stages	SE=93% SP=99%
Arco <i>et al.</i> , 2014	-	adaptive thresholding + hole filling, closing, regional minima	-	two (infected and noninfected)	Acc=96.46%
Das <i>et al.</i> , 2011	-	marker controlled watershed	opening, closing	two (infected and noninfected)	Acc=88.77%
Das <i>et al.</i> , 2013	-	marker controlled watershed	-	three (<i>P.falciparum</i> , <i>P.vivax</i> infected and noninfected) + three life-cycle-stages per species	Acc=84%
Das <i>et al.</i> , 2014	-	marker controlled watershed	-	three (<i>P.falciparum</i> , <i>P.vivax</i> infected and noninfected) + three life-cycle-stages per species	SE=99.72% SP=84.39%
Dave <i>et al.</i> , 2017	-	adaptive thresholding + erosion, dilation	-	two (infected and noninfected)	Acc=97.83% thin films, Acc=89.88% thick films
Devi <i>et al.</i> , 2017	-	marker controlled watershed	-	two (infected and noninfected)	Acc=98.02%
Diaz <i>et al.</i> , 2009	-	inclusion tree	-	two (<i>P.falciparum</i> infected and noninfected) + three life-cycle-stages	SE=94% SP=99.7% for detection, SE=78.8% SP=91.2% for life-stages
Di Ruberto <i>et al.</i> , 2002	area closing, opening	thresholding + granulometry, watershed transform	skeleton	two (<i>P.falciparum</i> infected and noninfected) + three life-cycle-stages	-
Elter <i>et al.</i> , 2011	-	thresholding + black top-hat, dilation	-	two (infected and noninfected)	SE=97%
Gonzalez-Betancourt <i>et al.</i> , 2016	erosion-reconstruction, dilation-reconstruction, closing	morphological filter, watershed transform	-	-	-
Ghosh <i>et al.</i> , 2011	-	thresholding + opening, closing	-	two (<i>P.vivax</i> infected and noninfected)	-
Kareem <i>et al.</i> , 2011, 2012	dilation, erosion	-	-	two (infected and noninfected)	Acc=88% SE=90% SP=86%

Khan <i>et al.</i> , 2011	area closing	thresholding + granulometry, opening, morphological reconstruction, gradient, dilation	-	five (<i>P.falciparum</i> , <i>P.vivax</i> , <i>P.ovale</i> , <i>P.malariae</i> infected, and noninfected)	Acc=81% SE=85.5%
Malih <i>et al.</i> , 2013	closing	-	area granulometry	two (infected and noninfected)	Acc=91% SE=80% SP=95.5%
Mushabe <i>et al.</i> , 2013	closing	thresholding + granulometry, dilation, erosion	-	two (infected and noninfected)	SE=98.5 SP=97.2%
Oliveira <i>et al.</i> , 2017	erosion	-	-	two (infected and noninfected)	Acc=91%
Reni <i>et al.</i> , 2015	new morphological filtering	-	-	-	-
Romero-Rondon <i>et al.</i> , 2016	dilation, opening	marker controlled watershed, erosion	-	-	-
Rosado <i>et al.</i> , 2017	-	adaptive thresholding + closing	-	four (<i>P.falciparum</i> , <i>P.ovale</i> , <i>P.malariae</i> infected, and noninfected) + three life-cycle-stages for species	SE=73.9-96.2% SP=92.6-99.3%
Ross <i>et al.</i> , 2006	area closing	thresholding + granulometry, opening, reconstruction, morphological gradient, closing, thinning thresholding + hole filling, watershed transform	-	five (<i>P.falciparum</i> , <i>P.vivax</i> , <i>P.ovale</i> , <i>P.malariae</i> infected, and noninfected)	SE=85% for detection, Acc=73% for classification
Savkare <i>et al.</i> , 2011a	-	thresholding + hole filling, watershed transform	-	two (infected and noninfected)	-
Savkare <i>et al.</i> , 2011b	-	thresholding + watershed transform	-	two (infected and noninfected)	SE=93.12% SP=93.17%
Savkare <i>et al.</i> , 2015	-	thresholding + watershed transform, erosion, dilation	-	two (infected and noninfected)	Acc=95.5%
Sheikhhosseini <i>et al.</i> , 2013	hole filling	thresholding + hole filling, opening	-	two (infected and noninfected)	Acc=97.25% SE=82.21% SP=98.02%
Somasekar <i>et al.</i> , 2015	erosion	fuzzy C-means clustering + erosion, hole filling	-	two (infected and noninfected)	SE=98% SP=93.3%
Somasekar <i>et al.</i> , 2017	-	thresholding + erosion, closing, hole filling	-	two (infected and noninfected)	average DSC=0.8
Soni <i>et al.</i> , 2011	-	thresholding + granulometry, morphological gradient, dilation	-	five (<i>P.falciparum</i> , <i>P.vivax</i> , <i>P.ovale</i> , <i>P.malariae</i> infected, and noninfected)	SE=98% for detection

Špringl, 2009	closing	thresholding + marker controlled watershed transform, hole filling, dilation, opening, erosion blob analysis + erosion, dilation, opening, closing, hole filling	-	two (infected and noninfected)	AUC=0.98
Sulistyawati <i>et al.</i> , 2015	-	-	-	two (infected and noninfected)	Acc=99.39%
Tek <i>et al.</i> , 2006	-	top-hat, infinite reconstruction	area granulometry	two (infected and noninfected)	SE=74% SP=98%
Tek <i>et al.</i> , 2010	closing, granulometry	thresholding + granulometry, area top-hat, closing	area granulometry	five (<i>P.falciparum</i> , <i>P.vivax</i> , <i>P.ovale</i> , <i>P.malariae</i> infected, and noninfected) + four life-cycle-stages for species	SE=72% SP=98%
Yunda <i>et al.</i> , 2012	-	thresholding + morphological gradient, erosion, dilation	-	three (<i>P.falciparum</i> , <i>P.vivax</i> infected, and noninfected) + two life-cycle-stages for <i>P.falciparum</i>	SE=77.19%

Table 1. Summary of analysed methods: morphological operations used in the main phases of analysis, kind of classification and performance measures (Sensitivity, Specificity, Accuracy, if reported).

568 Supplementary Materials: The following are available online at www.mdpi.com/link, Figure S1: title, Table S1: title, Video S1: title.

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571 you have received in support of your research work. Clearly state if you received funds for covering the costs to
572 publish in open access.

573 Author Contributions: For research articles with several authors, a short paragraph specifying their individual
574 contributions must be provided. The following statements should be used “X.X. and Y.Y. conceived and
575 designed the experiments; X.X. performed the experiments; X.X. and Y.Y. analyzed the data; W.W. contributed
576 reagents/materials/analysis tools; Y.Y. wrote the paper.” Authorship must be limited to those who have
577 contributed substantially to the work reported.

578 Conflicts of Interest: Declare conflicts of interest or state “The authors declare no conflict of interest.” Authors
579 must identify and declare any personal circumstances or interest that may be perceived as inappropriately
580 influencing the representation or interpretation of reported research results. Any role of the funding sponsors in
581 the design of the study; in the collection, analyses or interpretation of data; in the writing of the manuscript, or in
582 the decision to publish the results must be declared in this section. If there is no role, please state “The founding
583 sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing
584 of the manuscript, and in the decision to publish the results”.

585 Abbreviations

586 The following abbreviations are used in this manuscript:

MDPI	Multidisciplinary Digital Publishing Institute
DOAJ	Directory of open access journals
TLA	Three letter acronym
LD	linear dichroism

589 Appendix A

590 Appendix A.1

591 The appendix is an optional section that can contain details and data supplemental to the main text. For example,
592 explanations of experimental details that would disrupt the flow of the main text, but nonetheless remain crucial to understanding

593 and reproducing the research shown; figures of replicates for experiments of which representative data is shown in the main
594 text can be added here if brief, or as Supplementary data. Mathematical proofs of results not central to the paper can be added
595 as an appendix.

596 Appendix B

597 All appendix sections must be cited in the main text. In the appendixes, Figures, Tables, etc. should be labeled starting
598 with 'A', e.g., Figure A1, Figure A2, etc.

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714 **Sample Availability:** Samples of the compounds are available from the authors.

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