

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 recent 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>

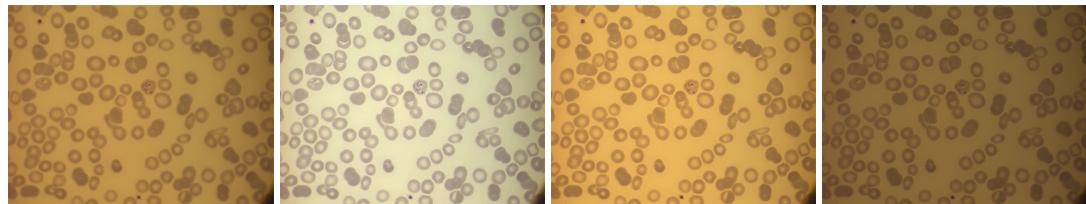


Figure 1. Different illumination conditions generate different images, because of the absence of a standardized acquisition procedure. From left to right: acquisition of the same smear with four microscope's brightness levels.

Courtesy of CHUV, Lausanne.

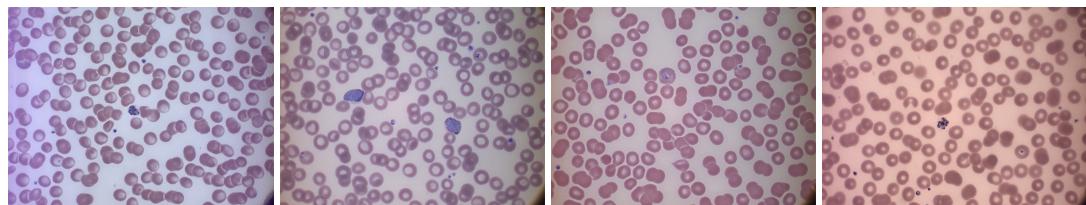


Figure 2. Types of human malaria: from left to right, *P. Falciparum* in its schizont stage, *P. Vivax* in two gametocytes specimens and one ring stage, *P. Ovale* in its ring stage, *P. Malariae* in its schizont stage. Courtesy of CHUV, Lausanne.

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 is not
 94 only a theory, but also a very powerful image analysis technique [5]. It was introduced by Matheron
 95 in 1964 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 [6]:

- 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.

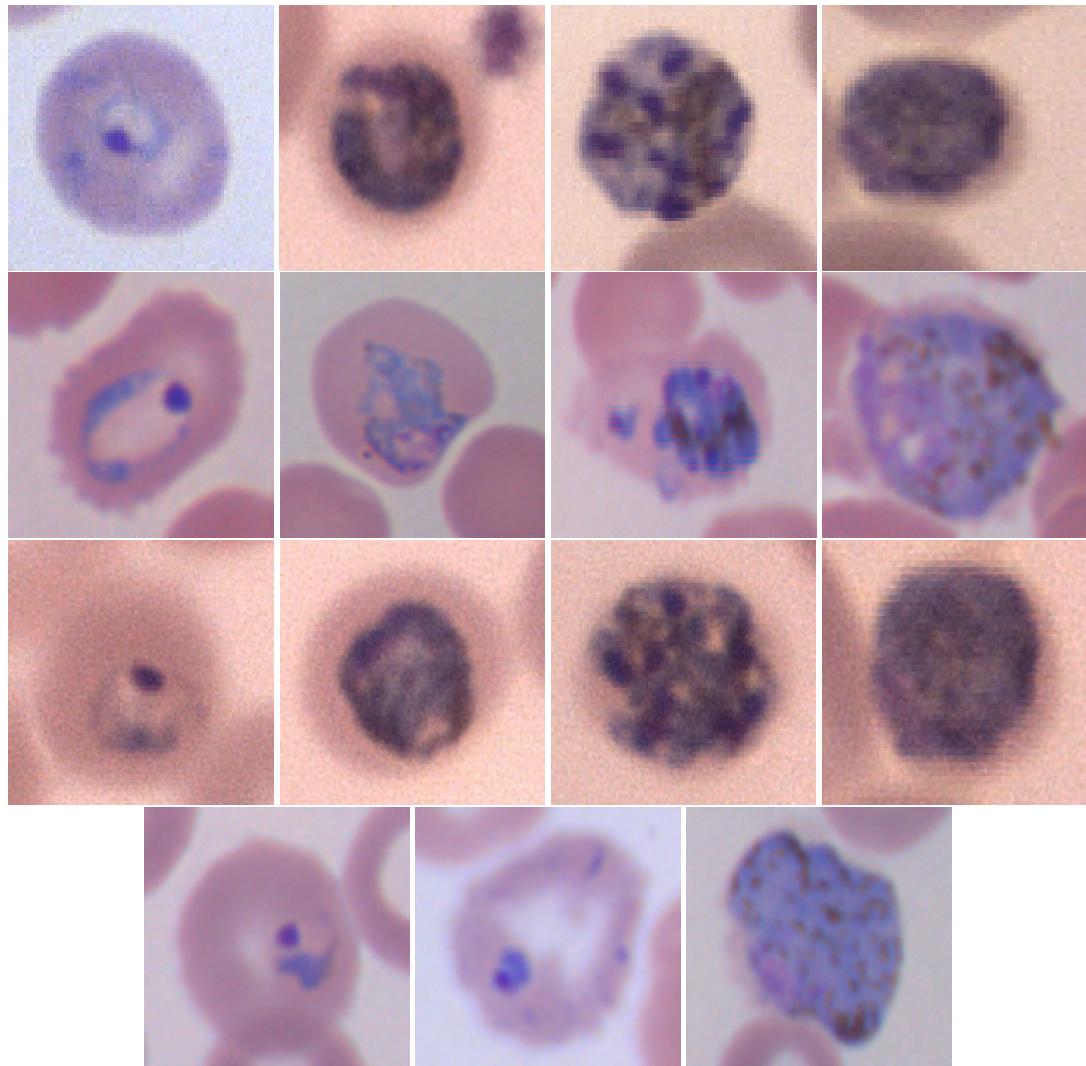


Figure 3. Examples of malaria parasite stages. First row, from left to right: *P.falciparum* ring, trophozoite, schizont, gametocyte; second row, from left to right: *P.ovale* ring, trophozoite, schizont, gametocyte; third row, from left to right: *P.malariae* ring, trophozoite, schizont, gametocyte; last row, from left to right: *P.vivax* ring, developed trophozoite, gametocyte.

Courtesy of CHUV, Lausanne.

- 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
112 of pixels of interest in the image. The structuring element has both a shape and an origin. From these
113 two basic operators, others have been derived (opening, closing, hit-or-miss). They can be applied to
114 extract image components useful in the representation and descriptions of region shapes, such as area
115 granulometry, boundaries, skeleton, or convex hull. Also, morphological operators can be used for
116 image preprocessing and postprocessing, such as morphological filtering, thinning, and especially for
117 segmentation.

118 2. Scope of this review

119 In this paper we present a review of computer-aided methods oriented to malaria parasites
120 detection and segmentation by mathematical morphology based techniques. Most of the studies were
121 followed Di Ruberto's work [7], which first proposed a system to evaluate parasitaemia in the blood.
122 The system was able to detect the parasites by using an automatic thresholding and morphological
123 operators. A morphological approach to cell segmentation which is more efficient than watershed
124 algorithm [5] was proposed. Finally, the parasites classification was still based on morphological
125 operators. Since then many systems for computer aided diagnosis of malaria have been proposed. Most
126 of them make use of mathematical morphology to process and analyse malaria-infected peripheral
127 blood cells images. The scope of this paper is to review and analyze the recent works of different
128 researchers in the area of malaria parasite recognition using computer vision which benefit from
129 mathematical morphology. Only few reviews exist in literature about microscopic image processing for
130 malaria parasites. However, they are not focused on MM techniques as they analyze generic computer
131 vision systems for malaria diagnosis, as in [8], [9] or [10]. Also, newer and promising approaches,
132 addressing for example the problem of malaria diagnosis in remote areas [11], [8], or improving
133 significantly both the detection and the classification performances [12], [13], [14] and [15], have not
134 been considered in the previous reviews.

135 The rest of the paper is organised as follows. Section 3 presents a review of the considered
136 works, according to a typical pipeline of a computer-aided image analysis process: preprocessing,
137 segmentation, feature extraction. All the considered works make use of morphological operators in at
138 least one of the phases of image analysis. Section 4 contains an overall discussion about the methods
139 and the conclusions are expressed in section 5.

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

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

- 144 1. Preprocessing.
- 145 2. Segmentation.
- 146 3. Feature extraction.
- 147 4. Classification.

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

152 Extensive search of articles has been made in PubMed and Google Scholar search engines based
153 on the keywords: "malaria, mathematical morphology, automated malaria diagnosis" up to October
154 2017. The search includes papers published in English and titles and abstracts of potentially relevant
155 studies were selected and presented from the most recent ones. Thereafter, the full texts of these studies
156 were evaluated as per the exclusion criteria.

157 Two main factors are generally considered if we refer to staining techniques: the type of
158 colouration, in which Giemsa and Leishman are the most common, and the thickness of blood slide,
159 which may be thick or thin. The majority of studies have been employed on thin blood smear images
160 (over two-third of the total count) while only a few have used thick blood smear images. Typically,
161 thin smears permit the identification of specific parasitic stage and quantification of malaria parasite;
162 on the other hand, thick smears are better if the target is to perform an initial identification of malaria
163 infection using blood pathology. Some examples are shown in fig. 4. Giemsa stained blood smear is
164 considered in most of the analysed literatures whereas Leishman stain is considered in few studies.
165 It is reported that Leishman stain has bigger sensitivity for parasite detection than Giemsa [16] and

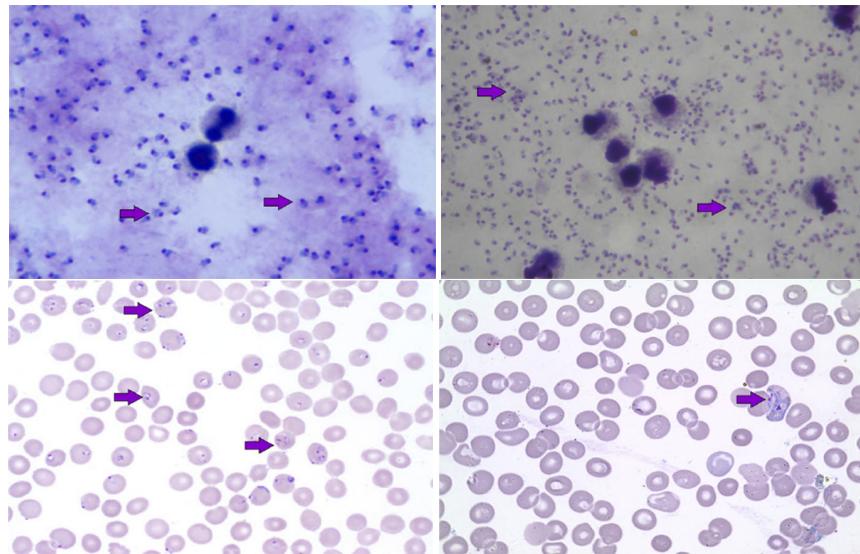


Figure 4. Malaria infected blood smear images. From top left, clockwise: thick smear with Giemsa stain, thick smear with Leishman stain, thin smear with Leishman stain, thick smear with Giemsa stain [9]. Arrows in top images indicate chromatin dots while, in the bottom ones, they show the infected erythrocytes.

166 is superior for visualization of red and white blood cell morphology [17]. On the contrary, Giemsa
 167 stain highlights both malaria parasites and white blood cells and, therefore, it is an additional issue
 168 to deal with. Giemsa stain is much costly and also time-taking procedure than Leishman. Moreover,
 169 magnification of 100X by using an oil immersion objective is used for capturing microscopic images of
 170 thin blood smear for identification of specific parasites and their infected stage.

171 3.1. Preprocessing

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

190 In [18] Gonzalez-Betancourt *et al.* proposed a system to determine markers for watershed
 191 segmentation based on the Radon transform and mathematical operators. In the first step of the
 192 process small irrelevant structures and part of the noise are eliminated by a morphological filter, in
 193 order to ensure the preservation of the cells edges. Image smoothing is performed by a morphological

erosion-reconstruction and dilation-reconstruction filter with a disk structuring element of radius equal to 20 pixels, which is 0.274 times smaller than the average radius of the RBCs. In this way the influences of the size and the shape of the structures can be separated in the smoothing process. At the same time the objects which are not eliminated remain unchanged. Also, a morphological closing is performed with a disk structuring element having radius smaller than half the average of the RBCs radii, in order to connect the possible (more than one) markers that can appear on a single cell.

In [19] Kareem *et al.* illustrated a morphological approach for blood cell identification and use the image features such as intensity, histogram, relative size and geometry for further analysis. Before the identification of blood cells, the authors propose a novel morphological filtering based on the size of RBC for platelets and/or artifacts elimination. A dilation is performed by a concentric ring structuring element and erosion by a disk-shaped structuring element. The radius of the structuring element depends on the radius of the RBCs, so that all the components smaller than the RBCs can be removed.

The system proposed in [11] by Oliveira *et al.* is based on image processing, artificial intelligence techniques and an adapted face detection algorithm to identify Plasmodium parasites. The latter uses the integral image and haar-like features concepts, and weak classifiers with adaptive boosting learning. The search scope of the learning algorithm is reduced in the preprocessing step by removing the background around blood cells by means of morphological erosions both for training and for testing.

Romero-Rondon *et al.* in [20] presented an algorithm that uses morphological operations, the watershed method, the Hough transform and the clustering method of k-means to detect overlapped RBCs. In the preprocessing stage white blood cells and platelets are removed before the segmentation task. During this step, some noise, the WBC cytoplasm and platelets still remain on the image. Therefore, the small objects are removed using a morphological opening and then the image is dilated with a disk-shaped structuring element.

Renì *et al.* in [21] described a new algorithm for morphological filtering of the blood images as a preprocessing tool for segmentation. Conventional morphological closing on blood images removes the unwanted components but also useful information. On the opposite the proposed method preserves the necessary information of foreground components while removing noise and artefacts.

In the method proposed in [22] by Sheikhhosseini *et al.* the first phase is the stained object extraction which detects candidates objects that can be infected by malaria parasites using intensity and colour. Before detecting the stained objects the method firstly extracts the foreground. Foreground image is a binary image which is produced after applying morphological hole filling on such pixels which have lower intensity value than average intensity value of green layer. After the stained objects extraction process, a series of morphological operations is also employed in order to eliminate small components and complete the final stained objects.

An edge-based segmentation of erythrocytes infected with malaria parasites using microscopic images is proposed by Somasekar *et al.* in [23]. A fuzzy C-means clustering is applied to extract infected erythrocytes, which is further processed for the final segmentation. A morphological erosion is used to erase some small noises and spots before the segmentation and holes inside the infected erythrocytes are filled using a morphological hole filling operation for the final segmentation.

In [24] Tek *et al.* presented a complete framework to detect and identify malaria parasites in images of Giemsa stained thin blood film specimens. Also, the system is able to identify the infecting species and life-cycle stages. The preprocessing step of the proposed method is applied to reduce the variations in the observed size, intensity, and colour of the cells and stained objects before the detection and classification steps. The aim is to correct the non-uniform illumination in the images. The estimation is based on a morphological closing operation using a sufficiently large structuring element. The sufficiently large size for an input image is determined automatically with respect to its average cell size computed from the area granulometry distribution.

242 3.2. Segmentation of RBCs and parasites

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

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

258 Arco *et al.* in [25] worked on thick blood films and proposed a method that uses an adaptive
259 thresholding based scheme, which also allows an effective classification of pixels. This means that the
260 election of whether a pixel belongs to the background or to the signal (parasites and white blood cells)
261 is only established by the pixels around it, that is its neighbourhood. Then, morphological methods
262 are applied to evaluate the area of connected components, labelling those belonging to parasites and
263 counting their number.

264 Anggraini *et al.* [26] proposed a method for separating blood cells, parasites and other components
265 from background in a microscopic field of a thin blood smear. They applied several global thresholding
266 methods and visually compared the results to qualitatively determine which technique yields the best
267 result. The binary image was then subjected to hole filling morphological operator and applied as
268 marker to label blood cells. From each identified cell (RBC and WBC), constituents of the parasite
269 (nucleus and cytoplasm) were extracted using multiple threshold.

270 Dave *et al.* in [12] performed image segmentation using histogram based adaptive thresholding
271 followed by mathematical morphological operations (erosion and dilation). The detection of infected
272 RBCs is based on a unsupervised learning technique.

273 The automated method proposed in [27] by Elter *et al.* for parasite detection and identification
274 worked on thin blood film acquired with Giemsa stain. The authors found that the G and B channels of
275 the RGB colour are very good features to identify objects containing chromatin in Giemsa stained blood
276 films, being not only considered highly discriminative but also almost independent of differences in
277 illumination and staining intensity. They transformed the colour input image into a monochrome
278 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,
279 mathematical morphology has been used with a black top-hat operator to separate MP from both
280 leukocytes and platelets, with a non-flat paraboloid structuring element of radius of 9 and a slope of 1
281 pixel. It should be taken into account that these fixed parameters might not be suitable for images with
282 different pixel resolutions. The black top-hat operator is followed by a thresholding operation with
283 a fixed threshold, which according to the authors is reliable given the independence of the G and B
284 channels with regard to illumination and staining intensity. However, the authors do not define the
285 value of this fixed threshold on the publication.

286 In [28] Ghosh *et al.* used divergence based threshold selection in order to segment P.vivax parasites
287 from Leishman-stained thin blood films. This method is based on Cauchy membership function [29]
288 and is applied to the C channel of CMYK colour space. Morphological operators of opening and
289 closing have been used for artefacts removal.

290 Kareem *et al.* in [30] used the Annular Ring Ratio transform method. Before applying it, a pre
291 processing phase for removing platelets, parasites and other artefacts in the image has been performed.

292 In the proposed method, the image after being converted to grayscale undergoes a morphological
293 opening similar to closing. Unlike conventional closing (dilation followed by erosion) which uses the
294 same structuring element, two different structuring elements are used, a concentric ring for dilation
295 and a disk for erosion. The inner and outer diameter of the dilation ring is set to 35% and 70% of
296 RBCs size, respectively and the erosion disk has the same diameter. Therefore, considering that fixed
297 manually defined parameters are used for this strategy, the results may substantially differ depending
298 on the image resolution. This approach results in locating only the stained components in the image
299 instead of all the cells and hence will not only speed up the operation but reduces the complexity.

300 Mushabe *et al.* [31] used morphological and statistical classification to detect malaria in blood
301 smears by identifying and counting red blood cells and Plasmodium parasites. Morphological
302 operations and histogram-based thresholding are used to extract RBCs and boundary curvature
303 calculations and Delaunay triangulation are used for splitting clumped RBCs. They worked on
304 Giemsa-stained thin blood smears.

305 In [32] Ross *et al.* proposed a method which provides a positive or negative diagnosis of malaria
306 and differentiates parasites by species. The segmentation step relies on a six steps thresholding selection
307 strategy. It aims to identify and segment potential parasites and erythrocytes from background.
308 Mathematical morphology has been used in several key steps of the procedure. Hole filling is used in
309 the first step in order to fill RBCs' binary masks obtained from a first thresholding. Afterwards,
310 step 4 employs RBCs' morphological reconstruction with parasites' mask, found in step 2, for
311 identifying infected cells. In step 5, a morphological opening filter, using a disk-shaped SE with
312 radius equal to the mean erythrocyte radius less the standard deviation, is applied to the grey-scale,
313 morphologically filtered, green component in order to remove any objects smaller than an erythrocyte.
314 The morphological gradient - difference between a dilation and erosion of the image - is then calculated
315 using a diamond-shaped SE with unity length. Finally, in step 6, the intersection of morphological
316 gradient image and the dilated cell cluster is calculated. This image is then transformed to a binary
317 image by thresholding any value greater than zero. A series of morphological operations, namely a
318 closing operation, thinning, and spur-removal are then applied to generate a contour of the segmented
319 erythrocytes. Contours are filled, and the segmented mask is again reconstructed with the valid
320 parasite marker image to result in a segmented mask of infected cells. RBCs and parasites masks are
321 consequently ready for next generation step.

322 Savkare *et al.* [33] worked on thin blood films with Giemsa staining and used global threshold
323 and Otsu threshold [34] on grayscale enhanced image (green channel) for separating foreground from
324 background. Hole filling has been performed on identified cells and morphological operators have
325 been used to identify overlapping cells. Then, watershed transform has been applied for separating
326 overlapped cells.

327 Also in the method proposed in [14] by Somasekar *et al.* the segmentation of the infected parasites
328 is based on thresholding. It is achieved in two stages by maximizing between-class variance of an
329 original image and consequently by an iterative threshold selection from a stage-one threshold image
330 with suitable stopping criteria. The segmented results are post processed to improve the accuracy of
331 malaria parasites detection by morphological operators (erosion and closing).

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

335 Di Ruberto *et al.* [7] aimed to detect the parasites by means of an automatic thresholding based
336 on a morphological approach applied to cell image segmentation, that is more accurate than the
337 classical watershed-based algorithm. They applied grey scale granulometries based on opening with
338 disk-shaped elements, flat and hemispherical. They used a hemispherical disk-shaped structuring
339 element to enhance the roundness and the compactness of the red cells improving the accuracy of the
340 classical watershed algorithm, while they have used a disk-shaped flat structuring element to separate

341 overlapping cells. These methods make use of the red blood cell structure knowledge, that is not used
342 in existing watershed-based algorithms.

343 Khan *et al.* in [35] presented a novel threshold selection technique used to identify erythrocytes and
344 possible parasites present on microscopic slides that greatly takes benefit of morphological operations,
345 such as granulometry and morphological reconstruction.

346 In [8] Rosado *et al.* proposed a system using supervised classification to assess the presence of
347 malaria parasites and determine the species and life cycle stage in Giemsa-stained thin blood smears.
348 For the RBCs segmentation, they used an adaptive thresholding approach followed by a closing
349 morphological operation with an elliptical structuring element.

350 In [24] Tek *et al.* the localisation of the parasites is achieved after a foreground and background
351 segmentation step. Firstly, a rough foreground image using morphological area top-hats (using the
352 average cell area value) is extracted. Then, from these rough foreground and background regions two
353 different threshold values are determined and used in morphological double thresholding of the input
354 grey level image to produce a refined binary foreground mask. From the foreground image the stained
355 pixels are detected using again a thresholding approach and finally used as markers to extract the
356 stained objects by morphological area top-hats based on the estimated average area value.

357 In [36] Yunda *et al.* proposed a method for P.vivax parasites detection. The segmentation phase
358 is a combination of border and region detection that allows rejection of the image background and
359 permits identifying each of the objects. Initially, the morphological gradient method is used to enhance
360 the borders of previously found objects. This is followed by a threshold detection stage using the
361 K-Median method. Furthermore, Laplacian operator was used to discriminate the pixels that are
362 interior or exterior in relation to the regions of the images and then erosion operation followed by two
363 dilations were applied to delete the pixels which did not make part of any object. In the end, Absence
364 of Gradients and Nernstian Equilibrium Stripping (AGNES) and K-Median techniques were applied
365 to assign the remaining number of pixels to each region, using the image regions previously identified
366 as objects and background as the starting point.

367 Several authors used marker controlled watershed [5] with morphological approach, as following
368 described.

369 Das *et al.* in [37], [38], [39], [9] segmented erythrocytes as aforesaid and then morphological
370 operators are used to eliminate unwanted cells like leukocytes and platelets. To conclude, overlapping
371 erythrocytes are segmented by using marker controlled watershed segmentation technique.

372 In the paper [13] Devi *et al.* proposed a computer assisted system for quantification of erythrocytes
373 in microscopic images of thin blood smears. The performance of the system in classifying the isolated
374 and clump erythrocytes by geometric features is evaluated for the different classifiers. The clump
375 erythrocytes are segmented using marker controlled watershed with h-minima as internal marker.

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

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

386 Khan *et al.* [35], among other experimentations, used it in order to try to separate overlapping
387 cells because, according to their statements, watershed transform can separate touching cells but it is
388 not sufficient for overlapping cells.

389 In the algorithm described by Romero-Rondon *et al.* in [20] the detection of overlapped RBCs is
390 still based on marker-controlled watershed transform. To define the suitable markers in watershed

391 transform they used three different approaches, based on a morphological erosion operation, on Hough
392 transform and on clustering method of K-means.

393 Savkare *et al.* in [42] segmented cells using K-mean clustering and global threshold. Overlapping
394 cells are separated using Sobel edge detector and watershed transform. Watershed transform is applied
395 on each cluster separately. Over-segmentation is minimized by series of morphological operations,
396 like erosion and dilation utilizing disk-shaped structuring elements.

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

400 In [44] Špringl performed red blood cell segmentation by using marker-controlled watershed
401 transformation based on the image gradient. Markers are computed as a combination of the binary
402 mask of the red blood cells and centres of the cells which are computed using a similar algorithm that
403 was utilized for the evaluation of the average cell radius. The binary mask is obtained by thresholding
404 the grey-scale image with an automatically estimated threshold using Otsu method [34].

405 In [15] Sulistyawati *et al.* combined morphological operations (erosion, dilation, opening and
406 closing) and blob analysis to segment and identify malaria parasites with a high degree of accuracy.

407 Tek *et al.* in [45] proposed a classifier-based method, for the segmentation stage, which relies
408 on a Bayesian pixel classifier to distinguish among stained and non-stained pixels. In particular,
409 they used a non-parametric method based on histograms in order to produce the probability density
410 functions of stained and non-stained classes. Stained pixels can belong to other components such
411 as WBCs, platelets or artefacts, in addition to the parasites and so the detection procedure requires
412 a further classification to distinguish among parasite and non-parasite pixels. However, the stained
413 pixels have to be represented as connected sets, representing stained objects, to extract features for the
414 classifier. Furthermore, top-hat extraction and infinite reconstruction were applied to find the regions
415 that include the objects.

416 To sum up, the analysed systems use mathematical morphology methods during or immediately
417 ensuing segmentation step for the following purposes:

- 418 • size evaluation of regions obtained from segmentation
- 419 • image cleaning and artefacts removal
- 420 • RBCs and parasites segmentation or separation
- 421 • improving parasites detection
- 422 • minimization of watershed over-segmentation.

423 3.3. Feature extraction

424 Feature extraction has the target of reducing the computational complexity of the subsequent
425 process and facilitating a reliable and accurate recognition for unknown novel data, considering
426 that the input data to an algorithm could be too large to be processed and it could be redundant
427 (e.g. repetitiveness of pixels patterns in an image). Moreover, the in-depth understanding of the
428 domain-specific knowledge gained by human experts on the problem being addressed can be of
429 extreme importance for the design of a reliable and effective feature extraction engine [46]. It starts
430 from determining a subset of the initial features and this procedure is called feature selection. The
431 selected features are expected to contain the relevant information from the input data, so that the
432 desired task can be performed by using this reduced representation instead of the complete initial data.

433 Malaria parasite infection causes micro structural changes in erythrocytes. The microscopic features
434 of the RBCs are usually specific to morphology, intensity and texture. They may also represent the
435 differences that occur among healthy and unhealthy cells. Most of the studies have reported both
436 textural and geometric features for describing malaria infection stages [9]. Generally speaking, features
437 may be distinguished according to the following characteristics: morphological features and textural
438 and intensity features.

439 It is a well known mathematical morphology approach to compute a size distribution of grains in binary

440 images, using a series of morphological opening operations. It is the basis for the characterization
441 of the concept of size. Some authors used area granulometry for preprocessing purposes in malaria
442 characterization [24] even though it is certainly effective for extracting cells size features information
443 [45], [47], [44]. In [24] local area granulometry combined with colour histogram are used as features.
444 The area granulometry feature is calculated locally on the binary mask of the stained objects, for the
445 RGB channels and then concatenated. Morphological features are also used in [37] (opening, closing)
446 and in [7] (skeleton) to classify parasites.

447 4. Discussions

448 In the review we have only considered the methods which employed mathematical morphology
449 in at least one step of the pipelines and it has been structured by considering the following information:
450 preprocessing, segmentation, features extraction. Most of the studies are based on *P. vivax* and/or
451 *P. falciparum* characterization. With regards to the showed approaches and related results, it is clear
452 that malaria parasites detection and segmentation techniques in microscopic images needs further
453 experiments and improvements. In general, the analysed works have been tested with a limited
454 number of images and the datasets are not publicly available; therefore, a comparison between
455 different approaches is very difficult. Despite promising results reported during the past years,
456 the great majority of the computer-aided methods found on the literature for malaria diagnosis are
457 based on images acquired under well controlled conditions and with proper microscopic equipment.
458 However, one should take into account that 80% of malaria cases occur in Africa, where this type of
459 equipment is scarce or even nonexistent in common healthcare facilities [8]. Moreover, this review
460 showed that *P. falciparum* is the most analysed if we refer to segmentation and detection, considering
461 that it is the most widespread among malaria parasite types. The majority of the works used thin
462 blood smear. It is typically used for identification of malaria infected stages, types of parasitic infection
463 and percentage of parasitemia, while thick blood smear is used for identification and quantification of
464 malaria parasite count against leukocyte count per microliter blood.

465 Preprocessing phase is typically taken on with filters and the most used in the analysed works is
466 certainly the median filter which permits to preserve sharp edges. Apart from the classic histogram
467 equalization and contrast stretching techniques, other filters have been employed, e.g., geometric mean
468 filter to remove Gaussian noise preserving edges, Laplacian filter, in order to find edges, and so on.
469 Median filter has been found to be effective for reducing impulse noises from the microscopic images,
470 even though recent studies have shown that geometric mean filter provides better performance than
471 the median filter [38], [9]. However, morphological operators have been greatly used with successful
472 performances, imposing themselves as powerful alternatives to more common and used techniques
473 for image enhancement and noise filtering ([7], [18], [30], [19], [47], [31], [11], [21], [20], [32] [22], [23],
474 [44], [24]).

475 Malaria parasites may be discriminated according to two different strategies: by segmenting the
476 whole erythrocyte from the blood smear image on the basis of which malaria infection is detected,
477 otherwise by segmenting chromatin dot or parasite infection region for characterizing parasite infection
478 stages based on some extracted target features. In general, thresholding-based approach is still widely
479 used for segmentation purposes. In particular, a lot of authors affirm that Otsu thresholding suffers
480 from limitations when textural variation is high, while histogram thresholding can not deal sufficiently
481 good in identifying valley regions in case of unimodal histograms. However, such a simple and fast
482 approach can greatly benefit from mathematical morphology as recent studies demonstrate, [26], [25],
483 [7], [27], [28], [30], [31], [8], [32], [33], [42], [14], [24]).

484 Another greatly used segmentation approach is clearly the watershed transform. The classic
485 watershed approach is reported to produce over segmentation results [33], whereas the marker
486 controlled approach does not suffer from this issue and it is reported to be very effective for overlapping
487 cells segmentation even though some authors affirm that it may fail to segment highly overlapped
488 cells ([37], [38], [39], [9], [13], [35], [20], [42], [43], [44]).

489 Other authors, [7], [35], [31], [32], [24]) employed granulometry and stated that it is very effective
490 to segment cells with regular size.

491 The analysed works performed classification phase for different purposes. The majority of them
492 aimed to distinguish among two classes only, malaria infected and noninfected RBCs, or to detect and
493 count parasites in a malaria blood image ([26], [25], [37], [12], [9], [7], [27], [28], [19], [16], [47], [31],
494 [11], [33], [43], [4], [23], [14], [15], [45]).

495 More complex classification strategies aimed to classify parasites into different classes, i.e. different
496 human parasites species [38], [39], [35], [24]), and/or different parasites life stages ([26], [38], [39], [7],
497 [41], [24]).

498 A summary of analysed methods is shown in Table 1. For each approach we report the processing
499 phase where MM is used (preprocessing and/or segmentation), which operators are applied, which
500 type of morphology (grayscale or binary), and shape and size of the used SE, if described. We detail
501 the kind of classification, i.e. if a method addresses the detection problem (infected and non infected)
502 only, if it faces the labelling of different parasites (*P.falciparum*, *P.ovale*, *P.malariae* or *P.vivax*) and, in
503 some cases, the different stages of life (ring, trophozoite, schizont, gametocyte). Finally, the measures
504 used for evaluating the system performance are reported, if present.

505 5. Conclusions

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

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

513 It is worth noticing that cells colours and the colour contrast between cells and background can
514 vary so often according to the different, existing staining techniques, thickness of smear, microscope
515 illumination and microscope's image acquisition procedure, as shown in fig. 1. A standardization
516 of the procedure should be really useful to avoid superfluous differences in similar images' features
517 and to have fair comparisons among the several proposed methods. The main efforts towards the
518 realization of a fully automatic blood cells segmentation and classification system cannot leave this
519 aspect out. Usually, any pattern recognition system is evaluated by performing tests using real set
520 of samples. In case of diagnosis this is a key aspect. Any system for diagnosis should be tested on
521 different images, acquired by different sources, and different specimens. This is crucial to guarantee
522 the diagnostic capability and usefulness of a computer vision system.

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

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

⁵³⁸ analysis, and using feature extraction including image morphological analysis, wavelet analysis, and
⁵³⁹ texture analysis for automated classification of renal cell [48].

⁵⁴⁰ Moreover, non-linear filtering has become increasingly important in many image processing
⁵⁴¹ applications. Initially, the attraction to non-linear filters was mostly limited to the impulse-removing
⁵⁴² and edge-preserving qualities of the median filter. However, as the number and sophistication of
⁵⁴³ non-linear filters have increased, so has the variety of applications for these filters. The shape-based
⁵⁴⁴ methods of mathematical morphology, in particular, are now used in a wide variety of medical
⁵⁴⁵ applications, including electrocardiography, ultrasound imaging, radiology, and histological image
⁵⁴⁶ analysis [49].

⁵⁴⁷ Furthermore, microscopic image analysis and, in particular, malaria detection and classification
⁵⁴⁸ can greatly benefit from the use of mathematical morphology. The interest in this approach to image
⁵⁴⁹ processing ad analysis is proved by the increasing number of works proposing methods for malaria
⁵⁵⁰ image analysis based on mathematical morphology techniques.

⁵⁵¹ In the end, it is worth considering that the development of new mobility-aware microscopic
⁵⁵² devices (and ideally low cost) is an area that can greatly improve the chances of the successful
⁵⁵³ deployment of computer vision CAD solutions for malaria diagnosis in the field. The mobile phone is
⁵⁵⁴ currently Africa's most important digital technology, and is boosting African health as it emerges as a
⁵⁵⁵ platform for diagnosis and treatment. Considering the recent significant improvements of the new
⁵⁵⁶ generation of mobile devices in terms of image acquisition and processing power, if a reliable automatic
⁵⁵⁷ diagnostic performance is ensured through the usage of those devices, one would dramatically reduce
⁵⁵⁸ the effort in the exhaustive and time consuming activity of microscopic examination. Moreover, the
⁵⁵⁹ lack of highly trained microscopists on malaria diagnosis in rural areas could then be complemented
⁵⁶⁰ by a significantly less specialized technician that knows how to operate the system and prepare blood
⁵⁶¹ smears. The usage of mobile devices in the system architecture can also bring significant improvements
⁵⁶² in terms of portability and data transmission, like the systems proposed by [11] and [8]. Finally, malaria
⁵⁶³ diagnosis might be just one element of a suite of diagnostic software tests running on this type of
⁵⁶⁴ system. Several other tests could simultaneously be carried out using the same images, for instance
⁵⁶⁵ cell counting or detection of other hemoparasites, like microfilaria or trypanosoma [50].

Authors	Preprocessing	Segmentation	MM/SE	Classification	Performance
Anggraini <i>et al.</i> , 2011	-	thresholding + hole filling	gray, bin	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	gray, bin/disk	two (infected and noninfected)	Acc=96.46%
Das <i>et al.</i> , 2011	-	marker controlled watershed + opening, closing	gray, bin	two (infected and noninfected)	Acc=88.77%
Das <i>et al.</i> , 2013	-	marker controlled watershed	gray	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	gray	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	bin	two (infected and noninfected)	Acc=97.83% thin films, Acc=89.88% thick films
Devi <i>et al.</i> , 2017	-	marker controlled watershed	gray	two (infected and noninfected)	Acc=98.02%
Diaz <i>et al.</i> , 2009	-	inclusion tree	gray	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	gray, bin/disk, flat and nonflat, with size depending on RBCs	two (<i>P.falciparum</i> infected and noninfected) + three life-cycle-stages	-
Elter <i>et al.</i> , 2011	-	thresholding + black top-hat, dilation	gray/disk, nonflat with size=9	two (infected and noninfected)	SE=97%
Gonzalez-Betancourt <i>et al.</i> , 2016	morphological filter, erosion-reconstruction, dilation-reconstruction, closing	watershed transform	gray/disk with size depending on RBCs	-	-
Ghosh <i>et al.</i> , 2011	-	thresholding + opening, closing	bin	two (<i>P.vivax</i> infected and noninfected)	-
Kamreem <i>et al.</i> , 2011, 2012	dilation, erosion	-	gray/concentric ring, disk with size depending on RBCs	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	gray	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%
Malihi <i>et al.</i> , 2013	closing	area granulometry	gray/disk with size depending on RBCs	two (infected and noninfected)	Acc=91% SE=80% SP=95.5%
Mushabe <i>et al.</i> , 2013	closing	thresholding + granulometry, dilation, erosion	gray, bin/disk	two (infected and noninfected)	SE=98.5 SP=97.2%
Oliveira <i>et al.</i> , 2017	erosion	gray, bin	-	two (infected and noninfected)	Acc=91%
Reni <i>et al.</i> , 2015	new morphological filtering	-	gray/anular ring, disk with size depending on RBCs	-	-

Romero-Rondon <i>et al.</i> , 2016	dilation, opening	marker controlled watershed, erosion	gray, bin/disk with size depending on RBCs	-	-
Rosado <i>et al.</i> , 2017	-	adaptive thresholding + closing	bin/elliptical with size=3	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	gray, bin/disk with size=6 and depending on RBCs, diamond with size=1	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	bin	two (infected and noninfected)	-
Savkare <i>et al.</i> , 2011b	-	thresholding + hole filling, watershed transform	bin	two (infected and noninfected)	SE=93.12% SP=93.17%
Savkare <i>et al.</i> , 2015	-	thresholding + watershed transform, erosion, dilation	bin/disk with size=2	two (infected and noninfected)	Acc=95.5%
Sheikhhosseini <i>et al.</i> , 2013	hole filling	thresholding + hole filling, opening	bin	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	bin/square with size=3	two (infected and noninfected)	SE=98% SP=93.3%
Somasekar <i>et al.</i> , 2017	-	thresholding + erosion, closing, hole filling	bin/square with size=3	two (infected and noninfected)	average DSC=0.8
Špringl, 2009	closing	thresholding + marker controlled watershed transform, hole filling, dilation, opening, erosion	gray, bin/disk with size depending on RBCs	two (infected and noninfected)	AUC=0.98
Sulistyawati <i>et al.</i> , 2015	-	blob analysis + erosion, dilation, opening, closing, hole filling	bin	two (infected and noninfected)	Acc=99.39%
Tek <i>et al.</i> , 2006	-	top-hat, infinite reconstruction, area granulometry	gray, bin	two (infected and noninfected)	SE=74% SP=98%

Tek <i>et al.</i> , 2010	closing, granulometry	thresholding + granulometry, area top-hat, closing, area granulometry	gray/disk with size depending on RBCs	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	bin	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, type of MM (gray or binary)/type and size of SE (if reported), kind of classification and performance measures (Sensitivity, Specificity, Accuracy, if reported).

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Abbreviations

The following abbreviations are used in this manuscript:

CBC	Complete Blood Count
WBC	White Blood Cell
RBC	Red Blood Cell
MM	Mathematical Morphology
MP	Malaria Parasite
SE	Structuring Element

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