Final Segmenting Schistosomiasis on Hyperspectral imaging

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Abstract: Schistosomiasis is a disease caused by parasitic worms and is also called as bilharzias or snail fever. To propose and validate an image segmentation algorithm designed to overcome the distinct challenges posed by schistosomes and macro parasites in general, including irregular shapes and sizes, dense groups of touching parasites and the unpredictable effects of drug exposure. Schistosomiasis is considered one of the Neglected Tropical Diseases. The combined concept will be based on a region-based distributing function with a novel edge detector which is derived from phase congruency and grayscale thinning by the threshold superposition. Image segmentation algorithm is designed in order to overcome the distinct challenges posed by schistosomes. Hyperspectral analysis of the parasite is made for the deeper analyzing of the bilharzia. The application of high-throughput screening method to the other parasitic disease. The highly conservative nature of grayscale morphological thinning by superposition is hosted collaboration system.

Keywords: High-throughput screening (HTS), Hosted Collaboration Solution (HCS), Hysteresis thresholding, Schistosomiasis, image segmentation, Neglected Tropical Diseases (NTD)

I. INTRODUCTION

Schistosomiasis is a chronic parasitic disease in tropical and subtropical regions and is associated with a variety of clinical syndromes that may lead to severe morbidity [1-2]. Over the past 25 years, therapy and control of schistosomiasis has come to rely heavily on one drug, praziquantel (PZQ) [29]. This reliance is of concern should widespread treatment failure arise, particularly as measures are being undertaken to increase PZQ's availability. In image processing and computer vision, gradient operators are widely used as a substrate for the detection of edges and estimation of their local orientation [22].The disease is spread by contact with water contaminated with the parasites. These parasites have been released from their fresh water snail hosts [30]. The disease is especially common among children in developing countries as they are more likely to play in contaminated water [16]. Application to discredited signals requires a new definition, or at the very least a consistent extension of the continuous definition. The disease is worse for children who can develop anemia, learning difficulties and malnutrition [12]. After years of infection eggs inflame organs such as the liver, bladder and lungs. If eggs end up in the brain or spinal cord, they can cause paralysis[20], seizures or inflammation of the spinal cord. Schistosoma species can migrate around and are not bound to just one location [11]. But each species has a preferred location.

The World Health Organization estimates that as many as 200 million people are infected in parts of South America, Africa and Asia [30]. Approximately 280 000 people die from schistosomiasis each year in sub-Saharan Africa and millions more are chronically ill [1]. Typical symptoms include abdominal pain, diarrhoea, fever, anaemia and fatigue [14]; the stunting of children's growth and cognitive development is another consequence of infection [13]. Schistosomiasis remains an important public health problem in developing countries [4]. It is difficult to devise reliable universal rules to merge the over-segmented regions in different cases [12]. The situation becomes even worse when the intensities vary within a large range .The detection of Schistosoma eggs in feces or urine is diagnostic of schistosomiasis. The extent of shedding of eggs may fluctuate widely, and as many as three specimens may be required in some patients.

II. LITERATURE SURVEY

Although occurrence of the disease in developed countries is extremely low, more than 200 million people are infected worldwide, with an additional 800 million at risk [30]. The chronic illness is caused by infection with one of several species of trematodes [24], chiefly Schistosoma mansoni, Schistosoma haematobium, and Schistosoma japonicum, which are carried to humans through water contaminated with their larvae [5]. Early on, infection is characterized by an inflammatory response to the parasites' eggs, eventually leading to fibrotic granulomas that can occlude the hepatic portal vein and cause hydronephrosis (kidney swelling from urine buildup) [28] and squamous cell bladder cancer [35]. Other effects of schistosomiasis include diarrhea, lesions in the central nervous system and genital sores which enhance the transmission of HIV [12]. Formulating the model in terms of level set functions and compute the associated Euler–Lagrange equations [17]. Edge detection methods that are used traditionally on the image gradient [10]. For nearly 40 years, the drug Praziquantel (PZQ) has provided what is essentially the only avenue of treatment for schistosomiasis.

While PZQ has some desirable properties—it is a single-dose drug effective against all major Schistosoma species which infect humans[26]—it also has a number of side effects, as well as a variable rate-of-cure as low as 60% and a lower activity against juvenile parasites [2].WHO considers schistosomiasis a disease for which new treatments are urgently needed [3]. Hyperspectral imaging (HSI) offers high potential as a non-invasive diagnostic tool for disease detection [18].Hyperspectral imaging proved to be highly suitable for the detection, identification and quantification of fungal disease [15].

III. METHODOLOGY

A. Existing Method

The preset methods have been introduced for screening drugs against helminthic diseases [11]. The only such screening system aside from our previous work does not employ a novel segmentation algorithm and in particular simply discards touching or highly irregular individuals. In contrast to parasites [20], segmentation and tracking of cells has been an active research area for some time [7], and several approaches undertaking the segmentation of touching cells have been proposed [27]. The general problem of defining feature similarity incorporating a variety of cues is not a trivial one [26]. The grouping cues could be of different abstraction levels and types and they could be in conflict with each other [3]. Furthermore, the weighting function could vary from image region to image region [38], particularly in a textured image. Some of these issues are addressed in [15]. The accompanying first-order differentiation filter is not necessarily optimal with respect to the first-order constraint in isolation [15]. The watersheds transform to derive minimal edges which reproduce the correct

topology while satisfying the principle of maximum parsimony [14]. Spectral graph theory provides us some guidance on the goodness of the approximation to the normalized cut provided by the second eigenvalue of the normalized Laplacian [22].

B. ***Proposed Method***

The proposed method includes a novel, high-sensitivity edge operator which combines phase congruency with ridge-detection by grayscale thinning [7]. The power and generality of the phase congruency approach to edge strength, and the highly conservative nature of grayscale morphological thinning by superposition[9], our detector has broad applicability in the relatively common case that there are edges at a wide range of phase angles[27], which may or may not have strong directional maxima across their entire contour [13]. Quantitative and qualitative analysis of segmentation results under multiple experimental conditions demonstrate the wide applicability of the algorithm [3]. The hyperspectral pixels in a small neighborhood around the test pixel are simultaneously represented by linear combinations of a few common training samples, which are weighted with a different set of coefficients for each pixel [19].

C. ***Watershed Algorithm***

S. Beucher and F. Meyer introduced in an algorithmic inter-pixel definition of the watershed, given the following procedure [15]:

1. Label each minimum with a distinct label. Initialize a set S with the labeled nodes.

2. Extract from S a node x of minimal altitude F, that is to say $F(x) = \min \{F(y)|y \in S\}$. Attribute the label of x to each non-labeled node y adjacent to x, and insert y in S.

Previous notions focus on catchment basins, but not to the produced separating line [13]. The topological watershed was introduced by M [29]. Couprie and G. Bertrand in 1997,[4] and beneficiate of the following fundamental property[24]. A function W is a watershed of a function F if and only if $W \leq F$ and W preserves the contrast between the regional minima of F; [10]where the contrast between two regional minima M1 and M2 is defined as the minimal altitude to which one must climb in order to go from M1 to M2[10]. Increasing the Level parameter merges segments in the original image to produce an output with fewer labeled regions [12]. To view segments with "softer" boundaries (often finer detailed structures), set the level to a lower value. Raise the Level parameter to capture grosser structures with more defined boundaries [14]. After a merge hierarchy has been created, changing the Level parameter can produce a new output in constant time as long as the Level is not raised above its initial setting [25].If F(x) and H(x) are the real and the imaginary component of spatial and imaginary frequencies then

$$E(x) = \sqrt{F^2(x) + H^2(x)} \quad \text{..... (3.4.1)}$$

The filter saves state between updates and only re-executes if the requested Level is not already in the hierarchy (or the input data has changed)[19]. Most of the complexity of the watershed algorithm is in the generation of the hierarchy, and experience shows that for many medical image data sets, only the first 10-20 percent of the complete hierarchy is of interest [11]. Setting the Level to a low value can therefore significantly save computation time [8]. The Segmentation is done by two main stages [19]. In the first stage connected plateaus of the pixels are explored [13]. Plateaus of minima are uniquely labeled while the distance to a lower border for pixels within plateaus of non-minima is computed [24]. This lower distance is used to transform the gradient image into a lower

complete one [20]. In the second stage a uniform rain over the topological surface is simulated. From each pixel a droplet starts sliding on the steepest slope line towards a minimum from which the label is propagated backwards along the whole path [22]. Hyperspectral imaging is an novel tool with high potential for non-invasive sensing of the physiological status of flora [12-14] and may allow an purpose and automatic assessment of the severity of plant diseases in combination with continuative data analysis methods[20].The Imaging sensor allow a pixel-wise attribution of disease-specific symptoms and healthy tissue and improve both[13], the specificity and sensitivity of disease detection by technical sensors[24].

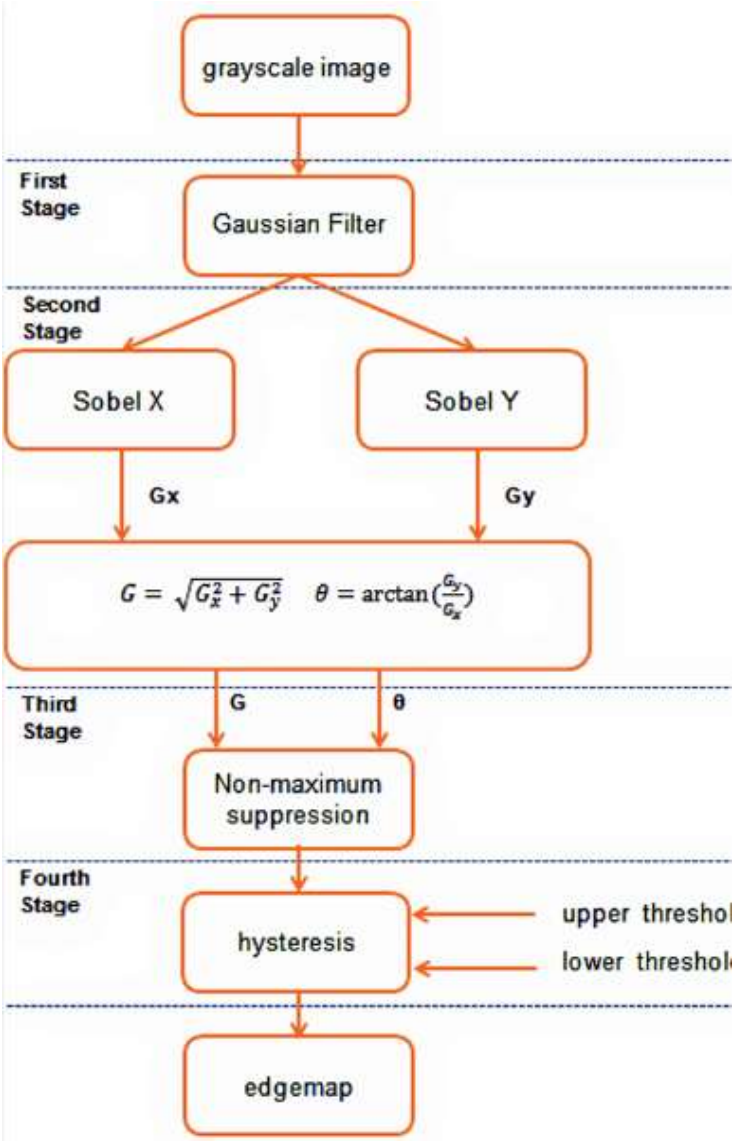

Figure 1: The Block Diagram of watershed segmentation

The figure 1 shows the gray scale image that is taken as input and it will be filtered using Gaussian filter and then it will be entering the second stage Sobel operation. Then it will enter the third stage where the non maximum suppression of the image will be processed. The fourth stage will be hysteresis stage and upper threshold and lower threshold. The output will be the edgemap.

D. *Advantages*

An important advantage of this watershed algorithm is its suitability for parallel implementation. While, immersion is a global method [24]. In topography, this occurs the point lies in the catchment basin of that minimum [13]. The final output image will be hyperspectralized with the image tool and it will made familiar and deeper understanding of the disease [5].Hyperspectral imaging acquires a three-dimensional dataset called hypercube, with the two spatial dimensions and one spectral dimension [18].Deeper analysis can be made by using the Hyperspectral tool and the output can be further made for the production of the medicine for curing this disease [25]. The measures can be taken for the formal detecting of the deeper and the needed in the watershed segmentation process [1].

IV. SCHISTOSOMIASIS LOCALIZATION

Schistosomiasis annoy more than 250 million people in regions of tropical and subtropical [17]. The disease is causing agents are blood flukes of the genus Schistosoma and infected by the contaminated water and the parasite pierce the skin [28]. Then migrating through the lungs and liver, the developing Schistosoma japonicum and S. mansoni parasites take up residence in the mesenteric veins, where male and female worms mature and reproduce [18]. Each day, female schistosomes produce numerous eggs which move through the intestinal wall into the lumen of the bowel and are shed with the feces [3].The pathology associated with schistosomiasis caused by S.japonica and S.mansoni is primarily a consequence of inflammatory responses to eggs inadvertently carried to the liver and other sites [16]. Female worms release thousands of eggs which are passed out of the body in the urine and feces [12]. If people urinate or defecate in bodies of freshwater, the eggs migrate to snails where they eventually hatch and begin the cycle again [17]. Some Schistosoma eggs, [24] however, remain trapped in the body and migrate to specific organs (depending on the type of parasite) where they can inflict major damage[23]. Urinary schistosomiasis causes scarring and tearing of the bladder and kidneys, and can lead to bladder cancer [19]. Hyperspectral imaging is expected to improve disease detection through a better examination of host-pathogen interactions [15,16]. Imaging sensor systems allow a pixel-wise attribution of disease-specific symptoms and healthy tissue and improve both, the specificity and sensitivity of disease detection by technical sensors [13].

V. EXPERIMENTAL RESULTS

The hyperspectral imaging data in the spectral angle classification algorithm that is used for the recognition of dissimilar subareas of disease-specific symptoms and their quantification [1]. The segmentation is largely accurate and most touching parasites are still split into discrete regions[19],attesting to the sensitivity of phase congruency to perceptual edge features[48], as well as to the robustness of the method as a whole against the prevalence of debris and other noise sources[30]. HSI generally covers a contiguous portion of the light spectrum with more spectral bands and higher spectral resolution than multispectral imaging [9]. HSI has the potential to capture the subtle spectral differences under different pathological conditions [19], while multispectral imaging may miss significant spectral information for diagnostics [23]. The filter saves state between updates and only re-executes if the requested Level is not already in the hierarchy (or the input data has changed)[30]. Most of the complexity of the watershed algorithm is in the generation of the hierarchy, and experience shows that for many medical image data sets [14], only the first 10-20 percent of the complete hierarchy is of interest [22]. Setting the Level to a low value can therefore significantly save computation time [17]. the segmentation is largely accurate and most touching parasites are still split

into discrete regions [26], attesting to the sensitivity of phase congruency to perceptual edge features, as well as to the robustness of the method as a whole against the prevalence of debris and other noise sources [10].The original image will be changed into the next gray level image on the basis of the hyper spectral image analysis. The need for the analysis will be based on the needed analysis of the parasitic disease. In the needed content of the basic use for the deeper and easier analyzing of the content to be made in the farther one in the hyper spectral images. The organization decomposes the hyperspectral image into a false color image, containing thematic information of the previously selected classes. The input hyperspecttral image is shown in figure 2 and then Region of Interest image is shown in figure 3.The internally analyzed hyper spectral image is shown in the figure 4. The segmented hyper spectral image is shown in figure 6.4.Then finally segmented hyper spectral image is shown in the figure 6.The measure over the processed hyper spectral image is shown in the figure 7.

VI. SCREEN SHOTS

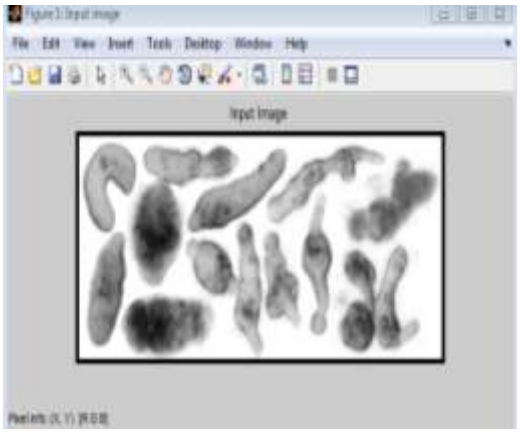

Figure: 2 Input hyperspectral image

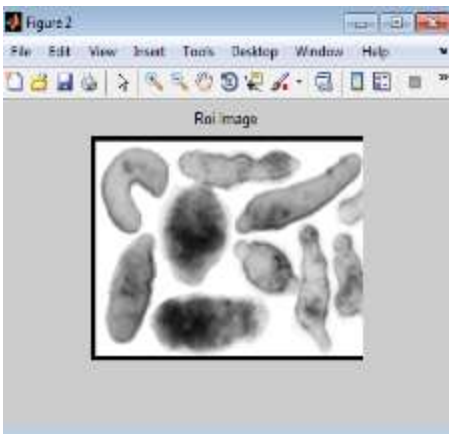

Figure: 3 ROI hyperspectral image

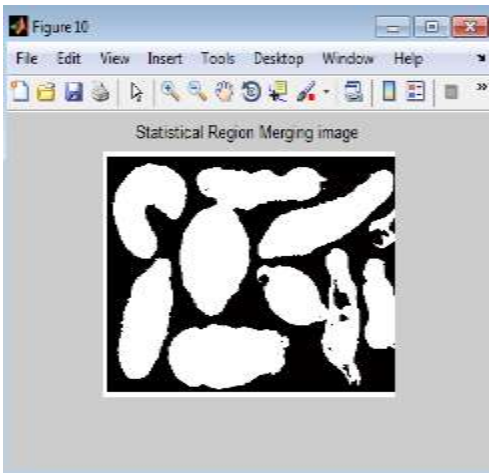

Figure: 4 Internal analyzed hyperspectral image

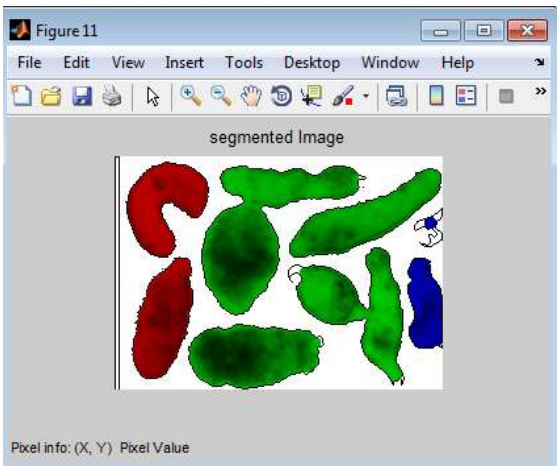

Figure: 5 Segmenting Hyperspectral image

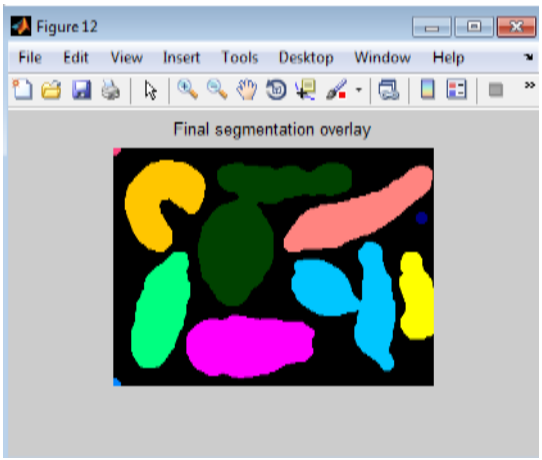

Figure: 6 Final Segmenting Hyperspectral image

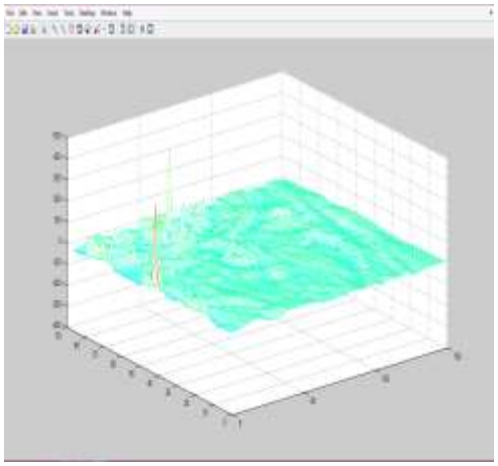

Figure: 7 Measure over the Processed Hyperspectral Image

VII. CONCLUSION

Abandoned diseases are a schistosomiasis which will represent a serious inclusive health issue. To present a segmentation algorithm designed specifically towards the segmentation of standard, bright-field microscopy images of schistosomes[1], which is robust against variegated natural and drug induced phenotypes, and which does not depend on any proprietary HTS systems[21]. The method includes a novel, high-sensitivity edge operator which, to the best of the knowledge, is the first to combine phase congruency with ridge-detection by grayscale thinning [10]. To submit that due to the power and generality of the phase congruency approach to edge strength[17], and the highly conservative nature of grayscale morphological thinning by superposition, our detector has broad applicability in the relatively common case that there are edges at a wide range of phase angles, which may or may not have strong directional maxima across their entire contour[19].The measure over the aspects of the Hyperspectral image make an aspect of the one that will provide the basis of the known type in the usefulness of the one which will make learn the details of the image[6]. The usefulness in the needed contents will make the note for the easier access of the watershed algorithm process.

VIII. FUTURE WORKS

The Hyperspectral analysis makes the useful access technique for the needed aspects of the parasite. Interms the proposed method will is truly high -throughput, phenotypic screen against schistosomiasis and lead both to the discovery of new drugs against this disease and lay ground work towards the application of HTS methods to other parasitic illnesses. We currently engaged with our collaborators in producing a publically available repository for data from HCS of parasites, and in developing publicly available software encompassing multiple stages of HCS data analysis, from segmentation to automated discovery of drug induced phenotypes. The time of computation is to be increased and the efficiency is also needed to be increased. The complexity of the watershed algorithm can be overcome and some of the new technique in the needed basis of the various details is detailed and it will be more helpful in the medical field.

IX. REFERENCES

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