MUSCLE INJURY DETERMINATION BY IMAGE SEGMENTATION

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Abstract—Congenital Muscular Torticollis (CMT) clinical examination is mainly carried out by ultrasound equipments. However, different subjectivities during diagnosis may result in wrong decisions. In this paper, we perform experiments on the animal muscle injury and propose an algorithm to derive an objective judgment on the fibrosis of muscle. In our implementation, we first apply the fast scanning algorithm for muscle image segmentation, and then analyze the segmentation results based on the proposed algorithm to determine the healthiness of muscle fibers. We furthermore propose a scoring criterion to evaluate the extent of injury. The experimental results show that the injury score determined by the proposed method can successfully help us to determine if the muscle is hurt or not and even infer the degree of fibrosis.

Keywords—image segmentation; ultrasonography; biomedical image processing; muscle injury; fibrosis

I. INTRODUCTION

In the past few decades, the ultrasonography played a very important role on clinical, e.g. internal medicine, gynecology and obstetrics. With the advance in technology, the probe head of the ultrasonic wave equipment has better and better performance. For the conventional diagnosis by X-ray, we cannot observe the slight muscle structure change as well as the pathological change of subcutaneous tissue. In contrast, the higher frequency launched from the ultrasonic probe head can capture more details of structure, e.g. muscle disorder, tumor, and tendon rupture in high-resolution supersonic diagnostic set.

The ultrasonography is the main method of the present diagnosis and the tracing studies of Congenital Muscle Torticollis (CMT) in children. Nevertheless, the operation of the ultrasonic diagnostic set and the interpretation of the acquired data require considerable experiences and training. In addition, different organisms have different body structures. Even for the same species, there exist several varieties. The professional knowledge cannot be learned in a short period.

Although CMT is a dynamic disease [1] and the neuromuscular composition is relatively complex, the echo intensity of ultrasound image has significant difference between the normal controls and patients with neuromuscular diseases, but no significant relationship with muscle thickness [2]. The smaller echo intensity represents the lower degree of muscle fibrosis [3] and presents white line in the ultrasound image. A white line is a healthy muscle fiber in the ultrasound image. As regards, an unhealthy muscle fiber must have been a complete healthy muscle fiber, but since the disease or hurt, a healthy muscle fiber will break into fractions of short fiber called unhealthy muscle fiber. The muscle fibrosis of CMT can be extended to the fibrosis of animal muscle injuries. The fibrosis theorems of CMT and animal muscle injuries are very similar. So that for convenience to do biopsy, we feed 18 mice for our simulations and propose an injury scoring method to infer the degree of muscle fibrosis. We expect this algorithm could also be applied to diagnose CMT in children. In order to avoid misdiagnosis caused by subjectivity, the healthy muscle and unhealthy muscle are shown in Fig. 1.

In our algorithm, we first apply the fast scanning algorithm [4] to segment the image of mouse muscle. The advantages of the fast scanning algorithm are that each cluster is connected and has similar pixel value. So based on the segmentation results of the fast scanning algorithm, we can directly find the healthy muscle fiber and the unhealthy muscle fiber in the ultrasound image, and then derive the injury score determined by the proposed method. According to the injury score, we can judge that if the muscle is hurt or not and even compare the injury score with the fibrosis determined by coloring agent (the fibrosis $\in [0, 1]$). The experiment of fibrosis determined by coloring agent is referred to [5]. Then we acquire a quadratic regression equation between the injury score and the fibrosis determined by color-
ing agent. This quadratic regression equation let us conjecture the fibrosis from the injury score.

This paper is organized as follows. In Section 2, we briefly review the concept of the fast scanning algorithm. In Section 3, we propose our algorithm about how to derive the injury score, and several simulation results in Section 4 show that our algorithm definitely determine the state of health of mouse. Conclusions are made in section 5.

II. FAST SCANNING ALGORITHM FOR IMAGE SEGMENTATION

We first apply a segmentation algorithm to the image of muscle. There are several methods of segmentation presented in [6], [7], [8], e.g. region growing, watershed, and K-means. However, we select the fast scanning algorithm for our implementation because of this algorithm is faster than other existing segmentation algorithm. Besides, the advantages of the fast scanning algorithm are that each cluster is connected and has similar pixel value. The concept of fast scanning algorithm is to scan from the upper-left corner to lower-right corner of the whole image and see if we can merge the pixel into an existed clustering. The merged criterion is based on our assigned threshold. If the difference between the pixel value and the average pixel value of the cluster is smaller than the threshold, then this pixel can be merged into the cluster. In this paper, we assign the threshold as 45. We describe the steps of the fast scanning algorithm as below.

**(Step 1):** Let the upper left pixel as the first cluster. Set the pixel \((x, 1)\) in the image as one cluster \(C_i\) and the pixel which we are scanning as \(C_j\).

**(Step 2):** In the first row, we scan the next pixel \((x, 1+1)\) and determine if it can be merged into the first cluster or be a new cluster according to the threshold. The judgments are in the following, where \(\text{mean} \) represents the average pixel value of cluster \(C_i\).

- If \(C_j - \text{mean}(C_i) \leq \text{threshold} \) then we merge \(C_j\) into \(C_i\) and recalculate the mean of \(C_i\).
- If \(C_j - \text{mean}(C_i) > \text{threshold} \) then we set \(C_j\) as a new cluster \(C_{i+1}\).

**(Step 3):** Repeat Step 2 until all the pixels in the first row have been scanned.

**(Step 4):** To scan the pixel \((x+1, 1)\) in the next row and compare this pixel with the cluster \(C_{i+1}\) which is in the upside of it. And determine if we can merge the pixel \((x+1, 1)\) into the cluster \(C_{i+1}\).

- If \(C_{j+1} - \text{mean}(C_{i+1}) \leq \text{threshold} \) then we merge \(C_{j+1}\) into \(C_{i+1}\) and recalculate the mean of \(C_{i+1}\).
- If \(C_{j+1} - \text{mean}(C_{i+1}) > \text{threshold} \) then we set \(C_{j+1}\) as a new cluster \(C_{n+1}\) where \(n\) is the cluster number so far.

**(Step 5):** Scan the next pixel \((x+1, 1+1)\) and compare this pixel with the cluster \(C_{n+1}\) and \(C_i\) which is in the upside of it and in the left side of it, respectively. And decide if we can merge the pixel \((x+1, 1+1)\) into anyone of two clusters.

- If \(C_j - \text{mean}(C_i) \leq \text{threshold} \) and \(C_j - \text{mean}(C_i) \leq \text{threshold} \) then we merge \(C_j\) into \(C_i\) and recalculate the mean of \(C_i\).
- Otherwise, set \(C_j\) as a new cluster \(C_{n+2}\) where \(n\) is the cluster number so far.

**(Step 6):** Repeat Step 4~5 until all the pixels in the image have been scanned.

**(Step 7):** Process the small cluster and let each pixel merge into the clusters adjacent to it.

III. PROPOSED METHOD FOR MUSCLE INJURY DETERMINATION

Conventionally, there are two methods that can determine whether the muscle is hurt and the degree of injury. The first one is to observe by eyes directly. However, this is too subjective and the result is not quantified.

Another method is to use the coloring agent. After the muscle is dyed by coloring agent, the size of the region with dark-blue color reveals the degree of fibrosis and the degree of fibrosis is closely related to the degree of injury. The method is useful in experiment. However it is impractical in diagnosis, since it is impossible to cut the muscle of a patient and dye the muscle.

Here, we proposed another method that uses the image segmentation algorithm in Section 2 together with the scoring method in Section 3 to determine whether the muscle is hurt and the degree of injury. This method can be automatically performed by computers and no coloring agent is required. The results are quantified and can be obtain within 2 seconds even using the Matlab.

A. Method of Finding the Healthy Muscle Fiber

The method to determine whether the muscle fiber of mouse broken or not is to analyze the texture of muscle fiber image. In general, the healthy muscle fiber has obvious white line texture in medical images. Consequently, the prior work is to use the fast scanning algorithm to get the clustering results \(C\) (which has \(N\) clusters) of the muscle fiber image, and search for the clusters which look like white line. However, the fast scanning algorithm may result in over-segmentation and divide a white-line-like cluster into several small clusters. In order to recover the desired white-line-like cluster, we have to merge these small clusters together based on their similarities, such as average intensity, distance, and orientation.
In Algorithm 1, we transform an RGB image to a gray level image and enhance the intensity contrast to generate a new image $I_g$ for the purpose of obtaining better segmentation results from the fast scanning algorithm.

After deriving the clusters of the segmentation results, we verify every cluster if anyone is similar to white line according to the average pixel value of cluster and two properties of line. The two properties of line are

\begin{align}
(1) \quad & \frac{\text{area}}{\text{length}} < 0.38 , \\
(2) \quad & \frac{\text{area}}{\text{length}} < 40 .
\end{align}

In the meanwhile, we check the clusters fitted the above properties whether there exist two or more clusters can be merged together.

**Algorithm 1: The fiber finding and merging method**

*Input:* The muscle fiber image of rat $I_{RGB}$.

*Initialization:*

(A) Transform an RGB image to a gray level image and enhance the intensity contrast to generate a new image $I_g$.

(B) $C := $ fastsegment($I_g$)

(C) Find the thresholding pixel value $M_0$.

(D) $Set_c$ is a set for storing the clusters which can be merged as fibers. The initial setting is $\{\}$.

(E) Set add as 0. add is for counting the number of clusters in $Set_c$.

for $i := 1$ to $N$

if $M_i > M_0$ then evaluate

a. $(m_{i,3}, n_{i,1})$: row coordinate value and column coordinate value of the leftmost point of $C_i$, respectively.

b. $(m_{i,2}, n_{i,2})$: the same as $(m_{i,1}, n_{i,1})$ but for the rightmost point of $C_i$.

c. $l_i$: the length of $C_i$.

d. $\text{angle}_i$: the angle between the direction of $C_i$ and the x-axis.

if cluster $C_i$ satisfies (1) & (2) then

if $\text{add} > 0$ then

find out if any cluster in $Set_c$ can merge with $C_i$ (determined by the process of white lines merging).

else then

$\text{add} := \text{add} + 1$;

$Set_c(\text{add}) := C_i$;

$Set_{l}(\text{add}) := (m_{i,1}, n_{i,1})$;

$Set_{r}(\text{add}) := (m_{i,2}, n_{i,2})$;

end

end

end

*The process of white lines merging:*

**Step 1:** Compute the coordinate differences between $C_i$ and $Set_c(j)$, where $j$ is 1 to $\text{add}$, as shown:

\begin{align}
q_1(j) &= \begin{bmatrix} \text{length} \\ \text{area} \end{bmatrix} = \begin{bmatrix} l_i(n_{j,1}) - n_{j,1} \\ l_i(m_{j,1}) - m_{j,1} \end{bmatrix} , \\
q_2(j) &= \begin{bmatrix} \text{length} \\ \text{area} \end{bmatrix} = \begin{bmatrix} r_j(n_{j,2}) - n_{j,2} \\ r_j(m_{j,2}) - m_{j,2} \end{bmatrix} .
\end{align}

**Step 2:** Rotating $q_1$ and $q_2$ according to $\text{angle}_i$, as shown as:

\begin{align}
q_1(j) &= \begin{bmatrix} \cos(\text{angle}_i) & \sin(\text{angle}_i) \\ -\sin(\text{angle}_i) & \cos(\text{angle}_i) \end{bmatrix} * q_1(j) , \\
q_2(j) &= \begin{bmatrix} \cos(\text{angle}_i) & \sin(\text{angle}_i) \\ -\sin(\text{angle}_i) & \cos(\text{angle}_i) \end{bmatrix} * q_2(j) .
\end{align}

\begin{align}
d_{-r_j} &= \max\left[ |q_1(j)(1)|, |q_2(j)(1)| \right] ,
\end{align}

where $d_{-r_j}$ means the maximum of the difference of row coordinate between $C_i$ and $Set_c(j)$.

**Step 3:** Find the cluster $k$ in $Set_c$, which satisfied

a. $d_{-r_j} < 35$.

b. One of types in Fig. 2.

if $k$ exists then

Merge $C_i$ into $Set_c(k)$.

Recalculate $Set_{l}(\text{add}) := (n_{k,1}, n_{k,1})$.

Recalculate $Set_{r}(\text{add}) := (n_{k,2}, n_{k,2})$.

end

end

Figure 2. Three types of two clusters, which can be merged together as a fiber.

In the following process, for verifying if any white lines in $Set_c$ can merge with $C_i$, we rotate the coordinate of the leftmost and rightmost point of lines in $Set_c$ according to the angle of $C_i$. This process makes it easy to compare with those lines based on $C_i$. The two merging rules are in Step 3.
The next work is to find the healthy muscle fiber. The healthy muscle fiber is decided by the length of fiber, which must exceed 80% of the width of the image. The algorithm is presented in Algorithm 2.

Algorithm 2: The healthy muscle fiber finding method

Initialization:
(A) $c := $ image column width.
(B) $h_{len} := 0$ presents the total length of healthy muscle fibers (sum over all fibers).

for $t := 1$ to $add$ do
  if the length of $Set_c(t) > 0.8* c$ then
    $h_{fiber} := h_{fiber} + 1$;
    $h_{len} := h_{len} + $ the length of $Set_c(t)$;
    exclude fiber $Set_c(t)$ from $Set_c$;
  elseif $Set_c(t)$ is one of type in Fig. 3 then
    exclude fiber $Set_c(t)$ from $Set_c$;
end

$NS := $ the size of $Set_c$;

We disregard the clusters in Fig. 3 because those fibers are much likely to be parts of the healthy muscle fibers which are not fully captured by the image, while directly using Algorithm 3 may misclassified them into unhealthy fibers. The summation of the length of healthy muscle fibers is for the purpose of computing injury score in final. The simulation results of Algorithms 1 and 2 are shown in Figs. 6, 10, 14, and 18.

B. Finding the Unhealthy Muscle Fiber

After deciding the healthy muscle fibers, the next step is to find the unhealthy muscle fibers. The unhealthy muscle fiber is composed of several short fibers, so the unhealthy muscle fiber finding method is based on the distance between any two fibers. In Algorithm 3, the distance between any two fibers considers both the horizontal distance and the vertical distance. The vertical distance will be amplified because two fibers in the same vertical position have more chance to compose an unhealthy muscle fiber. Furthermore, if the distance between two fibers is longer than half the image width, they cannot compose an unhealthy muscle fiber since we infer these fibers do not belong to a same healthy muscle fiber when the muscle is health. The simulation results of Algorithm 3 are shown in Figs. 7, 11, 15, and 19.

Algorithm 3: The unhealthy muscle fiber finding method

Initialization:
(A) According to $Set_c$, construct a $NS*NS$ matrix $dist$, which stores the minimum distance between any two fibers in $Set_c$. For example, $dist(p, q) =$ the minimum distance between fiber $p$ and $q$, where $1 \leq p \leq NS$ and $1 \leq q \leq NS$.
(B) Compute the area of each fiber in $Set_c$, called vector $area$.
(C) Compute the length of each fiber in $Set_c$, called vector $nh\_len$.
(D) $bs(p) := 0$ present the broken length of fiber $p$, while there exist elements in $dist < 0.5* c$ do
  Normalize $dist$: $ds(p, q) := \frac{dist(p, q)}{\sqrt{area(p)\cdot area(q)}}$.
  Find the minimum value $ds(u, v)$ in $ds$.
  $area(u) := area(u) + area(v)$;
  $nh\_len(u) := nh\_len(u) + nh\_len(v)$;
  $bs(u) := bs(u) + \text{the broken length between fiber } u \text{ and } v$;
  Merge $Set_c(u)$ into $Set_c(v)$ (delete $Set_c(u)$);
  Recalculate $dist$.
  if $Set_{roof}(nu2) - Set_{roof}(nu1) > 0.85* c$ then
    set the distance between fiber $u$ and other fibers as $c$.
    (means fiber $u$ cannot merge with others)
  end
end

Count the number of the unhealthy muscle fibers in $Set_c$, called $nh\_fiber$.

C. Injury Score

After deriving the healthy muscle fibers and the unhealthy muscle fibers, we can use the total number of fibers, summation of the broken length, and summation of the length of fibers to compute the injury score. So the injury score is presented as

$$Injury\ score = \frac{2*\text{sum}(bs)}{\text{Total length} \cdot \sqrt{\text{Total number}}}, \quad (7)$$

where \( \text{Total length} = \text{sum}(h_{len}) + \text{sum}(nh\_len) \),
\( \text{Total number} = h_{fiber} + nh\_fiber \).

IV. Simulation Results

In our experiment, we have 9 images of the healthy muscle and 9 images of the unhealthy muscle. We show two examples of the healthy muscle in Example 1 and 2, respectively. Furthermore, Example 3 and 4 show two examples of the unhealthy muscle, respectively.

We can choose the threshold as 0.1. If the injury score calculated from (7) is smaller than 0.1, then we can conclude that the muscle is healthy. Otherwise, we can conclude that the muscle is injured.
A. Example 1

Here, we present an image of healthy muscle. In Fig. 4, the left side image is the original image of the healthy muscle and we transform it into gray level image and enhance its intensity contrast. The processed image is shown in the right side.

Fig. 5 is the results of the fast scanning algorithm for the enhanced gray level image of the healthy muscle. The sub-images are sorted according to the size of cluster from large to small. The display order is from left to right and from up to down. We only show the first 20 large clusters in Fig. 5.

After deriving the results of fast scanning algorithm, we apply Algorithm 1 to find the fibers and merge some of them which look like in the same line. The fibers found by Algorithm 1 are shown in Fig. 6.

From Fig. 6, we can see that the first three larger fibers are in accordance with the healthy muscle fiber. The remaining five fibers are the short fibers which cannot be discriminated as the healthy muscle fibers and we have to be decided whether these fibers can be the part of the unhealthy muscle fibers.

Fig. 7 reveals the final results of fiber connection of the healthy muscle fibers and the unhealthy muscle fibers according to Algorithm 3. The first three larger fibers are the healthy muscle fibers and the last fiber is inferred as an unhealthy muscle fiber.

Finally, we can compute the injury score by (7) according to the results of Algorithm 3. The injury score is 0.0384. It is smaller than the threshold 0.1. Thus, we can conclude that the tested muscle in Fig. 4 is healthy.

B. Example 2

We show another image of the healthy muscle in Fig. 8. In Fig. 8, the right side image is the enhanced gray level result of the left side image.

Then we use the fast scanning algorithm to segment the enhanced gray level image of the healthy muscle. Fig. 9 shows the first 20 large segmentation results of Fig. 8.

After deriving the segmentation results in Fig. 9, we can use Algorithm 1 to find the clusters look like the fibers and merge the fibers which may be in a same line. The results are revealed in Fig. 10.

From Fig. 10, we can see that the first three larger fibers are in accordance with the healthy muscle fiber. The remaining two fibers are the short fibers which cannot be regarded as the healthy muscle fibers and we have to use Algorithm 3 to decide whether these fibers can be the part of the unhealthy muscle fibers.

Fig. 11 reveals the final results of fiber connection. The muscle fibers of Example 2 are discriminated as the healthy muscle fibers according to Algorithm 3. There does not exist any unhealthy muscle fiber in the image of Example 2.

In the final step, we can compute the injury score by (7) according to the results of Algorithm 3. The injury score is 0 for Example 2. It also reveals the fact that the tested muscle in Fig. 8 is healthy.

C. Example 3

In Example 2, we present an image of the unhealthy muscle. The operation of Fig. 12 is the same as Fig. 4. The right side image in Fig. 12 is the enhanced gray level result of the left side image.

Subsequently, we apply the fast scanning algorithm to the enhanced gray level image of the unhealthy muscle. The first 20 large clusters are shown in Fig. 13.

According to the results of Fig. 13, we can use Algorithm 1 to find the clusters look like the fibers and merge the fibers which may be in a same line. The results are revealed in Fig. 14.

From Fig. 14, we can discover that there does not exist any fiber in accordance with the healthy muscle fiber. All of them in Fig. 14 are the short fibers and some of them seem as fractions of the unhealthy muscle fibers. So after computing through Algorithm 3, the unhealthy muscle fibers are shown in Fig. 15.

Finally, we can compute the injury score by (7) according to the results of Algorithm 3. The injury score is 0.2756 for Example 3. It is larger than the threshold 0.1 and we can conclude that the tested muscle in Fig. 12 has been hurt.

D. Example 4

Example 4 is an image of the unhealthy muscle. The operation of Fig. 16 is the same as Fig. 4. The right side image in Fig. 16 is the enhanced gray level result of the left side image.

Then we apply the fast scanning algorithm to the enhanced gray level image of the unhealthy muscle. Fig. 17 shows the first 20 large clusters.

According to the results of Fig. 17, we can use Algorithm 1 to find the fiber-like clusters and merge the fibers which may be in a same line. Fig. 18 reveals the results of finding fiber of Algorithm 1.

Fig. 18 shows that there exists no healthy muscle fiber. All of the fibers in Fig. 18 may be fractions of the unhealthy muscle fibers. Then we apply Algorithm 3 to find out the unhealthy muscle fibers shown in Fig. 19.

Eventually, we can compute the injury score by (7) according to the result of Algorithm 3. The injury score is 0.3839 for Example 4. It is much larger than the threshold 0.1 and we can conclude that the muscle in Fig. 16 is injured.
Figure 4. The original image of healthy muscle of Example 1 and its enhanced gray level image.

Figure 5. The segmentation results (using the algorithm in [4]) of Fig. 4.

Figure 6. Sifting the fiber regions from Fig. 5 by Algorithm 1.

Figure 7. Finding the healthy or broken fibers from Fig. 6 by Algorithm 3.

Figure 8. The original image of healthy muscle of Example 2 and its enhanced gray level image.

Figure 9. The segmentation results of Fig. 8.

Figure 10. Sifting the fiber regions from Fig. 9 by Algorithm 1.

Figure 11. Finding the healthy or broken fibers from Fig. 10 by Algorithm 3.
Finding the healthy or broken fibers from Fig. 14 by Algorithm 3.

Figure 12. The original image of unhealthy muscle of Example 3 and its enhanced gray level image.

Figure 13. The segmentation results of Fig. 12.

Figure 14. Sifting the fiber regions from Fig. 13 by Algorithm 1.

Figure 15. Finding the healthy or broken fibers from Fig. 14 by Algorithm 3.

Figure 16. The original image of unhealthy muscle of Example 4 and its enhanced gray level image.

Figure 17. The segmentation results of Fig. 16.

Figure 18. Sifting the fiber regions from Fig. 17 by Algorithm 1.

Figure 19. Finding the healthy or broken fibers from Fig. 18 by Algorithm 3.
E. High Correlation between the Injury Score and the Fibrosis

From Figs. 4-19, we can see that the proposed algorithm will not produce misjudgment with the appearance of the healthy muscle fibers in the image of the unhealthy muscle. In Tables 1 and 2, we show the experiment results for other healthy and unhealthy muscle fibers, respectively. We show the injury scores calculated from (7) and compare it with the fibrosis determined by dyeing the coloring agent (it was described at the beginning of Section 3). We can see that the two data has very high correlation.

According to the experiment results in Table 1 and Table 2, we compute the quadratic regression equation as \( y = 0.4199x^2 + 1.1066x - 0.0352 \) in Fig. 20. Furthermore, the correlation coefficient between the injury score and the fibrosis determined by coloring agent is 0.8964. The high correlation proves the validness of the proposed method.

V. CONCLUSIONS

In this paper, we propose an algorithm to determine the number of healthy muscle fibers and the broken length of unhealthy muscle fibers. We first apply the fast scanning algorithm to segment the image into several clusters. Then we use the ratio of the area to the length to determine whether a region is a fiber. Then we use the broken lengths of fibers to compute the injury score, which reflects the degree of injury of the muscle.

The simulation results show that the proposed algorithm can determine whether a muscle fiber is the healthy or unhealthy validly. Furthermore, the injury score determined by the propose algorithm can also estimate the degree of fibrosis accurately. The result has very high correlation with the fibrosis determined by the conventional method using coloring agent.

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