**A concept for movement-based computerized segmentation of connective tissue in ultrasound imaging**

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**Abstract:**

This study proposes a concept for the computerized segmentation of ultrasound images of connective tissue based on movement. The information on movement is used in the segmentation of connective tissue instead of analysing a static image. Normalised cross-correlation is the algorithm used for the connective tissue segmentation based on movement. Tendons and ligaments are capable of almost frictionless movement relative to their neighbouring tissues making them good candidates for movement-based segmentation. To demonstrate this concept, a central cross section of the patellar tendon was imaged in the axial plane while movement was generated by manually pulling and pushing the skin close to the imaging area. Maps of internal movement were created for four representative pairs of consecutive images using normalised cross corelation. Thresholding followed by a series of morphological operations (k-clustering, blob extraction, curve fitting) enabled the extraction of the superficial-most tendon boundary. Comparison against manually segmented outputs indicated good agreement against ground truth (average±STDEV Bhattacharyya distance: 0.170±0.039). In contrast to the more superficial parts of the tissue, the applied method for motion generation did not result in clearly visible movement in the tissue areas deeper in the imaging window. The segmentation of the entire tendon will require movement patterns that involve equally the entire tendon (e.g., generated by a contraction of the in-series muscle). The results of this study offer an initial proof of concept that movement mapping could be used for the segmentation of connective tissue. Further research will be needed to identify the optimal way to use motion to complement existing segmentation approaches which are based on signal intensity, texture, and shape features.

**Keywords:** tendon, ligament, connective tissue, segmentation algorithm, normalized cross correlation, displacement map.

**1. Introduction:**

Ultrasound used for medical applications sends high frequency sound waves into the body through a transducer probe which is pressed against the skin with a coupling agent (e.g., an aqueous gel) applied on the surface of the skin. When these high frequency sound waves travel between tissue areas with different acoustic properties, they get reflected enabling the imaging of their internal structure.

Ultrasound is commonly used in clinical research and has been advocated by the World Health Organization for monitoring chronic diseases and for screening[1]. Its advantages relative to other imaging modalities include lower cost, high portability, patient/examiner safety (no harmful radiation used) and capacity for real time imaging. At the same time, ultrasound also has some significant drawbacks like: 1) Poor image quality due to image corruption by speckle noise, shadows and attenuation. 2) Dis-continuous boundaries due to orientation dependence during the acquisition of image. 3) Low contrast between nearby anatomical structures. According to literature the effect of these limitations of ultrasound can be minimised with the use of powerful algorithms for computerized segmentation of areas of interest[2].

In the case of connective tissue, computerized segmentation can improve research[3] on their biomechanics and help in the assessment and diagnosis of disease[4, 5]. Tendons and ligaments are both connective tissues characterized by high concentrations of collagen with a structured orientation. Their unique internal structure and composition also leads to a relatively distinctive presentation in ultrasound imaging as well as causing specific imaging artefacts (e.g. dependance of tissue echogenicity on the relative orientation between probe and collagen fibers) [6]. Tendons are connected to muscle and bone and their role is to facilitate movement while ligaments connect bones together to offer support. Even though their function is different their structure and appearance in ultrasound is similar. There is high acoustic impedance difference between connective tissue and the soft tissue that surrounds it leading to the creation of hyperechoic (bright) regions around tendons/ligaments. However, this bright region could expand within the connective tissue as well as in the surrounding soft tissue making the exact segmentation of the interface between tissues very challenging.

So far, the most common segmentation methodology used for ultrasound images of connective tissue are Model based segmentation, machine learning and deep learning methods. Even though these methods are algorithmicaly distinctive they all rely on the same type of input information and try to distinguish the region of interest based on an analysis of signal intensity, texture, and shape features. The process of distinguishing and labelling the region of interest based on signal intensity, texture and shape features is called as object recognition [7–10]. However, in the case of ultrasound imaging of connective tissue such information might not be sufficient for the accurate segmentation of the tissue’s boundaries. In such cases video analytics[11–14] where the pattern of movement is also considered could enhance the analysis[15], however this approach has not as yet been tested in the case of medical imaging.

To stimulate more research in this area, this paper proposes a concept of connective tissue segmentation based on movement. Following a brief presentation of existing methods that have been previously used for connective tissue, normalised cross-correlation (NCC) will be employed for segmentation based on movement. Finally, the application of this method will be demonstrated for a typical connective tissue (i.e., patellar tendon).

**2. Existing segmentation methodologies for connective tissue:**

A structured review of literature using PubMed on computerized segmentation of connective tissue revealed six papers on the segmentation of tendons [16–21] and three on the segmentation of ligaments [22–24]. The methods used in these studies included active contour approaches [17, 22, 25, 26], Chan-Vese [27], adaptive texture based active shape model [18], active shape models[28], curvelet transform [4], and convolutional neural networks (CNN) [29].

Sultan et.al. (2016) [16] segmented the finger extensor tendon from an ultrasound image using an active contour approach. The specific targeted application was for the assessment of rheumatoid arthritis. Rheumatoid arthritis affects the joints of the hand. This disease causes inflammation of the metacarpophalangeal joint present in the joint capsule region. Extensor tendons are structures present above the metacarpophalangeal joint. When the size of the joint increases due to arthritis, the distance between the joint and extensor tendon increases. Hence bone segmentation in joint and tendon segmentation is essential for inflammation assessment in the metacarpophalangeal joint. According to the method used by Sultan et al. [16] the ultrasound image was first converted into grey scale followed by inverting the image (converting black areas to white & vice versa). In the next step, pre-processing and enhancing the tendon region is performed by Log Gabor filters. At the end of this step, ridge like tendon structures were visualized above the metacarpal and phalangeal bone. Morphological thinning/ skeletonization was done to preserve the boundary and shape of the object while the structures belonging to adjacent to the tendon regions were removed using the median filter. Smoother tendon regions were obtained by further morphological operations (dilation followed by erosion) which join the disconnected boundaries followed by spline curve fitting. The resulted ridge-like structure was used as the first estimation of the tendon boundary to initialize the active contour segmentation process[16, 30]. Similarly, Martins et.al. (2018) [31] segmented the extensor tendon using phase symmetry pre-processing followed by segmentation using an active contour approach. Because the tendon was imaged in the longitudinal direction it could be assumed that its boundaries will be aligned in the horizontal direction of the image. Based on that, phase symmetry pre-processing was used to remove the vertical components present in the image. The resulted shape was then used as an initial contour for the active contour segmentation method[30, 31].

The active contour method was also used by Singh et.al. (2015)[22] to segment the anterior talofibular ligament[22, 30]. The overall process was done in three steps. In the first step, the region of interest was manually delineated (approximated by a rectangle, circle or a random shape). Then in the second step, optimization of the region of interest was accomplished using Darwinian particle swarm optimization [32] for the extraction of more specific ligament boundary. The contour obtained from the second step was given as the initial contour for contour deformation in the active contour method [30]. A similar approach was also used in Singh et.al (2017) [26] to segment the calcaneofibular ligament [26, 30]. However in this case, the optimization step was done using fractional order - Darwinian particle swarm optimization [33]. Fractional order - Darwinian particle swarm optimization reduces the number of iterations needed compared to Darwinian particle swarm optimization.

Among the major limitations of the active contour method is that edge/gradient information that is used to guide contour deformation is not reliable in ultrasound due to the presence of speckle noise and imaging artifacts[34]. To address this limitation a Chan-Vese approach was used in the segmentation of the anterior talofibular ligament[27, 35]. The overall process was done in three steps. In the first step, the region of interest was manually delineated. Then in the second step, optimization of the region of interest was accomplished using particle swarm optimization [36]. The contour obtained from the second step was used as the initial contour for contour deformation in the Chan-Vese method[37].

Chuang et.al. [18] (2014) also focused on the segmentation of finger tendons for the assessment of trigger finger pathology. In this case the tendon was imaged in the axial plane and segmentation was performed using adaptive texture based active shape model. This process consists of two phases training and segmentation. In the first phase, training dataset of manually segmented tendons was created with the help of experts. All the segmented contours were aligned to the same phase and then the mean of the contour was calculated. The point distribution model was created using principal component analysis. The point distribution model consists of a mean contour shape and tuneable parameters for defining the shape of the model to fit the target during the segmentation phase. Since the image quality in ultrasound is relatively poor in addition to the curvature and intensity feature in the energy function, texture information was also added to enhance the accuracy of the segmented output. A genetic algorithm[38] was used to help the model avoid getting stuck in local minima. One of the main disadvantages of this approach is that the combination of texture, shape and gradient information substantially increases computational complexity of the method. To address this issue, Ramakrishnan et.al. (2019) removed the texture information from the energy function[19]. Even though computational complexity was indeed reduced this was achieved at a cost to accuracy.

Gupta et.al. (2014)[4] segmented the supraspinatus tendon from an ultrasound image using curvelet transform [39]. In the first step, contrast enhancement was done using Rayleigh adaptive contrast enhancement [40]. This is because speckle noise (i.e. the dominant type of noise in ultrasound) follows the Raleigh distribution. Then the enhanced image was de-speckled with anisotropic diffusion [41] before feature extraction using curvelet transform. The coefficients of the curvelet transform were higher in the region surrounding the tendon than within the tendon. This enabled selecting the tendon area using a thresholding operation. Gupta et al. defined this threshold by analysing the pixel intensity values of the bursae and cortex area from more than 100 images[42]. Connected component analysis and area filtering were done in the following steps to remove blobs that are not part of the tendon. Morphological processing (dilation, erosion, 4th order polynomial curve fitting) was done after area filtering to produce a smoother tendon boundary.

Because of the computational complexity of ATASM, Kuok et.al. (2020) [21] performed automatic segmentation of finger tendon using deeply supervised dilated FC-Dense Net (D2FC-DN). Deeply supervised nets allow learning in a direct and transparent manner with training performed layer-wise to improve the classification accuracy. Deeply supervised nets were combined with dilated FC nets which use multi-scale feature information to maintain the resolution.

Even though these methods are algorithmically different, they are all affected by the inherent limitations of ultrasound imaging. For example, active contour, active shape and curvelet transform methods all rely on edge/gradient information to segment the region of interest. However this type of information is known to be very unreliable in ultrasound imaging due to the presence of speckle noise and imaging artifacts which in turn also reduce the accuracy of the segmented outputs[34, 43]. At the same time machine learning-based approaches require large training datasets of manually segmented images [44, 45]. However, the production of accurate training datasets is made very challenging by the speckle noise, discontinued boundaries, and low contrast of ultrasound images [46].

**3. Proposed movement-based methodology:**

To address this inherent problem of low image quality in ultrasound, this paper proposes to include information on movement in the segmentation for connective tissue. Instead of analysing a static image, movement-based segmentation analyses a series of images of a moving object to segment based on a movement differential between the targeted object and its background. Even though the analysis of videos can pose its own challenges[47–49] it also enables using motion as a feature for segmentation when the region of interest is unable to be differentiated from its surroundings based on colour, intensity, texture, gradient features[15]. Therefore, the application of such segmentation approaches relies on accurate methods for motion estimation. At the same time, the application of movement-based segmentation methods in ultrasound would also require reliable and reproducible methods for generating distinctive movement patterns in the targeted tissue.

**3.1 Movement generation**

Connective tissues are capable of almost frictionless movement relative to their neighbouring tissues. This unique feature makes them ideal for movement-based segmentation. However, to achieve that there is a need for a protocol to generate movement that does not significantly distort the tendon/ ligament and, at the same time, it generates a distinctive pattern of movement that highlights their boundaries. For relatively superficial tissues this movement protocol could be released by the examiner pulling and pushing the skin near the imaging area using gentle lateral movements. Such movements should move the subcutaneous soft tissue relative to the connective tissue. In this case movement mapping should reveal an abrupt change in displacement on the boundary between connective and subcutaneous tissue enabling its segmentation.

**3.2 Movement mapping**

The most common methods for the assessment of movement are sum of absolute differences [50], sum of squared differences [51], optical flow [52] and NCC [53]. Out of these methods, NCC was considered to be most the preferable. This is because of NCC’s ability to handle relatively large displacements and the fact that it has already been successfully used to analyse movement in tendon ultrasound images[54]. In this instance the remaining methods were not included in this analysis because of specific limitations which were likely to compromise their accuracy for the intended application. More specifically, optical flow is considered preferable in cases where the pixel displacement is small compared with the speckle size[55], which might not be the case here[54]. Sum of absolute differences cannot accurately handle the variations in spatial brightness we expect to find in an ultrasound image because of the lack of a normalization term[56]. Similarly, sum of squared differences cannot handle illumination changes which is handled in a robust manner by NCC [57].

NCC is used in the estimation of pixel displacement between two frames of a video to create a movement colour map[58]. A detailed flowchart of how NCC was utilised can be seen in figure I. Consider a pixel ‘l’ occupying a position (s, t) in the first frame. Determine its position in the successive frame of the video. First, a square window (kernel window) of size gh is created around the central pixel position ‘l’ in the first frame. Then again, a square window (search window) of size no is created around the same central pixel position in the next frame. The size of the search window is significantly greater than the kernel window. The NCC value is calculated for all possible positions of the kernel window within the search window. This results in a (g+n-1) (g+n-1) matrix where the highest value corresponds to the best prediction about the displaced position of the kernel window within the search window. If this maximum NCC value is higher or equal than 0.7 then it is concluded that the calculated displacement is reliable. NCC≥0.7 is used as the criterion for good cross correlation based on experiments on porcine and cadaveric tissues [53, 59].

In the present study, NCC between two windows f(g,h) and f(n,o) is determined by equation (1) []

Let f(g,h) denote the intensity value of the kernel window in the first frame of size Mg x Mh , where g g– 1}, h h -1} and f(n,o) denotes the intensity value of the search window in the second frame of size Nn x No , where n n -1},o o -1}.

----------------- (1)

Where f(g,h) – Intensity value of the kernel window of size Mg x Mh

f(n,o) - Intensity value of the search window of size Nn x No

– mean value of the first template

– mean value of the f(g,h) in the region under the second template f(n,o).

In this study both windows were assumed to be square matrices, in which case g=h and n=o.

This procedure is repeated for all pixels in the two frames keeping the size of the kernel and search windows constant. When the maximum NCC value satisfies the good cross correlation criterion (≥0.7), then the displaced pixel position (a, b) is recorded. The difference in coordinates along the depth (X axis) and along the width (Y axis) of the imaging window are stored in separate matrices (M1, M2 respectively). For M1 and M2 matrices, the convention will be that positive movement will be movement from right to left and from the bottom to the top of the image. The total absolute displacement between frames is also calculated (equation 2) and stored in a separate matrix (M3) (Figure II).

Total Displacement = -------------------- (2)

The size of the kernel and search windows are very important parameters for the reliable and computationally efficient use of this method. If the kernel window is too small, then the tracking process is likely to fail. If the kernel window is too large, then there is a probability of important features being missed during tracking. At the same time, the search window must be sufficiently larger than the kernel window to allow for tracking to take place. However, if it is too large then this will negatively impact the computational efficiency of the method and increase the risk of random erroneous results. In the present study the size of the kernel and search windows was decided through trial-and-error process. Their final sizes were 5x5 and 9x9 for kernel and search windows respectively.

At the end, the M1, M2 and M3 matrices are used to create colour maps of movement in the reference frame. Pixels where the good cross correlation criterion was not met are painted black.

Once the map of movement is produced, a segmentation process is used to extract the boundary of the tendon. In the present study this was done using a simple thresholding process followed by K-means clustering. K-means clustering classifies the input image into k number of clusters based on feature similarity. In our application, k=2 to obtain the dominant tissue region. In the next step, the output image from K-means clustering is converted to a binary image and the largest region is obtain using area filtering (blob-extraction). Finally, boundary tracing and curve fitting (6th order polynomial) enables the extraction of the boundary of the tissue of interest.

**4. Demonstration for the patellar tendon**

The proposed methodology was used for the patellar tendon to test the hypothesis that the boundary of connective tissue can be segmented based on movement.

* 1. **Methods**

The patellar tendon of a healthy volunteer (age:25y, weight:95kgr, height:170cm) was imaged using a linear array ultrasound probe (Esaote, LA435, 6-18MHz). During imaging the volunteer was in a seated position with both knees at 90deg. The examiner held the probe in the axial plane to image a central cross section of the left patellar tendon. Movement was generated by gently pushing and pulling the skin between the tendon and the ultrasound probe while ultrasound images were continuously recorded for 3 seconds at 38Hz (Supplementary material A). A stand-off material was used to improve docking between the ultrasound transducer and the surface of the knee.

The previously described computerized methodology was used to segment the patellar tendon based on movement. After visually inspecting the recorded images (115 frames in total) four pairs of consecutive frames were selected for analysis (pair A: frames 40-41, pair B: frames 52-53, pair C: frames 75-76, pair D: frames 109-110). What all these frames had in common was that they were recorded during the pull phase of the pull/push movement protocol and that internal movement could be visually detected. The first of each one of these pairs of frames was used as reference in the calculation of movement.

The accuracy of the computerized movement-based segmentation was assessed against manual segmentation. A bespoke graphical user interface (GUI) was created to facilitate this validation process. Starting from a reference image, the GUI continuously plays a short clip (10 frames) ending to the reference frame that enables visualising movement between the tendon and subcutaneous tissue. It then freezes the clip on the reference frame enabling the operator to place markers on the tendon boundary by clicking on the screen. This process can be done in iterations with the operator viewing the clip and gradually outlining the tendon. Once completed, the GUI automatically connects all manually placed markers with line segments to create a continuous contour. The bespoke GUI was used by a person with more than 5 years of experience on musculoskeletal ultrasound to segment the aforementioned reference frames.

The agreement of the computerized movement-based segmentation with the manually segmented tendon boundary was quantified using Bhattacharyya distance[60]. Bhattacharyya distance measures the amount of overlap/similarity between two probability distributions. To this end, each contour is considered as a probability distribution. The Bhattacharyya distance is defined by equation 3. The closer Bhattacharyya distance is to zero the higher the level of agreement between contours.

DB (l,m) = ----------------------------(3)

Where σl2, σm2 is the variance of lth and mth distribution respectively, µl, µm the mean of the lth and mth distribution respectively, and l, m are two contour distributions.

One sided students’ t-test was also used for the images with the lowest Bhattacharyya distance to test whether random removal of boundary points has a signifcant effect on the level of agreement with ground truth. To this end, twenty indepentent random samples of boundary points were created. During each sampling process, 5% of the total number of estimated tendon boundary points were removed and the Bhattacharyya distance was calcualted. After performing the random sampling twenty times, one sided students’ t-test was conducted with 5% level of significance over the computed distances. The null hypothesis and alternative hypothesis for the one-sided students’ t-test are as follows:

Null hypothesis () : Level of agreement between the ground truth and the algorithm estimated skin tendon boundary is not affected by random sampling.

Alternative hypothesis (): Level of agreement between the ground truth and the algorithm estimated skin tendon boundary is affected by random sampling.

The t-statistic is calculated by using (4)

t-statistic =(q-pm)/(std.dev./√(N-1)) ------------------------------------------------------------------------ (4)

where q and std.dev are the average and standard deviation of Bhattacharya distances obtained after random sampling respectively; pm is the population mean of Bhattacharya distance (without random sampling); N is the number of random samplings.

**4.2 Results**

Mapping of movement reveals a clear difference between the tendon and subcutaneous tissue in the Y direction (Figure II, M2 matrix). More specifically, during imaging the skin is pulled from left to right resulting in a negative displacement in the subcutaneous tissue of around ≈-1pixel (pixel size: 0.08mm0.08mm). At the same time the tendon appears to move in the opposite direction (displacement ≈+2pixel). Since the ultrasound probe was not rigidly fixed, this apparent positive displacement of the tendon can be explained by a lateral movement of the probe in the direction of pull. In the case of movement along the X axis, M1 reveals some movement near the edges of the tendon, with the subcutaneous tissue near the left tendon edge moving upwards (displacement ≈+1pixel) and tissue in the right tendon edge moving downwards (displacement ≈-2pixel). Even though there is a clear pattern of movement this does not seem to differentiate between tendon and its neighbouring tissues (Figure II). Similarly, total absolute displacement (M3) also does not appear to offer a clear picture of tendon boundaries. In this case the problem is the loss of information on the direction of movement. Detailed data on the calculated M1, M2 and M3 matrices for all analysed pairs of frames can be found in Supplementary material B.

The fact that tendon and subcutaneous tissue move in opposite directions means that a simple thresholding operation that isolates pixels with displacement higher than 0 pixels can provide a first definition of tendon outline. Postprocessing using thresholding, blob extraction, boundary tracing and curve fitting enables the extraction of tendon boundaries (Figure III).

Even though this process enabled the extraction of an estimated boundary for the entire tendon, movement could only be clearly visualised closer to skin. Based on that, it was decided the comparison against manual segmentation to focus only on the superficial-most tendon boundary.

Visual comparison between the computerized segmentation output and manual segmentation shows relatively good agreement for the superficial tendon boundary. However, some differences also appear close to the left/right edges of the tendon (Figure III). In quantitative terms the Bhattacharyya distance between computerized and manual segmentation was 0.136, 0.138, 0.202 and 0.206 for frames 40, 52, 75 and 109 respectively.

The obtained t-statitics for the effect of random sampling was 1.349 (frame 40). This was compared against the critical t-value with 5% level of signifcance and 19 degrees of freedom (1.729). Since the t-statistics is lower than the critical t-value the null hypothesis is accepted, namely the level of agreement between the ground truth and the movement-based estimated boundary is not affected by random sampling.

**5. Conclusions**

This research offers an initial proof of concept that movement mapping could be used to enhance the segmentation of connective tissue. The approach that is proposed here involves the manual generation of movement in the tissue and the use of NCC for the mapping of movement between consecutive ultrasound images.

In this study, movement was generated manually by pulling and pushing the skin near the imaged tissues. This movement pattern generated visible differences in displacement close to the skin surface between the patellar tendon and the subcutaneous tissue along the Y axis (i.e. the direction of the pull/push movement) enabling the accurate segmentation of the tendon’s superficial-most boundary. However, the used external movement pattern did not appear capable of generating substantial displacement deeper in the tissue, which will be a barrier for accurate movement-based segmentation of the tendon’s deeper-most boundary. The segmentation of the entire tendon will require movement patterns that affect equally the entire tendon outline (e.g. generated by a contraction of the in-series muscle).

Once the map of movement was calculated, then a series of postprocessing steps were followed to isolate and outline the tendon. The first step involved a simple thresholding operation. This was made possible because tendon and subcutaneous tissue appeared to move in different directions (Figure III,M2). The use of different movement patterns is also likely to require the use of different methods to map movement and of more sophisticated approaches for the segmentation of the map of motion. With regards to the method for movement mapping, the magnitude of displacements appeared to be low relative to pixel size, which means that other approaches such as optical flow could also be applicable.

In this study movement-based segmentation was used on its own to demonstrate the feasibility and potential value of this approach. Moving forward, further research will be needed to identify the optimal way to use motion to complement existing segmentation approaches which are based on signal intensity, texture, and shape features [4, 17, 18, 22, 25–29]. Even though the focus of this paper was on connective tissue, the concept of movement-based segmentation could be applicable in any tissue where a displacement differential can be generated on its boundary to significantly enhance computerized segmentation of ultrasound images.

**Declaration of Competing Interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

**Availability of data and material**

The video that is used in this study can be found in Supplementary material A. The calculated matrices for movement along the X axis (M1), Y axis (M2) as well as the absolute total displacement (M3) can be found in Supplementary material B.

**Code availability**

Available upon request

**Authors' contributions**

Ananth Hari Ramakrishnan and Panagiotis Chatzistergos developed the theoretical framework of the presented idea. All the authors were involved into the planning and implementation of the theoretical framework. Kannan Krithivasan and Madhusudhana Rao Nalluri verified the correctness of the proposed idea. Panagiotis Chatzistergos and Nachiappan Chockalingam collected the original ultrasound video of Patellar tendon that is used in the present study. Analysis on the results obtained and the inferences drawn from the analysis were critically evaluated by Panagiotis Chatzistergos. Ananth Hari Ramakrishnan wrote the manuscript and revising the manuscript critically for important intellectual content was done together by Panagiotis Chatzistergos and Muthaiah Rajappa. Muthaiah Rajappa supervised the entire work. Funding acquisition was done together by Panagiotis Chatzistergos, Nachiappan Chockalingam and Muthaiah Rajappa. All authors provided critical feedback and helped to shape the research, analysis and manuscript.

**Acknowledgment**

This work has been supported by the UK-India Education and Research Initiative (UKIERI) grant ‘Ultrasound based assessment of tissue biomechanics to enhance the clinical management of foot related pathologies’ (Project reference number: DST/INT/UK/P-145/2016). Financial support was also obtained from Department of Science and Technology (DST), New Delhi. The authors would also like to thank TATA Realty-IT City - SASTRA Srinivasa Ramanujam Research cell of SASTRA University.

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**Figure legends:**

Figure I: A flowchart of the application of NCC to produce a colour map of movement. Diagram

Description automatically generated

Figure II. Typical results for M1, M2 and M3 matrices quantifying displacement along the X direction, Y direction and the absolute total displacement respectively (frames 40-41). The direction of skin pull is also shown for reference.

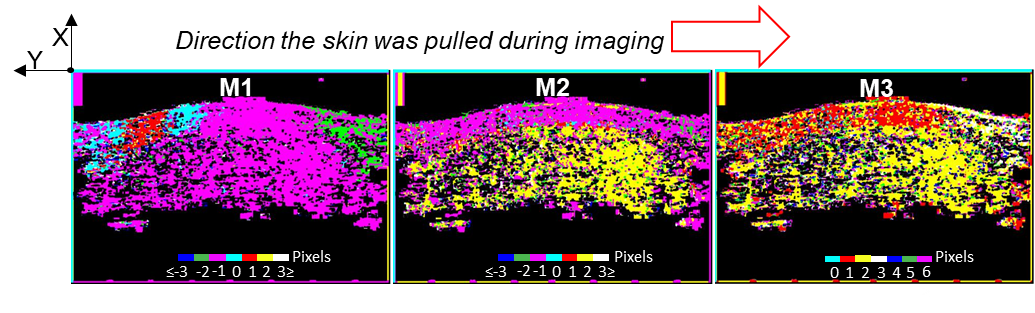


Figure III. The key postprocessing steps for computerized extraction of tendon boundaries based on movement. The manually segmented boundary is also shown for comparison.

