Classification of muscles from ultrasound image sequences

Master’s Thesis in Electrical Engineering

Affan Mustofadee
Abstract

The analysis of the health condition in Rheumatoid Arthritis (RA) remains a qualitative process dependent on visual inspection by a clinician. Fully automatic techniques that can accurately classify the health of the muscle have yet to be developed. The intended purpose of this work is to develop a novel spatio-temporal technique to assist in a rehabilitation program framework, by identifying motion features inherited in the muscles in order to classify them as either healthy or diseased. Experiments are based on ultrasound image sequences during which the muscles were undergoing contraction. The proposed system uses an optical flow technique to estimate the velocity of contraction. Analyzing and manipulating the velocity vectors reveal valuable information which encourages the extraction of motion features to discriminate the healthy against the sick. Experimental results for classification prove helpful in essential developments of therapy processes and the performance of the system has been validated by the cross-validation technique “leave-one-out”. The method leads to an analytical description of both the global and local muscle’s features in a way which enables the derivation of an appropriate strategy for classification. To our knowledge this is the first reported spatio-temporal method developed and evaluated for RA assessment. In addition, the progress of physical therapy to improve strength of muscles in RA patients has also been evaluated by the features used for classification.
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Mathematical Notation

The following designations of letters are used in this report to differentiate the three main types of mathematical functions, scalars, vectors and matrices.

1.) **Scalars**: normal or Italic, capital or small, eg., R, LS, s, v

2.) **Vectors**: bold and small, eg., v, r, s

3.) **Matrices**: bold and capital, eg., R, T, I
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1. Background

Human beings have suffered from diseases for thousands of years and the medical capability of stopping the spread of or curing disease once present has gradually developed over time. Although medical technology and knowledge concerning disease have progressed significantly over the past few decades, there are still a large number of diseases that cannot be completely eradicated. Examples of such diseases are cardiac failure, diabetes, and rheumatoid arthritis. These diseases are said to be chronic meaning that they persist for a long time, or worse still, a lifetime [2], [3], [4].

The kind of chronic disease studied in this project is Rheumatoid Arthritis (RA). The idea is to help RA patients who are suffering in their daily lives and are hoping that one day a perfect cure would exist so they can live a normal life in terms of occupation, family and social activities. Gaining more knowledge about the RA disease and especially how the muscles are affected by RA can help to develop more effective and individually-designed rehabilitation programs. An important amount of work has been devoted towards improving the existing process of rehabilitation. This research intends to pursue this line of work.

“Everyone is made of atoms. With every breath you take, some of my atoms are in it and become part of you and likewise yours become part of me. In this sense, we are all one!”[1]

The above fact gives a powerful impression of how atoms are recycled in the make-up of individual living being. It also explains how naturally we are connected to one another. Provided that we can, there is no good reason why we should not put our best efforts into helping patients suffering from complaints. Gaining a good background of the problem (in this case the disorder) is always an appropriate point of departure in any research project. For this reason a brief elaboration on the characteristics of RA disease is presented.

1.1 Rheumatoid Arthritis

The most basic question would be why this disorder is called Rheumatoid Arthritis. Simply put, Arthritis is inflammation of joints and Rheumatoid can be referred to muscles and bones. Combining these two words, Rheumatoid arthritis can be described as a disease that causes inflammation of joints, muscles, and it leads to destruction of the joint causing pain, swelling and loss of motion. This disease has been around for centuries and there is still little knowledge about what causes the development of the disease although numerous prospects have been contemplated over the years [2]. Presently, a cure for rheumatoid arthritis does not exist but fortunately it can, in some cases, be fully controlled. However, many different types of treatment can be used to alleviate symptoms or to amend the disease process. Until today, the utmost treatments can alleviate the suffering of the patient and prevent a further destruction of the joints. RA
tends to affect small joints particularly in hands, wrists and knees. In this study we concentrate on the joint and muscle affections in the hands.

The pressure that the deformity puts on surrounding tissues and muscles causes muscle weakness. RA muscle weakness is not only painful but can result in patients being unable to do simple tasks such as lifting items. During flares, RA patients experience difficulty in performing simple tasks of every day living such as lifting a cup of coffee or opening jars. The sign and symptoms of rheumatoid arthritis may come and go over time. They include:

- Pain and swelling in joints.
- Stiffness of the joints and muscles, especially after sleep.
- Lost of motion of the affected joints.
- Deformity of joints over time.
- General sense of not feeling well.

Typically, RA affected several joints at the same time especially the joints in the wrists, hands, feet and knees. Shoulders, elbows, hips, jaw and neck could become involve as the disease progresses. Although the exact causes of RA are uncertain, the following factor may increase the risk:

- Being female.
- Smoking cigarettes over a long period of time.
- Ageing.
- Inheriting specific genes which may increase susceptibility to RA.

We can summarize RA symptoms as follows:

1. RA can range from relatively mild to severe.
2. The outlook cannot be predicted for an individual when the disease starts.
3. RA can be treated to reduce pain, stiffness, and damage to joints.
4. Living a healthy lifestyle such as not smoking, eating healthily, taking regular exercise can help to reduce the risk of being affected.

Figure 1.1: A deformed hand due to RA
1.2 Motivation of research

The hand is used in many ways and in many different situations in our daily lives, and it has been well documented that injuries, disease and deformities of the hand affect the quality of life. In RA, which affects about 1% of the population in Sweden, the hands are frequently affected by pain, weakness and restricted mobility. RA is found throughout the world and affects all ethnic groups. It may strike at any age, but its prevalence increases with age; the peak incidence being between the fourth and sixth decades. The prevalence is about 2½ times higher in women than in men. RA patients experience both joint and muscle symptoms. Pain and tenderness of the joints are well described and documented [5], but there is less knowledge concerning how the muscles are influenced by the disease. An important part of hand function is based on the function of the muscles that are involved in finger and wrist motion and in the development of gripping force. The force that can be generated is dependent on the muscle architecture [6-8] including aspects such as muscle fibre length, muscle pennation angle, the contraction pattern, the muscle thickness and the muscle volume. These architectural parameters have not previously been examined or analysed in RA patients.

Several methods of evaluating hand and finger function are available [9], but these do not measure detailed changes in muscle architecture and function. Increased knowledge about muscle morphology and function in RA will allow better diagnosis and evaluation of interventions, such as surgical procedures, physiotherapy and/or pharmacological treatment. In the longer perspective it may be possible to establish a more efficient rehabilitation programme for RA patients.

1.3 Specific purpose of study/Research goal

The principal aim of this study is to classify the muscles by motion analysis in the forearms from ultrasound image sequences in the engineering point of view. These images correspond to both the healthy and the RA muscles. In this research we made a purposeful use of image analysis in medical study as it seems to be an appropriate technique for this task. The study of living tissues, commonly called in vivo, generally takes place within a living biological organism but with image analysis the study can be carried out secluded from the organs. Two well-known methods for capturing the in vivo activities are ultrasound imaging (US) and magnetic resonance imaging (MRI). These two medical imaging methods are necessary for in vivo biological study where in vitro these methods might not be as much needed since the study can be carried out in isolation from the organs. Why is classification necessary? Muscular motion is relatively complex and mere visual inspection from ultra-sound image sequences does not provide an extensive comprehension of the contraction pattern. A real understanding can only be acquired through a thorough examination and by classification we can at least extract some meaningful parameters of muscular health. To achieve the specified task, a system for muscle classification is to be developed. A system can be categorized into two types: 1) hardware realization – made up of physical components as in electrical, mechanical or hydraulic systems and 2) software realization-is an algorithm that computes an output from an input signal. This project aims at developing a software realization system which
focuses on algorithm development. Upon completion, this algorithm should be able to classify whether the input signal (muscle) is healthy or sick (RA). It is anticipated that the work in this research could at least help refine or increase the scientific knowledge in both the image analysis and medical fields which in turn can help RA patients.

2. Methodology

All image sequences and data come from the recorded ultrasound measurements of relevant subjects - see Table 1 in Appendix. All measurements and data recording were performed as in section 2.1.

2.1 Data capturing

According to [11], twenty healthy women and twenty unhealthy (RA) women aged 35-80 years were used as subjects. Ultrasound measurements were made in a relaxed position of the hand as well as in full contraction. Muscle cross-sectional area (CSA), pennation angle and contraction patterns were measured with ultrasound. Finger extension force was measured using a newly developed finger force measurement device. Figure 2.1 shows the measuring device and how fingers were placed for force measurement. To measure the force, each subject extended his/her fingers with as much force as possible against the wall of the device for a maximum period of four seconds. Ultrasound images were taken according to the position showed in Figure 2.2 in which the corresponding muscle is also shown. All ultrasound (US) examinations were performed with a Siemens Acuson Aspen system using a 7.5 MHz linear transducer (38 mm width). The dynamic images were recorded digitally as cine-loops.

Figure 2.1: Finger force measurement device

Each subject was supposed to take a measurement four times for the evaluation of the progress in the muscles after each successive therapy. That would provide 160 dynamic images for analysis from 40 subjects but there are only 137 images, 78 from the healthy subjects and 59 from the RA due to the occasional absence of some patients. Nonetheless, these sample images seem to be sufficient for the study. The information associated with
each image such as finger extension force, age of patient, size of image and number of frames can be manipulated in a way that facilitates the process of algorithm development.

Figure 2.2: US Scanning position and its corresponding image. The region within the white dots is used for analysis.

2.2 Basic Approach/Motion Analysis

When observing the image sequences, without applying image analysis, there is a similarity of the texture among healthy aged muscles and RA muscles and this similarity could complicate the classification task if texture analysis was to be carried out. On the other hand, there is a more noticeable distinction in motion between healthy and RA muscles, for all ages, serving to indicate that motion analysis could possibly be a suitable approach for classification.

Figure 2.3 illustrates the whole idea of the system to be trained. The system will be trained with a range of healthy and unhealthy image sequences in an attempt to provide the system with knowledge of motion pattern. Upon completion, motion features or parameters that distinguish between the healthy and sick should be uncovered and this system could be tested with arbitrary image sequences providing the output as for instance, the number 1 and 0 indicating either healthy or sick muscles respectively.

Motion determination, as in other areas of image processing, is swamped with a multitude of approaches [13] but due to the complex contraction pattern of muscles, relatively few approaches are suitable. Hence, seeking for appropriate methods can be considered a crucial step in this study.
Optical Flow

In image analysis, a common way to estimate the motion of an object in an image sequence is by computing the optical flow. Optical flow is often a convenient and useful image motion representation. In brief, optical flow is an estimation of the evident motion of objects in an image. The algorithm developed in the process can calculate the correlations between near frames in an image sequence. The result is a vector field originating or terminating at each pixel or region in a dynamic image. In actual fact, motion and gray value changes are not identical. The interpretation of intensity variation as pure relative motion is restrictive because velocity is a geometric quantity independent of illumination conditions. In essence, the optical flow can be defined as the flow of gray values in the image plane whereas a real motion of the object in a 3-D scene that is projected onto the image plane is referred to as “motion field”. Motion field in an image is the factual quantity we wish to extract from the image sequence but the optical flow is what we observe. It is reasonable to regard optical flow as motion field if and only if the irradiance (gray value) on the image plane of the moving objects does not change. However this is true only in very restricted circumstances. Two typical examples that demonstrate an inequality of motion field and the optical flow were presented by Horn [12]. Thus, it is entirely dependent on how significant the deviations are, in order that in practical situations the equivalence of optical flow and motion field is acceptable.

It is essential, at this point, to clarify the principal use of optical flow concept to achieve the objective of research. As pointed out in section 1.3, the research goal is to classify the muscle’s health; thus our main focus is to find the difference in motion of muscles between the healthy and RA subjects. As motion was projected onto a 2-D image plane by ultrasonic imaging, the analysis of motion is indeed an investigation of image flow in the sequence. As the goal is not to reconstruct 3D motion of the muscles, it has no
significant impact on our goal if optical flow could not accurately represent the true motion as long as it reflects the image changes due to motion during the time of the muscle’s contraction. Providing that the quality and resolution of ultrasonic image sequences of both the healthy and the RA are of a satisfactory level, we are allowed to apply Optical Flow techniques. However, the fact that image sequences were captured by the same ultrasonic equipment with the same scanning mode can decrease the gap between optical flow and motion field.

For the past few decades, many methods have been proposed for the computation of optical flow such as differential, tensor, correlation, and phase methods [13]. These four techniques are considered as elementary motion estimators. Due to the time constraint in acquiring a thorough comprehension of all techniques and time required for implementation, only differential and tensor methods described in [14] were put into practice.

Note that the two methods (Differential and Tensor) are based on direct manipulation of pixels in an image, thus they are in the category of spatial domain processing, where the term spatial domain refers to the image plane itself. The theoretical basis of both the methods is not entirely new and is now commonly accepted. Even so, this background material deserves a review because it is so crucial that all analysis carried out in this research involved velocity vectors estimated by the two methods. Thus understanding how these vectors are derived can help us to appreciate the physical meaning of numerical results.

2.3.1 Differential Method

Suppose that the image intensity is given by \( I(x,y,t) \) which is a function of time \( t \) as well as of the image coordinates \( x \) and \( y \). The intensity of the moving object at a small time later can be written as \( I(x + dx, y + dy, t + dt) \) where \( dx, dy \) denote an infinitesimal change of object’s position in the image plane by the elapsed time \( dt \).

The basic concept relies on the assumption that the intensity of the object remains constant in the image before and afterwards throughout the entire sequence. Provided that this is a justifiable assumption, we can then develop an algorithm for optical flow computation.

Based on this assumption,

\[
I(x + dx, y + dy, t + dt) = I(x,y,t) \quad \text{intensity remains unchanged} \quad (1)
\]

According to Taylor’s series theorem:

\[
f(x) = f(xo + h) = f(xo) + f' (xo) h + \frac{1}{2} f'' (xo) h^2 + \ldots \text{ where } h = x - xo
\]

Prime sign indicates partial derivative of \( f \).
The same concept of Taylor’s series is also valid for multivariable function as in our case the intensity function. As \( h \) approaches 0 we can now express the intensity in terms of its derivatives as

\[
I(x + dx, y + dy, t + dt) = I(x, y, t) + \frac{\partial I(x, y, t)}{\partial x} dx + \frac{\partial I(x, y, t)}{\partial y} dy + \frac{\partial I(x, y, t)}{\partial t} dt
\]

the second and higher order terms are assumed negligible.

In line with (1) we then have that,

\[
\frac{\partial I(x, y, t)}{\partial x} dx + \frac{\partial I(x, y, t)}{\partial y} dy + \frac{\partial I(x, y, t)}{\partial t} dt = 0
\]  

(2)

dividing (2) by \( dt \) gives

\[
\frac{\partial I(x, y, t)}{\partial x} \frac{dx}{dt} + \frac{\partial I(x, y, t)}{\partial y} \frac{dy}{dt} + \frac{\partial I(x, y, t)}{\partial t} \frac{dt}{dt} = 0
\]

(3)

The terms \( \frac{dx}{dt} \) and \( \frac{dy}{dt} \) stand for the speed of the object moving in x and y directions respectively.

Rearranging the equation in (3), and let \( V_x = \frac{dx}{dt} \), \( V_y = \frac{dy}{dt} \):

\[
-\frac{\partial I(x, y, t)}{\partial t} = \frac{\partial I(x, y, t)}{\partial x} V_x + \frac{\partial I(x, y, t)}{\partial y} V_y
\]

(4) BCCE

This is called the Brightness Constancy Constraint or BCC equation. \( \frac{\partial I(x, y, t)}{\partial t} \) tells us how fast the intensity is changing with time, whereas \( \frac{\partial I(x, y, t)}{\partial x} \) and \( \frac{\partial I(x, y, t)}{\partial y} \) correspond to the spatial rates of change of intensity across the image plane. These three quantities are assumed to be known at a given space-time x, y, t.

The starting point for differential methods begins at BCCE in which there are two unknown variables \( V_x \) and \( V_y \) respectively in a single scalar equation. Thus we can not determine the optical flow unambiguously with first-order derivatives at a single point in the space-time image. In place of a single point, we are allowed to use a small neighborhood to determine the optical flow assuming that BCCE holds in this region of image points at a given time t. However in this way we generally end up with an overdetermined equation system.
This system using the equation \( \mathbf{d} = -\mathbf{D} \mathbf{v} \) can not be solved exactly but only by minimizing an error functional. One type of standard solution is the method of Least-Square or LS, and can be obtained by multiplying the equation with \( \mathbf{D}^T \). From Linear Algebra we know that any matrix with dimension MxN multiplied by its transpose would result in a square matrix of dimension N, in this case a 2x2 matrix for solving the unknown \( \mathbf{v} = \begin{bmatrix} V_x \\ V_y \end{bmatrix} \).

\[
\begin{bmatrix}
\frac{\partial I(x_1, y_1, t_0)}{\partial t} \\
\frac{\partial I(x_2, y_2, t_0)}{\partial t} \\
\vdots \\
\frac{\partial I(x_n, y_n, t_0)}{\partial t}
\end{bmatrix} = -
\begin{bmatrix}
\frac{\partial I(x_1, y_1, t_0)}{\partial x} & \frac{\partial I(x_1, y_1, t_0)}{\partial y} \\
\frac{\partial I(x_2, y_2, t_0)}{\partial x} & \frac{\partial I(x_2, y_2, t_0)}{\partial y} \\
\vdots & \vdots \\
\frac{\partial I(x_n, y_n, t_0)}{\partial x} & \frac{\partial I(x_n, y_n, t_0)}{\partial y}
\end{bmatrix}
\begin{bmatrix}
V_x \\
V_y
\end{bmatrix}
\]

\( \mathbf{D}^T \mathbf{d} = -\mathbf{D}^T \mathbf{D} \mathbf{v} \) \hspace{1cm} (5)

\[
\mathbf{D}^T \mathbf{D} = 
\begin{bmatrix}
\sum_{i=1}^{N} \partial_x I(i) \partial_x I(i) & \sum_{i=1}^{N} \partial_x I(i) \partial_y I(i) \\
\sum_{i=1}^{N} \partial_y I(i) \partial_x I(i) & \sum_{i=1}^{N} \partial_y I(i) \partial_y I(i)
\end{bmatrix}
\]

N is the number of image points evaluated in a corresponding neighborhood.

Solving for velocity vectors,

\[
\mathbf{v} = [V_x \ V_y]^T = -(\mathbf{D}^T \mathbf{D})^{-1} \mathbf{D}^T \mathbf{d} \] \hspace{1cm} (6)

Note that \( \mathbf{D}^T \mathbf{D} \) is not always invertible and thus leads to ambiguity in determining optical flow. This ambiguity is commonly known as the “aperture problem” in motion analysis. The above equation is also a quantitative way to discuss about aperture problem.

1. If the matrix \( \mathbf{D}^T \mathbf{D} \) is of full rank, spatial gray value changes in all directions. Then both components of optical flow \( V_x \) and \( V_y \) can be determined.

2. If the matrix \( \mathbf{D}^T \mathbf{D} \) is of rank 1, one eigen value of \( \mathbf{D}^T \mathbf{D} \) is zero. Then only one component of optical flow can be determined (aperture problem).
3. If the matrix $D^T D$ is of rank 0, both the eigenvalues of $D^T D$ are zero. Then the equation can not be solved, no spatial gray value changes in both directions.

It is important to note that only the matrix $D^T D$ determines the type of solution of LS approach. This matrix contains only spatial derivatives; therefore temporal derivatives have less influence on the optical flow estimates. In this respect, the spatial structure of the image entirely determines whether and how accurately optical flow can be estimated.

### 2.3.2 Tensor Method

The tensor method for the analysis of motion constitutes locally oriented structure in space-time images; all that is required is to extend the differential method to three dimensions. Considering the structure tensor $T$, [14]

$$
\sum_{i=1}^{N} T(i) = \sum_{i=1}^{N} \left( \nabla I(i) \right)^T \left( \nabla I(i) \right) = \sum_{i=1}^{N} \left[ \begin{array}{c}
\partial_x I(i) \\
\partial_y I(i) \\
\partial_t I(i)
\end{array} \right] \left[ \begin{array}{c}
\partial_x I(i) \\
\partial_y I(i) \\
\partial_t I(i)
\end{array} \right]
$$

$$
= \left[ \begin{array}{ccc}
\sum_{i=1}^{N} \partial_x I(i) \partial_x I(i) & \sum_{i=1}^{N} \partial_x I(i) \partial_y I(i) & \sum_{i=1}^{N} \partial_x I(i) \partial_t I(i) \\
\sum_{i=1}^{N} \partial_y I(i) \partial_x I(i) & \sum_{i=1}^{N} \partial_y I(i) \partial_y I(i) & \sum_{i=1}^{N} \partial_y I(i) \partial_t I(i) \\
\sum_{i=1}^{N} \partial_t I(i) \partial_x I(i) & \sum_{i=1}^{N} \partial_t I(i) \partial_y I(i) & \sum_{i=1}^{N} \partial_t I(i) \partial_t I(i)
\end{array} \right]
$$

We can distinguish this technique from the differential method by considering the parameters to be estimated in the matrix $T$. The difference can be seen more clearly if the matrix $T$ is partitioned into rectangular smaller matrices generally called blocks, as set out below.

$$
T = \begin{bmatrix}
D^T D & D^T d \\
d^T D & \partial, \partial, I
\end{bmatrix}
$$

$T$ is a symmetric matrix with six regularized products of spatial and temporal derivatives. While the tensor method essentially performs an eigenvalue analysis of all six product terms which will be discussed shortly, the differential method uses the same products but only five of them selectively. Accordingly, the differential method does not take $\delta t \delta x \delta y$ into account. As will be explained, this additional term makes it possible for the tensor method to detect if the local neighbor illustrates a constant velocity or not, i.e. the possibility that differential method is deficient in.
By performing eigen value analysis of this 3x3 symmetric tensor, we can differentiate local structures in space-time images from different classes. There are four different classes of neighborhoods corresponding to a rank from 0 to 3.

**Class 1, Constant gray value:** All entries and eigen value of the structure tensor are zero or in other words $\text{Rank}(T) = 0$.

$$\lambda_1 = \lambda_2 = \lambda_3 = 0$$

No velocity or information on optical flow can be gained. In practice, this situation is easy to identify. The sum of all eigen values should be below a threshold $\varepsilon$ determined by the noise level in the image sequence. For any pixels where this condition is met the eigen value analysis can be skipped.

**Class 2, Spatial orientation and constant motion:** In this case only one eigen value is non zero as the gray value only change in one direction.

$$\lambda_1 > 0, \text{ and } \lambda_2 = \lambda_3 = 0$$

This means that $\text{Rank}(T) = 1$. We can use the ratio:

$$\frac{\lambda_1 - \lambda_2}{\lambda_1 + \lambda_2}$$

to check if this condition is satisfied. If this ratio is larger than a threshold $\gamma < 1$, the eigenvector $e_1 = [k_x, k_y, k_t]^T$ belonging to the largest eigen value $\lambda_1$ can be found. This eigenvector points in the direction of maximum change in gray values. This is in fact a linear symmetry of parallel planes or translating line case where only the normal velocity can be estimated due to the aperture problem. The normal velocity is given by [14],

$$v = -\frac{k_t}{k_x^2 + k_y^2} \left[\begin{array}{c} k_x \\ k_y \end{array}\right]^T$$

(7)

where $k$ denotes corresponding norm of eigen vectors with respect to its coordinate axes.

**Class 3, Distributed spatial structure and constant motion:** This is the case in which only one eigenvalue is zero.

$$\lambda_1, \lambda_2 > 0 \text{ and } \lambda_3 = 0$$

$\text{Rank}(T) = 2$, this is the case in which we have the most information about motion. The ratio below helps to check if this condition is met.

$$\frac{\lambda_1 - \lambda_3}{\lambda_1 + \lambda_3} > \gamma$$
The gamma $\gamma$ is the same as the one in class 2. This is a translating point case and the eigenvector $e_3 = [k_x, k_y, k_t]^T$ associated with the smallest eigenvalue points in the direction of constant gray values. We can track the moving point with the velocity vector computed as:

$$v = \begin{bmatrix} k_x & k_y \\ k_t & \end{bmatrix}^\gamma$$

(8)

Refer to [14] for derivation of the velocity vector.

**Class 4, Distributed spatial structure and non constant motion:** This case only occurs when all the eigenvalues are larger than zero.

$$\lambda_1, \lambda_2, \lambda_3 > 0$$

$\text{Rank}(T) = 3$, full rank. No useful information can be obtained in this case.

**3. Strategy proposals for features extraction**

Clearly even the best feature extraction technique would be weak if they cannot distinguish between healthy and RA muscles. A problem presented here in muscle feature studies is the classification of ambiguous condition in the health of muscles. In this work, we exploit the motion characteristics of a muscle from image sequences. In a motion analysis framework the following proposed strategies aim to extract recognized features of muscular health in order to deliver a prospective technique for classification.

The basic idea relies on the assumption that a 3D muscle’s contraction produces a special 2D motion which is concentrated in the central part (Fig. 2.2) compared to the outer regions.

There are two basic parameters used in extraction

1. **Velocity vectors**, $v$ – Obtained from OF computation, where

   $$\| v \| \Rightarrow \text{Speed of motion}$$
   $$\angle v \Rightarrow \text{direction of motion}$$

2. **Finger force** – External parameter obtained during the measurement process.

The features used to perform classification were extracted by manipulation of these two basic parameters.

Solution approaches include Speed/Direction estimation, Sequential Target Frames analysis, Co-operating Muscle fibers/Linear Symmetry, Local vector field analysis. Note that all OF computation follows the concept and theory described in section 2.3.1.
3.1 One target frame/Multi-frame sequential analysis

Features found to be useful for classification can be divided into two main types, one target frame feature and multi-frame feature. One target frame analysis is the investigation of velocity vectors of optical flow on a single frame in the image sequence as shown in Figure 3.1. Unlike one target frame, multi-frame sequential analysis is the investigation of variation of such vectors with time.

The analysis of both types of feature was carried out both in:

1) Global – Entire region of an image frame.
2) Local – An image frame is partitioned into smaller regions as shown in Figure 3.5. Each region is then analyzed separately.

3.2 One target frame and global feature

The following two techniques were exploited to find global features on a single target frame.

3.2.1 Speed/Dominant direction of motion

The first intuitive approach is to determine the speed and direction of muscle-motion in an image sequence. The determination of these features corresponds to computing the magnitude and trajectory of velocity vector, \( \mathbf{v} \), which represent spatio-temporal changes of gray value in the x and y directions, respectively. Assuming that healthy muscles exhibit rotational motion more than sick muscles do, we can relate the strength of muscles with motion trajectory. We justify this assumption by a mere observation of motion from two sample sequences, in healthy and RA muscles.

The magnitude of the velocity vectors \( \| \mathbf{v} \| \) denotes a speed of muscles’ motion at each computed point on the target image and it is measured in pixel-distance unit. We can find the dominant direction, \( R \), of motion by the following normalization:

\[
R = \frac{\sum_{i=1}^{N} V_{y_i}^2}{\sum_{i=1}^{N} V_{y_i}^2 + \sum_{i=1}^{N} V_{x_i}^2}, \quad \text{where} \quad 0 \leq R \leq 1 \quad \text{and} \quad N \quad \text{is the number of computed points}
\]

\[
R = 1 \leftrightarrow \text{is the dominant direction in y - direction}
\]

\[
R = 0 \leftrightarrow \text{is the dominant direction in x - direction}
\]

Thus \( R \) approaches to 1 is expected for healthy muscles and \( R \) approaches to 0 is expected for the sick.
The speed of muscles is determined by

\[ Speed = \sum_{i=1}^{N} \| v_i \| \]

where N is the number of computed velocity vectors in a frame. A large value of Speed is expected for healthy muscles. Dominant direction R and Speed in a frame may be rough and simple features, but it helps us to be aware of the difference between the two types of muscles.

### 3.2.2 Multiple views of motion

To explore Speed and R in a broader aspect, a computation of Optical Flow (OF) was applied to three different views of the sequence (Fig. 3.1→Fig. 3.3).

Magnitudes and directions are good descriptions of motion characteristics if a precise contraction instance is known. Unknown significant instance of motion results in a great difficulty in the selection of a target frame for the analysis, where only the right target image can display velocity vectors of overall motion. This problem arises from a variation of vector fields when different target frames were chosen. This implies that the motion of muscles is never constant in terms of speed and direction. Therefore, it is unlikely that one target image could give proper details of the overall motion.

- xy-space

![Figure 3.1: An xy-view image sequence illustrated with the target frame used for OF computation (marked in red).](image)
3.3 Multi-frame and global features

Instead of a single target frame, a sequence of target frames was investigated, thus giving an opportunity to record and analyze the changes of muscles’ motion with time. A sequentially storing statistical data computed each target frame such as:

- Speed in average direction, \( \text{Speed} = \frac{1}{N} \sum_{i=1}^{N} v_i \), \( v_i \) – velocity vector at each point

- Average direction, \( \Theta = \angle \sum_{i=1}^{N} v_i \)

- Maximum of speed, \( \text{maximum of} \{ \| v_i \| \}_{i=1}^{N} \)
are used to describe motion features. As each sequence comprises of approximately 30-40 frames, this results in a massive amount of data to be examined. Consequently, we need to apply statistical thinking using a data-oriented approach to understand the relation of the computed data.

### 3.3.1 Force/Total Speed

By making a careful observation about the relationship between force (described in section 2.1) and motion of the muscles, we found that healthy and sick muscles are well distinguished by the two parameters. We assigned to each muscle its generated finger force and its total speed.

\[
Total Speed = \frac{1}{t} \sum_{j=1}^{t} \sum_{i=1}^{N} |r_j|
\]

N = number of vectors in each target image.

\( t = \) number of frames used in the computation.

The computation of Total Speed is in fact the summation of speed described in section 3.2.1 over time.

### 3.3.2 Cooperating Muscle fibers/Linear Symmetry

After a thorough exploration of all statistical data computed in section 3.3, it was found that the variance in dominant direction of velocity vectors seem to be an appropriate feature for classification.

Figure 3.4: Illustration of linear symmetry of velocity vectors. Linear symmetry (LS) is indicated in the red rectangular.

On the assumption that each vector on the target image represents a muscle fibre or a tiny constituent of muscles, we can better perceive the way these minuscule pieces of muscle
co-operate with one another by looking at a vector field. In addition, a contraction pattern resulted from the extension force exerted by these muscle’s components could then be realized on the 2D image sequence. A dominant direction in which the majority of vectors pointed in the image indicates that muscle’s elements are most co-operative in this direction. Figure 3.4 illustrates an example of such co-operative vectors indicating in the red rectangle in which they are pointing to the right. We can estimate the amount of variance in velocity vectors by employing the linear symmetry (LS) approach.

In image analysis, the function \( f \) (an image) is called a linear symmetric image if its isocurves (curves or lines with invariant pixel values) have a common direction \([13]\). Our idea of using linear symmetry approach is to measure the number of velocity vectors having a common direction, not a common direction of isocurves of textures in an image. Although the object used for linear symmetry estimation in our situation is different from the definition, the goal nevertheless remains the same, to evaluate the degree of such a common direction.

\[
LS = \frac{\sum_{i=1}^{N} v_i}{\sum_{i=1}^{N} \|v_i\|}
\]

\(0 \leq LS \leq 1\) and is 1 only when all \(v_i\) in a frame have the same direction

It was believed that the more co-operative vectors in the image; the stronger the muscle is and for the weak muscle, the opposite is the case. In view of this position, we anticipated to see an image sequence either having a high linear symmetry throughout all frames or its average linear symmetry close to ‘1’ representing a sequence of a healthy muscle. An opposite characteristic of linear symmetry was expected for the sick muscles.

One important thing to note here before any further discussions is the use of word ‘collaboration’. This word is used with respect to its meaning described by Figure 3.4 and is also relied on some simplifications. First, it deals with feature vectors represented in the target image only. Second, it assumes velocity vector is a representation of muscle fiber. We justify these simplifications by regarding each pixel within the region of interest on the image as a muscle’s constituent. Therefore it should not be confused with the actual meaning of ‘collaboration of muscle fibers’ in the strict biological sense, as this involves complex biological structure of the tissues and a process of chemical reactions occurred within the organ.
3.4 Multi-frame and local feature

Section 3.3 focuses on the analysis of velocity vectors on the entire image, so it is a global analysis. The global features alone seemed to provide inadequate features and in fact, by far, only two features were observed to be suitable, Total Speed and LS of motion. This section presented another two features which were found to be very useful in classification and they were obtained by performing local analysis of velocity vectors. The term local in this case is defined according to Figure 3.5.

By performing the local analysis on each region shown in Figure 3.5, we could extract local features that once combined with the global features will give better results of classification. After several trial and error methods used in the analysis, two local features were then found to be useful:

3.4.1 Local feature 1, Mean of product of local variance in direction

First, the dominant direction of motion, R (see section 3.2.1), was computed at each region k on every frame t in the sequence denoted as \( R_k^t \), where t is the frame number in the sequence and k is the region. Thus there is a vector \( r_k = [R_k^1, R_k^2, \ldots, R_k^t]^T \) that indicates the variation of dominant direction, R, at each region. For each image sequence we have \( r_1, r_2, r_3, r_4, \) and \( r_5 \) where the subscript indicates the corresponding region. We can investigate the variation of \( R_k^t \) throughout all frames at each region from these five vectors as illustrated in Figure 4.11.
Second, we multiply all $r_k$ element-wise as follows:

$$
\mathbf{r}_{\text{mult}} = \begin{bmatrix}
\prod_{k=1}^5 r_k (1) \\
\prod_{k=1}^5 r_k (2) \\
\vdots \\
\prod_{k=1}^5 r_k (5)
\end{bmatrix}
$$

The local feature 1 is the mean of $\mathbf{r}_{\text{mult}}$:

$$
\mathbf{LF}_1 = \frac{1}{t} \sum_{i=1}^t \mathbf{r}_{\text{mult}} (i) \quad \text{where } \mathbf{LF}_1 \text{ represents local feature 1.}
$$

Therefore, there is one $\mathbf{LF}_1$ for each image sequence.

### 3.4.2 Local feature 2, Mean of mean of variation in angles

First angle of average direction of motion at each region $k$ was computed on every frame $t$ as:

$$
\theta_k^t = \tan^{-1} \left( \frac{\sum_{i=1}^N V_y^i}{\sum_{i=1}^N V_x^i} \right) \quad \text{where } N \text{ is the number of points in each region.}
$$

$\mathbf{\Theta}_k = [\theta_1^k, \theta_2^k, \ldots, \theta_5^k]^T$ is a vector where each element is the average direction of motion at each region on each frame. Thus we have $\mathbf{\Theta}_1, \mathbf{\Theta}_2, \mathbf{\Theta}_3, \mathbf{\Theta}_4,$ and $\mathbf{\Theta}_5$ where the subscript indicates the corresponding region.

Second, we find the mean of each $\mathbf{\Theta}_k$:

$$
\overline{\theta}_k = \frac{1}{t} \sum_{j=1}^t \mathbf{\Theta}_k (j)
$$

The final angle used as the local feature 2 is the mean of all $\overline{\theta}_k$.

$$
\mathbf{LF}_2 = \frac{1}{5} \sum_{k=1}^5 \overline{\theta}_k \quad \text{where } \mathbf{LF}_2 \text{ represents local feature 2.}$$
Therefore, there is one LF$_2$ for each image sequence. Figure 3.6 illustrated a sample of variation in angles of average direction $\Theta_k$.

![Figure 3.6: Variation of angles of average direction from frame to frame.](image)

These angles tell us how a direction of overall motion changed with respect to time. On average, an image sequence has a length of 4 seconds; this was the time taken for the measurement of the extension force by fingers. Since, there are about 41 frames for each sequence we could work out the time interval between two consecutive frames, as follow:

$$\Delta t = \frac{\text{duration of measurement}}{\text{number of frames in a sequence}}$$

$\Delta t$ time taken from one frame to another. In most cases, $\Delta t$ is approximately 97.56 ms. In relation to Figure 3.6 we could infer that a contraction of muscles within this short duration produces a continuous change of directions. $\Delta t$ also signifies a rapid change of angles. The information from both the graphs and the $\Delta t$ implies that our analysis of motion is in fact involved with very fast moving objects (the components of the muscle).

It is necessary to explain first, how angles in the graphs were presented. The value of angles presented in the graphs was measured in degree and each of their negative values was converted to a corresponding positive angle. This was to reduce a difficulty in picturing the change of direction form the positive to negative.
The concept used in the implementation of this conversion is simple. Velocity vectors resulted from the optical flow computation rotate in the range of 0 to 360 or 0 to -360 as illustrated on the above diagram. Depending on a choice of convenience, one can opt for either sort of range and eliminate the other. This can be done by performing modulo 360. However, this technique is typically performed on integer, but it is applicable to other types of numeric operands as well. Thus, we could apply the method in our computing numbers which are all non-integers. By applying this method of conversion, modulo function, it keeps our calculation simple.

3.5 Visualization tool

In fact all ideas of local features were obtained from the visualization tool (VT). This tool is a transformation of graphs into motion. Instead of looking at how magnitude, angle, LS etc change over time on the graphs, this tool shows all of these aspects of velocity vectors at each instant of motion on a single display. This is shown in Figure 3.7.

![Visualization tool (VT) of velocity vectors at each region of Figure 3.5.](image)

We can see the motion of the vectors in Figure 3.7 by displaying a sequence of images. This helps us to analyze the characteristics of motion of these vectors’ component in a more efficient way. Each vector corresponds to the motion at that region. Each vector in Figure 3.7 is computed as:

$$\sum_{j=1}^{N_k} v_i$$

maximum of \(\left\| \sum_{j=1}^{N_k} v_i \right\|\)^n

where n is the number of such vectors in the sequence and N_k is the number of vectors in a region k. Thus, each vector has a norm in the range [0 1] in all directions.
3.6 Classification Strategy

Each feature can be used as input to a classifier since it was carefully chosen to distinguish between healthy and sick muscles. The strategy used in each classifier step is to pass 100% healthy and reject sick subjects as far as possible; the rejection rate depends on the intrinsic feature of individual muscle. The general ideas to achieve this goal are

1) Cascade each classifier to gradually filter all sick muscles
2) If one feature is used in a classifier to perform classification, we can directly find the optimal threshold that could pass all healthy muscles.
3) If two features are used in a classifier we linearly transform 2D data into 1D. The threshold value can then be computed from the 1D data.

The following is an idea for computation of threshold values in each classifier.

-1 feature classifier

Figure 3.8 illustrated sample data that used mean and standard deviation to set the threshold value.

-2-features classifier

A computation of the threshold for 2-features classifier is not as trivial as the one in 1-feature classifier as it is now involved two classification parameters. However, we can reduce the dimension by linearly projecting all data down to 1D using

\[ y = w^T x \]
where \( w \) is the projection coefficients and \( x \) is the data point. It is now possible to set the threshold value on \( y \) and classify \( y > \text{threshold} \) as class 1, otherwise class 2.

The projection coefficient \( w \) should maximize the separation of the classes when projected onto \( y \). In this respect, we employed Fisher’s linear discriminant [15] to compute \( w \). The Fisher’s criterion \( J(w) \)

\[
J(w) = \frac{w^T S_B w}{w^T S_W w}
\]

is maximized when

\[
(w^T S_B w) S_w w = (w^T S_W w) S_B w
\]

this is obtained by differentiating \( J(w) \) with respect to \( w \) and set it to zero. \( S_B \) and \( S_W \) are _between-class_ covariance matrix and _within-class_ covariance matrix, respectively. The terms in the parentheses in the above equation is in fact the magnitude of \( w \), hence we can discard them as our aim is to find only the direction of projection. Furthermore, the _between-class_ covariance matrix \( S_B \) multiplied with \( w \) is always in the direction of \( (m_2 - m_1) \) where \( m_i \) is the mean vector of each class. Finally we obtained \( w \) as

\[
w \propto S_w^{-1} (m_2 - m_1)
\]

According to this equation, we need to find only the inverse of _within-class_ covariance matrix and the difference in vector means to obtain the best projection coefficients. \( S_w \) can be computed as

\[
S_w = \sum_{n \in C_1} [x_n - m_1][x_n - m_1]^T + \sum_{n \in C_2} [x_n - m_2][x_n - m_2]^T
\]

The threshold value is in this work computed as the average of the two projected means plus a small increment factor to raise the level.

\[
\text{Threshold} = \frac{m_{1_{\text{proj}}} + m_{2_{\text{proj}}}}{2} + \epsilon
\]

\( \epsilon \) is necessary to ensure 100% transit of healthy muscles.
4: Experimental results/Discussion

It is important to clarify that the tensor method for OF computation does not work well on the muscles’ texture. However, we could improve the tensor method’s algorithms so it is applicable to our analysis, but this is unnecessary as the differential method already gives a satisfactory result as shown in section 4.1.

4.1 Comparative evaluation of optical flow computation techniques

The implementation of both methods follows the concepts described in [12] in which a Gaussian filter is used for all tasks. Due to the problem with the application of the tensor method to the muscle’s texture in this particular case, only the differential method is a suitable approach for the analysis.

Figure 4.1: Results of optical computation with tensor approach, (left) point motion, (right) line motion.

Figure 4.2: Results of optical flow computation with differential approach

It is obvious from Figure 4.1 and Figure 4.2 that the differential method gives better results. Distributed spatial structure and non-constant motion are the intrinsic characteristics of muscles and this falls into class 4 of tensor method described in section
2.3.2. In this class, all eigen values are positive and no direction of motion could be computed. By comparing vector fields with the ultrasonic clip, the results obtained in Figure 4.2 seemed to comply with the real motion of the muscles.

4.2 One target frame and global features

![Image of velocity vectors for healthy and sick muscles](image)

**Figure 4.3:** Comparison of direction of velocity vectors between healthy (b) and sick (c) muscles.

It was presumed, in the beginning of the research, that healthy muscles contract more in the longitude direction (along y-axis in Fig. 4.1a) than they do in the latitude direction (along x-axis in Fig. 4.1a) whereas the sick muscles contract in the opposite manners. This presumption was based on the results obtained from a velocity vectors field of the optical flow from the first two sample image sequences (Fig. 4.1b, c).

These two image sequences were used as samples before all image sequences of patients and of healthy participants became available. The initial hypothesis has underestimated the complexity of a contraction of muscles. After we computed the optical flow on target images of each image sequence, in some cases, the contraction’s patterns tend to possess a rotational motion where in other cases, the average motion looks as if it swings back and forth for both the healthy and the sick muscles. The motion in the longitude direction occurred in both the healthy and the sick but for a very short instant (2 to 4 frames in the sequence). Velocity vectors were used as a measurement parameter to determine the overall motion. To estimate the overall motion, one frame in the sequence was selected as a target image for optical flow computation. One of the difficulties with this computation
is to decide which frame should be used as a target image to best represent the motion. The motion of muscles is never constant in terms of speed and direction. Therefore, it is unlikely that one target image could give details of the overall motion as the algorithm of this optical flow estimates the local motion of each pixel (few frames before and after the target image). In this respect, more target images are required to gain better insight into the motion.

The four images in Figure 4.4 demonstrated why longitude VS latitude direction approach can not be used for classification. These images were taken from the same sequence (RA patient) but different frame of target images. First, the predominant direction of motion varies from moment to moment; it depends entirely on the target image chosen to compute the optical flow. As can be seen from these four images that the angles of resultant velocities change from ~90 degree to ~45 degree indicating anti-clockwise upward rotation. In this case, the overall motion began in the vertical direction and slowly moved upward; thus we can not deduce direction on a whole unless we analyze it frame by frame. However, these images were taken from sick muscles, but the changes of angles and velocities are similar to those of the healthy subjects. These four images are ones of many examples (approximately 1000 images) which it is not feasible to present here. In some cases, only motion in the latitude direction exists, no motion in the longitude direction - according to the data these muscles are healthy.

For this reason, we can not find the right target image from both the healthy and the sick to make a comparison in the direction of the vector fields. The real contraction instance is unknown with the available data set, or else we could confine our attention to the significant moment of motion. As a result, motion analysis should be carried out more carefully with as many target images as possible. The idea is to compute and record some important features of velocity vectors such as speed in average direction, average direction, and maximum of speed presented on the vector field in each target image. These features can then be used to describe the motion in more details.

Before embarking on computing optical flow and registering the values of velocity’s features for approximately 1000 target images, the analysis in yt and xt views were first performed as this method needs only one target image per sequence. Provided that one target image is insufficient for this approach of analysis, this technique does not give a better way to estimate motion. Consequently the vast computation of velocity features is unavoidable. A clear justification for leaving out yt and xt analysis approach is addressed below.

**yt-view**

Figure 4.5 shows the difference of results in each case, healthy and diseased. The optical flows were computed from right to left (←) in the image sequence (see Figure 3.2). The assumption made at the initial state of this research regarding yt-view target image was that the velocity vectors field appear to point in the same direction and a large concentration of velocity vectors occurs within a short duration (frames 19-24 in Figure 4.5(top left)) for any chosen target images. We believed that these frames with the major
flow of velocity vectors implied a contraction instance in the sequence. The major flow is shown in the red ellipse for the healthy subjects. For the sick subjects, vectors point in the opposite direction to those of the healthy and the major flow can take place in any frames, shown in small red ellipses. These early results led to a spontaneous opinion that the target image of the healthy can be chosen from the frame which possesses most vectors in the large concentration area. Whereas, in the sick, the flow of vectors is randomly distributed throughout the entire image for any chosen target image, hence there is no particular target image for optical flow computation.

Figure 4.4: A sequential changes of direction of velocity vectors from frame to frame. (top left) frame 8, (top right) frame 9, (bottom left) frame 10, (bottom right) frame 11.

The assumption just stated is no longer valid when we made a comparison as in Figure 4.5. A large concentration of velocity vectors does not exist in this target image (top right) for the healthy, and the flow of velocity vectors is not truly random as we anticipated for the sick (bottom right). These are ones of many examples which verified that one target image is inadequate for this analysis approach. One possibility for remedying this situation is to have more target frames for computation, but a question now arose “Which analysis should we pursue, since both the yt-view and normal view (xy) requires more than one target image?” Intuitively thinking, the motion analysis across the xy-image plane through the time sequence is more natural and it aids visualizing actual motion of the muscles.
This approach of analysis is fairly similar to that of yt-view, except that now the computation is done from bottom to top instead of right of left (see Figure 3.3). The four images shown in Figure 4.6 are an example of disparity in results where the top two compared velocity vectors of the healthy and the bottom two compared velocity vectors of the sick. It is not necessarily to look for the right target image for comparison as we did not compare the vectors. What we tried to verify was the shape or feature of the overall vectors on the entire target image. To extract the true feature of motion, the majority of results of the target image should comply with one another but it did not happen in this case. Refer to the discussion of yt-view analysis for details clarifying that this approach of analysis should not be continued, since it encountered the same problem.
It is reasonable at this point to infer that global analysis of direction of velocity vectors in xy, yt, xt views as described in section 3.2 is not useful for classification. The speed of velocity vectors described in section 3.2 varies with a chosen target image; thus we can not gain any useful information of it.

4.3 Multi-frame and global features

With sequential target frame analysis in section 3.3 the computation of speed can be extended to obtain the total speed of muscles. The combination of Force and Total Speed features in section 3.3.1 could differentiate between the two classes of muscles, healthy and sick, as shown in Figure 4.7.

To find the optimal classifying threshold in Figure 4.7, we first applied the linear classification technique described in section 3.6 to find a specific choice of direction of projection of the data down to one dimension. The proportion of projected data per each projected value is displayed as a histogram in Figure 4.8. The projected data can be used to construct a discriminant by choosing the threshold so that we classify a new point as belonging to Healthy if \( y(x) > \text{threshold} \) and classify it as belonging to Sick otherwise. The threshold was then found as in section 3.6 with \( \varepsilon = -0.043 \) in this case.
According to Figure 4.8, we observed that approximately 50% of all sick muscles could be eliminated by Force/Motion classifier. However, we can filter the sick muscles that have not been eliminated by this classifier with another classifier in cascade.
Another global feature that could be used in a classifier is the Linear Symmetry of velocity vectors discussed in section 3.3.2. Information from a graph of linear symmetry (Fig. 4.9) tells how the fibres’ of collaborative muscle are, at each instant of motion, and a noticeable variation in both of the graphs signifies an inconstant collaboration of muscle fibres during contraction. This implies that our initial belief regarding linear symmetry and muscle’s health is no longer true. Accordingly, an analysis of linear symmetry alone did not turn out as expected, we were then urged to combine the linear symmetry with other features to be able to extract the motion’s feature.

![Figure 4.9: Plot of variation in LS of velocity vectors with time through the sequence, (left) healthy, (right) sick.](image)

According to Figure 4.9, we could notice the variation in time of LS and the figure also shows a high fluctuation of LS in the sick muscles compared to the healthy. This led to the assumption that both types of muscular fibres co-operated well over time during contraction but the co-operation of the diseased muscles is not so constant. Hence, variance of LS can be used as a 1-feature classifier.

\[
\sigma^2 = \frac{1}{t-1} \sum_{i=1}^{t} (LS_i - \bar{LS})^2 \quad \text{variance of LS, } t = \text{number of frames in the sequence}
\]

We can notice from Figure 4.10 that we can eliminate approximately 50% of the diseased muscles by this classifier. Refer to section 3.4 for the computation of the threshold value. It is important to note that the shift in level of the threshold depends on the observed data of the healthy muscle; in this particular case adding \(1\sigma\) to the mean of variance seems to perfectly give a proper threshold. However, \(2\sigma\) and \(3\sigma\) could be used as an increment factor instead if there exists a higher variance of the healthy than the highest one in Figure 4.10.
According to some experiments on the feature $R$ (section 3.2) and $\Theta$ (section 3.3) in the multi-frame sense, it was found that these two features cannot be used to distinguish between healthy and sick muscles. The local analysis performed on the image sequences is similar to those $R$ and $\Theta$ of the global analyses with minor alterations. Instead of investigating $R$ and $\Theta$ on the entire image, we applied the same approach to different regions shown in Figure 3.5 with the techniques discussed in section 3.4.1 and 3.4.2. The result of $LF_1$ is illustrated in Figure 4.11.
Figure 4.12: (Left) Plot of LF\textsubscript{1}. (Right) Plot of LF\textsubscript{1} VS LF\textsubscript{2}. The figure shows a better separation of data points in the combined features.

The results of local changes in angles of average direction $\Theta_k$ is very similar to the one for $r_k$ except that we take the mean of mean value of each graph not the mean of product of each graph. The combination of LF\textsubscript{1} and LF\textsubscript{2} could better isolate the healthy from sick and ease the classification task, Figure 4.12.

Figure 4.13: A scatter plot of LF\textsubscript{1} and LF\textsubscript{2} of healthy and sick muscles. The arrow indicates the direction of projection.

Figure 4.14: A histogram of projected data from Figure 4.13 using Fisher’s linear discriminant function. The threshold was computed as in section 3.6, $\varepsilon = -0.027$. 
A threshold value found to be suitably good to classify the data in Figure 4.13 is shown in Figure 4.14. The same linear classification approach used with Force/Total Speed was applied here again with a different value of $\varepsilon$. As can be seen from Figure 4.14 approximately 50% of sick muscles could be eliminated by this classifier. Healthy if $y(x) >$ threshold and sick otherwise.

### 4.5 Optimization of classifiers

It is evident from the results that each classifier could filter out approximately 50% of diseased muscles; thus we need to optimize these classifiers to achieve the best possible classification system. The four features from multi-frame analysis and the force were found to be useful:

1. Total Speed
2. Variance of LS
3. LF$_1$
4. LF$_2$
5. Force

These features need to be combined in favor of efficient classification. The diagram below demonstrated the promising cascaded classifiers.

Figure 4.15: A diagram showing the combination of classifiers. The system is divided into two stages 1D and 2D. The only input into each system is the components of velocity vectors, Vx and Vy which are matrices. Each element in the Vx and Vy corresponds to the speed of muscle in x and y direction respectively at the computed point. Each system tries to filter out the diseased and passes healthy muscles.

As can be seen from Figure 4.15 that variance of LS was placed first in the system. This is because 1D filter requires less computation compared to 2D filter. The muscles that can not pass var(LS) filter will be classified as sick directly without further proceeding. The performance of this system is evaluated in section 4.6.
4.6 System performance

The numerical results from each classifier, variance of LS, Total Speed/Force and LF₁/ LF₂ suggested a system design. Section 4.3 and section 4.4 illustrated that each classifier can filter out 50% of the sick muscles; thus we need to optimize these classifiers to achieve a better result. The most practical way found, was to cascade each classifier as discussed in section 4.5. A total of 36 healthy and 18 sick muscles were analyzed and classified by the classification system. Figure 4.16 shows the results of the classification in which we notice that all sick muscles were eliminated before reaching the output of the 3rd classifier. This is a satisfied result but it is important however to note that the system developed could 100% filter out the sick muscles with this specific training using data sets; therefore to generalize this classification technique, more muscles are required. Although the supply of data for training and testing is limited, we still can assess the performance of the system by cross-validation technique, called ‘leave-one-out’ [15]. Results of the cross-validation test are shown in Table A (page 40) where “1” means the muscle fulfill the classifying criterion of the system; thus it can proceed to the next system. Each muscle has to obtain three “1s” to be classified as healthy and any muscles that obtain a “0” are directly classified as sick. The cross-validation technique is a suitable validation when data is particularly scarce. The threshold values of all classifiers and the projection coefficient “w” for both the 2nd and 3rd classifiers were practically the average values obtained from “leave-one-out” training runs.

One important thing to note is the uncertainty at the border between healthy and sick muscles. The features used in the system did not give a sufficiently large separation gap; thus the muscles that lie near the threshold values are likely to fall in either of the two classes. This is a drawback of weak features used for classification, but in our case this problem has been taken care of by cascading each classifier as shown in Figure 4.15. For instance, if the sick muscle that is close to the threshold value of the 1st system, it might pass to the 2nd system. To pass to the 3rd system this muscle has to be in the healthy region or lie close to the threshold value again. Finally, to be classified as healthy this muscle has to pass the 3rd threshold. There are three threshold values specifically selected to satisfy healthy features and to kill off the diseased muscles. Therefore, the border problem does not give a great impact onto the system. To confirm that the system could perform well with a larger data set, we increased the number of data points of sick muscles. These data points were obtained from the same patient’s muscles. However this time each muscle was trained by the physical therapy process to improve the strength. The performance of the system (Table A) with these new data points was not as good as it was with the first data set which can eliminate all the sick muscles. This time the system achieved 86% accuracy as can be seen in Table A that three trained sick muscles were classified as healthy by the systems. However, we could think of this as a positive result because it shows that some sick muscles become healthier or stronger after the therapy. Figure 4.17 illustrates how the data points of the trained sick muscles moved into the healthy region and it also implies that the features used for classification are reliable. The improvement of muscles’ health can also be observed by comparing data points of diseased muscles in Figure 4.16 and Figure 4.17.
### Table A: Results of the Cross-validation test

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**100% accuracy**

**86% accuracy**
Figure 4.16: Result of each classifier, (top) 1\textsuperscript{st}, (middle) 2\textsuperscript{nd}, (bottom) 3\textsuperscript{rd}, the gray markers in the 1\textsuperscript{st} and 2\textsuperscript{nd} figures point out the survived sick muscles. There were 9 sick muscles surviving from the 1\textsuperscript{st} classifier, 3 of them were filtered out by the 2\textsuperscript{nd} classifier. The grey markers in the last figure are the same 6 surviving muscles from the 2\textsuperscript{nd} classifier. All of them are eliminated by the 3\textsuperscript{rd} classifier.
Figure 4.17: Scatter plots of the features used for classification. The plots show how data points of the trained sick muscles move into the healthy region.
5: Conclusion and future work

Classifying the muscles according to health using velocity vectors from optical flow is the main novelty of the proposed system. The health recognition is successful in separating healthy muscle sequence from RA diseased muscle sequence in motion, with 100% accuracy on the test data. Although restricted to small data base, the suggested system is able to deliver robust classification because the threshold levels were computed by linear classification techniques. These thresholds were also increased by corresponding factors to ensure 100% transition of healthy muscles; hence any muscles eliminated by the system can reliably be classified as sick. In addition, the results also reveal the effect of physical therapy process used to train the muscle of RA patients. As indicated in Figure 4.17, the sick muscles become stronger after they have been exercised by the process. One aspect I found very appealing is the physical meaning of numerical results which leads to deeper appreciation and easier comprehension of the muscle’s attributes, etc., inconsistent collaboration of muscle’s fibres during contraction.

We have developed a model which, we believe, helps in understanding features associated with tissue motion. We have illustrated the performance of the classifiers which are cascaded to achieve the best results. The results are quite promising and provide motivations for future studies on the property of classifiers and of features integration to construct the most advantageous classifier.

In this work we focused on the feature extraction technique with an application for muscle classification system. However, there are still many interesting problems left to investigate. Sample image sequences used to perform the analysis are handicapped by inadequate information in basic material. These include the following three aspects:

1. Finger force registration

To relate force with motion in a more efficient way we need to improve the measurement process and this can be accomplished as shown in the above diagram. The green ellipses indicate the duration in which force is being exerted; thus if this duration is precisely known we could concentrate our analysis of motion to these particular instances. The
force used in the analysis is the maximum force exerted by fingers with unknown instance.

2. Extraction of exact region

The real region of interest is the one surrounded by the white dot. The position of this region varies from muscle to muscle; thus it is not a trivial task to automatically extract such a region and moreover the region is sometimes invisible from the 2D image sequences. Consequently, we used the approximate area indicated in the red rectangular in the analysis instead. The results obtained may deviate from what we expected due to this unwanted portion.

3. 3D images

Motion of muscles can only be fully perceived from 3 dimensional image sequences, but what we have are 2 dimensional ones. This lack of one dimension causes loss of important information which resulted in inaccurate estimation.

Muscles vary in how fast they can contract and in how long they can continue to contract before they experience fatigue. These characteristics are influenced by muscle fiber type, load, and recruitment. Thus the only solution is to acquire more useful information than the available data (Table 1 in the Appendix). Much of the time and cost associated with the analysis and design of the classification system can be reduced by comprehensive information of measurement procedure. Lack of knowledge that generates the data results in a disadvantage when applying the image analysis technique.
### Table 1: Data on age, force and ultrasound codes.

Data about age, extension force (measurement occasion 1-4), US code

(M = healthy men, S = patient with RA, H = healthy women, n = subject code, last number = Occassion)

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