SEGMENTATION OF MEDICAL IMAGES
APPLICATIONS IN ECHOCARDIOGRAPHY AND NUCLEAR MEDICINE

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Abstract

Segmentation is an important task in all kinds of image analysis. In medical image analysis segmentation has a great clinical value since the aim could be to localize organs or pathologies in order to raise the quality of diagnoses. This thesis consists of three papers where different segmentation techniques have been applied to different imaging modalities. In the first paper a full computer assisted diagnosis system is presented where the aim is to find abnormal lesions in scintigraphy images of the kidneys. Here we have two segmentation parts; first segmentation of each kidney in the images using an active shape model and then localization of potential lesions using thresholding. In a test group of 56 patients the segmentations work very well just like the classification of lesions does. The second application is segmentation of the left ventricle in echocardiographic images. This segmentation is important when measuring the left ventricular function. The segmentation is done using a region based snake where the data term is driven by virtual image forces derived from the image intensities. To overcome problems with the cardiac valve opening and closing during the cardiac cycle, we annotate two anchor points, one on each side of the valve. We track these through the cycle in order to minimize user interaction and no segmentation is done over the valve. This method shows promising results. In the third paper we have developed a measure of the shape of the septum, the wall between the left and the right ventricle, to be used in echocardiographic images of patients with a mechanical pump attached to their heart as a bridge to transplantation. Such a measure can be useful when tuning the speed of the pump. Here the segmentation of the septum is achieved using the shortest path algorithm. The septum measure is then a measure of how much it deviates from a straight septum. Our septum measure corresponds in most cases to the assessments from a physician. These three applications show the usefulness of segmentation in a variety of applications within medical imaging.
Preface

This thesis is based on the following papers:


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Introduction

The main subject of this thesis is segmentation of medical images. Segmentation is an important task in image analysis where you want to divide an image into two or several different regions of interest. The application of segmentation in medical images can be to find a particular organ, tumors or other pathologies. There are several methods that solves this task and some of them will be presented later in this introduction. First an overview of medical image analysis in general is given.

1 Medical Image Analysis

Medical image analysis is a wide concept that includes several processing and analysis methods applied to a number of different imaging modalities. This image analysis can be divided into different subjects such as: image enhancement, segmentation, registration, quantification and classification. Then each imaging modality gives rise to a number of different examinations that can have different characteristics. The most common imaging modalities will briefly be presented below, followed by a short overview of medical image analysis.

1.1 Imaging Modalities

A short presentation of different imaging modalities will be given here, a more detailed description of the modalities can be found in for example [13].

Ultrasound

The sound frequencies used in ultrasound are above 1 MHz. A transducer positioned against the body surface emits the ultrasound and receives the reflected waves. When the waves reach an interface between tissues with different densities they can be scattered, absorbed, reflected or transmitted depending on the circumstances. The characteristics of the waves that
returns to the transducer forms the images. One special characteristic of ultrasound images is the speckle noise. It comes from the reflections back and forth between different tissues and makes the images quite noisy. There are three different presentation modes of ultrasound; A-mode, B-mode and M-mode. A-mode shows the echoes in the direction of the transducer, with amplitude on the y-axis and distance (assuming constant speed of sound) on the x-axis. In B-mode the sound beam is scanned across the patient and a two dimensional image is obtained. Echoes with a high amplitude are represented by high intensity values. M-mode shows each echo-producing interface as a function of time, which makes it possible to study movement of the structure. B-mode is the best known of the presentation modes, see an example image in Figure 1(a). Ultrasound is used e.g. in cardiology, gynecology, obstetrics, urology and neurology.

Figure 1: Examples of images from different modalities. (a) Ultrasound image, (b) CT image, (c) MR image [20] and (d) PET image.
1. Medical Image Analysis

X-rays

X-rays are electromagnetic radiation that attenuates different in different materials. There is a high attenuation in bones which means that a smaller amount of x-rays reach the detector behind the bones and they therefore show up clearly on the images. Different soft tissues in the body attenuate an equal amount of x-rays and it is hard to identify e.g. organs from each other. The lungs are visible because of the low attenuation in air compared to the attenuation in tissue. Some examples of examinations are skeletal x-ray, mammography and chest x-ray.

Computed Tomography

Computed tomography (CT) is an imaging technique where the x-ray tube rotates around the body and the rays are detected by a stationary circular array of detectors. The images are reconstructed using measurements of the transmitted x-rays through the body and mathematical models, see Figure 1(b) for an example of a CT image. In this way the body can be viewed in slices from different directions. There is a higher contrast resolution in CT images than in ordinary x-ray images which means that different organs can be separated in CT images. CT can be used for detecting tumors, head infarctions and abdominal diseases.

Magnetic Resonance Imaging

In magnetic resonance imaging (MRI) the body is put in a magnetic field. By introducing an electromagnetic field to get a resonance with the protons (mainly in water molecules in the body) a radio frequency signal is emitted and can be detected by a receiver coil. By mathematical models, these signals are transformed into cross-sectional images of the body. Particularly soft tissue is interesting in these images because of the high contrast resolution. In Figure 1(c) an MR image of the heart can be seen.

Nuclear Imaging

In nuclear imaging, photons from a radioactive substance are detected and then transformed into images. The radioactive substance is attached to a biological molecule that accumulates in the organ/tissue of interest after an injection into the blood. The detector can be a planar gamma camera and then the imaging technique is called scintigraphy. This gives two dimensional images and some applications are lung, bone and renal scintigraphy. Single photon emission computed tomography (SPECT) also uses a
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gamma camera but, as with ordinary CT, images from a number of angles are captured and reconstructed into a three dimensional data set. SPECT can be used for myocardial perfusion imaging and tumor detection. In positron emission tomography (PET) the detected radiation is annihilation radiation. This radiation occurs when positrons and electrons interact and the emitted photons are emitted in opposite directions. If a circular detector simultaneously detects photons in opposite directions it is assumed that the annihilation occurred on a straight line between the detectors. PET can for example be used in oncology and to diagnose Alzheimer’s disease. An example of a PET image can be seen in Figure 1(d).

1.2 Overview of Medical Image Analysis

The first clinical useful form of digital image analysis was developed in the early 1970s [8]. The ejection fraction (the volumetric fraction of blood pumped out of the left ventricle in one heartbeat) was computed from cardiac nuclear medicine images in a semi-automated manner [23]. This was an early form of quantification. When quantifying, you are interested in analyzing structure and function using features in the images. It can for example be blood flow, tissue shape, tissue texture and motion. These features are often extracted after some kind of segmentation process.

Another important part of medical image analysis is image enhancement. Medical images can be of bad quality for many reasons; superimposition of the surrounding tissue and Poisson noise from the photon emission in nuclear imaging are two of them. The image enhancement can for example be contrast enhancement, noise removal or sharpen details (e.g. edges) in order to make the analysis easier — both visually and in potential further image analysis. Contrast enhancement can be achieved by e.g. histogram equalization where the intensities are distributed over the histogram. Noise can be removed with different filters. A mean filter reduces the noise but has the disadvantage that the sharpness of edges is lost. A non linear filter that can be used for specific types of noise, as e.g. salt and pepper noise, is the median filter. This filter preserves edges. A Gaussian filter also removes noise and furthermore, it also blurs the image and should be used when details are not important.

Registration of images from different modalities was considered for the first time in the late 1980s [8]. One of the first attempts was matching the boundary surface of the brain that was manually segmented in CT, PET and MRI [19].
They used the Euclidean metric between landmarks to map the segmentations to each other. Registration between different modalities helps, for example, in the search for tumors. Tumors are visible in e.g. PET images, but it can be difficult to interpret the exact anatomical position in these images. CT images give a better anatomical view and by matching a CT image with a PET image, the location of the tumor can be identified, see for example [18, 22]. Registration can also be used to register images acquired at different times from the same patient or images from different patients in order to make comparisons. Most registration methods consist of some feature detection, feature matching, estimation of model parameters and finally image transformation.

An important application of medical image analysis is computer-aided diagnosis (CAD) systems. These systems are not intended to replace physicians, instead they are advisory. Such systems may contain all parts mentioned above and often also contain some kind of machine learning in order to be able to give a statement to the physician. There are several methods for machine learning, where the purpose is to train a system, for example to distinguish between an unhealthy and healthy defect from given data. Some methods that can be used are discriminant analysis, artificial neural networks, Bayesian networks and mixture models. One of the first fully automatic CAD systems came in the late 1980s for mammograms [8]. Data were acquired from the images by thresholding and feature detection. Then the data were analyzed with linear discriminant analysis in order to classify normal tissue and calcifications [2]. See [6] for several examples of CAD systems.

2 Segmentation Methods

As mentioned before, segmentation is the task of dividing an image into two or several regions of interest. There exist several segmentation methods and some of these methods will be presented thoroughly here.

2.1 Active Contour Models: Snakes

Active contour models, or more commonly named snakes, were first introduced by Kass, Witkin and Terzopoulos [16]. A snake is an energy minimizing spline that can be used for finding salient image contours. The models are called snakes because of the way the contour moves while searching for image edges and they are active since the energy is always minimizing which gives the models a dynamic
behavior. The snake needs to be initialized close to the contour of interest, but then finds its way to this contour by minimizing the energy.

The Classical Snake Model

A snake is a parametrized curve \( u : [0, 1] \to \mathbb{R}^2 \) such that the point of the curve \( u(s) = (x(s), y(s)) \) belongs to the image domain for all \( 0 \leq s \leq 1 \). The energy functional to be minimized consists of two parts, one expression for the internal energy and one expression for the external energy,

\[
E[u] = \frac{1}{2} \int_0^1 \alpha |u'(s)|^2 + \beta |u''(s)|^2 ds - \int_0^1 V(u(s)) ds,
\]

where \( u(s) \) is required to be a twice differentiable curve and \( V = V(x, y) \), is a potential function determined by the image.

The internal energy controls the shape of the snake and it depends only on the contour and not on the image data. The first term in (1), with the first derivative, makes the snake act like a string and the second term, with the second derivative, makes it act like a thin beam.

The function \( V \) in the external energy can be expressed in different ways depending on what you are looking for in the image. The simplest function is the image intensity, then the snake will be attracted to lines. Edges can be found in the image by using the gradient of the image intensities as a function. In this thesis, we are interested in snakes that are region based. This means that the external energy is driven by statistical properties of the image data inside and outside the contour, see later subsection for further explanation.

The segmentation is given by the curve \( \varphi \in C^2([0, 1], \mathbb{R}^2) \), which solves the variational problem

\[
E[\varphi] = \min_u E[u],
\]

where \( \varphi \) and \( u \) are subject to boundary conditions. For instance \( \varphi \) and \( u \) could be open curves with fixed end points or closed, simple curves.
Finding the Optimal Solution

From now on we consider the case $\beta = 0$ when the snake acts like a string. The snake energy may be expressed in the general form

$$E[u] = \int_0^1 L(u(s), u'(s)) ds, \quad (3)$$

which includes (1) if the Lagrange function $L$ is taken to be $L(u, u') = \frac{\alpha}{2} |u'|^2 - V(u)$. In this section we consider closed contours. That is, we minimize the functional (3) over the following set of admissible curves,

$$\mathcal{A} = \{ u \in C^1([0, 1], \mathbb{R}^2) : u(1) = u(0), u'(1) = u'(0) \}.$$

In order to minimize $E[u]$ we first look at the differential of $E$ defined as

$$dE[u; v] = \frac{d}{d\epsilon} E[u + \epsilon v] \bigg|_{\epsilon = 0}, \quad (4)$$

where $u + \epsilon v$ is a variation of $u$ and $u, v \in \mathcal{A}$. When computing the differential we find that it is

$$dE[u; v] = \frac{d}{d\epsilon} E[u + \epsilon v] \bigg|_{\epsilon = 0} = \frac{d}{d\epsilon} \int_0^1 L(u + \epsilon v, u' + \epsilon v') ds \bigg|_{\epsilon = 0},$$

$$= \int_0^1 \nabla_u L(u, u') \cdot v + \nabla_{u'} L(u, u') \cdot v' ds. \quad (5)$$

Now assume $u$ is a twice differentiable curve. Then by using integration by parts we can write the differential as:

$$dE[u; v] = \int_0^1 \{ \nabla_u L(u, u') - \frac{d}{ds} \nabla_{u'} L(u, u') \} \cdot v \ ds$$

$$= \langle \nabla_u L(u, u') - \frac{d}{ds} \nabla_{u'} L(u, u'), v \rangle_{L^2}$$

$$= \langle \nabla E[u], v \rangle_{L^2} \quad (6)$$

and in the last row we have defined the $L^2$-gradient of $E$ at $u$ as

$$\nabla E[u] = \nabla_u L(u, u') - \frac{d}{ds} \nabla_{u'} L(u, u'), \quad (7)$$
using the definition of an inner product: $\langle u, v \rangle_{L^2} = \int_0^1 u(s) \cdot v(s) \, ds$.

If $\varphi$ is a minimizer of $E[u]$ over $A$ then a necessary condition on $\varphi$ is Euler’s equation

$$\nabla \varphi L - \frac{d}{ds} \nabla \varphi L = 0,$$

(8)

where $\nabla \varphi L = \nabla_u L(\varphi(s), \varphi'(s))$ and $\nabla \varphi' L = \nabla_{u'} L(\varphi(s), \varphi'(s))$. Comparing with (7) we see that Euler’s equation can be written concisely as

$$\nabla E[\varphi] = 0.$$  

(9)

Applying our definition of the gradient of $E$ on the Lagrangian for our snake model (1), $L(u, u') = \frac{\alpha}{2} |u'|^2 - V(u)$, we get

$$\nabla E[u] = -\nabla V(u) - \alpha u''.$$  

(10)

The minimization is done using the method of gradient descent, which evolves a curve $u = u(s, t)$ with respect to a fictitious time parameter $t \geq 0$ according to the PDE

$$\frac{\partial}{\partial t} u = -\nabla E[u].$$

(11)

Thus we get the gradient descent scheme for the minimization of the snake functional $E$:

$$\begin{cases}
\frac{\partial}{\partial t} u(s, t) = \nabla V(u(s, t)) + \alpha u''(s, t), \\
u(s, 0) = u_0(s),
\end{cases}$$

(12)

where $u_0(s)$ is the initial contour specified by the user.

Region Based Snakes

As mentioned before, in this thesis we will consider snakes that are region based. We consider a closed curve $u \in A$ which is simple and we write our snake model as

$$E[u] = \int_0^1 \frac{\alpha}{2} |u'(s)|^2 \, ds - \iint_{\Omega(u)} W(x, y) \, dx dy,$$

(13)
where \( \Omega(\mathbf{u}) \) denotes the domain enclosed by \( \mathbf{u} \) with \( \partial \Omega \) oriented counter clockwise and \( W = W(x, y) \) is a function that depends on the image data.

Now we want to derive an expression for the gradient of \( E \) in (13), which can be used when minimizing the functional using the gradient descent method as described above. This has been done in [24] by using the divergence theorem of vector calculus. Another derivation, based on the interpretation for parametrized curves of the differential computed directly within the level-set framework, is given in [15]. In our approach we instead consider Green’s theorem

\[
\int_{\partial \Omega} P \, dx + Q \, dy = \iint_{\Omega} \left( \frac{\partial Q}{\partial x} - \frac{\partial P}{\partial y} \right) \, dxdy,
\]

and assume that we can find a vector field \((P, Q)\) such that \( \frac{\partial Q}{\partial x} - \frac{\partial P}{\partial y} = W \), e.g. by taking \( Q = 0 \) and \( P = -\int_0^y W(x, \hat{y}) \, d\hat{y} \). Our Lagrangian in the energy functional (3) can now be written as

\[
L = \frac{\alpha}{2} (x'^2 + y'^2) - P(x, y)x' - Q(x, y)y'.
\]

Here we used the fact that we can write our curve integral as

\[
\int_{\partial \Omega} P \, dx + Q \, dy = \int_0^1 P(x, y)x' + Q(x, y)y' \, ds.
\]

Now we write (7) component wise, \( \nabla E = ((\nabla E)_x, (\nabla E)_y) \), for easier computation when we have our region based term:

\[
(\nabla E)_x = \frac{\partial L}{\partial x} - \frac{\partial}{\partial s} \left( \frac{\partial L}{\partial x'} \right) = -\frac{\partial P}{\partial x} x' - \frac{\partial Q}{\partial x} y' - \alpha x'' + \frac{\partial Q}{\partial x} x' + \frac{\partial P}{\partial y} y' = -\alpha x'' - W y',
\]

and similarly,

\[
(\nabla E)_y = \frac{\partial L}{\partial y} - \frac{\partial}{\partial s} \left( \frac{\partial L}{\partial y'} \right) = -\frac{\partial P}{\partial y} x' - \frac{\partial Q}{\partial y} y' - \alpha y'' + \frac{\partial Q}{\partial x} x' + \frac{\partial Q}{\partial y} y' = -\alpha y'' + W x'.
\]
Summarizing this gives the gradient
\[
\nabla E[u(s)] = -\alpha u''(s) + W(u(s))\hat{u}'(s),
\]
where \(\hat{u}'(s) = (-y'(s), x'(s))\) is the inward unit normal vector to the curve \(u(s)\) since \(\partial \Omega\) is oriented counter clockwise, see Figure 2. The term \(W(u(s))\hat{u}'(s)\) can be interpreted as the force in the direction of the normal to the curve \(u(s)\).

Snakes have been used for example when segmenting tumors in MR images [12] and in CT images [17].

### 2.2 Active Shape Models

Active shape models (ASMs) have been described in [3]. The idea is that the contour should only be allowed to deform into shapes that are characteristic of the object of interest. To model the characteristic shapes of an object, a training set is needed. The contours are represented by a number of points, the \(i\)th contour denoted by the column vector \(x_i\). These points should be annotated in the same way for all shapes in the training set and then be aligned with for example Procrustes analysis [7]. By looking at the statistics of each point cloud, a Point
2. Segmentation Methods

Distribution Model can be derived. Each point cloud is modelled as a Gaussian distribution. The mean shape of \(N\) aligned shapes is given by

\[
\bar{x} = \frac{1}{N} \sum_{i=1}^{N} x_i. \tag{20}
\]

The major axes are found by Principal Component Analysis (PCA) of the data. The eigenvalues are calculated together with the corresponding eigenvectors of the covariance matrix,

\[
\Sigma = \frac{1}{N - 1} \sum_{i=1}^{N} (x_i - \bar{x})(x_i - \bar{x})^T. \tag{21}
\]

If the eigenvalues and eigenvectors are ordered as \(\lambda_j \geq \lambda_{j+1}\), then the first eigenvector represents the first principal axis, i.e. the direction where the points move the most. The eigenvalues show how much of the variance that is described by each principal axis. In most cases it is not necessary to use all principal axes in the model. It is enough to use the \(k\) first principal axes that describe a sufficiently large proportion of the total variance. Each shape in the training set can be written as

\[
x \approx \bar{x} + Vs, \tag{22}
\]

where \(V\) is a matrix with the \(k\) first principal axes as columns and \(s\) are a \(k\)-dimensional vector containing the weights. The weights can be computed by

\[
s = V^T (x - \bar{x}) \tag{23}
\]

and by varying the elements of \(s\) we can vary the shape \(x\) using (22). It can be shown that each eigenvalue of \(\Sigma\) is the variance of the corresponding weight, \(s_j\), and by restricting each weight to \(-3\sqrt{\lambda_j} \leq s_j \leq 3\sqrt{\lambda_j}\) it is ensured that the shape is similar to those in the training set, since most of a normal population lies within three standard deviations from the mean.

When using ASMs the object of interest is found in an iterative process. First, each point in the contour is moved to a position in its vicinity that better represents the object border. For example, if the border is an edge one can search for the strongest edge along the normal in each point. The second step is to ensure that the current shape is allowed. This is done by computing the weights, \(s\), using (23) and restrict each \(s_j\) to be in the interval \(-3\sqrt{\lambda_j} \leq s_j \leq 3\sqrt{\lambda_j}\)
as mentioned above. These two steps are repeated until there is a sufficiently low difference between two contour representations. In Figure 3 an example of how the contour adapts to the allowed kidney shape can be seen. The red contour represents the step where the object border is found and then, by the method described above, we obtain the cyan contour which is a more plausible shape of a kidney.

![Figure 3: An example of how active shape models work in an early stage of the iterations. The red contour is the best fit to the object boundary and the cyan contour is the adaptation of the red contour to a more plausible shape of a kidney.](image)

ASMs have been used in e.g. [9] where they do segmentation of different parts of the brain in MR images.

### 2.3 Shortest Path Problem

The shortest path problem arises in many applications, e.g. finding the shortest route from one city to another, but segmentation can also be formulated as a shortest path problem. The image is represented by a directed graph, \( G = \)
(\(V, E\)), where each vertex, \(v \in V\), corresponds to a pixel in the image. Neighboring pixels will be adjacent in the graph with an edge, \(e \in E\), connecting them. A neighborhood of a pixel can be defined in different ways in the 2D case; 4-connected and 8-connected, cf. Figure 4. Each edge has a weight, \(w\), that in the case of finding the shortest route between cities corresponds to distances between intersections. In the image case they can correspond to e.g. the intensity difference between pixels. The objective in the shortest path problem can be summarized as

\[
\min_p w(p) = \sum_{i=1}^{n} w(v_{i-1}, v_i),
\]

(24)

for a path \(p = (v_0, v_1, \ldots, v_n)\). Many of the algorithms that solve the shortest path problems rely on the property that each shortest path contains several shortest paths within it. This can be stated as in the following lemma:

**Lemma.** Given a weighted, directed graph \(G = (V, E)\) with weight function \(w : E \rightarrow \mathbb{R}\), let \(p = (v_0, v_1, \ldots, v_n)\) be a shortest path from vertex \(v_0\) to vertex \(v_n\).
and, for any $i$ and $j$ such that $0 \leq i \leq j \leq n$, let $p_{ij} = (v_i, v_{i+1}, \ldots, v_j)$ be the subpath of $p$ from vertex $v_i$ to vertex $v_j$. Then $p_{ij}$ is a shortest path from $v_i$ to $v_j$.

**Proof.** The path $p = (v_0, v_1, \ldots, v_n)$ can be decomposed into the subpaths $p_{0i} = (v_0, v_1, \ldots, v_i)$, $p_{ij} = (v_i, v_{i+1}, \ldots, v_j)$ and $p_{jn} = (v_j, v_{j+1}, \ldots, v_n)$ which gives $w(p) = w(p_{0i}) + w(p_{ij}) + w(p_{jn})$. Now assume that there is a path $p_{ij}'$ from $v_i$ to $v_j$ with $w(p_{ij}') < w(p_{ij})$ then the path $p_{0i} \rightarrow p_{ij}' \rightarrow p_{jn}$ is a path from $v_0$ to $v_n$ whose total weight, $w(p_{0i}) + w(p_{ij}') + w(p_{jn})$, is less than $w(p)$, which contradicts that $p$ is the shortest path from $v_0$ to $v_n$. \[\square\]

Shortest path algorithms have been used as segmentation method in, for example, mammograms [1] and live-wire implementations [11, 10] with applications in CT and MR.

**Algorithms**

There are some variants of the shortest path problem.

- **Single-source shortest paths problems**, where one wants to find the shortest path from a source vertex $s \in V$ to all other vertices in $V$.

- **Single-destination shortest paths problems**, here one wants to find the shortest path from each vertex in $V$ to a destination vertex $t$.

- **Single-pair shortest path problems**, find the shortest path from vertex $u$ to vertex $v$.

- **All-pairs shortest path problems**, find the shortest path from vertex $u$ to vertex $v$ for every pair of vertices $u$ and $v$.

There are a number of algorithms that solves these different variants. Some of them are Bellman-Ford, Dijkstra’s, Floyd-Warshall and Johnson’s algorithm which are described in e.g. [4]. Next we will describe Dijkstra’s algorithm in detail.

Dijkstra’s algorithm [5] can be used on a weighted, directed graph with non-negative weights. It solves the single-source variant of the shortest path problem. To describe the algorithm we introduce two attributes of each vertex $v$; $v.d$ which is an upper bound on the weight from the source $s$ to $v$ (a shortest path estimate) and $v.\pi$ which is assigned either NIL (no vertex) or another vertex and it is the predecessor of the current vertex $v$. In Algorithm 1 the outline of the algorithm can be seen. The first for loop initializes the attributes $d$ and $\pi$ for each vertex and
Algorithm 1 Dijkstra’s algorithm

1: for each vertex \( v \in G.V \) do
2: \( v.d = \infty \)
3: \( v.\pi = \text{NIL} \)
4: end for
5: \( s.d = 0 \)
6: \( S = \emptyset \)
7: \( Q = G.V \)
8: while \( Q \neq \emptyset \) do
9: \( u = \) the vertex \( v \) in \( Q \) with the lowest shortest path estimate
10: \( S = S \cup \{ u \} \)
11: for each vertex \( v \in G.\text{Adj}[u] \) do
12: \( \text{if } v.d > u.d + w(u,v) \) then
13: \( v.d = u.d + w(u,v) \)
14: \( v.\pi = u \)
15: end if
16: end for
17: \( Q = V \setminus S \)
18: end while

then the sets \( S \) (visited vertices) and \( Q \) (unvisited vertices) are initialized. In the while loop the algorithm picks out the closest vertex \( u \) and updates the adjacent vertices’ \( (G.\text{Adj}[u]) \) attributes if these edges make their shortest path estimate smaller. This will give the shortest path from \( s \) to each vertex. An example of execution of Dijkstra’s algorithm can be seen in Figure 5.

2.4 Thresholding

Thresholding is a quite simple segmentation method where an image, \( I(x, y) \), is divided into two regions, one below the threshold and one above. The thresholded image, \( T(x, y) \), can be defined as

\[
T(x, y) = \begin{cases} 
1, & I(x, y) \geq t \\
0, & I(x, y) < t 
\end{cases}
\]  

(25)

where \( t \) is the chosen threshold. Using several thresholds the image can of course be segmented into more than two regions. The threshold can be chosen in several
ways. One is to look at the histogram of the image. If the pixels corresponding to the object and background respectively, are grouped into two different groups the threshold is chosen as a value that separates the groups. Another way is to examine image intensities in the neighborhood of each pixel and calculating some statistics. Thresholding have, for example, been used for segmenting lymph nodes in CT images [21] and measuring ventricular volumes in MR images [14].

References

2. References


An Automated System for the Detection and Diagnosis of Kidney Lesions in Children from Scintigraphy Images

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Abstract:
Designing a system for computer aided diagnosis is a complex procedure requiring an understanding of the biology of the disease, insight into hospital workflow and awareness of available technical solutions. This paper aims to show that a valuable system can be designed for diagnosing kidney lesions in children and adolescents from 99mTc-DMSA scintigraphy images. We present the chain of analysis and provide a discussion of its performance. On a per-lesion basis, the classification reached an ROC-curve area of 0.96 (sensitivity/specificity e.g. 97%/85%) measured using an independent test group consisting of 56 patients with 730 candidate lesions. We conclude that the presented system for diagnostic support has the potential of increasing the quality of care regarding this type of examination.

1 Introduction

Proper medical treatment begins with a correct diagnosis. Medical imaging systems provide a wealth of information which provide possibilities as well as challenges for the interpreting physician. The processing of this information is a complex procedure, where collective knowledge in the field, familiarity with the specific examination procedure and technical equipment, patient history, and common sense come together in the formation of a diagnosis. Creating a fully automated system for processing information of this diversity is difficult; however there are situations where a computerized system can provide valuable diagnostic support. Computers excel at keeping track of large amounts of data and at performing time-consuming and tedious tasks quickly. The combination of a human interpreter and a computerized system can therefore improve diagnostic
accuracy [11]. The main contribution of such a system is to improve sensitivity, i.e. avoiding oversight. This paper presents a fully automated system for detecting and diagnosing kidney lesions from 2D scintigraphy images. There are two main contributions of this system. First, it eliminates time-consuming manual procedures in currently used systems such as the delineation of the kidneys. Second, it provides objective diagnostic support on a per-lesion basis to physicians with limited experience with this type of examination.

1.1 Clinical Background

One of the most common bacterial infections among children is urinary tract infection, caused by bacterial growth. This condition may develop into pyelonephritis\(^1\) which, left untreated, may cause scars in the parenchyma of the kidneys (cf. Figure A.1(a) for anatomical terms). Among the possible consequences of such lesions are future renal hypertension (high blood pressure) and renal failure [4].

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\(^1\)Inflammation in the renal pelvis.
Children with recurring infections are investigated for possible kidney lesions using an imaging method where a harmless agent known as dimercaptosuccinic acid (DMSA) is injected into the blood. DMSA accumulates in the kidneys and the local accumulation is proportional to the density of functional kidney cells [10, 8]. Low accumulation is therefore indicative of locally reduced kidney function. To make it possible to image the amount of accumulation, DMSA is combined with a radioactive molecule, $^{99m}$Tc, a weak gamma radiation emitter. A planar gamma detector is used to measure the amount of radiation emitted from the kidneys, thus forming an image of the renal function. The distribution of $^{99m}$Tc-DMSA in the kidneys are normally homogeneous. When a patient has had repeated urinary tract infections with lowered kidney function as a result, this can be seen as wedge-shaped areas of locally reduced intensity in the scintigraphy image [8], cf. Figure A.1(b).

1.2 Related Work

A segmentation method, specific to renal scintigraphy, is proposed in [9]. An automatic thresholding algorithm is used to segment each kidney. To avoid undersegmentation, pixels in an area around the initial boundary are classified as kidney pixels or background. This method does, however, not consider the fact that diseased kidneys may show lower uptake in wedge-shaped areas around its boundary. The paper also proposes a system for diagnosing the entire kidney as normal or abnormal based on a boundary curvature measure. The sensitivity and specificity of this method was 88% and 96% respectively.

A commercial $^{99m}$Tc-DMSA analysis program is available from Hermes Medical Solutions [1]. This software presents various kidney-specific measurements and presents a statistical map of uptake deviations.

2 Methods

An overview of our system can be seen in Figure A.2 and the different steps are explained in more detail below.

2.1 Kidney Segmentation

To segment and classify lesions we require some knowledge of relevant kidney anatomy; for instance we wish to build a map of normal $^{99m}$Tc-DMSA uptake
Figure A.2: An overview of the system components, from input image to a lesion-based classification.

and to measure the size of a lesion relative to the entire kidney. As is evident from Figure A.1(b), delineating the outer borders of the kidneys is a relatively easy task, the kidneys are mostly of high intensity while the background is considerably darker. However, lesions commonly distribute along the border, creating wedge-like regions of low intensity. To recover a plausible kidney border in such areas, strong prior information on the kidney shape must be incorporated. We believe that Active Shape Models (ASMs) [3] are a suitable approach for this purpose. An ASM models the distribution of landmarks along the boundary of a structure as a multivariate Gaussian distribution by means of a principal component analysis on the concatenated $x$- and $y$-coordinates of all shapes. Tuning the parameters of this model to fit an object in a given image is carried out in an alternating fashion. First, each landmark of the model is moved to a position in its vicinity which most likely represents the object border. Then, the landmark configuration is relaxed using information from the statistical landmark model to ensure that the resulting shape is anatomically plausible.

To create the statistical model of kidney anatomy, a training set of 40 kidneys were annotated with 14 landmarks along the boundary. The model is of a right kidney; left kidneys were mirrored to be incorporated in the model. By mirroring the model, we obtain a segmentation tool which can be used on both kidneys under the assumption of no consistent difference between left and right kidneys [9]. The resulting shape model uses 10 principal axes which captures 95% of the training set variation.

Successful delineation of a kidney using the ASM scheme requires an initial estimate of the segmentation which is reasonably close to the actual structure. A bounding box containing the kidney to segment is easily obtained from the marginal image histograms. The position, size and rotation of this kidney is then estimated by computing the centroid and principal axes for the coordinates corresponding to pixels above a foreground intensity threshold. Using this infor-
mation, the mean shape is translated such that its centroid coincides with the estimated kidney centroid. The shape is then rotated according to the principal axes. Finally, the shape is scaled in the directions of the principal axes according to the variance explained along each axis. Results of this initialization can be seen in the upper row of Figure A.3.

![Figure A.3: Example of segmentations with the initialization in the upper row and the final segmentation in the lower row. In the fourth example from the left it can be seen that the segmentation algorithm recovers the low-intensity upper and lower kidney poles.](image)

The ASM search for an improved fit from the initial segmentation guess is based on image edge information. Applying an edge detection algorithm on the raw image data is unwise; scintigraphy images exhibit uneven intensities due to the underlying Poisson process of nuclear decay. Neighboring pixels representing the same tissue type may display vastly different intensity levels just by chance. To reduce this effect while preserving more global edge structures we apply a bilateral image filter [13]. Bilateral filters are similar to standard Gaussian blurring with the modification that the Gaussian bell is weighted in each position by the photometric distance between the central pixel and its neighbors. This has the effect of smoothing homogenous regions while preserving structure. As a final preparatory image modification, we encourage the ASM to disregard edges enclosed in bright areas to some extent by taking the square root of all intensity values, thus focusing more on the background/foreground edges of interest.

When moving a landmark to a new position, we search among 30 samples along profiles perpendicular to the shape as suggested in [3]. From these candidate positions, we select the one which maximizes the difference between the mean of
inside samples and the mean of outside samples. An advantage of this formulation is that it considers edges with background on the outside and foreground on the inside of the shape model, rather than any image edges. The algorithm is run until the landmark difference between iterations is sufficiently low. The second row of Figure A.3 shows examples of resulting segmentations.

2.2 Boundary representation

As stated above, the kidney shape model consists of 14 landmarks placed along the kidney image boundary. This results in a rather course representation of the outline. However, a larger number of landmarks is difficult to achieve since the kidney exhibits few distinctive anatomical points of reference as projected in $^{99m}$Tc-DMSA images. Instead, we rely on a suitable interpolation technique to connect the landmarks accurately. The boundary is represented by a simple closed curve, making the use of Fourier descriptors [12] suitable. This boundary representation uses a combination of the discrete Fourier transform and Fourier series to calculate the Fourier coefficients $c_k$ and to recover a continuous boundary curve representation $f(t)$ respectively,

$$c_k = \frac{1}{n} \sum_{j=0}^{n-1} e^{-2\pi i jk/n} f_j, \quad f(t) = \sum_{k=-n/2}^{n/2} c_k e^{ikt}.$$

Here $n = 14$ is the number of landmarks, $f_j = x_j + iy_j, \ j = 0 \ldots n - 1$ represents the set of input landmarks, and $i$ is the complex unit. The complex boundary function $f(t)$, here sampled at 200 points, is a sum of harmonics of differing phase and frequency which leads to a globally smooth boundary suitable for describing the kidney boundary. Further, there exists convenient analytical expressions for the area and the centroid of the resulting shape [12]. The outlines in Figure A.3 are interpolated using this technique; note how it better handles the curvedness of the outline than line segments would.

2.3 Background removal

The background radiation present in the $^{99m}$Tc-DMSA kidney images is due to partial uptake in the blood and other organs. This also occurs behind and in front of the kidneys, as viewed from the gamma detector. This effect can be substantial and must be taken into account for accurate estimation of the kidney-specific
2. Methods

$^{99m}$Tc-DMSA uptake. Our approach is to create a smooth surface representing how the background radiation varies over the kidney, based on background samples outside, but close to, the kidney. We then subtract the intensities implied by this surface from the kidney area and a result of this can be seen in the top row of Figure A.5.

To represent a smoothly varying surface without sudden kinks or excessive bending, we use a smoothing thin-plate spline [2]. To obtain a smooth estimate of the background uptake, and avoid fitting the surface to noise, we choose to regularize the thin-plate spline rather than smoothing the image background samples. The resulting surface solves

$$\arg \min_{f} \sum_{i=1}^{n} (z_i - f(x_i, y_i))^2 + \lambda \iint \left( \left( \frac{\partial^2 f}{\partial x^2} \right)^2 + 2 \left( \frac{\partial^2 f}{\partial x \partial y} \right)^2 + \left( \frac{\partial^2 f}{\partial y^2} \right)^2 \right) \, dx \, dy,$$

where $\{z\}$ is the set of background samples outside the kidney, $\{x, y\}$ is the set of image coordinates of these samples, $f(x, y)$ is the thin-plate spline approximant and $\lambda \in [0, \infty)$ determines the stiffness of the plate. There exists a closed-form solution for solving this problem via a linear system of equations [2].

2.4 Candidate Lesion Segmentation

The most distinctive image feature of kidney lesions is reduced uptake of $^{99m}$Tc-DMSA. We therefore base our lesion segmentation approach on a pixel-wise statistical map of uptake in healthy kidneys and classify areas of a kidney as candidate lesions which exhibit significantly lowered uptake, measured on the 5% level. In order to create a map of normal uptake, we created a database of normal kidneys; six patients where both kidneys are considered normal, eleven patients with normal left kidneys, and 17 patients with normal right kidneys — a total of 40 samples. Since kidneys have different shapes and sizes they must be transformed to a common frame of reference where we obtain an approximate pixel-wise anatomical correspondence. We use thin-plate spline interpolation of the 14 corresponding outline landmarks to this end where each warp is represented by a pair of thin-plate splines taking care of landmark deflections in the $x$ and $y$ directions respectively.
Besides this spatial normalization the images also require photometric normalization by an unknown multiplicative factor. This is a general challenge in many investigations in nuclear medicine as absolute uptake depends on many unknown biological and technical parameters. Our normalization approach matches image \( A \) to image \( B \) by multiplying \( A \) by a factor such that the median of regions of \( A \) with high intensities (almost certainly healthy) matches the median of the corresponding regions in \( B \). In the normal database, all samples are normalized with respect to an arbitrarily chosen normal sample.

Empirical experience shows that a normal distribution is sufficiently accurate to describe the distribution of intensities. The parameters of these pixel-wise distributions are estimated by computing the mean and standard deviation of all normalized normal samples. Figure A.4 shows the mean uptake and its 95% confidence interval. The middle row of Figure A.5 shows the resulting statistical maps of \( z \)-values where tones of yellow towards red indicate regions lower than \(-2\) standard deviations (\(-2\sigma\)).

Figure A.4: The middle image shows the mean uptake of \(^{99m}\)Tc-DMSA and the two outer images shows the uptake at the borders of the confidence interval.

### 2.5 Classification

The essence of a system for computer aided diagnosis (CAD) is a classification into normal or abnormal, or gradings thereof, either on a per-lesion basis or regarding the patient as a whole. Here, we classify each lesion as either normal (blue) or abnormal (red). Typically, such systems are tuned such that very few actual lesions are classified as normal (high sensitivity). This gives the interpreting physician the possibility to focus on lesion candidates classified as abnormal, thus streamlining the work and reducing the risk of oversight.
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Figure A.5: Top row shows the resulting intensities when the background radiation has been subtracted. In the middle row a statistical maps of $z$-values for the selection of samples can be seen. Yellow towards red indicate areas lower than $-2z$. Bottom row shows example of classification with LDA, the red areas are classified as scars and the blue ones are classified as healthy.

We conducted experiments with three classifiers, two relatively simple baseline classifiers and one state-of-the-art approach. For baseline experiments, we used linear and quadratic discriminant analysis (LDA, QDA), and the more advanced approach is represented by an artificial neural network (ANN). A set of features is calculated from each potential lesion in order to perform the classification. These relate both to the lesion shape and texture, as well as to the kidney and patient as a whole. The following set of features were used here:

**Lesion edge closeness** This feature measures the distance from the lesion to the kidney edge. For each pixel position along the contour of the lesion, the distance to the closest point on the continuous kidney perimeter is found using numerical optimization. The smallest such distance, measured in millimeters, is returned.

**Lesion major and minor axis length** Length in millimeters of the principal axes of the ellipse with the same second moments as the lesion.

**Relative lesion area** The area of the lesion divided by the kidney area.
Lesion sum of z-scores The sum of the z-values within a lesion. The z-values are obtained by subtracting the lesion normal database mean image and dividing by the database standard deviation image, making each lesion pixel \( N(0, 1) \)-distributed.

Lesion relative sum of z-scores The sum of lesion z-values divided by the area of the lesion. Measured in z-scores per square millimeter.

Lesion localization These two features measure the position of the lesion centroid relative to its bounding box in the x- and y-directions. Since the scars are often located at the lateral wall of the kidney this measure can be an important addition to lesion edge closeness. Measures range from 0 to 1 with 1 corresponding to the most lateral/caudal positions and 0 corresponding to the most medial/cranial positions.

Lesion eccentricity This feature measures the elongation of the lesion as the eccentricity of the ellipse with the same second moments as the lesion. Values range from 0 to 1, where 0 represents a circle and 1 represents a line segment.

Lesion rate of extreme database deviation This feature measures the proportion of the lesion which falls under 4 standard deviations when compared to the normal database.

Kidney separate function This important measure quantifies the functional relation between the two kidneys of a patient. With equally functioning kidneys, this measure is at 50%. Lower numbers indicate loss of kidney function.

Kidney length This feature is of importance since partially damaged kidneys are likely to suffer from impaired growth. Measured in millimeters.

Kidney area Another way of measuring kidney growth. Measured in square millimeters.

Patient age Age can be an important factor to control for as kidneys develop much during childhood.

To train the classifiers we created a training set consisting of 36 patients with a total of 483 candidate lesions. These lesions were classified as normal or abnormal.
by a leading specialist on interpreting $^{99m}$Tc-DMSA renal scintigraphy images. The prevalence of lesions was 12%. Separate from this training set, we created a test set from 56 patients with a total of 730 candidate lesions. The prevalence in the test set was 8%.

Under the assumption that the vector of features for a patient follows a multi-dimensional Gaussian distribution, LDA and QDA provide optimal classification in terms of minimizing error rate [7]. Further, LDA assumes that normal and abnormal candidate features share the same covariance matrix while QDA allow for different such matrices. LDA and QDA assign a candidate lesion to the class $k$ that maximizes

$$\delta_k = x^T \Sigma_k^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma_k^{-1} \mu_k + \log \pi_k,$$  \hspace{1cm} (A.1)

and

$$\delta_k = -\frac{1}{2} \log |\Sigma_k| - \frac{1}{2} (x - \mu_k)^T \Sigma_k^{-1} (x - \mu_k) + \log \pi_k$$  \hspace{1cm} (A.2)

respectively, where $k \in \{\text{normal, abnormal}\}$, $x$ represents the input feature vector to test for, $\Sigma$ represents a covariance matrix, $\mu_k$ is the mean feature vector for class $k$, and $\pi_k$ is the prior probability for class $k$.

The ANN classification model was implemented as an ensemble of multi-layer perceptrons (MLP), where each MLP consisted of one hidden layer (7 nodes). Training was carried out by minimizing a cross-entropy error with an additional weight elimination term [6] to allow for a possible regularization of the ensemble. Four-fold cross validation was used during the model selection phase and the final ensemble model used on the test set was created using 3-fold cross splitting, repeated 10 times, resulting in an ensemble of size 30. The average output of the MLPs was used as the ensemble prediction.

Examples of lesions classified by LDA can be seen in the bottom row of Figure A.5.

3 Results

The segmentation works well both on kidneys with normal $^{99m}$Tc-DMSA uptake and on kidneys with lower uptake, cf. Figure A.3. The shape model also makes sure that the shape of a kidney is maintained. The segmentation has been evaluated on 40 kidneys and the rate of acceptable segmentations is around 95%. Most of the unacceptable segmentations have minor errors; most common is an unsatisfying segmentation of the upper and lower pole of the kidney.
The lesion segmentation algorithm based on the database of normal uptake detected 100% of diagnosed lesions in the training and test data sets. We did not have the opportunity to assess the accuracy of candidate lesion geometry.

The classification was validated on a test set of 730 possible lesions and the performance of the different classifiers can be seen in Table A.1. We fixed the sensitivity at a high value, here 96.5%, since this lessens the risk of classifying an actual lesion as normal while maintaining reasonable specificity. LDA and ANN show similar performance with high specificity and negative predictive value. QDA has notably lower specificity and positive predictive value as well as a larger misclassification rate. Receiver Operating Characteristic (ROC) curves for each classifier can be seen in Figure A.6.

Table A.1: Classification results as measured on the test set of 730 candidate lesions.

<table>
<thead>
<tr>
<th></th>
<th>LDA</th>
<th>QDA</th>
<th>ANN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area under ROC curve (AUC)</td>
<td>0.964</td>
<td>0.935</td>
<td>0.960</td>
</tr>
<tr>
<td>Sensitivity (%)</td>
<td>96.5</td>
<td>96.5</td>
<td>96.5</td>
</tr>
<tr>
<td>Specificity (%)</td>
<td>84.8</td>
<td>61.2</td>
<td>83.4</td>
</tr>
<tr>
<td>Positive Predictive value (%)</td>
<td>35.0</td>
<td>17.4</td>
<td>32.9</td>
</tr>
<tr>
<td>Negative Predictive value (%)</td>
<td>99.7</td>
<td>99.5</td>
<td>99.6</td>
</tr>
<tr>
<td>Mis-classification rate (%)</td>
<td>14.2</td>
<td>36.0</td>
<td>15.6</td>
</tr>
</tbody>
</table>

The program has been developed using MATLAB. The computation time for the analysis of one patient ranged from 5-9 seconds when running on a 2.2 GHz Windows PC with 1.5 Gb of RAM.

4 Discussion

We have shown that an accurate system for the diagnosis of kidney lesions can be created. Similar systems have previously been shown to increase diagnostic accuracy in practice, particularly by increasing sensitivity [11]. This means that physicians are less likely to miss non-conspicuous lesions. In contrary to many presently used systems, our approach is fully automatic and quick. This has the potential of increasing care effectiveness and relieving the interpretation from some of its inherent subjectiveness.

In our classification experiments, linear discriminant analysis performed at least as good as the more flexible alternatives. Cross-validation results for the
4. Discussion

Figure A.6: ROC curves for LDA (blue), QDA (red), and ANN (green). LDA and ANN perform similarly while QDA does slightly worse.

The lesion detection system detected 730 lesions in the test material — 8% of these represented actual lesions. This stresses the importance of offering classification of detected findings. The work involved in classifying 730 findings from scratch is far greater than reviewing around 60 candidates classified as abnormal paired with a quick review of remaining lesions.

In this paper, we have used data from a single hospital. In future work we will evaluate the method on material from more centers and a bigger variety of cameras. Further, we wish to develop the user interface to better fit typical hospital workflow, including integration with image storage and retrieval systems, and to
provide a system for (semi-)automatic reporting. One may also consider providing a diagnosis for the patient as a whole, based on the diagnoses of the individual lesions, in order to quantify the risk of future renal malfunction.

References


Paper B
Segmentation of the Left Heart Ventricle in Ultrasound Images Using a Region Based Snake

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Abstract: Ultrasound imaging of the heart is a non-invasive method widely used for different applications. One of them is to measure the blood volume in the left ventricle at different stages of the heart cycle. This demands a proper segmentation of the left ventricle and a (semi-) automated method would decrease intra-variability as well as workload. This paper presents a semi-automated segmentation method that uses a region based snake. To avoid any unwanted concavities in the segmentations due to the cardiac valve we use two anchor points in the snake that are located to the left and to the right of the cardiac valve respectively. For the possibility of segmentations in different stages of the heart cycle these anchor points are tracked through the cycle. This tracking is based both on the resemblance of a region around the anchor points and a prior model of the movement in the y-direction of the anchor points. The region based snake functional is the sum of two terms, a regularizing term and a data term. It is our data term that is region based since it involves the integration of a two-dimensional subdomain of the image plane. A segmentation of the left ventricle is obtained by minimizing the functional which is done by continuously reshaping the contour until the optimal shape and size is obtained. The developed method shows promising results.

1 Introduction

In this section a short background about ultrasound images in general will be given. Then some related work will be presented and finally a motivation for our approach is given.

1.1 Ultrasound Images

Ultrasound imaging is routinely used for a number of examinations in different fields such as cardiology, gynaecology, obstetrics, neurology, urology etc. When it is used for imaging the heart, it is called echocardiography. It can be used for a number of different examinations: heart development, cardiac structure and function as well as changes in normal physiologic states and pathologic condi-
tions. Left ventricular function can for example be obtained via two-dimensional ultrasound images by computing the ejection fraction. This is done by using Simpson’s biplane rule for estimating the end-diastolic and end-systolic left ventricle volumes [8].

The ultrasound frequencies used are in the range 2–10 MHz. When the sound travels from a tissue with a certain density to a tissue with a different density (e.g. from myocardium to blood), some of the sound waves are reflected. The reflected waves are received by the transducer where they are turned back to electrical energy and then displayed as an image. Depending on where on the body the user positions the transducer, different views of the heart can be obtained. Some of the most common are: long axis view of the left atrium and the left ventricle, short axis views of the heart in planes from the base of the heart to the apex and the four chamber view, see Figure B.1 [8].

![Schematic image of the different views used in echocardiography. Image reprinted with permission of Amra Jujic, Skåne University Hospital, Sweden.](image)

**Figure B.1:** Schematic image of the different views used in echocardiography. Image reprinted with permission of Amra Jujic, Skåne University Hospital, Sweden.

### 1.2 Related Work

There has been quite a lot of work done on segmentation of the ventricles in the heart in different views. The properties of ultrasound images almost demands custom-made methods for this application. Some of these methods are presented
Kucera et al. proposed a method with a region based external force in their early work on segmentation of the left ventricle [7]. This force is used in an active contour 3D model with time as one dimension. Their method is fairly reliable on both short axis and long axis views of the heart. Sarti et al. also used a region based approach in their segmentation model where they incorporate the a priori knowledge of the statistical distribution of grey levels [14]. The level set method is used to drive the curve evolution to achieve a maximum likelihood segmentation of the target, with respect to the statistical distribution law of image pixels. When comparing the area enclosed by the resulting contours from this method with manually outlined contours the correlation is excellent. A region based segmentation has also been done by Boukerroui et al. in their adaptive segmentation algorithm [3]. They use a weighting function that takes both local and global statistics into account during the segmentation process. The results of the segmentation of the left ventricle shows good results when compared with manual outlines by a medical expert.

Mishra et al. use an active contour model when segmenting the left ventricle in short axis view [10]. They solve the optimization problem using a Genetic Algorithm (GA) and the performance is comparable with inter-observer variations. A multiscale approach to the contour optimization is done by Mignotte and Meunier [9]. Their external energy in the snake energy function is also region based. They show some segmentation results for short axis views that are qualitatively good. Chen et al. constructed a geometric active contour model with a shape and an intensity prior [4]. The results of applying the method to a two chamber view are promising.

Bosch et al. developed an Active Appearance Motion Model (AAMM) that were used to do a segmentation of the left ventricle [2]. This is an extension of Active Appearance Models (AAM) and they did an automated segmentation over the full heart cycle. Their results are comparable with inter-observer variations. Mitchell et al. did a fully three dimensional AAM with time as one of the dimensions in the ultrasound images [11]. They got a correlation coefficient of 0.79 when comparing the area of the left ventricle defined by their method and an observer respectively.

Several other methods have also been evaluated for this segmentation problem, including artificial neural networks [1, 13], a fuzzy multiscale edge detector [15] and a Kalman filter based tracking method [5]. All of these methods give
acceptable segmentations of the left ventricle in long axis and/or short axis views.

1.3 Motivation for Our Method

The purpose of this work has been to develop a semi-automated segmentation method that segment the left ventricle in ultrasound images of the heart. A region based snake is used for the segmentation and it is specially designed to overcome some of the problems that are encountered in ultrasound images. Two anchor points are used in the snake and a tracking algorithm with a prior model for the movement of these from frame to frame are constructed. The proposed method performs a segmentation over the full cardiac cycle with only an initialization in the first frame.

2 Methods

The methods used in our segmentation algorithm will be described in this section. First some necessary user inputs are presented and the tracking algorithm for the anchor points is described. Then the classical snake model is explained as well as a region based snake model with anchor points. The section ends with a short step by step overview of the algorithm.

2.1 User Inputs

At the beginning of the algorithm, the user has to provide with some inputs that are presented here. In the first frame the user should annotate two points – one on each side of the cardiac valve, cf. Figure B.2. These are denoted $a^* = (a_1^*, a_2^*)$ and $b^* = (b_1^*, b_2^*)$ and are called anchor points, see the next section for more details. The user should also, by cycling through the frames, indicate the vertical position, $p$, of the cardiac valve when the heart is at most contracted. This value is used for computing the mean position of the cardiac valve as

$$h = \frac{a_2^* + b_2^*}{2} + p,$$

which is needed later for the prior model. To get the correct number of steps in the prior model, the user also needs to specify the length of one heart cycle.
2. Methods

2.2 Anchor Points

Since the cardiac valve can cause the snake to get stuck with a concavity in the cranial part of the left ventricle, two anchor points are used – one on each side of the valve, cf. Figure B.2. This means that no segmentation is done over the valve, instead a straight line is drawn between the anchor points. Since the segmentation is done in several frames, it is desirable to track the anchor points in the entire cycle in order to reduce the interaction with the user who annotates them in the first frame. The known anchor points in the previous frame are denoted \( \mathbf{a} = (a_1, a_2) \) and \( \mathbf{b} = (b_1, b_2) \). It will be described below how anchor point \( \mathbf{a} \) is tracked from one frame to the next, anchor point \( \mathbf{b} \) is tracked in the same way. We search for anchor point \( \mathbf{a}' \) in the current frame in a bounding box of size \( 25 \times 25 \) pixels around the position of anchor point \( \mathbf{a} \) in the previous frame. The tracking is based on the following three parts.

![Figure B.2: Two anchor points marked with a dot inside a diamond.](image-url)
• **Image resemblance**

It is reasonable to assume that the intensity distribution is fairly identical around an anchor point from one frame to the next. To get a value of how good the resemblance is, the sum of squared error is computed as

\[
R = \sum_{i=1}^{N} (L_i - C_i)^2, \quad (B.2)
\]

where \(L_i\) is the \(i\)th pixel in a \(5 \times 5\) window around the previous anchor point \(a\) and \(C_i\) is the \(i\)th pixel in a \(5 \times 5\) window around the current, not yet determined, anchor point \(a'\).

• **Distance**

It is very likely that an anchor point does not take a major leap from one frame to another and hence a measure for this is included too

\[
D = \beta |a' - a| = \beta \sqrt{(a'_1 - a_1)^2 + (a'_2 - a_2)^2}, \quad (B.3)
\]

where \(\beta\) is a constant.

• **Prior model**

A prior model of the movement in the vertical direction of the anchor points has been constructed. By manually tracking two anchor points in three patients a polynomial model, \(m\), of degree 5 that describes the movement in one cycle as a deviation from the mean position of the anchor points is obtained. The model can be seen in Figure B.3. The comparison is then done by computing the following expression:

\[
P = \gamma |a'_2 - M(t)|^2, \quad (B.4)
\]

where \(\gamma\) is a constant, \(M(t) = h + m(t)\) (where \(h\) is defined in (B.1)) and \(t\) is an index for the current frame.

To find the anchor point in the next frame the following expression is minimized

\[
\min_{a'} \{M = R + D + P\} \quad (B.5)
\]

to get the position of the anchor point \(a'\) in the current frame.
2. Methods

Figure B.3: The prior model of the movement in the vertical direction of the anchor points as the solid line and the data that the model is based on is marked with dots.

2.3 Snake Model

In the first two paragraphs of this section the classical snake model is recalled together with its extension to region based data terms. In the third paragraph it is explained how the region based model is adapted to our problem.

The Classical Snake Model

The snake model was first introduced in 1987 by Kass, Witkin and Terzopolous [6] as a means of synthesizing the noisy filter-response coming from an edge-detector into a coherent delineation of a perceived edge in the image, such as the boundary separating two image regions with distinct grey level characteristics.

Let us recall the classical snake model: A grey scale image $I$ is a real-valued function $I : \Omega \to [0, 1]$ defined for every point (pixel) $\mathbf{x} = (x, y)$ in the image domain $\Omega \subset \mathbb{R}^2$. The latter is usually a rectangle. The corresponding function value $I(\mathbf{x})$, is called the grey level at the pixel $\mathbf{x}$. Mathematically, a snake is given by a differentiable parametrized curve $\mathbf{u} : [0, 1] \to \mathbb{R}^2$, where each point of the
curve $u(s) = (x(s), y(s))$, $0 \leq s \leq 1$ is a pixel in the image domain $\Omega$. With each snake is a snake energy associated, given by

$$E[u] = \alpha \int_0^1 \frac{1}{2} |u'(s)|^2 \, ds + \int_0^1 g(u(s)) \, ds.$$  \hspace{1cm} (B.6)

Here the first term is a regularisation term and the second one is a data term. The function $g(x) : \Omega \to \mathbb{R}$ is an edge map. A typical example of an edge map is

$$g(x) = \frac{\epsilon}{\sqrt{\epsilon^2 + |\nabla I(x)|^2}},$$  \hspace{1cm} (B.7)

where $\epsilon > 0$ is a parameter. The regularisation term is smaller for shorter curves than for longer curves. At the same time the data term is smaller when the snake $u(s)$ is situated near an edge, where image gradients are large. Therefore the best delineation of an edge is defined, by the snake model, as the curve $u^*$ for which the snake energy is minimized,

$$E[u^*] \leq E[u] \quad \text{for all admissible curves } u.$$

The set of curves which are deemed admissible depends on the application at hand. In their original paper Kass, Witkin and Terzopolous [6] considered the delineation of incoherent edges from noisy edge-detection signals. They considered as admissible all differential curves $u : [0, 1] \to \mathbb{R}^2$ with fixed end-points $u(0) = a$ and $u(1) = b$, specified by the user. The minimizer $u^*$ of $E$ in this class of curves then gives the image edge through the points $a$ and $b$ and consistent with the image data. In other applications, such as segmentation of an image into foreground and background, one may consider as admissible the set of all simple closed differentiable curves in the plane. The curve which optimizes the snake energy then defines the boundary between foreground and background.

**Region Based Snake Models**

A region based snake model is an active contour where the segmentation is driven by the statistical properties of the image data inside and outside the contour. This is in contrast to the classical snake model where the contour is controlled by edge-forces derived from the shift in grey levels at perceived edges in the image. One of the most commonly used region based snake models is one in which the grey levels at each pixel in the image $I$ is assumed to follow a Gaussian distribution.
with a common variance $\sigma^2$ but with two distinct mean values: $\mu_0$ if the pixel belongs to the background and $\mu_1$ if it belongs to the object. The snake problem then becomes the optimization of the functional,

$$E[u, \mu_0, \mu_1] = \alpha \int_0^1 \frac{1}{2} |u'(s)|^2 \, ds + \int_{\text{ext}(u)} (I(x) - \mu_0)^2 \, dx$$

$$+ \int_{\text{int}(u)} (I(x) - \mu_1)^2 \, dx,$$

(B.8)

where $\text{ext}(u)$ denotes the set of points (pixels) $x$ on the outside of the contour given by $u$, and $\text{int}(u)$ the set of pixels inside the contour. This model can be seen as the snake formulation of the piecewise constant Mumford-Shah model [12] with two regions. This and similar region based snake models have been studied by Tsai in his thesis [16], see also Tsai et al. [17]. The functional $E[u, \mu_0, \mu_1]$ has to be minimized both with respect to the mean grey levels $\mu_0, \mu_1$ and the active contour $u$. It follows directly from the definition of $E$ that, for any fixed contour $u$, the optimal mean grey levels correspond to the mean intensity of the image $I$ on the outside and the inside of the contour, respectively. The optimal active contour is found by applying a gradient descent PDE associated with $E$ to an initial contour supplied by the user.

Region based snake models, such as the above, can be rewritten (up to a fixed additive constant) in the form

$$E[u, \mu_0, \mu_1] = \alpha \int_0^1 \frac{1}{2} |u'(s)|^2 \, ds + \int_{\text{int}(u)} V(x) \, dx,$$

(B.9)

where $V : \Omega \to \mathbb{R}$ is a potential function derived from the data-term. For the piecewise constant Mumford-Shah model above one can take $V(x) = (I(x) - \mu_1)^2 - (I(x) - \mu_0)^2$. This form is practical if we want to derive the gradient descent equations of motion of our active contour. The idea of the gradient descent procedure is to gradually change the shape of the snake, hence the name active contour, in such a manner that its energy steadily decreases. This is described mathematically by a snake $u = u(s, t)$ which depends on a (fictitious) time parameter $t \geq 0$. The motion of the snake is then dictated by the gradient descent PDE, which can be written formally as

$$\left\{ \frac{\partial}{\partial t} u = -\nabla E[u],
\right.$$

$$u(\cdot, 0) = u_0(\cdot).$$

(B.10)
Here $\nabla E[u]$ is the $L^2$-gradient of the functional $E$ computed at the contour $u$. Using methods from the calculus of variations it is possible to show that $L^2$-gradient for the region based snake at the contour $u = u(s)$ is

$$
\nabla E[u](s) = -\alpha u''(s) + V(u)\hat{u}'(s), \quad 0 \leq s \leq 1. \tag{B.11}
$$

Here $\hat{u}'(s) = (-u_2'(s), u_1'(s))$ is the $\pi/2$ radians counter-clockwise rotation of the tangent vector $u'(s)$ of the contour. As usual, $u'(s) = \partial u(s)/\partial s$. Therefore the gradient descent PDE for the minimisation of the region based snake model becomes,

$$
\begin{cases}
\frac{\partial}{\partial t} u = \alpha u''(s) - V(u)\hat{u}'(s), \\
u(\cdot, 0) = u_0(\cdot),
\end{cases} \tag{B.12}
$$

where $u_0$ is the initial contour. This PDE describes a time-evolution of the contour $u$ which we follow until convergence,

$$
u_*(s) = \lim_{t \to \infty} u(s, t), \tag{B.13}
$$

in which case $\nu_*$ satisfies the Euler equation $0 = \nabla E[\nu_*] = -\alpha \nu_*''(s) + V(\nu)\hat{\nu}_*(s)$, so that $\nu_*$ is a strong local minimum of the functional $E$.

For the region based snake given by $E$, the evolution defined by the descent PDE (B.12) has an interesting further property, namely that the contour always moves perpendicular to itself. Therefore the quantity $\frac{1}{2}|\nu_*(s)|^2$ is constant along the optimal contour, i.e., for all $s$, $0 \leq s \leq 1$. If the model is discretized, this property ensures that the control points of the contour will remain equidistant along the contour throughout its evolution.

**Region Based Snake Model with Anchor Points**

In this paper a region based snake model with two fixed anchor points $a$ and $b$ is considered. The required closed contour is the union of two arcs. The first arc is the snake $u : [0, 1] \to \Omega$ running counter-clockwise, inside the left ventricle, from one anchor point $u(0) = a$ to the other anchor point $u(1) = b$. The second arc is formed by the straight line running from $b$ to $a$, thus completing the contour. In our application we use the simple data term,

$$
V(x) = I(x) - \mu, \tag{B.14}
$$
where the constant $\mu$, $0 < \mu < 1$, is chosen by the user for optimal performance. If we take $\mu = 1/2$, our model corresponds to the piecewise constant Mumford-Shah model with the fixed choice of grey levels $\mu_0 = 0$ inside the snake (supposed to be inside the left ventricle where the image is black) and $\mu_1 = 1$ outside the snake. The snake's initial position $u_0(s)$ is supplied by the user (or by the solution to a previous instance of the same problem). The corresponding snake energy is minimized by evolving the snake according to the PDE,

\[
\frac{\partial}{\partial t} u(s, t) = \alpha u''(s, t) - V(u(s, t))u'(s, t), \quad t > 0, 0 < s < 1,
\]

\[
u(0, t) = a, \quad \text{and} \quad u(1, t) = b \quad \text{for all } t > 0,
\]

\[
u(s, 0) = u_0(s) \quad \text{for } 0 \leq s \leq 1.
\]

(B.15)

This problem is solved iteratively using a semi-implicit finite-difference discretization of the derivatives. The algorithm is terminated when the change in the solution, from one iteration to the next, is less than a given tolerance.

2.4 Algorithm

The segmentation of the left ventricle follows these steps:

1: The user annotates two anchor points, one at each side of the cardiac valve. The length of one cardiac cycle is also indicated as well as the position of the cardiac valve when the heart is contracted.

2: The anchor points are tracked through the cycle using the method described in section 2.2.

3: The segmentation begins in the first frame where an initialization of the snake is done. The region based snake, described in section 2.3, iterates until a tolerance level is reached and a segmentation is obtained in that frame.

4: For the next frame the segmentation in the last frame is used as initialization for the snake and then it iterates until the tolerance level is obtained.

5: Then item number 4 is repeated for the rest of the heart cycle.
3 Results

The proposed method has been tested on a sequence of ultrasound images and the results from some frames can be seen in Figure B.4. Both the tracking of the anchor points as well as the segmentations of the left ventricle can be studied here. The method was implemented using MATLAB. The computation time for performing the segmentation in each frame in one cardiac cycle is approximately 40 seconds when running on a 3.20 GHz Windows PC with 64 Gb of RAM.

![Figure B.4: The anchor points and resulting segmentations at different frames.](image)
4 Discussion & Conclusions

As can be seen in Figure B.4 our algorithm captures the edges of the left ventricle quite well for different levels of heart contraction. The choice of a region based snake seems to be good.

The tracking of the anchor points also seems to work well. The use of a prior model turned out to be necessary when testing the tracking algorithm without it. With no prior model the anchor points have a tendency to wander away or not follow the cardiac valve back when the heart relaxes.

One problem with our method is that the left ventricle stretches out to the apex of the heart, which is located in the top of the images in Figure B.4, and this is not captured so well by our method. The reason is the high intensity levels in that part of the image that is due to the closeness to the transducer. One idea to overcome this problem is to insert an anchor point in the apex to force the snake to stay there. This is something that will be investigated in the future.

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References


A Measure of Septum Shape using Shortest Path Segmentation in Echocardiographic Images of LVAD Patients

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Abstract: Patients waiting for heart transplantation due to a failing heart can get a left ventricular assist device (LVAD) implanted through open chest surgery. The device consists of a pump that pumps blood from the left ventricle into the aorta. To get the correct rotation speed of the pump, the physicians consider a number of measurements as well as a sequence of echocardiographic images. The important information obtained from the images is the shape of the inter-ventricular septum. For instance, if the septum bulges towards the left ventricle the speed is too high and it might harm the right ventricular function. To get a measure of the shape of the septum, which can be incorporated in a decision support system, we perform a segmentation of the septum using a shortest path method. To reduce user interaction, the user only needs to annotate two anchor points in the first frame. They mark the endpoints of the septum and they are tracked through the sequence with our tracking algorithm. After the segmentation the septum is divided into two regions, the one closest to the right ventricle and the one closest to the left ventricle, and the desired measure is the difference between the areas of these regions divided by the total septum area. The segmentation shows promising results and the obtained septum measure corresponds in most cases to the assessments from a physician.

1 Introduction

In this section we will give an introduction to echocardiography and a short clinical background in order to justify the need of a septum measure. Some related work on septum segmentations and other applications of shortest path segmentations will also be presented.

1.1 Echocardiography

Echocardiography is the acquisition of ultrasound images of the heart. There are a number of different examinations of the heart that can be done with echocardiography, e.g. studying heart development, cardiac structure and function as well as changes in normal physiologic states and pathologic conditions. The ultrasound
frequencies used are in the range 2–10 MHz. When the sound travels from a tissue with a certain density to a tissue with a different density (e.g. from myocardium to blood), some of the sound waves are reflected. The reflected waves are received by the transducer where they are turned back to electrical energy and then displayed as an image. Depending on where on the body the user positions the transducer, different views of the heart can be obtained. Some of the most common are: long axis view of the left atrium and the left ventricle, short axis views of the heart in planes from the base of the heart to the apex and the apical four chamber view [9], see Figure C.1. Here we also observe the location of the inter-ventricular septum and that the left ventricle (LV) is to the right and the right ventricle (RV) is to the left in the apical four chamber view that we will use.

1.2 Clinical Background

A left ventricular assist device (LVAD) is a mechanic pump designed to maintain adequate cardiac output in patients with severe heart failure, primarily as a bridge to transplantation. The LVAD is implanted through open chest surgery and supports the left ventricle by mechanically pumping blood from the left ventricle into the aorta. The device is located outside the heart and connected through cannulas
into the apex of the left ventricle and into the ascending aorta [1], see Figure C.2.

Figure C.2: Description of the LVAD system. *Reprinted with the permission of Thoratec Corporation.*

Since the use of LVAD is increasing the need for optimal evaluation of how these devices impact cardiac morphology, physiology, and function also increases. When adjusting the rotation speed (effect) of the pump in order to optimize treatment it is crucial to find a balance where the left ventricle gets unloaded without a negative effect of the right ventricle. If the effect of the LVAD is too high, left ventricular size will decrease predominantly caused by a leftward shift of the inter-ventricular septum. This will have a negative effect on the right ventricular function as well as on the tricuspid valve (i.e. increased valvular regurgitation). In contrast, if the effect of the LVAD is low, the inter-ventricular septum will shift towards the right ventricle. Both of these suboptimal settings result in decreased
cardiac output and the rotation speed therefore has to be adjusted [1].

The most important, non-invasive imaging tool for evaluating these parameters is echocardiography. Presently several echocardiographic measurements have been studied in order to optimize the LVAD output but none has proven clinically sufficient [11, 14, 13, 10]. None of these studies have a specific measurement for septum shape, but [14, 13, 10] mentions the importance of a straight septum and performs a visual examination of the septum shape.

1.3 Related Work

Segmentation in any kind of ultrasound images are difficult because of the characteristic noise called speckle. A method for inter-ventricular septum segmentation based on non-local spatio-temporal priors was proposed by [7]. These priors are used in the energy term in an active contour representation. They tested their method on 32 patients in the parasternal long axis (PLAX) view and got a satisfactory segmentation in 93% of the cases with a mean error of 1.8949 mm. In [12] they proposed a method for automated septum thickness measurement. The segmentation of the septum was done by searching for 1D functions that minimizes an energy that includes intensity distribution and a width constrain. The method was evaluated on images in PLAX view and compared with two cardiologists’ measurements and gave successful segmentations in 89/82% of the cases for each cardiologist respectively. Segmentation of the septum has also been done by [4]. Their method is a level set framework where they use a shape prior. The application of their method is high frame rate (150–350 fps) echocardiography and they evaluated it on a sequence acquired in apical four-chamber view. The resulting segmentation was positively evaluated visually by a cardiologist.

Shortest path segmentation has been used in other medical applications. For example it has been used in live wire implementations [5, 6] with applications in e.g. CT and MR images. [2] used shortest path to segment the pectoral muscle in mammograms and [8] used it when segmenting the myocardium in MR images.

The methods mentioned above that segments the septum have not done the segmentation with the purpose to use it on LVAD patients but for other clinical applications. We have developed a new echocardiographic algorithm based on inter-ventricular septal shift for optimizing the effect of the LVAD. This is a semi-automated algorithm where input is needed only in the first frame.
2. Methods

The images used in this work are sequences of echocardiographic images obtained in patients when tuning the pump speed. Each sequence consists of two-three cardiac cycles and the image size is $716 \times 956$ pixels.

The user has to provide some initial input to the segmentation algorithm. Two points have to be annotated in the first frame, one in the basal part of the septum and one in the apical part, cf. Figure C.3. These are called anchor points and are denoted $\mathbf{a} = (a_1, a_2)$ and $\mathbf{b} = (b_1, b_2)$ respectively. The anchor points are used to determine the position of the start and end points of the shortest path algorithm. In the next subsection it will be described how they are tracked through the image sequence in order to reduce user interaction.

![Figure C.3: The anchor points marked with two red stars.](image)

2.1 Tracking of Anchor Points

We track the anchor points from one frame to the next. The search for the new anchor point $\mathbf{a}'$ in the current frame is done in a bounding box of size $25 \times 25$ pixels around the position of anchor point $\mathbf{a}$ in the previous frame ($\mathbf{b}'$ is found in the same manner). The first part of the tracking algorithm is a measure of intensity resemblance around the anchor point and the sum of squared error is...
computed as

$$R = \sum_{i=1}^{N} (L_i - C_i)^2,$$

(C.1)

where $L_i$ is the $i$th pixel in a $5 \times 5$ window around the previous anchor point $a$ and $C_i$ is the $i$th pixel in a $5 \times 5$ window around the current, not yet determined, anchor point $a'$. There is not much movement in the septum so the distance the anchor point moves from one frame to the next is also taken into account,

$$D = |a' - a| = \sqrt{(a'_1 - a_1)^2 + (a'_2 - a_2)^2}. \quad \text{(C.2)}$$

The anchor points should not be too close to any edge of the septum so a measure that controls this is also included in the tracking algorithm,

$$E = |(|a'_1 - e_1| - |a'_1 - e_2|)|. \quad \text{(C.3)}$$

Here $e_1$ and $e_2$ are the approximate edges of the septum found by computing the derivative of the image in the horizontal direction and finding the closest maximum on both sides of $a'$. To get the position of $a'$ in the current frame, the following expression is minimized,

$$\min_{a'} \{ R + \beta D + \gamma E \}.$$

(C.4)

Here $\beta$ and $\gamma$ are weight parameters. After testing different values these parameters have been set to $\beta = \gamma = 1/12$.

### 2.2 Shortest Path Segmentation

In a shortest path segmentation the aim is to find the path between two nodes in a graph that minimizes the sum of the weights of the edges. There are a number of standard algorithms that solves this problem and we have used Dijkstra's algorithm [3]. In our case, each pixel is a node and there are edges between neighbouring pixels (horizontally and vertically). We form the weights on each edge by first filter the image with a Gaussian kernel and then compute the derivative in the horizontal direction, $I_x$. The derivative is then squared, normalized between 0 and 1 and after this called $h$. The weight on the edge between node $i$ and node $j$ is

$$w_{ij} = \frac{(1 - h_i) + (1 - h_j)}{2}. \quad \text{(C.5)}$$
We have defined the problem to always start in the basal part of septum going to the apical part since the septum is more distinct in the basal part. To avoid going in the other direction, an extra weight is put on those edges corresponding to the downward direction. Using a threshold on $h$, we also put extra weight on edges in regions above the threshold which are not likely to be the septum edges.

The anchor points are used for the start and end positions of the shortest path algorithm as mentioned earlier. However, we want one path along the septum edge closest to the right ventricle and one path along the edge closest to the left ventricle. So we want to find the edges of the septum in the vicinity of the anchor points. This is done as described in the explanation of (C.3).

The two edges of the septum are segmented separately and to avoid that the segmentation is too narrow or that the paths cross we do the segmentation iteratively. If the distance between the two paths becomes too narrow at some vertical level, the segmentation up to the previous vertical level is saved. Then the shortest path algorithm starts again, jumping five pixels in the direction of the end position to get a new start position, and finds the new shortest path. This is done until the end positions are reached.

### 2.3 Septum Measure

When we have our segmentation of the septum, we can divide it into two parts by drawing a straight line between our anchor points. Then the septum is divided into one part closest to the right ventricle (yellow) and one part closest to the left ventricle (blue), cf. Figure C.4. The septum measure we compute in each frame is

$$s = \frac{r_1 - r_2}{r_1 + r_2}, \quad (C.6)$$

where $r_1$ is the area of the region marked with yellow and $r_2$ is the area of the region marked with blue in Figure C.4. The measure showed to the user is then the mean value of the whole sequence of images chosen (e.g. one cardiac cycle). The measure is 0 if the septum is straight, a negative value if it bulges towards the left ventricle and a positive value if it bulges towards the right ventricle. It is also possible to show the variations of the septum measure during a sequence in a graph.
3 Results & Discussion

The tracking of anchor points has been visually evaluated and it works well in most cases. Three examples of the shortest path segmentation can be seen in Figure C.5. It can be seen here that the paths follow the edge between the septum and ventricle well despite varying intensity levels due to noise. In Figure C.5(c) the segmentation fails on the edge between the right ventricle and the septum. This is because the echoes of the septum are too low and it is hard to distinguish between septum and the right ventricle.

The whole algorithm described in the last section was tested on four patients with a total of 38 examinations and the resulting septum measures can be seen in Figure C.6. The professional assessments on the horizontal axis was obtained from medical records. As can be seen in this figure, there are not many examples of a septum that bulges towards the left ventricle. The reason is that it is not desirable to put these patients in that condition since it may be harmful for the heart. When an adequate pump speed is found, you stay there and do not try any higher speed. Despite this fact it is possible to see a trend for our septum measures with negative values when the septum bulges towards the left ventricle and large positive values when it bulges towards the right ventricle. This is also confirmed by the red line in Figure C.6 that corresponds to a least squares approximation.
Figure C.5: Three examples of the shortest path segmentation. The segmentation works fine in (a) and (b). Due to a lot of noise the segmentation goes wrong in (c).

of the measured values where the slope of the line is 0.3. The values of a straight septum which in theory would be around zero tends to be in the interval 0-0.5 where we have the majority of measurements and the value for our least squares approximation is 0.31 for this assessment.

In Figure C.7 we have three examples of patients with straight septum according to their assessment and where our algorithm gives a septum measure between 0.035 and 0.279. These examples are quite easily interpreted as straight even for an untrained eye. There are two examples in Figure C.8(a) and C.8(b) that really looks like they bulge towards the right ventricle and our septum measure gives a mean value around 0.90 but the assessment is that the septum is straight. The reason for this may be that the physician has taken some other information from the images into account when interpreting or maybe the annotation of the anchor points is not entirely correct and really needs to be done by an experienced user. Another thing that can give a septum measure that indicates that the septum bulges in some direction is the case in Figure C.8(c), where the septum is thicker towards one of the ventricles compared to the other. Here we get a septum measure of 0.522.

Two examples of septums that bulge towards the right ventricle and where our septum measure also gives a large positive value can be seen in Figure C.9(a) and C.9(b). Here we get a septum measure of 0.817 and 0.896. In Figure C.8(d) we get a negative value on a sequence where the assessment is that the septum
Figure C.6: The septum measure of 38 examinations on four patients. Each column of dots within each assessment corresponds to the same patient (LV = left ventricle, RV = right ventricle). The red line is a least squares approximation. Note that when we do the least squares approximation the measurements within each assessment has the same x-coordinate [-1,0,1].

bulges towards the right ventricle. This might be caused by the difficulties to annotate and track the anchor points correctly. The anchor point in the apical part is certainly not easy to position correctly since it is quite a lot of noise there. Also the segmentation has some difficulties to find the border between the septum and the right ventricle.

In Figure C.9(c) and C.9(d) we see the two examples of a septum that bulges towards the left ventricle and here we also get a negative septum measure. The segmentation of the case in Figure C.9(c) works quite well even though it is hard to see the septum because the left ventricle has decreased in size. The exact assessment of Figure C.9(d) is that it strikes against the left ventricle during some parts of the cardiac cycle. This is probably why we do not get such a large negative value since in other parts of the cycle it is more straight. This is one problem that can occur with taking the mean value of the septum measure. A good idea is therefore to present both the mean value of the septum measures as well as a curve of how it varies during the cardiac cycle.
4. Conclusion

The proposed method for segmenting the septum in echocardiographic images has turned out to work quite well. Some further work need to be done in order for the segmentation to be more robust to the noise in the echocardiographic images. The measure of septum shape that we have developed seems to be a good indicator on whether the pump speed is too high or too low. This can be of great clinical value for patients with an LVAD.

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Figure C.8: Four visualizations of the septum measure when the it disagrees with the assessments. In (a) $\bar{s} = 0.903$ (assessment: straight), in (b) $\bar{s} = 0.896$ (assessment: straight), in (c) $\bar{s} = 0.522$ (assessment: straight) and in (d) $\bar{s} = -0.114$ assessment: bulges towards the right ventricle).
Figure C.9: Four visualizations of the septum measure on patients with a septum that bulge towards the right ventricle in (a) and (b) and bulge towards the left ventricle in (c) and (d). In (a) $\bar{s} = 0.817$, in (b) $\bar{s} = 0.896$, in (c) $\bar{s} = -0.225$ and in (d) $\bar{s} = -0.085$. 

4. Conclusion
References


