The use of a body-wide automatic anatomy recognition system in image analysis of kidneys

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Summary

English:
In this thesis developed at MIPG, Upenn, we adapted, tested, and evaluated methods and algorithms for body-wide fuzzy modeling and automatic anatomy recognition (AAR) developed within MIPG in image analysis of kidneys. We built a family of body-wide fuzzy models, at a desired resolution of the population variables (gender, age), completed with anatomic, and organ geographic information. The implemented AAR system will then automatically recognize and delineate the anatomy in the given patient image(s) during clinical image interpretation. My training also included gaining proficiency in large software systems called 3DVIEWNIX and CAVASS which had an incorporation of all these developments.
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1. Introduction

1.1. Basic concept of quantitative medical Imaging

In this day and age, practice of Radiology is mostly qualitative. The physicians visualize the images to make a clinical decision at individual patient level. Also, the accuracy of disease recognition and reporting have been done by using biomarkers, and gathering volumes of image information which could be time consuming and not very cost effective. Quantification is a different approach to assess the normal values of anatomical sections of different parts of the human body. As an analogy, blood sample analysis represents different numbers that in turn indicates various parameters in the blood ranging from normal to abnormal. Obviously, the number out of range can be detected as an abnormality (1).

1.2. Motivation: Why Quantitative Radiology (QR)?

The main motivation of this thesis is to study the applications of Quantitative Radiology (QR) in clinical practice. Quantification has been investigated in clinical research, however only descriptive and qualitative radiology is used for the patients in the hospitals. Through my thesis I would like to prove that QR can be implemented in clinical practice as it can help improve early diagnosis, standardize object (also referred to as organs) management, improve understanding of normal disease processes, report and discover new biomarkers and to handle large volumes of image data effectively. This project helps visualizing more extensive knowledge in image processing, object identification and delineation as it can have some clear cut advantages in routine clinical practice for physicians and for the health care system. If QR can be adapted to clinical practice, it can improve the diagnostic values which are determined by sensitivity, specificity and accuracy.

Why Automatic Anatomy Recognition (AAR)?

AAR is computerized automatic anatomy recognition during radiological image reading. In order to achieve Quantitative Radiology we need body-wide Automatic anatomy recognition (AAR) to make it more objective, improve specificity and sensitivity for disease detection. Automatic recognition of the human inner organs from medical imaging data can make the quantitative radiology feasible. Automatic anatomy detection which is based on fuzzy object models (2-7) can provide the appropriate mathematical tools for creating fuzzy models which
can make it possible to extract the 3D models of organs from medical imaging data. Fuzzy and probability principles start off with different axioms and use different mathematical constructs and lead to different algorithms in images. Our motivation for using fuzzy objects modeling principle is to find natural and getting object information extraction from images as realistically as possible. In this thesis the focus was to see whether we can automatically recognize the kidney and delineate the anatomy of the kidney, then the quantification is easy to take. We are using AAR methodology to automatically detect kidney and study the kidneys.

Why kidney?
In clinical radiology practice, the interpretation of CT, MRI and PET images is typically descriptive, qualitative or semi-quantitative at best. Although some approaches may be useful to describe gross abnormalities that are present, they are often unable to detect early disease states that may be present in tissues of the body, and are frequently unable to sufficiently characterize disease conditions with high specificity. As such, quantitative assessments are required in order to improve diagnostic assessment of imaging datasets obtained in the clinical setting.

The kidneys may be affected by various disease conditions, including benign focal lesions such as cysts, oncocytomas, angiomyolipomas; malignant lesions such as renal cell carcinoma, lymphoma, or metastases; infection (i.e., acute pyelonephritis); vascular disease such as by vasculitis and infarction; and medical renal disease such as in relation to diabetes mellitus, hypertension, glomerular disease, drug-induced nephropathy, amongst others. In the present study, we are interested in applying quantitative assessment to abdominal MRI examinations in order to better characterize focal lesions that occur in the kidney. The main reasons to perform quantitative assessment in this clinical situation are to better characterize focal renal lesions as benign or malignant, and to improve the ability to determine the histological type of focal renal malignancy when present in order to optimize pretreatment planning and to prognosticate patient outcome.

1.3. Hypothesis:

From the existing body-wide AAR system, we can quickly adapt to specific applications in different body regions. Particularly in this project we are focusing on kidney and our claim is that the AAR system can be adapted to recognize and segment the kidneys from datasets in abdominal region. You do not have to start from the scratch to see how to segment the kidneys. Therefore this thesis can lead to a better approach for kidney segmentation.

Specific hypothesis:
One of the inputs of the model used for the AAR’s fuzzy model training is the hierarchical relationship of organs that are distinguishable for the model. This hierarchical graph plays an important role in the model and helps the recognition results to improve significantly. It is claimed that a more detailed anatomical hierarchy improves the position error between the predicted binary image produced by the AAR algorithm and the manually obtained one. This hypothesis is tested for the data set comprised of CT images of abdomen with the kidney as a target organ. It is claimed that the results are improved by adding an extra node (display children of top most parent in views) to the anatomical hierarchy. This extra node could be a combination of the target organ with some other organs. In this case both kidneys form a single node in the hierarchy as parent node for each one of them which are the target organs. When we have bilateral organs which means they are on both sides of the body having a hierarchy where two are combined in one object and then subsequently separated to the individual objects will give a better result. Results show a significant improvement although its cost in computation consuming time is negligible.

Different hierarchies may not give the same result for recognition.

When you have an AAR system, it can be adapted to different modalities like MRI very quickly.

1.4. Purposes and research topic:

Overall aim of this thesis is to adapt AAR methodology to the specific organ segmentation problem which is our broad aim, which can be subdivided in several components: (A1) gathering the training CT datasets for the different body regions – thorax (on computed tomography (CT)), abdomen (on CT and magnetic resonance imaging (MRI)), (A2) gathering MRI datasets for kidneys in abdominal region (A3) generate fuzzy model for these body regions especially for abdomen because kidneys are located in the abdominal region (A4) investigating different hierarchies to find out which hierarchies are most effective for the kidneys.

1.5. Literature review:

Several investigations (8-15) in kidney segmentation using both semi-automatic (9, 11, 12, 13) and fully automatic methods (8, 10, 14, 15) have been carried on CT and MRI images. Despite the important role of segmentation in medical imaging, difficulties are encountered due to the associated variations in image quality. For example, certain conventional methods as thresholding and region growing approaches (16) are often corrupted by noise, which can cause difficulties in applying these methods. Among these methods, for the semi-automatic kidney segmentation, they use optimal surface search with graph construction (11), segmentation of kidney from high-resolution multi-detector tomography images that uses a graph cuts technique
In the fully automatic methods, a constrained morphological 3D h-maxima transform approach (8), graph cuts framework for kidney segmentation with prior shape constraints (14), fully renal cortex segmentation on CT data sets using leave-one-out strategy (15).

Different approaches in the model processing part

Using the models including the prior information about shape and location of organs has been considered in order to constrain the variations in the whole model processing (17, 18). Different approaches have been reported in the whole model processing such as statistical theoretical framework, statistical shape modeling (19), statistical atlases (20), and not taking a fuzzy approach, except (2,3), both in the brain only. The novelty in our method is determined in the following considerations: (A) focusing on a particular organ system in image analysis, which are the kidneys. (B) Using fuzzy object models (2-7), which can provide the appropriate mathematical tools to extract three-dimensional models of organs from medical imaging datasets. Fuzzy set concepts have been used greatly, fuzzy modeling approaches allow bringing anatomic information in an all-digital form into graph theoretic frameworks designed for object recognition. (C) Modeling a more detailed anatomical hierarchy, which plays an important role in the model leading ultimately to the production of an effective AAR system. (D) Organizing kidneys, left kidney, and right kidney in a hierarchy, encoding kidneys relationship information in to the hierarchy. And (E) using optimal threshold-based recognition method, which is powerful concept with consequence in the kidneys recognition and delineation.

There are several steps involved in the Automatic Anatomy Recognition of the kidneys (AAR-QR) project; 1- collecting whole body imaging data from normal subjects 2- building and assessing fuzzy models 3- applying these fuzzy models in order to recognize and delineate anatomy in a certain diseased subject. (2-7)

In this project, we evaluated different organs to create several object’s models in this age group. Modeling processes had to be done with care, because it is problematic that many of these organs have no proper definition of the boundary in a mathematical sense. For example, we all understand what kidney means but when it comes to identifying kidneys’ boundary on CT or MRI images as a specified object becomes really challenging, even for some well-defined objects like liver. The problem is not only with kidney, but all open objects in the thorax and abdomen. Therefore, the first thing is to define the exact thoracic and abdomen regions, where it starts and where it ends. Then, work through all these areas, and come up with an overall definition that is comprehensible by physicians and radiologists.

In organ like kidney, there are vessels and lymphatic system which can potentially cause some issues while defining the boundary. Therefore, in order to avoid this, an expert has to define the boundary of the object and come up with some operation definition that could be applied to all the subjects in a very consistent manner.
Thus, it is very crucial to follow these steps to build a fundamental method to automatically process the modeling, recognition and delineating the anatomy in patient’s images. The modeling is based on hierarchy, which divides the body into separate parts like thorax and abdomen. It has been clear that there is no way to define the best hierarchical manner in the whole body, so certain organ hierarchy leads to obtain better results. Regarding this point the anatomical and computational organizations are not necessarily the same. For building this model, there are specialized tools that have already been developed for both thorax and abdomen called the 3DVIEWNIX.

Regarding the object definition and variation, there are also variations in the whole model processing itself. Bigger people may not necessarily have larger organs. The anatomy of some organs is independent of the size of the person. Some of them are symmetrical. For example, left and right kidney is considered as pair of organs with a fixed relationship, correlating among object size. They often have a high correlation in size. It means that, if one gets bigger then the other also becomes bigger, however these do not apply to all organs. Some organs even show no correlation or negative correlation, in geographic terms we can consider the relationship of the organs.

The scene is an image, which is the main type of data. It refers to multidimensional images like 2 dimensional (2D), 3D, 4D, and all the data that are handled in 3D. Fuzzy boundary is represented in different ways. For example, there is some source of the object in the image where it is not possible to make a hard decision, for doing segmentation in unclear objects; we have uncertainty, which typically is the region of boundary with pixel values. Fuzzy modeling approach allows capturing information about uncertainties at the patient level (e.g., partial volume effect) and organizing this information within the model.

1.6. MIPG perspective and 3DVIEWNIX

3DVIEWNIX has been developed and maintained by the Medical Image Processing Group. It has been employed by hundreds of sites. It is a powerful instrument which provides a variety of sophisticated approaches to manipulate, visualize and quantify structure information captured in multimodality image data. The operators will be able to employ a various processing paths through 3DVIEWNIX to achieve their study aims. (21)

3DVIEWNIX is based on the UNIX operating system, X-Window, and the C programming language. The basic philosophy of 3DVIEWNIX is that we have focused in medical images which are applicable in 2 dimensional (2D), 3D and 4D, in fact it is set up for n dimensional images. Some operations can do for 2 and 3 dimensional and some of them for 4D. You can consider images with the same body region but using deferent modality like CT and MRI since they give different types of information.

You need to define the object in images, for instance preprocessing can do this with defining the object, segmenting it explicitly or improving the object information by enhancing object information in different ways.
2. Automatic Anatomy Recognition methodology

The AAR methodology is graphically summarized in Figure 1. The body is separated into \( M \) body regions \( B_1 \ldots B_M \). Models are constructed for each specific body region and each population group \( G \). Three main blocks in Figure 1 correspond to model building, object recognition, and object delineation. A fuzzy model \( FM(O_\ell) \) is constructed separately for each object \( O_\ell \) in \( B, \ell=1, \ldots, L \), and these models are integrated into a hierarchy selected for each specific body region \( B \). The output of the first step is a fuzzy anatomic model \( FAM(B) \) of the body region \( B \). This model is employed to recognize objects in a given case image \( I \) of the specific body region \( B \) belonging to the specific population group \( G \) in the second step. The hierarchical relationship of organs is tracked in this process. The output of this step is the set of transformed fuzzy models \( FM^T(O_\ell) \) corresponding to the state when the objects are recognized in \( I \). These adapted models and the image \( I \) form the input to the third step of object delineation which also tracks the hierarchical relationship of organs. Finally the delineated objects are output as Images (2-7) (cf. fig. 1).
There are three components from our perspective. Describing concepts, methods and algorithms, and also in the given image how one can recognize and delineate automatically. Once you recognize and delineate the anatomy, quantification is easy to make.

2.1 What is segmentation?

Segmentation consists of assigning a label to every pixel in an image such that pixels with the same label share the same characteristics, like being part of the same organ. In fact, outlining images can be done either in hard or fuzzy way. It is very difficult to do fuzzy way for human; it
should be done only in the hard way. Segmentation consists of two tasks, recognition and delineation. Recognition is the high level task and is done with determining the object whereabouts in the scene, usually humans are more efficient than the computers to get this high level knowledge, but in delineation which is to determine the objects spatial extent and composition in the scene which is a low level task and very detailed quantitative task, usually computers do better than humans.

There is a large amount of publications about segmentation since image processing started. The method can be classified into three groups:

First, PI (purely image based) approach (6): Collecting the whole available information in an image and determining the best way of performing recognition and delineation. In most methods, recognition is done manually which actually specifies something and delineating is done automatically which mostly relies on available information in the given image only. (22-28)

The second method is shape model based (SM) approach (29-32): employing models to code object family shape information, recognition is based on model and it can be manual or the combination of both, the whole idea is to bring the model to perform recognition and delineation.

The third method is Hybrid approach: which is the combination of PI and SM approaches, in this method recognition is based on the model and can be done automatically. (33-36)

2.2. Fuzzy modeling

**Notation:** We will use the following notation throughout this thesis. G: the population group under consideration. B: the body region of focus. O₁...Oₗ: L objects (also referred to as organs) of B (such as kidney, liver, etc. for B= Abdomen) considered in B for AAR. We are focusing on fuzzy model and fuzzy model steps in a set of images and different subjects (N) because we are building the model for the normal subjects. I₁ ............Iₙ: Images for body region (B) and subjects all from a particular population group G. Iᵣ,传媒: the binary image representing the delineation of object Oₗ in the image I. FAM(B): Fuzzy anatomic model of the whole object assembly in the body region B with respect to its hierarchy since each specific body region has its own hierarchy. FMᵀ(Oₗ): Transformed FM(Oₗ) corresponding to the state when Oₗ is recognized in a given patient image I.

Gathering image database for B and G

Gathering body wide group wise image data for normal subjects, our essential ponder is that model should reflect what is normal based on our experience working in different applications and modalities. Normality is easier to model and the images were of high quality and visually appeared radiologically normal for the body region, that is why we are focusing on normal datasets. Our modeling schema is such that the population variables can be defined at higher “resolution” in the future and the model can then be updated when more data are added. For the
thoracic and abdominal body regions, a board certified radiologist selected all image data (CT and MRI) from our health system patient image database.

Delineating objects of B in the Images

There are two parts to this task – forming an effective definition of the specific body region B and the organs in B in terms of their precise anatomic extent, and then delineating the objects following the effective definition.

Delineation of objects: We can use some interactive tools, some manual tools and also some automatic tools. Through a combination of methods including live wire, iterative live wire (40) thresholding, and manual painting, tracing and modification. For instance, in the abdomen, to delineate kidney as an object by using the iterative live wire method. (Iterative live wire is a version of live wire in which once the object is segmented in one slice, the user commands next slice, the live wire then runs automatically in the next slice, and the process is continued until automatic outlining fails when the user resort to iterative live wire again, and so on). In MRI images, the same approach works if background non-uniformity correction and intensity standardization (41) are applied first to the images.

All segmentation results of the objects were examined for accuracy by several checks – generating 3D surface renditions of objects form each subjects in different objects combination as well as a slice-by-slice confirmation of the delineations overlaid on the gray images for all images.

Constructing fuzzy object models

The Fuzzy Anatomy Model FAM (B) of body region B for G is defined to be a quintuple: (2-7)

\[
\text{FAM (B)} = (H, M, \rho, \lambda, \eta).
\]  

[1]

Briefly, the overall definition of the five elements of FAM(B) is as follows. The first item is hierarchy (H) of the objects in the specific body region B. M is a set of fuzzy models; one fuzzy model associated with each object in B. ρ defines the parent-to-offspring relationship in hierarchy H over the specific population group G. λ expresses a set of scale factor ranges indicating the size variation of each object Oℓ over the population group G. η represents a set of measurements pertaining to the organs assembly in B (η could be used to measure the volume of the objects). A detailed explanation of these elements is presented below.

Hierarchy: H is expressed as a tree, of the objects in B. The idea is that, the whole body itself has middle tree, a root of the tree and different body region are different aspects and within these concepts each body region has its own hierarchy. For example, for thorax the root is the skin
boundary and everything else means other organs within the body region, there are some other hierarchy that can be used for the specific task of segmenting one or two specific objects like the kidneys.

\[ M = \{FM(O_\ell): 1 \leq \ell \leq L\} \] is a set of fuzzy models, one model per object. We are given the segmented images then they are outlined for object then fuzzy model expresses the fuzzy set that is the value of the voxel and indicates membership, so fuzziness that comes from the fact that these are for instance fifty different livers or lungs or kidneys, they are identical in size, position, orientation and shape, the idea of creating the fuzzy is to average them, so overlapped areas, maximize membership. (2-7)

\[ \rho \] describes the parent-to-offspring relationship in H over G: \[ \rho = \{\rho_{\ell,k}: O_\ell \text{ is a parent of } O_k, 1 \leq \ell, k \leq L\}. \] It also encodes whole body to body region relationships. If you take the center of \( O_\ell \) and center of \( O_k \) there are certain relationship geometrically.

\( \lambda \) is a set of scale ranges \( \lambda = \{\lambda_\ell=[\lambda_{b,\ell},\lambda_{h,\ell}]: 1 \leq \ell \leq L\} \) indicating the size variation of each object \( O_\ell \) over G. The size of the object can be expressed in a number. We can resize all of them to the same size. If you take one number, one possibility is the volume and scale factor. In scale factor, if you come up with one idea in the size of the object, you find the mean size and then scale everyone to the mean size so that it gives you the scale factor for every object. Also for every subject, so that scale factor has a variation over the population that can be different for every object. This information is made use of recognizing \( O_\ell \) in a given image to limit the search space for its pose. \( \eta \) represents a set of measurements pertaining to the objects in B. For details, see (2-7).

2.3 Recognition

Recognition is a high-level process of determining the whereabouts of an object in the image.

The second step is recognition. The goal of recognition is to determine where objects \( O_\ell \) are in a given test image I, to determine the best pose (location, orientation, and scale factor) of \( FM(O_\ell) \) in I, \( 1 \leq \ell \leq L \). We recognize the root object first in the hierarchy H. There is an initial global recognition step whose goal is an initial pose of FAM(B) in I in close to the known true objects in the binary images. This process is adjusted consequently hierarchically by using the parent-to-offspring relationship \( \rho_{\ell,k} \). The children \( O_k \) are recognized by knowledge of the pose of their already recognized parent \( O_\ell \). Root object should be used in the model for the given image. The best status of the position and orientation are known in the recognition. Then we can follow the hierarchy and parent’s objects relationship and the scale information. During the offspring object recognition, object’s root recognition is different with the recognition of the objects in the hierarchy; in fact we have several methods to do this.
There are many techniques for recognition depending on the types of objects such as: b-scale method, Fisher linear discriminate, optimum threshold and hierarchical registration. (37, 38, 39) For all of them we search the optimal method and also the optimal position for each case, depending on definition of the automation criteria. We have tested three methods and optimum threshold is the best one. If you do the recognition then you know that for every object in a given image position, orientation and size should be considered, once you provide that information then you need to do delineation.

2.4. Anatomic definition for thoracic and abdominal objects

We have conducted detailed analysis and review of the thoracic objects; there are numerous disparities and inconsistencies found, in the segmentation of various thoracic objects. To correct this issue and ensure consistency of the objects throughout all the subjects, we have refined the anatomic boundaries and definition of various thoracic objects. The 13 objects in the thoracic region are illustrated below in hierarchy (cf. fig. 2).

Figure 2 the 13 objects in the thoracic region are illustrated in hierarchy: tskin: thorax skin boundary; tb: trachea and bronchi; lps: left pleural space; rps: right pleural space; pc: pericardium; tsk: thoracic skeleton (previously bone); as: arterial system; vs: venous system; e: esophagus; rs: respiratory system (lps+rps+tb); ims: internal mediastinum (pc+as+vs+e); tscr: spinal cord; stmch: stomach.

This expresses the outline of the important correction and refinement made to the objects. The anatomic boundary of the thoracic region can be simply defined as the region starting from the base of the lung, all the way up to the apices of the lungs. More precisely, the inferior anatomic extent of the thoracic region, starts from 1 standard CT-axial slice below the first
appearance of the lung. Equals 5 mm below the first appearance of the lung, and the superior anatomic extent is defined up to, 3 standard CT–axial slices, above the apices of the lung (equal 15 mm above the apex of the lung). One slice in our axial CT patient images corresponds to 5 mm. in all images the slices go up from the base of the lungs to their apex (cf. fig. 3).

Figure.3 the anatomic boundary of the thoracic region

Tskin–thorax skin

The skin is segmented following the anatomic boundaries of the thoracic region, as described before. So, the inferior extent of segmentation for skin starts from one slice below the first appearance of the lungs. And the superior extent is marked by 3 standard CT–axial slices above the apices of the lungs. More precisely, the inferior extent anatomical bottom-most) of skin, is marked by 1 standard CT–axial slice, below the first appearance of the lung, (equals 5 mm below the first appearance of the lung) and the superior anatomic boundary for skin is all the way up to three standard CT axial slices above the apices of the lungs (cf. fig. 4).
RS – respiratory system

The respiratory system is an combined object of the individual objects namely, LPS – left plural sac, RPS– right plural sac and TB – trachea bronchi (cf. fig. 5).
The inferior extent of the left plural sac is defined by the base of the lung, the first appearance of the left plural sac, on the bottom-most slice, and the superior extent is defined by the apex of the left lung (cf. fig. 6).

Figure 5 (a) the axial CT slice with overlaid rs segment (b) 3D rendered rs object. LPS – left plural sac

Figure 6 the axial CT slice with overlaid lps segment.

RPS – right plural sac
The inferior extent of the right plural sac is defined by the base of the lung, the first appearance of the right plural sac, on the bottom-most slice, and the superior extent is defined by the apex of the right lung (cf. fig. 7).

(a)                                                                     (b)

Figure 7 (a) the axial CT slice with overlaid rps segment (b) 3D rendered rps object.

Trachea and bronchi – tb

The superior/top anatomic boundary for segmentation of tb would be marked by the last axial slice, in the upper thoracic region, where the trachea is visible. And the tb is segmented all the way down, towards the inferior boundary, including the branching of trachea into the left and right bronchi. The main structure of left and right bronchioles is included, whereas the secondary branches and bronchioles are excluded. From a simple visual perspective, the ‘general upside-down Y’ structure was included with all the additional branches cut off/excluded. The superior boundary is marked by the superior anatomic delimiting plane for tb, i.e. until trachea is visible in the upper thoracic region (cf. fig. 8).
Figure 8 (c) the axial CT slice with overlaid tb segment (d) 3D rendered tb object.

Tsk –bone

The bone is segmented all the way through the body region, from the posterior to anterior boundary of the skin (cf. fig. 9).

Figure 9 (e) 3D rendered tsk object, (f) the axial CT slice with overlaid tsk segment

Ims –internal mediastina system

The ims is a combined object, which includes the following objects pc -pericardium, e – esophagus, a –arterial system and vs –venous system (cf. fig. 10).
Pericardium – pc

In theory, pericardium is a double-walled sac containing the heart and the roots of the great vessels (cf. fig. 11a). But, in the reality, the vessels that emerges out of the pericardium and are seen more visibly as discrete structures and the enclosing sac is not always explicitly visible on the axial CT slices. We have decided to consistently define the pericardium by tracing the actual boundary-pericardial sac itself.

The top boundary or the extent to which the vessels are to be included and the anatomic point of reference for the anterior-top boundary will be marked by the plane/axial slice where the pulmonary trunk starts to branch out to the right/left pulmonary artery. (cf. fig. 11b).
Esophagus

The segmentation of esophagus starts in the inferior/bottom section, from the first slice of the thoracic region and all the way to the top superior/top section, until the plane/axial –slice where the trachea is visibly seen. In other words, the superior/top anatomic boundary of the object tb is also considered the superior delimiting point of reference or the upper cut-off point for esophagus.

In anatomic terms, the anterior extent of esophagus is segmented from the very first bottom-most slice of the thoracic region all the way through up until the superior/top anatomic boundary of trachea –i.e., until trachea is visible. (cf. fig. 12).
Figure 12 (g) the anatomical information of the e object, (h) 3D rendered e object.

Arterial system – as

The inferior anatomic boundary, for segmenting as, starts from the first slice of the thoracic region (anatomically bottom-most), and the superior/top anatomic boundary is the anatomic extent to which, the three arteries that arise from the aortic arch, are included into as. In abstract terms, we include the aorta, ascending aorta, the aortic arch and the three arteries that rise from above the aortic arch. In the superior extent of as, the brachiocephalic artery, left common carotid artery and left subclavian artery should be included all the way until the plane/axial –slice where any of them start to branch out. In other words, the axial-plane at which any of these three arteries starts to branch out acts as our cut-off point for the superior section or boundary. The inclusion of pulmonary trunk starts from the plane/axial –slice where the ascending aorta first appears. In fact traversing from the inferior to superior section in while segmenting, the appearance of ascending aorta acts as our anatomic point of reference to start tracing the pulmonary trunk. (cf. fig. 13).
Figure.13 (a) the anatomical information of the as object, (b) 3D rendered as object.

Venous system –vs

The inferior extent of segmentation of vs starts from first (anatomically bottom- most) slice, where the azygos vein is visible. And the superior/top anatomic boundary or the cut-off would be the plane/axial-slice where the secondary branches on the brachiocephalic veins start. vs segment would include the azygos vein (the azygos branches and sub-branches are not included), superior vena cava and right and left brachiocephalic vein, where one of the brachiocephalic veins is separating into two or more branches. (cf. fig. 14).
All the above defined objects, for n= 50 subjects, have been refined and corrected accordingly. These revisions and refinements to the anatomic boundaries and definitions of the thoracic objects would facilitate the accomplishment of more consistency thorough the objects, thereby producing crisper models.

We have conducted analysis for most of the abdominal objects. To ensure consistency of the objects throughout all the subjects, we have refined the anatomic boundaries and definitions of various abdominal objects, which are outlined in this document (cf. fig. 15).
Figure 15 (a) the 11 objects in the abdominal region are illustrated in hierarchy. aia: aorta until bifurcation to iliac arteries; asft: abdominal soft tissue (mscl + spln + rkld + lkd + aia + ivc); ask: abdominal skeleton; askin: abdominal skin; ivc: inferior vena cava; lvr: liver; lkd: left kidney; mscl: muscle; rkld: right kidney; spln: spleen; sat: subcutaneous adipose tissue.

Definition of abdominal region:

The inferior anatomic boundary of the abdominal region can be simply defined by the plane/axial slice where the union of the right and left common iliac arteries is anatomically represented by the top-most, axial slice that marks the top/superior aspect of the liver (cf. fig. 16).
Figure 16 the anatomic boundary of the abdomen region

Askin-abdominal skin

The skin is segmented following the anatomic boundaries of the abdominal region, as described before. So, the inferior extent of segmentation for skin starts from the slice where the common iliac arteries unite and form the aorta. And the superior extent is marked by the axial slice, where the superior part/top of the liver is seen in the upper abdominal region (cf. fig. 17).

Figure 17 the anatomic boundary of the askin object
Abdominal skeleton – ask

The segmentation of ask is in below. (cf. fig. 18).

Figure.18 3D rendered ask object

Asft, this is a combined object obtained by including the individual objects namely, Muscle, spleen, right kidney, left kidney, Aorta and iliac artery, inferior vena cava.

Lvr- liver

The superior anatomic boundary for the segmentation of liver, would lie on the plane/axial-slice where the top-most part of liver appears. And the inferior anatomic boundary would be defined by the plane/axial-slice, where the liver first starts to appear. The portal and hepatic arteries and veins are included when approaching and entering into the liver and extraneous extensions are excluded (cf. fig. 19).
Sat, the subcutaneous adipose tissue (sat), refers to the layers of fat, right beneath the skin. The sat is segmented using the following approaches:

To segment subcutaneous adipose tissues as an object, the skin outer boundary (as an object) is first segmented by using the iterative live wire method (40). Subsequently, the interface between the subcutaneous and visceral adipose compartments is delineated by using also the iterative live wire method. Once these two object boundaries are delineated, the subcutaneous and visceral components are delineated by using thresholding and morphological operations. (cf. fig. 20).
Spl-spleen

The superior and inferior extent for the object, spleen, is defined by the extent of boundary of the object itself. In other words, the spleen is segmented from and to where it actually starts and ends on the axial slices. The actual sac like, physical spleen structure cleanly segment from the start to end of the object, the extraneous structures like the vessels which enter into and come out of the spleen, are excluded (cf. fig. 21).

![3D rendered spl object](image)

Figure.21 3D rendered spl object

Rkd- right kidney and lkd- left kidney

The superior and inferior anatomic boundary for both right and left kidneys is defined by the superior and inferior boundaries of the individual objects itself. In other words, the right kidney is segmented from the inferior boundary of the right kidney all the way up to the superior boundary of the right kidney. The same applies to the left kidney as well. Based on review, we have decided that the segmentation would follow and include the actual bean shaped structure of the kidney. All the other external blood vessels (viz, renal arteries, renal veins) are excluded (cf. fig. 22)
Aorta and iliac arteries

The superior and inferior boundaries of the aia are defined by the pre-defined boundary of the abdominal region. Anatomically, aia includes the abdominal aorta, from the point of union of common iliac arteries, all the way up to the aorta, delimited by the superior boundary of the
abdominal region. We include only the structure of aorta through this region and the branches/sub-branches of arteries are not included (cf. fig. 24).

![Diagram showing abdominal aorta and inferior vena cava with important branches.](image)

Figure 24 (e) the anatomical information of the aorta and iliac arteries objects, (f) 3D rendered aia object

IVC – inferior vena cava

Anatomically, ivc includes the inferior vena cava, from the point of union of iliac veins, all the way up, until the delimitation by the superior boundary of the abdominal region. We only include the actual structure ivc; the branches/sub-branches of veins, are not included (cf. fig. 25).
Figure.25 3D rendered ivc object

Muscle -mscl (cf. fig. 26).

Mscl is delineated by using thresholding and morphological operations as the same procedure for sat.

Figure.26 3D rendered mscl object
3. Adaptation of AAR to kidney segmentation

3.1. About kidney

The kidneys are a pair of organs located in the back of the abdomen the size of each kidney is about 4 or 5 inches long [length – about 12 cm breath- about 6 cm thickness], the average weight of a normal, healthy adult kidney is approximately 120-140 grams. The kidney helps maintain a constant environment within the body and also the kidney regulates water and electrolyte levels within narrow limits and removes waste metabolic products and foreign toxin. The kidney regulates Red blood cell concentration and maintains blood pressure in our body. They are essential in the urinary system and serve the body as a natural filter of the blood.

There are different types of kidney diseases and also different types of kidney cancer exist like renal cell carcinoma which is one of the most common cancers.

Figure.27 the anatomical information of kidney object

Location and structure
Regarding to the abdominal cavity the right kidney is slightly lower than the left kidney and also left kidney is located more centered than the right. The relationship between right kidney and liver and also left kidney and spleen is really interesting, according to our data base in most subject the liver hugs the right kidney and the spleen is like a roof at the top of the left kidney. Both right and left kidney moves down on inhalation. The kidney has a bean shape structure and each kidney has a convex and concave surfaces.

![Diagram of kidney and related structures](image)

Figure.28 the anatomical information of kidney object

3.2. Automatic recognition strategies

As I explained before, we have different types of hierarchies, the fuzzy model and the result is based on this hierarchy; askin, kidneys (which is the combination of left kidney and right kidney), left kidney (lkd) and right kidney (rkd) as shown below. Different hierarchies are tested for the data set comprised of CT images of abdomen with the kidneys as target organs. It is shown how the results are improved by adding an extra node to the anatomical hierarchy and also different types of hierarchies may not give the same result for recognition (cf. fig. 29).
Figure 29 the 4 objects in the abdominal region are illustrated in hierarchy. Askin; kidneys (which is the combination of left kidney and right kidney); left kidney (lkd) and right kidney (rkd).

The recognition result is based on optimal thresholding which is an important concept. Meaning that optimization is a vast branch of mathematics. The hierarchical order also is followed in this method. Optimal thresholding method uses known (learned) fixed object threshold interval and minimal false positive and false negative of the threshold image with respect to FM(O₁) for best recognition. For MRI images for this approach to make sense, it is essential to correct for background intensity non-uniformities arising from magnetic field inhomogeneity first, followed by intensity standardization (40). So in this context the root object is recognized first, for the hierarchy shown in Figure 28, the root object is the skin outer boundary. There is a global approach, which does not involve searching for the best pose. We call this the One-Shot Method which is used as initialization for a more refined optimal thresholding method. (2-7)

One-Shot Method

We know approximately what the threshold for the root object O₁ is (by applying a threshold to I), and then from that approximate threshold you can roughly segment O₁ to produce a binary Image. The goal of the one-shot method is to find the mean relationship, estimated from the
training images, between the roughly segmented $O_1$ and the true segmentation of $O_1$. This estimation can be specified by the geometric center from the set of 1-voxels of any binary image and the eigenvectors derived from $X$ via principle component analysis. Similar thresholding is performed on each gray image $I_n$ in the training datasets to acquire a rough segmentation of $O_1$. The mean, of such estimation over all training images is done at the model building stage of AAR. The pose of all other objects are adjusted consequently hierarchically by using parent-to-offspring relationship $\rho_{\ell,k}$.

Optimal thresholding method

This is a method to refine the result found from the one-shot method, starting from the initial pose obtained by the one-shot method, a search is made within the pose space for an optimal pose of the fuzzy model that yields the smallest sum of the volume of false positive and false negative regions. It should be considered that the model itself is taken as the reference for defining false positive and false negative regions. As the model is fuzzy so at every voxel there is a membership, therefore when you find the threshold for given interval you get the binary image, in this context the false positive and false negative correspond to the disagreement between the membership of the fuzzy model and the thresholding result. The search space to find an optimal pose is limited to a region around the initial pose. This region is determined from a knowledge of $\rho_{\ell,k}$ and its variation and the scale factor range $\lambda$.

Determining the optimal threshold interval at the model building stage

Suppose we already built fuzzy model and estimated $\rho$ and $\lambda$. We run the recognition process on the training datasets. Since we still do not know the optimal threshold but have the true segmentations made by a person. The process is to test out recognition ability for each of a number of threshold intervals and then select the threshold interval that yields the best match of the model with known true segmentation for each object.

To summary, the optimal threshold method of recognition consists of three steps: (a) starts the search process from the initial pose indicated by the one-shot method. (b) It uses the optimal threshold values determined from the training datasets for each object. And (c) finds the best pose for $\text{FM}(O_\ell)$ in the given image $I$ by optimally matching the model with thresholded image $I$.

3.3 Image data

CT datasets: We focused on males aged 50-60 years old with normal hospital data base in thorax and abdomen. The images are acquired using breath-hold CT, they were contrast enhanced, their size and their level of digitization was 0.9*0.9*5 mm, the slice basing (basis) was 512*512*80 pixels/voxels. The number of subjects was 50.
For those regions in 50-60 subjects, we have used half of the data base for creating the model and the other half for testing it.

MRI datasets: we focused on males and females aged 28-78 years old with various focal renal pathologies (normal, cysts, angiomyolipomas, and renal cell carcinomas of different types) in abdomen with the kidneys as target organs. They were T1-weighthed, axial post contrast enhanced, delayed phase, their size and their level of digitization was 0.7*0.7*4-5mm, the slice basing (basis) was 512*512*40-69 pixels/voxels. Manufacturer: GE medical systems, manufacturer’s model name: GENESIS_SIGNA, magnetic field strength: 15000, spacing between slices: 7. Repetition time TR: 1210.54 msec. Eco time TE: 183.55 msec. In the case of MRI, the resulting images are processed, first to suppress background non-uniformities and subsequently to standardize the image intensities (41). Standardization is done separately for each MRI case. The number of subjects was 17.

3.4 Experiments

These are some examples of thorax and abdomen objects that we have used in the model building FM(O). Since the volumes are fuzzy, they are volume rendered by using an appropriate opacity function. The objects that we have considered look like a picture collection. It is important to understand the relationship between the objects and the way the objects fit together in terms of relationships and also core identifications. It looks like they enfold each other; there is a lot of prior information about object’s specific relationship for every subject consistently. For example, in the aorta and inferior vena cava and the kidneys how the same angles in to the same cross, and also spleen and left kidney enfold each other very nicely, and muscle and soft tissue. (cf. fig. 30).
Figure 30: Renditions of objects used for modeling from two body regions (abdomen and thorax)
3.5 Results and discussions

Results for recognition are summarized in Figures 32-33 and Tables 1-4 for the kidneys as target organs. The recognition accuracy is expressed in terms of position and size. Values 0 and 1 for the two measures, respectively, indicate perfect recognition. The position error is expressed as the distance between the geometric centers of the known true objects in the binary images and the center of the adjusted fuzzy model $FM^T(O_i)$. The size error is expressed as a ratio of the estimated size of the object at recognition and true size.
Figure 3.2 sample recognition results for some of the tested organs for Abdomen on CT images based on optimal thresholding method. Cross sections of the model are shown overlaid on test image slices. (a) skin, (b) kidneys, (c) right kidney (rkd) and (d) left kidney (lkd).

<table>
<thead>
<tr>
<th>subjects</th>
<th>Position Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abd-CT001</td>
<td>2.3258000</td>
</tr>
<tr>
<td>Abd-CT002</td>
<td>11.3573000</td>
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<tr>
<td>Abd-CT003</td>
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<tr>
<td>Abd-CT004</td>
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</tr>
<tr>
<td>Abd-CT005</td>
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</tr>
<tr>
<td>Abd-CT006</td>
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<td>Abd-CT007</td>
<td>4.3550000</td>
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<td>Abd-CT008</td>
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<td>Abd-CT010</td>
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<td>Abd-CT011</td>
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<td>Abd-CT012</td>
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<tr>
<td>Abd-CT015</td>
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<tr>
<td>Abd-CT016</td>
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<td>Abd-CT017</td>
<td>9.1735000</td>
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<tr>
<td>Abd-CT018</td>
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<tr>
<td>Abd-CT019</td>
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</tr>
<tr>
<td>Abd-CT020</td>
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<tr>
<td>Mean(mm)</td>
<td>7.3747750</td>
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<tr>
<td>SD(mm)</td>
<td>5.08798396</td>
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</tbody>
</table>

Table 1: recognition results (mean, standard deviation) for some of the tested organs for Abdomen on CT images, skin, kidneys, left kidney (lkd) and right kidney (rkd)
<table>
<thead>
<tr>
<th>subjects</th>
<th>Scale factor error as size ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abd-CT001</td>
<td>1.014400 1.041300 0.872700 1.023900</td>
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<td>Abd-CT002</td>
<td>1.007300 0.813200 0.918000 0.778300</td>
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<td>Abd-CT004</td>
<td>1.018500 0.928100 0.794900 0.787300</td>
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<td>Abd-CT020</td>
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**mean**  
<table>
<thead>
<tr>
<th>skin</th>
<th>kidneys</th>
<th>lkd</th>
<th>rkd</th>
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<tbody>
<tr>
<td>1.026625</td>
<td>0.9312100</td>
<td>0.9210200</td>
<td>0.9271000</td>
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<tr>
<td>SD</td>
<td>0.01457947</td>
<td>0.14344882</td>
<td>0.11001672</td>
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Table.2 scale factor error as size ratio for some of the tested organs for Abdomen on CT images, askin, kidneys, left kidney (lkd) and right kidney (rkd).

For those subjects from MRI datasets, we have used the CT data base for creating the model and we have tested result for recognition on MRI. The results are shown below (cf. fig. 33) and (cf. tb. 3-4).
Figure 3.3 sample recognition result for some of the tested organs on MRI datasets for Abdomen based on optimal thresholding method. Cross sections of the model are shown overlaid on test image slices. (e) Askin, (f) kidneys, (g) right kidney (rkd) and (h) left kidney (lkd)

<table>
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<tr>
<th>MRI-1</th>
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<td>3.7500000</td>
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<td>MRI-3</td>
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<td>MRI-4</td>
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<td>MRI-5</td>
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<td>MRI-7</td>
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<td>MRI-9</td>
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<td>MRI-11</td>
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<td>MRI-15</td>
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<td></td>
<td>MRI-16</td>
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<tr>
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<td>--------</td>
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<tr>
<td>Mean(mm)</td>
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<table>
<thead>
<tr>
<th></th>
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<tr>
<td>mean</td>
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<tr>
<td>SD</td>
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<td>0.08158655</td>
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Table 3 recognition results (mean, standard deviation) for some of the tested organs for Abdomen on MRI images, askin, kidneys, left kidney (lkd) and right kidney (rkd).

Table 4 scale factor error as size ratio for some of the tested organs for Abdomen on MRI images, askin, kidneys, left kidney (lkd) and right kidney (rkd).

The size error is always close to 1 for most of the objects, the position error is between 1-3 voxels. The result from CT and MRI datasets are good enough for delineation which is the next
step. The results from MRI data sets are remarkable since the results are generated by using the models built at a different modality, namely CT, and for a different group with an age difference of about 28-78 years.

4. Conclusions

It is possible to design, adapt, test and evaluate methods and algorithm for body wide fuzzy modeling and automatic anatomy recognition (AAR) system in Image analysis of kidneys.

In this thesis I have taken a fuzzy approach to modeling and some aspects of the fuzzy model building operation (2-7). I have considered the hierarchical organization H of the kidneys, the hierarchical information in the building process. It is shown how the results are improved by adding an extra node to the anatomical hierarchy.

<table>
<thead>
<tr>
<th>Position Error (mm)</th>
<th>Askin</th>
<th>lkd</th>
<th>rkd</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.37</td>
<td>14.56</td>
<td>5.08</td>
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<tr>
<td>5.08</td>
<td>13.43</td>
<td>8.70</td>
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</tr>
<tr>
<td>Size Error</td>
<td>1.02</td>
<td>0.90</td>
<td>0.91</td>
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<td>0.01</td>
<td>0.90</td>
<td>0.08</td>
<td>0.03</td>
</tr>
</tbody>
</table>

Table.5 Recognition accuracy (mean, standard deviation) for some of the tested organs shown in Figure 34 for Abdomen on CT images

Figure.34 the 3 objects in the abdominal region are illustrated in hierarchy. Askin; left kidney (lk); and right kidney (rkd)
Table 6 Recognition accuracy (mean, standard deviation) for some of the tested organs shown in Figure 35 for Abdomen on CT images

Figure 35: The 4 objects in the abdominal region are illustrated in hierarchy: Askin; kidneys (which is the combination of left kidney and right kidney); left kidney (lkd) and right kidney (rkd).

Positional recognition accuracy for skin, kidneys, left kidney and right kidney is good enough for delineation TP(true positive) and FP(false positive) of ≥ 90% and ≤ 0.5% See References (42-44) for delineation result. Our data sets have 4-5 mm slice spacing, which means that objects recognition accuracy in position is within about 1-3 voxels.

The AAR methodology can be applied to different modalities like CT and MRI and also different body region such as thorax and abdomen. In order to recognize the anatomy of the kidney in a certain diseased subject; future studies will include extension of developed algorithms into different modalities like MRI with different protocols and PET.

5. Acknowledgement

- I would like to express my great appreciation to Dr. Jayaram K. Udupa for approving my application to perform my master thesis in his MIPG section and also for his guidance and constant supervision. The supervision and support that he gave truly help the progression and smoothness of the project.
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I wish to acknowledge the help provided by Dewey Odhner in the MIPG section.
I wish to thank my family for their tremendous contributions and support.

6. REFERENCES


43. Tong, Y., Udupa J.K., Odhner, D., Sin, S., Arens, R., “Recognition of Upper Airway and