MEDICAL IMAGE UNDERSTANDING USING ANATOMICAL MODELS : APPLICATION TO CHEST X-RAYS

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ABSTRACT: A comprehensive "expert assistant" system is being developed with initial application to chest X-rays. This system is characterised by the use of explicit anatomical models for reasoning about the anatomy, and for visualising the anatomical structures identified in the image segmentation. The overall strategy is to compare a modality-independent model with the image(s) by way of an intermediate feature space. The system is implemented to identify major structures on chest X-rays, mainly using long edges. An explicit three-dimensional anatomical model forms a major system component, and the object-oriented structure of this model permits adaptation and anatomical reasoning. The system is implemented in a frame structure using LISP, and features automatic and interactive segmentation of major landmarks in chest X-rays.

1. OVERVIEW OF THE SYSTEM

A role is emerging for "expert assistant" software for medical imaging workstations [13]. Image processing, high-level concepts and prior knowledge are essential components of such systems. Medical image processing systems are diverging from methodologies drawn from computer vision since many of the underlying assumptions of computer vision are not applicable in medical imaging. For example, the segmentation of a scene as objects v. ground is rarely appropriate, especially in the case of projection modalities. Multiple views of the anatomy are frequently obtained by disparate imaging modalities where data fusion cannot be achieved by image registration. But at an expert human level they can be perceived as representations of the same underlying anatomy. It is the underlying thesis of this paper that anatomical reasoning is the basis of modality-independent knowledge, and that explicit anatomical

Y. Bizais et al. (eds.), Information Processing in Medical Imaging, 239–250.

models are an essential component of a medical image understanding system, and therefore of an expert assistant system.

Anatomical knowledge is commonly introduced into medical image segmentation by means of elastic matching to anatomical atlases [1]. When performed in two dimensions such systems commonly encounter difficulty with anatomical variations, particularly those in which three-, rather than two-dimensional deformations are required for a complete description. For these reasons, this work has addressed the use of three-dimensional anatomical models in medical image interpretation. Such modelling as a strategy in image interpretation sets out to capture aspects of the human expert's reasoning, particularly those aspects which occur at the "expert" level, rather than at the level of simple object segmentation. It is believed that the reasoning process of clinicians takes place in "anatomical space", where concepts such as spatial relationships, connectivities, ranges of normality define the metric. The hierarchical, systematised nature of anatomical knowledge is compatible with computer knowledge databases [12], while links to visualisations and interactivity are readily incorporated. Systematic concepts which may be incorporated into an anatomical model include tissue and organ types described through inheritance. For spatial reasoning, the model must be deformable in an anatomically consistent fashion, maintaining, for example, invariant connections between organs. Thus it is not essential that the model represents a detailed normal atlas; however, the model must be deformable to actual anatomies. In practice, an initial state of the model close to average anatomy minimises the "distance" of the excursion in anatomical space from the initial point to an instantiated anatomy.

For compactness, the model needs to be hierarchical and parameterised. One way of achieving this is through Lindenmayer systems ("L-systems") [7,8], an iterative description of complex structures previously applied to plants and described in detail in Section 3. This allows complex structures to be described using a small number of anatomically significant parameters. Shape descriptions need to incorporate a trade-off between the compactness of parametric descriptions and the explicitness of vertex descriptions.

The ability to describe anatomical relationships in natural language [10] is achieved by an object-oriented structure. The principal invariance property is connectedness, that is, the connections between organs must be maintained. A second property, defined as adjacency, refers to contact between organs which may allow them to slide over one another. The description needs to be embedded in a knowledge system where relationships more complex than spatial relationships may be explored, including functional relationships invoked in testing disease hypotheses.

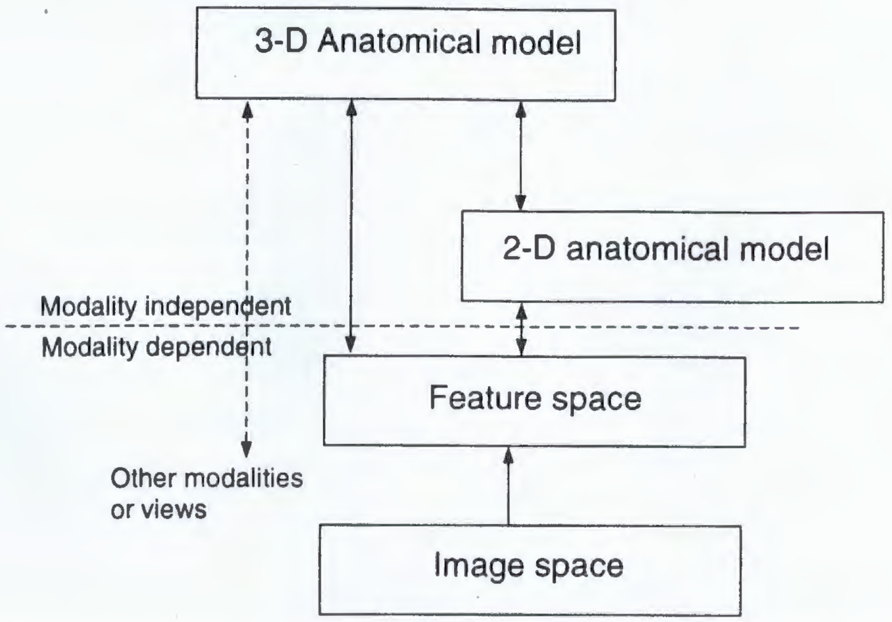

Fig. 1. The relationships between the pixel-based image space, "anatomical space" as defined by two and three dimensional models, and the intermediate feature space.

While several systems exist for describing anatomy using object-oriented models (e.g. Schubert et al., [12]), linking such a system to medical images is a distinguishing feature of the present system (see also [10]). A prime requirement of the system is that the model itself is independent of imaging modality. This requires the intermediate stage of a modality-dependent feature space description which contains symbolic information about image-space features such as edge character and location, textures and multiple relationships among them (Fig. 1). Image segmentation proceeds on an iterative basis, with refinements to the segmentation being based on crude models, which progressively refine the 3-D model.

The system has initially been implemented on posterior-anterior chest X-rays [2]. This clinical problem was chosen as an ideal application for an "expert assistant" because of the large throughput of chest X-rays in most radiology practices [5]. The X-ray projection process superimposes contributions from the whole of the anatomy, requiring 3-D anatomical knowledge. While many lung diseases are diagnosed on the basis of texture changes within the lung fields, the approach in this project has been to restrict the scope to abnormalities more readily described as anatomical or structural variations. This has effectively restricted the diagnoses to identifying abnormalities of long, smooth edges.

2. IMPLEMENTATION

The software has been implemented on a Silicon Graphics Iris Indigo workstation, using LISP for high-level control, and Iris Inventor for model visualisation. A user interface has been designed using the GL Library and resembles a standard PACS user interface, so that interactivity can be investigated by clinicians unfamiliar with image processing interfaces. "Features" not available in conventional workstations, but made possible by the image-understanding capabilities, include anatomical visualisation, automatic and interactive image segmentation, a report on abnormalities of major structures and automatic measurement of lung field sizes and the cardio-thoracic ratio.

Extensive use is made of frame structures for knowledge management [9]. Features of the frame structure include the following:
(1) Each frame is associated with a specific entity such as an organ, organ spatial relationship, image feature etc.
(2) Slots, which contain specific pieces of information related to an instantiation of the frame such as spatial coordinates, names etc.
(3) Procedures which modify slots, create frames according to defined algorithms or translate model knowledge into constraints in blackboard frames.

The frame structure is ideal for organising information in several domains in the current system, and specific applications include the following:
(1) "Blackboard" architecture [9] which is implemented for the feature space description. This is a network of frames with variable slots, in which, for example, edges may be identified from their binary relationships (e.g. "Edge A is to the left of edge B") with these relationships themselves occupying slots. The relationships are stored as fuzzy membership values of sets.

(2) The anatomical model itself stored in a frame-based structure. Slots include name of organ, pointers to parameters defining the organ shape, information about connectivities and adjacencies, X-ray attenuation and collision resolution procedure. Procedures include:

(1) Modifying anatomy of a particular organ to match an image feature;
(2) Modifying nearby organs to maintain adjacency and connectivity;
(3) Generating feature-space information from the model, such as edge positions.

Images are derived from conventional X-ray films digitised using a Lumisys 100 digitiser which records images at up to 50 μm spatial resolution, 12 bit dynamic range.

3. ANATOMICAL MODEL

Organ shape descriptions have received much attention in the literature [3,4,11]. The shape descriptions used for image matching have some strict requirements:

(1) They should be "natural" in order to express variations in anatomy, even at the level of basic topology.

(2) They must be expressible in terms of a small number of parameters which can be varied to match the image to organ shape. Editing organ shape should be intuitive: for example, an extended organ (such as a blood vessel or a stomach) should be movable without affecting its diameter.

(3) Deriving image parameters from the model must be computationally efficient, so that an iterative matching process can be invoked. For projection imaging, this requires rapid re-calculation of the edge locations; for cross-sectional imaging, rapid calculation of arbitrary sections is essential.

(4) A vertex representation of the anatomy must be derivable from the parametric description. This assists both in visualisation, and in invoking the adjacency, connectedness and collision procedures which maintain anatomical consistency.

Most organs are defined in terms of a natural medial axis, usually the embryological axis from which organ growth actually took place. The axis shape can be defined parametrically as a spline curve, or iteratively through L-systems [7,8]. At several points along the medial axis, cross-sections are defined. These are parameterised using Fourier descriptors in polar coordinate space. The axial variation of the Fourier descriptors themselves may be parameterised as, for example, polynomial curves, although this removes the local nature of individual parameters.

Positions, relationships and shapes of organs are influenced by gravity, internal pressures, elasticity and growth patterns. Organ shapes may be influenced by adjacent organs. For example, the shape of the lung is determined almost exclusively by the size and positions of surrounding organs. The concept of organ "indentation", where organs adopt shapes determined by those of the surrounding organs is a well-established anatomical concept, as is "displacement", where organs are moved from their original position, retaining their shape. The space-filling property of anatomical structures implies that each part of an organ surface is shared between two organs, and after collision and space-filling constraints have been satisfied, the vertex representations of organ shapes is highly redundant (in theory by a factor of 2). This used when defining a rank order of organs such that organ i usually indents or displaces organ $i+1$. In the chest, this is achieved by the sequence:

$i=$	1	2	3	4	5
Organ type	Bones	Diaphragm	Heart	Vessels	Lungs

Lung shape descriptors are therefore not included, the lung surfaces being defined by the mediastinum, diaphragm and costal pleurae.

Organ shapes and connectivities may be described in a compact and parametric form using an L-systems description, as used by Lindenmayer for describing plant growth [7,8]. This is an iterative symbolic description in which elements such as generalised cylinders are progressively added to form a complex system, the accretion process mimicking physical growth. This approach has been found to be particularly useful in describing skeletal structures, as shown in Fig. 2.

Organs with more complex shapes can be described by a combination of the L-system representation, with cross-sectional boundaries represented by Fourier contour descriptors. Parametrically the x and y coordinates of each contour in the set can be represented as follows:

$$x = r(c,s)\cos(\theta(c,s))$$
$$y = r(c,s)\sin(\theta(c,s)) \qquad \text{(Eq. 1)}$$
$$z = s$$

Fig 2. Model of the skeletal structures in the chest, generated using an iterative 9-parameter L-systems approach.

where r is the distance from the centroid and is a function of two parameters: c for points on the contour plane, and s for points on the surface resulting from the ensemble of contours or slices. To achieve a more parametric representation of an individual contour $r(c)$, the discrete Fourier descriptors are obtained as:

$$a_k = \frac{1}{M}\sum_{m=0}^{M-1} r(c)\exp(-2j\pi km / M) \qquad k = 0,\cdots,M-1 \qquad \text{(Eq. 2)}$$

where M is the number of vertices in the contour, and a_k are the Fourier descriptors of the contour. M can be small, typically 4, for relatively simple objects such as the heart. The resulting volume can be represented by the matrix:

$$O = \begin{bmatrix} a_{0,1} & \cdots & a_{M-1,1} \\ \vdots & \cdots & \vdots \\ a_{0,N} & \cdots & a_{M-1,N} \end{bmatrix} \qquad \text{(Eq. 3)}$$

where N is the number of slices. Further economy of parameters can be achieved if each individual column in O is modelled by a polynomial. A model of the heart, derived from this model using a total of 12 parameters, is shown in Fig. 3.

All parameters associated with the prototype anatomy (based on normal CT data) and the instantiated anatomy are stored in a frame structure for incorporation into the feature-space reasoning described below.

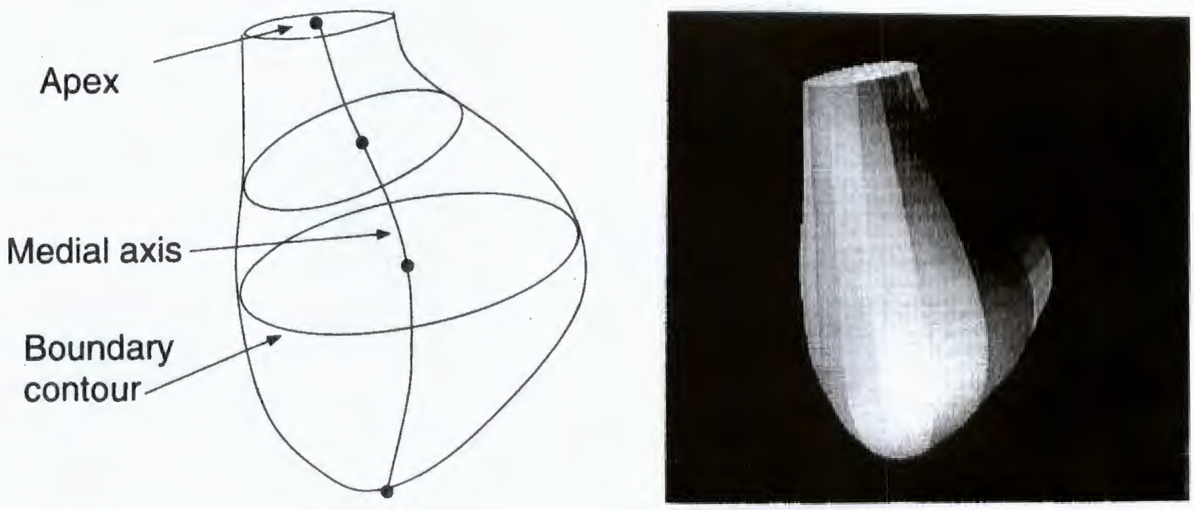

Fig 3 (Left) Fourier-based shape description. The heart surface is described by a series of curves, with a specific orientation and scale relative to its predecessor, starting at the apex. (Right) Rendered 12-parameter model of the heart.

4. FEATURE EXTRACTION AND FEATURE SPACE REASONING

The architecture for reasoning about image data is shown in Fig. 1, i.e. a 2D model used for large-scale landmarking, and a 3D model used for finding more subtle structures such as hila and pulmonary vessels. The features identified during the major landmarking are the edges forming the boundaries of the lung fields, i.e. mediastinum, diaphragm, apices and costal margins. In the 2D model these are represented by line segments to describe shape, and pairwise spatial relationships. Lengths and orientations of line segments and their relationships are described using fuzzy membership values into the "normal" set, which translate into confidence values of normality. The feature space currently contains only edges since complete or partial edges are a significant feature used by radiologists in interpreting projection-based images.

Translating image-based information to feature space begins with midline determination based on a minimum-cost path across the image, locating the mediastinum. Pixel-based processing then produces a large number of candidate edges. The first stage is a Laplacian-of-Gaussian (LoG) operation, followed by a tracking operation on the zero-crossing LoG pixels which establishes the presence of "long" edges. Labelling these edges involves checking their locations and spatial relationships against their positions predicted by the 2D model.

Reasoning in feature space is achieved by a blackboard architecture implemented as a network of frames where each edge (feature) predicted by the model has its own frame in the blackboard (Fig. 4). The blackboard frame stores knowledge about position, length and orientation of edges derived from the model, as well as spatial relationships to other edges. These relationships form the links between frames in the network and, as an edge is identified, the links indicate which other frames' edges are to be updated based on the new information.

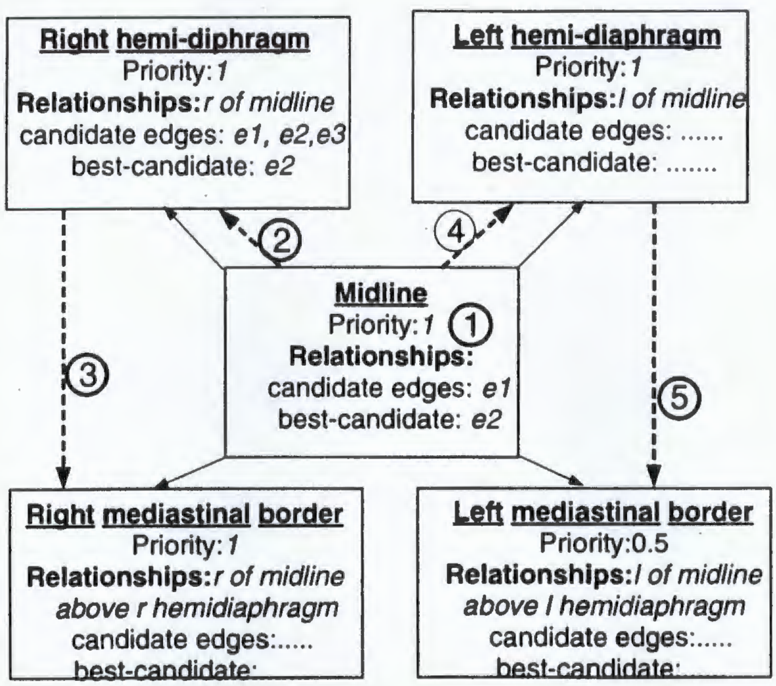

Fig. 4 A network of frames comprising a "blackboard" for image segmentation. The solid arrows represent influence relationships. Dotted arrows represent the order of segmentation. The network is shown immediately after identification of the right hemi-diaphragm. "Priority" refers to the number of established relationships necessary for segmentation of a feature.

Outlines in X-rays are often partial or indistinct due to projection and superposition, so it is difficult to identify edges with certainty. The inference engine is able to entertain multiple edge-labelling hypotheses and that which seems most consistent can be selected using confidences based on fuzzy membership values, and then changed if necessary in the light of further information. Since each constraint imposed by the model generates a confidence value, we can also be specific as to the nature of abnormalities and if the inference engine is not confident about a decision it has made, then it can report the exact reason for this lack of certainty.

The final stage consists of active contour ("snake") refinement of the edges [6]. Edges resulting from the LoG operation are tortuous and affected by overlying structures such as ribs. The active contours refine the edge positions based on the energy function :

$$E_{total} = E_{internal} + E_{image} + E_{model} \qquad \text{(Eq. 4)}$$

Internal forces are heavily constrained for low curvature, and the edge features are selected so that "cusps" (e.g. the costo-phrenic junctions) lie at the junctions of the snakes. External forces are (1) image-based, which attract the snake to areas characterised by large gradients, and (2) model-based, influencing the contour position directly from the currently instantiated two- or three-dimensional model. This is the most direct way of allowing a three-dimensional anatomical model to influence image segmentation. Alternatively, snake contours may be entered manually at the conclusion of the automatic segmentation.

5. CURRENT SYSTEM AND FUTURE DEVELOPMENTS

The current system relies more heavily on two-dimensional than three-dimensional models. However, full 3-D anatomical descriptions have been incorporated into the frame structure, with generation of two-dimensional image space (synthetic X-rays) and feature space (symbolic descriptions) of the three-dimensional anatomical instantiations, and realistic visualisations. A high-level two-dimensional feature space description has been incorporated, which currently provides:

(a) Segmentation of right and left hemi-diaphragms, heart, costal margins, apices.

(b) Report on nature (sharpness etc), location and size of the above features.

(c) Interactive refinement of selected edges using active contours.
(d) Automatic measurement of dimensions such as cardio-thoracic ratio.
In a preliminary sample of 14 patients with abnormal lung anatomy, no feature was misidentified, even with major abnormalities (such as in Fig. 5). However, the system occasionally reported a failure to identify a structure, usually due to an edge being very indistinct.
The result of a segmentation is shown in Fig. 5.

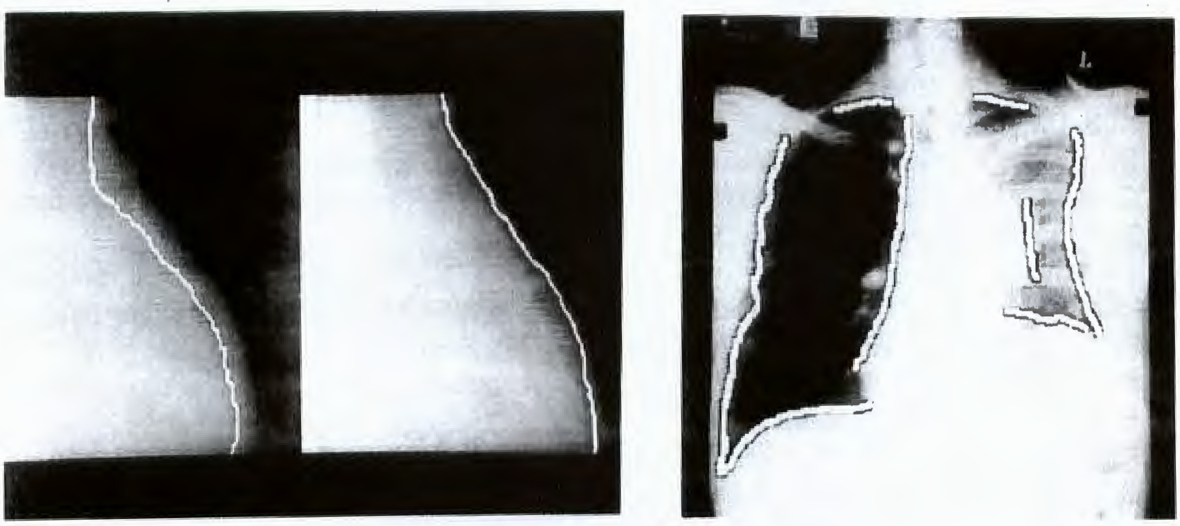

Fig 5. (Left) Refinement of the heart outline using an active contour.
(Right) Result of an image segmentation, showing a normal right lung and left lung affected by consolidation and displaced boundaries. Apices, hemidiaphragms, mediastinal and lateral boundaries are correctly identified.

The three-dimensional model is being introduced progressively to the system; at present it guides the identification of heart boundaries, by optimising the model shown in Fig. 3, and subsequently contributing to the model-based energy terms in Eq. 4.

Thus the system has been successful in coarse-scale image segmentation in chest X-rays in the presence of abnormalities and has already been received well by radiologists. More complete implementation, with full incorporation of a 3-D model, will allow the system to realise its full capabilities. Further enhancement will include other views (notably lateral X-rays) and other modalities, which will take full advantage of high-level, three-dimensional anatomical knowledge incorporated into an expert assistant workstation.

ACKNOWLEDGMENTS

The authors thank George Kossoff, David Robinson, Mark Berman, Leanne Bischof, Yuchong Jiang, Rosemary Irrgang, John Hiller, Claude Sammut, Tatjana Zrimec and an anonymous reviewer for their contributions to this work.

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