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Medical X-ray Images of the Human Thorax

Segmentation, Decomposition
and Reconstruction

PHD THESIS

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To Cat

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ABSTRACT

Medical image segmentation methods have been developed for different anatomical structures using image data acquired from a variety of modalities. This thesis presents fully automated computer algorithms to segment, decompose and reconstruct medical X-ray images of the human thorax. Focus is on postero-anterior (PA) chest radiographs and computed tomography (CT) images.

Two segmentation methods are proposed to accurately identify the unobscured regions that define the lung fields in digital PA chest radiographs. The first approach is a contour delineation method that uses an optimal path finding algorithm based on dynamic programming. The second approach is a non-rigid deformable registration framework, where the lung field segmentation is reformulated as an optimization problem. A flexible optimization strategy based on genetic algorithms is adopted. Both methods can be used in computer-aided diagnosis systems by providing the required pre-processing step before further analysis of such images can be applied successfully.

Algorithms for the construction of 3D patient-specific phantoms from volumetric CT images of the human thorax are also provided. Based on material basis decomposition applied to CT numbers, CT images are decomposed into known intervening materials, providing voxelized anthropomorphic phantoms suitable for several computer simulations in diagnostic radiology and nuclear medicine. The method is extended for extracting the lung region of interest usually required by most pulmonary image analysis applications. A robust 3D optimal surface detection algorithm is used for accurately separating the lungs.

Lastly, a methodology for recovering the 3D shape of anatomical structures from single radiographs is presented. Voxelized phantoms resulting from CT image decomposition are used to simulate radiological density images and reconstruct estimated thickness maps of the structures to be recovered. A formal relationship between CT data and radiographic measurements is derived to support the design of subtraction and tissue cancellation algorithms.

RESUMO

Inúmeros métodos de segmentação de imagens médicas têm sido desenvolvidos para diferentes estruturas anatómicas usando dados provenientes de diversas modalidades. Esta tese apresenta algoritmos computacionais automáticos para segmentar, decompor e reconstruir imagens médicas do tórax humano, nomeadamente radiogramas torácicos em incidência postero-anterior (PA) e tomogramas computadorizados (TC).

Dois métodos de segmentação são propostos para identificar as regiões que definem os campos pulmonares em radiogramas digitais PA do tórax. O primeiro método consiste em delinear os contornos pulmonares usando um algoritmo de pesquisa do trajecto óptimo baseado em programação dinâmica. O segundo é baseado no alinhamento não-rígido de um modelo deformável formulando a segmentação dos campos pulmonares num problema de optimização. Para o efeito, é usada uma estratégia flexível de optimização baseada em algoritmos genéticos. Ambos os métodos podem ser usados em sistemas computacionais de apoio ao diagnóstico médico, fornecendo o pré-processamento necessário para que a análise à posteriori de tais imagens possa ser aplicada com sucesso.

Algoritmos para a construção de fantasmas 3D específicos de cada paciente resultantes de tomogramas volumétricos são providos. Baseado na decomposição em materiais de base aplicada aos números de TC, estas imagens são decompostas em materiais conhecidos, fornecendo fantasmas antropomórficos voxelizados, apropriados para diversas simulações computacionais com aplicações na radiologia diagnóstica e medicina nuclear. Uma outra aplicação deste método é a extração da região de interesse pulmonar, requerida pela grande maioria das aplicações de análise de imagem pulmonar. É ainda proposto um algoritmo robusto de detecção óptima de superfície 3D para a separação rigorosa dos pulmões.

Por último, é apresentada uma metodologia para a reconstrução 3D da forma de estruturas anatómicas partindo de apenas um radiograma. Fantasmas voxelizados resultantes da decomposição de imagens TC são usados para simular imagens radiológicas de densidade e estimar mapas de espessuras de cada estrutura que se pretende reconstruir. A relação formal entre dados TC e medidas radiológicas é deduzida viabilizando a implementação de algoritmos de eliminação e subtração de tecidos.

RESUMÉ

Quelques méthodes de segmentation d'images médicales ont été développées pour différentes structures anatomiques en utilisant des données d'image acquises d'une variété de modalités. Cette thèse présente des algorithmes d'ordinateur entièrement automatisés pour segmenter, décomposer et reconstruire des images médicales aux rayons X du thorax humain. L'étude est centrée sur les radiographies postéro-antérieures (PA) et les images volumétriques de tomographie calculée (TC).

On propose deux méthodes de segmentation pour identifier les régions qui définissent les poumons en radiographies digitales PA. La première approche est une méthode de délimitation de contours qui emploie un algorithme optimal de conclusion de chemin basé sur la programmation dynamique. La deuxième approche considère un alignement non-rigide d'un modèle déformable, où la segmentation des poumons est reformulée comme un problème d'optimisation. Une stratégie flexible d'optimisation basée sur des algorithmes génétiques est adoptée. Les deux méthodes peuvent être employées dans les systèmes de diagnostic assisté par ordinateur en fournissant l'étape de prétraitement exigée avant que davantage d'analyse de telles images puisse être appliquée avec succès.

Des algorithmes pour la construction de fantômes 3D spécifiques du patient à partir d'images volumétriques de TC du thorax humain sont également fournis. Suivant la décomposition de matériaux de base appliquée aux données de TC, des images de TC sont décomposées en matériaux intervenants connus, fournissant des fantômes anthropomorphes voxelisés appropriés à plusieurs simulations sur ordinateur dans la radiologie diagnostique et la médecine nucléaire. La méthode est étendue pour extraire la région d'intérêt des poumons habituellement exigée par la plupart des applications d'analyse d'images pulmonaire. Un algorithme robuste de détection optimale de surface 3D est employé pour séparer les poumons.

Pour finir, on présente une méthodologie pour reconstruire la forme 3D de structures anatomiques à partir de simples radiographies. Des fantômes de voxélisés résultant de la décomposition d'image de TC sont employés pour simuler des images radiologiques de densité et estimer l'épaisseur des structures prétendues. Un rapport formel entre les données TC et les mesures radiographiques est dérivé pour permettre le développement d'algorithmes de soustraction de tissus.

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LIST OF ABBREVIATIONS

2D	Two Dimensional
3D	Three Dimensional
CR	Computed Radiography
CT	Computed Tomography
DOF	Degree of Freedom
DR	Digital Radiography
DRR	Digital Reconstructed Radiograph
DP	Dynamic Programming
FFD	Free Form Deformation
FLTK	Fast Light Toolkit
FN	False Negative
FP	False Positive
GA	Genetic Algorithm
HPH	Hospital Pedro Hispano
HSJ	Hospital São João
ITK	Insight Segmentation and Registration Toolkit
JSRT	Japanese Society of Radiological Technology
MRI	Magnetic Resonance Imaging
MIP	Maximum Intensity Projection
MC	Monte Carlo
PDM	Point Distribution Model
PA	Postero-Anterior
PCA	Principal Component Analysis
RCGA	Real Coded Genetic Algorithm
SA	Simulated Annealing
SRG	Seeded Region Growing
TPS	Thin Plate Spline
TP	True Positive
TN	True Negative
VTK	Visualization Toolkit

NOTATION

E	Energy
h	Planck's constant
ν	Frequency
c	Speed of light
λ	Wavelength, path length
γ	Reduced energy
m_0	Mass of electron at rest
A	Atomic mass
Z	Atomic number
u	Atomic mass unit
N_A	Avogadro's number
σ_{atom}	Total cross-section per atom
N_g	Electron mass density
μ	Linear attenuation coefficient
ρ	Mass density
α, β, ξ	Material, mixture, compound
ε	Absorption ratio (efficiency)
t	Time
I	Intensity
T	Transmission
D	Optical density
R	Radiological density
H	CT number
k, K	Calibration constants

OXYZ	Physical space coordinate system
O	Space origin
X, Y, Z	Direction (axis)
dX, dY, dZ	Pixel/voxel/node spacing
$\Delta X, \Delta Y, \Delta Z$	Physical extent
x, y, z	Cartesian coordinates
r, θ, ϕ	Polar/Spherical coordinates
Ω	Solid angle
d	Length, distance
V	Volume
$\mathbf{X}(x, y)$	2D digital grid/image/graph
$\mathbf{H}(x, y, z)$	3D digital grid/image/graph
$\mathbf{p} = (x, y)^T$	2D point/pixel/node
$\mathbf{p} = (x, y, z)^T$	3D point/voxel/node
$\mathbf{P} = \{\mathbf{p}_n\}$	Set of N points, $n = 0, 1, \dots, N - 1$
$\otimes$	Convolution operation
$\mathcal{R}$	Rotation transformation
$\mathcal{A}$	Affine transformation
$\mathcal{T}$	Thin-Plate Spline transform
$\mathcal{N}$	Normal distribution
σ	Standard deviation
δ, Δ	Perturbation, displacement, variation
u	Random number

Chapter 1

INTRODUCTION

Diagnostic imaging is an invaluable tool in medicine today. Computed Radiography, Computed Tomography, Digital Mammography and Magnetic Resonance Imaging are, among others, medical imaging modalities that provide effective means for mapping the anatomy of a subject. These technologies have greatly increased knowledge of normal and diseased anatomy and are a critical component in diagnosis and treatment planning.

Medical images can be used qualitatively for aid in making a diagnosis. However, their use in medical research requires extraction of quantitative and objective information from images. Several rather distinct entities can be measured quantitatively. These include measuring physical properties or characterizing shape of anatomical structures. Of course, before any values can be computed, structures of interest must be delineated. With the increasing size and number of medical images, the use of computers in facilitating their processing and analysis has become necessary. In particular, *image segmentation* computer algorithms for the delineation of anatomical structures of interest are a key component in assisting and automating specific radiologic tasks.

1.1 Motivation

There is currently no single segmentation method that yields acceptable results for every medical image. Methods do exist that are more general and can be applied to a variety of data. Selection of an appropriate approach to a segmentation problem can therefore be a difficult dilemma.

Image segmentation can be, in principle, performed manually by a trained clinician with suitable equipment. However, manual segmentation has several drawbacks. First, the amount of acquired data is enormous and performing the structure extraction manually, or even semi-automatically, can be costly, if feasible at all. Second,

when several experts are processing the images, the reproducibility and the comparability of the processed images are reduced. This is simply due to the divergent opinions and the individual working habits of the people involved.

These considerations call for automatic methods to perform the structure extraction. In particular, the automated segmentation of anatomical structures in chest radiographs and thoracic CT images, such as the lung region of interest, is of great importance for the development of dedicated Computer-Aided Diagnosis (CAD) systems. As CAD in chest radiography and computed tomography becomes the focus of researchers, X-ray image segmentation methods have received a considerable amount of attention in the literature.

Automation of medical image analysis is complicated and requires advanced techniques, because 1) intensity values in an image do not solely define the (biologically meaningful) structure of interest, as their spatial organization is also very important; 2) images are characterized by individual variability. The spatial relationships between different structures in a medical image are often *a priori* known based on existing anatomical knowledge. This has to be taken into account when segmenting images. Methods that are specialized to particular applications often achieve better performance by taking into account this available source of information. The high-level prior knowledge simplifies the segmentation problem, but at the same time algorithms capable of utilizing it can become more complicated than segmentation algorithms relying only on the image data.

1.2 Main Contributions

In order to contribute to the required methodological knowledge, our efforts have been directed towards the development of fully automated computer algorithms to segment, decompose and reconstruct medical X-ray images of the human thorax. The main contributions of this thesis, focused on postero-anterior (PA) chest radiographs and volumetric computed tomography (CT) images, can be summarized as follows:

- Two methods to segment the lung fields in digital standard PA chest radiographs. The complete lung boundaries, including the costal, mediastinal, lung top sections and diaphragmatic edges are delineated by using a contour delineation method based on dynamic programming. The second approach is a non-rigid deformable registration method. The segmentation of the lung fields

is reformulated as an optimization problem solved with a flexible optimization strategy based on genetic algorithms. Both methods can be used in CAD systems by providing the required pre-processing step before further analysis of such images can be applied successfully.

- The construction of 3D patient-specific phantoms from volumetric CT images of the human thorax. Based on dual-energy principles, the mathematical framework that reflects material basis decomposition applied to CT numbers is derived, providing a method for CT image decomposition into known intervening materials. Voxelized anthropomorphic phantoms that result from the proposed algorithms are suitable for several computer simulations in diagnostic radiology and nuclear medicine.
- A method for extracting the lung fields from CT images. This is an extension of the proposed method for decomposing CT images that results in the accurate delineation of such anatomical region of interest, usually required by most pulmonary image analysis applications in CAD. The segmentation algorithm provides also a valuable visualization tool.
- The implementation of a robust algorithm for separating the right and left lungs. A 3D optimal surface detection algorithm is suggested for accurately separating the lungs, once they have been segmented. The algorithm provides the proper means for simultaneously detecting the anterior and posterior junctions lines.
- A methodology for recovering the 3D shape of anatomical structures of interest from single radiographs. Voxelized anthropomorphic phantoms are used to simulate radiological density images and reconstruct estimated thickness maps. The physical relationship between CT data and radiographic measurements is formally derived to provide the adequate methodology to develop chest radiograph enhancement techniques based on tissue cancellation algorithms.

1.3 Outline of the Thesis

This thesis is organized as follows.

Chapter 2 describes the fundamental concepts underlying the image formation in Digital Radiography and Computed Tomography. Medical X-ray imaging systems are characterized in terms of their physical and geometrical properties and

several topics on radiation physics, such as medical X-ray production, interaction of radiation with matter and image receptors are briefly discussed to provide the basic understanding of X-ray physics in diagnostic radiology. Attenuation coefficients are discussed in detail and the principles of dual-energy radiography are described to introduce the concept of material basis decomposition, which should prove particularly useful in Chapter 5 and Chapter 6.

Chapter 3 reviews standard image processing techniques. Special emphasis is given to those that support the proposed methods for segmenting planar radiographs and volumetric CT images of the human thorax, described in Chapter 4 and Chapter 5, respectively. The construction of a prior geometrical lung contour model is explained in detail and model-based image segmentation approaches based on statistical shapes and deformable models are presented. Several optimization strategies, namely dynamic programming, genetic algorithms and simulated annealing are briefly described and similarity measures are defined to evaluate the performance of the segmentation algorithms.

Chapter 4 presents two segmentation approaches to automatically extract the lung fields from PA chest radiographs, namely the contour delineation method based on dynamic programming and the model-to-image registration method based on genetic algorithms. A detailed description of both methods is provided and experimental results are reported after applying them on two different image databases. Performance analysis is done by comparing the computer-based segmentation outputs with results obtained by manual analysis.

Chapter 5 is dedicated to the segmentation of CT images of the human thorax. Fully automated segmentation algorithms are described to decompose such volumetric images and construct realistic computer models of the thoracic anatomy. Experimental results of phantom construction obtained from a private image database are reported and qualitatively evaluated. A method for extracting the lung region of interest in thoracic CT images is also explained in detail. Quantitative analysis of the performance of such procedure is provided by comparing segmentation outputs with those obtained from manual contouring, for which inter-human variability is also investigated.

Chapter 6 addresses the problem of the 3D shape recovery of anatomical structures of interest from single planar radiographs. Simulation of the medical X-ray systems described in Chapter 2 is now considered and the methods presented in Chapter 4, for segmenting 2D chest radiographs, and Chapter 5, for decomposing 3D CT images, are integrated into a unique inter-modality registration framework.

The general characteristics of the Monte Carlo and ray casting techniques are briefly presented as possible methods to generate simulated radiographs and create thickness maps. The 3D reconstruction from a single radiograph is finally illustrated for a simple case, by recovering the lungs, the body and the patient itself.

The main contributions of this thesis are finally summarized in Chapter 7 and future directions are pointed out.

Chapter 2

MEDICAL X-RAY IMAGING SYSTEMS

Many medical imaging systems measure the transmission of X-rays through the human body. In this Chapter, we review the underlying X-ray physics of diagnostic radiology. The fundamental principles of radiation physics, such as medical X-ray production, interaction of radiation with matter and image receptors are briefly discussed to provide the basic information of the formation of the radiological image. Analytical expressions that describe the resultant image in terms of physical parameters are derived through a simple and formal mathematical structure which should prove useful in further, more detailed analysis.

2.1 Background

Electromagnetic radiation used in diagnostic imaging include, among others, γ -rays emitted by radioactive atoms for imaging the distribution of a radiopharmaceutical in nuclear medicine, X -rays, used in Digital Radiography and Computed Tomography, and *radiofrequency* radiation as the transmission and reception signal for Magnetic Resonance Imaging. The electromagnetic spectrum illustrated in Figure 2.1 shows these different categories of radiation.

Electromagnetic radiation can exhibit particle like behavior. The energy of these particles, *photons* or *quanta*, is given by

$$E = h\nu = h\frac{c}{\lambda}, \quad (2.1)$$

where h is the Planck's constant and c , λ and ν are, respectively, the speed, wavelength and frequency of the radiation, with $c = \lambda\nu$. The energy of a photon is usually expressed in *electron-volt*, eV. One electron-volt is defined as the energy

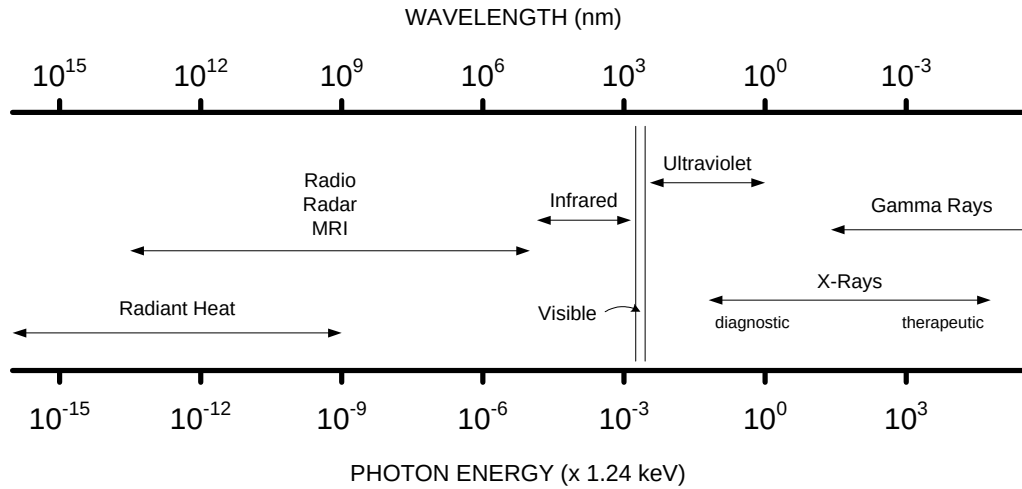


Figure 2.1: The electromagnetic spectrum.

acquired by an electron as it traverses an electric potential difference of 1 volt (V) in vacuum. Multiples of the eV common to medical imaging are the keV and MeV. The Planck's constant is $h = 6.62 \times 10^{-34} \text{ J} \cdot \text{s} = 4.13 \times 10^{-18} \text{ keV} \cdot \text{s}$.

2.2 Medical X-ray Production

The apparatus for X-photon production is a typical electronic vacuum tube containing cathode and anode. In clinical terminology, the anode of the X-ray tube is frequently referred to as the target, while the cathode is sometimes called the filament. The heating of the filament results in the emission of electrons and the high voltage between cathode and anode causes the electrons to be accelerated towards the target. The X-ray energy results from collisional interactions between the accelerated electrons and the atoms of the target material being bombarded. The X-ray tube has shown sufficient intensity to provide usable images in reasonable exposures for medical applications.

The interactions of the incoming electron striking an atom of the target material are diagrammed in Figure 2.2. Two possibilities for interaction are common. The first and most frequent interaction is termed *Bremsstrahlung* or "braking" radiation (Figure 2.2(a)). In this interaction, the accelerated electron passes relatively close to the nucleus of the atom. The path of the accelerated electron is affected by the nucleus with a resulting change in direction and dissipation of energy. The difference in the kinetic energy before and after interacting with the nucleus is

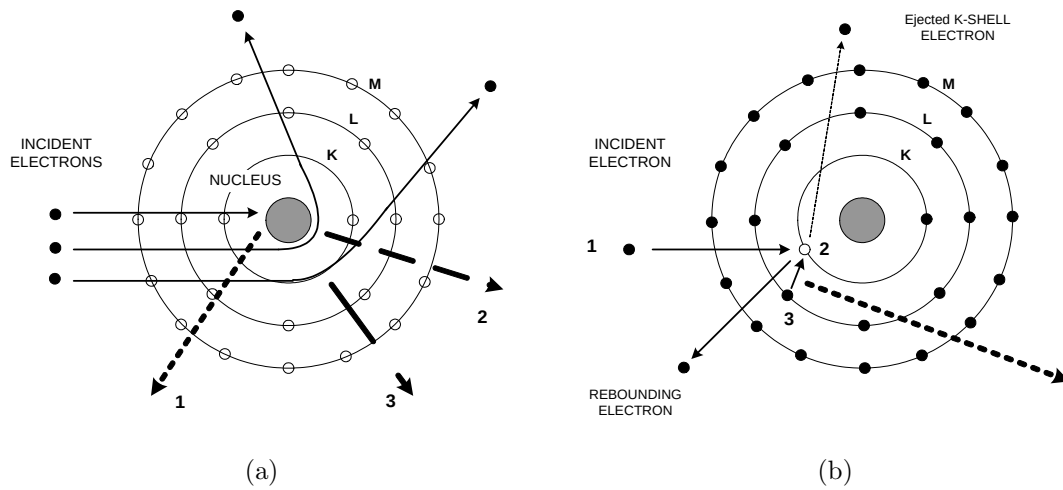


Figure 2.2: (a) Bremsstrahlung ("braking" radiation): incident electron impact with the nucleus of the atom target results in the maximum energy of the X-ray photon (1); Close and distant interactions yield photons with moderate (2) and low (3) energies, respectively; (b) Characteristic radiation emission results from electronic decays between orbital shells: (1) incident electron, (2) ejected electron, (3) radiative decay.

radiated as an X-ray photon. Bremsstrahlung interactions can result in photons of almost any energy, limited only by the tube potential. In the second interaction, the accelerated electron interacts directly with an electron in an orbital shell of the target atom (Figure 2.2(b)). The orbital electron is displaced but the orbital gap is rapidly filled by an electron from a more distant orbit. The difference in the energies of the two electron orbits is radiated as an X-photon with an energy that is characteristic for the specific element and the specific orbital shell. This results in superimposed *characteristic* photon spikes to the Bremsstrahlung radiation spectrum.

A typical radiation spectrum from a medical X-ray tube is illustrated in Figure 2.3. The anode voltage actually corresponds to a photon energy distribution, whose maximum allowed photon energy is the electron energy E_{max} . Typical values are $E_{max} = 25$ keV in mammography and $E_{max} = 125$ keV in digital chest radiography and computed tomography. As seen from the spectrum, the most frequent photon energy is approximately one third of the tube potential voltage.

2.3 Interactions of X-rays with Matter

This Section discusses the nature of the different interaction processes between X-rays and matter. A large number of processes have been postulated, but only some

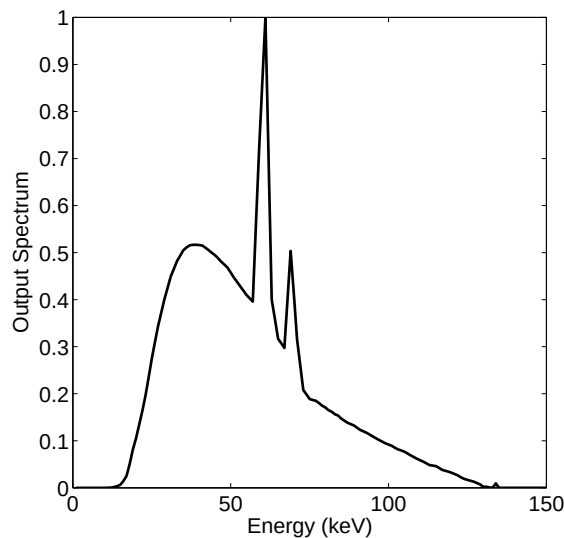


Figure 2.3: Medical X-ray production. Typical output spectrum of a X-ray tube used in medical imaging applications. Bremsstrahlung (smooth curve) and characteristic radiation (spikes). The maximum energy of a photon is limited by the tube voltage.

of them have any relevance to diagnostic radiology and will be considered here.

2.3.1 Photoelectric Absorption

In the case of photoelectric interaction, the incoming photon is absorbed by transferring all of its energy to a tightly bound electron, which is ejected from the atom. The photoelectric effect is illustrated in Figure 2.4(a). The resulting vacancy is then filled in a very short period of time by an electron falling into it, usually from the next shell. This is accompanied by the emission of characteristic X-ray photons called *fluorescent radiation*, as shown in Figure 2.4(b). In order to photoelectric absorption occur, the energy E of the incident photon must be greater than or equal to the binding energy E_0 of the orbital electron. The kinetic energy $\Delta E = E - E_0$ of the ejected *photo-electron* is dissipated in the surrounding matter. Photoelectric absorption dominates in materials with higher atomic number. Lower energy radiation is absorbed in the M and L shells, while higher-energy excitation is absorbed in the inner K shell.

2.3.2 Compton Scattering

Compton scattering, also called inelastic, incoherent or non classical scattering, is the predominant interaction of X-ray photons in the diagnostic energy range with

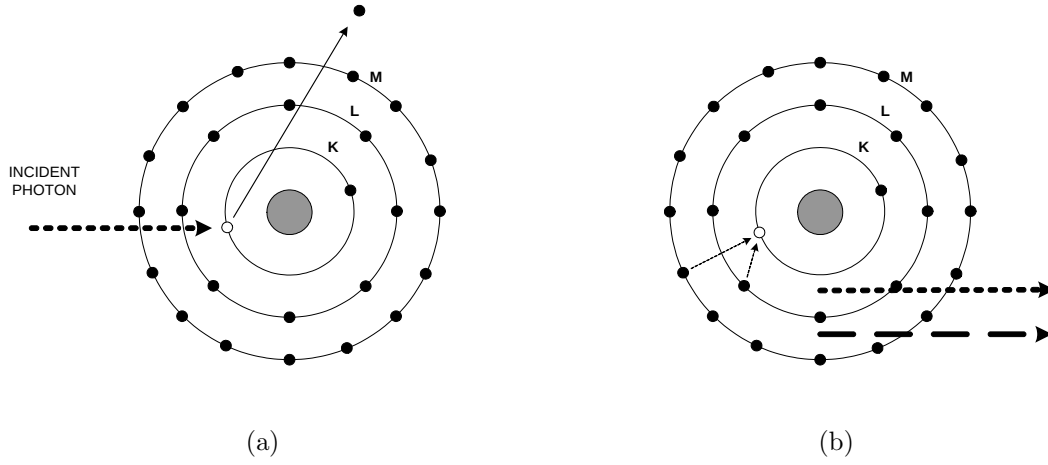


Figure 2.4: Photoelectric absorption. Schematic representation of (a) *Photo-electron* ejection; (b) characteristic radiation emission.

soft tissues. This interaction, illustrated in Figure 2.5(a), is most likely to occur between photons and valence shell electrons. In Compton scattering, a fraction of the incident photon energy is transferred to the atomic electron, resulting in the ionization of the atom and the scattering of the incident photon. The kinetic energy of the ejected electron is lost via excitation and ionization of atoms in the surrounding material.

As with all types of interactions, both energy and momentum must be conserved. The binding energy of the electron that was ejected is comparatively small and can be ignored. The energy of the incoherent scattered photon, E' , depends upon the initial photon energy E and is related to the scattering angle θ relative to the incident path, according to the Compton Angle-Wavelength relation,

$$E' = \frac{E}{1 + \gamma(1 - \cos \theta)}, \quad (2.2)$$

where $\gamma = E/m_0c^2$ is the *reduced energy* and m_0c^2 is the rest mass of the electron (510.975 keV).

As the energy of the incident photon increases, both scattered photons and electrons are scattered more towards the forward direction. The Compton scattered photons may traverse the medium without interaction or may undergo subsequent interactions such as photoelectric absorption, Compton scattering or Rayleigh scattering.

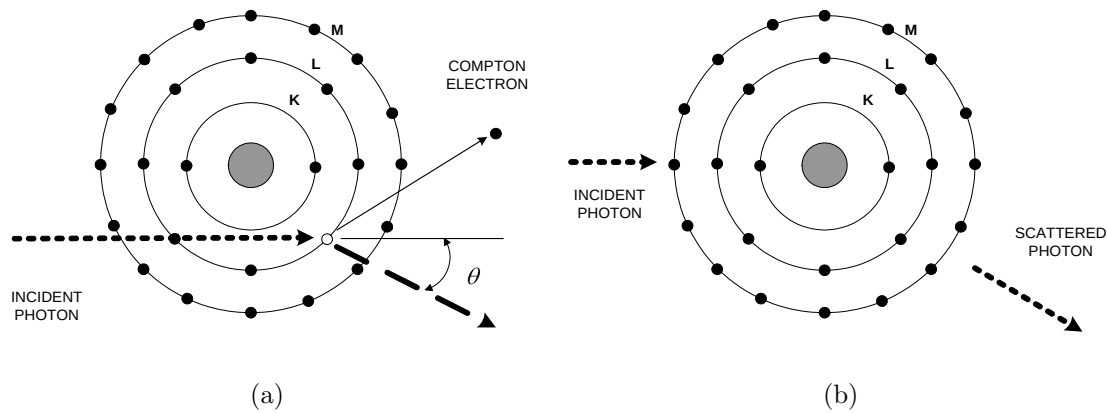


Figure 2.5: Schematic representation of (a) Compton scattering; (b) Rayleigh scattering.

2.3.3 Rayleigh Scattering

Coherent or Rayleigh scattering is the apparent deflection of X-ray beams caused by atoms being excited by the incident radiation. The incoming photon interacts with and excites the total atom, as opposed to individual electrons as in Compton scattering or photoelectric effect. During the Rayleigh scattering event, the electric field of the incident photon's electromagnetic wave expands energy, causing all of the electrons in the scattering atom to oscillate in phase. The atom's electron cloud immediately radiates this energy, by emitting a photon of the same energy but in a slightly different direction, as shown in Figure 2.5(b). In this interaction, electrons are not ejected and thus ionization does not occur. Coherent scattering only results in a change in the direction of the photon since the momentum change is transferred to the whole atom.

This interaction occurs mainly with very low energy diagnostic X-rays, as used in mammography (15 to 30 keV). Compton and Rayleigh scattering have deleterious effect on image quality. In X-ray transmission imaging, scattered photons are much more likely to be detected by the image receptor, thus reducing the image contrast.

2.4 X-ray Attenuation

The total attenuation of a X-ray beam when passing through matter is illustrated using the simple geometry of Figure 2.6, where a parallel beam of X-ray photons traverses a slab of a given material. The beam is partially absorbed and scattered

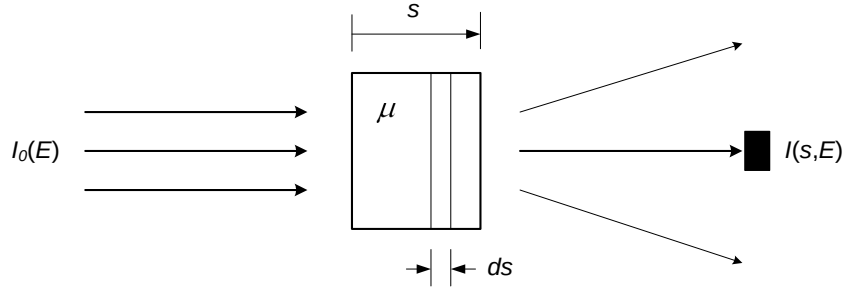


Figure 2.6: Schematic representation of the parallel beam geometry for measuring X-ray attenuation.

in the slab with the remaining transmitted energy traveling in straight lines to the detector plane. In this geometry, a collimated X-ray source is assumed such as would be produced by a point source at infinity. The assumption of a parallel geometry avoids the geometrical distortions due to a finite source close to the object.

Let N be the photon flux of the incident beam, defined as the number of photons passing through a unit cross-sectional area of the slab, per unit time. The photon flux, typically expressed in $\text{photons} \cdot \text{cm}^{-2} \cdot \text{s}^{-1}$, decreases as the beam penetrates a layer of material. The number of photons dN interacting with particles of matter and removed from the beam, in a layer of thickness ds , is given by

$$dN = -\mu N ds, \quad (2.3)$$

where μ is a constant of proportionality known as the *linear attenuation coefficient*. The number of photons interacting is proportional to the incident flux, the interacting distance and the material. The probability of a photon interaction is the total cross-section per atom σ_{atom} that is related to the density ρ of the material according to

$$\mu = \frac{\rho}{uA} \sigma_{atom}. \quad (2.4)$$

In the above equation, $u = 1.6605402 \times 10^{-24}$ g is the atomic mass unit and A is the relative atomic mass of the material. Attenuation coefficients will be discussed in more detail in the Section 2.4.1.

If N_{in} is the incident flux of a narrow beam of monoenergetic photons, the number of transmitted photons N_{out} emerging from the slab of thickness s is computed from Eq. 2.3 as

$$\int_{N_{in}}^{N_{out}} \frac{dN}{N} = -\mu \int_0^s ds. \quad (2.5)$$

By solving Eq. 2.5, the total attenuation of the beam is given by the classical exponential attenuation law

$$N_{out} = N_{in} \exp(-\mu s). \quad (2.6)$$

The intensity I of a beam is defined as the energy flux and can be expressed in terms of the photon flux weighted by the energy per photon E . In the more general case, the incident beam is polyenergetic since its spectrum contains different energies. Since attenuation coefficients, photon interaction cross-sections and related quantities depend on the photon energy, the intensity $I(s)$ at the detector plane is given by

$$I(s) = \int_0^{E_{max}} I_0(E) \exp \left[- \int_0^s \mu(E) ds \right] dE, \quad (2.7)$$

where $I_0(E)$ is the incident spectral intensity of the beam and $\mu(E)$ is the linear attenuation coefficient as a function of the energy, at each position within the object of interest. In Eq. 2.7, the integral is computed from 0 to E_{max} , the maximum photon energy emitted by the X-ray source (see Section 2.2).

At the detector, the bracketed term in Eq. 2.7 represents the X-ray transmission T through a thickness s of the slab at each photon energy E , as given by

$$T(s, E) = \exp \left[- \int_0^s \mu(E) ds \right]. \quad (2.8)$$

As μ is uniform throughout the slab, Eq. 2.8 becomes, for a particular energy E_0 ,

$$T(s, E_0) = \exp[-\mu(E_0)s], \quad (2.9)$$

where $\mu(E_0)$ is the linear attenuation coefficient at E_0 .

2.4.1 Attenuation Coefficients

The total cross-section σ_{atom} for an interaction by the photon can be written as the sum over independent contributions from the principal attenuation mechanisms (see Section 2.3). In the diagnostic range of energies, the total linear attenuation coefficient expressed by Eq. 2.4 can be decomposed into

$$\mu(E) = \mu_{photo} + \mu_{incoh} + \mu_{coh}, \quad (2.10)$$

where μ_{photo} , μ_{incoh} and μ_{coh} are the photoeffect, Compton and Rayleigh attenuation contributions, respectively. For composite materials, the analytical expressions for the various components as a function of energy and specific material characteristics, namely the atomic number Z , take the form

$$\mu(E) = \rho N_g \left\{ f_C(E) + C_P \frac{\bar{Z}_P^m}{E^n} + C_R \frac{\bar{Z}_R^k}{E^l} \right\}, \quad (2.11)$$

In the above equation, C_P and C_R are the magnitudes of the photoelectric and Rayleigh components, $f_C(E)$ is the energy-dependent Compton scattering function, E is the photon energy in keV and N_g is the electron mass density or electron per gram,

$$N_g = \sum_i N_{gi} = N_A \sum_i \omega_i \frac{Z_i}{A_i}, \quad (2.12)$$

where ω_i is the fraction by weight of the i th constituent of the composite material and $N_A = 6.022045 \cdot 10^{23} \text{ mol}^{-1}$ is the Avogrado's number. In this material, $\bar{Z}_R$ and $\bar{Z}_P$ are the effective atomic numbers as given by

$$\bar{Z}_R = \left(\sum_i \alpha_i Z_i^k \right)^{\frac{1}{k}}, \quad \bar{Z}_P = \left(\sum_i \alpha_i Z_i^m \right)^{\frac{1}{m}}, \quad (2.13)$$

and α_i is the electron fraction of the i th element

$$\alpha_i = \frac{N_{gi}}{\sum_j N_{gj}}. \quad (2.14)$$

In Eq. 2.11 and Eq. 2.13, the exponents in the Rayleigh and photoelectric components have been experimentally determined as $k = 2.0$, $l = 1.9$, $m = 3.8$ and $n = 3.2$, and the constants as $C_R = 1.25 \times 10^{-24}$ and $C_P = 9.8 \times 10^{-24}$ [1].

The Compton scattering function $f_C(E)$, which is independent of the atomic number Z , can be given with a high degree of accuracy by the Klein-Nishina function [2]:

$$f_C(E) = \frac{1+\gamma}{\gamma^2} \left[\frac{2(1+\gamma)}{1+2\gamma} - \frac{1}{\gamma} \ln(1+2\gamma) \right] + \frac{1}{2\gamma} \ln(1+2\gamma) - \frac{(1+3\gamma)}{(1+2\gamma)^2}, \quad (2.15)$$

where γ is the reduced energy, as in Eq. 2.2.

One important attenuation mechanism in the diagnostic energy range is the photoelectric component having a very strong atomic number Z dependence. The

attenuation due to photoelectric absorption varies approximately as the third power of the atomic number of the material so that the linear coefficient attenuation will vary approximately as the fourth power. Thus photoelectric absorption becomes increasingly important with higher atomic number materials. Photoelectric absorption dominates the lower energies while the Z independent Compton scattering component dominates the higher energies.

2.4.2 X-ray Tables

The linear attenuation coefficient μ of all materials depends on the photon energy of the beam and the atomic number of the elements that compose the mixture. In Eq. 2.4 and Eq. 2.11, μ is linearly dependent on the density ρ of the material. Since it is the mass of the material itself that provides the attenuation, attenuation coefficients are often characterized by μ/ρ , the *mass attenuation coefficient*, usually expressed in cm^2g^{-1} . These coefficients are then multiplied by the density to get the linear attenuation coefficient μ in cm^{-1} .

Figure 2.7 shows the total mass attenuation coefficients of water and cortical bone plotted as a function of photon energy, from 1 keV to 1 MeV. The PC based program XCOM¹ [3] was used to compute the cross-section data (mass attenuation coefficients) of these mixtures, by considering Eq. 2.11 through the following relation

$$\frac{\mu(E)}{\rho} = \sum_i \omega_i \frac{\mu_i(E)}{\rho_i}, \quad (2.16)$$

where ω_i is the fraction by weight of the i th element that compose the mixture, as specified in ICRU Report 44 [4].

The relative strengths of the photon interactions versus energy show two distinct regions of single interaction dominance: the photoelectric effect is mainly below while Compton effect is above 30 keV. Rayleigh attenuation process is relatively unimportant in the energies used in diagnostic radiology. *De facto*, this type of interaction has a low probability of occurrence in the diagnostic energy range, as seen in Figure 2.7. In water, coherent scattering accounts for less than 5% of X-ray interactions above 70 keV and at most only accounts for 12% of interactions at approximately 30 keV.

¹ XCOM (also called NIST Standard Reference Database 8 XGAM) can be used to calculate photon cross sections for scattering, photoelectric absorption and pair production, for any element, compound or mixture, at energies from 1 keV to 100 GeV. Web version of XCOM: <http://physics.nist.gov/PhysRefData/Xcom/Text/XCOM.html>

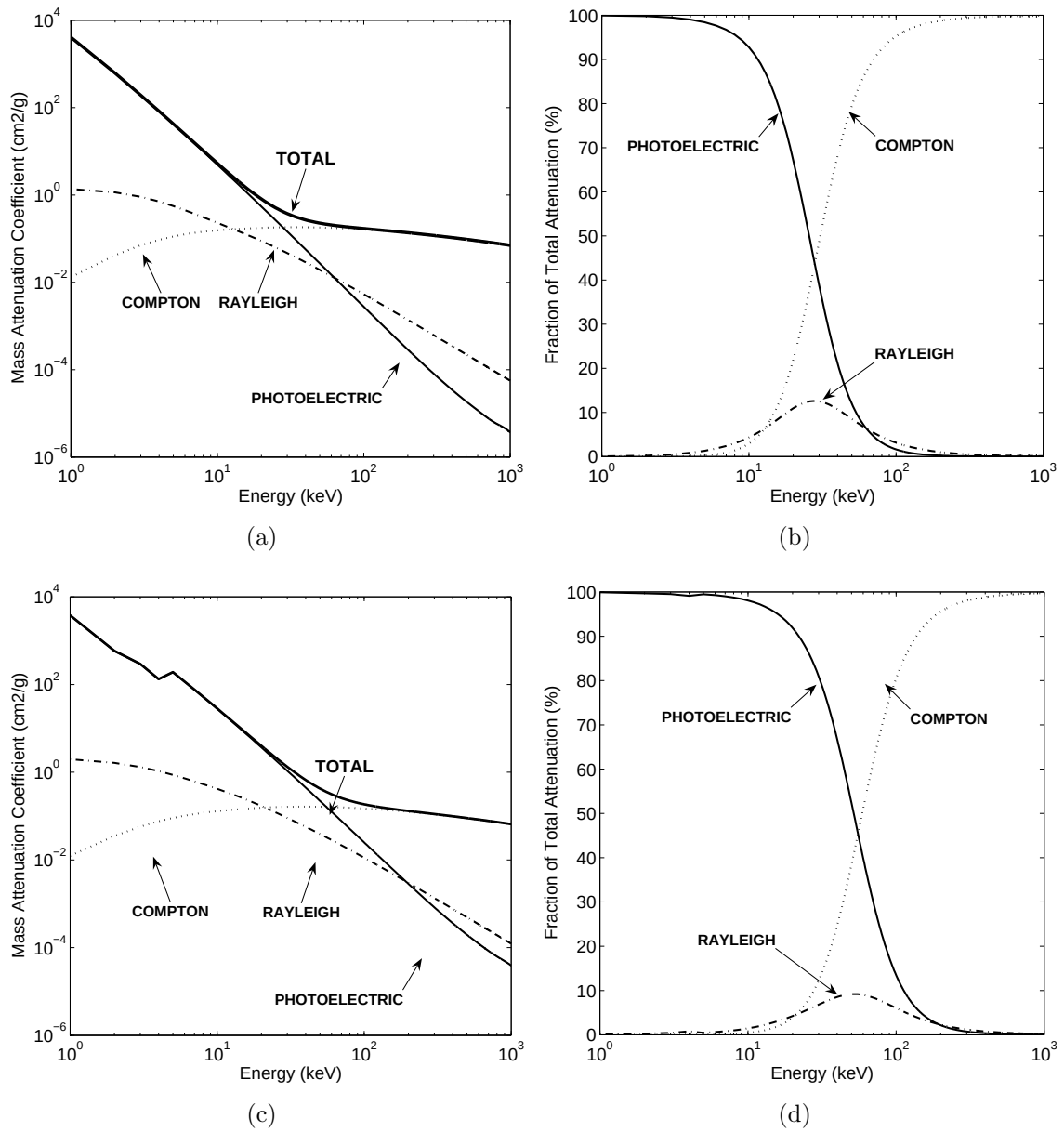


Figure 2.7: X-ray mass attenuation coefficients. The components (left column) and relative contribution of each process (right column) of photon cross sections, are plotted as function of the photon energy, in the diagnostic range from 1 keV to 1 MeV, for water (first row) and cortical bone (second row).

Values of attenuation coefficients can be expressed in *barns* (e.g. data from Storm and Israel [5]). The appropriate conversion between cm^2g^{-1} and *barns* can be made using the following expression [6],

$$\frac{\mu(E)}{\rho} (\text{cm}^2\text{g}^{-1}) = \frac{N_0}{A} \frac{\mu(E)}{\rho} (\text{barns}), \quad (2.17)$$

where $N_0 = N_A \times 10^{-24}$ and N_A is the Avogadro's number. Attenuation coefficient data can show quite large variations as compared to others. A comparison of some data tables can be found in [6].

2.5 Projection Radiography

In this Section, we will describe a physical model for simulating imaging systems based on the measurement of X-ray transmission. The basics concepts and geometrical aspects involved in these systems are described to provide a good understanding of the imaging process involved in X-ray projection radiography.

2.5.1 X-ray Source Simulation

Computer simulation of X-ray spectra is one of the most important tools in diagnostic radiology for characterizing the quality of imaging systems. Accurate methods for simulating of X-ray spectra are still needed owing to the fact that experimental measurements requires special equipment.

X-ray spectral reconstruction from transmission data has been achieved by using spectral algebra [7], and general purpose Monte Carlo computer codes have been used for the simulation of X-ray spectra in diagnostic radiology [8] and mammography [9]. Bremsstrahlung and characteristic X-ray production were considered in these works. The use of Monte Carlo methods is the most accurate means of predicting the X-ray spectra even in complex geometries owing to more accurate physics modeling and incorporation of appropriate interaction cross-section data. The principles of these methods applied to radiation transport simulations will be discussed in Section 6.2.1.

The simulation of various target/filter combinations is also required in the diagnostic radiology energy range. For investigating the effect of tube voltage, target material and filter thickness, the code described in [10] was used to generate Tungsten anode X-ray spectra. Different values of added Aluminum filtration thickness,

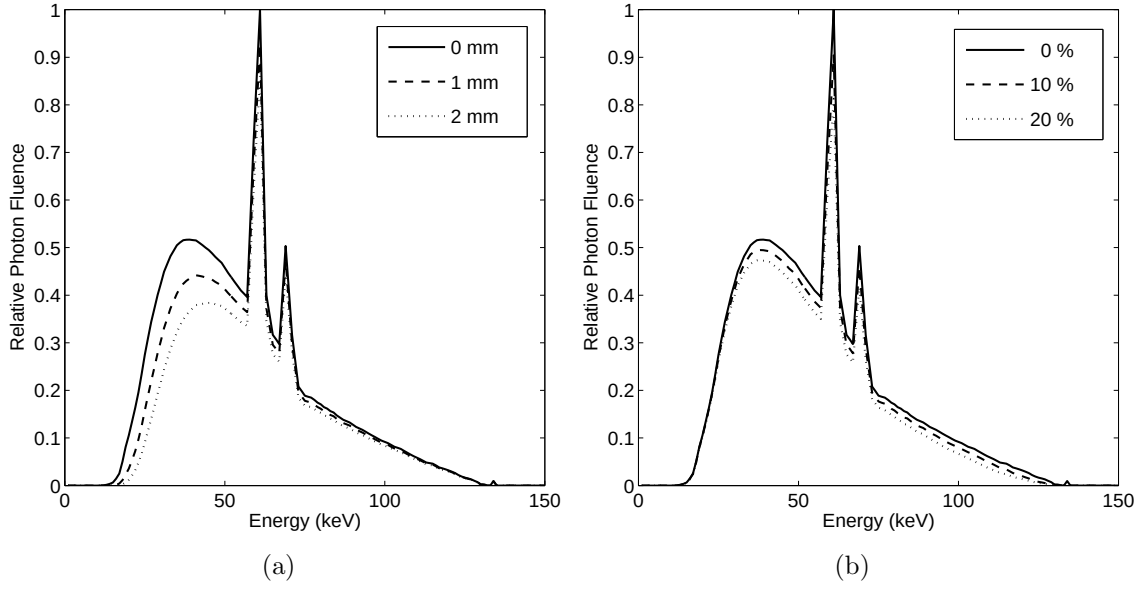


Figure 2.8: Computer generated X-ray spectra, simulated for different values of (a) Aluminum added filtration and (b) % of voltage ripple.

in mm, and voltage ripple of the source, in percent, were considered to simulate the spectra plotted in Figure 2.8. In all cases, the input tube voltage was set to $V_{tube} = 150$ kV and the output is an array containing the generated spectrum expressed in photons $\cdot \text{cm}^{-2}$ per energy bin, with the energy E , in keV, corresponding to the index number. For example, at energy $E = 50$ keV, the output contains the X-ray photon fluence (number of emitted photons per unit area) for that spectrum in the energy region 49.5 keV to 50.5 keV.

2.5.2 Imaging System Geometry

For studying the geometrical properties of a projective X-ray imaging system with respect to the image distortion and resolution, the *point source geometry* of Figure 2.9 is usually adopted. The system is formed by an ideal point source, $\mathbf{s}$, of X-ray photons, located at $(0, 0, d)$, defined in a cartesian coordinates system OXYZ, lying on the Z (optical) axis at a distance $z = +d$ from the origin O. The output of the system, measured at each point $\mathbf{p}_d = (x_d, y_d, 0)^T$ of image plane OXY perpendicular to the optical axis, is given by the line integral of the linear attenuation coefficient $\mu(x, y, z, E)$ of the various rays.

For convenience, a monoenergetic X-ray source is assumed. This represents no loss of generality since we can return to the general relationship as expressed in

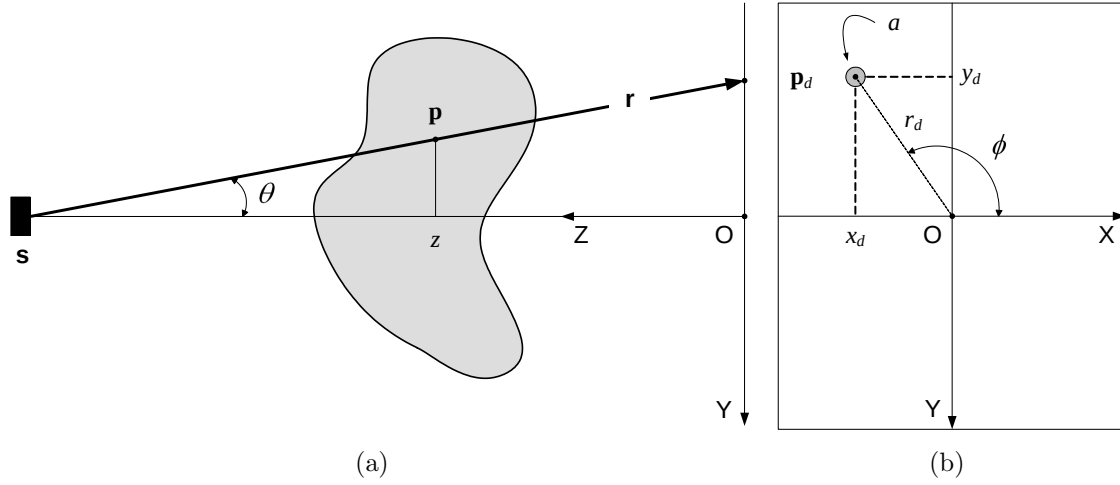


Figure 2.9: (a) Schematics representation of an imaging system using the point source geometry. (b) Image (detector) plane with a centered-image coordinate system OXY .

Eq. 2.7. The detector output $I_d(x_d, y_d)$ is given by

$$I_d(x_d, y_d) = I_i(x_d, y_d) \exp \left[- \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r} \right], \quad (2.18)$$

where $I_i(x_d, y_d)$ is the intensity of the beam incident on the detector plane in the absence of any attenuating object and $\mu(x, y, z, E_0)$ is the linear attenuation coefficient at energy E_0 , at a given point $\mathbf{p} = (x, y, z)^T$. The integral is performed over the straight line from the point source $\mathbf{s}$ and to the detector point $\mathbf{p}_d$, as given by

$$\int_{\mathbf{s}}^{\mathbf{p}_d} d\mathbf{r} = r = \sqrt{x_d^2 + y_d^2 + d^2}, \quad (2.19)$$

where d is the distance from the source to the image plane, considered to be constant, and r is the *radiologic path* defined as the distance from point $\mathbf{s}$ to point $\mathbf{p}_d$.

The intensity $I_i(x_d, y_d)$ in the absence of any attenuating object can be evaluated with the aid of Figure 2.10. Let the source be a point radiator emitting N photons per second isotropically during the exposure interval. The intensity at a point $\mathbf{p}_d$ in the detector plane is proportional to the number of photons per unit area at that point, as given by

$$I_i(x_d, y_d) = N(E) E \frac{\Omega}{4\pi a}, \quad (2.20)$$

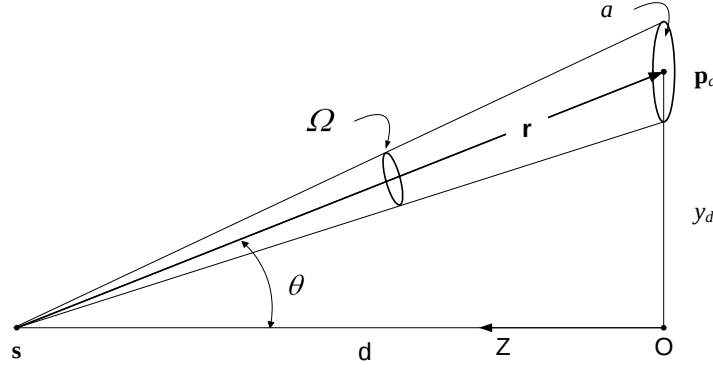


Figure 2.10: Point source geometry intensity falloff.

where Ω is the solid angle intercepted by the incremental area a defined as

$$\Omega = \frac{a \cos \theta}{r^2}. \quad (2.21)$$

The intensity $I_i(x_d, y_d)$ can be specified in terms of I_0 , its value at the origin O , where $\theta = 0$, as

$$I_0 = \frac{N(E) E}{4\pi d^2}. \quad (2.22)$$

Since $\cos \theta / r^2 = \cos^3 \theta / d^2$, the incident intensity at point $\mathbf{p}_d$ is expressed as

$$I_i = I_0 \cos^3 \theta = I_0 \frac{1}{(1 + r_d^2/d^2)^{3/2}}, \quad (2.23)$$

with $r_d^2 = x_d^2 + y_d^2$. In the above equation, the term $\cos^3 \theta$ is interpreted as the product of an inverse square falloff with distance, providing a $\cos^2 \theta$ dependence, multiplied by a $\cos \theta$ dependence due to the obliquity between the rays and the detector plane.

Thus far the source has been assumed to be monoenergetic. For a polychromatic source, the detector output becomes

$$I_d(x_d, y_d) = \int_0^{E_{\max}} I_i(x_d, y_d, E) \exp \left[- \int_s^{\mathbf{p}_d} \mu(x, y, z, E) d\mathbf{r} \right] dE. \quad (2.24)$$

Beam Hardening

Low-energy photons are preferentially absorbed when passing through matter. As a result, the energy spectrum is shifted towards higher photon energies. This produces the well known *beam hardening effect*, where thick or dense body regions transmit photons with a "hardened" spectrum, having a larger proportion of higher energy photons, in comparison with low-attenuating or thin regions. Beam hardening can introduce contrast variations that depend on the choice of the radiologic path through a region of the body, rather than by the local tissue characteristics of the region itself.

2.5.3 X-ray Detectors Considerations

In diagnostic X-ray imaging, one of the important factors that affects image quality is degradation of contrast due to scattered radiation. The most commonly used antiscatter method is insertion of a grid between the patient and the recording system. The grid selectively absorbs a larger amount of scattered radiation than primary radiation. Thus, the detected primary exposure is reduced by a factor equal to the primary transmission of the grid.

Let $E_{ps}(x_d, y_d)$ be the total energy imparted to the detector screen incident on the area around the point $\mathbf{p}_d$. $E_{ps}(x_d, y_d)$ contains both primary and scatter components. The primary component $E_p(x_d, y_d)$ is determined by subtracting a scatter estimate E_s from the total energy:

$$E_{ps} = E_p + E_s. \quad (2.25)$$

In practice, the primary $E_p(x_d, y_d)$ represents the total radiation one expects to be detected Following Eq. 2.24,

$$E_p = I_d a \Delta t, \quad (2.26)$$

where a is the exposed area during the time Δt of the radiographic examination. The theoretical value of the imparted energy is then rewritten as a function of the

incident spectral intensity $N'(E) = dN(E)/dE$ as

$$E_p(x_d, y_d) = \frac{\cos^3 \theta}{4\pi d^2} a \Delta t \cdot \int_0^{E_{\max}} N'(E) E \varepsilon(E) \exp \left[- \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E) d\mathbf{r} \right] G(E) dE. \quad (2.27)$$

In Eq. 2.27, $\varepsilon(E)$ is the absorption ratio of the detector and $G(E)$ the transmission ratio of the grid for primary photons of energy E . In the absence of attenuating material, the expected imparted energy takes the form

$$E_{pi}(x_d, y_d) = \frac{\cos^3 \theta}{4\pi d^2} a \Delta t \int_0^{E_{\max}} N'(E) E \varepsilon(E) G(E) dE. \quad (2.28)$$

The *optical density* is the log of the inverse of the transmitted intensity relative to the intensity incident on the film, $D = \log [1/T]$ and is often related to the imparted energy E_p through the relationship

$$D(x_d, y_d) = \eta_1 \log [\eta_2 E_p(x_d, y_d)], \quad (2.29)$$

where η_1 and η_2 are related to the detector response. For conventional radiographic systems, the exposure incident on the detector has to be increased when a grid technique is employed so that the proper optical densities of the film are maintained. This results in an increase in patient exposure. For digital radiographic systems, the increase of incident exposure is not necessary when a grid is used, since the detected signal may be amplified optical or electronically by the system before being processed and displayed. The use of an antiscatter grid in a digital imaging system thus need not cause an increase in patient exposure.

2.5.4 Digital Radiography

The process of digitalization results in a digital image, or planar radiograph. Planar radiographs can be thought of as two-dimensional (2D) arrays of gray values. Each array element or *pixel* (picture element) represents exactly one image point of the detector, which gray level encodes the optical density as given by Eq. 2.29, related to the amount of the transmitted energy imparted at the corresponding pixel area. At each pixel location it is assumed that the 2D digital image $\mathbf{X}(x_d, y_d)$ is linearly

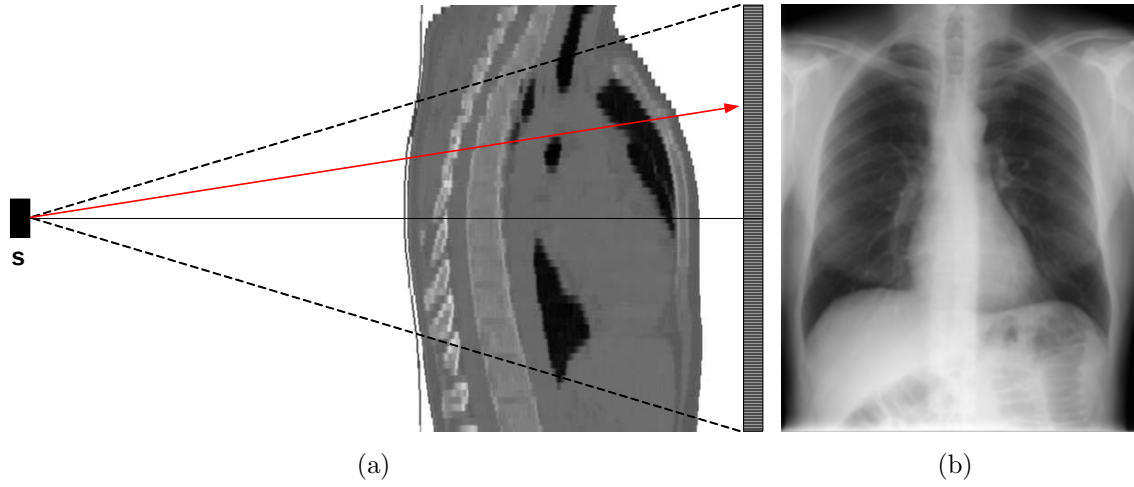


Figure 2.11: (a) Schematic representation of the X-ray imaging system for digital PA chest radiography. (b) The digital image (planar radiograph) is of size $N_X \times N_Y = 1760 \times 2144$ pixels, in X and Y direction, respectively with isotropic resolution (pixel spacing) $dX = dY = 0.200$ mm. The physical extent of the image is $\Delta X \times \Delta Y = 35.2 \times 43.0$ cm and corresponds to a standard screen size.

related to the transmission, such that

$$\mathbf{T}(x_d, y_d) = c_1 \mathbf{X}(x_d, y_d) + c_2. \quad (2.30)$$

where c_1 and c_2 are constants determined by system calibration.

A typical digital PA chest radiograph is shown in Figure 2.11. PA stands for posterior-anterior which means that the patient faces the observer (the radiation passes through the patient from back to front). By convention, the brightness indicates absorbed radiation.

2.6 Computed Tomography

In single projection radiography the three-dimensional (3D) anatomy of the patient is reduced to a 2D projection image. The optical density and therefore the intensity transmission at a given pixel represents the X-ray attenuation properties within the patient along a line, or *ray*, between the X-ray focal spot of the source $\mathbf{s}$ and the point $\mathbf{p}_d$ on the detector. The resultant image is the superposition of all the planes normal to the direction of X-ray emission, through the information along the direction parallel to the X-ray beam is lost. This fact difficulties diagnosis of the characteristics of a section at a given depth plane. This is particularly true

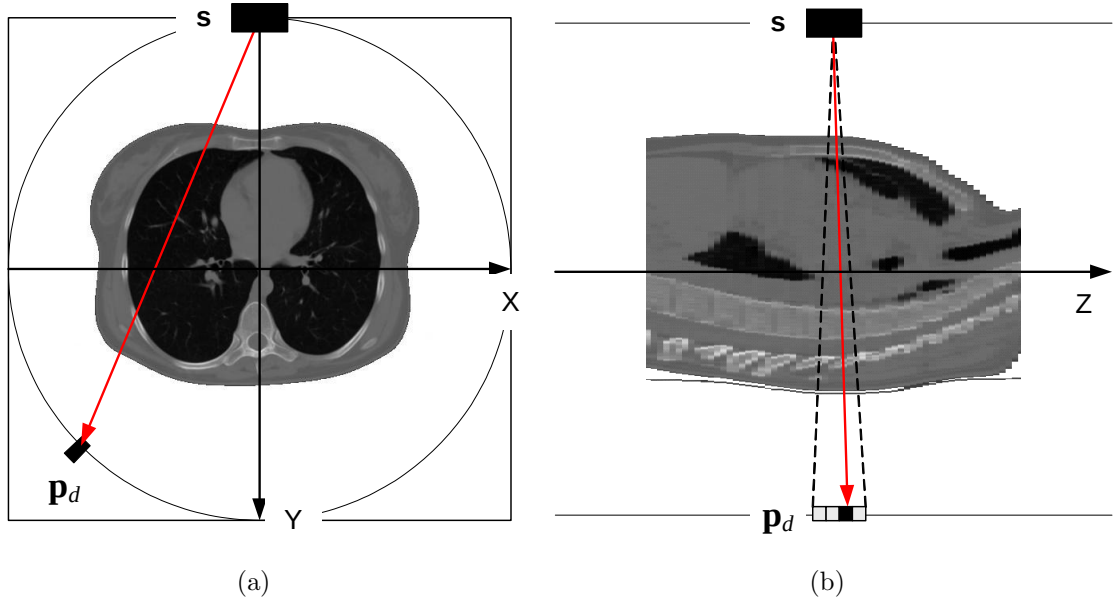


Figure 2.12: Computed Tomography. Schematic representation of (a) fan beam geometry and (b) helical CT scanner with multi-row detector.

in pulmonary imaging, where the visualization of lung lesions is obscured by the superimposed rib structures.

Computed Tomography (CT) is a well established process of generating a patient-specific attenuation coefficients map by using an external source of radiation. Projection data acquired by the CT scanner are used by image reconstruction algorithms to recover 3D information of the patient anatomy, thus providing a distinct improvement in the ability to visualize structures of interest. CT scanner technology today is used not only as a diagnostic tool in medicine, but in many other applications, such as non destructive testing and soil core analysis [11].

The basic principles involved in the image acquisition and reconstruction from projection data in X-ray CT imaging are now discussed.

2.6.1 Image Acquisition Principles

All modern CT scanners incorporate the *fan beam geometry* in the acquisition and reconstruction process. This imaging geometry is illustrated in Figure 2.12(a), where the X-ray source is collimated into a narrow beam and scanned through the plane of interest (OXY). CT scanners have been developed and evolved to incorporate *slip ring* technology that allows the gantry to rotate freely and continuously throughout the entire patient examination.

CT scanners are designed to acquire data while the table of the scanner is moving; as a result, the X-ray tube moves in a helical pattern around the patient. Avoiding the time required to translate the patient table, the total scan time required to image the patient can be much shorter. Entire scans can be performed within a single breath-hold, avoiding inconsistent levels of inspiration. An important consideration is the speed of the table motion relative to the rotation of the CT gantry, described by a parameter known as *pitch*. State-of-the-art CT scanners use multi detector arrays. With the introduction of multi detector arrays, the slice thickness is determined by the detector size and not by the collimator. This represents a major advance in CT technology.

2.6.2 Tomographic Imaging

Consider the imaging geometry of Figure 2.13 in which radiation of an external X-ray source with incident intensity I_i is transmitted through the object of interest represented by a 2D distribution of linear attenuation coefficients $\mu = \mu(x, y)$. As the radiation passes through the scanned volume of the patient, the transmitted intensity distribution $I_d(x', \phi)$ is recorded on a scanning detector at each position of the scan. The acquisition of a single axial CT image or axial *slice* involves a large number of transmission measurements. This process is repeated at multiple angles ϕ , measured with respect to the X-axis of the object.

Eq. 2.18 is now used to relate the acquired detector signals I to the linear attenuation coefficient. Considering the logarithmic transmission and assuming a monoenergetic photon source E_0 ,

$$p(x', \phi) = \ln \left(\frac{I_i}{I_d(x', \phi)} \right) = \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, E_0) dy', \quad (2.31)$$

where $p(x', \phi)$ is the projection, or *sinogram*, of the acquired data (Figure 2.13(a)) and the integration is performed along the radiologic path (Y' axis) from the X-ray source $\mathbf{s}$ to the detector point $\mathbf{p}_d$. The integral equation represented by Eq. 2.31 is known as the X-ray or Radon transform [12].

2.6.3 Reconstruction Algorithms

Recent advances in acquisition geometry, detector technology, multiple detector arrays and X-ray tube design have led to scan times that allows computerized recon-

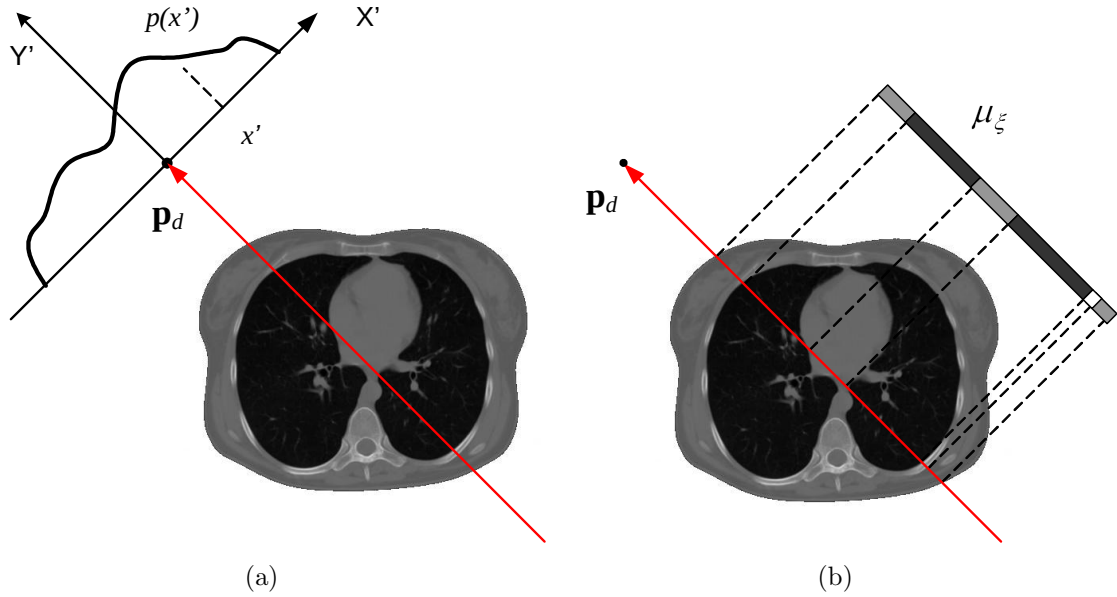


Figure 2.13: Tomographic Imaging. (a) Projection data; (b) Cross-section reconstruction.

struction of the image data essentially in real time. The raw data acquired by a CT scanner is preprocessed before reconstruction through numerous filtering steps. Calibration data are used to adjust and correct the gain of each detector in the array, and electronic detector systems produce a digitized data set that is easily processed by a computer. Tomographic reconstruction performs the inverse operation of Eq. 2.31. The image reconstruction problem is therefore to obtain an estimate of the linear attenuation coefficient distribution $\mu = \mu(x, y)$ from the set of all projections $p(x', \phi)$ and form a cross-sectional image of the patient (Figure 2.13(b)).

Tomographic reconstruction is a well-understood problem. The most straightforward, although computationally inefficient solution involves linear algebra. An initial distribution is assumed and it is compared with the measured projections. Using iterative algorithms, either additive or multiplicative, each reconstructed element or pixel is successively modified. This method is known as the *Algebraic Reconstruction Technique* [2, 13, 14].

The best known solution of the reconstruction problem is the *filtered back projection algorithm* [15]. This approach is a direct reconstruction method based on the central section theorem. Each projection is individually transformed, weighted, inverse transformed and back projected, using the convolution theorem of Fourier transforms [16, 17].

Other reconstruction methods, usually iterative, include mathematical models of the underlying physics of the image acquisition process including photon attenuation, Poisson statistics, scatter radiation and the geometric response of the detector. These methods have been considered in Positron Emission Tomography, to improve the signal-to-noise radiation of the reconstructed image [18, 19].

CT Numbers

As discussed in Section 2.5.2, beam hardening leads to transmission images in which the reconstructed attenuation value of a tissue depends on the location within the patient. Beam hardening effects are corrected to a high degree of accuracy in all modern CT scanners [20]. Calibration data are usually determined from AIR scans and do not result in absolute calibration of the reconstructed attenuation coefficients $\mu(x, y)$. The 3D CT image $\mathbf{H}(x, y, z)$ is reconstructed inside the field of view (FOV) of the scanner by assigning to each point $\mathbf{p}$ located at spatial coordinates (x, y, z) a gray value or *CT number*. For a given material ξ , the corresponding CT number H_ξ is defined as

$$H_\xi = \left(\frac{\mu_\xi}{\mu_w} - 1 \right) K, \quad (2.32)$$

where μ_ξ and μ_w are the linear attenuation coefficients of material ξ and water, respectively, and K is a calibration constant. CT numbers are often scaled as Hounsfield Units (HU) by setting, in Eq. 2.32, $K = 1000$ which is the standard means of representing CT images from clinical scanners. Air has a value near $H = -1000$ HU and, following Eq. 2.32, water corresponds to $H = 0$ HU. Tissues denser than water have values $H > 0$, such as soft tissues, blood, muscle and compact bone, whereas fat (adipose) tissues, for example, typically has values near $H = -100$ HU.

As planar radiographs, X-ray CT image data sets are provided in digital format organized as a stack of axial slices, defining a 3D volume array or rectangular grid of voxels. Each voxel represented by the point $\mathbf{p} = (x, y, z)^T$ within the 3D or volumetric image displays the average X-ray attenuation of the material ξ in that voxel, for which the corresponding gray level is the CT number H_ξ . A reconstructed cross section of the human thorax is shown in Figure 2.14(a). The image $\mathbf{H}(x, y, 0)$ corresponds to an axial slice (plane OXY) reconstructed at $E_0 = 125$ keV, with a slice thickness of $dZ = 5.0$ mm. Multi Planar Reconstruction (MPR) techniques are used to display the spatial distributions of CT numbers $\mathbf{H}(x, 0, z)$ and $\mathbf{H}(0, y, z)$. These are the *coronal* (plane OXZ) and *sagittal* (plane OYZ) views of a CT scan, as illustrated in Figure 2.14(b) and (c), respectively.

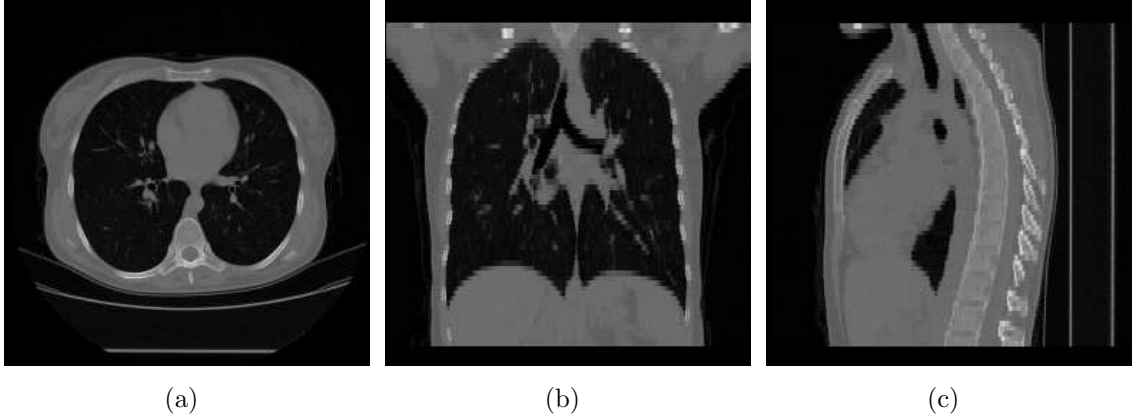


Figure 2.14: Multi planar reconstructions. 2D views of (a) axial, (b) coronal and (c) sagittal planes of a volumetric CT dataset of the human thorax.

2.7 Dual-Energy Radiography

Dual-energy radiography is an effective technique proposed by Alvarez and Macovsky [21] and Lehmann *et al.* [1], that allows removal of contrast between pairs of materials by a linear combination of two images acquired at different energies (low and high energy). In this way, it is possible to display details of interest by removing the background.

2.7.1 Basis Material Decomposition

The dual-energy procedure relies on the physical property that the X-ray mass attenuation coefficient of any material can, to a good approximation, be written as a linear combination of two energy dependent basis functions f_P and f_C . These functions characterize the principal means of attenuation in the diagnostic energy range: photoelectric absorption and Compton scatter. Neglecting the relatively small Rayleigh component discussed in Section 2.4.2, and following Eq. 2.11, the attenuation coefficient of any material can be expressed as

$$\frac{\mu(E)}{\rho} \simeq a_C f_C(E) + a_P f_P(E). \quad (2.33)$$

In the above equation, the constant coefficients a_C and a_P are the Compton and photoelectric components. Since the basis functions f_P and f_C are linearly independent, the mass attenuation coefficient of a given material ξ can be written, within a particular energy range, as a linear combination of the mass attenuation

Table 2.1: Comparison of accuracies of material basis decomposition using Aluminum (α) and PMMA (β) as basis materials (least squares fit, energy range: 40 - 110 keV).

Material ξ	Decomposition reported in [1]			Decomposition computed with XCOM [3]		
	a_1	a_2	rms (%)	a_{1calc}	a_{2calc}	rms (%)
Aluminum	1.0000	0.0000	0.000	1.0000	0.0000	0.000
PMMA	0.0000	1.0000	0.000	0.0000	1.0000	0.000
Muscle	0.9496	0.0803	0.039	0.9483	0.0804	0.004
Bone	0.2369	0.8325	0.259	-0.1510	1.2360	0.001
Water	0.9679	0.0708	0.053	0.9645	0.0731	0.000
Tissue	-	-	-	0.9476	0.0811	0.000
Iodine	-58.664	68.074	2.737	-50.291	61.070	0.234

coefficients of two other materials, α and β , also called *basis set materials* [1]. From Eq. 2.33,

$$\frac{\mu_\xi(E)}{\rho_\xi} \simeq a_1 \frac{\mu_\alpha(E)}{\rho_\alpha} + a_2 \frac{\mu_\beta(E)}{\rho_\beta}, \quad (2.34)$$

where a_1 and a_2 can be computed from Eq. 2.11 through Eq. 2.15, as given by

$$a_1 = \frac{N_{g\xi}(Z_\xi^m - Z_\beta^m)}{N_{g\alpha}(Z_\alpha^m - Z_\beta^m)}, \quad (2.35a)$$

$$a_2 = \frac{N_{g\xi}(Z_\xi^m - Z_\alpha^m)}{N_{g\beta}(Z_\beta^m - Z_\alpha^m)}. \quad (2.35b)$$

To experimentally validate the approximation used in Eq. 2.34, Table 2.1 illustrates the accuracy to which the basis decomposition holds over the range of energies from 40 to 110 keV, for 1 keV steps, using Aluminum and polymethyl methacrylate (PMMA) as the chosen basis materials. The coefficients a_{1calc} and a_{2calc} are the results of a least squares fit of the total mass attenuation coefficients values, taken from the tables produced by XCOM [3]. The results obtained by Lehmann *et al.* [1] are compared, considering the same basis materials and energy range. In all cases, the root mean square (*rms*) error is less than 3%.

Partial results of bone decomposition are presented in Table 2.2 using the least square fit of Table 2.1. Aluminum and PMMA have been used in the past as basis

Table 2.2: Actual and fitted mass attenuation coefficients of bone (material ξ) decomposition using Aluminum (α) and PMMA (β) as basis materials.

E (keV)	$\frac{\mu_\xi(E)}{\rho_\xi}$ (cm ² g ⁻¹)	$a_1 \frac{\mu_\alpha(E)}{\rho_\alpha} + a_2 \frac{\mu_\beta(E)}{\rho_\beta}$ (cm ² g ⁻¹)
40	0.66560	0.66706
50	0.42420	0.42365
60	0.31480	0.31431
70	0.25700	0.25685
80	0.22290	0.22298
90	0.20080	0.20101
100	0.18550	0.18583
110	0.17430	0.17465

materials [1] because they encompass the range of atomic numbers of organic tissues in general diagnostic radiology. The physical properties of these materials are similar to bone and soft tissue and they can be easily fabricated for calibration. Linear combinations of other basis functions such as the mass attenuation coefficients of tissue and bone can be also chosen as a new basis [22]. A dual energy procedure for signal-to-noise ratio evaluation in mammography with synchrotron radiation is reported in [23], where PMMA and polyethylene were chosen as basis materials α and β in order to discriminate breast tissues.

2.7.2 Single Projection Imaging

The convenience of identifying a material ξ in terms of its density ρ_ξ and thickness t_ξ is now described. Multiplying both terms of Eq. 2.34 by the thickness and density of the material, the logarithmic transmission (see Eq. 2.8 and 2.9) is expressed as the combination of the linear attenuation coefficients of the basis materials α and β , as given by

$$R = t_\xi \mu_\xi(E) = A_1 \mu_\alpha(E) + A_2 \mu_\beta(E), \quad (2.36)$$

where, from Eq. 2.34,

$$\begin{aligned} A_1 &= t_\xi a_1 \frac{\rho_\xi}{\rho_\alpha}, \\ A_2 &= t_\xi a_2 \frac{\rho_\xi}{\rho_\beta}. \end{aligned} \quad (2.37)$$

The coefficients A_1 and A_2 have dimension of length. Lehmann *et al* [1] have

shown the convenience of representing the logarithmic transmission of the material ξ by a vector in a two-dimensional basis plane. In this plane, the cartesian axes are associated with the base materials, and A_1 and A_2 are the projection of the vector R on the two axes. The length of the vector is therefore $|R| = \sqrt{A_1^2 + A_2^2}$, which is proportional to the thickness of the material ξ . The *characteristic angle* of the material in the basis plane can be defined from Eq. 2.35 and 2.37 as

$$\theta_\xi = \tan^{-1} \left(\frac{A_2}{A_1} \right) = \tan^{-1} \left[\frac{\rho_\alpha N_{g\alpha} (Z_\alpha^m - Z_\xi^m)}{\rho_\beta N_{g\beta} (Z_\xi^m - Z_\beta^m)} \right], \quad (2.38)$$

and depends only on the material's atomic number Z_ξ and the basis plane definition.

The dual-energy problem is to determine the values of A_1 and A_2 . These constants can be found by measuring (or simulating) the logarithmic transmission of a monochromatic X-ray beam at two different energies, namely low energy E_l and high energy E_h . From Eq. 2.36, the following relations are obtained:

$$\begin{aligned} R_l &= A_1 \mu_\alpha(E_l) + A_2 \mu_\beta(E_l), \\ R_h &= A_1 \mu_\alpha(E_h) + A_2 \mu_\beta(E_h). \end{aligned} \quad (2.39)$$

The solutions of the above linear system are

$$\begin{aligned} A_1 &= \frac{R_h \mu_\beta(E_l) - R_l \mu_\beta(E_h)}{\mu_\alpha(E_h) \mu_\beta(E_l) - \mu_\beta(E_h) \mu_\alpha(E_l)}, \\ A_2 &= \frac{R_l \mu_\alpha(E_h) - R_h \mu_\alpha(E_l)}{\mu_\alpha(E_h) \mu_\beta(E_l) - \mu_\beta(E_h) \mu_\alpha(E_l)}. \end{aligned} \quad (2.40)$$

The display of A_1 and A_2 , at every point, produces two *basis images* containing all the energy information inherent in the initial X-ray image. When the vector (A_1, A_2) is projected onto the unit vector directed outwards from the basis plane origin at angle ϕ , as illustrated in Figure 2.15(a), and the length of the projection C is displayed at every point, the resulting image is called a *basis projection image*, computed through the following relation

$$C = A_1 \cos(\phi) + A_2 \sin(\phi). \quad (2.41)$$

The effective atomic number of an unknown sample of material can be identified by computing basis projection images and varying the angle ϕ until $C = 0$ at every pixel. Then, ϕ is perpendicular to the characteristic angle θ_ξ of the unknown.

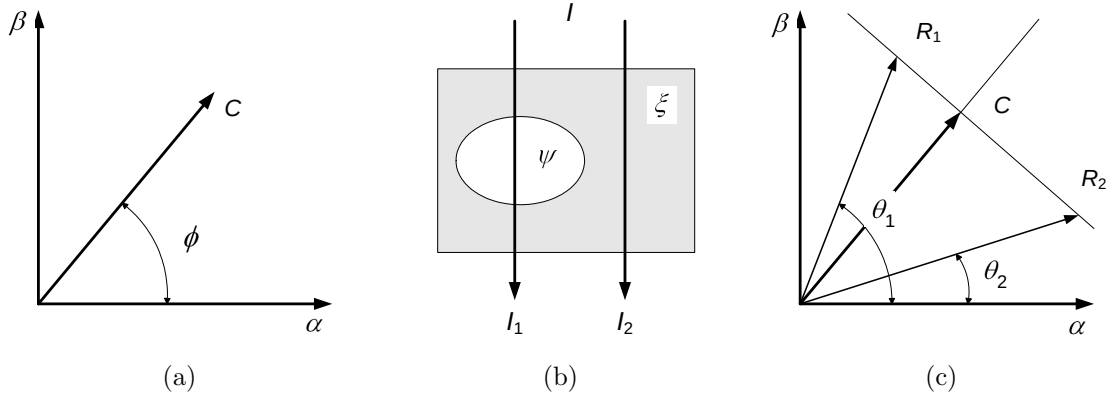


Figure 2.15: Dual Energy Radiography. (a) Basis Plane Representation; (b) Intensity transmission through different combinations of materials; (c) Logarithmic transmission represented in the basis plane.

2.7.3 Contrast Cancellation

The selective cancellation of unwanted tissues can be accomplished using dual energy radiography principles. Consider a material ψ embedded in a volume of material ξ as illustrated in Figure 2.15(b). An incident monochromatic X-ray beam is attenuated in different ways depending on the relative thickness of the two materials. Thus, a given logarithmic transmission R can correspond to many possible thickness combinations of the materials ψ and ξ . Figure 2.15(b) shows an example of two beams I_1 , transmitted through material ψ and ξ , and I_2 transmitted only through material ξ . If the logarithmic transmission is represented in the basis plane as shown in Figure 2.15(c), the vertex of the corresponding vectors R_1 and R_2 lies on the same line. This line is called the *iso-transmission* line [24] and describes all logarithmic transmission vectors.

Associating a gray level with the length of each vector, a radiographic image is obtained. If the vectors R_1 and R_2 are projected on a direction C defined by the angle ϕ , with C being perpendicular to the iso-transmission line, all the projected vectors have the same modulus. The gray levels associated with the projected vectors results then in a homogeneous basis projection image, C , where the contrast between materials ψ and ξ is forced to vanish. In this particular case, the angle ϕ is the so-called *contrast cancellation angle*.

Both simulated and experimental transmission data can be used to perform dual-energy decomposition calculations. A comparison of four different methods is reported in [24] and further details about the contrast cancellation algorithm

can be found in [25]. Dual-energy has not entirely evolved into a routine clinical examination because of the limitations of conventional imaging systems. Due to the broad band of energy spectrum of conventional X-ray source, a true separation between the low and high energy is not possible. Two approaches [26, 27, 28] have been taken so far: the kVp imaging in which the X-ray generator tube potential is switched between two voltages, and single exposures with a filter that preferentially filters out low energy radiation.

2.8 Summary

In this Chapter, we have presented a simple and formal description of the underlying physics in medical X-ray imaging systems, such as digital chest radiography and computed tomography. X-ray imaging systems were characterized in terms of their physical and geometrical properties. Medical X-ray production, interaction of radiation with matter and image receptors are topics covered in this Chapter. Attenuation coefficients are discussed in detail and the principles of dual-energy radiography are described to introduce the concept of material basis decomposition, which should prove particularly useful in Chapter 5 and Chapter 6.

Chapter 3

IMAGE PROCESSING TECHNIQUES

Image segmentation is an essential process for most subsequent image analysis tasks. In particular, many of the existing techniques for image description and recognition [29] and image visualization [30] highly depend on the segmentation results. Many techniques have been proposed to deal with the image segmentation problem [31]. Since a large amount of literature has been published on this topic [12, 32, 33] the discussion presented in this Chapter is restricted to some of the most frequently used algorithms with emphasis on the ones that will be applied to medical X-ray images of the human thorax, as discussed in Chapter 4 and 5.

3.1 Image Representation

The individual position of a pixel inside the image is identified by a unique index. An index is an array of integers that defines the position of the pixel along each coordinate dimension of the image. Figure 3.1 illustrates the main geometrical concepts associated with a digital image. Pixel spacing is measured between the pixel centers, represented as circles and can be different along each dimension. The image origin is associated with the coordinates of the first pixel in the image. A pixel is considered to be the rectangular region surrounding the pixel center holding the data value.

3.2 Image Filtering and Processing

3.2.1 Smoothing and Resampling

X-ray image data has a level of uncertainty that is manifested in the variability of measures assigned to pixels. This uncertainty, mainly due to scattered radiation in X-ray images, can be interpreted as noise and considered an undesirable component

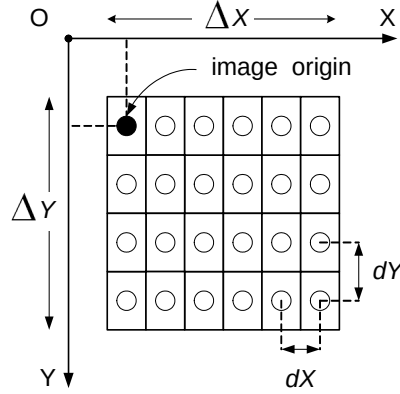


Figure 3.1: Geometrical concepts associated with a digital image (adapted from [34]).

of the image data. Several methods that can be applied to reduce noise on images, by attenuating high spatial frequencies of the image spectrum. It is usually implemented in the form of the input image convolution with a *kernel* filter. Given a 2D digital input image $\mathbf{I}_0(x, y)$, the filtered image $\mathbf{I}(x, y)$ is available by computing the convolution of the image with a kernel $\mathbf{G}(x, y)$, denoted as

$$\mathbf{I} = \mathbf{G} \otimes \mathbf{I}_0, \quad (3.1)$$

where $\otimes$ denotes the spatial convolution operator of image $\mathbf{I}_0$ with the kernel filter $\mathbf{G}$, as given by

$$\mathbf{G}(x, y) \otimes \mathbf{I}_0(x, y) = \iint \mathbf{G}(x' - x, y' - y) \mathbf{I}_0(x, y) dx' dy'. \quad (3.2)$$

Smoothing an image can be performed in different manners since different kernels attenuate the spatial frequencies in different ways. One of the most commonly used kernels is the Gaussian defined in terms of its standard deviation σ_0 as

$$\mathbf{G}_{\sigma_0}(x, y) = \frac{1}{\sigma_0 \sqrt{2\pi}} \exp \left[- \left(\frac{x^2}{2\sigma_0^2} + \frac{y^2}{2\sigma_0^2} \right) \right]. \quad (3.3)$$

The classical method of smoothing an image by convolution with a Gaussian kernel slows down when the standard deviation σ_0 increases. This is due to the larger size of the kernel, which results in a higher number of computations per pixel.

Image resampling is a common operation which varies the sampling grid spacing. It is usually combined with prior smoothing in order to generate a new image with different resolution without changing its physical extent. The image filtering

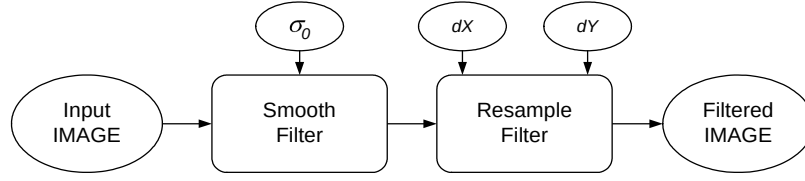


Figure 3.2: Collaboration diagram (pipeline) of the image smoothing/resampling algorithm.

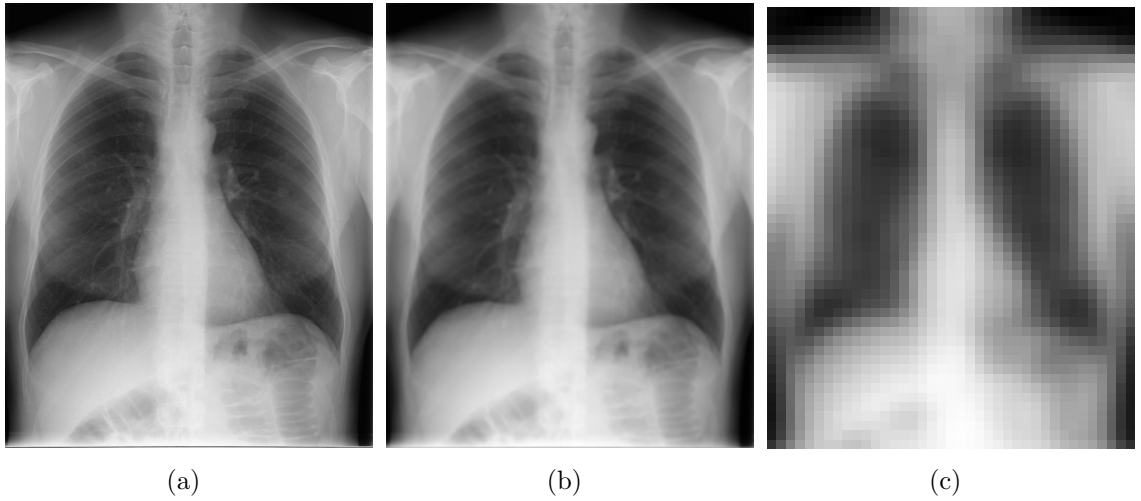


Figure 3.3: (a) PA Chest radiograph with pixel spacing $dX = dY = 0.2$ mm; Effects of smoothing and resampling with parameters set to (b) $\sigma_0 = dX = dY = 1.0$ mm, and (c) $\sigma_0 = dX = dY = 9.0$ mm. Images have been resized for display. True sizes (horizontal $\times$ vertical) are 1760×2144 , 352×428 and 39×47 pixels, respectively.

pipeline for image smoothing/resampling is shown in Figure 3.2. The resolution of the resulting image is selected by fixing the pixel spacing dX and dY of the output image. One can select different combinations of the values of dX and dY , as well as the standard deviation σ_0 for smoothing. When $dX = dY$, the input image is resampled isotropically. Consider the X-ray chest image displayed in Figure 3.3(a). The image is of size 1760×1760 pixels and spatial resolution or pixel spacing 0.2×0.2 mm. The following parameters $\sigma_0 = dX = dY = 1.0$ mm and $\sigma_0 = dX = dY = 9.0$ mm were used to produce, respectively, the results of Figure 3.3(b) and (c).

The discretization of the image is more visible on the output image in Figure 3.3(c) due to the choice of a low resolution, while the effects of smoothing are more pronounced by choosing higher values of σ_0 of the Gaussian kernel. Smoothing and resampling are optional image processing steps and therefore can be omitted in

the following discussion. By considering images with lower resolutions, computation time of further image processing tasks on the filtered image can be reduced.

3.2.2 Image Feature Extraction

The borders between anatomical structures observed in chest radiographs often largely coincide with image edges and ridges. Compared to other medical image modalities such as CT or MRI, edges are more difficult to extract from X-ray projection images. This Section provides a description of the proposed image processing for enhancing such features. Image enhancement is performed in analogy with the processing of stimuli by retinal and simple cells present in the human visual cortex, as described next.

Receptive Fields and Filter Kernels

Several filters have been proposed as convolution kernels for extracting visual features from an image. The shape and size of the kernel attempt to simulate the receptive field function of retinal cells. The receptive field (RF) of a cell in the visual system is defined as the region of the retina over which one can influence the firing of that cell [35]. RF of retinal ganglion cells are circular with either an ON center (excitatory) and an OFF (inhibitory) surround, or the reverse (center OFF - surround ON), thus presenting two types of polarity. As illustrated in Figure 3.4, Gaussian functions $\mathbf{G}_\sigma(x, y)$ were used in Eq. 3.3 as kernel filters to simulate these type of RF and used in the filtering step described in Section 3.2.1. An ON response is characterized by an increased firing rate of the cell to a light stimulus: a spot of light filling the ON center causes the cell to fire vigorously. Cells of the lateral geniculate body or LG neurons, have characteristics similar to retinal ganglion cells, since the receptive field of these cells is concentric and has an ON or OFF center with reverse type of surround. Ganglion cells and LG neurons are also called center-surround cells [35].

Directional Filtering

Simple cortical cells have elongated RF and respond better to oriented stimuli such as lines and bars within the image. Linear and complex Gabor functions [36, 37] have been proposed as computational models of simple cells. Several parameters, such as the orientation of the filter and spatial aspect ratio, are tuned to determine the preferred orientation and ellipticity of the receptive field of a particular

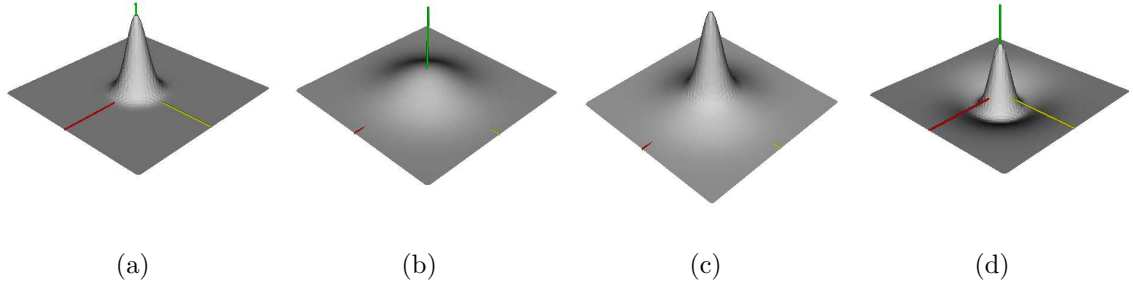


Figure 3.4: 3D view of Gaussian functions $\mathbf{G}_\sigma(x, y)$ simulating the receptive field of center-surround cells. (a) $\mathbf{G}_A = \mathbf{G}_{\sigma_A}(x, y)$ with standard deviation $\sigma_A = 1.0$ mm and (b) $\mathbf{G}_B = \mathbf{G}_{\sigma_B}(x, y)$ with $\sigma_B = 3.0$ mm. (c) Sum of Gaussians, $\mathbf{G}_A + \mathbf{G}_B$ and (d) difference of Gaussians, $\mathbf{G}_A - \mathbf{G}_B$.

cell. Gabor filters have been used in several computer vision tasks, including image enhancement [38] and edge detection [39].

Directional filtering was performed in 2 directions, namely X (horizontal) and Y (vertical) directions, to provide the means for enhancing anatomical structures such as the lung fields and their boundaries. For simplicity, 2D Gaussian functions were used for extracting image features from the input chest radiograph to be segmented, although other type of filters can be used as well. The choice of a Gaussian kernel is based on the reduction of the number of parameters, since only one is needed to define it. We presented in [40] results of processing chest radiographs with Gabor filters.

Several features $\mathbf{I}_1(x, y)$ were computed by convolving the input X-ray image with spatial derivatives of Gaussian filters, as given by

$$\mathbf{I}_1(x, y) = \mathbf{G}_{nm,\sigma}(x, y) \otimes \mathbf{I}(x, y), \quad (3.4)$$

where $\otimes$ denotes the spatial convolution operation of the input image $\mathbf{I}(x, y)$ with the 2D Gaussian kernel $\mathbf{G}_{nm,\sigma}$ as defined by

$$\mathbf{G}_{nm,\sigma}(x, y) = \frac{\partial^n}{\partial x^n} \frac{\partial^m}{\partial y^m} \mathbf{G}_\sigma(x, y). \quad (3.5)$$

The parameters n and m of the filter are, respectively, the order of the derivatives in X and Y directions, and σ is the standard deviation of the Gaussian function. Examples of such kernels are shown in Figure 3.5. Smoothing the image by convolving it with a Gaussian kernel before applying a differential operator is less sensitive to

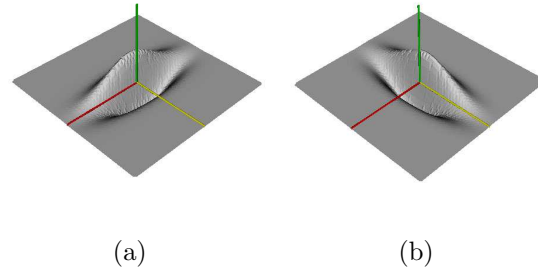


Figure 3.5: Example of derivatives of Gaussian functions $G_{nm,\sigma}(x, y)$ used for directional filtering of planar radiographs. 3D view of first order derivative (a) $G_{01,\sigma}$ and (b) $G_{10,\sigma}$, with standard deviation $\sigma = 1.0$ mm.

noise and more suited to relatively large features than alternatives such as Robert's cross or Sobel operators based on local differences.

The order of the Gaussian derivatives, n and m , determines the nature of the detected structures in the output image $\mathbf{I}_1(x, y)$ computed through Eq. 3.4. Using zero order derivatives, i.e. $(n, m) = (0, 0)$, light from dark regions are distinguished in the image (see Figure 3.4). Directional filtering is achieved when considering higher derivative orders. The combinations $(n, m) = (1, 0)$ and $(n, m) = (0, 1)$ yield edges from dark to bright regions, or vice versa, in X and Y directions, respectively (see Figure 3.5). When second order derivatives are used, i.e. by setting $(n, m) = (2, 0)$ and $(n, m) = (0, 2)$ one detects bright and dark line structures, perpendicular to the direction along which the derivative is performed.

Image filtering was performed in both horizontal and vertical directions by using Gaussian filter kernels with different scales. By choosing a particular value for the standard deviation σ of the Gaussian, an associated scale is selected. Instead of using a unique σ value, usually selected empirically, a multiscale approach was adopted. 3 different scales, namely $\sigma_1 = 1.0$ mm, $\sigma_2 = 3.0$ mm and $\sigma_3 = 9.0$ mm, were used for the 5 combinations of derivative orders (n, m) above mentioned. This results in 15 ($= 5 \times 3$) image features computed from Eq. 3.4.

Response Normalization

A normalization is included at this stage to adjust the intensity level of each convolution output. This step is important since we intend to combine such image features. First, the gray level intensity of the output of the Gaussian filters are normalized to zero mean and unit standard deviation. The transformation is denoted

by $\mathbf{I}_1(x, y) \rightarrow \mathbf{I}_2(x, y)$, where $\mathbf{I}_1(x, y)$ is the output of the convolution operation as given by Eq. 3.4. Then, a non-linear intensity mapping is performed on the image $\mathbf{I}_2$ by using a standard Sigmoid filter. A flexible implementation of this filter [34] includes several parameters that can be tuned to select its input and output intensity ranges. The following equation represents the Sigmoid intensity transform $\mathbf{I}_2(x, y) \rightarrow \mathbf{I}_3(x, y)$ applied pixel-wise:

$$\mathbf{I}_3(x, y) = (b - a) \frac{1}{1 + e^{-\frac{\mathbf{I}_2(x, y) - c}{d}}} - a. \quad (3.6)$$

In the above equation, the parameters a and b are the minimum and maximum values of the output image $\mathbf{I}_3$, d defines the width of the input intensity range and c defines the intensity around which the range is centered. The parameters were set to $a = -1$, $b = 1$, $c = 0$ and $d = 1$, such that $-1 \leq \mathbf{I}_3(x, y) \leq 1$.

The normalization includes a final step that incorporates an analog threshold element. This element has been previously suggested as part of a multilayered network for visual feature extraction [41]. Here, the function of such element was considered equivalent to that of a neuron. The output of a threshold element is an analog value, positive or zero, linearly proportional to the input providing that is greater than the threshold. The threshold value was set to $c = 0$, as in Eq. 3.6. More precisely, we defined the non-linear characteristic transfer function of the analog threshold element as follow:

$$\mathbf{R}_{nm,\sigma}^{(p)}(x, y) = \max\{0, (-1)^p \mathbf{I}_3(x, y)\}, \quad p = \{0, 1\}. \quad (3.7)$$

The image features extraction step is a composition of a convolution operation and normalization. From Eq. 3.4, 3.6 and 3.7, this step is described by the following processing pipeline: $\mathbf{I}(x, y) \rightarrow \mathbf{G}_{nm,\sigma} \rightarrow \mathbf{I}_1 \rightarrow \mathbf{I}_2 \rightarrow \mathbf{I}_3 \rightarrow \mathbf{R}_{nm,\sigma}^{(p)}(x, y)$. A schematics of this pipeline is shown in Figure 3.6.

The output of the analog element is a normalized response $\mathbf{R}_{nm,\sigma}^{(p)}$ with positive values, such that $0 \leq \mathbf{R}_{nm,\sigma}^{(p)}(x, y) \leq 1$. The thresholding operation described by Eq. 3.7 is actually equivalent to a half-wave rectification.

Since the Sigmoid transform results in images $\mathbf{I}_3$ with both positive and negative values, two opposite contrast polarities were used by including the parameter p in Eq. 3.7. By switching this parameter, $p = \{0, 1\}$, each convolution of the input chest radiograph with a particular filter $\mathbf{G}_{nm,\sigma}$ yields two normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}$, one for each value of p . Responses with opposite polarities were constructed

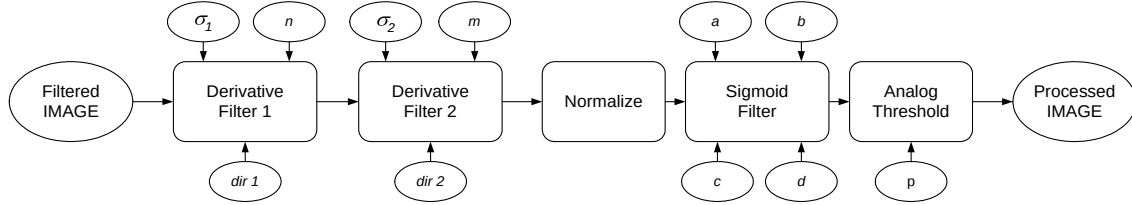


Figure 3.6: Collaboration diagram (pipeline) of the image feature extraction algorithm. The input image of the pipeline is a filtered version of the digital chest radiograph (see Figure 3.2).

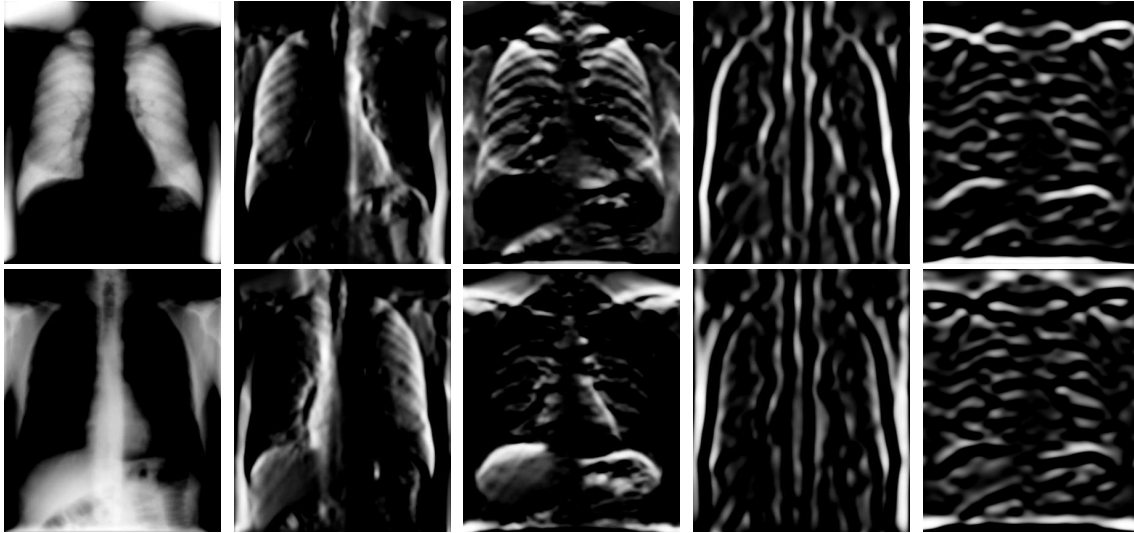


Figure 3.7: Examples of normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}(x, y)$, using the image processing pipeline of Figure 3.6. The chest radiograph of Figure 3.3(b) (filtered image) was processed with different derivatives of 2D Gaussian convolution kernels. σ is the width of the Gaussian and n and m are the order of the derivatives in X (horizontal) and Y (vertical) directions, respectively. From left to right: $\mathbf{R}_{00,1}$, $\mathbf{R}_{10,3}$, $\mathbf{R}_{01,3}$, $\mathbf{R}_{20,9}$ and $\mathbf{R}_{02,9}$. First row displays responses with polarity $p = 0$, while second row corresponds to $p = 1$. All response intensity values range between 0 (black) and 1 (white), that is, $0 \leq \mathbf{R}_{nm,\sigma}^{(p)}(x, y) \leq 1$.

to distinguish light from dark regions and discriminate light-dark from dark-light transitions.

Since 15 image features were extracted and 2 opposite polarities are considered, a total of 30 normalized responses were computed for each input radiograph to be segmented. Some responses $\mathbf{R}_{nm,\sigma}^{(p)}$ are displayed in Figure 3.7. Each response correspond to a particular combination of the Gaussian filter parameters n , m and σ . For each case, responses are shown for the two opposite polarities p .

3.3 Image Segmentation

Medical image segmentation plays a crucial role in many imaging applications by automating or facilitating the delineation of anatomical structures and other regions of interest. The general segmentation problem involves the partitioning of an input image into a number of homogeneous segments, such as contours and surfaces, that define the region of the object of interest as spatially connected groups of pixels. Alternatively, segmentation can be considered as a pixel labeling process in the sense that all pixels that belong to the same homogeneous region are assigned the same label.

3.3.1 Optimal Thresholding

Thresholding is used to change or identify pixel values based on specifying one or more values, called the threshold values. When more than one threshold value is considered we have a multithresholding technique [42]. The easiest method of grouping pixels into coherent regions is simply to threshold their gray values so that all pixels whose values are in a given range fall into the same class. More often, thresholding is used to binarize images so that the image foreground is separated from its background. Binary images are created by turning all pixels below a certain threshold to zero and all pixels above that threshold to one. In particular, the output of the analog threshold element $\mathbf{R}_{nm,\sigma}^{(p)}$ as given by Eq. 3.7, is a thresholded version of the image $\mathbf{I}_3$ at threshold T . For polarity $p = 0$ and threshold $T = 0$, Eq. 3.7 can be rewritten as

$$\mathbf{R}_{nm,\sigma}^{(0)}(x, y) = \begin{cases} 1, & \text{if } \mathbf{I}_3(x, y) \geq T, \\ 0, & \text{otherwise.} \end{cases} \quad (3.8)$$

The gray level distribution characterized by the image *histogram* is used for

computing the threshold. Local maxima of the histogram generally correspond to objects of interest in the image scene so that threshold values are best placed at local minima of the histogram to separate such objects.

Although this approach is quite effective in many cases, the choice of the threshold value is difficult and may lead to strange and unacceptable results. Often thresholding is not fully automatic as the choice of the threshold requires manual intervention. Several *unsupervised clustering* methods have been devised for selecting automatically the threshold. One of the most well known algorithm is the *isodata* [43]. The *isodata* clustering is an iterative algorithm that searches for suitable cluster centers (usually in good agreement with the local maxima of the image histogram) such that the distances between the cluster centers and the members of the cluster are minimized. A fixed number of clusters to be detected must be initially provided. The procedure is then repeated until the cluster centers remain stable. A proof of the convergence of the *isodata* algorithm is given in [44]. For bi-level thresholding, the optimal threshold [45] can be computed as follow. Let $T^{(i)}$ be the segmentation threshold at step i . To choose a new threshold value, the image is thresholded using $T^{(i)}$ in Eq. 3.8 to separate background from foreground pixels. Let $\bar{H}_1^{(i)}$ and $\bar{H}_2^{(i)}$ be the mean gray-level of the groups after segmenting a given image $\mathbf{H}$ with threshold $T^{(i)}$. Then the new threshold for step $i + 1$ is

$$T^{(i+1)} = \frac{\bar{H}_1^{(i)} + \bar{H}_2^{(i)}}{2}. \quad (3.9)$$

This iterative threshold update is repeated until there is no change in the threshold, i.e., $T^{(i+1)} = T^{(i)}$. This method works well if the spreads of the distributions are approximately equal, but it does not handle well the case where the distributions have differing variances.

Another criterion for classifying pixels is to minimize the error of misclassification. The goal is to find a threshold that classifies the image into two clusters such that we minimize the area under the histogram for one cluster that lies on the other cluster's side of the threshold. This is equivalent to minimizing the within class variance or, equivalently, maximizing the between class variance of foreground and background pixels. Using discriminant analysis, the method proposed by Otsu [46] defines the between-class variance σ_b^2 of the thresholded image as

$$\sigma_b^2(T) = n_1(T) n_2(T) [\bar{H}_2(T) - \bar{H}_1(T)]^2. \quad (3.10)$$

where $n_1(T)$ and $n_2(T)$ are the number of background and foreground pixels. For bi-level thresholding, Otsu verified that the optimal threshold T^* is chosen so that the between-class variance σ_b^2 is minimized, that is,

$$T^* = \arg \min_T \{ \sigma_b^2(T) \}. \quad (3.11)$$

Eq. 3.10 shows that the threshold depends only on the difference between the means of the two clusters. The optimal threshold is computed by updating $n_1(T)$ and $n_2(T)$ and the respective cluster means $\bar{H}_1(T)$ and $\bar{H}_2(T)$ as pixels move from one cluster to the other as T increases. Using simple recurrence relations the between-class variance is updated as each threshold is successively tested:

$$\begin{aligned} n_1(T+1) &= n_1(T) + n(T) \\ n_2(T+1) &= n_2(T) - n(T) \\ \bar{H}_1(T+1) &= \frac{n_1(T) \bar{H}_1(T) + n(T) T}{n_1(T+1)} \\ \bar{H}_2(T+1) &= \frac{n_2(T) \bar{H}_2(T) - n(T) T}{n_2(T+1)} \end{aligned} \quad (3.12)$$

Whereas the Otsu's method separates the two clusters according to the threshold and try to optimize some statistical measure, *mixture modeling* assumes that there already exists two distributions. The image histogram is usually considered as being the sample probability density function of a mixture of Gaussians and therefore the segmentation problem is reformulated as one of parameter estimation followed by pixel classification [33].

Thresholding considers only the value of all the pixels, not any *contextual* relationship between them, and thus, there is no guarantee that the pixels identified by the thresholding process are contiguous. This cause it to be sensitive to noise and image inhomogeneities. These artifacts essentially corrupt the histogram of the image making the separation more difficult. When the distribution of the pixel values is noisy, the image (or its histogram) is usually smoothed before trying to find separate modes or clusters. A survey on thresholding techniques is provided in [42]. More recently, a quantitative performance evaluation of thresholding methods has been presented in [47].

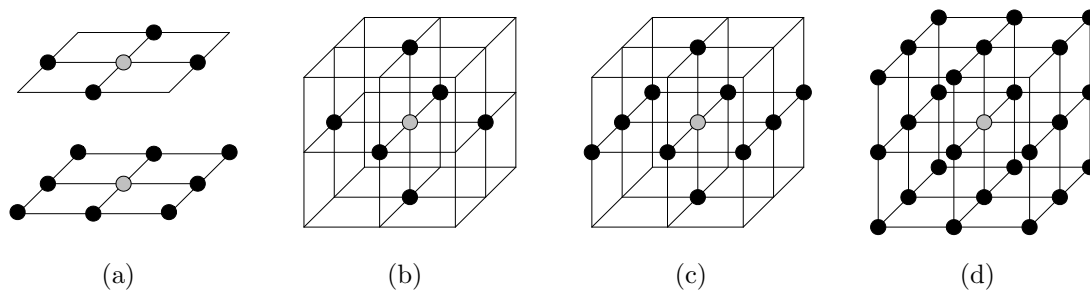


Figure 3.8: Pixel and voxel connectivity. (a) 4 and 8 pixel connectivity (2D); (b) to (d) 6, 10 and 26 voxel connectivity, respectively (3D).

3.3.2 Region Growing Techniques

Region growing algorithms have proven to be an effective approach for image segmentation. Region growing is a procedure that group pixels or sub regions into larger regions based on a predefined criteria. The basic approach is to start with a set of *seed* points and from these grow regions by appending to each seed those neighboring pixels that have properties similar to the seed. The selection of a set of one or more starting points and similarity criteria is often based on the nature of the problem. Region growing algorithms vary depending on the criteria used to decide whether a pixel should be included in the region or not, the type connectivity used to determine neighbors, as illustrated in Figure 3.8, and the strategy used to visit neighboring pixels.

The initialization of a Seeded Region Growing (SRG) algorithm requires, at least, one seed point. It is convenient that this point be placed in a typical region of the anatomical structure to be segmented. A simple similarity criterion for including connected pixels in the region is based on their gray level so that pixels having gray level $\mathbf{I}(x, y)$ in the same interval receive the same class label. If T_L and T_U are the lower and upper thresholds that define that interval, the region growing algorithm includes those pixels $\mathbf{p} = (x, y)^T$ connected to the seed that satisfy

$$T_L \leq \mathbf{I}(x, y) \leq T_U. \quad (3.13)$$

The lower and upper thresholds T_L and T_U define the interval in which pixel values should fall in order to be included in the region. Setting the threshold values too close will not allow enough flexibility for the region to grow. Setting them too far apart will result in a region that engulfs the image.

Criteria based on statistics of the current region may be used [33]. In the simplest

case, the algorithm first computes the mean m and standard deviation σ of values for all the pixels currently included in the region. By providing a factor k to define a range around the mean, neighbor pixels whose values fall inside the range are accepted and included in the region, that is,

$$m - k\sigma \leq \mathbf{I}(x, y) \leq m + k\sigma. \quad (3.14)$$

When no more neighbor pixels are found that satisfy the criterion, the algorithm is considered to have finished its first iteration. At that point, the mean and standard deviation of the intensity levels are recomputed using all the pixels currently included in the region. This mean and standard deviation defines a new intensity range that is used to visit current region neighbors and evaluate whether their intensity falls inside the range. This iterative process is repeated until no more pixels are added or the maximum number of iterations is reached. The number of iterations is specified based on the homogeneity of the intensities of the anatomical structure to be segmented. Highly homogeneous regions may only require a couple of iterations. Noise present in the image can reduce the capacity of the SRG algorithm to grow large regions. When faced with noisy images, it is usually convenient to pre-process the image by using an edge preserving smoothing filter.

A close variant of the SRG technique is illustrated in Figure 3.9. If two seeds, $\mathbf{p}_1$ and $\mathbf{p}_2$, and a lower threshold T_L are provided, the algorithm can be applied to grow a region connected to the first seed and not connected to the second one. In order to do this, the iterative procedure finds a value that could be used as upper threshold for the first seed. A binary search is used to find the value that separates both seeds. Major anatomical structures can be segmented by providing seed pairs in the appropriate locations. Selecting one seed in one structure and the other seed in the adjacent structure creates the appropriate setup for computing the threshold T_U that will separate both structures. As an example, consider the input image Figure 3.9(a), filtered as described in Section 3.2.1. The image is of size 352×428 pixels with gray levels ranging from 0 to 1024. The two seeds (white circles) $\mathbf{p}_1$ and $\mathbf{p}_2$ defined by the pair of coordinates $(x_1, y_1) = (8, 5)$ and $(x_2, y_2) = (103, 137)$ were manually identified in the right side of the image, and T_L was set to 0. The segmentation output of the SRG algorithm, shown in Figure 3.9(b) and (c) for which $T_U = 437$ was computed, are binary images with zero-value pixels everywhere except on the extracted regions. The same algorithm was applied to the left side, and $T_U = 403$ was found for the pair of seeds $\mathbf{p}_3$ and $\mathbf{p}_4$, $(x_3, y_3) = (342, 8)$

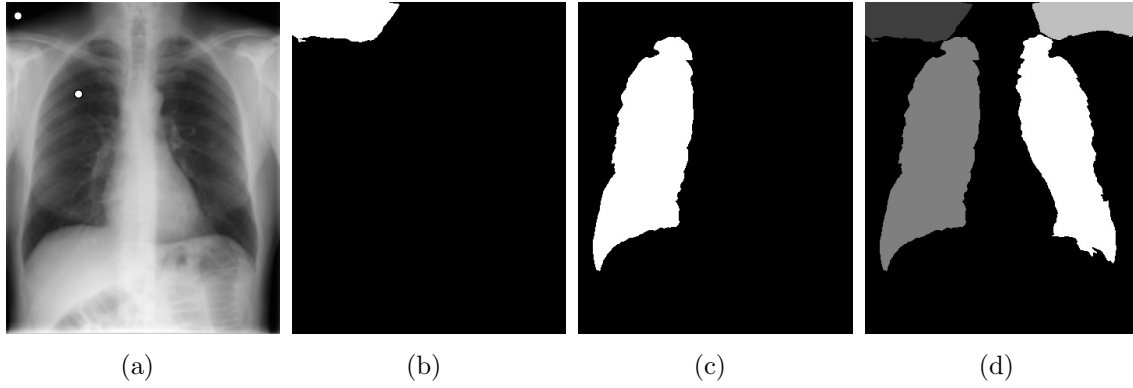


Figure 3.9: Example illustrating the seeded region growing (SRG) technique. (a) Filtered input image with seeds p_1 and p_2 (white circles); (b) Segmented region connected to seed p_1 and (c) connected to seed p_2 but not connected to p_1 . (d) Resulting image labeling after applying SRG on both sides of the image. Input values range from 0 to 1024 and the threshold is $T_U = 437$ and $T_U = 403$ for the right and left side, respectively.

and $(x_4, y_4) = (233, 137)$. This algorithm is intended to be used in cases where adjacent anatomical structures are difficult to separate. Applying twice the SRG algorithm results in the segmentation output shown Figure 3.9(d). As illustrated by the example, this technique provides a suitable method for separating the lung fields from the supra-clavicular region of the thorax.

Image segmentation using SRG should be performed on smoothed version of the image since the distribution of pixel values could be quite different from that of the input (non-filtered) image. Like thresholding, region growing is sensitive to noise and is not often used alone but within a set of image processing operations. Fuzzy analogies with region growing have also been developed [48].

3.4 Model-Based Image Segmentation

3.4.1 Lung Contour Model

A simple geometrical model of the lungs was adopted by defining a set of landmarks to describe conveniently its shape. Connecting the landmarks will result in several *segments* that are used to represent the boundaries between the lung regions and other anatomical structures observed in chest radiographs. The landmarks were chosen to reflect as much as possible the location of prominent visual features within the image. As shown in Figure 3.10(a), the selected landmarks, labeled from A to E , were superimposed on a PA chest radiograph to illustrate their anatomical

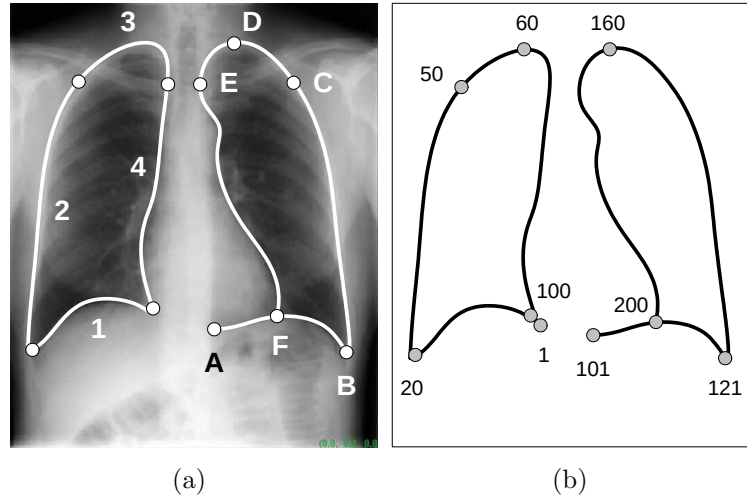


Figure 3.10: Lung contour model for PA chest radiograph segmentation. (a) The model is constructed by defining several segments (1 to 4) between landmarks (A to F), with anatomical correspondence. (b) A set of (200) interpolated points representing a template of the lung shape, manually delineated on the corresponding image.

correspondence.

A lung contour model is easily constructed, for each lung, by considering four segments: the hemidiaphragm (segment 1 - AFB), the costal edges or rib cage (segment 2 - BC), the lung top section or lung apex (segment 3 - CDE) and the mediastinal edges (segment 4 - EF). The junction of these four segments forms a closed contour denoted by the sequence $[FBCDE]$, that represents the unobscured region of the lung.

Defining several paths that contain at least one segment (or part of a segment) of the contour model, a method for segmenting the lung fields is proposed and explained in detail in Chapter 4, Section 4.3. The method is based on the automated and accurate delineation of such paths, based on the observation that the lateral edges (segments 2 and 4) are nearly vertical while, on the other hand, the hemidiaphragms (segments 1) are nearly horizontal and the lung top sections (segment 3) are approximately circular.

3.4.2 Dynamic Programming

The detection of optimal paths can be achieved by using an optimization algorithm based on dynamic programming we now introduce. Dynamic programming is a method of finding the global optimum of multistage processes. It is based on Bellman's principle of optimality [49] which state that *the optimum path between*

two given points is also optimum between any two points lying on the path. Typical applications of the use of dynamic programming in boundary tracking problems are tracing borders of elongated objects like roads and rivers in aerial photographs and the segmentation of handwritten characters. Medical applications include the segmentation of mammographic masses [50] and boundary detection in ultrasonic images [51] for automated measurement of the carotid artery [52]. Boundary delineation based on dynamic programming can be formulated as a graph searching problem where the goal is to find the optimal path between a set of starting nodes and a set of ending nodes. The optimal path is defined as the minimum cost path and the cumulative cost of a path (cost path) is the sum of the local costs of each pixel on the path. Application of the local cost to all pixels results in the so-called cost function. More details on constructing *cost images* are found in Section 4.2.3.

3.5 Statistical Shape Models

We now describe how to construct a 2D statistical shape model of the lungs from PA chest radiographs. The resulting model is intended to be used in a model-to-image registration algorithm for segmenting the lung fields from unseen images. The complete description of the proposed method is provided in Section 4.4.

Statistical shape models capture shape information from the set of labeled training data. A prerequisite for such models is a set of points located at corresponding positions on all training shapes. A popular method to describe shapes of objects is the Point Distribution Model (PDM), where each training shape is specified by a set of points lying on the contour or surface of the object [53, 54]. This particular multivariate model has proven to be especially useful for medical image segmentation.

3.5.1 Point Distribution Models

To construct the model, the outline of each lung field were hand traced on each digital chest radiograph of a private database by an experienced radiologist. A software system was specifically developed to perform this task. The software consists on a mouse-controlled graphical user interface that allows outlining/editing of 2D points and contours. Image contouring was performed at the lower resolution ($\sigma_0 = dX = dY = 1.0$ mm), by first delineating the right lung, then the left lung, according to the following sequence: hemidiaphragm (1), costal edge (2), lung top (3) and

mediastinal edge (4), as illustrated in Figure 3.10(a). Each lung is annotated by manually placing points around its border and spline interpolation was used to define the corresponding contour. Manual contours were stored in separated files and later used as the "gold standard" to evaluate the performance of the automated lung field detection algorithms.

The lung shape is represented by a set of N points $\mathbf{P} = \{\mathbf{p}_n\}$, $n = 0, 1, \dots, N-1$, where $\mathbf{p}_n = (x_n, y_n)^T$ is a point of the lung contour interpolated from the points provided by the user. Figure 3.10(b) shows an example of image contouring for which some contour points are indicated. The model was constructed such that, for each lung, 20, 40 and 40 points were interpolated to delineate, respectively, the segments AB , BD and DF . The total number of points of the resulting contour model is therefore $N = 200$. Note that due to the bilateral symmetry observed in chest radiographs, points $\mathbf{p}_n$ and $\mathbf{p}_{n+N/2}$, $n = 0, 1, \dots, N/2 - 1$, can be defined as points with symmetry correspondence.

Mean Shape

From the set of points $\mathbf{P}$ we are able to derive a *template* of the shape. By concatenating the coordinates for each point into a shape vector, we can represent every template with a single location $\mathbf{x}$ in a $2N$ -dimensional space:

$$\mathbf{x} = (x_0, y_0, x_1, y_1, \dots, x_{N-1}, y_{N-1})^T. \quad (3.15)$$

If the object is three-dimensional, then the space is $3N$ -dimensional. Some areas of the space (the shape-space) spanned by these vectors will be more densely populated than others and, by taking several examples of the input class, we can infer a model of the distribution, the point distribution model. Once the corresponding points in all the contours are constructed, each template is represented by a shape vector and the mean shape is given by

$$\bar{\mathbf{x}} = \frac{1}{S} \sum_{s=0}^{S-1} \mathbf{x}_s, \quad (3.16)$$

where S is the number of examples in the training set. Figure 3.11(a) shows the lung contours manually extracted from a dataset of $S = 39$ chest radiographs. From this training set, the mean shape plotted in Figure 3.11(b) was computed and clearly exhibits the expected bilateral symmetry of the human anatomy observed in PA chest radiographs.

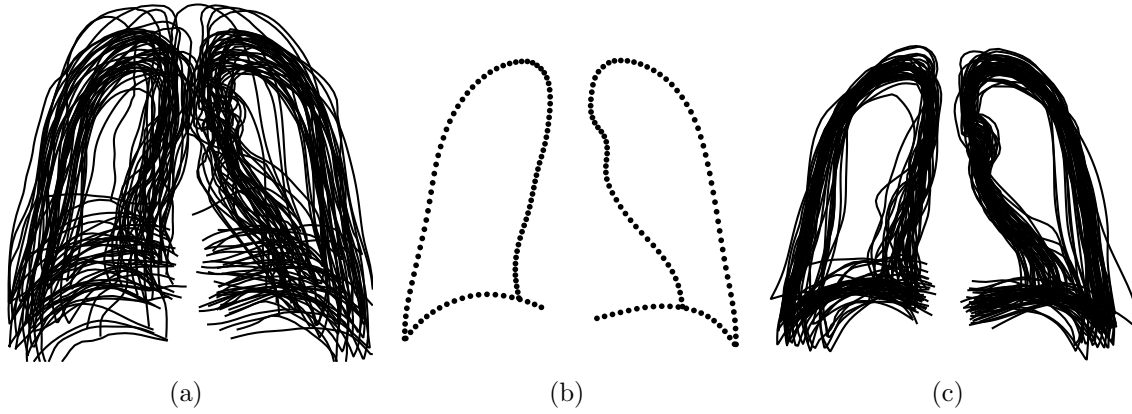


Figure 3.11: Point distribution model of the lungs. (a) Unaligned training shapes (contours) used to construct the mean shape (b), the lung contour model; (c) same contours after alignment using the Procrustes algorithm.

When modeling the different shapes of the templates it is usual to remove the spurious effects of the template location and orientation before transforming the examples into the space. This can be done by using the Procrustes algorithm [55, 56] to align all the shapes before the mean shape is produced. Aligned training shapes using the Procrustes algorithm are plotted in Figure 3.11(c).

3.5.2 Principal Component Analysis

The analysis of the shape vectors derived manually from the set of training examples gives insight in the typical variations in shape of the lungs and their correlation. The modes of variation, the way in which the model points tend to move together, can be found by applying the Principal Component Analysis (PCA) to the deviation from the mean shape as follow. The covariance matrix $\mathbf{C}$ of the training data is first computed using

$$\mathbf{C} = \frac{1}{S-1} \sum_{s=0}^{S-1} (\mathbf{x}_s - \bar{\mathbf{x}}) (\mathbf{x}_s - \bar{\mathbf{x}})^T. \quad (3.17)$$

The covariance matrix $\mathbf{C}$ is a matrix of size $2N \times 2N$ and describes the modes of variation of the points of the shape. $\mathbf{C}$ is eigen-decomposed to give a set of unit eigenvectors $\mathbf{e}_k$, $k = 0, 1, \dots, 2N-1$, and the corresponding eigenvalues λ_k , $\lambda_k \geq \lambda_{k+1}$, such that

$$\mathbf{C}\mathbf{e}_k = \lambda_k \mathbf{e}_k, \quad (3.18a)$$

$$\mathbf{e}_k^T \mathbf{e}_k = 1. \quad (3.18b)$$

The shape modes are not of equal importance. It can be shown that the eigenvectors of the covariance matrix corresponding to the largest eigenvalues describe the most significant modes and that the proportion of the total variance explained by each eigenvector is equal to the corresponding eigenvalue [57].

In many cases, a relatively small number of modes m ($m < 2N$) is used to approximate the original data while still representing a large fraction of its variation. The value of m can be determined by the number of principal components that are required to account for a sufficiently large proportion of λ_T , typically between 90% and 99%, of the total variance of all the variables, where

$$\lambda_T = \sum_{k=0}^{2N-1} \lambda_k. \quad (3.19)$$

The corresponding eigenvectors allow us to approximate any member of the original data set and can be treated as deformations of the whole model. New shapes $\tilde{\mathbf{x}}$ are generated by combining vectors, one for each mode, using an m -dimensional vector $\mathbf{b}$:

$$\tilde{\mathbf{x}} = \bar{\mathbf{x}} + \Phi \mathbf{b}, \quad (3.20)$$

where $\Phi = (\mathbf{e}_0, \mathbf{e}_1, \dots, \mathbf{e}_{m-1})$ is the matrix of the first m eigenvectors and $\mathbf{b} = (b_0, b_0, \dots, b_{m-1})^T$ is a vector of weights, one for each eigenvector, controlling the modes of shape variation. Since the eigenvectors are orthogonal, $\Phi^T \Phi = 1$ and

$$\mathbf{b} = \Phi^T (\tilde{\mathbf{x}} - \bar{\mathbf{x}}). \quad (3.21)$$

The above equation allows to generate new examples of the lung shape by varying the parameters $\mathbf{b}$ with suitable limits so that the new shapes can be considered as extracted from the training set.

Another way of visualizing which parts of the objects exhibit most shape variation is the independent PCA, applied to each model point $\mathbf{p}_n = (x_n, y_n)^T$, by considering $\mathbf{x} = \mathbf{p}_n$ in Eq. 3.15. In this case, the dimension of the shape vectors is reduced to $N = 2$, the dimension of the points. The result is displayed in Figure 3.12, where independent PCA has been applied without and with Procrustes alignment of the training set, as illustrated in Figure 3.12 (a) and (b), respectively. In both cases, the spread of each model point $\mathbf{p}_n$ is described by an ellipse with center at $\mathbf{p}_n$, whose semi-axis have the directions of the computed eigenvectors $\mathbf{e}_0$ and $\mathbf{e}_1$ and length equal to $b_k = \sqrt{\lambda_k}$, $k = 0, 1$, where λ_k is the corresponding eigenvalue

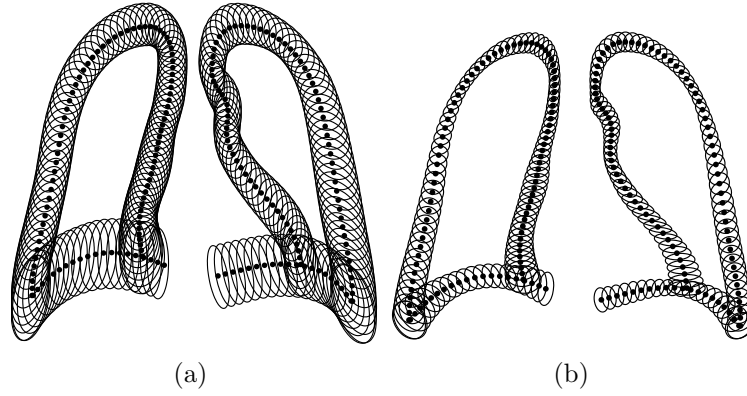


Figure 3.12: Independent principal component analysis for visualizing the spread of each point of the lung contour model, (a) before and (b) after alignment of the training shapes.

of $\mathbf{e}_k$.

3.5.3 Mean Shape Triangulation

The mean shape computed from the PDM described above is a geometrical representation that results in the partitioning of a given chest radiograph. In fact, beside the delineation of the lung fields, this approach is suitable to describe other general anatomical structures as connected regions within the thorax. For example, considering the landmarks A , F and E of both lungs (see Figure 3.10(a)), the model defines the cardiac silhouette as the closed contour $[(AFE)_r (EFA)_l]$, where the subscripts r and l stand for right and left. This is actually equivalent to the region defined between the mediastinal edges, below the lung top sections and above the hemidiaphragms. Similarly, connecting the landmarks $[(BFA)_r (AFB)_l]$ will result in the subdiaphragmatic region of the patient.

For each anatomical structure, the corresponding region can be described by a set of points, uniformly sampled in its interior. First an initial distribution of equilateral triangles is first created within the region by choosing the initial edge length of the triangles. Then, the resulting mesh is iteratively smoothed until the mesh points move less than a given tolerance. Figure 3.13 shows the result of such triangulation. The specification of the triangulated mean shape is reported in Table 3.1, and will be denoted as the parametric representation $\mathbf{p}_m = (\hat{x}_m, \hat{y}_m)^T$, $m = 0, 1, \dots, M-1$, corresponding to the set $\mathbf{P} = \{\mathbf{p}_m\}$ of M points, $M \geq N$, where N is the number of interpolated points that define the mean shape.

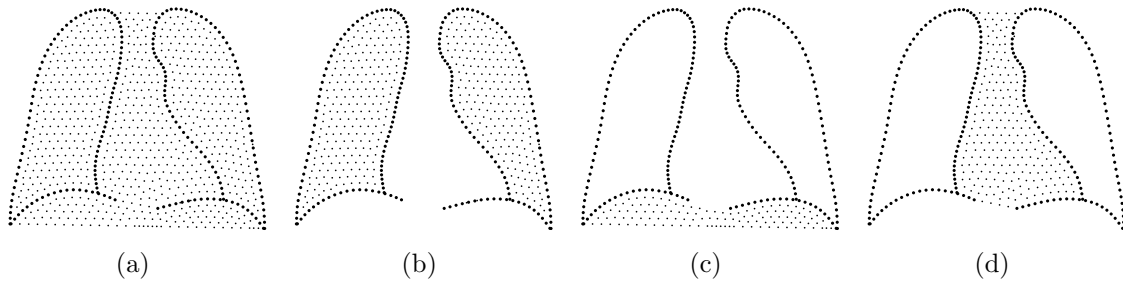


Figure 3.13: Mean Shape Triangulation. (a) Lung mean shape triangulated with initial edge length 10.0 mm and distance tolerance 0.01 mm; Anatomical regions corresponding to (b) interior of the lungs, (c) subdiaphragmatic region of the patient and (d) mediastinum.

Table 3.1: Specification of the lung contour model (triangulated mean shape) of Figure 3.13(a).

Image Database	HSJ	(private)	
Images in training set	S	39	(all)
Contours in image (lung fields)		2	(manual)
Segments in contour (both fields)		3	
Points in segments (one field)		20, 40, 40	(interpolated)
Points in contour model	N	200	(interpolated)
Initial edge length		10	mm
Edge tolerance		0.01	mm
Points inside right lung		207	(triangulated)
Points inside left lung		185	(triangulated)
Points below hemidiaphragms		119	(triangulated)
Points inside mediastinum		202	(triangulated)
Points in triangulated model	M	913	(total)

3.6 Deformable Models

Two and three-dimensional objects, such as surfaces and contours, can be manipulated in the normal ways. *Linear transforms* include translation, rotation and scaling. These are all operations that take place on the vertices of the model alone, since the connectivity of the points remains unchanged. Any set of such linear transforms can be encapsulated in a 4×4 transform matrix, by making use of homogeneous coordinates. Others operations, namely reflection and shearing, are also possible within such a framework but will not be considered here. *Non-linear transforms*, on the other hand, can change not only the position and orientation of objects but also their shape. By definition, two objects have the same shape if there exists a linear transform that exactly maps one onto the other. One of the many ways to specify a linear transformation is to give two sets of points and use the transform that maps one to the other. In general there will not exist a linear transform that exactly maps the points onto one another and so an error term must be minimized to find the best solution.

Two non-linear transforms are presented, namely the Free Form Deformation (FFD) and the Thin-Plate Spline (TPS) transform. FFD is a method for non-rigid warping with local control, through the use of cubic B-splines, while, by contrast, TPS does a global nonrigid warping controlled by a set of landmarks. Landmark-based transform will be used in Section 4.4 for the automated lung field segmentation of PA chest radiographs using a model-to-image registration framework.

3.6.1 Free Form Deformation

The deformation of a prior model can be accomplished using Free Form Deformation (FFD), a popular deformation technique in computer graphics [58]. The FFD is controlled by a rectangular deformation grid, of size $N_x \times N_y$, that surrounds the model (or just a portion of it). The grid is defined by the lattice or set of control points $\mathbf{U} = \{\mathbf{u}_{ij}\}$, $i = 0, 1, \dots, N_x - 1$, $j = 0, 1, \dots, N_y - 1$, and, when one or more points of the grid are moved to new positions, the model is deformed correspondingly.

Consider a geometrical model defined by the set of points $\mathbf{P} = \{\mathbf{p}_m\}$, $m = 0, 1, \dots, M - 1$, where $\mathbf{p}_m = (\hat{x}_m, \hat{y}_m)^T$. To deform the model using FFD, the local coordinates $(\hat{s}_m, \hat{t}_m)$, $0 \leq \hat{s}_m, \hat{t}_m \leq 1$, of each point $\mathbf{p}_m$ in the model point set are first computed with respect to the undisplaced FFD grid $\mathbf{U}$. The new position $\mathbf{q}_m$ of each point m in the deformed model, after moving the control points $\mathbf{u}_{ij} = (\hat{x}_{ij}, \hat{y}_{ij})^T$ to new positions $\mathbf{v}_{ij} = (x_{ij}, y_{ij})^T$, can be calculated using a bivariate tensor product:

$$\mathbf{q}_m = \sum_{i=0}^{N_x-1} \sum_{j=0}^{N_y-1} B_{i,N_x}(\hat{s}_m) B_{j,N_y}(\hat{t}_m) \mathbf{v}_{ij}, \quad (3.22)$$

where $B_{i,N}(s)$ is the Bernstein polynomial blending function of degree N , defined as

$$B_{i,N}(s) = \frac{N!}{i!(N-i)!} s^i (1-s)^{N-i}. \quad (3.23)$$

The deformation of the model depends on the displacement of each control point denoted $\Delta \mathbf{u}_{ij} = (\Delta x_{ij}, \Delta y_{ij})^T$, for which $\mathbf{v}_{ij} = \mathbf{u}_{ij} + \Delta \mathbf{u}_{ij}$. FFD is then represented by the set of displacement vectors $\Delta \mathbf{U} = \{\Delta \mathbf{u}_{ij}\}$, $i = 0, 1, \dots, N_x - 1$, $j = 0, 1, \dots, N_y - 1$, also called the *displacement vector field*.

3.6.2 Thin-Plate Splines

One particular and useful non-linear transform is the Thin-Plate Spline (TPS) [59]. TPS is frequently found in image analysis. For example, this transform has been used with velocity encoded MR images [60], to calculate cardiac strain from MR images [61], and analyzing bone structure on radiographs [62]. As with the landmark transform, a TPS transform is specified by two sets of corresponding points. With TPS, one of the sets of landmarks, the *source landmarks*, is exactly mapped onto the other, the *target landmarks*, and a deforming transform is interpolated between them. The interpolation is chosen such that it minimizes a bending energy, ensuring that the deformation is smooth and no discontinuities appear. Since we will make use of this *landmark transforms* at many stages, the algorithm is herein presented.

Consider the triangulated geometrical model of Figure 3.14(a), defined by the set of points $\mathbf{P} = \{\mathbf{p}_m\}$, $m = 0, 1, \dots, M - 1$, where $\mathbf{p}_m = (\hat{x}_m, \hat{y}_m)^T$. Let $\mathbf{m} = \{m_l\}$, $l = 0, 1, \dots, L - 1$, be a set of parameters which generates $L \leq M$ sequentially given source landmarks $\mathbf{u}(m_l)$ in the model. We assume that those landmarks represent the shape well. For simplicity, denote $\mathbf{u}(m_l) = \mathbf{u}_l$ and $\mathbf{U} = \{\mathbf{u}_l\}$ the set of the source landmarks. The target landmarks $\mathbf{v}_l$ form the set $\mathbf{V} = \{\mathbf{v}_l\}$ and represent the deformed model. According to the statistical shape theory [63], $\mathbf{U}$ and $\mathbf{V}$ can be regarded as the landmark representation of the shape and the deformed shape, respectively.

The TPS transform is specified by mapping the source landmarks $\mathbf{U}$ to the corresponding target landmarks $\mathbf{V}$. The deformation is characterized by the transform

$\mathcal{T} = (f, g)^T$, such that $\mathbf{V} = \mathcal{T}(\mathbf{U})$, i.e., $\mathbf{v}_l = \mathcal{T}(\mathbf{u}_l)$, $l = 0, 1, \dots, L-1$, where

$$f(\mathbf{u}) = a_0 + a_1\hat{x} + a_2\hat{y} + \sum_{l=0}^{L-1} c_l U(\mathbf{u}, \mathbf{u}_l), \quad (3.24a)$$

$$g(\mathbf{u}) = b_0 + b_1\hat{x} + b_2\hat{y} + \sum_{l=0}^{L-1} d_l U(\mathbf{u}, \mathbf{u}_l), \quad (3.24b)$$

and U is the basis function. In 2D we use $U(r) = r^2 \log r$, while in 3D we simply use $U(r) = r$. In Eq. 3.24, the parameters $\mathbf{a} = (a_0, a_1, a_2)^T$, $\mathbf{b} = (b_0, b_1, b_2)^T$, $\mathbf{c} = (c_0, c_1, \dots, c_{L-1})^T$ and $\mathbf{d} = (d_0, d_1, \dots, d_{L-1})^T$ can be calculated by solving the following matrix equation

$$\begin{pmatrix} \mathbf{K} & \mathbf{Q} \\ \mathbf{Q}^T & \mathbf{0} \end{pmatrix} \begin{pmatrix} \mathbf{c} & \mathbf{d} \\ \mathbf{a} & \mathbf{b} \end{pmatrix} = \begin{pmatrix} \mathbf{x} & \mathbf{y} \\ \mathbf{0} & \mathbf{0} \end{pmatrix}, \quad (3.25)$$

where, $\mathbf{K}_{ij} = U(\mathbf{u}_i, \mathbf{u}_j) = \|\mathbf{u}_i - \mathbf{u}_j\|^2 \log \|\mathbf{u}_i - \mathbf{u}_j\|$, $i, j = 0, 1, \dots, L-1$, $\mathbf{Q} = (1, \hat{\mathbf{x}}, \hat{\mathbf{y}})$ and $\mathbf{0}$ is an array of zeroes.

Note that in the above equation, $\mathbf{x} = (x_0, x_1, \dots, x_{L-1})^T$, $\mathbf{y} = (y_0, y_1, \dots, y_{L-1})^T$, $\hat{\mathbf{x}} = (\hat{x}_0, \hat{x}_1, \dots, \hat{x}_{L-1})^T$ and $\hat{\mathbf{y}} = (\hat{y}_0, \hat{y}_1, \dots, \hat{y}_{L-1})^T$, where $\mathbf{u}_l = (\hat{x}_l, \hat{y}_l)^T$ and $\mathbf{v}_l = (x_l, y_l)^T$ are corresponding landmarks of $\mathbf{U}$ and $\mathbf{V}$, respectively. It can be shown that the TPS transform minimizes the following so-called bending energy function [59]

$$E(\mathcal{T}) = \iint_{\mathbb{R}^2} (L(f) + L(g)) dx dy, \quad (3.26)$$

where

$$L(\cdot) = \left(\frac{\partial^2}{\partial x^2} \right)^2 + 2 \left(\frac{\partial^2}{\partial x \partial y} \right)^2 + \left(\frac{\partial^2}{\partial y^2} \right)^2. \quad (3.27)$$

Substituting Eq. 3.24 and Eq. 3.25 into Eq. 3.26 yields

$$E(\mathcal{T}) = \mathbf{c}^T \mathbf{K} \mathbf{c} + \mathbf{d}^T \mathbf{K} \mathbf{d}. \quad (3.28)$$

The thin-plate bending energy E is invariant to affine transforms and makes TPS especially suitable for describing nonrigid shape deformations in biological and medical applications. In the image analysis domain, thin-plate splines provide a natural way to move from point correspondences to entire image warps.

The TPS warping function is the transform that minimizes the bending energy (Eq. 3.26, 3.28) and simultaneously maps all points $\mathbf{p}_m$ of the undeformed model

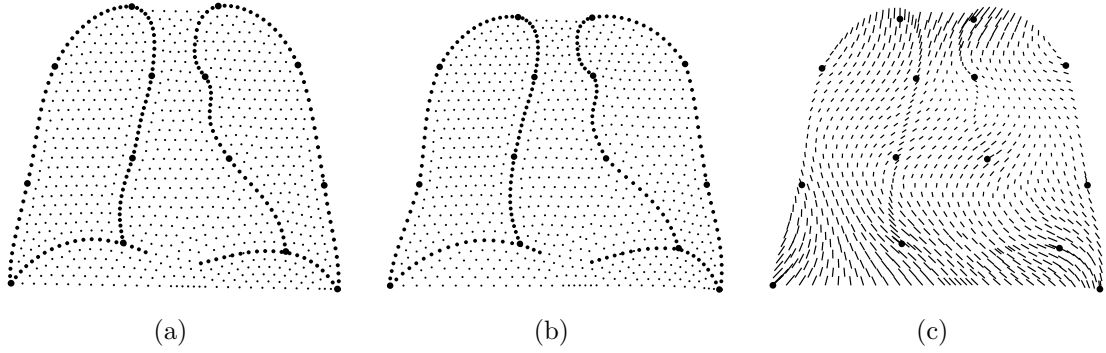


Figure 3.14: Lung model deformation using thin-plate splines (TPS) transform. (a) Undeformed model (triangulated mean shape) with a set of 14 *source* landmarks selected on the lung contour; (b) The model deformation using thin-plate splines is achieved by mapping the source landmarks to the corresponding *target* landmarks (source landmarks randomly displaced from their original position); (c) Corresponding displacement vector field, shown for all points of the triangulated model.

exactly onto their corresponding points $\mathbf{q}_m$ in the deformed model:

$$\mathbf{q}_m = \mathcal{T}(\mathbf{p}_m). \quad (3.29)$$

An example of the lung model deformation using TPS is illustrated in Figure 3.14, where the source landmarks $\mathbf{u}_l$ were selected from the points of the lung contour model (Figure 3.14(a)) and randomly displaced from their original position (Figure 3.14(b)) to create the target landmarks $\mathbf{v}_l$. As for FFD, model deformation using TPS defined by the corresponding sets of source and target landmarks can be represented by $\mathbf{v}_l = \mathbf{u}_l + \Delta\mathbf{u}_l$, where $\Delta\mathbf{u}_l = (\Delta x_l, \Delta y_l)^T$ is the displacement of the landmark $\mathbf{u}_l$. Again, the deformation is described by the corresponding displacement vector field $\Delta\mathbf{U} = \{\Delta\mathbf{u}_l\}$, $l = 0, 1, \dots, L - 1$, where L is the number of landmarks. Note that, as illustrated in Figure 3.14(c), the vector field can be computed from all the undeformed and transformed model points and therefore the displacements correspond to the vectors $\Delta\mathbf{p}_m = \mathbf{q}_m - \mathbf{p}_m$, $m = 0, \dots, M - 1$.

3.7 Optimization Techniques

This Section describes the basic principles of two common optimization techniques, namely genetic algorithms (GA) and Simulated Annealing (SA). Both search algorithms can be used as an optimizer in the model-to-image registration method reported in Section 4.4.1 for segmenting the lung fields from PA chest radiographs.

A proposed GA implementation is provided in Section 4.4.2.

3.7.1 Genetic Algorithms

In *The Origin of Species* [64], Charles Darwin stated the theory of natural evolution. Over many generations, biological organisms evolve according to the principles of natural selection like "survival of the fittest" to reach some remarkable forms of accomplishment. GA were originally devised as a model of adaptation in an artificial system by Holland [65].

Genetic Algorithms are probabilist search algorithms characterized by the fact that a number C of potential solutions $\mathbf{w}_c$ of the optimization problem simultaneously sample the search space of all possible individuals. This population $\mathbf{W} = \{\mathbf{w}_c\}$, $c = 0, 1, \dots, C-1$, is modified according to the natural evolution process: after initialization, selection and recombination are executed in a loop until some termination criteria is reached. Each run of the loop is called a generation and $\mathbf{W}^{(t)}$ denotes the population at generation t .

The flow chart of a *simple* GA is diagrammed in Figure 3.15(a). It is assumed that selection and recombination are done sequentially: first, a selection phase creates an intermediate population, $\mathbf{W}'$, and then recombination is performed with a certain probability on the individuals of this intermediate population to get the population $\mathbf{W}^{(t+1)}$ for the next generation. Mimicking the natural selection and reproduction, an initial population $\mathbf{W}^{(0)}$ can be evolved to the best solution $\mathbf{w}^*$ of the problem.

The selection operator is intended to improve the average quality of the population by giving individuals of higher quality a higher probability to be copied into the next generation. Selection thereby focuses the search on the exploration of promising regions in the search space. Recombination changes the genetic material in the population, either by crossover or mutation, in order to exploit new points in the search space. A schematic representation of standard recombination operators is given in Figure 3.15(b).

Solution Representation and Evaluation

In a standard GA, a solution is encoded as a string of *genes* to form a *chromosome* $\mathbf{w}$ representing an individual in the population. Each gene can take one or several values or *alleles*. Holland [65] showed that long chromosomes, with few alleles per gene are preferable to shorter chromosomes with many alleles per genes. This

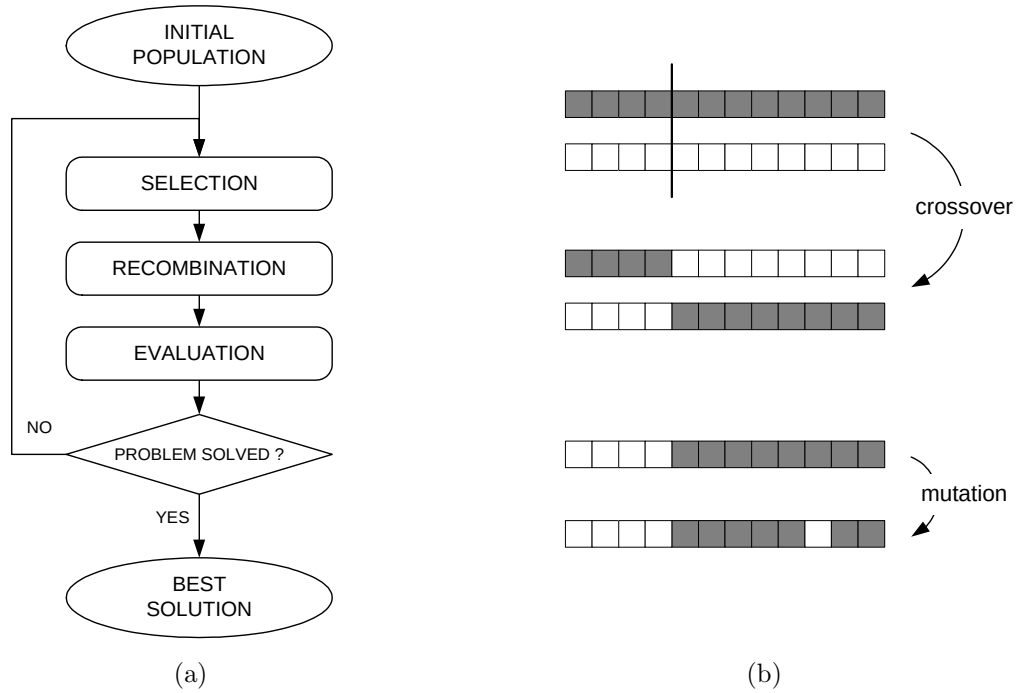


Figure 3.15: (a) Flow chart of a *simple* genetic algorithm. (b) Standard recombination operators, crossover and mutation, applied to chromosomes with binary alleles.

imply that the optimal case is to consider binary alleles. Consequently, in many optimization problems involving real-valued variables, the chromosomes are simply bit strings.

The quality of an individual is measured by an objective function, f_c , which can decode the chromosome $\mathbf{w}_c$ and assign a *fitness* value to the individual the chromosome represents. In many applications, the fitness is simply the objective function evaluated at the point in the search space represented by the chromosome.

Selection Functions

There are several schemes for the selection process, such as roulette wheel selection and its extensions, scaling techniques, tournament, elitist models and ranking methods [66, 67]. For selection only the fitness value of the individuals are taken into account. Hence, the state of the population is completely described by the fitness function.

Roulette wheel - A problem is the possible existence of a *super individual* in the population, i.e., an individual with an unusually high fitness. With fitness-proportionate selection this individual will get many copies in successive generations

and rapidly come to dominate the population thus causing premature convergence to a possibly local optimum. It is possible to partially avoid this effect by suitably scaling the evaluation function which amounts to the use of a modified fitness measure. Several scaling methods have been suggested [66]. Another approach to mitigate the above effect is to use selection methods that do not allocate trials proportionally to fitness, such as common methods described next.

Linear ranking - In this selection, the individuals are sorted by fitness. A rank C is assigned to the best individual and the rank 1 to the worst individual. Thus, the best individual receives a predetermined multiple of the number of copies than the worst one. The selection probability is linearly assigned to the individuals according to their rank. Rank selection reduces the dominating effects of super individuals without need for scaling and, at the same time, it exacerbates the difference between close fitness values, thus increasing the selection pressure in stagnant populations.

Tournament - This type of selection runs a *tournament* among a few individuals: at generation t , a number k of individuals is selected randomly from the population $\mathbf{W}^{(t)}$ with uniform probability, and the best one among them, the one with the highest fitness from this group, is copied into the intermediate population $\mathbf{W}'$. The winner can also be chosen probabilistically. The process is then repeated C times, the constant number of individuals in the population. A widely used tournament is held only between two individuals (binary tournament with $k = 2$) but a generalization is possible to an arbitrary group size k called *tournament size*. A 1-way tournament of size $k = 1$ is equivalent to random selection. The selection pressure is proportional to the tournament size. The chosen individual can be removed from the population that the selection is made from if desired, otherwise individuals can be selected more than once for the next generation. Tournament selection has the advantage that it need not be global so that local tournaments can be held simultaneously in a spatially organized population.

Truncation - In truncation selection with threshold T only the fraction T best individuals can be selected and they all have the same selection probability.

Recombination Operators

Recombination includes crossover and mutation or any operator that changes the genetic material of the chromosomes. Crossover is the process whereby two selected *parent* chromosomes are combined together to create *offspring*. This operator mimics

the genetic crossover of DNA¹ in nature and serves to increase the variety in the population, allowing the algorithm to explore most of the search space. In this way, the GA manages to find the approximate global optimum in very large search spaces in relatively short times. Mutation is a background operator which selects a gene at random on a given individual and mutates the allele for that gene (for bit strings the bit is complemented). Mutation is used to reintroduce alleles which may have been lost from the population for purely stochastic reasons. Schematics of these operators are given in Figure 3.15(b) for the case of binary alleles.

The balance between exploitation and exploration can be adjusted either by the selection pressure of the selection operator or by the recombination operator, e.g. the probability of crossover p_{cross} and mutation p_{mut} . As this balance is critical for the behavior of the GA, the properties of selection and recombination operators are of great interest to understand their influence on the convergence speed.

GA have been quite successful in optimization problems, especially when standard mathematical methods are hard to apply e.g. for noisy, discontinuous or non-differentiable functions. GA have shown to solve linear and nonlinear problems by exploring all regions of the state space and exponentially exploiting promising areas through the selection and recombination operations. A more complete discussion of genetic algorithms, including extensions and related topics can be found in the books by Davis [68], Goldberg [66], Michalewicz [67] and a useful tutorial is provided in Whitley [69].

3.7.2 Simulated Annealing

Simulated annealing [70] is a stochastic decent technique derived from statistical mechanics. When crystalline material is slowly cooled through its melting point, highly ordered, low-energy crystals are formed. The slower the cooling, the lower the final lattice energy. This physical process is a natural optimization method where the lattice energy E is the objective function to be minimized. Numerical systems can be run through a similar optimization process if the parameters of the system are identified with state space variables, and the objective function of the optimization problem with the energy E .

Thermal fluctuations in the system are simulated by randomly perturbing its parameters, and the size of the fluctuations are controlled by a temperature parameter T . If a system is at equilibrium at temperature T , the probability that the system

¹ Deoxyribonucleic Acid

is in a particular atomic configuration is

$$p(E) = \exp\left(-\frac{E}{k_B T}\right), \quad (3.30)$$

where E is the energy of the configuration and k_B is the Boltzmann constant. Simulated annealing attempts to reach the minimum energy state through a series of atomic reconfigurations or local perturbations which are accepted if the energy is decreased, and accepted with probability $p(\Delta E) = \exp(-\Delta E/k_B T)$ if the energy is increased. For $T > 0$, there is always some probability that a detrimental step will be accepted, thus allowing the algorithm to escape from local minima.

In contrast to simulated annealing which uses an analogy with a physical optimization process, GA are based on the genetic processes of biological evolution. A good comparison of these optimization algorithms with Monte Carlo techniques is given in [71].

3.8 Validation

In order to quantify the performance of a segmentation method, validation experiments are necessary. Validation is typically performed using one of two different types of truth models. The most straightforward approach to validation is by comparing the automated segmentation with manually obtained segmentations. This approach does not guarantee a perfect true model since an operator's performance can also be flawed. The other common approach to validating segmentation methods is through the use of physical phantoms [72] or computational phantoms [73]. Physical phantoms provide an accurate depiction of the image acquisition process but typically do not present a realistic representation of anatomy. On the other hand, computational phantoms can be more realistic in this latter regard but often simulate the image acquisition process using only simplified models.

Once a truth model is available, a figure of merit must be defined for quantifying the performance [74, 75, 76]. The choice of the performance measure is dependent on the application and can be based on region information such as the number of pixels misclassified, or boundary information such as distance to the true boundary. A survey on this topic is provided in [77].

The proposed methods for automated lung field extraction from chest radiographs and volumetric CT images, as described respectively in Chapter 4 and Chapter 5, are expected to produce binary masks as the final segmentation output. The

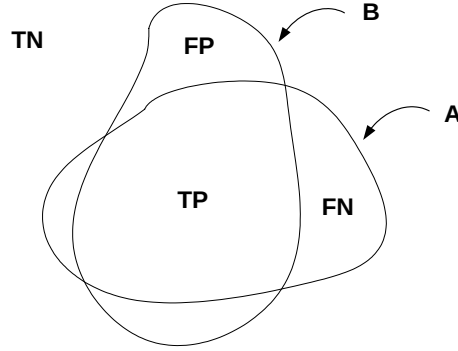


Figure 3.16: Confusion Matrix. Binary images A and B are compared pixel-wise to classify each pixel as true positive (TP), true-negative (TN), false-positive (FP) and false-negative (FN), when considering the contour in A as the reference.

binary images were compared pixel-wise with the corresponding hand-segmented images to classify each pixel in the image in one of four categories, as illustrated in Figure 3.16: true positive (TP) where both the algorithm and the human observer considered the pixel to be within the lung; true-negative (TN) where both considered the pixel to be outside the lung; false-positive (FP) where the computer found the pixel inside the lung and the observer did not; and false-negative (FN), where the observer detected the pixel in the lung but the algorithm did not. The number of pixels N in each category was found as a fraction of the total number of pixels in the image. These quantities were used to calculate the classical accuracy [78],

$$\text{accuracy} = \frac{N_{\text{TP}} + N_{\text{TN}}}{N_{\text{TP}} + N_{\text{TN}} + N_{\text{FP}} + N_{\text{FN}}}, \quad (3.31)$$

to measure the segmentation performance. The sensitivity and specificity are defined per convention:

$$\text{sensitivity} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FN}}}, \quad (3.32a)$$

$$\text{specificity} = \frac{N_{\text{TN}}}{N_{\text{TN}} + N_{\text{FP}}}. \quad (3.32b)$$

Considering the problem as the segmentation between lung and background and following the approach introduced in [79], we computed the accuracy, sensitivity and specificity to compare our results with other studies reported in the literature [80, 81, 82, 83].

Other methods can be used to evaluate the performance of segmentation algo-

rithms. Among them, we focused on two standard performance indicators, namely degree of overlap and F-score [84]. The degree of overlap was also used to evaluate the results of a segmentation method applied to digital lateral chest radiographs [85] and mammograms for detecting mass lesions [50]. These two additional measures were considered for comparative purposes. Unlike accuracy, as given by Eq. 3.31, they are independent of the true negative fraction, the part of the image correctly classified as background.

The degree of overlap between the two segmentation masks was computed as the ratio:

$$\text{overlap} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FP}} + N_{\text{FN}}} = \frac{|A \cap B|}{|A \cup B|}. \quad (3.33)$$

where A and B are respectively the segmented lung region or set of non-zero pixels in the first and second binary mask. In Eq. 3.33, $\cap$ represents the intersection and $\cup$ the union of two sets, and the operator $|\cdot|$ represents the size (number of pixels) of a set. N_{TP} is the part of the image that have been correctly classified as lung and therefore $N_{\text{TP}} = |A \cap B|$. With this definition, the overlap represents also the true positive fraction relative to $|A \cup B|$.

By computing the area of the respective lungs, $|A|$ and $|B|$, for both the manual and automated segmentation, the precision and recall were calculated as follows:

$$\text{precision} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FP}}} = \frac{|A \cap B|}{|B|}, \quad (3.34a)$$

$$\text{recall} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FN}}} = \frac{|A \cap B|}{|A|}. \quad (3.34b)$$

Note that *recall* defined by Eq. 3.34b is actually *sensitivity* as given by Eq. 3.32a. Taking the weighted average of precision P and recall R leads to the F-score,

$$F = \frac{PR}{\alpha P + (1 - \alpha) R} = \frac{|A \cap B|}{\alpha |A| + (1 - \alpha) |B|}, \quad (3.35)$$

where α is a parameter to the F-score used to control the weight assigned to precision and recall. We used $\alpha = 0.5$, a value often used [86, 87], to determine the relative importance of each term, by expressing no preference for either. For this particular case, and following Eq. 3.35, the measure is computed as $F = 2 |A \cap B| / (|A| + |B|)$.

3.9 Final Remarks

This Chapter focused on the presentation of basic techniques for the analysis of 2D and 3D images. Generally, solutions to practical segmentation problems are obtained by applying such methods in sequence. For the sake of simplicity, they have been illustrated for 2D images although some of them are easily generalized to 3D. For instance, elementary algorithms such as smoothing, resampling and directional filtering were introduced to extract prominent visual features in chest radiographs and compute normalized responses suitable for detecting the borders between anatomical structures that largely coincide with edges and ridges in such images.

Optimal thresholding and region growing present some limitations for performing segmentation by itself. These limitations are particularly noticeable in noisy images and in images lacking spatial uniformity, as is the case with planar radiographs. However, such techniques will prove particularly useful for extracting anatomical structures of interest from volumetric CT images.

Based on prior knowledge, we have described the construction of a statistical shape model of the lungs. A main drawback of the approach is the point correspondence problem in the model construction phase. On every training sample, points have to be placed in a consistent manner. In order to describe the lung shape and its variations correctly, points on all training samples have to be located at corresponding anatomical positions. Although the number of training shapes is small, the geometrical model reflects well the expected reflectional symmetry observed in PA chest radiographs and will be used as the basis of model-based segmentation methods, namely contour delineation based on dynamic programming and model-to-image registration based on genetic algorithms. For the latter, the deformation of the model was considered by means of landmark-based non-rigid transforms, such as Free-Form Deformations and Thin-Plate Splines.

Finally, several figures of merit were defined for quantifying the performance of segmentation methods. These measures are mainly based on a pixel-wise comparison of binary masks that correspond to the region of segmented objects.

Chapter 4

SEGMENTATION OF 2D PA CHEST RADIOGRAPHS

Several toolkits were used to develop the computer algorithms that support the proposed segmentation methods, namely the Insight Segmentation and Registration Toolkit (ITK), for image filtering and processing, the Visualization Toolkit (VTK), for image display and visualization and the Fast Light Toolkit (FLTK) for constructing graphical user interfaces. A brief description of the toolkits is provided in Appendix A.

4.1 Introduction

The automatic segmentation of anatomical structures from medical images provides useful information required by many computer-aided diagnosis (CAD) systems. In chest radiography, CAD schemes are mainly developed for automated detection of abnormalities. Most of the techniques for segmenting the lung region from thoracic images have in mind as ultimate goal the identification of pulmonary nodules [88, 89, 90, 91]. The delineation of the boundaries of the lungs have also been used as indicators of cardiomegaly [92, 93, 94] or pneumothorax [95]. Accurate identification of the lung fields is thus an essential pre-processing step before further analysis of thoracic images can be applied successfully. It is also a useful tool for automatic region-based image processing and data compression [96].

Region-based and edge-based image segmentation methods have been applied to solve the lung field segmentation problem in conventional chest X-ray images [97]. The first category assigns each pixel to a particular object or region. Examples are split-and-merge algorithms and region growing techniques. The second category are edge-based algorithms. Instead of dividing the image into object and background pixels, the boundary of the object is detected by first constructing the so-called

edge-image. In the edge image each pixel is assigned a value according to the edge strength. Based on this image, pixels with strong edge are selected and linked to each other. The linked pixels often represent object boundaries.

The methods use two general approaches that have been classified as rule-based reasoning and pixel classification [83]. Rule-based systems apply a sequence of algorithms consisting of a series of image processing operations such as image linear combination, spatial filtering, thresholding, and morphological operations to delineate the lung field boundaries. Each of these steps contain specific processing and, usually, certain adjustable parameters. For the segmentation of lung fields, such schemes have been proposed by several authors [98, 99, 100, 101, 102], by using heuristic edge-tracing approach [79], a technique for thresholding chest images on the basis of global gray-level histogram analysis [85], or the detection of rib cage boundaries and diaphragm edges on the basis of a derivative method [103]. A system to extract lung edges that employs reasoning mechanisms has been presented in [104]. The thoracic cage boundary has also received some attention [103, 105], since it delimits the area of search of the ribs. The derivative-based approach for detecting rib cage boundaries [92, 103, 100] based on the second derivatives of the image profiles were used to detect the edges of the ribcage and polynomial curve fitting was applied to detected edges to estimate the complete rib cage. A method based on image features extraction and edge detection from derivatives of image profiles is also reported in [81].

In pixel classification, each pixel in the image is individually classified as lung or non-lung based on features such as image data magnitude, location, and local texture measures [106]. Lung segmentation by pixel classification using neural networks has also been investigated [89, 107, 108, 109]. The use of an adaptive-sized hybrid neural network [96] has also been proposed for segmenting chest radiographs. Other approach considers a pixel classifier for the identification of lung regions using Markov random field modeling [80, 110]. A hybrid segmentation scheme that combines the strengths of a rule-based approach and pixel classification was also proposed [83].

Either approaches can utilize global knowledge, such as human thorax anatomy, implicitly through constraints and tests in the algorithm logic, and explicitly through a series of rules expressed as logical constraints [104] or with statistical shape models trained on hand digitized contours [111]. A comparative study on a public database on the segmentation of anatomical structures in chest radiographs using supervised methods is provided in [94].

Most of the published work focus on automated segmentation of lung fields in standard PA chest radiographs. An overview of the literature on lung field segmentation, rib detection and methods for selection of lung nodule candidates can be found in [112]. Segmentation approaches applied to lateral chest images can be found in [85, 102]. Dual-energy chest X-ray images have also been used to develop and test a method for delineating the lung fields [82]. The segmenting method exploits the characteristics of dual-energy subtraction images [1] to improve lung field segmenting performance, by using soft-tissue and spatial frequency-dependent, background-subtracted images. The soft-tissue images provided by dual-energy technology eliminate ribs, which are a major source of errors in these CAD systems.

Since chest radiographs are projection images, the lung fields contain several superimposed structures, such as lung vasculature, posterior and anterior ribs, and clavicles. Image analysis should differentiate between these structures that do not make up the borders of the lung fields, as opposed to other structures such as the mediastinum and the diaphragm. This is only possible by the incorporation of knowledge. Knowledge-based processing is thus mandatory to solve the task of segmenting planar radiographs. Beside the nature of projection images, large anatomical variations from person to person and different levels of inspiration of the subject(s) during the examination make the automatic segmentation of chest radiographs a hard problem from a computer vision point of view. The accurate segmentation of anatomical structures in chest X-ray images is still an open problem and manual extraction is often considered as the most reliable technique.

4.2 Segmentation Methods

4.2.1 Anatomical Model

A tutorial on chest anatomy is beyond the scope of this Chapter. We only briefly present the anatomy of the human thorax to provide some minimal knowledge of chest images. A normal PA chest radiograph is shown in Figure 4.1 with several normal structures labeled. The left side of the image shows the right lung. The right and left lungs are radiolucent since they are mainly composed of air and therefore show up as black in the image. A darker vertical stripe indicates the trachea. Within the lung fields, only bony structures and blood vessels are visible, such as the heart, the aortic arch where the aorta bends and the hilum where the arteries and veins enter the lungs. The posterior ribs in the back of the patient are usually visible more

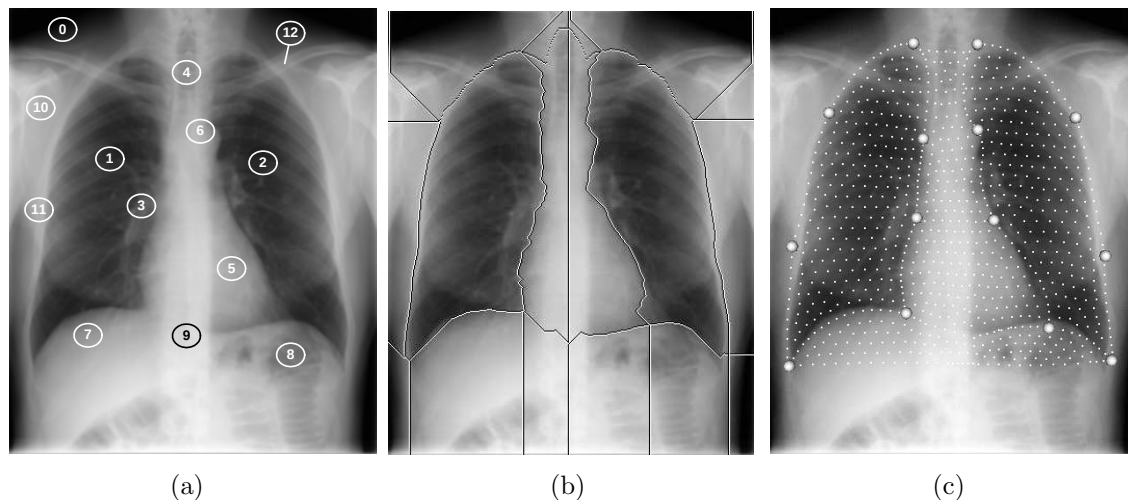


Figure 4.1: Normal anatomy of the human thorax observed in a 2D PA chest radiograph: (0) AIR outside the patient, (1) right lung, (2) left lung, (3) right hilum (lung root), (4) large airways (trachea), (5) mediastinum (left ventricle), (6) aortic arch, (7) right hemidiaphragm, (8) stomach gases, (9) spine, (10) shoulderblade, (11) posterior ribs turning into the anterior ribs, (12) clavicle (see also Figure 5.1). Typical lung field segmentation output of the proposed methods: (b) contour delineation method based on dynamic programming and (c) model-to-image registration based on genetic algorithms.

clearly than the anterior ribs. If there is enough contrast in the mediastinum (the area projected between the lung fields) the spine may be visible. Below the lung fields diaphragm starts. Usually stomach gases can be seen in the left diaphragm.

As noted elsewhere [80, 83], the lung boundaries define actually the regions of the lungs not obscured by the mediastinum, heart, or diaphragm. It has been estimated [113] that approximately 26% of the lung volume and 43% of the total projected area is obscured by one of these structures. Therefore, when focusing on segmentation of standard PA chest radiographs, the lung fields are defined as those regions of the image for which the radiation has passed through the lungs. Methods to segment and process the remaining parts of the lungs are important. Unfortunately, segmenting the total projected area of both lungs from a chest radiograph is substantially more difficult than segmenting the unobscured regions and it is the subject of ongoing research [88].

4.2.2 Proposed Algorithms

The two methods reported herein are segmentation schemes that accurately segment the lung fields from standard PA chest radiographs. Actually, two approaches are

proposed to achieve this goal:

- **Contour Delineation** (method 1) - Based on the contour model defined in Section 3.4.1, the complete lung boundaries, including the costal, mediastinal and diaphragmatic edges are depicted by using an edge tracing algorithm based on dynamic programming (DP) (see Section 3.4.2). This technique is typically used as a search method for border detection. A description of the method is presented in Section 4.3 and a typical output of the method is given in Figure 4.1(b).
- **Model-to-Image Registration** (method 2) - Using the prior geometrical model (statistical shape) of the lungs (see Section 3.5 and Section 3.6), this method treats the lung field segmentation as an optimization problem using a genetic algorithm (GA) (see Section 3.7). The approach is based on a non-rigid deformable model to image registration framework described in Section 4.4, and a typical output is shown in Figure 4.1(c).

Both image segmentation methods are model-based approaches that consist on several algorithms applied sequentially. A schematic of the image processing pipeline is shown in Figure 4.2 and the corresponding list of steps is given below.

```
// Algorithm - Lung Field Segmentation
// -----
1. Read input IMAGE (planar radiograph)
2. Smooth and resample IMAGE (optional)
3. Process IMAGE and compute normalized RESPONSES
4. Combine RESPONSES and construct COST images:
5. Segment lung fields based on:
   - Contour Delineation, using DP
   AND/OR
   - Model-to-Image Registration, using GA
```

The segmentation procedure is constructed in such a way that both approaches share the same initial steps. These correspond to the image processing steps presented in Section 3.2: first, an optional image filtering step is performed to smooth and resample the input chest radiograph (see Section 3.2.1), then, based on the convolution of the image with derivatives of a Gaussian, image features are extracted from the filtered image resulting in normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}(x, y)$ as described in Section 3.2.2.

The common steps are intended to provide *cost images*. Actually, four cost images were computed for segmenting the lungs. As described below, these images are

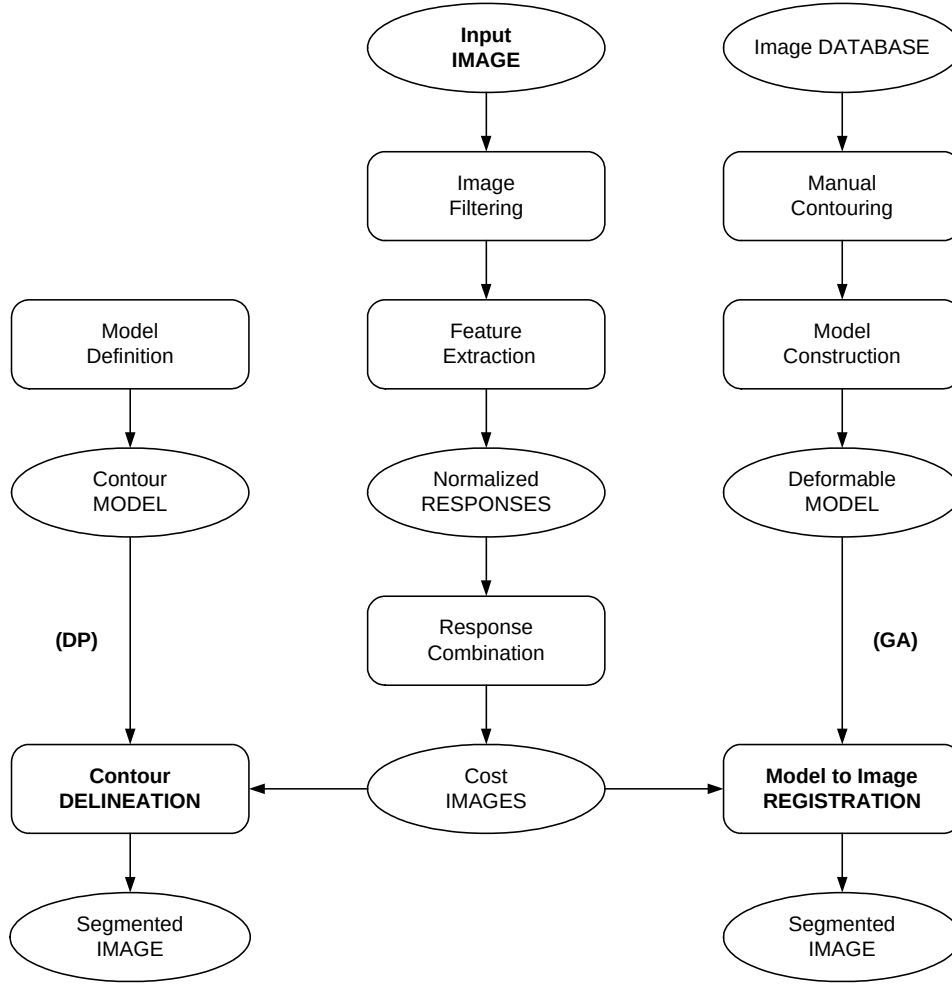


Figure 4.2: Proposed methods for automated lung field segmentation from PA chest radiographs. The contour delineation method is based on dynamic programming (DP) while a genetic algorithm (GA) is used by the model-to-image registration method. A typical output of both methods is shown in Figure 4.1(b) and (c), respectively.

suitable for applying an optimal path finding algorithm based on dynamic programming when method 1 is chosen. If method 2 is adopted, cost images are used to compute the objective function in a registration framework using an optimization genetic algorithm.

4.2.3 Cost Images

The cost function is defined as a weighted sum of terms that include local measurements such as pixel intensity, gradient intensity of the image or geometrical constraints of the shape of the detected border [50]. Local costs assigned to each pixel in the image should embody the notion of a good boundary, that is, pixels that reflect many characteristics of the searched boundary correspond to low costs and vice versa. As most lung contours exhibit strong edges, we want to assign a low cost to pixels with strong image features. Here, we propose a different way of computing *cost images* by combining multiple normalized responses, based on a winner-takes-all, multiscale approach. Three cost images were computed for locating and delineating all the segments of the lungs. An additional cost image was built for detecting the thorax centerline.

For one particular structure, the associated cost image $\mathbf{c}(x, y)$ is computed as follows. We first determine the normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}(x, y)$ that should be considered, or not, for computing the corresponding cost image. Then, the selected responses were combined pixel-wise according to the following equation:

$$\mathbf{c}(x, y) = \begin{cases} \omega \mathbf{R}_{nm,\sigma}^{(p)}(x, y) & , \quad \text{if } \mathbf{R}_{nm,\sigma}^{(p)}(x, y) > |\mathbf{c}(x, y)| \\ \mathbf{c}(x, y) & , \quad \text{otherwise} \end{cases} \quad (4.1)$$

where the weighting factor ω has been included to distinguish *excitatory* from *inhibitory* responses. The pixel value of the cost image $\mathbf{c}(x, y)$ is initially set to zero and sequentially updated through Eq. 4.1 by considering all the selected responses, one at a time. Since all response intensity values $\mathbf{R}_{nm,\sigma}^{(p)}(x, y)$ range between 0 and 1, any cost image computed via Eq. 4.1 is such that $-1 \leq \mathbf{c}(x, y) \leq 1$.

The selection of a given response is motivated by visual inspection of Figure 3.7, depending on its brightness characteristics. A response $\mathbf{R}_{nm,\sigma}^{(p)}(x, y)$ is excitatory ($\omega = -1$) or inhibitory ($\omega = \{0, 1\}$), if its brightness should assign to pixels (x, y) in the final cost image $\mathbf{c}$ a lower or higher cost, respectively. When a multiscale approach is adopted, the above equation is applied for any σ value of the Gaussian kernel filters used for computing the normalized responses. We recall that, since

Table 4.1: Combination of selected normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}(x, y)$ for constructing the cost images $\mathbf{c}(x, y)$ shown in Figure 4.3, with Eq. 4.1. When the index σ is omitted, all scales of the response $\sigma_1 = 1$, $\sigma_2 = 3$ and $\sigma_3 = 9$ (mm) are considered.

Structure	Cost Image	Normalized Response $\mathbf{R}_{nm}^{(p)}$		
		$\omega = -1$	$\omega = 0$	$\omega = 1$
Thorax centerline	$\mathbf{c}_0$			$\mathbf{R}_{00}^{(0)}, \mathbf{R}_{10,9}^{(0)}, \mathbf{R}_{10,9}^{(1)}$
Hemidiaphragms	$\mathbf{c}_1$	$\mathbf{R}_{01}^{(1)}$	$\mathbf{R}_{00}^{(1)}$	$\mathbf{R}_{00}^{(0)}$
Costal edges Top sections	$\mathbf{c}_2$	$\mathbf{R}_{20,9}^{(0)}, \mathbf{R}_{02,9}^{(0)}$	$\mathbf{R}_{00}^{(1)}$	$\mathbf{R}_{00}^{(0)}$
Right mediastinal edge	$\mathbf{c}_3$	$\mathbf{R}_{10}^{(1)}$		$\mathbf{R}_{10}^{(0)}$
Left mediastinal edge	$-\mathbf{c}_3$	$\mathbf{R}_{10}^{(0)}$		$\mathbf{R}_{10}^{(1)}$

responses are combined together, the normalization algorithm included in the image feature extraction step (see Section 3.2.2) is mandatory.

Many combinations of responses are possible to construct a single cost image and therefore several tests were performed to evaluate the output of Eq. 4.1. We noted that, as expected, some combinations are more indicated for visually detecting one or another anatomical structure. The chosen combinations and corresponding weights ω are reported in Table 4.1, where the index σ has been omitted when all scales were considered in Eq. 4.1 for computing the cost image.

The resulting cost images are shown in Figure 4.3. Figure 4.3(a) displays the cost image $\mathbf{c}_0(x, y)$ where the thorax centerline is easily detected as low cost pixels lying on a nearly vertical axis centered in the image. The hemidiaphragms correspond to prominent visual features on the cost image $\mathbf{c}_1(x, y)$, displayed in Figure 4.3(b), while the right and left costal edges and top sections of both lungs are visually identified as ridges on the single cost image $\mathbf{c}_2(x, y)$, as shown in Figure 4.3(c). As reported in Table 4.1, no first order responses was used ($n, m \neq 1$) to construct $\mathbf{c}_2$. Finally, the cost image $\mathbf{c}_3(x, y)$, shown in Figure 4.3(d) is suitable for detecting both the right and left mediastinal edges. Since these edges are of the same nature but opposite polarities (dark to light and light to dark transitions), the image $\mathbf{c}_3$ and its symmetric $-\mathbf{c}_3$ were used for detecting them. Note that for computing $\mathbf{c}_1$ and $\mathbf{c}_3$, only responses of zero and first orders ($n, m \neq 2$) were selected since these edge structures correspond to dark to light transitions.

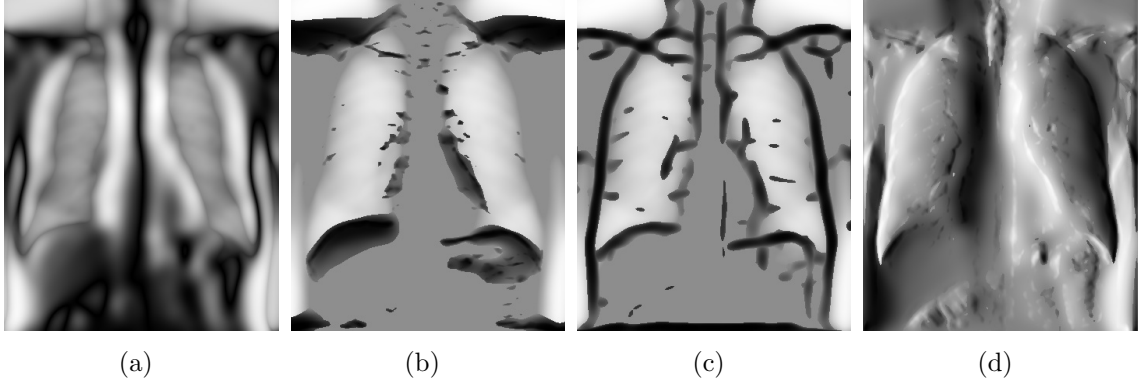


Figure 4.3: Cost images computed from the selected normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}$ of Figure 3.7 (see also Table 4.1). (a) The cost image $\mathbf{c}_0(x, y)$ is computed for detecting the thorax centerline corresponding to the bilateral symmetry axis of the image. (b) to (d) The cost images $\mathbf{c}_1(x, y)$, $\mathbf{c}_2(x, y)$ and $\mathbf{c}_3(x, y)$ are used for delineating, respectively, the hemidiaphragm edges, the costal edges and lung top sections, and the right and left mediastinal edges. All cost image values range between -1 (black) and 1 (white), that is, $-1 \leq \mathbf{c}(x, y) \leq 1$.

4.3 Contour Delineation

The following steps summarize the proposed method for lung field segmentation using dynamic programming (DP):

```
// Algorithm - Contour Delineation (DP)
// -----
1. Detect SYMMETRY axis, using  $\mathbf{c}_0(x, y)$ 
2. Optimal PATH finding algorithms
   - HEMIDIAPHS delineation, using  $\mathbf{c}_1(x, y)$ 
   - RIGTH/LEFT COSTOS delineation, using  $\mathbf{c}_2(x, y)$ 
   - TOP POLAR delineation, using  $\mathbf{c}_2(r, \theta)$ 
   - RIGTH/LEFT HEART delineation, using  $\pm \mathbf{c}_3(x, y)$ 
3. Create segmentation OUTPUT
   Relabel IMAGE as LUNG if pixel is:
   - left of RIGTH COSTO PATH and right of RIGTH HEART PATH
   - left of LEFT COSTO PATH and right of LEFT HEART PATH
   - below TOP PATH
   - above HEMIDIAPHS PATH
```

In the following, we will assume that the upper left corner of any cost image $\mathbf{c}(x, y)$ corresponds to its origin and coincides with the origin of the coordinate system OXY. The entire image is the spatial region located in positive x and y , such that for any point $\mathbf{p}$ located at coordinates (x, y) within the image, $0 \leq x \leq x_{\max}$ and $0 \leq y \leq y_{\max}$. The algorithms that compose the segmentation method are now described.

4.3.1 Symmetry Axis Detection

The thorax centerline is detected as the straight line corresponding to the bilateral symmetry axis observed in PA chest radiographs. The centerline separates the right from left side of the patient and, more often, it has been selected at the largest pixel value near the center of the horizontal profile of the input image. This approach presents some limitations when a large lateral inclinations of the patient are observed.

In [114], we described an iterative method based on genetic algorithms to overcome this problem. Here, we describe a simpler technique to detect the symmetry axis by using the associated cost image $\mathbf{c}_0(x, y)$ (see Figure 4.3(a)). In this image, straight lines were constructed by connecting points $\mathbf{p}_1$ lying on the X axis for which $y_1 = 0$, to points $\mathbf{p}_2$ lying on the bottom border of the image such that $y_2 = y_{\max}$. The symmetry axis is then selected as the line, denoted $x = f_0(y)$, $0 \leq y \leq y_{\max}$, joining $\mathbf{p}_1$ to $\mathbf{p}_2$ for which the mean gray scale value of the profile computed from the cost image $\mathbf{c}_0$ is minimum. This exhaustive search was restricted to straight lines, nearly vertical, by considering points $\mathbf{p}_1$ and $\mathbf{p}_2$ for which $0.25x_{\max} \leq x_1, x_2 \leq 0.75x_{\max}$. The result of detecting the centerline is shown in Figure 4.4(a).

4.3.2 Optimal Path Finding

An optimal path finding algorithm was developed to accurately detect the segments that make up the lung contour model defined in Section 3.4.1. The delineation of the searched segments is based on optimal graph searching techniques by first defining several paths that contain at least one segment (or part of a segment) in the model. For each segment, the algorithm considers the corresponding cost image (see Table 4.1) as a 2D graph in which dynamic programming should find the optimal path. The graph nodes correspond to image pixels and, to each node, a local cost is assigned. The optimal path is found by selecting those nodes (pixels) that linked (connected) together form the path with the lower cost.

Hemidiaphragms

The delineation of the right and left hemidiaphragms is based on the observation that these two segments are nearly horizontal. Therefore, the optimal path finding algorithm is applied on the cost image $\mathbf{c}_1(x, y)$ to search for a single path, denoted

$\mathbf{p}_1 \rightarrow \mathbf{p}_2$, running in the horizontal direction, that includes the hemidiaphragm of both lungs. We define *horizontal* paths by connecting a point $\mathbf{p}_1$ lying on the Y axis and a point $\mathbf{p}_2$ lying in the right border of the image, for which $x_1 = 0$ and $x_2 = x_{\max}$, respectively. Note that the searched path can be represented as the function $y = f_1(x)$, $0 \leq x \leq x_{\max}$.

Border detection based on dynamic programming requires the choice of starting points and ending points. To delineate a horizontal path, from left to right, the pixels of the first column of the cost image $\mathbf{c}_1$ represent the starting nodes, whereas the ending nodes are represented by the pixels in the last column of the image. The cumulative cost of each path is stored in a cumulative cost matrix $\mathbf{C}_1(x, y)$. The construction of the matrix $\mathbf{C}_1$ involves two steps: first, the cumulative cost of pixels in the last column are set to the cost of these pixels $\mathbf{C}_1(x_{\max}, y) = \mathbf{c}_1(x_{\max}, y)$, then the cumulative cost for other pixels is calculated, from the right to the left side of the image, through the following recursive relation:

$$\mathbf{C}_1(x, y) = \mathbf{c}_1(x, y) + \min_{\tilde{y} \in [y - kdY, y + kdY]} \{\mathbf{C}_1(x + dX, \tilde{y})\}, \quad (4.2)$$

where dX and dY are the pixel spacings in X and Y direction, respectively. The additional cost of a segment of a path, $y = f_1(x)$, from (column) x to (column) $x + dX$, depends only on the local cost value of the pixel (x, y) . In the above equation, the parameter k is used to control the smoothness of the path. This connectivity constraint, expressed as $|f_1(x + dX) - f_1(x)| \leq kdY$, is introduced to guarantee the continuity of the contour in 2D. The optimal path $\mathbf{p}_1^* \rightarrow \mathbf{p}_2^*$ is found by backtracking the path from the starting pixel with the lower cumulative cost, $\mathbf{p}_1^*$, to one of the pixels $\mathbf{p}_2^*$ in the last column. The result of such procedure is shown in Figure 4.4(b), for which $k = 1$, such that the pixels belonging to the path are 8-connected.

Costal Edges

For detecting the costal edges, the same reasoning is adopted. Each of these segments is approximately vertical. The optimal path finding algorithm is then applied to search for paths running along the Y direction by constructing the cumulative cost matrix $\mathbf{C}(x, y)$ through the following expression, similar to Eq. 4.2:

$$\mathbf{C}(x, y) = \mathbf{c}(x, y) + \min_{\tilde{x} \in [x - kdX, x + kdX]} \{\mathbf{C}(\tilde{x}, y + dY)\}. \quad (4.3)$$

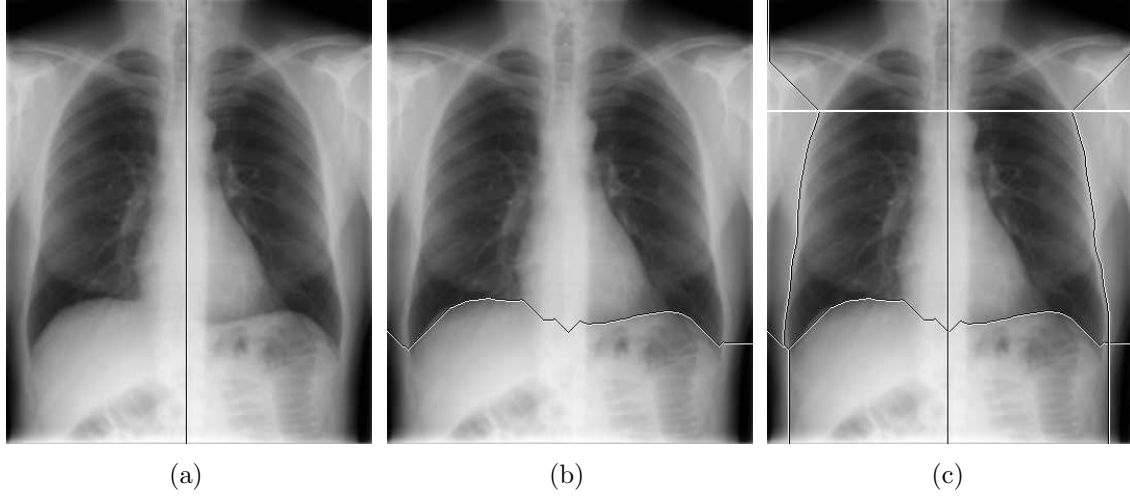


Figure 4.4: Lung contour delineation using the optimal path finding algorithm. (a) Detected thorax centerline corresponding to the bilateral symmetry axis of the PA chest radiograph. Output of the optimal path finding algorithm based on dynamic programming for delineating (b) the hemidiaphragms and (c) the costal edges, below the (white) horizontal line $y = 0.25y_{\max}$. Above this line, the lungs are delimited by their top sections.

Note that the cumulative cost given by Eq. 4.3 is computed from bottom to top, by setting $\mathbf{C}(x, y_{\max}) = \mathbf{c}(x, y_{\max})$, and used to delineate paths $\mathbf{p}_1 \rightarrow \mathbf{p}_2$ that connect the points $\mathbf{p}_1$ and $\mathbf{p}_2$, for which $y_1 = 0$ and $y_2 = y_{\max}$, respectively. Each costal edge is then included in a path assuming the form $x = f_2(y)$, $0 \leq y \leq y_{\max}$.

From Table 4.1, the delineation is achieved by considering $\mathbf{c}(x, y) = \mathbf{c}_2(x, y)$ in Eq. 4.3. Before the optimal path finding algorithm is applied, additional search constraints have been included. The local cost of all nodes (x, y) located below the detected path $y = f_1(x)$ (hemidiaphragms), and within the upper region of the image above the line $y = 0.25y_{\max}$ is set to zero, that is, $\mathbf{c}_2(x, y) = 0$, $0 \leq y \leq 0.25y_{\max}$, $f_1(x) \leq y \leq y_{\max}$. In this region, we assume that the lungs are delimited by their top sections.

Figure 4.4(c) shows the optimal paths that result from the dynamic programming algorithm, applied once on each side of the image for delineating sequentially the right and the left costal edges. With a connectivity parameter $k = 1$, the optimal paths $\mathbf{p}_1^* \rightarrow \mathbf{p}_2^*$ were found by backtracking the paths in the cumulative cost matrix $\mathbf{C}_2(x, y)$ from a starting pixel located at one of the upper corners of the image, $\mathbf{p}_1^* = (0, 0)^T$ (for the right costal edge) and $\mathbf{p}_1^* = (x_{\max}, 0)^T$ (for the left costal edge), to one of the pixels $\mathbf{p}_2^*$ in the last row.

Lung Top Sections

To apply dynamic programming to find the lung top sections, we notice that they are approximately circular. This circularity constraint is implemented by carrying out the calculations in polar space. The transform is restricted to a rectangular region of interest (ROI) in the cost image $\mathbf{c}_2(x, y)$. The ROI is the region where the top sections are expected to appear and includes all pixels (x, y) lying above the line $y = 0.25y_{\max}$. The polar transform is applied with the center $(x_c, y_c) = (x_c, 0.25y_{\max})$ lying on the symmetry axis, with $x_c = f_0(y_c)$, and radius $r_{\max}$.

The center defines the origin for the coordinate transform and the radius should be chosen large enough to allow application of the algorithm within the ROI. A radius $r_{\max} = 0.5y_{\max}$ was considered. All pixels inside the ROI in the original cost image $\mathbf{c}_2(x, y)$ are transformed to the polar ROI $\mathbf{c}_2(r, \theta)$ shown in Figure 4.5(a-top). The horizontal axis in the polar image represents the angle θ from π to 2π (from right to left) measured with respect to the X axis of the image, and the vertical axis represents the radius from 0 to $r_{\max}$ (from bottom to top).

The dynamic programming algorithm is applied to the polar ROI by constructing the cumulative cost matrix $\mathbf{C}_2(r, \theta)$, shown in Figure 4.5(a-bottom), and the optimal path is found by backtracking the path from one of the pixels in the first column to one of the pixels in the last column. Actually, this procedure is analogous to that used for delineating the hemidiaphragms. Following Eq. 4.2,

$$\mathbf{C}_2(r, \theta) = \mathbf{c}_2(r, \theta) + \min_{\tilde{r} \in [r-kdr, r+kdr]} \{ \mathbf{C}_2(\tilde{r}, \theta + d\theta) \}, \quad (4.4)$$

where $d\theta$ and dr are the pixel spacings of the polar image along the horizontal and vertical direction, respectively. The optimal path is finally transformed back to rectangular coordinates in the original image providing the segmentation shown in Figure 4.5(b).

To guarantee the continuity of the top sections and lateral segments of the lung contour, the optimal path $\mathbf{p}_1^* \rightarrow \mathbf{p}_2^*$ is calculated under the constraint that the starting point $\mathbf{p}_1^*$ and the ending point $\mathbf{p}_2^*$ belong to the right and left costal edge, respectively. Since for any pixel (x, y) in the path that includes the right costal edge, $x = f_2^{(r)}(y)$, this is accomplished by choosing the starting point $\mathbf{p}_1^* = (r_1, \theta_1)^T$ such that $\theta_1 = \pi$ and $r_1 = x_c - f_2^{(r)}(y_c)$. Then the optimal path is found by backtracking the path to the ending point $\mathbf{p}_2^* = (r_2, \theta_2)^T$ in the last column, for which $\theta_2 = 2\pi$. The optimal path is forced to end at point $\mathbf{p}_2^*$ by adding extra cost to all points in

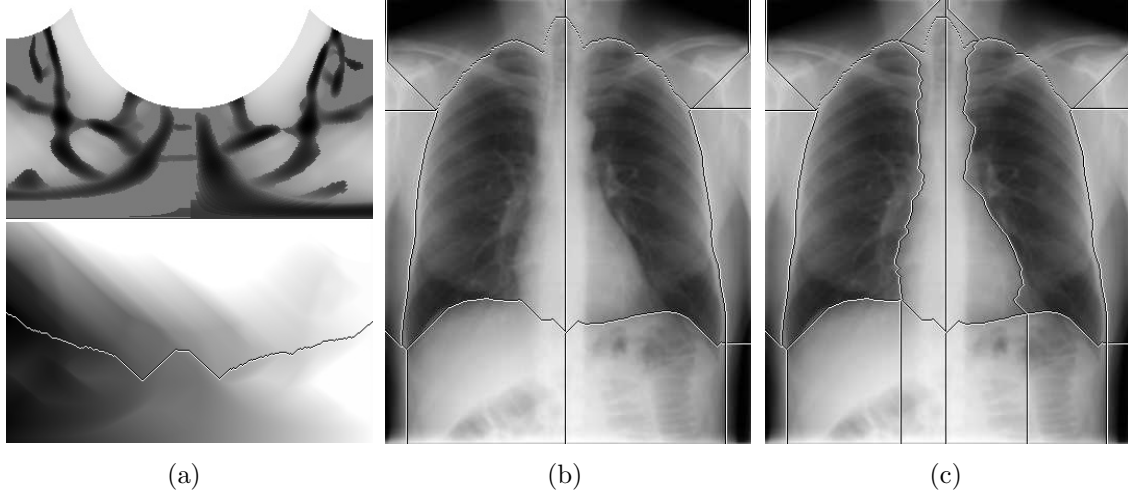


Figure 4.5: Lung contour delineation using the optimal path finding algorithm. (a) Top sections delineation using the polar transform: cost image $\mathbf{c}_2(r, \theta)$ in polar coordinates (top) and corresponding cumulative cost image $\mathbf{C}_2(r, \theta)$ (bottom) showing the detected optimal path. (b) Resulting lung top sections superimposed on the input chest radiograph; (c) Mediastinal edges delineated from top to bottom of the image, using the same algorithm.

the last column of the cost matrix except to point in row r_2 . Since $\mathbf{p}_2^*$ belongs to the left costal edge (path), $r_2 = f_2^{(l)}(y_c) - x_c$.

Mediastinal Edges

The detection of the right and left mediastinal edges is achieved with the aid of the cost image $\mathbf{c}_3(x, y)$. We assume these segments are part of vertical paths described by, respectively, the functions $x = f_3^{(r)}(y)$ and $x = f_3^{(l)}(y)$, $0 \leq y \leq y_{\max}$. The same approach used for delineating the costal edges is now adopted and therefore these boundaries are detected by using Eq. 4.3 for computing the cumulative cost matrix. For the right segment the image $\mathbf{c}_3(x, y)$ is used while $-\mathbf{c}_3(x, y)$ is considered for the left part of the contour.

Before the cumulative matrix is computed search constraints can be applied. In each case, the local cost was set to zero except in a central region of the image: for all pixels (x, y) below the detected hemidiaphragms $f_1(x) \leq y \leq y_{\max}$ (as for the costal edges) and above the delineated top sections $0 \leq y \leq f_2^{(\theta)}(x)$, $\mathbf{c}_3(x, y) = 0$. The resulting optimal paths, backtracked from top to bottom, are shown in Figure 4.5(c).

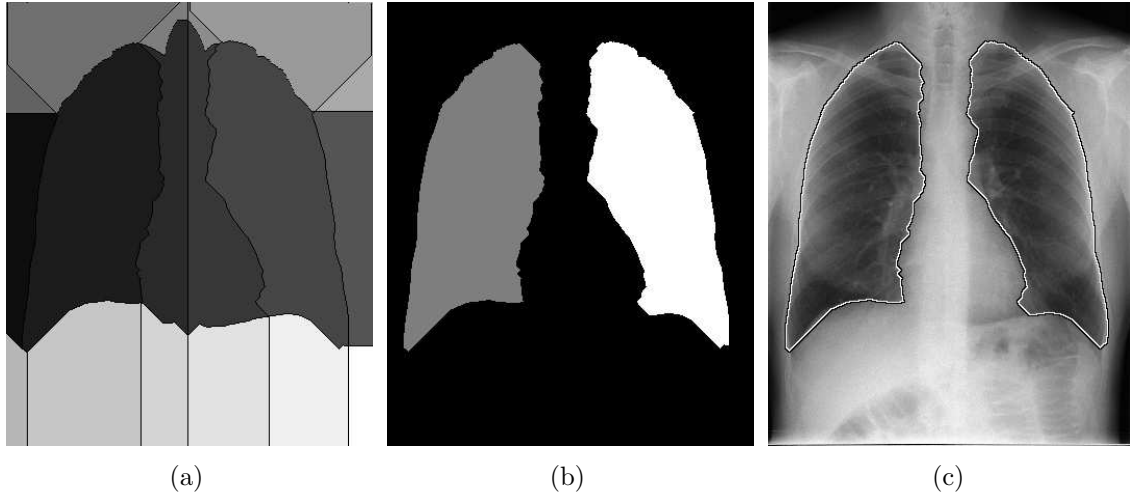


Figure 4.6: Lung field segmentation from PA chest radiographs using the contour delineation method based on the optimal path finding algorithm (dynamic programming). (a) Resulting labeled image; (b) Extracted lung fields; (c) Final segmentation output.

4.3.3 Segmentation Output

Figure 4.6(c) shows the final results of applying sequentially the optimal path finding algorithm for delineating all the segments defined in the lung boundary model. The contour delineation method allows to represent the chest radiographs as the partitioning of the image into connected regions with anatomical correspondence. The corresponding labeled chest radiograph is displayed in Figure 4.6(a), where the lung fields are easily extracted as the region defined in between the costal and mediastinal edges, above the hemidiaphragms and below the top sections. The segmentation output is then created either as the mask shown in Figure 4.6(b) or as the corresponding borders seen in Figure 4.6(c).

4.4 Model-to-Image Registration

Image registration emerged in medical image processing to match two independently acquired images. To register images, the geometrical relationship between them has to be determined. Matching all the geometric data available for a patient (intra-patient registration) provides better diagnostic capability, better understanding of data, and improves surgical and therapy planning and evaluation. In particular, an application for matching radiographs of the same patient taken at different times in order to investigate interval change has been reported in [115, 116]. Although

matching to atlases has been applied to several problems in medical image processing, less effort have been dedicated to chest radiographs. A detailed survey on registration techniques is provided in [117].

We propose a method to accurately identify the lung fields from chest radiographs by matching a prior geometrical model to the image to be segmented. This method is inspired on the approach we described in [40]. The registration task is seen as an optimization problem where the goal is to find the transformation matching the model to the image, maximizing or minimizing one or more *objective* functions. To solve this problem, instances of a deformable model are projected into the image until one well supported by the observed data is found.

4.4.1 Registration Framework

The general workflow of the registration is shown in Figure 4.7. The main components of the registration framework are a deformable model of the lungs, a transformation model to constrain the allowable deformations, a registration criterion or metric to judge the goodness of fit and a suitable optimization strategy. As described below, the transform parameters are adjusted such that the fitness of the corresponding deformed model is maximized. The fitness value is computed from image features (the cost images) previously extracted from the input chest radiograph (see Section 4.2.3). The following steps summarize the proposed method using a global optimization technique based on genetic algorithms (see Section 3.7.1) and will be described in detail in the next Sections.

```
// Algorithm - Model-to-Image Registration (GA)
// -----
1. Construct lung deformable MODEL
2. Compute COST images of IMAGE
3. Define TRANSFORM of MODEL
4. Define CODING/DECODING of chromosome CHROM
5. Define FITNESS function (metric)
6. Run GA (Genetic Algorithm)
```

Because the application involves nonrigid matching of a model and images in 2D, the description is worked out in 2D, although extension to 3 or more dimensions is straightforward. For convenience, as opposed to the contour delineation method, the calculations are now performed in a 2D image centered coordinate system OXY, and therefore the origin of the images coincides with their center. Consequently, the cost images define the spatial region that includes the points (pixels) located at

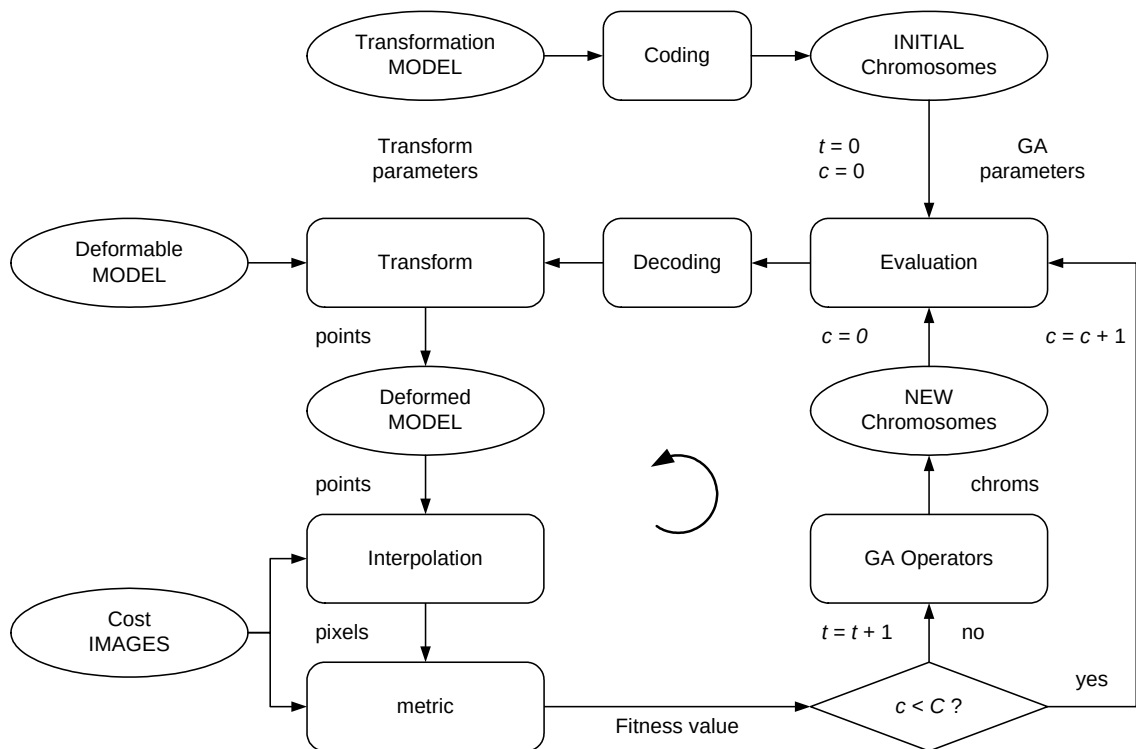


Figure 4.7: Lung field segmentation from PA chest radiographs using the model-to-image registration method. The registration task is an optimization problem solved with a genetic algorithm (GA), where C solutions are encoded as chromosomes (chroms), each representing a solution (transformation parameters) in the search space. The optimal solution is obtained by evolving an initial population of random solutions.

coordinates (x, y) for which $-\Delta X/2 \leq x \leq \Delta X/2$ and $-\Delta Y/2 \leq y \leq \Delta Y/2$, where ΔX and ΔY are the physical extent of the images along the X and Y direction, respectively. Before the registration is performed, the center of the bounding box of the model is automatically computed and moved to coincide with the center of the image.

Transformation Model

We have proposed an approach to warp a model to chest radiographs in [40] which is based on Free Form Deformation (see Section 3.6.1). Here, the adopted parametrization of the deformation model is based on the Thin Plate Splines transform (see Section 3.6.2) we now described.

In Section 3.5, we have presented the construction of a 2D statistical shape model of the lungs. The resulting lung mean shape (lung contour) is now used as the deformable model, represented by the set of N points $\mathbf{P} = \{\mathbf{p}_n\}$, where $\mathbf{p}_n = (x_n, y_n)^T$, $n = 0, 1, \dots, N-1$, is a point of the lung contour.

To deform the model, L source landmarks $\mathbf{u}_l = (\hat{x}_l, \hat{y}_l)^T$, $l = 0, 1, \dots, L-1$, are selected from the contours of both lungs to form the set $\mathbf{U} = \{\mathbf{u}_l\}$. Moving the landmarks to new position $\mathbf{v}_l = \mathbf{u}_l + \Delta\mathbf{u}_l$ results in the set of target landmarks $\mathbf{V} = \{\mathbf{v}_l\}$, $\mathbf{v}_l = (x_l, y_l)^T$, where the displacement vectors $\Delta\mathbf{u}_l$ represent the deformation field of the transform denoted by $\Delta\mathbf{U} = \mathbf{V} - \mathbf{U} = \{\Delta\mathbf{u}_l\}$. In 2D, the deformation field can be parametrized by the $2L$ -dimensional vector

$$\Delta\mathbf{U} = (\Delta x_0, \Delta y_0, \Delta x_1, \Delta y_1, \dots, \Delta x_{L-1}, \Delta y_{L-1})^T. \quad (4.5)$$

As discussed in Section 3.6.2, the TPS transform, denoted $\mathbf{V} = \mathcal{T}(\mathbf{U})$, is computed from the sets of source and target landmarks and allows to generate instances of the deformable model.

Ideally, the transformation model should allow just enough degrees of freedom (DOF) to model any physical transformation. Because the training set of manual contours with and without global rigid alignment can be used to construct the lung mean shape, an affine transformation component $\mathcal{A}$ is included in the transformation model. This transform can be parametrized as a set of vectors $\mathbf{A} = \{\mathbf{a}_i\}$, $i = 0, 1, 2$. In 2D, and introducing a 0 element for convenience, $\mathbf{A}$ is the set of parameters

$$\mathbf{A} = \{s_X, s_Y, \theta_Z, 0, d_X, d_Y\}. \quad (4.6)$$

The affine transformation $\mathcal{A} = (\mathcal{A}_2 \circ \mathcal{A}_1 \circ \mathcal{A}_0)$ is an ordered concatenation of 5 rigid model transformations, namely anisotropic scaling in X and Y directions, rotation around the Z axis and translation along X and Y directions, with translation parameters $\mathbf{a}_2 = (d_X, d_Y)^T$, in mm, rotation parameter $\mathbf{a}_1 = (\theta_Z, 0)^T$, in radian, and $\mathbf{a}_0 = (s_X, s_Y)^T$ as scaling factors. In 3D, 9 parameters are used to described $\mathcal{A}$.

The transformation model is now completely characterized by combining the Thin Plate Splines and affine components. Following Eq. 3.29, the final transform is the point-to-point correspondence

$$\mathbf{q}_n = (\mathcal{A} \circ \mathcal{T})(\mathbf{p}_n), \quad (4.7)$$

defining the N contour points $\mathbf{q}_n$ of the deformed model.

Solution Coding/Decoding

To search for the optimal transformations $\mathcal{T}$ and $\mathcal{A}$, a genetic algorithm (GA) was used, where allowable transforms are described by a population (or set) of C individuals (solutions), $\mathbf{W} = \{\mathbf{w}_c\}$, $c = 0, 1, \dots, C - 1$. The proposed GA considers each chromosome $\mathbf{w}_c$ (the genotype) as a single solution (the phenotype) in the search space of the deformable registration problem. For a particular transform $(\mathcal{A} \circ \mathcal{T})_c$ the corresponding chromosome $\mathbf{w}_c$ is constructed by concatenating the parameters of the TPS and affine components,

$$\mathbf{w}_c = \{\Delta \mathbf{U}_c, \Delta \mathbf{A}_c\} = \{\Delta \mathbf{u}_{lc}, \Delta \mathbf{a}_{ic}\}, \quad (4.8)$$

where $\Delta \mathbf{U}_c$ is the deformation field and $\Delta \mathbf{A}_c$ represent the deviation of the affine parameters from their default values $\bar{\mathbf{a}}_0 = (1, 1)^T$ (scaling), $\bar{\mathbf{a}}_1 = (0, 0)^T$ (rotation) and $\bar{\mathbf{a}}_2 = (0, 0)^T$ (translation).

A key feature of genetic algorithms is the representation of physical variables of interest by a simple string data structure. In the GA, the chromosome $\mathbf{w}_c$ representing the transform parameters $\Delta \mathbf{u}_{lc}$ and $\Delta \mathbf{a}_{ic}$ is rewritten as the string of genes $\mathbf{w}_c = \{u_{cg}\}$, $g = 0, 1, \dots, G - 1$. From Eq. 4.5 and Eq. 4.6, the coding results in a vector of G alleles:

$$\mathbf{w}_c = (u_{c0}, u_{c1}, \dots, u_{cg}, \dots, u_{c,G-1})^T. \quad (4.9)$$

When a number L of landmarks are chosen and the registration is performed in 2D, the chromosome length is $G = 2L + 6$. For the 3D case, $G = 3L + 9$, accounting for 9 parameters (DOFs) of the affine component.

Binary coding has been the usual individual representation in genetic algorithms for a long time. Binary strings are sufficiently general but they are not always the more natural or the more adequate representation. This is especially important with deformable models because meaningful but random initial populations are hard or even impossible to construct. Instead of the traditional binary coding, a Real-Coded Genetic Algorithm (RCGA) is used [118]. With RCGA implementations a more natural floating point representation is adopted and therefore it is possible to define recombination operators that can do well in a particular problem domain.

The RCGA representation was used to codify the transform parameters. This approach allows to decode in a straightforward manner a particular chromosome $\mathbf{w}_c$ back to the transform $(\mathcal{A} \circ \mathcal{T})_c$ it represents. Given $\mathbf{w}_c = \{u_{cg}\}$ with G alleles, the deformation field $\Delta \mathbf{U}_c = \{\Delta \mathbf{u}_{lc}\}$ and therefore the TPS transform are obtained by first defining, for each landmark l , a local *perturbation*. The perturbation $\delta \mathbf{u}_{lc}$ is a gene with 2 alleles (in 2D) that is related to the displacement vector of the landmark $\mathbf{u}_{lc}$.

If the perturbation is the displacement itself, $\Delta \mathbf{u}_{lc} = \delta \mathbf{u}_{lc}$ resulting in 2D in the simple decoding of the deformation field:

$$\delta \mathbf{u}_{lc} = (u_{cg}, u_{c,g+1})^T, \quad (4.10)$$

where $g = 2l$ and $l = 0, 1, \dots, L-1$ (for 3D, $g = 0, 3, \dots, 3L-1$). The parameters $\mathbf{a}_0$ (scaling), $\mathbf{a}_1$ (rotation) and $\mathbf{a}_2$ (translation) are given by the last $G - 2L$ alleles of the chromosome and, From Eq. 4.6, the decoding of the affine component is performed by introducing the perturbation vector $\delta \mathbf{a}_{ic}$ where, for $i = 0, 1, 2$,

$$\delta \mathbf{a}_{ic} = (u_{c,2L+i}, u_{c,2L+i+1})^T. \quad (4.11)$$

Performing independent PCA to all contour points in the model as described in Section 3.5.2 allows to take into account the spread of each landmark coordinate observed in the training set. In fact, the perturbation can be seen as the vector of weights, $\mathbf{b}_{lc}$, controlling the modes of variation of a single landmark. Instead of using Eq. 4.10, and following Eq. 3.20, we propose to decode the TPS component as

$$\Delta \mathbf{u}_{lc} = \Phi_l \delta \mathbf{u}_{lc}, \quad (4.12)$$

where we consider $\Phi_l = (\sqrt{\lambda_g} \mathbf{e}_g, \sqrt{\lambda_{g+1}} \mathbf{e}_{g+1})$ and, as before, $g = 2l$ and $l = 0, 1, \dots, L-1$. The matrix Φ_l is related to the principal directions (eigenvectors $\mathbf{e}$)

of the landmark displacement and corresponding amplitudes (eigenvalues λ). When constructing the statistical lung model, alignment of the training contours can be done before the mean shape is computed and similar component analysis can be performed to the affine parameters. The corresponding decoding is given by

$$\Delta \mathbf{a}_{ic} = \mathbf{\Omega}_i \delta \mathbf{a}_{ic}, \quad (4.13)$$

where $i = 0, 1, 2$ and $\mathbf{\Omega}_i = (\sigma_{i0}, \sigma_{i1})$ is a 2D vector describing the variation of the parameters of each affine transformation $\mathbf{a}_i$. Note, from Eq. 4.6, that $\sigma_{11} = 0$. Decoding the chromosome $\mathbf{w}_c$ results in the final affine transform components given by $\mathbf{a}_{ic} = \bar{\mathbf{a}}_{ic} + \Delta \mathbf{a}_{ic}$.

Fitness and Objective Functions

When GA is running, an objective function f is supplied which decodes the chromosomes and assign a *fitness*, f_c , to the individual the chromosome $\mathbf{w}_c$ represents. During evolution, at a given generation t , the fitness is computed for all the chromosomes in the population $\mathbf{W}^{(t)}$ by evaluating the objective function at samples points in the search space of transformations. To solve the problem of registering the lung model to a chest radiograph, all the N points on the lung contour are selected and deformed for computing the fitness according to

$$\mathbf{q}_{nc}^{(t)} = (\mathcal{A} \circ \mathcal{T})_c^{(t)}(\mathbf{p}_n), \quad (4.14)$$

where $\mathbf{q}_{nc}^{(t)}$ is the deformed model point $\mathbf{p}_n$ at time t , given by Eq. 4.7 after the chromosome is decoded.

To perform the experiments described below a simple metric was used. Given the chromosome $\mathbf{w}_c^{(t)}$, the following fitness function is proposed to evaluate the goodness of the corresponding solution:

$$f_c^{(t)} = 0.5 \left(1 - \frac{f_{1c}^{(t)} + f_{2c}^{(t)} + f_{3c}^{(t)}}{N} \right), \quad (4.15)$$

where each component of the fitness, a time dependent objective function, is computed by using the cost images $\mathbf{c}(x, y)$ (see Section 4.2.3) as

$$f_{1c}^{(t)} = \sum_{n=0}^{n_1-1} \mathbf{c}_1(\mathbf{q}_{nc}^{(t)}) + \sum_{n=0}^{n_1-1} \mathbf{c}_1(\mathbf{q}_{n+N/2,c}^{(t)}), \quad (4.16a)$$

$$f_{2c}^{(t)} = \sum_{n=n_1}^{n_2-1} \mathbf{c}_2(\mathbf{q}_{nc}^{(t)}) + \sum_{n=n_1}^{n_2-1} \mathbf{c}_2(\mathbf{q}_{n+N/2,c}^{(t)}), \quad (4.16b)$$

$$f_{3c}^{(t)} = \sum_{n=n_2}^{N/2-1} \mathbf{c}_3(\mathbf{q}_{nc}^{(t)}) - \sum_{n=n_2}^{N/2-1} \mathbf{c}_3(\mathbf{q}_{n+N/2,c}^{(t)}), \quad (4.16c)$$

and $\mathbf{c}(\mathbf{q}_n) = \mathbf{c}(x_n, y_n)$ denotes the cost value interpolated in the image $\mathbf{c}$ at point $\mathbf{q}_n$. An interpolator based on the nearest point was used since it reduces the overall time of registration.

When the fitness is used to evaluate instantiations of the deformable model, one seeks to minimize the objective functions (Eq. 4.16) or maximize the fitness (Eq. 4.15), thus favouring solutions for which the deformed contour points have low cost. Note that the same reasoning was adopted in the contour delineation method, using the same cost images.

The objective functions in Eq. 4.16 are defined as follows. The first terms of each function is the contribution of model points $\mathbf{q}_n$, $n = 0, 1, \dots, N/2 - 1$, that belong to the right contour of the deformed model. Based on the reflectional symmetry of chest radiographs, the second terms evaluate the corresponding points $\mathbf{q}_{n+N/2}$ of the left lung. Alternatively, Eq. 4.15 could be expressed as the sum of two terms, one for each lung contour. The function f_1 evaluates the hemidiaphragm segments by considering, in Eq. 4.16a, the first $n_1 = 20$ model points and the cost image $\mathbf{c}_1(x, y)$ corresponding to this structure. Similarly, for computing f_2 using Eq. 4.16b, $n_2 = 65$ was used to interpolate 2×45 points within $\mathbf{c}_2$ corresponding the costal and lung top sections segments. Finally, the mediastinal edges are evaluated in $\mathbf{c}_3$ (Eq. 4.16c) with the remaining 70 points of both lung contours. For any cost image $-1 \leq \mathbf{c}(x, y) \leq 1$, and the fitness is constrained to the values $0 \leq f_c^{(t)} \leq 1$. If the transformed point falls outside the spatial region of the image, a *violation* as occurred and the cost is set to $\mathbf{c}(\mathbf{q}_n) = 1$. Actually, introducing this *penalty* function forces the deformable model to remain within the spatial region of interest during the optimization process.

4.4.2 Genetic Algorithm Implementation

Although well suited for multi-objective optimization, the registration problem is solved with a simple genetic algorithm. The following pseudo-code summarize the proposed lung field segmentation method based on this global optimization technique, diagrammed in the right side of Figure 4.7:

```
// Genetic Algorithm Optimization (Run GA)
// -----
// population W with C chromosomes
// tmax = -1 for continuous optimization

t = 0
Generate initial POP W(0) with C random CHROMS
Evaluate initial POP W(0) (all CHROMS)
Copy POP W(0) to POP W(t)

// Main loop of GA
while ( t > tmax )
    Generate NEW POP W(t+1) from POP W(t)
    Evaluate NEW POP W(t+1) (all CHROMS)
    Get best CHROM w* from W(t+1)
    Copy POP W(t) to POP W(t+1)
    t = t + 1
end

// Generate NEW POP W(t+1) from POP W(t)
select C CHROMS from POP W(t) to POP W'
recombine CHROMS from POP W' to POP W(t+1)

// Evaluate POP (all CHROMS)
c = 0
while ( c < C )
    decode CHROM to TRANSFORM
    deform MODEL with TRANSFORM
    compute FITNESS of CHROM
    c = c + 1
end
```

Initial Population

At $t = 0$, the GA begins with an initial population $\mathbf{W}^{(0)}$ of C individuals representing random transformations. The strategy proposed in this study is to construct each chromosome, $\mathbf{w}_c^{(0)}$, $c = 0, 1, \dots, C - 1$, by sampling alleles, the components of perturbation vectors $\delta \mathbf{u}_c$ and $\delta \mathbf{a}_{ic}$, from a normal distribution with zero mean and unit standard deviation:

$$u_{cg}^{(0)} = \mathcal{N}(0, 1), \quad (4.17)$$

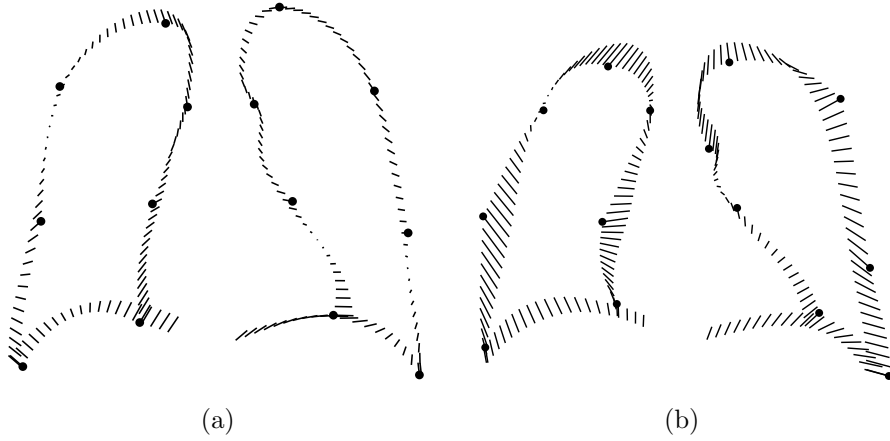


Figure 4.8: Deformable model under random transformations. A set of landmarks is used to deform all contour points. The transformation of the model is coded as local perturbations of each landmark around their original position. (a) Random displacements of the landmarks are used to deform the model under TPS; (b) A combination of TPS and affine transformation applied to the prior model.

with $g = 0, 1, \dots, G - 1$. Once the initial population has been created, all chromosomes $\mathbf{w}_c^{(0)}$ are decoded by using Eq. 4.12 and Eq. 4.13 (the PCA decoding) and the model points $\mathbf{p}_n$ are deformed with the corresponding transform $(\mathcal{A} \circ \mathcal{T})_c^{(0)}$, as given by Eq. 4.14. Instances of the deformable model under random transformations are illustrated in Figure 4.8. Next, initial solutions are evaluated by computing their fitness value with the aid of Eq. 4.15. The best chromosome $\mathbf{w}^*$ encoding the optimal solution $(\mathcal{A} \circ \mathcal{T})^*$ is then obtained by evolving $\mathbf{W}^{(0)}$, until some criterion has been reached.

Selection

The selection process identifies individuals in a current population $\mathbf{W}^{(t)}$ as the parents based on their fitness to participate in the reproduction. Many methods of selection exist in genetic algorithms and tournament selection was chosen. This technique runs a "tournament" among k individuals chosen at random from the population and selects the winner, the one with the best fitness, for crossover (see Section 3.7.1). Tournament selection has several benefits: it is efficient to code and allows the selection pressure to be easily adjusted by changing the tournament size k . If the tournament size is larger, weak individuals have a smaller chance to be selected. The selected parents are copied to an intermediate population $\mathbf{W}'$ where suitable recombination operators can be applied to produce the randomness

in shapes.

Recombination

The selected parents of the intermediate population $\mathbf{W}'$ will take part in the reproduction to create new individuals with crossover probability p_{cross} and form the population $\mathbf{W}^{(t+1)}$ for the next generation. In [114], we proposed a method for detecting the symmetry axis in chest radiographs based on a probabilistic genetic algorithm, where an Unimodal Normal Distributed Crossover operator (UNDX) was used to create offspring normally distributed around the mean vector determined by parents. Other similar schemes exist, such as the Simplex Crossover operator (SPX) for which the offspring are uniformly distributed around the mean vector within the predefined space, and the Parent-centric Crossover operator (PCX), where the offspring have more probability to be distributed around each parent.

By introducing the notion of *interval* schemata for RCGA [119], a blend crossover (BLX- α) operator was suggested and will be used for the experiments. For two parent solutions $\mathbf{w}_1^{(t)}$ and $\mathbf{w}_2^{(t)}$ selected at random from $\mathbf{W}'$, and assuming that $\Delta u_g^{(t)} = u_{2g}^{(t)} - u_{1g}^{(t)} > 0$, the BLX- α randomly creates the solution $\mathbf{w}^{(t+1)} = \{u_g^{(t+1)}\}$ such that

$$u_{1g}^{(t)} - \alpha_{cross} \Delta u_g^{(t)} \leq u_g^{(t+1)} \leq u_{2g}^{(t)} + \alpha_{cross} \Delta u_g^{(t)}, \quad (4.18)$$

where $\alpha_{cross} \geq 0$. The above equation can be rewritten in a more convenient form to express the child solution. If r is a random number between 0 and 1, then

$$u_g^{(t+1)} = (1 - \gamma_{cross}) u_{1g}^{(t)} + \gamma_{cross} u_{2g}^{(t)}, \quad (4.19)$$

where $\gamma_{cross} = (1 + 2\alpha_{cross})r - \alpha_{cross}$. Note that the factor γ_{cross} is uniformly distributed for a fixed value of α_{cross} . If $\alpha_{cross} = 0$, the crossover operator creates a random solution such that $u_{1g}^{(t)} \leq u_g^{(t+1)} \leq u_{2g}^{(t)}$. The BLX- α has an interesting property: the location of the child solution depends on the difference in parent solutions. This is clear if Eq. 4.19 is rewritten as

$$u_g^{(t+1)} - u_{1g}^{(t)} = \gamma_{cross} (u_{2g}^{(t)} - u_{1g}^{(t)}) = \gamma_{cross} \Delta u_g^{(t)}. \quad (4.20)$$

If the difference between the parent solutions is small, the difference between the child and parent solutions is also small. This is an essential property for any search algorithm to exhibit self-adaptation, since the spread of the current population dic-

tates the spread of solutions in the resulting population.

The choice of value of the BLX- α crossover is a trade off between computation time and the goodness of the result. Better optimization results may be achieved at the expense of longer computation time by increasing α_{cross} .

We assume that mutation can occur, with constant probability p_{mut} , by randomly selecting one parameter (allele) from the transformation vector of each parent, replacing it with random number as given by Eq. 4.17, while keeping other parameters unchanged. If p_{mut} is high, a lot of the computation time is wasted by evaluating mutated models that are of irregular shape and hence have low fitness.

Fitness Evolution

The number of chosen landmarks is a trade-off between computation time and the number of DOFs of the deformation. To perform the registration, $L = 14$ source landmarks were selected from the contour model resulting in $G = 2L + 6 = 34$ transform parameters (alleles) to optimize. Several tests were performed to judge for the best combination of selection and recombination operators. Some comparative results are plotted in Figure 4.9 where tournament and roulette-wheel were used as selections schemes. Experiments with the tournament selection were performed with the size $k = 3$, corresponding to 6% of the constant number C of individuals in the population. The BLX- α was compared with standard crossover operators, such as the one-point crossover (illustrated in Figure 3.15(b)). We believe that a good compromise between exploration of the search space and computation time of the algorithm is achieved by setting $\alpha_{cross} = 0.3$ when using BLX. Two different probabilities were considered, namely $p_{cross} = 1$ and $p_{cross} = 0.8$ for crossover and $p_{mut} = 0$ and $p_{mut} = 0.005$ for mutation.

The registration output corresponding to the fitness evolution of Figure 4.9(a) is shown in Figure 4.10 for which the genetic operators and related parameters are listed in Table 4.2. By comparing the tested combinations, these were considered as representing the best behavior of the proposed GA.

GA Parameters

For the GA parameters, we have employed standard values, namely a population of $C = 50$ individuals. In general, a fixed maximum number of fitness function evaluations is allowed. Here, the number of generations (iterations of the GA) was set to $t_{max} = 100$ corresponding to 5000 evaluation for the main loop, plus 50 to take

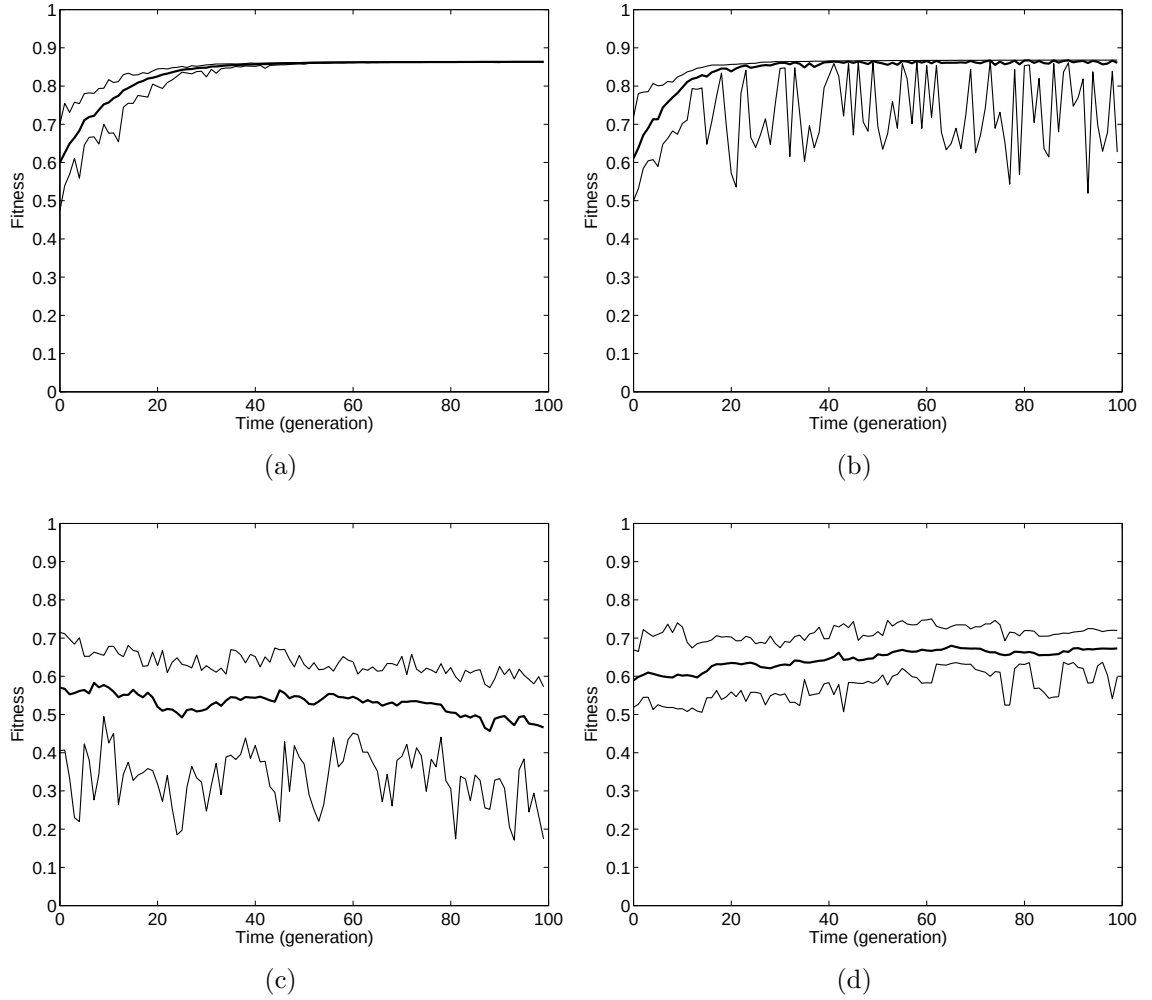


Figure 4.9: Fitness evolution of the model-to-image registration using a genetic algorithm. The size of the population is $C = 50$ individuals with chromosome length $G = 34$ ($L = 14$ model landmarks, 6 affine parameters), and $t_{\max} = 100$ generations were simulated with different combination of selection and recombination operators, with probabilities p_{cross} and p_{mut} . (a) Tournament, BLX- α , $p_{\text{cross}} = 1$, $p_{\text{mut}} = 0$ (see Figure 4.10 for the registration output); (b) Tournament, BLX- α , $p_{\text{cross}} = 0.8$, $p_{\text{mut}} = 0.005$; (c) Roulette-wheel (fitness-proportionate selection), BLX- α , $p_{\text{cross}} = 1$, $p_{\text{mut}} = 0.005$; (d) Roulette-wheel, one-point crossover, $p_{\text{cross}} = 1$, $p_{\text{mut}} = 0.005$. A tournament size $k = 3$ (6% of C) was used and $\alpha_{\text{cross}} = 0.3$ for BLX crossover. In all cases, the upper and lower curves correspond to the maximum and minimum fitness value observed in the population.

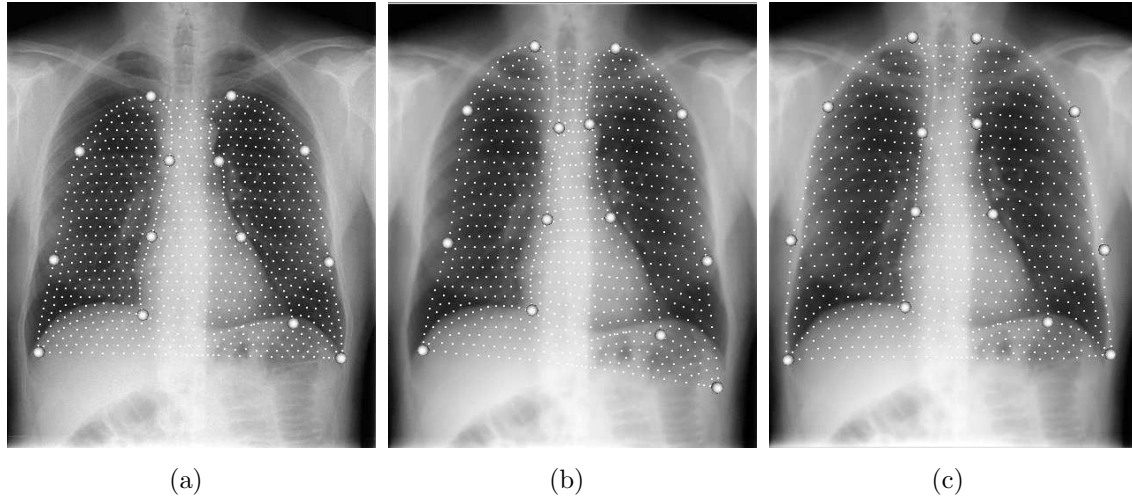


Figure 4.10: Lung field segmentation from PA chest radiographs using the model-to-image registration method. This optimization problem is solved with a genetic algorithm (GA). (a) Undeformed lung model; (b) Instance of the deformable model during optimization (evolution); (c) Final model best fitted to image after 100 iterations (generations). GA parameters are reported in Table 4.2 and the corresponding fitness evolution is plotted in Figure 4.9(a).

into account the population $\mathbf{W}^{(0)}$. All the parameters are listed in Table 4.2 (see the results of the segmentation shown in Figure 4.10. and the corresponding fitness evolution, $f^{(t)}$, plotted in Figure 4.9(a)). Analysis of the computation time of the whole registration process (about 1 min for one chest radiograph) was performed with the FLTK time probes utility (see Appendix A, Section A.3).

4.5 Experimental Results

To evaluate the performance of the proposed methods, the lung contour delineation and model-to-image registration were performed on two different image databases described in the next Sections.

4.5.1 Image Databases

Public Database (JSRT)

The JSRT database was established by the Japanese Society of Radiological Technology. This is a publicly available database with 247 PA chest radiographs collected from 13 institutions in Japan and one in the United States. 154 images contain exactly one pulmonary lung nodule (LN) each; the other 93 images contain no lung

Table 4.2: Lung field segmentation from PA chest radiographs using the model-to-image registration method. Genetic algorithm parameters. These were used to produce the segmentation output of Figure 4.10 resulting in the fitness evolution plotted in Figure 4.9(a).

Points in contour model	N	200
Number of landmarks	L	14
Affine parameters		6
Random generator seed		0.8346
Chromosome length	G	34
Population size	C	50
Tournament size	k	3
BLX- α crossover	α_{cross}	0.3
Crossover probability	p_{cross}	1.0
Mutation probability	p_{mut}	0.0
Number of generations (stopping criterion)	t_{max}	100

nodules (NN). The images were scanned from films to a size of 2048 by 2048 pixels, a spatial resolution of 0.175 mm/pixel and 12 bit gray levels. More details about the database can be found in [120].

Used in many studies on nodule detection on chest radiographs, the JSRT database has been established to facilitate comparative studies on segmentation of the lung fields in standard PA chest radiographs. In each image the lung fields have been manually segmented by two observers to provide a reference standard. The segmentations of the first observer are taken as reference standard. The independent segmentations from the second observer can be compared to segmentations by a computer algorithm to allow for comparisons between human and computer results.

Private Database (HSJ)

Our image database contains 39 adult standard PA chest radiographs collected from the computed radiography unit of the Radiology Department of the Hospital S. João (HSJ), in Porto. All images were acquired with a tube voltage of 125 kV and 180.0 cm focus-detector distance. The size of the images is either 1760×2144 (horizontal $\times$ vertical) or 1760×1760 pixels, corresponding to standard screen formats of 35.0×35.0 cm² and 35.0×43.0 cm², respectively. The radiographs were digitized

Table 4.3: Lung field segmentation from PA chest radiographs. Experiments were performed on a public image database (JSRT) and a private database (HSJ) to evaluate the performance of the proposed methods based on dynamic programming (DP) and genetic algorithms (GA).

Method	Database	Images				
		#	Original		Filtered	
			size (pixel)	spacing (mm)	size (pixel)	spacing (mm)
DP	JSRT	247	2048×2048	0.175	348×348	1.0
DP	HSJ	39	1760×2144	0.200	352×428	1.0
			1760×1760		352×352	
GA	HSJ	39	1760×2144	0.200	352×428	1.0
			1760×1760		352×352	

with a DIGISCAN 2T Plus imaging plate system (Siemens, Erlangen, Germany) and provided in DICOM format with a pixel resolution of $0.200 \text{ mm} \times 0.200 \text{ mm}$, and 10 bits per pixel. These images are a reasonable representation of both normal and abnormal radiographic findings, from both genders, showing regular and irregular lung shapes and abnormalities such as enlarged heart size, lung consolidation and emphysema, among others (see Appendix B). We did not exclude any image for which our rule-based segmentation scheme could fail to produce any acceptable output, since robust segmentation methods should give good performance on abnormal images as well.

4.5.2 Experiments

Experiments are reported in Table 4.3. For the registration method, the parameters listed in Table 4.2 were used. The original images were previously smoothed and reduced in format for segmentation as described in Section 3.2.1. For both databases, the images were subsampled to a resolution of $\sigma_0 = dX = dY = 1.0 \text{ mm}$, in both the horizontal (X) and the vertical (Y) directions. We used one implementation of Gaussian smoothing available in the ITK toolkit [34]. This filter implements an approximation of convolution with the Gaussian and its derivatives and requires a constant number of operations regardless of the σ_0 value [121, 122]. The standard deviation of the Gaussian filter kernel was set to $\sigma_0 = 1.0 \text{ mm}$, the value of the final pixel spacing dX . For the HSJ database, this corresponds to a reduction by a

factor of 5. The original gray level range of the lower spatial resolution images was maintained. The smoothing/resampling step was performed to reduce the amount of data for each radiograph in order to speed up the computational process while preserving enough resolution to identify the lung fields.

All the images of the JSRT database have been considered and subdivided in two folds. To ensure the integrity of the results, the images and reference standard in one fold (fold 1 - all odd numbered images) were used to train and tune the algorithms of the contour delineation method, applied to segment the images in the other fold (fold 2 - all even numbered images).

4.5.3 Validation

Segmentation performance was assessed by comparing the output of the automatic computer based segmentation methods with results obtained by manual analysis of a human observer. For that purpose, a dedicated algorithm was developed. For each subject, the program reads the file containing the point coordinates of the manual contours and constructs a binary image, with zero-value pixels everywhere except on the region enclosed by each lung contour. The output of the automated method is provided as a second binary image, where the non-zero pixels correspond to segmented lung fields. A pixel by pixel analysis was then performed to measure the similarity between the set of non-zero pixels of the two segmentation masks (see Section 3.8).

The computed measures used to evaluate the performance of the proposed segmentation schemes are reported Table 4.4, Table 4.5 and Table 4.6. The results are discussed in the following Section. Separate analysis was performed for the right lung and the left lung, by computing the accuracy, degree of overlap and F-score. For each experiment listed in Table 4.3, the average (mean), standard deviation (std), minimum (min) and maximum (max) values of each measure were computed and can be used as a figure of merit regarding the performance of the corresponding method. The results are reported and discussed in the next Section. We assumed equal importance of recall and precision when computing F-score. The sensitivity, specificity, precision and recall (= sensitivity) are also listed for comparison. All similarity measures range from 0 to 1.

4.6 Discussion

Accuracy, sensitivity, and specificity have been used or can be calculated from results reported in several studies. A range of accuracies for several lung field segmenting methods reported in the literature is listed in [83] where a table of their values is provided. In this study, the highest attainable accuracy of a segmenting method was estimated as the inter-observer variability, mainly due to the difficulty in assessing the exact borders of mediastinum. An accuracy of 0.9846 ± 0.0048 is provided as the theoretical upper bound. Based on these measures, the results presented here show that the proposed segmentation methods, surprisingly with the same mean accuracy of 0.98, perform better than the reported methods. In a more recent study [94], several schemes were applied to the JSRT (public) image database and comparison was made by using the degree of overlap as the reference figure of merit. The value of 0.946 ± 0.018 was obtained when quantifying inter-human variability. Characterized by a mean overlap of 0.91 and 0.90 for, respectively, the right lung and left lung, our contour delineation method compares favorably with the reported results.

Performance measures computed in the first experiment (DP/JSRT) are reported in Table 4.4. These correspond to the lung contour delineation method based on dynamic programming, using the JSRT image database. The results reflect a similar performance for both lungs, as illustrated in Figure 4.11(a), where the similarity measures were sorted in ascending order for the 247 images. To place the results in perspective, Figure 4.11(b) shows the histograms of the degree of overlap for the right and left lung fields. Figure 4.12 shows the lung contours generated by the proposed method superimposed on the original images, corresponding to the best and worst 3 segmentation outputs. In Appendix B, similar results are shown for 20 images. Clearly, the optimal path finding algorithm failed when detecting the costal edges. Since the cost images computed for delineating such segments depend on the first order derivative along the horizontal direction, unexpected high values of this feature due to the borders of the image confuse the algorithm. Although less noticeable, a similar error occurs in both sides of the image due to the breast, as seen in some images presented in Appendix B. Consequently, the method is expected to perform differently, depending on the gender of the patient being examined.

In the second and third experiments, both the contour delineation and the model-to-image segmentation method based on genetic algorithms were applied to the same private image database. Results of comparing the methods with manual analysis

Table 4.4: Lung field segmentation from PA chest radiographs. Performance measures of the contour delineation method based on dynamic programming (DP), using the public image database (JSRT). Best and worst segmentation outputs (overlap) are shown in Figure 4.12 (see also Appendix B).

Measure	Right Lung			Left Lung		
(DP/JSRT)	min	max	mean $\pm$ std	min	max	mean $\pm$ std
accuracy	0.88	0.99	0.98 ± 0.01	0.87	0.99	0.98 ± 0.01
sensitivity	0.76	1.00	0.96 ± 0.03	0.78	1.00	0.97 ± 0.02
specificity	0.85	1.00	0.99 ± 0.01	0.86	1.00	0.99 ± 0.01
overlap	0.63	0.96	0.91 ± 0.04	0.51	0.96	0.90 ± 0.06
precision	0.64	0.99	0.95 ± 0.04	0.51	0.98	0.92 ± 0.06
recall	0.76	1.00	0.96 ± 0.03	0.78	1.00	0.97 ± 0.02
F-score	0.78	0.98	0.95 ± 0.02	0.67	0.98	0.95 ± 0.04

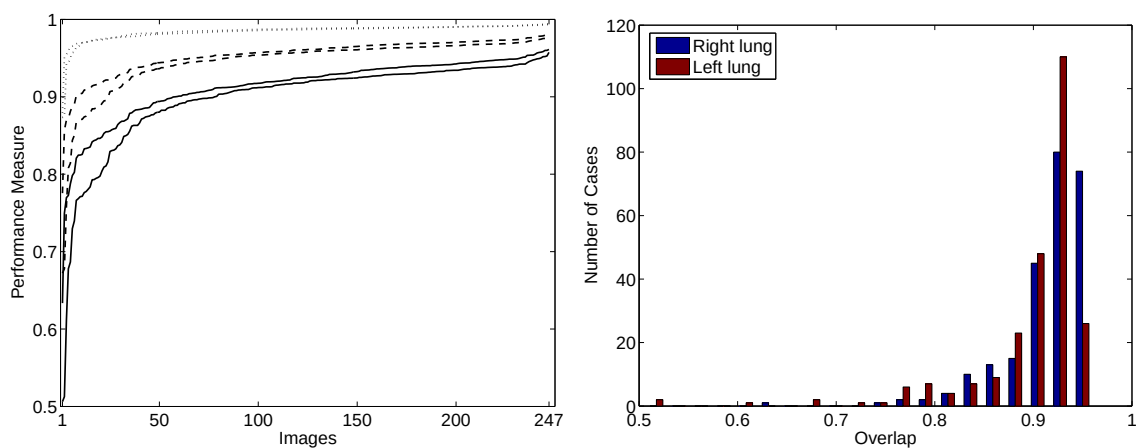


Figure 4.11: Performance measures of the contour delineation method using the public image database (DP/JSRT). (a) The measures are sorted in ascending order for the 247 images: accuracy (dotted lines), F-score (dashed lines) and overlap (solid lines). For each measure, the upper and lower curves correspond to the right and left lung, respectively. To the left of the graph, where images are hard to segment, the differences between the various measures are most clear. (b) The distribution of overlap values for both lungs (see also Table 4.4).

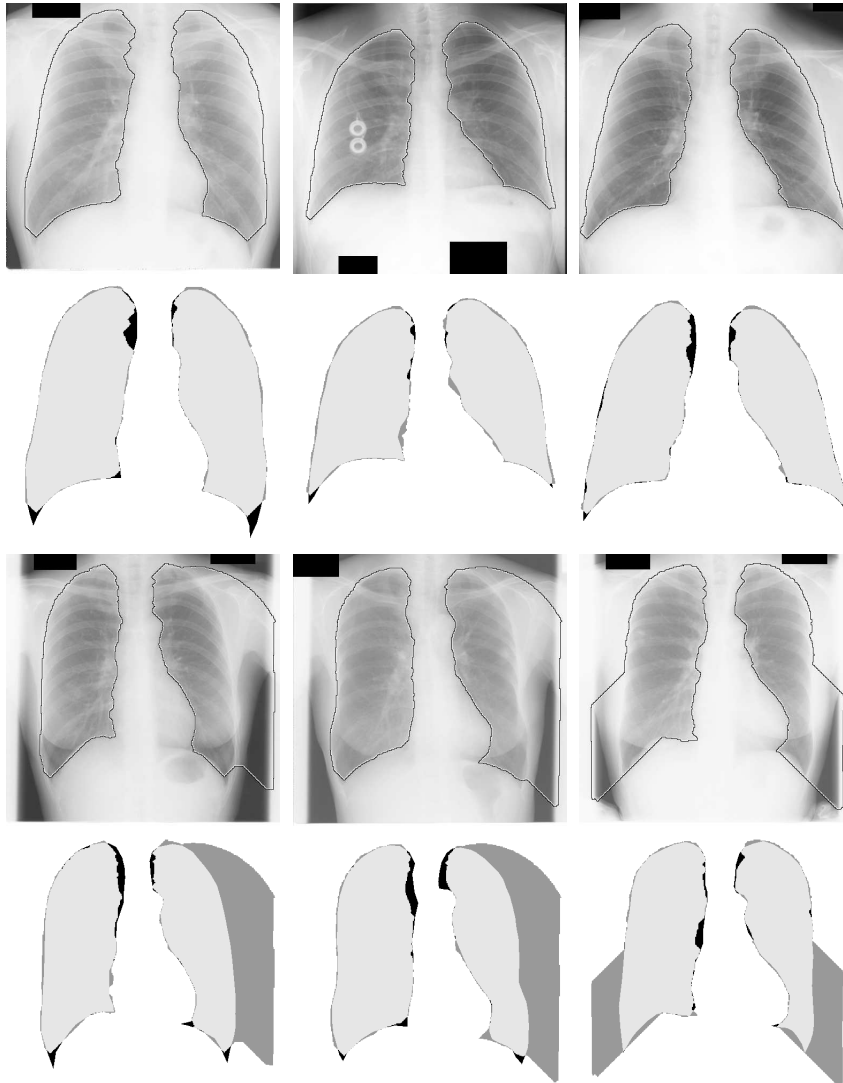


Figure 4.12: Segmentation outputs (contours and confusion matrix) of the contour delineation method using the public image database (DP/JSRT). Results are shown for the best (first rows) and worst (last rows) 3 of 247 images. True negative pixels (TN) are white, true positive (TP) light gray, false positive (FP) dark gray, and false negative (FN) black (see also Appendix B).

are reported in Table 4.5 and Table 4.6, respectively. It is interesting to note that delineation and registration perform equally, although one could expect to obtain such results since both methods are based on the same image features and therefore the same cost images for computing either the cumulative cost of a path or the fitness of an instance of the deformable model.

Performance measures computed in these experiments can be loosely compared with those obtained in the first one. Strict comparison is not possible since they were applied on different data sets. Actually, the JSRT database contains images of good technical quality, and very few images with gross abnormalities. Since segmentation errors are more likely to occur when the image contains pathology or unusual anatomy, we believe that some images of the private database are much harder to segment.

In order to identify the main sources of the errors of computer algorithms, the worst results were presented to a radiologist who rated the performance on a qualitative scale. The best and worst 3 segmentation outputs obtained by using the contour delineation method and the model-to-image registration approach are presented, respectively, in Figure 4.13 and Figure 4.14. Examples of following wrong edges are evident. This is due to severe pathologies present in such images, namely consolidation of the right lung and cardiomegaly observed, respectively, in the first and all images of Figure 4.13. These radiological findings result in the loss of an edge-like appearance of the hemi-diaphragms and a poor definition of the cardiac silhouette, corresponding to the border between heart and lung.

Results of segmenting all images of the private images database are reported in Appendix B. In a few cases, the detection of the lung apices has failed. To solve this problem, the proposed contour-based approach can be combined with the strength of a region growing technique. In fact, in PA chest radiographs the lung fields and the supraclavicular regions are adjacent, and both regions correspond to low intensity pixels. We believe that their separation could be effectively achieved by using the ISRG algorithm, as suggested by the example provided in Figure 3.9. Therefore this algorithm is suggested to constrain or even correct the vertical position of the lung top sections. Alternatively, ISRG could be used as a robust initialization when detecting this particular segment. Note that this error has not been observed when applying the model-to-image registration method.

Table 4.5: Lung field segmentation from PA chest radiographs. Performance measures of the contour delineation method based on dynamic programming (DP), using the private image database (HSJ). Best and worst segmentation outputs (overlap) are shown in Figure 4.13 (see also Appendix B).

Measure	Right Lung			Left Lung		
(DP/HSJ)	min	max	mean $\pm$ std	min	max	mean $\pm$ std
accuracy	0.86	0.99	0.98 ± 0.02	0.93	1.00	0.98 ± 0.01
sensitivity	0.81	0.97	0.92 ± 0.04	0.77	0.97	0.92 ± 0.05
specificity	0.85	1.00	0.99 ± 0.02	0.94	1.00	0.99 ± 0.01
overlap	0.38	0.95	0.87 ± 0.09	0.62	0.95	0.87 ± 0.09
precision	0.40	1.00	0.94 ± 0.09	0.71	1.00	0.93 ± 0.08
recall	0.81	0.97	0.92 ± 0.04	0.77	0.97	0.92 ± 0.05
F-score	0.55	0.97	0.93 ± 0.07	0.77	0.97	0.93 ± 0.05

Table 4.6: Lung field segmentation from PA chest radiographs. Performance measures of the model-to-image registration method based on genetic algorithm (GA), using the private image database (HSJ). Best and worst segmentation outputs (overlap) are shown in Figure 4.14 (see also Appendix B).

Measure	Right Lung			Left Lung		
(GA/HSJ)	min	max	mean $\pm$ std	min	max	mean $\pm$ std
accuracy	0.94	0.99	0.98 ± 0.01	0.96	0.99	0.98 ± 0.01
sensitivity	0.87	0.99	0.93 ± 0.03	0.85	0.98	0.93 ± 0.03
specificity	0.93	1.00	0.99 ± 0.01	0.96	1.00	0.99 ± 0.01
overlap	0.58	0.93	0.86 ± 0.08	0.65	0.93	0.87 ± 0.07
precision	0.62	1.00	0.92 ± 0.08	0.67	0.99	0.93 ± 0.08
recall	0.87	0.99	0.93 ± 0.03	0.85	0.98	0.93 ± 0.03
F-score	0.74	0.97	0.92 ± 0.05	0.79	0.97	0.93 ± 0.04

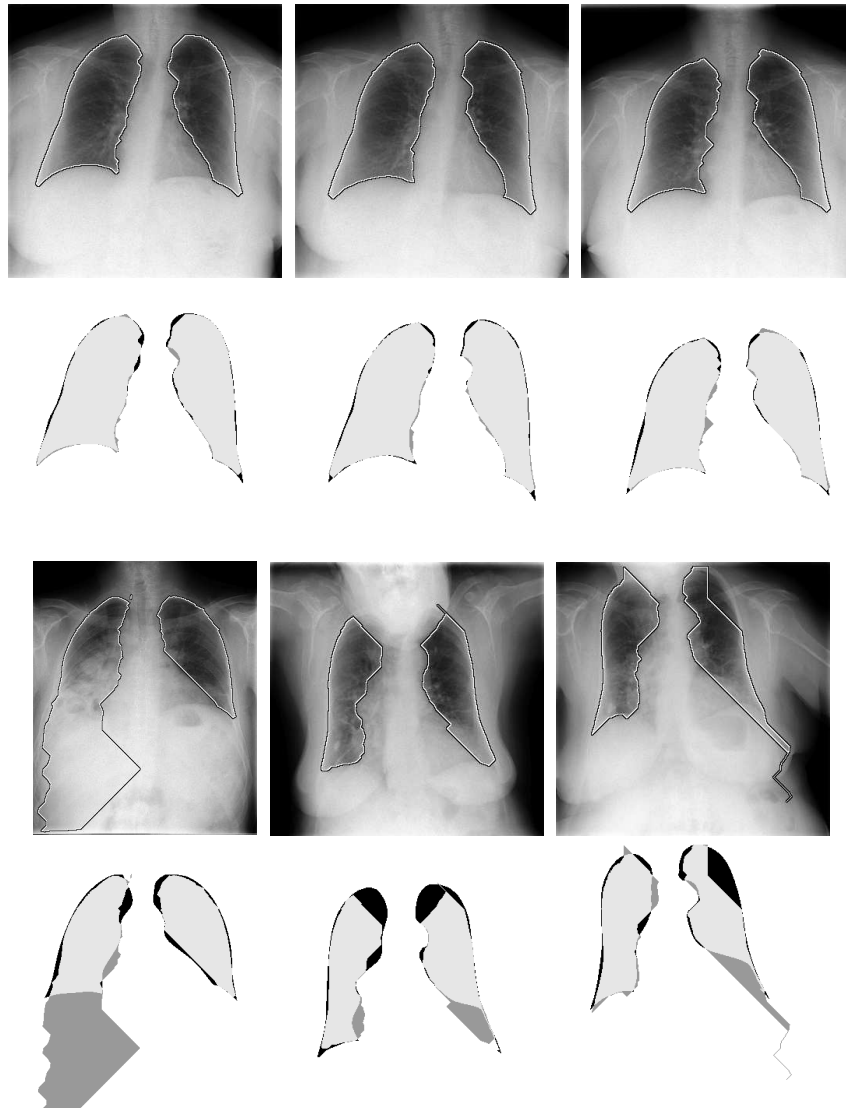


Figure 4.13: Segmentation outputs (contours and confusion matrix) of the contour delineation method using the private image database (DP/HSJ). Results are shown for the best (first rows) and worst (last rows) 3 of 39 images. TN - white, TP - light gray, FP - dark gray, FN - black (see also Appendix B).

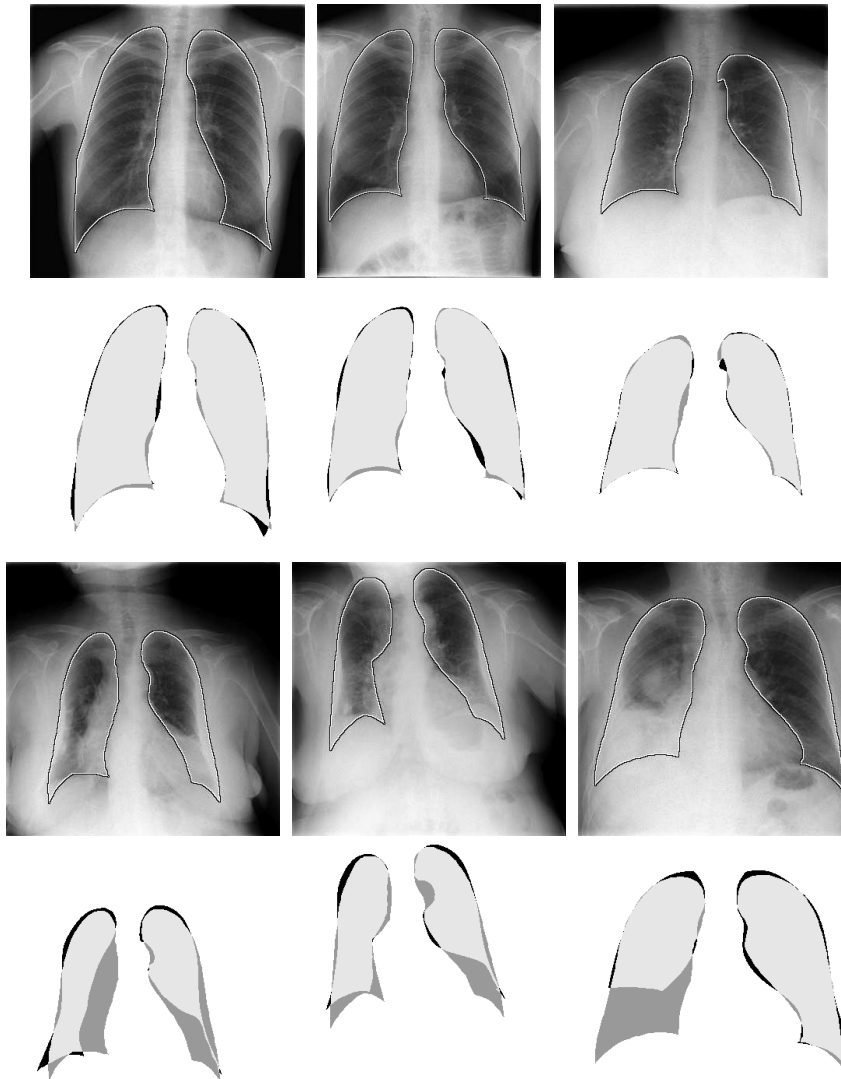


Figure 4.14: Segmentation outputs (contours and confusion matrix) of the model-to-image registration method using the private image database (GA/HSJ). Results are shown for the best (first rows) and worst (last rows) 3 of 39 images. TN - white, TP - light gray, FP - dark gray, FN - black (see also Appendix B).

4.7 Conclusions

In this Chapter, we described two fully automated segmentation methods for accurately extracting the lung fields on digital standard PA chest radiographs. The proposed approaches are model-based image segmentation methods that consist on several algorithms applied sequentially. The segmentation framework was designed in such a way that both methods use the same cost images. To compute such cost functions, one for each of the segments defined in the lung contour model, we proposed a combination of multiple normalized image feature based on a winner-takes-all, multiscale approach.

The first method is a contour delineation method, for which an optimal path finding algorithm was developed to accurately detect the segments that make up the lung contour model. Based on dynamic programming, this border detection algorithm is a simple and effective technique that provides with a complete lung boundary description, including the costal, mediastinal, lung top sections and diaphragmatic edges. The second scheme employs a non-rigid deformable model-to-image registration framework. The construction of the deformable model is based on standard techniques by using a training set of templates manually delineated. The point distribution model was adopted to represent the lung mean shape, allowing the incorporation of statistical information about its expected variation. Thin-Plate Splines are then used to define a model transformation and the lung field segmentation is reformulated as an optimization problem to search for the best transformation parameters. Due to their flexibility, genetic algorithms were chosen as the optimization tool to solve the problem.

Experimental results are reported after applying them on two different image databases and performance analysis was done by comparing the computer-based segmentation outputs with results obtained by manual analysis. Several similarity measures were considered and qualitative evaluation of segmentation outputs was made to identify possible source of errors. The accuracy of the proposed segmentation schemes is comparable to other methods published so far, reflecting their applicability in CAD systems.

Chapter 5

DECOMPOSITION OF 3D CT IMAGES

In this Chapter, we present a method for segmenting anatomical structures from thoracic CT images. The approach is based on the principles of material basis decomposition described in Chapter 2 and integrates several image processing techniques described in Chapter 3.

5.1 Introduction

Models of the human anatomy serve an important role in several aspects of diagnostic and therapy related image processing. Transmission X-ray computer tomography supplies the required high resolution 3D human anatomy necessary to create a computerized 3D volume array modeling all major internal structures of the body. Computerized anthropomorphic phantoms can either be defined by mathematical (analytical) functions or digital voxel-based volume arrays where each voxel of the volume contains a label or index number designating it as belonging to a given organ or internal structure [123]. This volume models the human anatomy and can serve as a patient-specific voxel-based phantom suitable for many computer-based modeling and simulation. Computer models have been applied to better understand the image formation process in diagnostic radiology, particularly for analyzing scatter and attenuation problems in nuclear medicine. Compared to dosimetry calculations, much higher statistics are necessary to perform imaging simulations. In the field of oncology, internal and external radiotherapy sources have become more sophisticated in their design and application. The calculation involved in clinical therapy planning can be more effectively investigated with computerized realistic human models.

Another application of CT imaging lies in the broader context of the development of computer aided diagnosis (CAD) systems to detect the presence of pulmonary disease, quantify and follow-up its evolution. Therefore, accurate and robust segmentation of the lung fields from X-ray CT images is a prerequisite for most pulmonary

image analysis applications. The immediate goal of the lung segmentation algorithm is to separate lung voxels from surrounding anatomy. Robust and accurate algorithms that require minimal (semi-automated methods) or no human interaction (fully automated methods) must be designed to identify the precise boundaries of the lungs.

In earlier works, a single segmentation threshold was selected to segment the lungs as low-density cavities inside of the patient [124, 125]. Lung contours have been extracted in 2D, using a slice by slice analysis [124, 126, 127], thus not considering the hypothesis that more than one contour could be needed for delineating each lung in a particular slice of the volumetric image. Several studies published so far [126, 128] have considered lung region segmentation without extracting the trachea or large airways. Knowledge-based segmentation algorithms that use explicit anatomical knowledge such as the expected size, shape, relative positions and expected X-ray attenuation coefficients of objects have also been proposed [129, 130, 131] for segmenting dynamic chest CT images. Most of the proposed techniques for segmenting the lung region are developed for lung nodule detection [124, 126, 128, 131, 132]. In fact, CAD methods are effective for assisting radiologists as a viable alternative to double reading in the early detection of lung cancer in thoracic CT scans. Several schemes have been proposed to automatically evaluate the growth of pulmonary nodules by quantifying their volume and change over time [133, 134]. This goal can be achieved by means of registration and matching of lung surfaces [135, 136] in temporal CT scans. Methods for matching thoracic structures across individuals were used to create a normative human lung atlas [137]. Other applications that require the accurate lung region segmentation as the basis for computer assisted techniques include quantitative analysis of emphysema [138] and differential lung function [127, 139]. The segmentation of the lung fields from High-Resolution Computed Tomography (HRCT) scans has been considered [140]. The use of anatomic pulmonary atlas to automatically segment the oblique lobar fissures in HRCT has been demonstrated in [141]. The goal of the pulmonary atlas used in this method is not to precisely represent all of the pulmonary anatomy, but simply to initialize the subsequent fissure detection. A review of the literature on computer analysis of the lungs in CT scans addressing the segmentation of various pulmonary structures, registration of chest scans, and applications aimed at detection, classification and quantification of chest abnormalities is presented in [142].

Aside from its applications as a pre-processing step for CAD methods, the automated lung field segmentation may be used for image data visualization. A single

thoracic CT examination may result in acquisition of more than 300 sections for 1 mm reconstruction intervals. The interpretation of such amount of data requires the radiologist to mentally reconstruct a three dimensional representation of the patient anatomy. In this context, CT image segmentation can be required for the surface/volume rendering of structures of interest as a visual aid for the radiologist's diagnostic task.

In an effort to contribute to the required methodological knowledge, we describe fully automated segmentation algorithms for decomposing volumetric CT images into several anatomical structures. A voxel classification strategy is adopted to construct a 3D patient-specific anthropomorphic phantom and accurately extract the lung region of interest. The proposed method follows a hierarchical representation of the patient anatomy. First, the thorax of the patient is segmented from the surrounding background image and decomposed into *body* and *lung* structures. Then, the large airways are identified and extracted from the lung parenchyma. Since the method can be specifically directed towards CAD applications, the lung fields are finally extracted and the corresponding mask is created as the final output of the segmentation procedure.

There are several distinctions between our method and previous work. The method is based on the principle of dual-energy radiography [1, 21] discussed in Section 2.7. This novel approach explores the concept of material decomposition applied to CT numbers and provides a simple anatomical model describing the major structures of the human thorax in terms of their composition and physical properties. This is particularly important when constructing realistic computer models. The segmentation procedure results in a set of automatically computed threshold values that reflects the gray-scale characteristics of a specific dataset. Instead of using a unique fixed threshold value, two thresholds are used to segment the lung region from CT images. We also propose the use of an optimal surface detection algorithm based on dynamic programming for separating the left and right lungs. Our automatic computer-based segmentation was tested on several images of a private database and compared with results obtained by manual analysis. Preliminary results of the method based on material decomposition are reported in [143].

5.2 Basis Set Decomposition

As discussed in Section 2.7.1, the principle of dual-energy radiography allows to express the mass attenuation coefficient μ_ξ/ρ_ξ of a given material ξ of density ρ_ξ ,

in terms of the mass attenuation coefficients of two basis materials α and β . For a particular photon energy E within the diagnostic energy range $[E_{\min}, E_{\max}]$,

$$\frac{\mu_{\xi}(E)}{\rho_{\xi}} = a_1 \frac{\mu_{\alpha}(E)}{\rho_{\alpha}} + a_2 \frac{\mu_{\beta}(E)}{\rho_{\beta}}. \quad (5.1)$$

Introducing the energy dependency of the linear attenuation coefficient, the CT number H_{ξ} corresponding to the material ξ , Eq. 2.32 is now rewritten as

$$H_{\xi}(E) = \left(\frac{\mu_{\xi}(E)}{\mu_w(E)} - 1 \right) K. \quad (5.2)$$

We define the CT number H_{ξ} as a function of the attenuation of materials α and β by considering the material decomposition expressed by Eq. 5.1:

$$H_{\xi}(E) = \left[\frac{K}{\mu_w(E)} \left(a_1 \frac{\mu_{\alpha}(E)}{\rho_{\alpha}} + a_2 \frac{\mu_{\beta}(E)}{\rho_{\beta}} \right) \right] \rho_{\xi} - K, \quad (5.3)$$

In terms of H_{α} and H_{β} , the CT numbers of materials α and β , respectively, the above equation assumes a more convenient form,

$$H_{\xi}(E) = a_1 \frac{\rho_{\xi}}{\rho_{\alpha}} H_{\alpha}(E) + a_2 \frac{\rho_{\xi}}{\rho_{\beta}} H_{\beta}(E) + \left(a_1 \frac{\rho_{\xi}}{\rho_{\alpha}} + a_2 \frac{\rho_{\xi}}{\rho_{\beta}} - 1 \right) K, \quad (5.4)$$

or, equivalently,

$$H_{\xi}(E) = b_1 H_{\alpha}(E) + b_2 H_{\beta}(E) + (b_1 + b_2 - 1) K, \quad (5.5)$$

where $b_1 = a_1 (\rho_{\xi}/\rho_{\alpha})$ and $b_2 = a_2 (\rho_{\xi}/\rho_{\beta})$ are energy independent. Since a_1 and a_2 represent fraction by weight (see Eq. 2.16 and 2.34), the coefficients b_1 and b_2 represent fraction by volume.

The *mean CT number* $\bar{H}_{\xi}$ of a given material ξ is now computed. In CT the detector signal and therefore the CT numbers in the image depend on the incident spectral intensity $N'(E)$ of the external source and the average absorbed energy $E\varepsilon(E)$ for X-ray photon of energy E [144, 145]. The intrinsic efficiency $\varepsilon(E)$ denotes the fraction of detected photons (see Section 2.5.3). The mean CT number $\bar{H}_{\xi}$ is computed by integrating Eq. 5.5 over the chosen diagnostic energy range for which

material decomposition as given by Eq. 5.1 is considered valid,

$$\bar{H}_\xi = \int_{E_{\min}}^{E_{\max}} N'_0(E) E \varepsilon(E) H_\xi(E) dE, \quad (5.6)$$

where $N'_0(E)$ is the relative spectral intensity of the source. From Eq. 5.5

$$\bar{H}_\xi = b_1 \bar{H}_\alpha + b_2 \bar{H}_\beta + (b_1 + b_2 - 1) K. \quad (5.7)$$

The condition $b_1 + b_2 = 1$ is satisfied since b_1 and b_2 are volume fractions and therefore the mean CT number of any material ξ can be expressed independently of the calibration constant K of the scanner, as a linear combination of the mean CT numbers $\bar{H}_\alpha$ and $\bar{H}_\beta$ of basis materials α and β :

$$\bar{H}_\xi = b_1 \bar{H}_\alpha + b_2 \bar{H}_\beta, \quad (5.8a)$$

$$b_1 + b_2 = 1. \quad (5.8b)$$

The above expressions reflect the material decomposition applied to CT numbers and can be applied to any voxel $\mathbf{p}$ located at coordinates (x, y, z) in a CT image $\mathbf{H}(x, y, z)$.

Consider now a structure (as well as the CT image itself) made up of material ξ with corresponding mean CT number $\bar{H}_\xi$ and enclosing a volume V_0 . If n_0 is the total number of voxels in the structure ξ , then $V_0 = n_0 dV$, where $dV = dXdYdZ$ is the volume of one voxel $\mathbf{p}$. Material decomposition of the volumetric structure ξ into basis materials α and β can therefore be applied to all the voxels inside ξ and following Eq. 5.8,

$$n_0 \bar{H}_\xi = n_1 \bar{H}_\alpha + n_2 \bar{H}_\beta, \quad (5.9a)$$

$$n_1 + n_2 = n_0, \quad (5.9b)$$

where n_1 and n_2 are defined as the total number of voxels of two non-overlapping regions of volume V_1 and V_2 , within the decomposed structure ξ made up of material α and β , respectively. Using Eq. 2.38, the material ξ can be represented by its characteristic angle θ_ξ in the basis plane. It is interesting to note that θ_ξ is simply given by

$$\tan \theta_\xi = \frac{n_2}{n_1} = \frac{b_2}{b_1} = \frac{a_2}{a_1}. \quad (5.10)$$

The material decomposition described above will be used to guide the segmentation of CT images, as explained in the following Sections, where different combinations or contents of basis materials are considered to define and compute the composition/decomposition of several thoracic structures of interest.

5.3 CT Image Segmentation

5.3.1 Anatomical Model

As for chest radiographs, a simple anatomical model is adopted for describing the major internal structures of interest that are found in thoracic CT images. Figure 5.1(a) displays the normal anatomy of the human thorax expected to be observed in a volumetric CT image, for one slice at the level of the carina where the trachea divides into the main bronchi. The adopted anatomical model is shown in Figure 5.1(b) and includes a hierarchical description of anatomical structures within the patient, approximately centered inside the field of view (FOV) of the scanner. The lungs are the region of interest in pulmonary applications, mainly composed by AIR and LUNG tissue. We assume that they include the right lung, the left lung and the large airways containing the trachea and main bronchi. The body of the patient represents dense structures, mainly composed by FAT, SOFT tissue and BONE structures such as mediastinum, muscles and ribcage.

Each structure described in the model is assumed to be a combination of the intervening *materials* reported in Table 5.1. Equivalently, each structure can be decomposed into these materials, as illustrated in Figure 5.1(b). For each material, Eq. 5.2 and Eq. 5.6 were used to compute the corresponding mean CT number, by using the photon cross-section libraries published by NIST [3] and considering tissue composition taken from ICRU-44 [4]. The diagnostic energy range was defined from $E_{min} = 40$ keV to $E_{max} = 150$ keV. In Eq. 5.6, the weighting function $N'_0(E)$ corresponds to the simulated X-ray source spectrum, generated with the code described in [10]. Al-added filtration of 1 mm and no voltage ripple were used (see Section 2.5.1 and Figure 2.8). An ideal CT detector was considered by setting the absorption efficiency $\varepsilon = 1$. For comparison purpose, the mean CT numbers computed for a monochromatic beam of $E = 125$ keV are also listed.

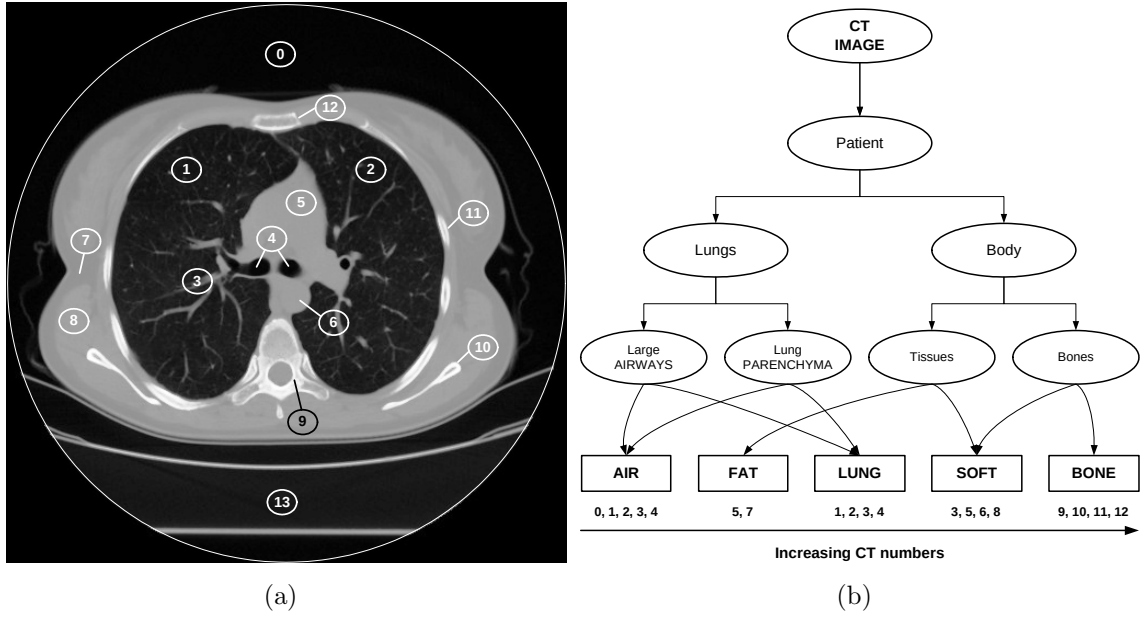


Figure 5.1: (a) Normal anatomy of the human thorax observed in a single slice of a thoracic CT image at the level of the carina: (0) AIR outside the patient, (1) right lung, (2) left lung, (3) right hilum (lung root), (4) large airways (main bronchi), (5) mediastinum (great vessels), (6) descendant aorta, (7) FAT tissue, (8) SOFT tissue, (9) spine, (10) scapula, (11) rib, (12) sternum, (13) table of the scanner (see also Figure 4.1); (b) 3D patient-specific phantom construction: hierarchical representation of anatomical structures and corresponding material composition/decomposition.

Table 5.1: Material specification of the anatomical model used for decomposing CT images. Mean CT numbers $\bar{H}_\xi$ are computed from Eq. 5.6.

Material ξ	Designation (ref. [4])	Density ρ_ξ (gcm ⁻³)	Mean CT Number $\bar{H}_\xi$	
			(40 – 150 keV)	(125 keV)
AIR	Air (sea level)	0.001	−999	−999
FAT	Adipose Tissue	0.950	−92	−55
WATER	Water Liquid	1.000	0	0
LUNG	Lung Tissue	1.050	+48	+42
SOFT	Soft Tissue	1.060	+55	+51
BONE	Cortical Bone	1.920	+2032	+953
least squares			991.2	994.4
without	$\bar{H}_\xi = m\rho_\xi - K$	K	1002.7	999.9
BONE		r ²	0.998	0.999

5.3.2 Proposed Algorithms

A schematic of the image processing pipeline of the proposed method for decomposing CT images is given in Figure 5.2. The automated segmentation and decomposition is achieved by means of several algorithms discussed below. To describe the patient anatomy, a computerized 3D volume array or rectangular grid of voxels of the same size and spacial resolution of the input CT image is first created. A voxel classification strategy is then adopted to classify each voxel of the grid by an indexing number, or *label*, designating it as belonging to a given structure of the anatomical model defined in the previous Section. Actually, two main outputs are expected from the decomposition of a single CT image:

- **3D Patient-Specific Phantom** (algorithms I or II, III and IV): this sequence provides a method for decomposing the whole patient into known materials. The computerized 3D volume array is labeled accordingly and results in a suitable voxelized phantom for computer simulations. A description of the method is given in Section 5.4.
- **Lung Region of Interest** (algorithms I or II, III, V and VI): this sequence corresponds to the lung field segmentation from CT images and provides the means for defining the lung region of interest, specifically dedicated to pulmonary imaging applications. The proposed segmentation method is described in Section 5.5.

Both methods correspond to a rule-based combination of material decompositions applied to CT numbers with different image processing techniques described in Chapter 3, namely histogram analysis, global thresholding and seeded region growing. The proposed algorithms correspond to a step by step procedure and each algorithm results in the segmentation of at least one of the structure of interest defined in the thoracic model.

5.4 3D Patient-Specific Phantom

5.4.1 Patient Segmentation

The distribution of CT numbers is typically bimodal in thoracic CT images since they contain mainly two types of voxels: 1) *low* density or attenuation voxels, within the lung parenchyma, large airways and air surrounding the subject, and 2) *high*

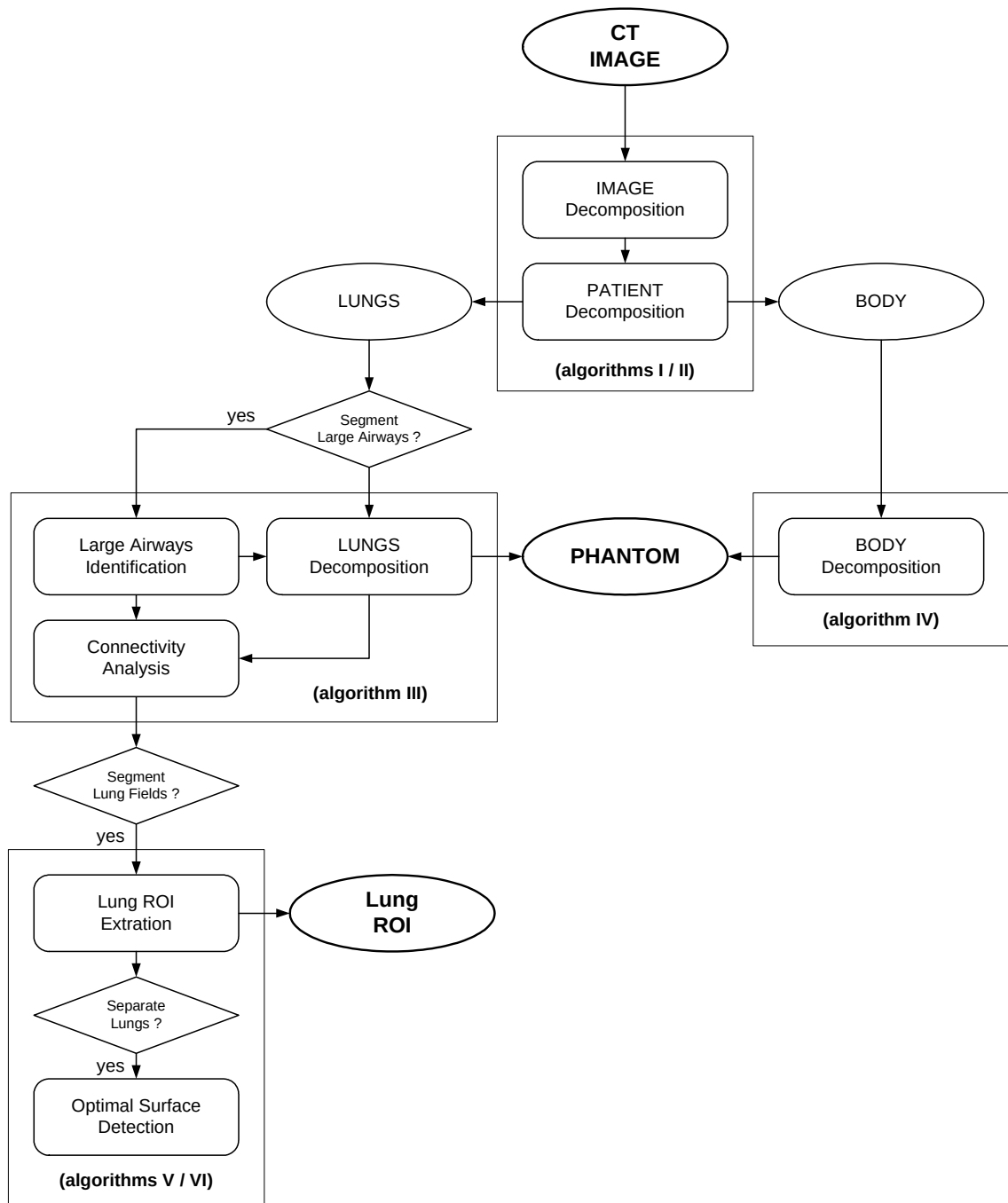


Figure 5.2: CT image segmentation and decomposition pipeline. For the 3D patient-specific phantom construction, the large airways identification step is not necessary. The optimal surface detection algorithm is intended to separate the right and left lungs. It represents an optional step in the lung field segmentation algorithm.

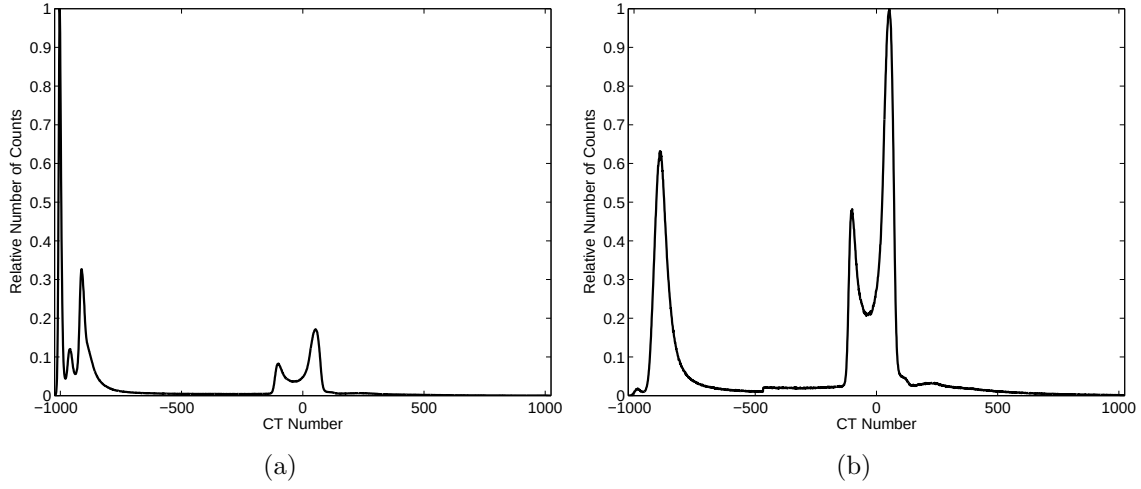


Figure 5.3: CT number distribution (image histogram) of gray levels considering (a) all voxels within the whole CT image; (b) all voxels that belong only to the thoracic region of the patient in the scanned volume.

density voxels, corresponding to the dense structures of the thorax. Because materials with higher densities will contrast more with background voxels, a simple histogram analysis can be used to identify all voxels belonging to the patient from the surrounding background image.

Consider a CT image $\mathbf{H}(x, y, z)$ and its gray-level histogram shown in Figure 5.3(a). The histogram was constructed by considering all image voxels, including those lying outside the FOV. Figure 5.3(b) shows the histogram of the same image, restricted to the thoracic region of the patient, once segmented as described next. Note that the distributions are similar except for that region of low attenuation, corresponding to the background image. For display purposes, only values between -1000 and +1000, previously normalized, are plotted.

From the CT number distribution of the image, *low* and *high* density voxels are separated according to a particular segmentation threshold T_0 . The expected value of T_0 should fall into the region between two main peaks of the histogram. Equivalently, if $\bar{H}_\alpha$ and $\bar{H}_\beta$ denote, respectively, the mean CT number of *low* and *high* density voxels, T_0 should satisfy $\bar{H}_\alpha(T_0) \leq T_0 \leq \bar{H}_\beta(T_0)$. Two optimal thresholding techniques, namely Otsu's method and the *isodata* algorithm (see Section 3.3.1) were used to automatically compute T_0 . Both techniques use an iterative procedure and provided the same optimal threshold, $T_0 = (\bar{H}_\alpha + \bar{H}_\beta)/2$.

Once T_0 has been computed, the body of the patient is extracted from *high* density voxels, using a threshold-based 3D seeded region-growing (SRG) technique.

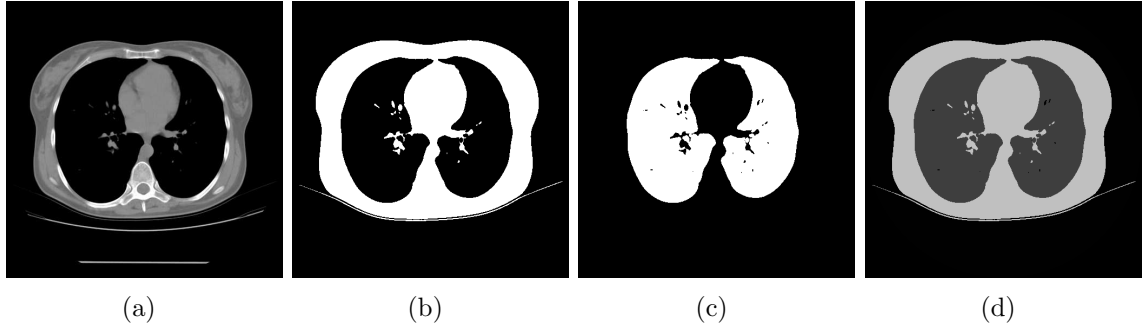


Figure 5.4: Patient segmentation without background extraction. (a) Middle slice of 3D input CT image; (b) Body and (c) lungs, segmented from (a) using 3D SRG. The lungs are both connected through the large airways; (d) image voxels labeled as body (light gray), lungs (dark gray) and background (black) surrounding the patient (see also Figure 5.5).

From a starting voxel or seed point $\mathbf{s}_0$, this recursive procedure involves checking its 26-connected neighbors: any voxel with CT number greater than T_0 , previously computed, is included in the body, its neighbors are also checked, and so on (see Section 3.3.2). The seed $\mathbf{s}_0$ is automatically selected from the base axial slice $\mathbf{H}(x, y, 0)$ of the CT image. The slice is iterated from its center until a pixel with CT number above T_0 is found, and this pixel is selected as the seed. The 3D SRG algorithm is applied repeatedly until every one-voxel is included in the contiguous set. As a result, the binary image shown in Figure 5.4(b) is constructed such that all pixels connected to $\mathbf{s}_0$ are turned "on" (i.e. assigned the value 1: white pixels) and all other pixels are turned "off" (value 0: black pixels).

To discriminate the lungs from other *low*-density regions within the patient, another 3D SRG is applied to connect voxels of the input image with CT numbers below T_0 . A new seed, $\mathbf{s}_1$, is automatically selected from the middle slice $\mathbf{H}(x, y, z_{\max}/2)$ of the image (see Figure 5.4(a)), providing that its CT number is lower than T_0 . Starting from $\mathbf{s}_1$, both lungs are segmented as a single structure since they are expected to be connected through the large airways. The result of the 3D SGR algorithm is shown in Figure 5.4(c), for one slice of the CT image.

The following steps summarize the proposed algorithm:

```
// Algorithm I - Patient Segmentation
// -----
1. Construct histogram of whole CT IMAGE (compute  $T_0$ )
2. Find seed  $\mathbf{s}_0$  and connect BODY (3D SRG using  $T_0$ )
3. Find seed  $\mathbf{s}_1$  and connect LUNGS (3D SRG using  $T_0$ )
4. Label IMAGE voxels as BODY and LUNGS
5. Label remaining IMAGE voxels as BACKGROUND
```

By performing two 3D SGR based on the same threshold value T_0 , the patient segmentation algorithm results in voxel labeling of the input CT image into three different structures: body, lungs and background, as shown in Figure 5.4(d).

Ideally a threshold value equal to the average of densities of the body and lungs should be used to decompose the segmented patient. Therefore, the use of a new threshold value T_1 is suggested to connect the lungs. From Figure 5.4(b), the background is first identified as regions that include the corners of the image. Once more, 3D SGR is used to connect these regions. A logical NOT operation is then performed on the background mask and used to label image voxels as belonging to the thoracic region of the patient, as shown in Figure 5.5(a) and (b), respectively. The optimal threshold T_1 is now computed by using the same clustering techniques as before. This time, only voxels that belong to the patient are considered to construct the histogram plotted in Figure 5.3(b). Connected lungs using T_1 are shown in Figure 5.5(c) and the resulting image labeling is displayed in Figure 5.5(d).

The patient segmentation algorithm, including the background identification, is finally rewritten as follow:

```
// Algorithm II - Patient Segmentation
// -----
1. Construct histogram of whole CT IMAGE (compute  $T_0$ )
2. Find seed  $s_0$  and connect BODY (3D SRG using  $T_0$ )
3. From corners of IMAGE, connect BACKGROUND (3D SRG using  $T_0$ )
4. Label IMAGE voxels as BACKGROUND
5. Label remaining IMAGE voxels as PATIENT
6. Construct histogram of PATIENT (compute  $T_1$ )
7. Find seed  $s_1$  and connect LUNGS (3D SRG using  $T_1$ )
8. Relabel PATIENT voxels as BODY and LUNGS
```

By restricting the region of interest to the patient, the optimal threshold T_1 is a better estimate than T_0 , that was computed using all image voxels. Although the resulting image labeling provided by the two algorithms is visually very similar, as seen through comparison of Figure 5.4(d) and Figure 5.5(d), thresholds T_0 and T_1 are quite different, as observed in experimental results. In the present example, optimal values $T_0 = -467$ and $T_1 = -409$ were obtained.

5.4.2 Lung Decomposition

The lungs segmented from the previous algorithms contain the trachea and main stem bronchi that define the large airways. The remaining part of the lungs is the

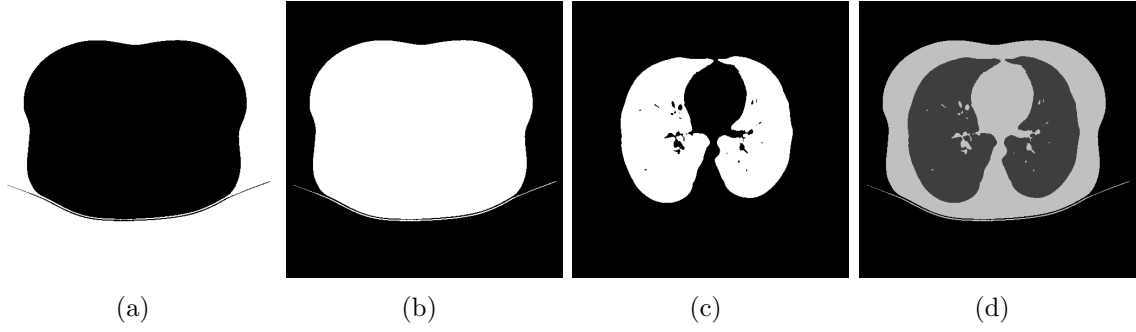


Figure 5.5: Patient segmentation with background extraction. (a) Connected background (white) by applying 3D SGR from the corners of the image; (b) Segmented patient (negation of the background); (c) Connected lungs using 3D SRG; (d) Corresponding image labeling: body (light gray), lungs (dark gray) and background (black) surrounding the patient (see also Figure 5.4).

lung parenchyma that contains the right and left lungs. All structures included in the lungs are expected to contain air-filled regions surrounded by a tissue with higher density. Consequently, AIR and LUNG tissue were chosen from Table 5.1 as the basis materials to decompose the lungs. As explained later in Section 5.5.2, the large airways should be detected and separated from the lung parenchyma to improve the robustness of the right and left lung separation algorithm.

In this Section, two different material decompositions applied to lung voxels are considered and included into a single algorithm. The first decomposition is performed to identify AIR within the large airways, while the second decomposition is used to distinguish AIR from LUNG tissue within the whole lungs.

Large Airways Identification

Let n_0 be the total number of voxels labeled as lungs and $\bar{H}_\xi$ the mean value of CT numbers observed in the segmented patient (see Figure 5.5(b)). Using the data listed in Table 5.1, the material decomposition of lung voxels, with CT number $\bar{H}_\xi$, into AIR (material α) and LUNG tissue (material β) is performed by setting in Eq. 5.9a, $\bar{H}_\alpha = -999$ and $\bar{H}_\beta = +48$. Respecting Eq. 5.9b, the number of AIR voxels within the decomposed lungs is computed as $n_1 = n_0(\bar{H}_\xi - \bar{H}_\beta)/(\bar{H}_\alpha - \bar{H}_\beta)$. This number is now related to a new threshold value T_2 that is determined from the gray-level histogram $n(H)$ of the segmented lungs as

$$T_2 = \arg \max_T \left\{ \sum_{H=H_{\min}}^T n(H) \leq n_1 \right\}, \quad (5.11)$$

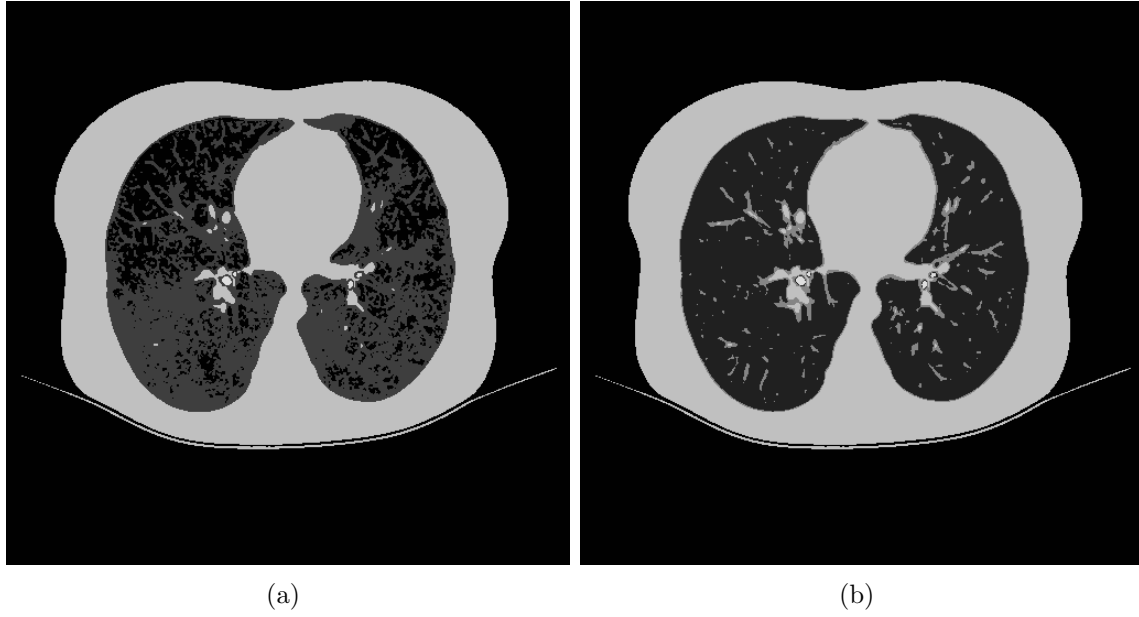


Figure 5.6: Material decomposition of the lungs into AIR (black) and LUNG tissue (dark gray). Results are shown after performing (a) a first decomposition for identifying AIR inside the large airways (white) and (b) a second decomposition for identifying AIR inside the whole lungs (see also Figure 5.7).

where $H_{\min}$ the minimum CT number found inside the lungs. Consequently, lung voxels with CT number below T_2 are relabeled as being composed of AIR, as shown in Figure 5.6(a) and 5.7(a). Following the example, $\bar{H}_\xi = -261$ (segmented patient) and $T_2 = -897$ were obtained, corresponding to the volume fraction $b_1 = n_1/n_0 = 0.29$ (AIR). Equivalently, one can consider that 29% of voxels within the lungs are *pure* AIR.

To identify the large airways, a seed $\mathbf{s}_2$ is automatically selected from the top slice $\mathbf{H}(x, y, z_{\max})$ of the CT image, where one expects the trachea to appear as a large, circular, air-filled object near the center of the body. The top slice is iterated until a pixel currently labeled as AIR is found. From the starting pixel $\mathbf{s}_2$, the 3D SRG algorithm is used to grow the large airways based on T_2 , by selecting among AIR voxels those connected to the seed. The corresponding result is shown in Figure 5.7(b), for a single slice of the volumetric image.

Parenchyma Decomposition

The above decomposition represents only an intermediate algorithm for identifying the large airways among AIR voxels within the lungs. Actually, if the decomposition

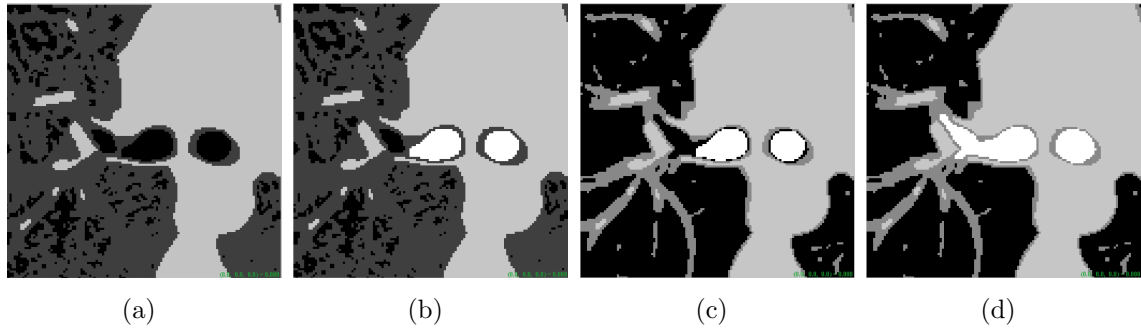


Figure 5.7: Large airways identification. Results are shown after performing, (a) first decomposition of the lungs, (b) 3D SRG for connecting AIR inside the large airways (white), (c) second decomposition and (d) relabeling based on connectivity and topological analysis. Note that, as expected, air-filled regions (black) within the lung parenchyma are separated by LUNG tissue (dark gray) from the segmented body of the patient (light gray) (see also Figure 5.6).

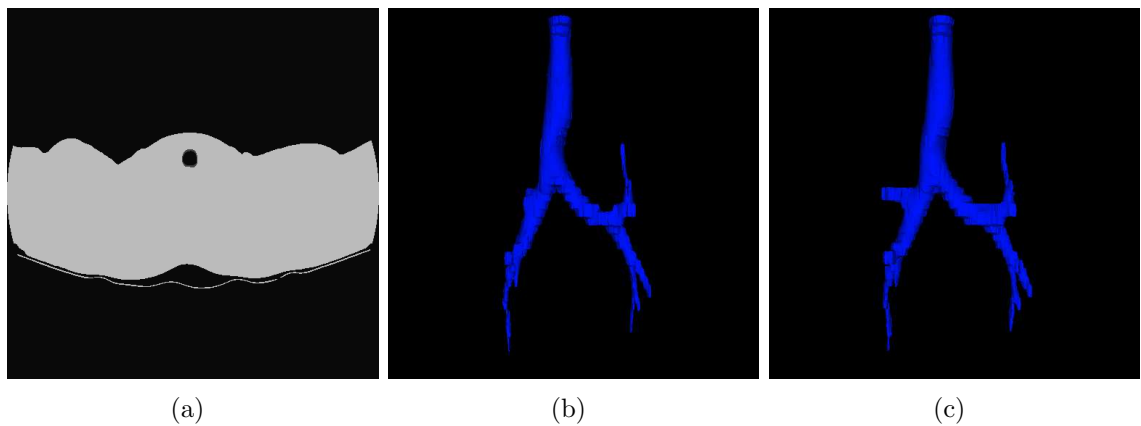


Figure 5.8: Large airways segmentation results. (a) A seed is automatically found in top slice of CT image for connecting, using 3D SRG, AIR voxels corresponding to the large airways; Surface rendering of the segmented large airways (b) before and (c) after connectivity and topological analysis (see also Figure 5.7).

of a CT image is performed for constructing a 3D patient-specific phantom, this algorithm can be considered as optional.

Actually, the lungs should be more accurately decomposed if only voxels belonging to that structure are used to compute its mean CT number. Therefore, material decomposition is now performed by first computing the mean CT number $\bar{H}_\xi$ of lungs voxels, and considering again AIR and LUNG tissue as the basis set. A new threshold T_3 is computed by using Eq. 5.11 to identify, this time, AIR from LUNG tissue voxels within the parenchyma. Results of the second decomposition are displayed in Figure 5.6(b). In this example, the mean CT number $\bar{H}_\xi = -850$ (segmented lungs) and threshold $T_3 = -794$ were computed, corresponding to the volume fractions $b_1 = 0.86$ (AIR) and $b_2 = 0.14$ (LUNG tissue).

The segmentation of the large airways is finally achieved through connectivity and topological analysis: small objects labeled as AIR after the second decomposition and connected to the large airways, as illustrated in Figure 5.7(c), are included in this structure and relabeled accordingly. The final result is illustrated in Figure 5.7(d).

The following steps summarize the large airways identification and parenchyma decomposition algorithms:

```
// Algorithm III - Lung Decomposition
// -----
1. Construct histogram of LUNGS

// Large Airways Identification - 1st decomposition:
2. Compute mean CT number of PATIENT
3. Decompose LUNGS as AIR and LUNG tissue (compute T2)
4. Relabel LUNGS voxels as AIR ( $H < T_2$ )
5. Find seed S2 and connect LARGE AIRWAYS (3D SRG using T2)
6. Relabel AIR voxels as LARGE AIRWAYS

// Parenchyma Decomposition - 2nd decomposition:
7. Compute mean CT number of LUNGS
8. Decompose LUNGS as AIR and LUNG tissue (compute T3)
9. Relabel LUNGS voxels as AIR ( $H < T_3$ )
10. Relabel remaining LUNGS voxels as LUNG tissue

// Connectivity and Topological Analysis:
11. Relabel AIR voxels as LARGE AIRWAYS
```

The steps are applied sequentially, as illustrated in Figure 5.7(a) to (d) for the central region of a slice at the level of the carina. Other results of the proposed algorithm are presented in Figure 5.8. The top slice of the CT image is displayed in Figure 5.8(a) where the seed s_2 was automatically selected and used to grow the

large airways. Surface rendering of such structure, before and after connectivity and topological analysis is shown in Figure 5.8(b) and (c) respectively.

5.4.3 Body Decomposition

The final algorithm for constructing a 3D patient-specific phantom is now described. It represents the decomposition of the body into FAT (adipose) tissue, SOFT tissues (including blood) and higher density structures herein referred to as *bones*, corresponding mainly to the whole skeleton of the patient (see Figure 5.1). The bones are expected to include the spine, ribs, clavicles, scapula and sternum, as well as bone marrow (soft tissue filling spaces within some bones).

The first step of the algorithm consists of separating *bones* from *non-bones* structures. To achieve this goal, a segmentation threshold T_4 is used to distinguish low density from high density voxels within the segmented body. Ideally, the threshold value should be chosen (or computed) such that: 1) voxels with CT number below T_4 (low density voxels) should correspond to spatial regions made up of FAT and SOFT tissue only, and 2) bone structures should be identified as voxels with CT number above T_4 (high density voxels). Based on a few experiments performed on some CT images, the value $T_4 = +140$ was selected for thresholding the body and relabel its voxels as bones and non-bones. To ensure that the condition 1) is fulfilled, the regions currently labeled as bones are further dilated. The dilatation was performed using a $3 \times 3 \times 3$ structuring element and the *dilated bones* were relabeled accordingly. As visualized in a single axial slice of the labeled CT image, displayed in Figure 5.9(a), this operation tends to merge the vertebral column, ribs and skeletal muscles into a single 3D connected region.

Once identified, non-bones structures are decomposed into FAT and SOFT tissues. Material decomposition expressed by Eq. 5.9 is now performed by considering, respectively, $\bar{H}_\alpha = -93$ and $\bar{H}_\beta = +55$ as the mean CT number of these two basis materials (see Table 5.1) and $\bar{H}_\xi$ the mean CT number computed within the non-bones region being decomposed. As a result, a decomposition threshold T_5 is automatically computed and used to relabel non-bones voxels as FAT or SOFT tissue, if their CT number is below or above T_5 , respectively. Figure 5.9(b) shows an example of such decomposition, for which $\bar{H}_\xi = -20$ (non-bones), $T_5 = +12$, $b_1 = 0.51$ (FAT) and $b_2 = 0.49$ (SOFT).

The last step of the algorithm is based on the assumption that the dilated bones can be expressed as a combination of bone and SOFT tissue, erroneously included due

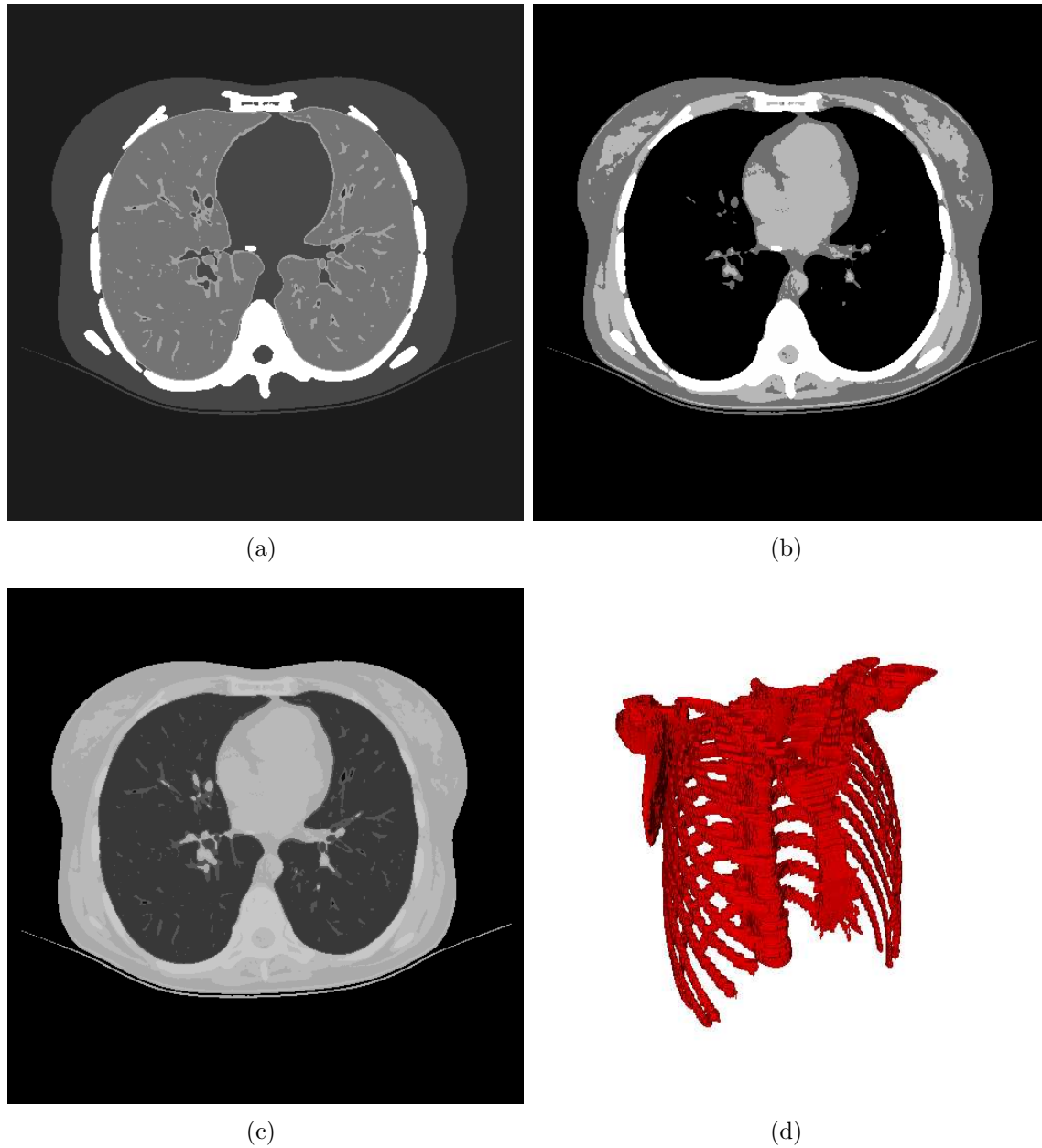


Figure 5.9: Body decomposition. (a) Dilated bones, in white, after body thresholding; (b) Decomposition of non-bones voxels within the body, into FAT and SOFT tissues; (c) Dilated bones decomposition into SOFT tissue and bones structures forming the skeleton; (d) Surface rendering of the segmented bone structures.

to the dilatation. Based on material decomposition, we finally separate these two groups of voxels according to a new threshold T_6 . In this case, $\bar{H}_\alpha = +55$ (for SOFT tissue) and $\bar{H}_\beta$ should reflect as much as possible the contents of bone. To compute this value, the dilated bones are first eroded (actually, this is a closing operation) and the mean CT number $\bar{H}_\beta$ is then estimated within the resulting region. Using the computed threshold, voxels with CT number below T_6 are relabeled as SOFT tissue. The whole decomposition of the body is illustrated in Figure 5.9(c). In the provided example, $\bar{H}_\xi = +231$ (dilated bones), $\bar{H}_\beta = +362$ (closed bones) and $T_6 = +133$ were computed, corresponding to the volume fractions $b_1 = 0.43$ (SOFT) and $b_2 = 0.57$ (bones). Surface rendering of the segmented bones is shown in Figure 5.9(d).

The proposed algorithm for decomposing the body of the patient is described by the following steps:

```
// Algorithm IV - Body Decomposition
// -----
1. Construct histogram of BODY
2. Set threshold value T4 = 140
3. Relabel BODY voxels as BONES (H > T4)
4. Dilate BONES and create BONES_DILATED
5. Relabel BODY voxels as NON-BONES

// 1st Material Decomposition:
6. Decompose NON-BONES as FAT and SOFT tissue (compute T5)
7. Relabel NON-BONES voxels as FAT tissue (H < T5)
8. Relabel remaining NON-BONES voxels as SOFT tissue

// 2nd Material Decomposition:
9. Erode BONES_DILATED and create BONES_CLOSED
10. Compute mean CT number of BONES from BONES_CLOSED
11. Decompose BONES_DILATED as SOFT tissue and BONES (compute T6)
12. Relabel BONES_DILATED voxels as SOFT tissue (H < T6)
13. Relabel remaining BONES_DILATED voxels as BONES
```

5.5 Lung Field Segmentation

A 3D region or volume of interest that includes the lung parenchyma is usually required by most pulmonary image analysis applications. In this Section, a method for segmenting such region of interest is described. The proposed method consists of a sequence of algorithms (see Figure 5.2) that include, at first, the patient segmentation (Section 5.4.1) and the large airways identification algorithms (Section 5.4.2).

5.5.1 Lung Region of Interest Extraction

To identify the lung region of interest (lung ROI) a constrained dilatation is performed on the two segmented regions that actually contain AIR within the lungs: AIR within the large airways and AIR within the lung parenchyma. These AIR-filled regions are shown in Figure 5.10(a) and result from the large airways identification. The dilatation is performed as follow. First, the large airways are dilated: any voxel labeled as LUNG tissue within the 26-neighborhood of the connected large airways is included in such structure and relabeled accordingly. Next, the same rule is applied when considering the neighborhood of AIR voxels within the lungs. This sequential procedure is applied repeatedly until all LUNG tissue voxels have been relabeled as belonging to large airways or lung parenchyma (Figure 5.10(b) and (e)).

The constrained dilatation is then followed by a 2D connectivity analysis, performed in each slice of the CT image, to identify and eliminate small unwanted interior cavities inside the lung parenchyma (Figure 5.10(c) and (f)). These steps actually correspond to a 2D filling operation of the lung parenchyma (Figure 5.10(d) and (g)). The final output of the lung ROI extraction step is a 3D connected and filled region, displayed in Figure 5.11(a) as a binary mask for one slice of the image. Figure 5.11(b) shows the corresponding lung ROI extracted in the same slice of the original CT image, while the surface rendering of such structure is shown in Figure 5.11(c).

The steps that follow summarize the lung region of interest extraction algorithm:

```
// Algorithm V - Lung Field Segmentation
// -----
1. Find voxels borders of AIR and LARGE AIRWAYS
2. Dilate LARGE AIRWAYS and AIR, by "conquering" LUNG tissue
3. Compute statistics of LARGE AIRWAYS and lung PARENCHYMA
4. Connect BODY in 2D slices (2D SRG)
5. Fill PARENCHYMA (2D SRG)
6. Extract lung ROI
7. Compute statistics of ROI
```

The mean CT numbers of the segmented lung structures are finally updated. In this example, the following values were obtained: $\bar{H}_\xi = -862$, $\bar{H}_\xi = -850$ and $\bar{H}_\xi = -846$ within, respectively, the dilated large airways, lung parenchyma and the extracted lung ROI. Note that beside AIR surrounded by LUNG tissue, the lung ROI contains additional SOFT tissue, such as arteries and veins, due to the filling operation and therefore the mean density of this structure is slightly increased.

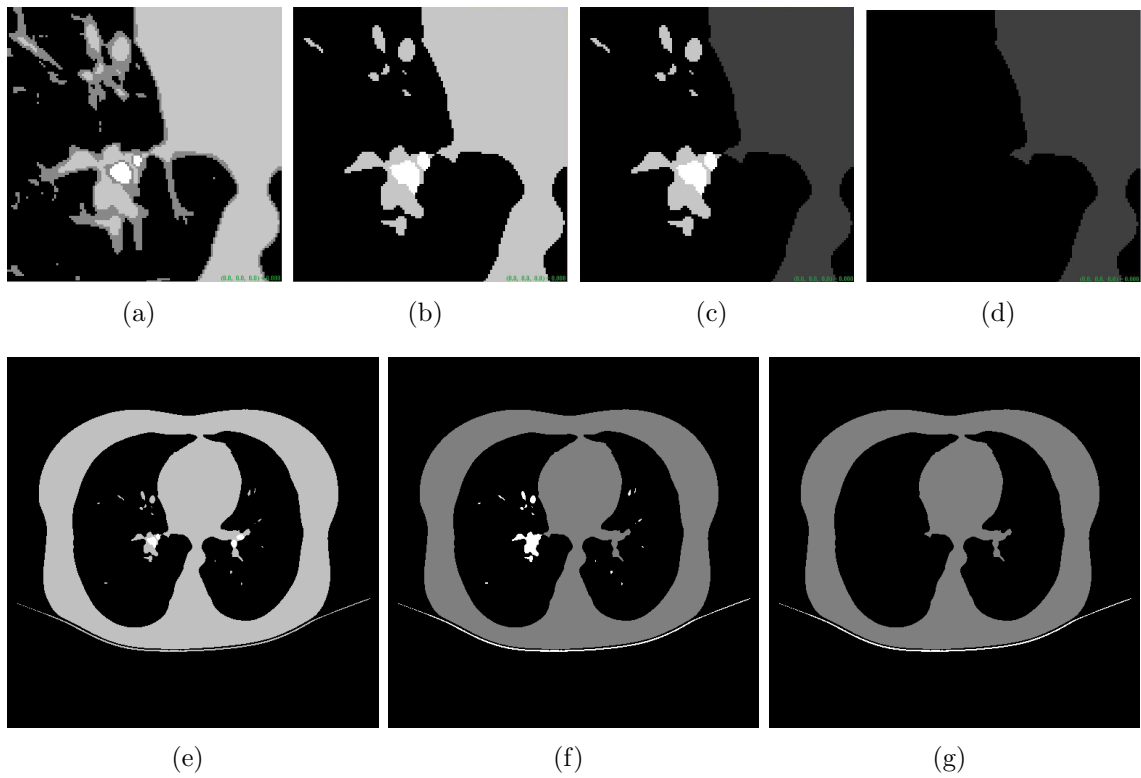


Figure 5.10: Lung region of interest extraction. (a) CT image labeling after the patient segmentation and large airways identification algorithms. (b) Results of dilating AIR voxels of large airways and lung parenchyma. A 2D connectivity analysis is performed to (c) identify and (d) eliminate small interior cavities within the lungs; (e) to (g) Same results as (b) to (d), respectively, shown for the entire slice.

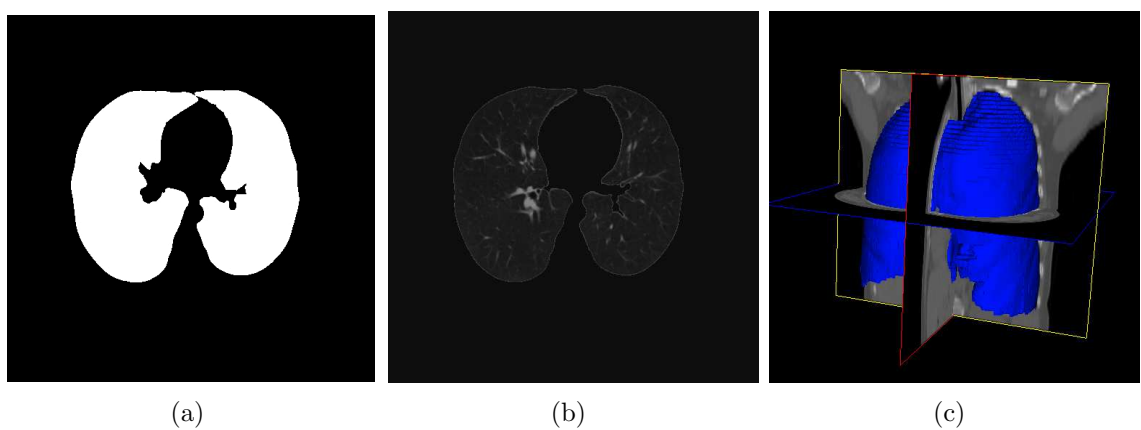


Figure 5.11: Lung region of interest extraction results. (a) Binary mask defining the extracted lung ROI in one slice; (b) Corresponding ROI in the original CT image (same slice); (c) Surface rendering of the lung ROI.

5.5.2 Right and Left Lung Separation

Since many lung diseases show specific regional distribution or preferences, the lung region of interest extraction includes an additional step to separate the left and the right lung. The anterior and posterior junction lines separating the lungs can be very thin. The attenuation of this interface may be reduced such that the corresponding CT numbers, along such junction lines, fall below the threshold T_1 . Remember from Section 5.4.1 that T_1 was automatically computed for segmenting the whole lungs within the patient.

The goal of the lung separation algorithm is to identify a 3D surface representing the boundary between the left and right lung. Therefore, an optimal 3D surface detection algorithm [45] is suggested for simultaneously delineating the anterior and posterior junction lines in each axial slice (OXY plane) of the joining region. Since the searched surface is expected to be approximately parallel to the sagittal (OYZ) plane, it assumes the form $x = f(y, z)$.

Let $\mathbf{H}(x, y, z)$ be a 3D CT image defined in its physical extents $\Delta X = x_{\max} - x_{\min}$, $\Delta Y = y_{\max} - y_{\min}$ and $\Delta Z = z_{\max} - z_{\min}$ in the coordinate system OXYZ. The optimal surface detection algorithm considers a 3D graph that represents the image $\mathbf{H}$ with the same size. The graph nodes, $\mathbf{p} = (x, y, z)^T$, correspond to CT image voxels and, to each node, a local cost $\mathbf{c}(x, y, z)$ is assigned. The construction of the optimal surface is based on optimal graph searching techniques and consists of selecting those voxels that linked together form the surface with the lowest cost. The total cost $\mathbf{c}_f$ associated with the surface $f(y, z)$ is calculated as the sum of individual costs of all nodes forming the surface,

$$\mathbf{c}_f = \sum_{y=y_{\min}}^{y_{\max}} \sum_{z=z_{\min}}^{z_{\max}} \mathbf{c}(f(y, z), y, z), \quad (5.12)$$

where $\mathbf{c}(f(y, z), y, z)$ is the local cost of the node located at (x, y, z) in the CT image, for which $x_{\min} \leq x \leq x_{\max}$, $y_{\min} \leq y \leq y_{\max}$ and $z_{\min} \leq z \leq z_{\max}$.

The legality of the surface is defined by 3D surface connectivity requirements that depend on the application at end. The connectivity constraint is introduced to guarantee surface continuity in 3D. In the following, the parameter d represents the maximum allowed change in the x coordinate of the surface along the unit distance (pixel spacings) dY and dZ in the Y and Z directions, respectively. If d is small, the legal surface is stiff and the stiffness decreases with larger values of d . For all nodes

of the surface, the connectivity constraint is expressed as follow:

$$\begin{aligned} |f(y, z) - f(y - dY, z)| &\leq d, \\ |f(y, z) - f(y, z - dZ)| &\leq d. \end{aligned} \quad (5.13)$$

The cumulative surface cost is defined as the sum of the local cost associated with the node (x, y, z) and the sum of the two cost minima identified in the two lines constructed in the 3D graph that represent the immediate predecessors:

$$\begin{aligned} \mathbf{C}(x, y, z) &= \mathbf{c}(x, y, z) \\ &+ \min_{\tilde{x} \in [x-d, x+d]} \{ \mathbf{C}(\tilde{x}, y - dY, z) \} \\ &+ \min_{\tilde{x} \in [x-d, x+d]} \{ \mathbf{C}(\tilde{x}, y, z + dZ) \}. \end{aligned} \quad (5.14)$$

The graph is searched starting from the line with coordinates $(x, y_{\min}, z_{\max})$ for which $\mathbf{C}(x, y_{\min}, z_{\max}) = \mathbf{c}(x, y_{\min}, z_{\max})$, in X-Z-Y coordinate order, towards the line $(x, y_{\max}, z_{\min})$. The optimal surface construction proceeds in the reversed X-Y-Z order and propagation of the connectivity constraint guarantees the legacy of the resulting surface. The x coordinate of the optimal surface-node in the line (y, z) , denoted by $f^*(y, z)$, is defined as

$$f^*(y, z) = x \quad : \quad \mathbf{C}(x, y, z) = \min_{\tilde{x} \in [x_1, x_2]} \{ \mathbf{C}(\tilde{x}, y, z) \}, \quad (5.15)$$

where

$$\begin{aligned} x_1 &= \min(x_{\max}, f^*(y + dY, z) + d, f^*(y, z - dZ) + d), \\ x_2 &= \max(x_{\min}, f^*(y + dY, z) - d, f^*(y, z - dZ) - d), \end{aligned} \quad (5.16)$$

and the backtracking process continues until the optimal node is found in the line $(x, y_{\min}, z_{\max})$.

To reduce the computational time of the graph-searching algorithm, the optimal 3D surface was detected only in a region that corresponds in size with the bounding box of the lung ROI, once segmented as explained in Section 5.5.1. The bounding box is automatically computed to define the points $(x_{\min}, y_{\min}, z_{\min})$ and $(x_{\max}, y_{\max}, z_{\max})$. Within this spatial region, the local cost of a node is the gray level or CT number of the corresponding voxel. If the voxel is labeled as belonging to the body, the local cost is set to zero.

The steps below summarize the optimal surface detection algorithm used for separating right and left lungs.

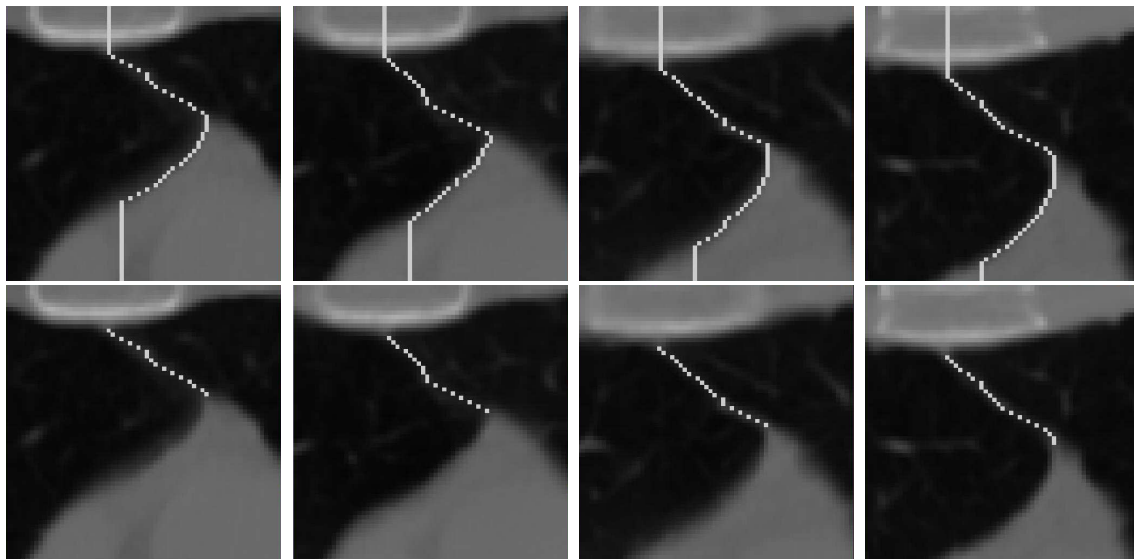


Figure 5.12: 3D optimal surface detection. First row: borders between the right and left lungs forming the optimal 3D surface are shown in four consecutive slices of a CT image; Second row: anterior line junction detected on the same slices.

```
// Algorithm VI - Lung Separation
// -----
// Optimal Surface Detection
1. Find bounding box of lung PARENCHYMA
2. Compute 3D COST image (GRAPH)
3. Compute CUMULATIVE COST from GRAPH
4. Construct OPTIMAL SURFACE from CUMULATIVE COST
5. Relabel OPTIMAL SURFACE voxels as JUNCTIONS
6. Relabel lung ROI as RIGHT lung and LEFT lung
```

Figure 5.12 (first row) illustrates the output of the optimal 3D surface detection algorithm. The results are shown in four consecutive slices where the lines forming the surface were superimposed. The connectivity constraint was applied by considering $d = \max(dX, dY, dZ)$, where dX , dY and dZ are the pixel spacings along the X, Y and Z directions, respectively. In the example, $d = dZ = 5$ mm, the slice thickness, and $dX = dY = 0.702$ mm. Consequently, the maximum allowed change in the x coordinate of the surface was approximately 7 pixels in axial planes. After the optimal surface has been constructed, voxels lying on this surface and previously labeled as body are identified as the junction lines, as shown in Figure 5.12 (second row). Figure 5.13(a) illustrates the corresponding image labeling of lung voxels as belonging to the right and left side of the patient. Figure 5.13(b) displays the resulting surface rendering while volume explosion of the lungs is shown in Figure 5.14.

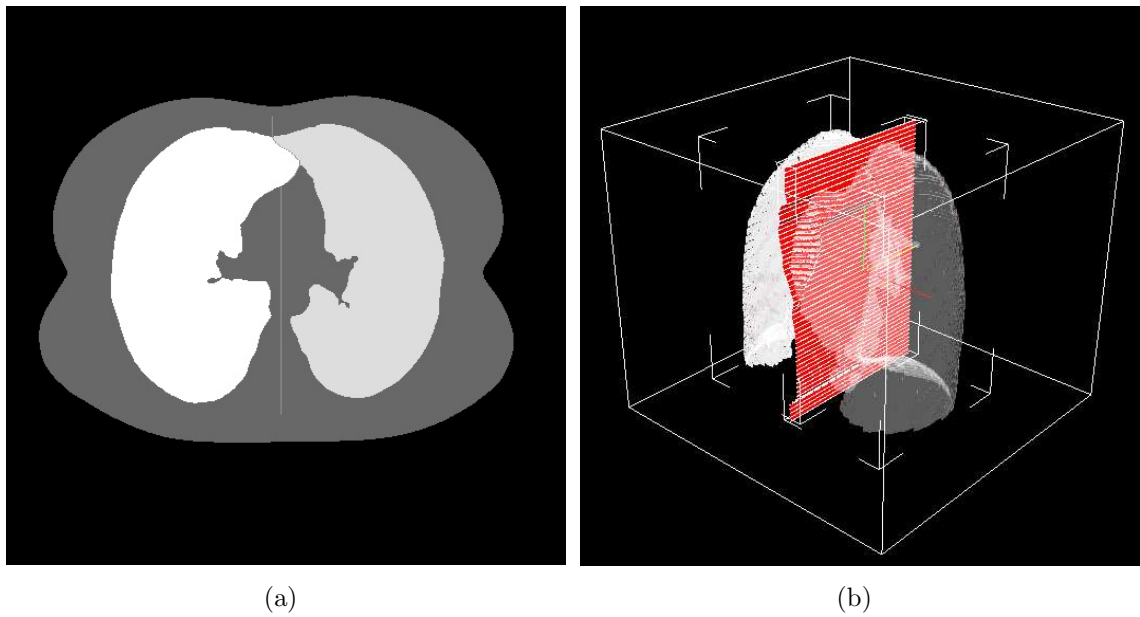


Figure 5.13: Right and left lung separation. (a) Segmented structures defining the lung ROI: right lung (white) and left lung (light gray). (b) The lungs are separated by the 3D optimal surface detection algorithm. The optimal surface (red) is searched within the bounding box of the ROI (the outline of the CT image is also shown).

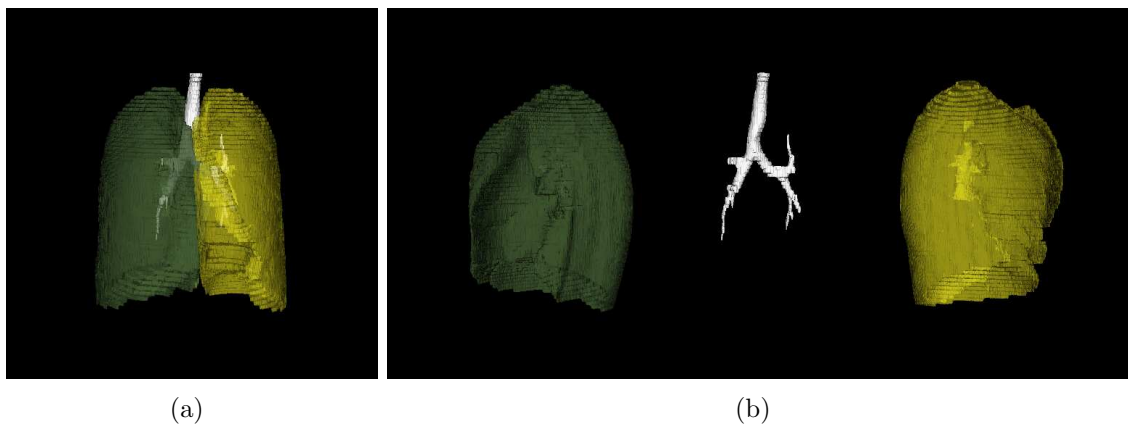


Figure 5.14: Lung field segmentation from CT images. (a) Surface rendering of segmented lung structures: large airways (white), right lung (green) and left lung (yellow); (b) Corresponding volume explosion.

5.6 Experimental Results

In this Section, experimental results of the 3D patient-specific phantom construction and the lung region of interest extraction are reported.

5.6.1 CT Image Database

The proposed segmentation algorithms were evaluated on a private image database that consists on 3D X-ray CT images acquired from 30 subjects using a *LightSpeed CT* scanner (GE Medical Systems; Milwaukee, WI) from the Radiology Department of the Hospital Pedro Hispano (HPH), in Matosinhos. Each volume in the database contains a stack of 45 to 74 contiguous axial slices. Each slice is a matrix of 512×512 square pixels, with a resolution (pixel spacing) ranging from 0.514 to 0.811 mm per pixel (mean value 0.702 mm). The slice thickness of 5 mm is the same for all the CT images in our database. The data sets are provided by the scanner in DICOM format and 16 bits per pixel are used to express CT numbers. It is assumed that the calibration of the scanner reflects the mean CT number of each material listed in Table 5.1, thus ignoring the small variation in tissue densities expected across the population of subjects that were included in the database.

The FOV corresponds to the reconstruction of the scanned patient in supine position. Although cross-sections of the patient thorax are not always completely inside the FOV, all thoracic 3D CT images include the entire lung region of interest to be segmented.

5.6.2 Computed Threshold Values

The threshold values automatically computed by the proposed segmentation method are reported in Table 5.2. Mean values and standard deviations (std) are listed in the same sequence they were computed for each image of the database. Each algorithm results in the segmentation of at least one particular structure previously defined in the anatomical model. The CT image itself and the patient are segmented with optimal thresholds, while material decomposition is used for the lungs and the body.

The thresholds T_0 and T_1 were computed for segmenting the patient from the image background (T_0) and for separating the lungs from the body within the patient (T_0 or T_1). The corresponding segmentation algorithms are provided in Section 5.4.1. Both algorithms were tested by using two different techniques for computing optimal threshold values and, for each input CT image to be segmented, equal values of T_0

Table 5.2: 3D patient-specific phantom construction. Computed threshold values for CT image decomposition. Mean values and standard deviations (std) were computed from the 30 images of the database (see also Table 5.3).

Segmented Structure		Computed Threshold			
Algorithm	ξ	Type	$\bar{T}$	mean	std
I	CT Image	optimal	$\bar{T}_0$	-468	13
II	Patient	optimal	$\bar{T}_1$	-399	28
III	Lungs	(decomposition)	$\bar{T}_2$	-886	25
		decomposition	$\bar{T}_3$	-772	26
IV	Body	fixed	$\bar{T}_4$	+140	
	Non-Bones	decomposition	$\bar{T}_5$	+6	10
	Dilated Bones	decomposition	$\bar{T}_6$	+128	8

Table 5.3: 3D patient-specific phantom construction. Material decomposition of structures segmented from 3D CT images. Mean values and standard deviations (std) were computed from the 30 images of the database (see also Table 5.2).

Decomposed			Material Decomposition				
Structure			Basis Materials		Volume Fractions		
ξ	$\bar{H}_\xi$	std	α	β	$\bar{b}_1$	$\bar{b}_2$	std
CT Image			Background	Patient	0.50	0.50	0.08
Patient	-216	39	Lungs	Body	0.28	0.72	0.05
Lungs	(Patient)		AIR	LUNG	0.26	0.74	0.04
	-829	33			0.84	0.16	0.03
Large Airways	-863	22					
Parenchyma	-828	33					
Lung ROI	-822	33					
Body	+23	25	Non-Bones	Dilated Bones	0.82	0.18	0.09
Non-Bones	-16	19	FAT	SOFT	0.48	0.52	0.13
Dilated Bones	+196	41	SOFT	Bones	0.46	0.54	0.07
Fat tissue	-93	7					
Soft tissue	+44	5					
Bones	+339	53					

and T_1 were obtained. Considering the 30 images, the mean values $\bar{T}_0 = -468$ and $\bar{T}_1 = -399$ were obtained. The threshold T_0 depends on the value of all voxels in the image, including those lying outside the FOV. The corresponding CT number of these voxels is dependent of the scanner used to acquire the data and usually equal to $H = -1024$ or $H = -3071$. Consequently, a pre-processing algorithm was included to correct properly this value to $\bar{H} = -999$, the CT number of AIR expected to be found in the entire background. T_1 should be used instead of T_0 for identifying the lungs since, by considering the patient region, T_1 only depends on the scanned volume of interest and provides a better estimate of the volume fractions of lungs and body within the segmented patient. The value of $\bar{T}_1 = -399$ (quite different from $\bar{T}_0$) is actually coherent with a study from Kemerink [138] that investigates the influence of the threshold and shows the value of -400 (HU) as adequate in most of the cases.

As described in Section 5.4.2, the segmentation of the large airways was achieved by computing the threshold T_2 (first material decomposition), while another value T_3 was used to decompose the lung parenchyma into materials AIR and LUNG tissue (second decomposition). Considering all images, $\bar{T}_2 = -886$ and $\bar{T}_3 = -772$, as reported in Table 5.2. These thresholds are patient-dependent (as $\bar{T}_0$ and $\bar{T}_1$) and reflect the variability of the large airways and lung parenchyma composition within the database. The first decomposition is optional since the segmentation of this structure is only needed for extracting the lung ROI. The 3D patient-specific phantom can be constructed by simply decomposing the lungs as AIR and LUNG tissue.

The final algorithm of the phantom construction consists on decomposing the body to identify non-bones from bone structures. To achieved this goal, the same fixed value $T_4 = +140$ was used for all images. Note that this threshold is only used for initializing the whole body decomposition process, since the mean CT number of bone structures is updated after the closing operation is performed, as explained in Section 5.4.3.

5.6.3 Phantom Composition

The 3D patient-specific phantom construction from a single CT image results in the sequential decomposition of the structures previously defined in the model. Applying the proposed algorithms to all the images in the database, the mean CT number $\bar{H}_\xi$ and therefore the expected composition, the volume fraction b , of each anatomical

structure can be computed. Mean values and standard deviation (std) are reported in Table 5.3. Note that the corresponding material decompositions are such that α (β) corresponds to a basis material with density lower (higher) than the decomposed structure ξ .

The first material decomposition corresponds to the segmentation of the CT image for separating the patient from the image background. This step was achieved by computing the optimal threshold T_0 (see Table 5.2). We note that the resulting mean volume fractions $\bar{b}_1$ and $\bar{b}_2$ are 50% for both structures. Although the values are the same, we believe there is no particular reason for that occurrence. In fact, the volume fraction b_2 (patient) observed in the database can be as high as 65% ($T_0 = -497$), while the minimum value found is $b_2 = 34\%$ ($T_0 = -468$).

The next algorithm (algorithm II) was performed on the segmented patient to decompose it as non-overlapping regions, namely the lungs and the body. The results reported were obtained by using T_1 as the segmentation threshold. As expected, the lungs are characterized by a lower density $\bar{H}_\alpha = -829 \pm 33$ than voxels labeled as body inside the patient, $\bar{H}_\beta = +23 \pm 25$. From the experiments, one can conclude that, since the lungs are 0.28% of the scanned volume (patient), they only account for 0.14% of the entire volumetric CT image, including voxels outside the FOV of the scanner. Actually, this is a surprising result since most applications focus on the analysis of this particular structure.

We assumed that the lungs are composed of AIR and LUNG tissue. As described in Section 5.4.2, the large airways were identified as *pure* air voxels within of the whole lung region. About 28% of lung voxels are candidates for being part of the large airways. The *true* lung decomposition is achieved when using its mean CT number. In this case, mean values of 84% of AIR and 16% of LUNG tissue were obtained in the database. Of all the computed volume fractions, these values represent the contents that show the lowest variation. The lung parenchyma was defined as the lungs without the large airways and its CT number should increase. The same is expected to happen when segmenting the lung region of interest since pulmonary veins and arteries have been included due to the filling operation (see Section 5.5.1).

Material decomposition allows to predict the contents of FAT tissue, SOFT tissue and bone structures within the segmented body of a patient. First, non-bones are identified and further decomposed, resulting into FAT and SOFT volume fractions of 48% and 52%, respectively. Table 5.3 shows that the variation of these contents is the highest value. We believe this is a consequence of the variability of the amount of FAT tissue among all the patients in the population. In fact, decompositions



Figure 5.15: 3D patient-specific phantom construction. Surface rendering of segmented structures labeled as bones, for 3 different CT images of the database.

resulting in 22% and 78% (FAT/SOFT) and 77% and 23% were observed.

The final decomposition is performed on the highest attenuation voxels in the entire CT image. The body include the *dilated bones*, expected to contain only SOFT and bone structures such as the skeleton of the patient, as show in Figure 5.15. Note that the corresponding mean CT number, $\bar{H}_\xi = +339 \pm 53$, shows the largest standard deviation when computed from the database. This is quite acceptable since these are high density structures that include CT numbers up to +3071.

Basis Plane Representation

As discussed in Section 2.7.2, all the segmented structures ξ that compose a given CT image can be conveniently represented in the basis plane. The volume fractions b_1 and b_2 of the corresponding intervening materials α and β define the structure ξ in the plane by the vector (b_1, b_2) . From Eq. 5.10, the characteristic angle is then computed as $\theta_\xi = \tan^{-1}(b_2/b_1)$, under the condition $b_1 + b_2 = 1$. Considering the volume fractions listed in Table 5.3, θ_ξ can be computed for each decomposition. The following values were obtained: $\theta_0 = 45.0^\circ$ (CT image), $\theta_1 = 68.7^\circ$ (patient), $\theta_3 = 10.8^\circ$ (lungs), $\theta_4 = 12.4^\circ$ (body), $\theta_5 = 47.3^\circ$ (non-bones) and $\theta_6 = 49.6^\circ$ (dilated bones). Note that θ_i corresponds to the characteristic angle of the structure decomposed by using the segmentation threshold T_i , reported in Table 5.2. Figure 5.16 shows the resulting basis plane representation of CT image decomposition. Similar representation could be drawn for a single CT image. Each intervening materials is separated geometrically and, since all the segmented anatomical structures are non-overlapping regions, the overall vector sum is the volumetric CT image itself.

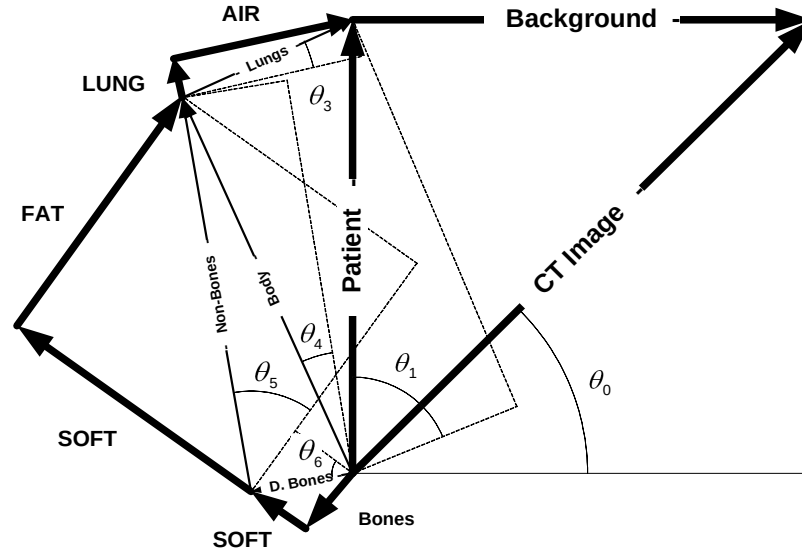


Figure 5.16: Basis plane representation of CT image decomposition. Each structure in the anatomical model is defined as a vector in the plane, whose components correspond to the contents (fraction by volume) of the intervening materials of that structure. The characteristic angles are: $\theta_0 = 45.0^\circ$ (CT image), $\theta_1 = 68.7^\circ$ (patient), $\theta_3 = 10.8^\circ$ (lungs), $\theta_4 = 12.4^\circ$ (body), $\theta_5 = 47.3^\circ$ (non-bones) and $\theta_6 = 49.6^\circ$ (dilated bones). Note that SOFT tissue is identified by decomposing both non-bones and dilated bones. (see also Table 5.3).

5.7 Validation

5.7.1 Large Airways

Surface rendering of the large airways segmented from all images of the database can be visualized in Appendix C. These segmentation outputs were qualitatively evaluated by an experienced radiologist. By visual inspection, the best and worst results were selected to judge for the performance of this particular extraction algorithm. The selected outputs are presented in Figure 5.17. In all cases, the trachea and main stem bronchi have been correctly identified by the computer.

5.7.2 Lung Region of Interest

Some results of the lung field segmentation algorithm are given in Figure 5.18. The performance of the method was assessed by comparing the automatic computer-based segmentation with results obtained by manual analysis. For this purpose, two image data sets, set 1 and set 2, were taken from the database. The pixel spacing (resolution) in each slice of both datasets is $dX = dY = 0.702$ mm, actually the

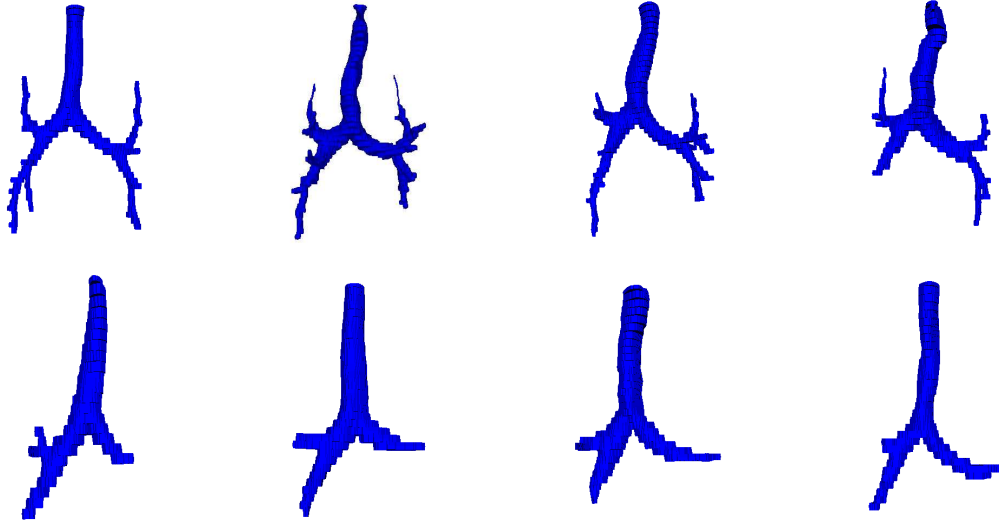


Figure 5.17: Large airways segmentation results (surface rendering). The results, qualitatively evaluated by an experienced radiologist, are shown for the best (first row) and worst (last row) 4 of 30 CT images of a private database (HPH) (see also Appendix C).



Figure 5.18: Lung field segmentation results shown for 3 different images of the database: surface rendering of the large airways (white), right lung (green) and left lung (yellow).

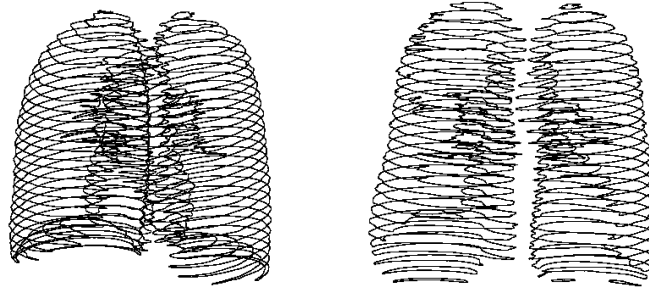


Figure 5.19: Manual contouring of the lung region of interest (ROI). The lung ROI manually delineated by an experienced radiologist (human A) in two images of the database: set 1 (left) and set 2 (right). In each case, the results of manual contouring are shown for even numbered slices only.

mean value across the image database. This represents the unique criterion used for choosing these images. Although the number of slices in the volumes is different (64 for set 1 and 57 for set 2), quantitative comparison of the corresponding segmentation outputs is independent of the image resolution. One experienced radiologist A and two image analysts B and C manually traced the lung borders on every slice of the two chosen sets. The operators worked independently of each other using the same software system specifically developed to perform manual analysis. Overall, each human operator traced lung borders on 121 slices. In each slice, more than one contour could be delineated for each lung and manual contours were then stored for later evaluation. The manual delineation of the lung ROI performed by A on the two images is shown in Figure 5.19. For display purposes, only contours of even numbered slices are shown.

We evaluated the performance of the method by using the same similarity measures as for the case of chest radiographs, namely accuracy, degree of overlap and F -score (see Section 4.5.3). The degree of overlap corresponds to the true positive volume fraction, as given by Eq. 3.33. Results of comparing the proposed method with manual analysis are reported in Table 5.4. When computing the accuracy, sensitivity and specificity, the segmentation performed by the observers is considered as the ground truth, while equal importance of recall and precision is assumed for calculating the F -measure.

Although the variability that occurs when comparing the automated segmentation with human delineations is very small, the results serve to lower the measures at which the proposed computerized scheme may be expected to perform. From

Table 5.4: Lung field segmentation from CT images. Performance measures of the lung ROI extraction algorithm computed for two CT images of a private database (HPH). The segmentation output of the computer-based method is compared with the manual contours performed by three different humans (A, B and C) on every slice of both images. See Table 5.5 for inter-human variability.

Measure	CT Image 1			CT Image 2		
	A	B	C	A	B	C
accuracy	0.997	0.997	0.997	0.994	0.995	0.995
sensitivity	0.988	0.985	0.986	0.985	0.981	0.980
specificity	0.998	0.999	0.999	0.996	0.997	0.997
overlap	0.975	0.978	0.977	0.961	0.963	0.964
precision	0.986	0.993	0.991	0.975	0.982	0.984
recall	0.988	0.985	0.986	0.985	0.981	0.980
F-score	0.987	0.989	0.989	0.980	0.981	0.982

Table 5.5: Lung field segmentation from CT images. Analysis of inter-observer variability. Performance measures were computed by comparing manual segmentation of the lung ROI delineated on two CT images of a private database (HPH). Manual contouring was performed by three different human operators (A, B and C) on every slice of the 3D images. See Table 5.4 for comparing with the performance measures of the proposed computer-based segmentation method.

Measure	CT Image 1			CT Image 2		
	A/B	A/C	B/C	A/B	A/C	B/C
accuracy	0.997	0.996	0.997	0.995	0.995	0.996
sensitivity	0.991	0.989	0.987	0.990	0.989	0.987
specificity	0.997	0.997	0.999	0.996	0.996	0.998
overlap	0.973	0.972	0.978	0.969	0.964	0.973
precision	0.981	0.983	0.991	0.978	0.975	0.986
recall	0.991	0.989	0.987	0.990	0.989	0.987
F-score	0.986	0.986	0.989	0.984	0.982	0.987

Table 5.4, and considering the overlap as the reference measure, 96.1% of voxels identified by the radiologist have been correctly labeled by the computer as belonging to the lung region of interest. This is the worst case when evaluating the method with set 2. We also evaluated the variability that occurs between the manual segmentation performed by the three observers. Results of such analysis are reported in Table 5.5. When computing the accuracy, sensitivity and specificity, the segmentation performed by the radiologist (observer A) is considered as the ground truth (when comparing B and C, B is the gold standard).

5.7.3 Lung Separation

To evaluate the optimal surface detection algorithm, junction lines positioning accuracy was assessed by computing a distance-based metric. For each voxel $\mathbf{p}_n^* = (x, y, z)^T$ that belongs to one of the detected junction lines, as shown in Figure 5.12 (first row), the closest points $\mathbf{p}_n^{(r)}$ and $\mathbf{p}_n^{(l)}$ are identified on the contours manually delineated for the left and the right lung, respectively. By computing the distance $d(\mathbf{p}_n^*)$ between the node $\mathbf{p}_n^*$ and the midpoint lying between $\mathbf{p}_n^{(r)}$ and $\mathbf{p}_n^{(l)}$, we defined the positioning accuracy as the mean distance $\bar{d} = \sum_{n=0}^{N-1} d(\mathbf{p}_n^*) / N$, where N is the total number of voxels on the computer-defined junction lines. The optimal surface detection accuracy was computed by considering the contours delineated by the human operators A, B and C. The mean values and standard deviations, expressed in percent of the pixel spacing dX are, respectively, $\bar{d}_A = 0.71 \pm 0.57$, $\bar{d}_B = 0.62 \pm 0.51$ and $\bar{d}_C = 0.92 \pm 0.70$. In all cases, $\bar{d}$ is less than $dX = 0.702$ mm, the image resolution in the axial plane. The accuracy was only computed for set 1, since no junction lines were detected in set 2.

5.8 Conclusions

In this Chapter, a fully automated method for segmenting volumetric CT images was described. The proposed method is based on a simple description of the thoracic anatomy and contains knowledge specific to the CT modality. We have applied the method on 30 CT images of a private image database. Providing a reproducible set of threshold values, the decomposition of a given CT image results in the identification of several structures of the human thorax, namely the central tracheo-bronchial and lung parenchyma, fat and soft tissues within the body and bone structures such as the skeleton of the patient. Each segmented structures have been specified in terms

of its mean CT number and volume fraction within the image.

Using dual-energy principles applied to CT numbers, the concept of basis material decomposition was explored to provide the means for constructing 3D patient-specific voxel-based phantoms from CT scans. Anthropomorphic phantoms have several applications in the radiologic sciences. In the field of diagnostic imaging, such segmented data can be used to create realistic digital reconstructed radiographs which closely resemble clinical data. They also prove especially interesting in testing and improving tomographic reconstruction algorithms.

In CAD systems, the lungs are the structure of interest for most diagnostic purposes in thoracic CT imaging. Because of the large amount of data acquired during in a single CT scan, it is critical to develop an efficient method that does not require human interaction for accurately delineate such organs. Several algorithms were included in the segmentation framework to extract the lung region of interest, and segmentation outputs were compared with manual analysis. Because it is fully automated it can be applied to a CT data set prior to clinical review, and the computation time is acceptable for most of pulmonary applications. With the additional step of lung separation, the method can also provide functional information about the individual right and left lung.

Chapter 6

3D SHAPE RECONSTRUCTION FROM SINGLE RADIOGRAPHS

In this Chapter, we describe a strategy to solve the problem of recovering the 3D shape of anatomical structures from single planar radiographs. The proposed approach is based on the simulation of X-ray images and addresses the problem of registering CT images to planar radiographs by directly exploiting the relationship between the two imaging modalities.

6.1 Introduction

Registration of medical data from different imaging devices has proven to be an important tool in the field of computer-aided surgery and image-guided therapy [146, 147]. A crucial module of many 2D-3D registration algorithms is the generation of simulated X-ray images or Digitally Reconstructed Radiographs (DRRs), often compared to radiographs or portal images. Since registration is usually an iterative process, fast generation of DRRs is desired. To compute such virtual images, DRR volume rendering, also called simulated X-ray volume rendering, has been used as a direct volume rendering technique that consists of simulating X-rays passing through the reconstructed CT volume thus generating an X-ray like image. During the last two decades, lots of volume rendering techniques were proposed. However, rendering of large medical datasets is still a challenge due to the fast development of scanning techniques. For an $N \times N \times N$ volume, most volume rendering techniques, such as ray casting [148] or splatting [149, 150], have $O(N^3)$ time complexity, which makes these algorithms not efficient for large datasets. Siddon's method [151] is essentially a ray-casting technique that takes the points of intersection between the ray and planes as sample points instead of intersection between the ray and voxels. Although it improves the speed of sampling, its computation complexity is still

$O(N^3)$. A recent DRR generation technique is the adaptive Monte Carlo Volume Rendering [152]. In this method the entire volume domain is adaptively divided into sub-domains using importance separation and then sampling is performed in these sub-domains. It is based on the conventional Monte Carlo volume rendering [153, 154] that is very efficient for large medical datasets since the involved projection process is independent of the size of the datasets.

Computer simulations of medical imaging systems that make use of the Monte Carlo algorithm are also particularly useful and efficient experimentation tools in the study of image quality parameters in diagnostic radiology. In this context, the Monte Carlo method has been extensively used to study contrast, noise, absorbed dose and grid performance [155]. Monte Carlo simulations have been performed to yield diagnostically realistic images of internal distribution of radiopharmaceuticals [156]. Since we are able to model a known source distribution and known attenuation distribution, dose calculations for internal and external radiation sources using anthropomorphic phantoms can give new insights in the field of health physics and therapy. Overviews of the Monte Carlo method and its applications in different fields of radiation physics are found in [157, 158]. A useful review of Monte Carlo techniques in medical radiation physics, including diagnostic radiology, radiotherapy and radiation protection can be found in [159] and methodologies applied to nuclear medicine problems are outlined in [160].

In X-ray projective imaging, an important source of 3D information is available: the selective absorption of X-ray photons by the different tissues being imaged. Such source of information is used in CT for the reconstruction of a density image from a complete set of projections. Unfortunately, when the number of projections available is small, image reconstruction becomes an extremely ill-posed problem. Here, we address the most interesting possibility of recovering the 3D shape of anatomical structures of interest starting from a single conventional radiograph.

The shape reconstruction strategy hereafter proposed considers as input a digital 2D PA chest radiograph, from which several thoracic structures are to be recovered. Based on a geometrical representation of the imaging system, the computation of DRRs from previously segmented volumetric CT images are used for registering X-ray CT data with the planar radiograph. The registration is achieved through the delineation of the lung fields in the real and simulated images. We assume that a segmentation method is available to delineate such regions, providing a point-to-point correspondence between the resulting contours.

The proposed approach involves several steps. First, 3D patient-specific phan-

toms constructed from CT images are used for computing DRRs. The construction of the phantoms is described in Chapter 5. We are currently developing a X-ray simulation tool based on the Monte Carlo algorithm to provide the necessary simulated images. Although no experimental results will be reported herein, the formal description of the adopted models for performing these simulations is given in the next Section, providing the necessary information to understand the details of the algorithm. Next, *radiological density* images are computed, from which we estimate the thickness of each structure we intend to recover from the original image. Instead of using Monte Carlo simulations, volume rendering based on ray casting techniques was implemented to achieve this task. Finally, a proper linearization algorithm of the original radiograph is described and the 3D shape recovery algorithm is illustrated for a simple case.

6.2 Digitally Reconstructed Radiographs

In this Section, the general characteristics of the Monte Carlo simulation of photon transport are briefly presented. For the sake of simplicity, the discussion is limited to the conventional method where all the interaction events experienced by a photon are simulated in chronological succession.

6.2.1 Monte Carlo Simulations

The Monte Carlo simulation of radiation transport is a stochastic method based on the random sampling of variables from a probability distribution. It is used to follow a large number of photon histories in order to determine the spatial, directional and spectral distribution of the radiation. The history or track of a particle is viewed as a random sequence of free flights that end with an interaction event where the particle changes its direction of movement and loses energy. To simulate these histories an interaction model of the relevant interaction mechanisms is used to determine the probability distribution functions (PDF) of the random variables that characterize a track: 1) free path between successive interaction events, 2) type of interaction taking place and 3) energy loss and angular deflection in a particular event. Once these PDFs are known, random histories can be generated by using appropriate sampling methods. If the number of generated histories is large enough, quantitative information on the transport process may be obtained by simply averaging over the simulated histories. The simulation of a single photon history requires the following

steps described next.

```
// Algorithm - Monte Carlo Photon Transport Simulation
// -----
1. Sampling for source photon energy
2. Sampling for emission direction (laboratory frame)
3. Sampling for path length
4. Calculation of position using direction and path length
5. Sampling for interaction process
6. Sampling for new photon energy
7. Calculation of polar angle (scattering)
8. Sampling for azimuthal angle (scattering)
9. Calculation of the new photon direction (laboratory frame)
10. Loop back to step 3.
```

Source Photon Energy and Emission Direction

Each particle track starts off at a given position, with initial direction and energy in accordance with the characteristics of the source. In radiation-transport theory, the direction of motion of a particle is usually described by a unit vector $\mathbf{e}$. Given a reference coordinate system OXYZ, the direction $\mathbf{e}$ can be specified by giving either its direction cosines (e_x, e_y, e_z) , i.e. the projections of $\mathbf{e}$ on the directions of the coordinate axes, or the polar angle θ and the azimuthal angle ϕ , defined as illustrated in Figure 6.1(a),

$$\mathbf{e} = (e_x, e_y, e_z)^T = (\sin \theta \cos \phi, \sin \theta \sin \phi, \cos \theta)^T. \quad (6.1)$$

If the emission is simulated for the isotropic case, the direction vector can be regarded as a point on the surface of the unit sphere and the polar and azimuthal angles are uniformly sampled such that $0 \leq \theta \leq \pi$ and $0 \leq \phi \leq 2\pi$.

For generating a photon beam, we are currently simulating the anode X-ray tube with the Tungsten anode X-ray spectrum of Figure 2.8. Figure 6.1(b) shows the sampled source spectrum using the rejection method [160] and, by using a point source geometry, the spatial distribution of the imparted energy at the detector plane is shown in Figure 6.1(c), for which a source-to-detector distance of $d = 1800\text{mm}$ and a typical value of the anode angle $\theta_{\max} = \pi/15$ ($\sim 10^\circ$) were considered. For each emitted photon, the polar and azimuthal angles of the emission direction were randomly sampled as $\theta = \pi - u\theta_{\max}$ and $\phi = 2\pi u$. Hereafter, u stands for a random number uniformly distributed in the interval $[0, 1]$.

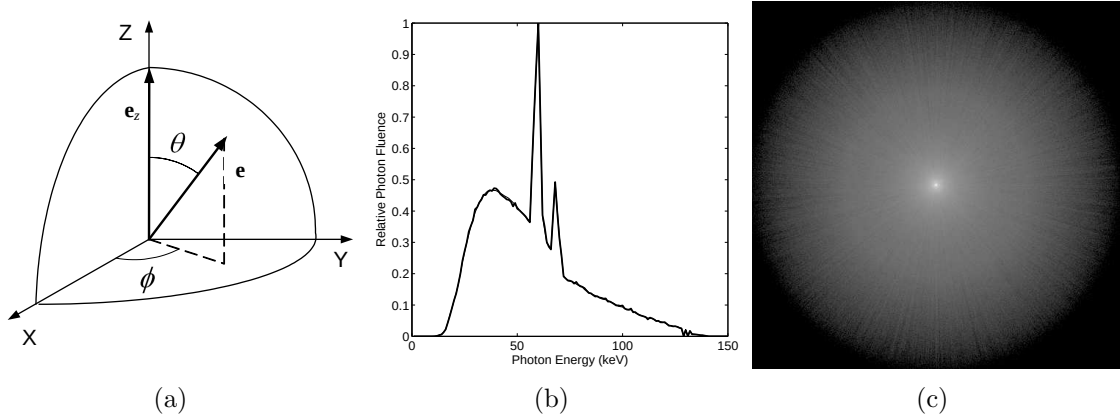


Figure 6.1: (a) Polar and azimuthal angles, θ and ϕ , of a direction vector $\mathbf{e}$. (b) Source sampling of the simulated Tungsten anode X-ray spectrum of Figure 2.8, using the rejection method (spectral distribution of 0.18×10^6 photons accepted from 10^6 sampled photons); (c) Energy imparted on the detector plane (source-to-detector distance $d = 1800$ mm, anode angle $\theta_{max} = \pi/15$).

Selection of Photon Interaction

The probability for a certain type of interaction to occur is given by the partial attenuation coefficients as given by Eq. 2.10,

$$\mu(E) = \mu_{photo} + \mu_{incoh} + \mu_{coh}, \quad (6.2)$$

where only the principal attenuation mechanisms in the diagnostic energy range are considered: partial contribution for photoelectric effect (μ_{photo}), incoherent or Compton interaction (μ_{incoh}) and coherent or Rayleigh interaction (μ_{coh}). We are actually using the photon cross-section libraries and parameterizations published by NIST [161], already discussed in Section 2.4.2. These are also implemented in simulation packages such as GEANT [162] and PETSIM [163].

During the simulation of a single photon, a uniform random number u is sampled to select a particular interaction type. If the condition $u < \mu_{photo}/\mu$ is true, then a photoelectric interaction has occurred, otherwise the same value of u is used to test whether $u < (\mu_{photo} + \mu_{incoh})/\mu$. If this is true, then one continues with a Compton interaction. If not, a coherent interaction has taken place. In the case of photoelectric absorption, the photon is discarded while scattered photons proceed to the next step.

The energy of an incoherent scattered photon, E' , depends upon the initial photon energy E and the scattering angle θ (relative to the incident path), according to the

Compton Angle-Wavelength relation described by Eq. 2.2:

$$E' = \frac{E}{1 + \gamma(1 - \cos \theta)}, \quad (6.3)$$

where $\gamma = E/m_0c^2$ is the reduced energy. One very commonly used method to sample the energy and direction of Compton scattered photon is the algorithm developed by Kahn [164]. Kahn's sampling method is based on a mixed method and given by the following set of statements [157, 160]:

```
// Algorithm - Kahn's Sampling Method
// -----
// function t = kahn(gama,test)
gama = E/(m0*c*c)
test = (2*gama + 1) / (2*gama + 9)
r = 2*u1
if ( u2 < test ) {
    UU = 1 + gama*r
    if ( u3 > 4*(UU - 1)/(UU*UU) )
        t = kahn(gama,test)
    t = 1 - r
}
else {
    UU = (2*gama + 1)/(gama*r + 1)
    t = 1 - (UU - 1)/gama
    if ( u4 > (0.5*t*t + 1/UU) )
        t = kahn(gama,test)
}
```

Photon Path Length

Once the interaction type has been selected, the polar scattering angle θ and the energy loss W are sampled and the azimuthal scattering angle is generated according to the uniform distribution in $[0, 2\pi]$, as $\phi = 2\pi u$. The state of a particle immediately after an interaction (or after entering the sample or starting its trajectory) is defined by its position coordinates $\mathbf{p} = (x, y, z)^T$, energy E and direction cosines of the direction of flight, i.e., the components of the unit vector $\mathbf{e} = (e_x, e_y, e_z)^T$, as seen from the laboratory frame OXYZ. Each simulated track is thus characterized by a series of states $\mathbf{p}^{(t)}$, $E^{(t)}$, $\mathbf{e}^{(t)}$, where $\mathbf{p}^{(t)}$ is the position of the scattering event at time t , and $E^{(t)}$ and $\mathbf{e}^{(t)}$ are the energy and direction cosines of the direction of movement just after that event.

Let us assume that a track has already been simulated up to a state $\mathbf{p}^{(t)}$, $E^{(t)}$, $\mathbf{e}^{(t)}$. The length λ of the photon path to the next collision is then calculated to

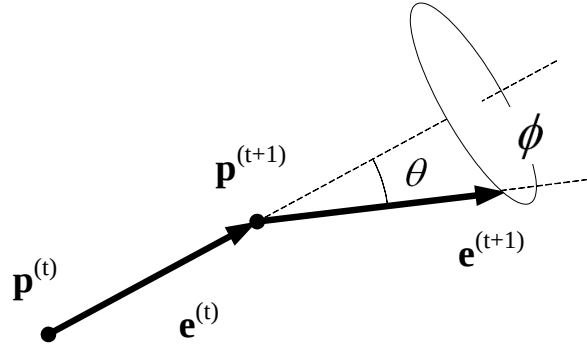


Figure 6.2: Angular deflections in single-scattering events.

determine the next point of interaction in the material. This distance depends upon the photon energy E , the material density ρ and linear attenuation coefficient $\mu(E)$ (see Section 2.4). If the probability function of the photon path length x is $p'(x) = \mu \exp(-\mu x)$ then the probability that a photon will travel a distance λ or less is given by the cumulative distribution function constructed from the integral of $p'(x)$ over the interval $[0, \lambda]$:

$$p(\lambda) = \int_0^{\lambda} p'(x) dx = 1 - \exp(-\mu\lambda). \quad (6.4)$$

To sample the path length a uniform random number u is substituted for $p(\lambda)$ and Eq. 6.4 is solved for λ :

$$\lambda = -\frac{1}{\mu} \ln(1 - u) = -\frac{1}{\mu} \ln u. \quad (6.5)$$

Since $1 - u$ is also a random number with the same distribution as u , the calculation is simplified according to Eq. 6.5.

Coordinate Calculations

If the photon is at position $\mathbf{p}^{(t)}$ in the material, the coordinates $\mathbf{p}^{(t+1)}$ of the next point of interaction are computed by geometrical considerations from the photon path length λ and direction cosines $\mathbf{e}^{(t)}$, according to

$$\mathbf{p}^{(t+1)} = \mathbf{p}^{(t)} + \lambda \mathbf{e}^{(t)}, \quad (6.6)$$

where λ is the distance between the previous point $\mathbf{p}^{(t)}$ and the new position $\mathbf{p}^{(t+1)}$. The energy of the particle is reduced, $E' = E - W$, and the direction of movement after the interaction, $\mathbf{e}^{(t+1)} = (e'_x, e'_y, e'_z)^T$ is obtained by performing a rotation of $\mathbf{e}^{(t)} = (e_x, e_y, e_z)^T$ (see Figure 6.2). The rotation matrix $\mathcal{R}(\theta, \phi)$ is determined by the polar and azimuthal scattering angles. To explicitly obtain the direction vector $\mathbf{e}^{(t+1)} = \mathcal{R}(\theta, \phi) \mathbf{e}^{(t)}$ after the interaction, we first note that, if the initial direction is along the Z axis, $\mathbf{e}^{(t)} = \mathbf{e}_z = (0, 0, 1)^T$, the direction after the collision is

$$\begin{pmatrix} \sin \theta \cos \phi \\ \sin \theta \sin \phi \\ \cos \theta \end{pmatrix} = \mathcal{R}_Z(\phi) \mathcal{R}_Y(\theta) \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix}, \quad (6.7)$$

where

$$\mathcal{R}_Y(\theta) = \begin{pmatrix} \cos \theta & 0 & \sin \theta \\ 0 & 1 & 0 \\ -\sin \theta & 0 & \cos \theta \end{pmatrix}, \quad \mathcal{R}_Z(\phi) = \begin{pmatrix} \cos \phi & -\sin \phi & 0 \\ \sin \phi & \cos \phi & 0 \\ 0 & 0 & 1 \end{pmatrix}, \quad (6.8)$$

are rotation matrices corresponding to active rotations of angles θ and ϕ about the Y and Z axes, respectively. On the other hand, if Θ and Φ are the polar and azimuthal angles of the initial direction

$$\mathbf{e}^{(t)} = (\sin \Theta \cos \Phi, \sin \Theta \sin \Phi, \cos \Theta)^T, \quad (6.9)$$

the rotation $\mathcal{R}_Y(-\Theta) \mathcal{R}_Z(-\Phi)$ transforms the vector $\mathbf{e}^{(t)}$ into $\mathbf{e}_z$. It is then clear that the final direction vector $\mathbf{e}^{(t+1)}$ can be obtained by performing the following sequence of rotations of the initial direction vector: 1) $\mathcal{R}_Y(-\Theta) \mathcal{R}_Z(-\Phi)$, which transforms $\mathbf{e}^{(t)}$ into $\mathbf{e}_z$; 2) $\mathcal{R}_Z(\phi) \mathcal{R}_Y(\theta)$, which rotates $\mathbf{e}_z$ according to the sampled polar and azimuthal scattering angles; and 3) $\mathcal{R}_Z(\Phi) \mathcal{R}_Y(\Theta)$, which inverts the rotation of the first step. Hence

$$\mathcal{R}(\theta, \phi) = \mathcal{R}_Z(\Phi) \mathcal{R}_Y(\Theta) \mathcal{R}_Z(\phi) \mathcal{R}_Y(\theta) \mathcal{R}_Y(-\Theta) \mathcal{R}_Z(-\Phi). \quad (6.10)$$

The final direction vector is

$$\mathbf{e}^{(t+1)} = \mathcal{R}(\theta, \phi) \mathbf{e}^{(t)} = \mathcal{R}_Z(\Phi) \mathcal{R}_Y(\Theta) \begin{pmatrix} \sin \theta \cos \phi \\ \sin \theta \sin \phi \\ \cos \theta \end{pmatrix}, \quad (6.11)$$

and its direction cosines are

$$\begin{aligned} e'_x &= e_x \cos \theta + \sin \theta (e_z \cos \phi \cos \Phi - \sin \phi \sin \Phi), \\ e'_y &= e_y \cos \theta + \sin \theta (e_z \cos \phi \sin \Phi + \sin \phi \cos \Phi), \\ e'_z &= e_z \cos \theta - \sin \theta (\sin \Theta \cos \phi). \end{aligned} \quad (6.12)$$

The simulation of the track then proceeds by repeating these steps. A track is finished either when the photon hits the detector, leaves the material system or when its energy becomes smaller than a given energy, which is the energy where particles are assumed to be effectively stopped and absorbed in the medium.

In order to reduce the statistical noise to an acceptable level, the number of photon histories must usually be large, hence leading to a heavy computational load, still not acceptable in our applied research. The necessity to have a practical simulation tool at disposal lead to the development of an alternative solution based on ray tracing techniques we describe next.

6.2.2 Ray Casting Techniques

Volume rendering is typically used to generate images that represent an entire 3D image dataset in a 2D image. Image-order volume rendering [165], often referred to as ray casting or ray tracing, is a flexible technique that can be used to render any volumetric 3D image dataset and can produce a variety of images. The basic idea is to determine the value of each pixel in the image by sending a ray through the pixel into the volume according to the geometry parameters of the imaging system. The data encountered along the ray is evaluated by using some specified function in order to compute the pixel value.

Using a parallel beam geometry in which all rays are parallel to each other and perpendicular to the image plane, the Maximum Intensity Projection (MIP) is probably the simplest way to visualize volumetric data. This case is the standard orthographic projection where the ray function determines the maximum value along the ray producing an image that provides an intuitive understanding of the underlying data. Examples are shown in Figure 6.3 where the projections were obtained from a thoracic CT image from which the patient has been previously segmented as described in Section 5.4.1. One problem with the MIP is that it is not possible to tell where the maximum value occurred along the ray.

We now consider ray casting applied to more realistic imaging systems, as illustrated in Figure 6.4, corresponding to the point source geometry. The simulated

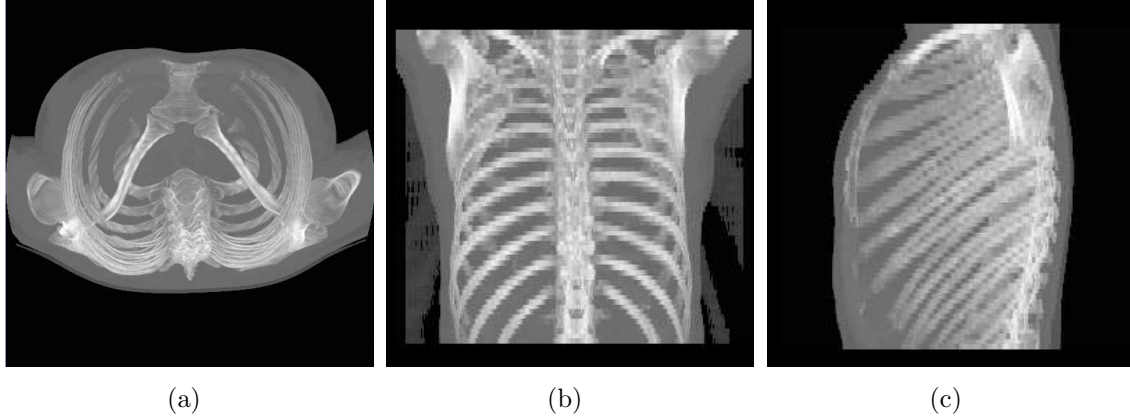


Figure 6.3: Maximum intensity projections of a thoracic CT image along a direction perpendicular to the (a) axial, (b) coronal and (c) sagittal plane.

imaging system considers the source, $\mathbf{s}$, located at coordinates $(0, 0, d)$, lying on the Z axis at a distance d from the origin of the laboratory frame OXYZ. Based on Eq. 2.18, the simplified monoenergetic case, one can develop a more useful formulation which directly illustrates the distortion due to the point source geometry. The detector output measured at a point $\mathbf{p}_d = (x_d, y_d)^T$ lying in the image plane OXY is given as a function of the logarithmic transmission, also referred to as the *radiological density* [166],

$$\mathbf{R}_{\text{ct}}(x_d, y_d) = \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z) dr, \quad (6.13)$$

where $\mu(x, y, z)$ is the linear attenuation coefficient of the tissue at coordinates (x, y, z) within a given CT image $\mathbf{H}(x, y, z)$. In Eq. 6.13, dr is the line integral element, $dr = \sqrt{dx^2 + dy^2 + dz^2}$ and the ray cast or line integration from $\mathbf{s}$ to $\mathbf{p}_d$ takes place along a line defined as

$$\begin{aligned} x &= \frac{d - z}{d} x_d, \\ y &= \frac{d - z}{d} y_d. \end{aligned} \quad (6.14)$$

The 2D transmission function at any plane z is therefore magnified by $(d - z)/d$ at the detector plane.

To compute Eq. 6.13, the size and resolution of the output DRR image is first specified. The coordinates (x_d, y_d) for each of the pixels $\mathbf{p}_d$ in the output image are first generated and used to determine, from Eq. 6.14, the equation of each

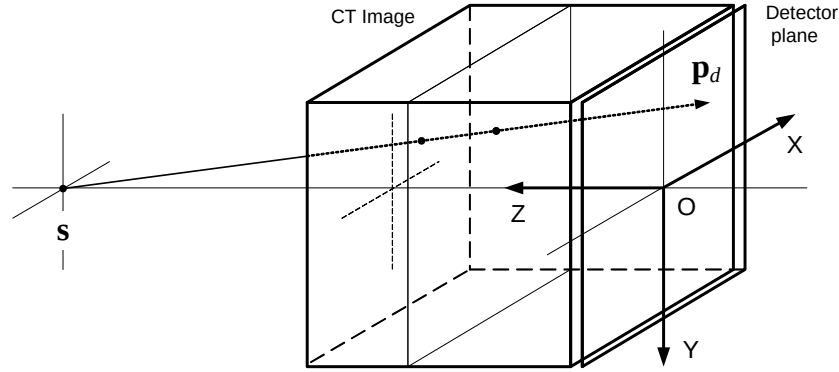


Figure 6.4: Schematic representation of volume rendering using the ray casting technique.

corresponding ray which is cast through the input volume. The position of the CT volume $\mathbf{H}$ between the ray source and screen is such that the normal from the image plane to the ray source passes directly through the center of the DRR. The ray is then uniformly sampled and the value of μ is interpolated at intersections of the ray with equally spaced, parallel planes z . For each ray, the radiological density can be rewritten in terms of each anatomical structure ξ contained in the volume,

$$\mathbf{R}_{\text{ct}}(x_d, y_d) = \sum_{\xi} \mu_{\xi} \mathbf{M}_{\xi}(x_d, y_d), \quad (6.15)$$

where $\mathbf{M}_{\xi}(x_d, y_d)$ denotes the total thickness of the structure ξ along the ray of projection that crosses the image plane in $\mathbf{p}_d$.

Using the method described in Chapter 5, thoracic CT images of a private image database (HPH) were previously segmented in several anatomical structures within the patient (body and lungs) and further decomposed into known materials ξ , namely AIR, LUNG tissue, FAT tissue, SOFT tissue and bones structures. Since the linear attenuation μ_{ξ} of these intervening materials is available (see Table 5.1), realistic radiographic images can be obtained by using the simple ray casting technique.

6.3 Shape from Radiological Density

3D shape recovering of anatomical structures from a single planar radiograph is an inverse, severely ill-posed problem that has an infinite number of solutions. To transform it into a problem with a single solution, the typical characteristic of the structures to be recovered must be taken into account. Therefore, the first step of

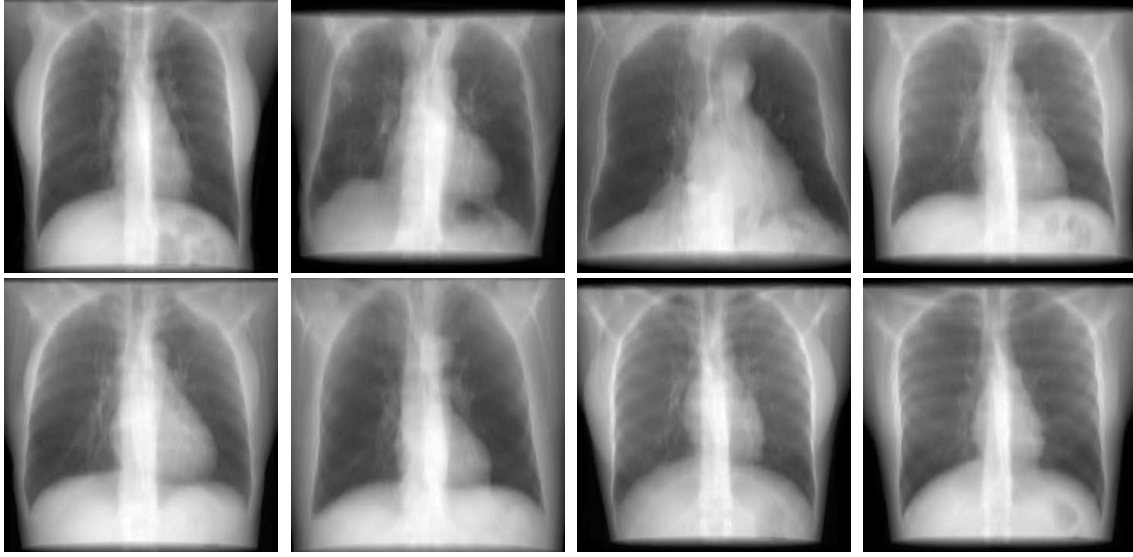


Figure 6.5: Radiological density images $\mathbf{R}_{\text{ct}}^{(s)}(x_d, y_d)$ generated from 3D patient-specific voxelized phantoms using the ray casting technique. The phantoms correspond to segmented CT images of a private database (HPH) using the method based on material decomposition described in Section 5.4.

the proposed reconstruction method is the estimation of *thickness maps* whose gray level at every pixel in the image plane is the expected thickness of the anatomical structures of interest along the ray of projection that crosses that pixel. Such maps can be computed as follows.

6.3.1 Thickness Maps

Let $\mathbf{H}^{(s)}(x, y, z)$, $s = 0, 1, \dots, S - 1$, be a volumetric CT image of the database containing S images. For each volumetric image $\mathbf{H}^{(s)}$, volume rendering was implemented to generate DRR images from the corresponding 3D patient-specific voxelized phantom obtained after the material decomposition has been applied. From Eq. 6.15, the DRR output is the radiological density image computed as

$$\mathbf{R}_{\text{ct}}^{(s)}(x_d, y_d) = \sum_{\xi} \mu_{\xi} \mathbf{M}_{\xi}^{(s)}(x_d, y_d). \quad (6.16)$$

Results of such projections are shown in Figure 6.5 for some CT images of the database. The simulated images, of size 352×352 and pixel spacing $dX = dY = 1.0$ mm, were obtained with a source-to-detector distance $d = 1800$ mm. The thickness maps $\mathbf{M}_{\xi}^{(s)}(x_d, y_d)$ corresponding to the 4 images of the first row are shown in Figure 6.6 and Figure 6.7. The maps were computed for all structures ξ segmented

in the patient during the 3D phantom construction algorithm. Figure 6.6 shows the maps corresponding to the intervening materials of the lung structures, namely AIR within the lung parenchyma, AIR contained in the large airways and LUNG tissue. For the body of the patient, mainly composed of FAT tissue, SOFT tissue and bones structures, the results are shown in Figure 6.7 for the same volumetric datasets.

Let suppose that the model-to-image registration method described in Section 4.4 is now applied for segmenting the lung fields in each of the radiological density images $\mathbf{R}_{\text{ct}}^{(s)}$. Using the mean shape to represent these regions in each simulated image, a point-to-point correspondence exists between the detected lung contour points and simulated images can be warped to each other. This is a typical model-to-model registration problem with point correspondence from which *mean* thickness maps are now computed for each structure. Consider now the lung deformable model represented by its mean shape, the set of N points $\mathbf{P} = \{\mathbf{p}_n\}$, where $\mathbf{p}_n = (\hat{x}_n, \hat{y}_n)^T$, $n = 0, \dots, N-1$, is a point of the lung contour. The lung field segmentation from the radiological density image $\mathbf{R}_{\text{ct}}^{(s)}(x_d, y_d)$ results in the deformed model $\mathbf{Q}^{(s)} = \{\mathbf{q}_n^{(s)}\}$, such that $\mathbf{q}_n^{(s)} = (x_n^{(s)}, y_n^{(s)})^T$ corresponds to the deformed point $\mathbf{p}_n$. The point correspondence between the two sets $\mathbf{P}$ and $\mathbf{Q}^{(s)}$ allows to specify a Thin-Plate Spline (TPS) transform $\mathcal{T}^{(s)}$ that maps exactly the set of source landmarks $\mathbf{p}_n$ onto the set of target landmarks $\mathbf{q}_n^{(s)}$, that is,

$$\mathbf{q}_n^{(s)} = \mathcal{T}^{(s)}(\mathbf{p}_n). \quad (6.17)$$

Computing S TPS transforms, the simulated images $\mathbf{R}_{\text{ct}}^{(s)}$ are warped to a common space, the model space, defined as a rectangular grid of points $\mathbf{p}_d$ coincident with the pixels in the image plane. The mean radiological density image $\bar{\mathbf{R}}_{\text{ct}}(x_d, y_d)$ is then computed for all pixels $\mathbf{p}_d$ as

$$\bar{\mathbf{R}}_{\text{ct}}(\mathbf{p}_d) = \frac{1}{S} \sum_{s=0}^{S-1} \mathbf{R}_{\text{ct}}^{(s)}(\mathbf{q}_d^{(s)}), \quad (6.18)$$

where $\mathbf{R}_{\text{ct}}^{(s)}(\mathbf{q}_d^{(s)})$ is the density value interpolated in the image $\mathbf{R}_{\text{ct}}^{(s)}$, at location $\mathbf{q}_d^{(s)}$, for which $\mathbf{q}_d^{(s)} = \mathcal{T}^{(s)}(\mathbf{p}_d)$. From Eq. 6.16, the above expression becomes

$$\bar{\mathbf{R}}_{\text{ct}}(\mathbf{p}_d) = \frac{1}{S} \sum_{s=0}^{S-1} \sum_{\xi} \mu_{\xi} \mathbf{M}_{\xi}^{(s)}(\mathbf{q}_d^{(s)}), \quad (6.19)$$

or

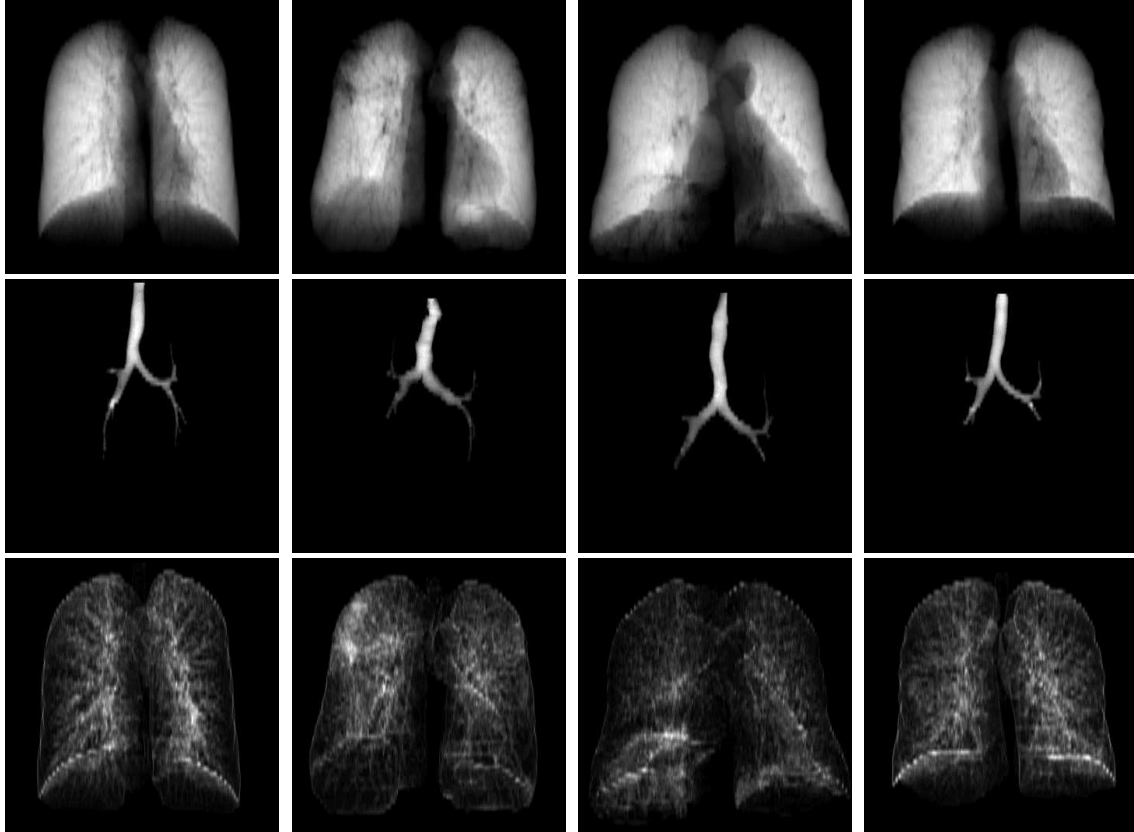


Figure 6.6: Thickness maps $M_{\xi}^{(s)}(x_d, y_d)$ of segmented lung structures generated from 4 different 3D patient-specific voxelized phantoms using the ray casting technique. The phantoms correspond to segmented CT images of a private database (HPH) (see Section 5.4). First row: AIR within the lung parenchyma; Second row: AIR within the large airways; Last row: LUNG tissue.

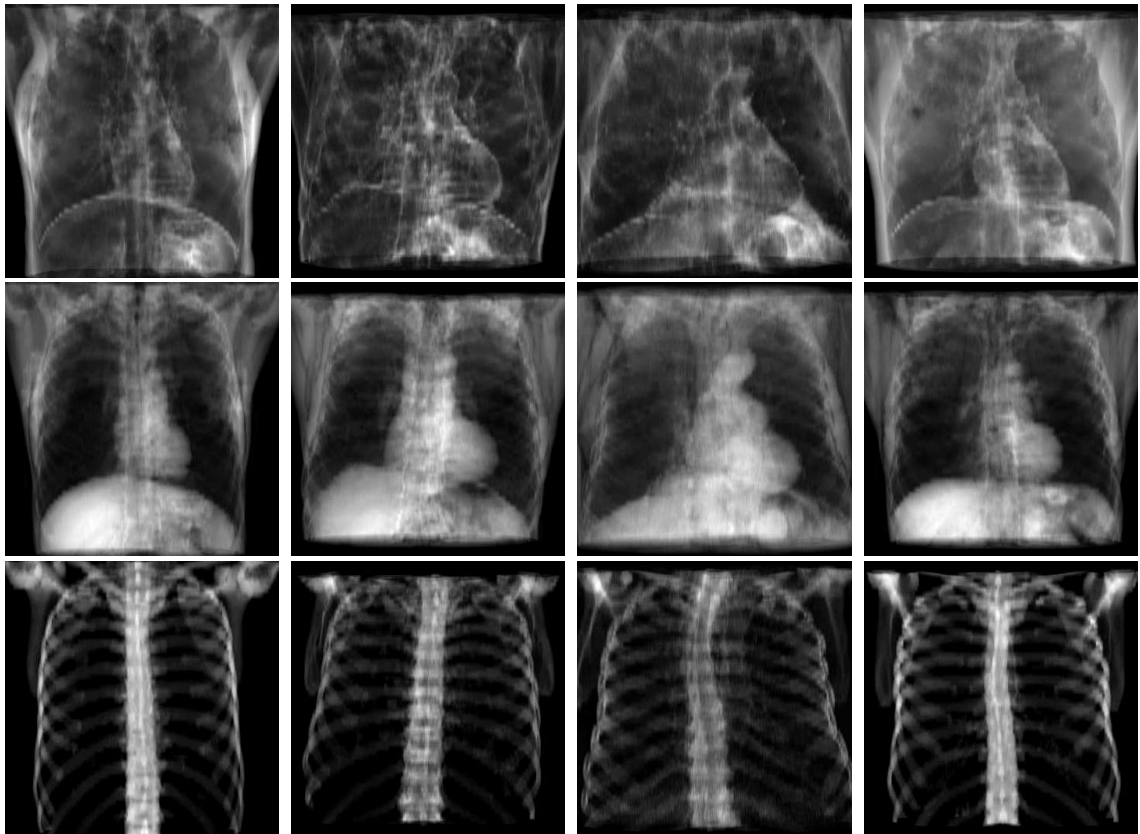


Figure 6.7: Thickness maps $M_{\xi}^{(s)}(x_d, y_d)$ of segmented body structures generated from 4 different 3D patient-specific voxelized phantoms using the ray casting technique. The phantoms correspond to segmented CT images of a private database (HPH) (see Section 5.4). First row: FAT tissue; Second row: SOFT tissue; Last row: bone structures.

$$\bar{\mathbf{R}}_{\text{ct}}(\mathbf{p}_d) = \sum_{\xi} \mu_{\xi} \left[\frac{1}{S} \sum_{s=0}^{S-1} \mathbf{M}_{\xi}^{(s)}(\mathbf{q}_d^{(s)}) \right], \quad (6.20)$$

and, considering Eq. 6.18,

$$\bar{\mathbf{R}}_{\text{ct}}(\mathbf{p}_d) = \sum_{\xi} \mu_{\xi} \bar{\mathbf{M}}_{\xi}(\mathbf{p}_d). \quad (6.21)$$

As expected, the mean radiological density $\bar{\mathbf{R}}_{\text{ct}}(x_d, y_d)$ is calculated from the mean thickness map $\bar{\mathbf{M}}_{\xi}(x_d, y_d)$ determined for each structure ξ . These maps are shown in Figure 6.8. The results were obtained by considering 30 decomposed CT images of the database. Actually, manual contouring was performed in the corresponding simulated images for delineating the lung fields. Although the model-to-image registration method has not been tested yet in such images, an automatic segmentation algorithm should be used when a larger database is available to compute thickness maps. Nevertheless, manual delineation has the advantage of reducing misregistration errors that could result from a poor computer-based segmentation.

6.3.2 3D Shape Recovery

The 3D reconstruction of anatomical structures of interest from an input digital chest radiograph $\mathbf{X}$ is now considered. We assume that this *real* image is defined in the same plane as the simulated images discussed above. We can also hypothesise that the same intervening materials ξ that define the 3D voxelized phantoms constructed from CT images are present in the planar radiograph $\mathbf{X}$. Therefore, a similar expression to Eq. 6.21 can be used to express the corresponding radiological density:

$$\mathbf{R}_{\text{xray}}(x_d, y_d) = \sum_{\xi} \mu_{\xi} \mathbf{M}_{\xi}^{(\mathbf{X})}(x_d, y_d). \quad (6.22)$$

The 3D shape recovery is then formulated as the problem of computing, in the above equation, the maps $\mathbf{M}_{\xi}^{(\mathbf{X})}$ at each pixel (x_d, y_d) in the image, i.e., the total thickness of each material or structure ξ at that pixel.

We will only consider the simple case of 3D shape recovery, for which a small and negligible inter-patient variability is assumed. Under this approximation, the mean thickness maps $\bar{\mathbf{M}}_{\xi}$ in Eq. 6.21 are the solution of the problem and the 3D patient anatomy is reconstructed by using a point-to-point correspondence. Suppose that

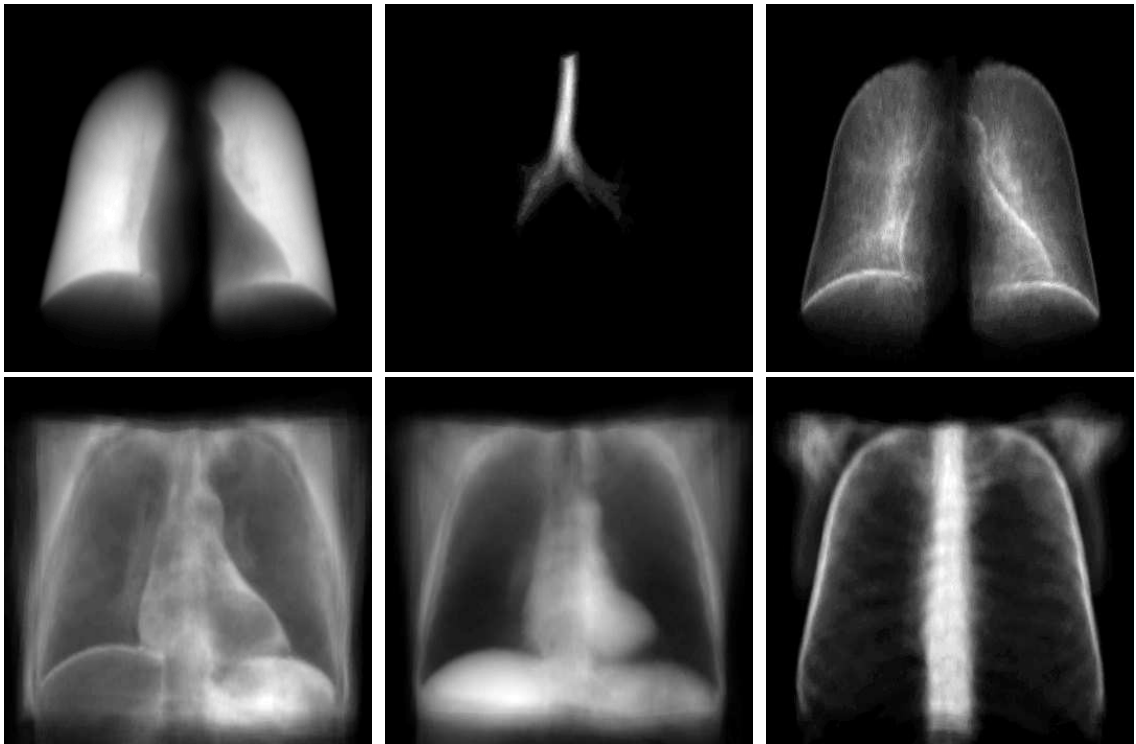


Figure 6.8: Mean thickness maps $\bar{M}_\xi(x_d, y_d)$ generated from 30 patient-specific voxelized phantoms using the ray casting technique. First row: mean thickness maps of segmented lung structures: AIR within the lung parenchyma; AIR within the large airways and LUNG tissue; Second row: mean thickness maps of segmented structures within the body of the patient: FAT tissue, SOFT tissue and bone structures.

the lung fields have been previously segmented from the chest radiograph $\mathbf{X}$. Using the model-based segmentation method, the deformed model $\mathbf{Q} = \{\mathbf{q}_n\}$ is obtained and the set of source landmarks $\mathbf{q}_n$ defines the TPS transform $\mathbf{p}_n = \mathcal{T}(\mathbf{q}_n)$ that maps each point $\mathbf{q}_n$ to the corresponding point $\mathbf{p}_n$ in the undeformed lung model. Consequently, the approximate reconstruction is equivalent to assume that

$$\mathbf{R}_{\text{xray}}(\mathbf{q}_d) \simeq \bar{\mathbf{R}}_{\text{ct}}(\mathbf{p}_d), \quad (6.23)$$

where $\mathbf{p}_d = \mathcal{T}(\mathbf{q}_d)$, for each point $\mathbf{p}_d$ in the model space, and one solution of the reconstruction problem is given by

$$\mathbf{M}_{\xi}^{(\text{X})}(\mathbf{q}_d) \simeq \bar{\mathbf{M}}_{\xi}(\mathbf{p}_d). \quad (6.24)$$

Results of such reconstruction are shown in Figure 6.9. The surfaces represent the total thickness of the lungs (i.e., the sum of AIR and LUNG tissue thicknesses), the body (FAT, SOFT tissue and bones structures) and the patient (lungs and body). For each of these structures, the corresponding surface is a function assuming the form $z_{\xi} = f(x_m, y_m)$, where z_{ξ} is the value interpolated at point $\mathbf{p}_m$ in the map $\bar{\mathbf{M}}_{\xi}(\mathbf{p}_m)$, that is, the thickness $\mathbf{M}_{\xi}^{(\text{X})}(\mathbf{q}_m)$ is interpolated at the corresponding point $\mathbf{q}_m$. Actually, the surfaces were reconstructed at each point $\mathbf{p}_m$ of the triangulated mean shape of the lung model, although the location of pixels in the entire image could be considered as well. Note that since the original structures are non-symmetric, the recovered surfaces are only an approximation of such structures. However, some properties such as the volume are preserved. It should be noted that if additional projections of the imaged structures are available, asymmetry constraints can be directly derived from these images and added to the reconstruction process.

6.3.3 System Calibration

In order to investigate the goodness of the approximation expressed by Eq. 6.23, the theoretical relationship between the radiological density $\mathbf{R}_{\text{xray}}(x_d, y_d)$ and the gray level $\mathbf{X}(x_d, y_d)$ of any pixel in digital planar radiograph, measured at the detector plane, was first derived. The following expression was obtained and reflects the relationship between these two physical quantities:

$$\mathbf{R}_{\text{xray}}(x_d, y_d) = k_3 \{ \ln [\mathbf{X}(x_d, y_d) + k_1] + k_2 \}. \quad (6.25)$$

The above equation is derived in Appendix D, where k_1 , k_2 and k_3 are defined

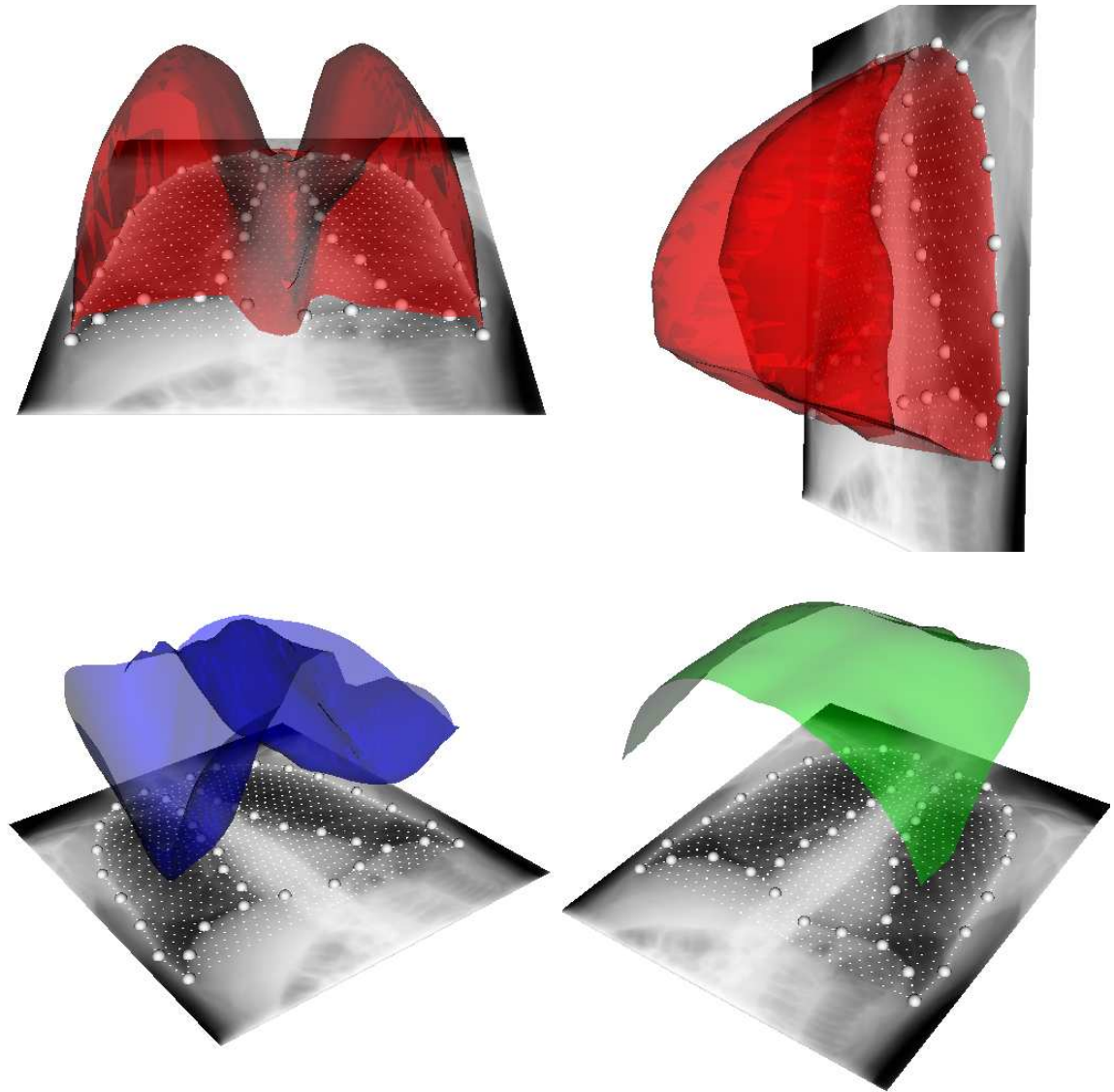


Figure 6.9: 3D shape recovery from single radiograph. Different views of the recovered lung shape (red), body (blue) and patient (green). The thickness of each structure is only reconstructed in the region corresponding to the lung fields of the PA chest radiograph. Some landmarks (white spheres) of the segmented lung contour, using the model-to-image registration method, are also shown.

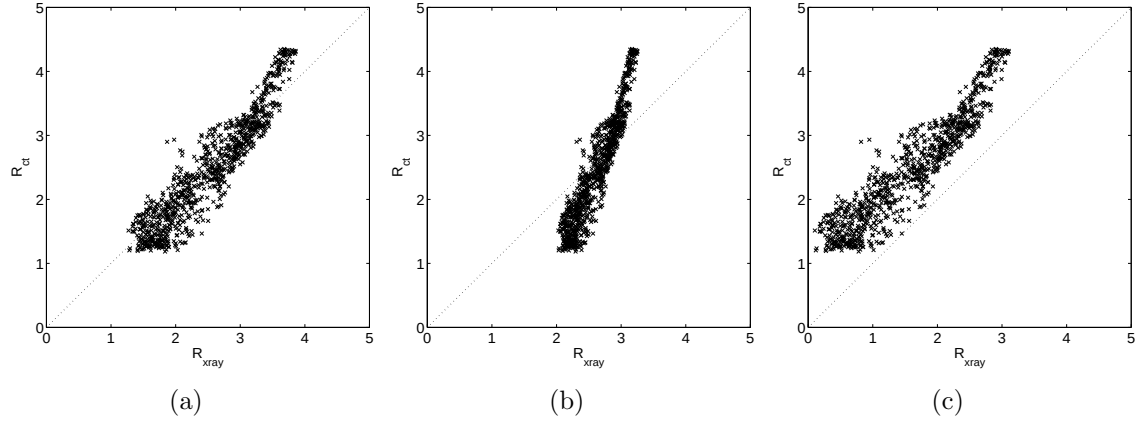


Figure 6.10: Radiological density correspondence between calibrated values computed from a real planar radiograph, $\mathbf{R}_{\text{xray}}(x_m, y_m)$, and simulated mean values computed from CT, $\bar{\mathbf{R}}_{\text{ct}}(x_m, y_m)$. Correspondence is plotted for the 913 points $\mathbf{p}_m$ of the triangulated mean shape of the lung model for different sets of calibration parameters (k_1, k_2, k_3) : (a) $(1.01, 0.11, 5.26)$, (b) $(1.01, 0.68, 2.49)$ and (c) $(0.81, 0.08, 5.26)$.

as calibration constants related to the physical and geometrical parameters of the X-ray imaging system used to acquire the original radiograph.

Once the image formation has been linearized, different sets of calibration parameters (k_1, k_2, k_3) were used to evaluate Eq. 6.25. The radiological density images were matched point-wise by plotting the pairs $(\mathbf{R}_{\text{xray}}, \bar{\mathbf{R}}_{\text{ct}})$ for each point $\mathbf{p}_m$ of the triangulated mean shape of the lung contour. Figure 6.10 illustrates the resulting correspondence, for which the constants were manually set to $k_1 = 1.01$, $k_2 = 0.11$, $k_3 = 5.26$ (Figure 6.10(a)), $k_1 = 1.01$, $k_2 = 0.68$, $k_3 = 2.49$ (Figure 6.10(b)), and $k_1 = 0.81$, $k_2 = 0.08$, $k_3 = 5.26$ (Figure 6.10(c)). For the case of perfect match, one should obtain $\mathbf{R}_{\text{xray}} = \bar{\mathbf{R}}_{\text{ct}}$ for each point $\mathbf{p}_m$. Actually, the constants should be experimentally determined by using precisely manufactured calibration objects.

6.4 Concluding Remarks

We have proposed a method for estimating the thickness of the major anatomical structures present in a single PA chest radiograph. To recover the 3D shape of such structures, volume rendering of segmented CT images was performed to obtain realistic simulated radiological density images. Taking into account the characteristics of the X-ray imaging system used to acquire the input radiograph, such DRRs contain the necessary information of the anatomy. A potentially significant difference between simulated and real radiographs can arise because of changes or differences

in the patient or environment.

Although the proposed algorithm was illustrated for a simple case, we believe that the adopted approach for 3D shape recovery from a single radiograph is promising. Incorporating dual-energy radiography principles, algorithms for selective cancellation of unwanted tissues are currently under development. Experimental calibration of the medical X-ray imaging system is still needed.

Chapter 7

GENERAL CONCLUSIONS AND FUTURE DIRECTIONS

The work presented in this thesis is centered on the segmentation of medical X-ray images of the human thorax for which knowledge-based approaches were adopted and fully automated computer algorithms were developed. These are now discussed in the light of the results reported in the thesis which has focused on the lung field extraction from standard PA chest radiographs and the material decomposition of volumetric CT images. Exploiting the relationship between CT data and radiographic measurements, 3D reconstruction algorithms were designed to integrate such imaging modalities into a single application for recovering the 3D shape of anatomical structures from single radiographs.

In Chapter 4, two methods were presented to accurately identify the unobscured regions that define the lung fields in digital PA chest radiographs. The proposed methods exploit both the strength of model-based approaches and optimization techniques. The first method is a contour delineation method for which an optimal path finding algorithm based on dynamic programming was implemented. The second approach consists on a model-to-image registration framework where genetic algorithms are used as a global optimization technique.

Several aspects are common to both methods. First, they are based on the same geometrical model that defines the lung region of interest. From a training set of manually contoured images, a point distribution model, the lung contour model, was constructed to reflect the normal anatomy of such structure observed in chest radiographs. The optimal path finding algorithm was used to search for the segments defined in the contour model and non-rigid deformations of the same model were considered in the registration method. Second, the same cost images were used to compute the cumulative cost of the searched paths and define the fitness functions of the genetic algorithm, in order to evaluate each individual in the population.

The construction of the cost images, as well as the geometrical model, is based on the characteristics of the detected lung borders. To compute these images, a multi-resolution bank of Gaussian filters was used although other kernel filters could be considered as well. Since this processing step is time consuming, directional filtering was performed on the input radiograph by using only 2 directions and 3 different scales. Image features resulting from this step, previously normalized, were finally combined to compute the cost images.

The main difference between the two proposed segmentation methods is that dynamic programming is applied to search for each optimal path, one-by-one, while the genetic algorithm is used to search for the best location of anatomical landmarks and therefore the position of all the model points simultaneously.

Using the contour delineation method, segments are detected by using the same sequence adopted for manually delineating lung contours in the training set: first, hemi-diaphragms, then costal edges, lung top sections and lastly mediastinal edges defining the borders of heart and lung. Once a path has been detected, spatial constraints were included to search for the remaining segments, by simply masking their corresponding cost images. Although defined in different directions, optimal paths should be more dependent to each other by applying harder geometrical constraints.

To implement the model-to-image registration a real coded genetic algorithm was adopted. We proposed a very simple representation of initial solutions: strings of random numbers sampled from a normal distribution. In fact, this approach is intuitive and naturally encodes instances of the deformed model by defining landmarks displacements as local random perturbations. Using this representation, decoding is straightforward and statistical information derived for each landmark during the model construction step is easily added. To deform the model, a thin-plate splines landmark-based transform was used. The choice of the number of landmarks is a compromise between the number of degrees of freedom of the deformable model and the time spent to segment a chest radiograph. Actually, this is the main bottleneck in terms of execution speed of the segmentation-by-registration method.

The model-to-image registration method is flexible enough to consider other transformation models, optimizers and metrics. With genetic algorithms, additional care is required since the evolution of the registration process highly depends on the choice of recombination operators. Some improvements in the design of such optimization technique are currently being investigated. For example, implementations of new crossover and mutation operators based on the bilateral symmetry observed in PA chest radiographs have already been included in the proposed segmentation

method. These are under evaluation. We are also considering the incorporation of local hill climbers. Because principal component analysis was used to construct the statistical shape model, we believe that active shape models can be included into the registration method in a straightforward manner.

Evaluated on the private image database, the two proposed segmentation methods performed equally. An interesting observation is that, for the same radiograph, different types of segmentation failures occur. This suggests the implementation of a mixed method that exploits the strength of both approaches, although none of the methods was designed to take into account possible abnormal findings. In fact, lung pathologies such as cardiomegaly and lung consolidation, as observed in the private database, has negative influence on the performance of lung fields segmentation schemes. The age of the patient also has a large impact on the appearance of the anatomy. Therefore, specific classes of images should be treated separately. The use of different specific databases for different patient groups e.g. based on age and sex should also improve the performance of such segmentation algorithms.

Although the applicability of the proposed segmentation methods has proven to be effective in standard PA chest radiographs, the methods are sufficiently general to be applied in lateral radiographs as well. Both the contour delineation method and the model-to-image registration approach are intended to be used in such images, by taking into account most of the considerations above mentioned.

In Chapter 5, fully automated segmentation algorithms for decomposing volumetric CT images into several anatomical structures are presented. Based on material decomposition applied to CT numbers, a voxel classification strategy was adopted to construct a 3D patient-specific anthropomorphic phantom from a single CT image. The resulting voxelized phantom is suitable for radiotherapy planning and image guided surgery. It is also well indicated for performing several computer simulations, namely in diagnostic radiology and nuclear medicine. Applications specifically directed towards CAD were also considered and the method was extended to accurately extract the lung region of interest from CT images as the final output of the segmentation procedure.

The proposed decomposition method follows a hierarchical representation of the patient anatomy. First the thorax of patient is separated from the background image and, within the patient, the lungs from the body. Combinations of global thresholding and seeded region growing techniques were used to achieve this goal. These structures were further decomposed into known intervening materials, namely air, lung, fat and soft tissues and bony structures, defined in a simple anatomical

model. Such decomposition was conveniently illustrated by using the basis plane representation. The identification of high density structures containing the skeleton is one of the final steps of the segmentation method. We plan to include suitable algorithms to further decompose the skeleton into its different components such as the scapula, vertebrae and individual ribs. The segmentation of other structures like the sternum could represent a harder task since the corresponding CT numbers are often similar to those of soft tissues. It is also our intention to obtain a more realistic representation of the human thorax by including other anatomical structures in the model. For example, a specific algorithm should be designed to delineate the mediastinum and therefore distinguish it from other soft tissues lying outside the thoracic cage.

We are currently collecting several thoracic CT datasets into a single image database. Although a small number of images is available at the moment, results of applying the proposed method to all of them reflect its robustness. A set of reproducible segmentation thresholds was obtained. Although different threshold values were used to separate the patient from the background image and extract the lungs from the body, local thresholding techniques applied near the boundary of such adjacent structures should be used to improve the detection of the corresponding interfaces.

Voxelized phantoms were used to characterize each of the segmented anatomical structures in terms of their physical and geometrical properties, by computing their mean CT number and volume fraction. Using such information, the construction of realistic physical phantoms for the calibration and optimization of medical X-ray imaging systems is under consideration.

In the broader context of CAD, the method was extended for extracting the lung fields, providing an accurate delineation of such anatomical region of interest usually required by most pulmonary image analysis applications. Here, we implemented an algorithm to identify and extract the large airways from the lung parenchyma. This was used to improve the separation of the right and the left lung, by means of a robust 3D optimal surface detection algorithm based on dynamic programming.

Chapter 6 exploits the relationship between CT data and radiographic measurements. Several reconstruction algorithms are proposed to integrate such imaging modalities into a single application for recovering the 3D shape of anatomical structures from single radiographs. To achieve this goal, CT images were previously decomposed and the resulting voxelized phantoms were used to create realistic digitally reconstructed radiographs. The proposed reconstruction approach is based on

thickness maps estimated for each structure to be recovered. Preliminary results of the 3D shape recovery algorithm are reported. In order to perform a reasonable reconstruction, all the geometry and the calibration of the original X-ray imaging device has to be known precisely. For the latter, a formal relationship was derived to establish the correspondence between the radiological density and the gray level of any pixel in digital planar radiograph.

Recovering the shape of anatomical structures from single radiographs will likely produce a number of different radiological images. Statistical models of the appearance of normal chest radiographs may be fitted to input images and subtracted to enhance possibly abnormal structures. In many digital chest units it is technically feasible to make two radiographs with different energies at the same time and to subtract these in order to obtain a dual energy subtraction image in which the bony structures or other unwanted tissue are virtually invisible. Such images have not been used in clinical practice, although we believe that sophisticated subtraction algorithms are likely to become extremely useful and a standard in pre-processing for CAD in chest radiography.

Appendix A

C++ OPEN SOURCE TOOLKITS

The decision to use the following toolkits was taken due to the quantity of segmentation and visualization tools they offer. As the libraries are implemented in C++ they can be used on most platforms such as Linux, Mac OS and Windows.

A.1 ITK - The Insight Segmentation and Registration Toolkit

All the computer algorithms presented in the thesis that support the proposed method were implemented in C++, using the Insight Segmentation and Registration Toolkit (ITK). ITK is an open-source cross-platform toolkit containing a large collection of C++ standard template libraries for medical data representation and processing. It has been developed since 1999 on the initiative of the US National Library of Medicine, and can be downloaded freely from the ITK web page¹. Currently under active development, ITK employs leading-edge segmentation and registration algorithms in two, three, and more dimensions [167]. It follows a data-flow approach that is based on *data* objects for (image representation) that are manipulated by *filter* objects (image processing).

Example Code

The following example code can be used for computing the normalized responses $\mathbf{R}_{nm,\sigma}^{(p)}$ (Eq. 3.4 to Eq. 3.7). The corresponding image processing pipeline is diagrammed in Figure 3.6. For different values of the parameters σ , n and m , several output image features are extracted, as shown in Figure 3.7.

¹ <http://www.itk.org/>

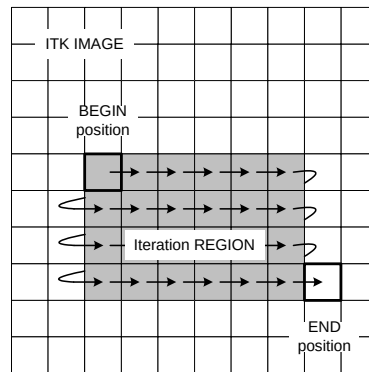


Figure A.1: ITK iterator traversing every voxel within a region of interest in the image.

```
// Algorithm - Image Feature Extraction
// -----
// Filters:
GaussianType::Pointer smoother1 = GaussianType::New();
GaussianType::Pointer smoother2 = GaussianType::New();
NormalizeType::Pointer normalize = NormalizeType::New();
SigmoidType::Pointer sigmoid = SigmoidType::New();
ThresholdType::Pointer threshold = ThresholdType::New();
// parameters:
smoother1 -> SetSigma( 1.0 );           // sigma (mm)
smoother2 -> SetSigma( 1.0 );
smoother1 -> SetOrder( GaussianType::ZeroOrder ); // n
smoother2 -> SetOrder( GaussianType::FirstOrder ); // m
sigmoid -> SetOutputMinimum( -1.0 ); // a
sigmoid -> SetOutputMaximum( 1.0 ); // b
sigmoid -> SetBeta( 0.0 ); // c
sigmoid -> SetAlpha( 1.0 ); // d
threshold -> SetOutsideValue( 0 );
threshold -> ThresholdAbove( 0 ); // p
// pipeline:
smoother1 -> SetInput( resampler -> GetOutput() );
smoother2 -> SetInput( smoother1 -> GetOutput() );
normalize -> SetInput( smoother2 -> GetOutput() );
sigmoid -> SetInput( normalize -> GetOutput() );
threshold -> SetInput( sigmoid -> GetOutput() );
threshold -> Update();
```

Image Iterators

One of ITK's extremely useful features are *image iterators*. Iterators allow to traverse every voxel (and possibly its neighborhood) of an image quickly to apply any treatment such as voxel count and average gray level within a region of interest. Iterators were mainly used in this work for image labeling. A schematic representation of one of many image iterators provided by the toolkit is given in Figure A.1.

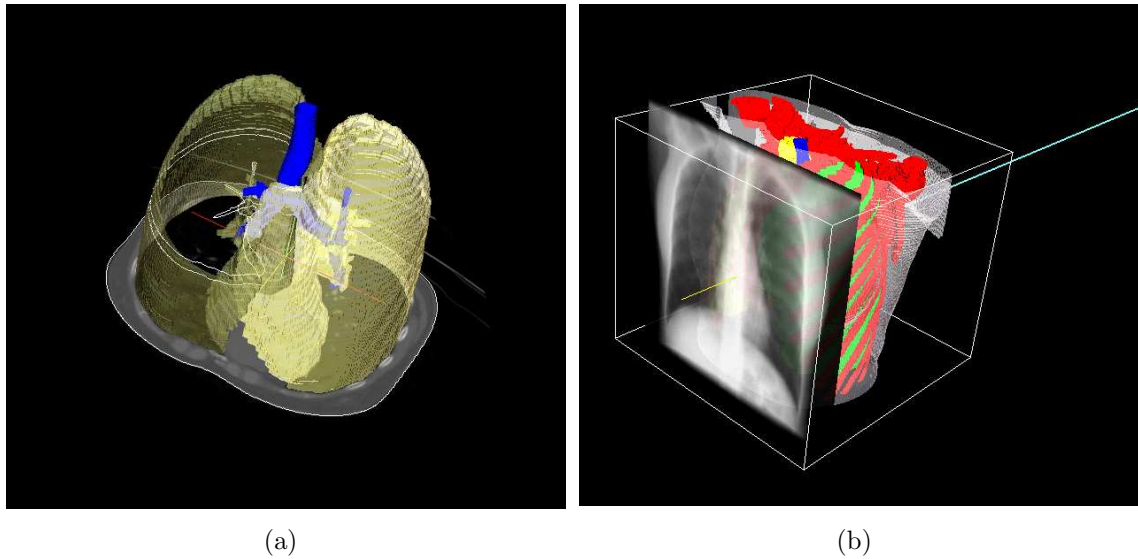


Figure A.2: Visualization examples using VTK. (a) Surface rendering of the segmented lung parenchyma from a CT image: large airways (blue), lung right (green) and left lung (yellow). Surface clipping of the segmented patient is also shown in the central axial slice of the image. (b) Visualization of the simulated medical X-ray imaging system for DRR generation.

A.2 VTK - The Visualization Toolkit

However, ITK lacks visualization capabilities as its focus is on segmentation and registration. The ITK framework has a layer that allows it to integrate the Visualization Toolkit (VTK), an open-source, freely available² software system for 3D computer graphics, image processing, and visualization [165]. As ITK, VTK consists of a C++ class library designed to support an object oriented paradigm which allows base *image filters* to be chained together in a program. VTK was used in particular pieces of the processing pipeline to produce the image displays and surfaces rendering presented in this thesis. Examples illustrating the VTK capabilities are shown in Figure A.2.

A.3 FLTK - The Fast Light Toolkit

The Fast Light Toolkit (FLTK), a C++ open-source toolkit freely available³, was used for constructing the graphical user interface displayed in Figure A.3. The application was developed for the automated segmentation of the lung fields from

² <http://www.vtk.org/>

³ <http://www.fltk.org/>

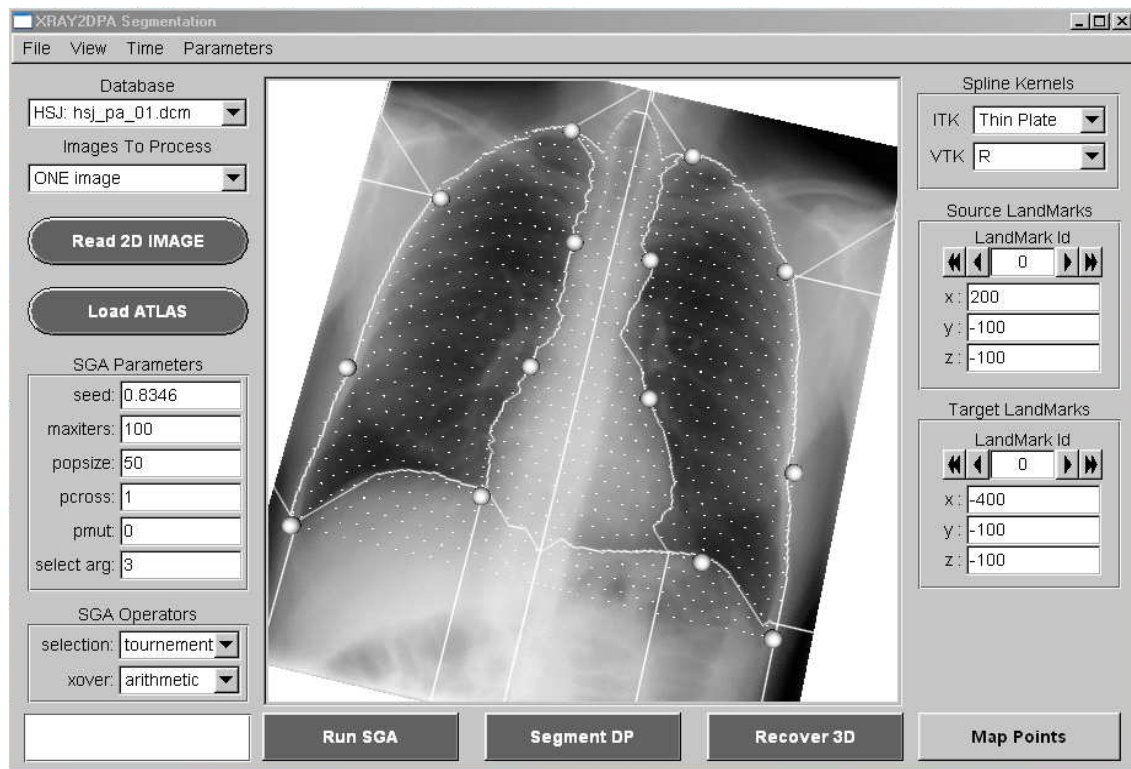
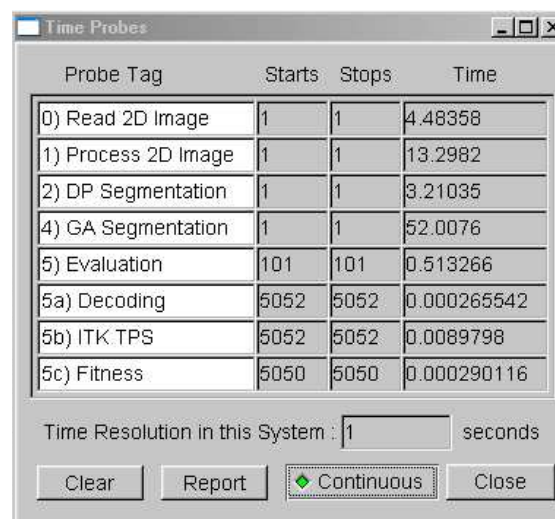


Figure A.3: Lung field segmentation from PA chest radiographs. FLTK graphical user interface of the application.

chest radiographs to perform the experiments reported in Table 4.3.

The user is allowed to choose one of the two segmentation methods described in Chapter 4, namely contour delineation (Section 4.3), based on dynamic programming (**Segment DP**) and model-to-image registration (Section 4.4) based on genetic algorithms (**Run SGA**). As described in Section 4.5.1, two image databases are currently available.

The FLTK time probes utility, shown in Figure A.4, was particularly useful to evaluate the computation time performance of the iterative registration method. The displayed output and time probes were obtained with the parameters (left side of the application) listed in Table 4.2. The corresponding fitness evolution is plotted in Figure 4.9(a).



Probe Tag	Starts	Stops	Time
0) Read 2D Image	1	1	4.48358
1) Process 2D Image	1	1	13.2982
2) DP Segmentation	1	1	3.21035
4) GA Segmentation	1	1	52.0076
5) Evaluation	101	101	0.513266
5a) Decoding	5052	5052	0.000265542
5b) ITK.TPS	5052	5052	0.0089798
5c) Fitness	5050	5050	0.000290116

Time Resolution in this System : 1 seconds

Clear Report  Continuous Close

Figure A.4: FLTK time probes utility.

Appendix B

2D PA CHEST RADIOGRAPH SEGMENTATION RESULTS

The results of the proposed segmentation methods of PA chest radiographs (see Section 4.3 and 4.4) are presented in this Appendix and correspond to the experiments reported in Table 4.3. The results of the contour delineation (DP) and model-to-image registration (GA) methods using the image databases HSJ and JSRT are organized as follow:

- **DP/JSRT**: Table B.1 and Figure B.1 (best 20 of 247 images)
- **DP/JSRT**: Table B.2 and Figure B.2 (worst 20 of 247 images)
- **DP/HSJ** : Table B.3, Figure B.3 and Figure B.5 (all 39 images)
- **GA/HSJ** : Table B.4, Figure B.4 and Figure B.6 (all 39 images)

The segmentation performances are expressed in percent and represent the true positive fraction (TPF), actually the degree of overlap defined by Eq. 3.33, false negative fraction (FNF) and false positive fraction (FPF):

$$\text{TPF} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FP}} + N_{\text{FN}}} = \frac{|A \cap B|}{|A \cup B|}, \quad (\text{B.1a})$$

$$\text{FNF} = \frac{N_{\text{FN}}}{N_{\text{TP}} + N_{\text{FP}} + N_{\text{FN}}} = \frac{|A \cap B^c|}{|A \cup B|}, \quad (\text{B.1b})$$

$$\text{FPF} = \frac{N_{\text{FP}}}{N_{\text{TP}} + N_{\text{FP}} + N_{\text{FN}}} = \frac{|A^c \cap B|}{|A \cup B|}, \quad (\text{B.1c})$$

where A^c denotes the set of all pixels not belonging to A . In the above equations, A and B are the segmented lung region (set of non-zero pixels) resulting from the manual contouring and the automated methods, respectively. $\cap$ represents the intersection, $\cup$ the union of two sets and the operator $|\cdot|$ represents the size (number of pixels) of a set (see Section 3.8).

Table B.1: Lung field segmentation from PA chest radiographs. Segmentation performance of the contour delineation method using the public image database (DP/JSRT, best 20 of 247 images). Segmentation outputs are shown in Figure B.1 .(see also Table 4.4).

Image	Right Lung			Left Lung			Both Lungs		
	TPF	FNF	FPF	TPF	FNF	FPF	TPF	FNF	FPF
NN089	0.95	0.03	0.02	0.95	0.02	0.03	0.95	0.03	0.02
NN044	0.94	0.01	0.05	0.95	0.01	0.04	0.95	0.01	0.04
NN032	0.95	0.03	0.02	0.95	0.02	0.03	0.95	0.03	0.02
NN030	0.96	0.01	0.03	0.95	0.01	0.04	0.95	0.01	0.04
NN020	0.95	0.03	0.02	0.95	0.02	0.03	0.95	0.02	0.03
LN147	0.96	0.03	0.01	0.94	0.01	0.05	0.95	0.02	0.03
LN132	0.96	0.01	0.03	0.93	0.01	0.06	0.95	0.01	0.04
LN129	0.94	0.03	0.03	0.95	0.01	0.04	0.95	0.02	0.03
LN107	0.96	0.02	0.02	0.94	0.02	0.04	0.95	0.02	0.03
LN092	0.94	0.04	0.02	0.96	0.01	0.03	0.95	0.03	0.02
NN086	0.94	0.03	0.03	0.95	0.01	0.04	0.94	0.02	0.04
NN077	0.94	0.01	0.05	0.94	0.01	0.05	0.94	0.01	0.05
NN069	0.94	0.03	0.03	0.94	0.00	0.06	0.94	0.02	0.04
NN063	0.94	0.02	0.04	0.94	0.02	0.04	0.94	0.02	0.04
NN061	0.94	0.02	0.04	0.94	0.02	0.04	0.94	0.02	0.04
NN060	0.95	0.02	0.03	0.92	0.02	0.06	0.94	0.02	0.04
NN059	0.93	0.03	0.04	0.94	0.01	0.05	0.94	0.02	0.04
NN054	0.94	0.03	0.03	0.94	0.01	0.05	0.94	0.02	0.04
NN051	0.95	0.02	0.03	0.94	0.01	0.05	0.94	0.02	0.04
NN049	0.95	0.01	0.04	0.94	0.03	0.03	0.94	0.02	0.04

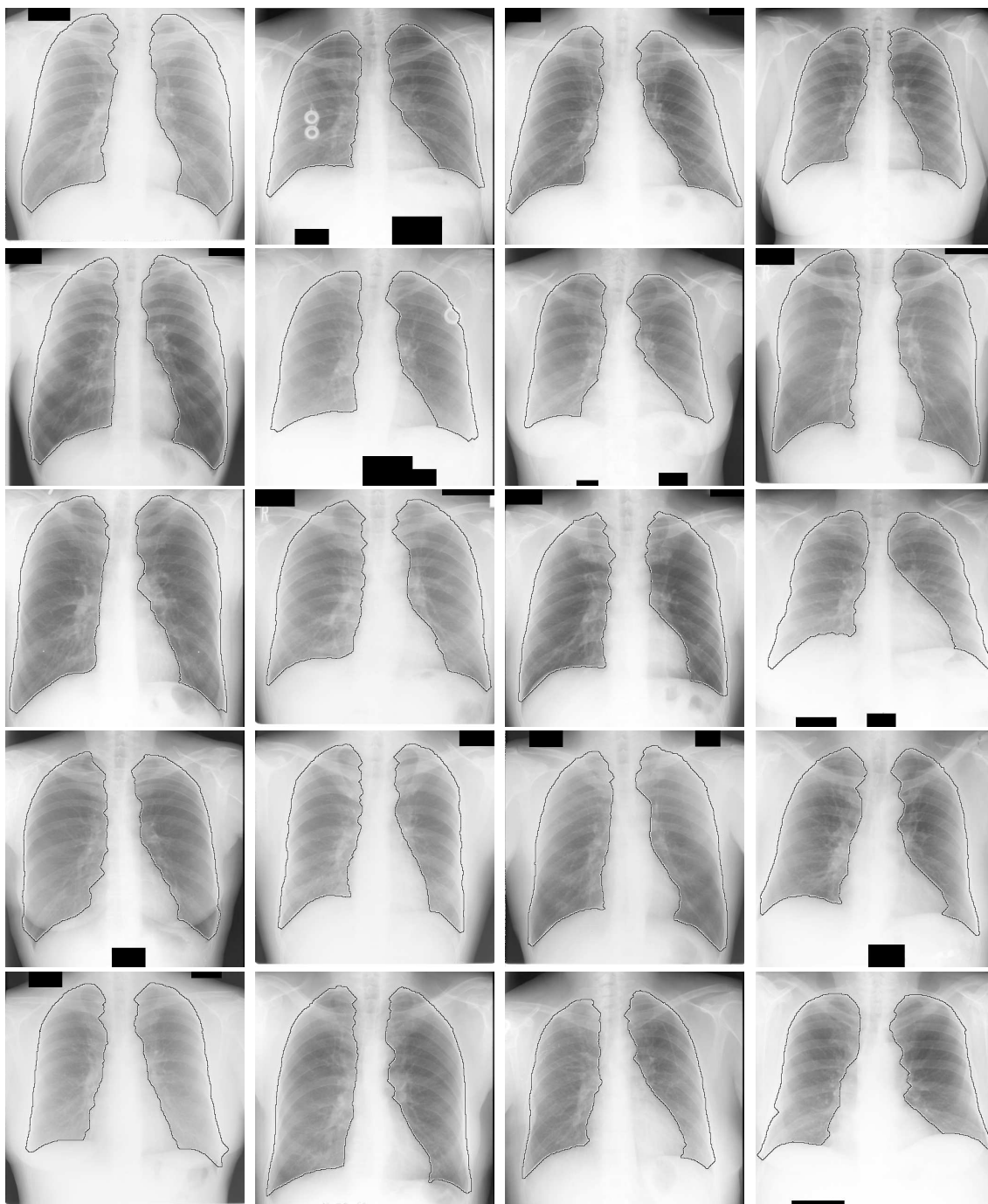


Figure B.1: Segmentation outputs of the contour delineation method using the public image database (DP/JSRT, best 20 of 247 images). Performance measures are reported in Table B.1.

Table B.2: Lung field segmentation from PA chest radiographs. Segmentation performance of the contour delineation method using the public image database (DP/JSRT, worst 20 of 247 images). Segmentation outputs are shown in Figure B.2 (see also Table 4.4).

Image	Right Lung			Left Lung			Both Lungs		
	TPF	FNF	FPF	TPF	FNF	FPF	TPF	FNF	FPF
LN077	0.93	0.04	0.03	0.51	0.01	0.48	0.68	0.02	0.30
LN021	0.94	0.04	0.02	0.51	0.02	0.47	0.69	0.03	0.28
LN034	0.77	0.02	0.21	0.69	0.01	0.30	0.73	0.01	0.26
LN103	0.63	0.02	0.35	0.92	0.05	0.03	0.74	0.03	0.23
LN048	0.87	0.12	0.01	0.61	0.02	0.37	0.75	0.07	0.18
LN044	0.77	0.05	0.18	0.77	0.01	0.22	0.77	0.04	0.19
LN010	0.82	0.03	0.15	0.78	0.07	0.15	0.80	0.05	0.15
LN029	0.83	0.01	0.16	0.77	0.01	0.22	0.80	0.01	0.19
LN090	0.93	0.04	0.03	0.68	0.10	0.22	0.80	0.07	0.13
LN128	0.82	0.02	0.16	0.80	0.03	0.17	0.81	0.02	0.17
NN066	0.80	0.04	0.16	0.83	0.02	0.15	0.81	0.03	0.16
LN004	0.85	0.02	0.13	0.78	0.03	0.19	0.82	0.02	0.16
LN043	0.83	0.04	0.13	0.80	0.07	0.13	0.82	0.05	0.13
LN071	0.93	0.04	0.03	0.73	0.02	0.25	0.82	0.03	0.15
NN007	0.75	0.24	0.01	0.90	0.03	0.07	0.82	0.15	0.03
LN006	0.85	0.03	0.12	0.81	0.02	0.17	0.83	0.03	0.14
LN137	0.83	0.11	0.06	0.83	0.12	0.05	0.83	0.11	0.06
LN154	0.90	0.07	0.03	0.74	0.21	0.05	0.83	0.13	0.04
LN110	0.84	0.03	0.13	0.83	0.01	0.16	0.84	0.02	0.14
NN087	0.79	0.13	0.08	0.91	0.02	0.07	0.84	0.08	0.08



Figure B.2: Segmentation outputs of the contour delineation method using the public image database (DP/JSRT, worst 20 of 247 images). Performance measures are reported in Table B.2.

Table B.3: Lung field segmentation from PA chest radiographs. Segmentation performance of the contour delineation method using the private image database (DP/HSJ, all 39 images). Segmentation outputs are shown in Figure B.3 and Figure B.5 (see also Table 4.5).

Image	Right Lung			Left Lung			Both Lungs		
	TPF	FNF	FPF	TPF	FNF	FPF	TPF	FNF	FPF
HSJ01	0.87	0.10	0.03	0.92	0.07	0.01	0.89	0.09	0.02
HSJ02	0.91	0.04	0.05	0.95	0.02	0.03	0.93	0.03	0.04
HSJ03	0.91	0.04	0.05	0.87	0.04	0.09	0.89	0.04	0.07
HSJ04	0.95	0.03	0.02	0.95	0.03	0.02	0.95	0.03	0.02
HSJ05	0.77	0.18	0.05	0.69	0.15	0.16	0.73	0.17	0.10
HSJ06	0.82	0.11	0.07	0.90	0.10	0.00	0.86	0.10	0.04
HSJ07	0.85	0.08	0.07	0.62	0.19	0.19	0.73	0.14	0.13
HSJ08	0.91	0.05	0.04	0.90	0.04	0.06	0.91	0.04	0.05
HSJ09	0.94	0.04	0.02	0.95	0.03	0.02	0.94	0.03	0.03
HSJ10	0.89	0.06	0.05	0.89	0.05	0.06	0.89	0.05	0.06
HSJ11	0.86	0.09	0.05	0.88	0.08	0.04	0.87	0.09	0.04
HSJ12	0.92	0.04	0.04	0.93	0.04	0.03	0.92	0.04	0.04
HSJ13	0.95	0.03	0.02	0.94	0.04	0.02	0.95	0.03	0.02
HSJ14	0.87	0.04	0.09	0.69	0.02	0.29	0.78	0.03	0.19
HSJ15	0.92	0.05	0.03	0.92	0.03	0.05	0.92	0.04	0.04
HSJ16	0.91	0.06	0.03	0.91	0.04	0.05	0.91	0.05	0.04
HSJ17	0.93	0.05	0.02	0.85	0.04	0.11	0.89	0.04	0.07
HSJ18	0.93	0.04	0.03	0.93	0.05	0.02	0.93	0.04	0.03
HSJ19	0.92	0.05	0.03	0.88	0.06	0.06	0.90	0.06	0.04
HSJ20	0.89	0.07	0.04	0.69	0.08	0.23	0.80	0.07	0.13
HSJ21	0.87	0.07	0.06	0.90	0.07	0.03	0.88	0.07	0.05
HSJ22	0.90	0.05	0.05	0.91	0.06	0.03	0.90	0.06	0.04
HSJ23	0.93	0.05	0.02	0.93	0.04	0.03	0.93	0.05	0.02
HSJ24	0.81	0.18	0.01	0.92	0.04	0.04	0.87	0.11	0.02
HSJ25	0.83	0.05	0.12	0.89	0.05	0.06	0.86	0.05	0.09
HSJ26	0.90	0.05	0.05	0.88	0.10	0.02	0.89	0.07	0.04
HSJ27	0.85	0.09	0.06	0.90	0.05	0.05	0.88	0.07	0.05
HSJ28	0.84	0.06	0.10	0.65	0.09	0.26	0.74	0.08	0.18
HSJ29	0.83	0.16	0.01	0.89	0.09	0.02	0.86	0.13	0.01
HSJ30	0.89	0.08	0.03	0.81	0.12	0.07	0.85	0.10	0.05
HSJ31	0.89	0.09	0.02	0.73	0.21	0.06	0.81	0.15	0.04
HSJ32	0.88	0.11	0.01	0.92	0.07	0.01	0.90	0.09	0.01
HSJ33	0.86	0.05	0.09	0.77	0.10	0.13	0.81	0.07	0.12
HSJ34	0.85	0.04	0.11	0.87	0.12	0.01	0.86	0.08	0.06
HSJ35	0.88	0.04	0.08	0.92	0.05	0.03	0.90	0.05	0.05
HSJ36	0.88	0.05	0.07	0.90	0.08	0.02	0.89	0.07	0.04
HSJ37	0.83	0.13	0.04	0.90	0.09	0.01	0.86	0.11	0.03
HSJ38	0.84	0.15	0.01	0.88	0.11	0.01	0.87	0.13	0.00
HSJ39	0.38	0.04	0.58	0.89	0.11	0.00	0.52	0.06	0.42

Table B.4: Lung field segmentation from PA chest radiographs. Segmentation performance of the model-to-image registration method using the private image database (GA/HSJ, all 39 images). Segmentation outputs are shown in Figure B.4 and Figure B.6 (see also Table 4.6).

Image	Right Lung			Left Lung			Both Lungs		
	TPF	FNF	FPF	TPF	FNF	FPF	TPF	FNF	FPF
HSJ01	0.90	0.07	0.03	0.87	0.05	0.08	0.89	0.06	0.05
HSJ02	0.93	0.01	0.06	0.92	0.02	0.06	0.92	0.02	0.06
HSJ03	0.90	0.06	0.04	0.93	0.05	0.02	0.91	0.05	0.04
HSJ04	0.93	0.01	0.06	0.92	0.04	0.04	0.93	0.02	0.05
HSJ05	0.83	0.12	0.05	0.79	0.06	0.15	0.81	0.09	0.10
HSJ06	0.58	0.07	0.35	0.65	0.03	0.32	0.61	0.05	0.34
HSJ07	0.79	0.05	0.16	0.70	0.05	0.25	0.74	0.05	0.21
HSJ08	0.88	0.09	0.03	0.92	0.05	0.03	0.90	0.07	0.03
HSJ09	0.93	0.02	0.05	0.93	0.03	0.04	0.93	0.02	0.05
HSJ10	0.91	0.05	0.04	0.90	0.03	0.07	0.91	0.04	0.05
HSJ11	0.83	0.05	0.12	0.84	0.03	0.13	0.83	0.04	0.13
HSJ12	0.89	0.06	0.05	0.89	0.04	0.07	0.89	0.05	0.06
HSJ13	0.92	0.05	0.03	0.92	0.04	0.04	0.92	0.04	0.04
HSJ14	0.81	0.05	0.14	0.85	0.05	0.10	0.83	0.05	0.12
HSJ15	0.93	0.03	0.04	0.92	0.05	0.03	0.93	0.04	0.03
HSJ16	0.90	0.03	0.07	0.89	0.06	0.05	0.90	0.05	0.05
HSJ17	0.85	0.12	0.03	0.90	0.08	0.02	0.87	0.10	0.03
HSJ18	0.87	0.12	0.01	0.91	0.05	0.04	0.89	0.09	0.02
HSJ19	0.85	0.10	0.05	0.86	0.05	0.09	0.86	0.08	0.06
HSJ20	0.83	0.06	0.11	0.69	0.06	0.25	0.77	0.06	0.17
HSJ21	0.86	0.04	0.10	0.78	0.12	0.10	0.82	0.08	0.10
HSJ22	0.92	0.06	0.02	0.93	0.03	0.04	0.92	0.05	0.03
HSJ23	0.93	0.04	0.03	0.93	0.03	0.04	0.93	0.04	0.03
HSJ24	0.88	0.10	0.02	0.92	0.04	0.04	0.90	0.07	0.03
HSJ25	0.86	0.06	0.08	0.91	0.03	0.06	0.88	0.05	0.07
HSJ26	0.91	0.04	0.05	0.88	0.09	0.03	0.90	0.06	0.04
HSJ27	0.90	0.03	0.07	0.91	0.06	0.03	0.91	0.05	0.04
HSJ28	0.81	0.07	0.12	0.92	0.06	0.02	0.86	0.07	0.07
HSJ29	0.87	0.13	0.00	0.89	0.10	0.01	0.88	0.12	0.00
HSJ30	0.76	0.04	0.20	0.78	0.06	0.16	0.77	0.05	0.18
HSJ31	0.86	0.11	0.03	0.86	0.11	0.03	0.86	0.11	0.03
HSJ32	0.88	0.11	0.01	0.86	0.12	0.02	0.87	0.12	0.01
HSJ33	0.88	0.05	0.07	0.91	0.08	0.01	0.90	0.06	0.04
HSJ34	0.91	0.07	0.02	0.87	0.13	0.00	0.89	0.10	0.01
HSJ35	0.85	0.10	0.05	0.84	0.15	0.01	0.85	0.13	0.02
HSJ36	0.88	0.07	0.05	0.89	0.09	0.02	0.89	0.08	0.03
HSJ37	0.86	0.10	0.04	0.88	0.06	0.06	0.87	0.08	0.05
HSJ38	0.60	0.03	0.37	0.90	0.09	0.01	0.75	0.06	0.19
HSJ39	0.84	0.03	0.13	0.82	0.06	0.12	0.83	0.05	0.12

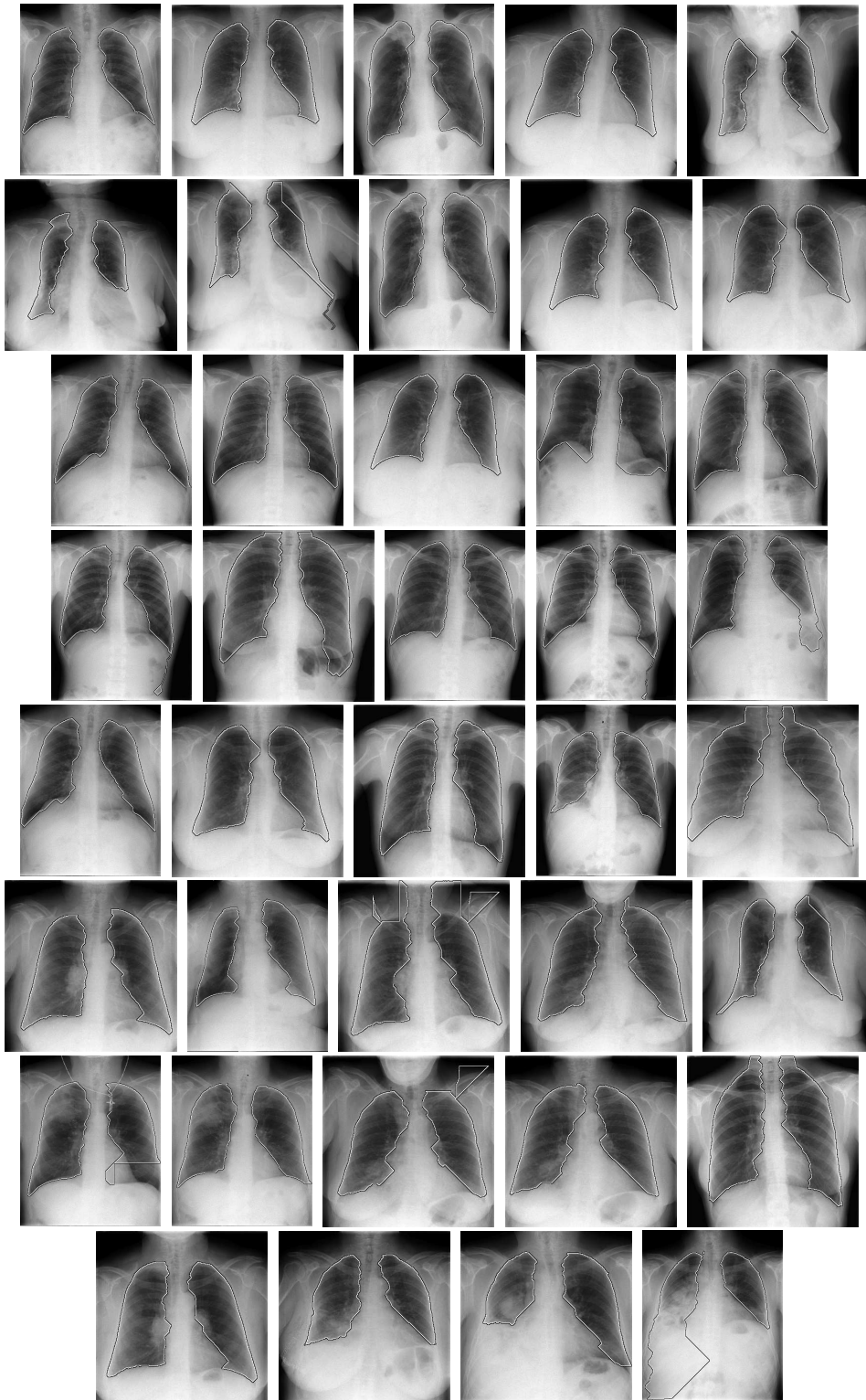


Figure B.3: Segmentation outputs of the contour delineation method using the private image database (DP/HSJ, all 39 images, contours). Performance measures are reported in Table B.3.

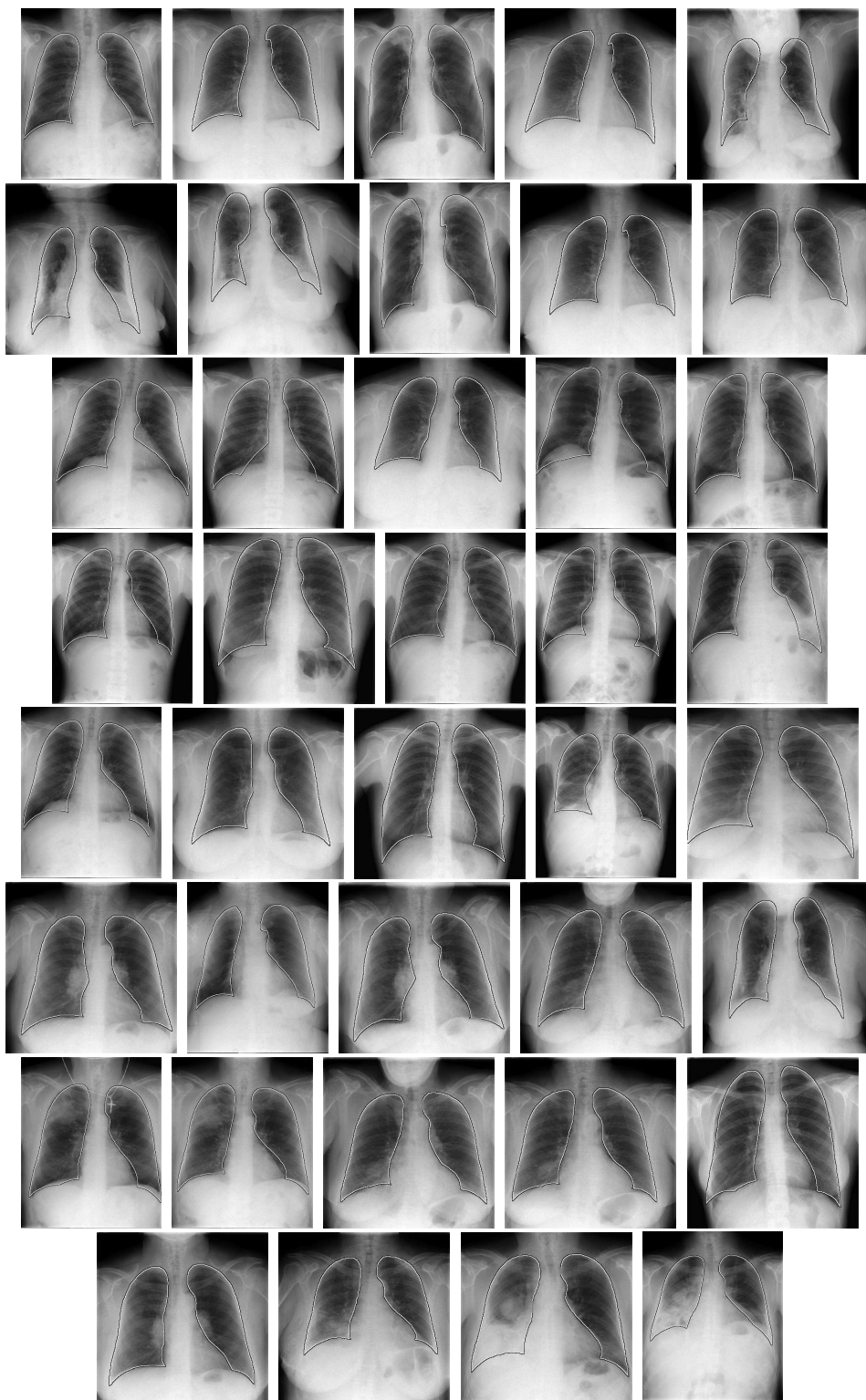


Figure B.4: Segmentation outputs of the model-to-image registration method using the private image database (GA/HSJ, all 39 images, contours). Performance measures are reported in Table B.4.

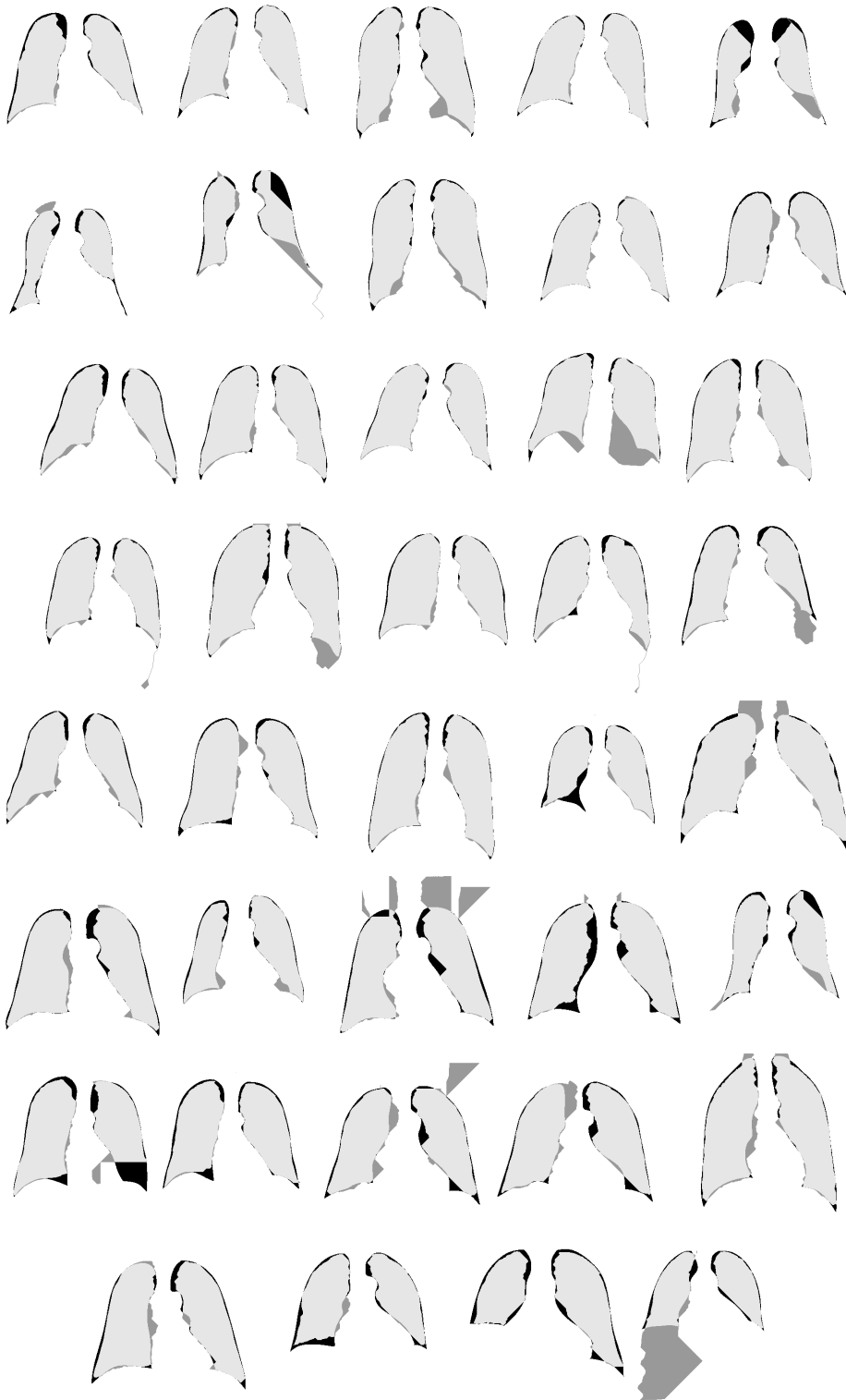


Figure B.5: Segmentation outputs of the contour delineation method using the private image database (DP/HSJ, all 39 images, confusion matrix). Performance measures are reported in Table B.3.

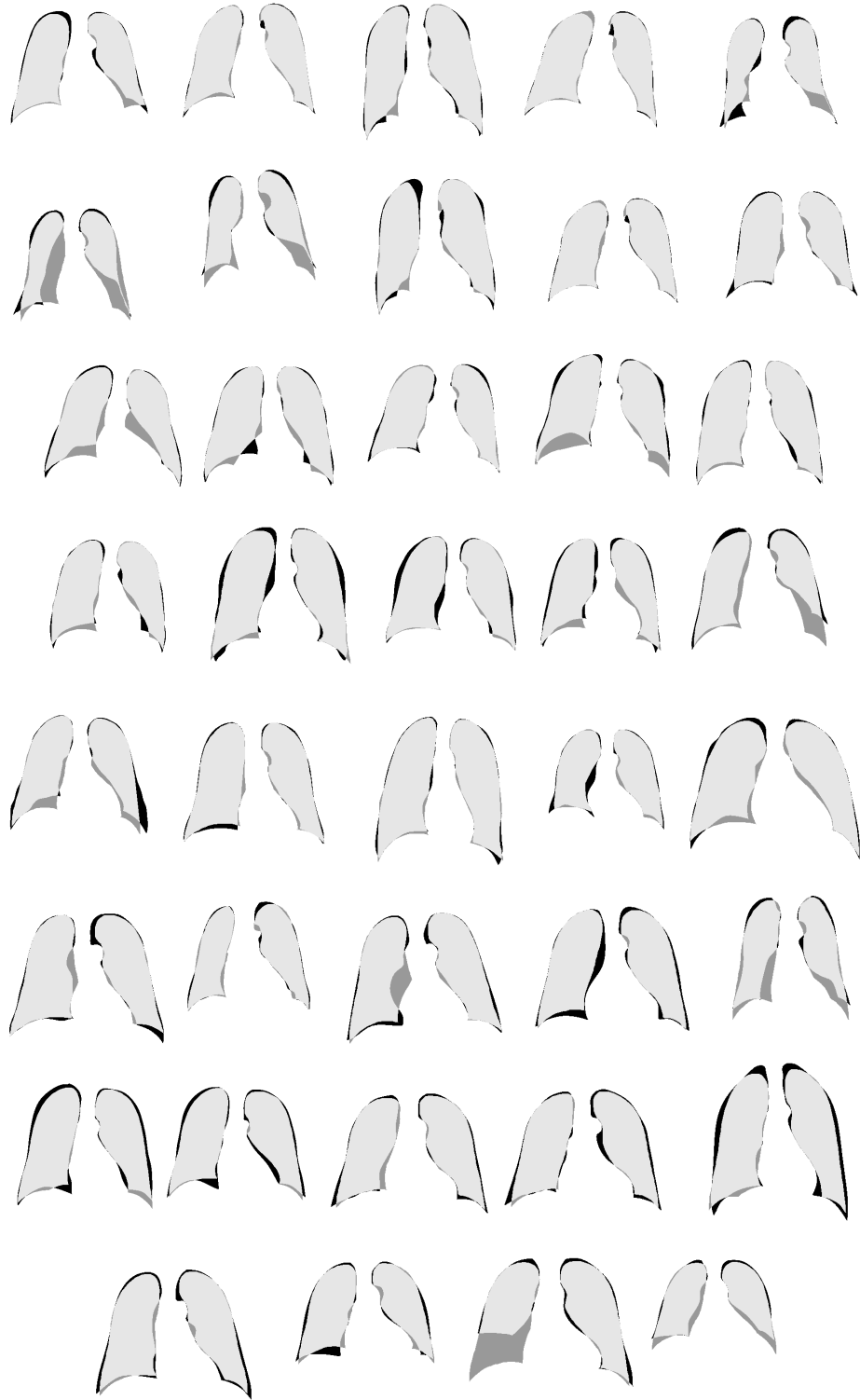


Figure B.6: Segmentation outputs of the model-to-image registration method using the private image database (GA/HSJ, all 39 images, confusion matrix). Performance measures are reported in Table B.4.

Appendix C

3D CT IMAGE SEGMENTATION RESULTS

In this Appendix, segmentation outputs of the large airways identification algorithm are presented. The results, shown in Figure C.1, were qualitatively evaluated by an experienced radiologist to select the best and worst segmentation results from CT images of a private database (HPH).

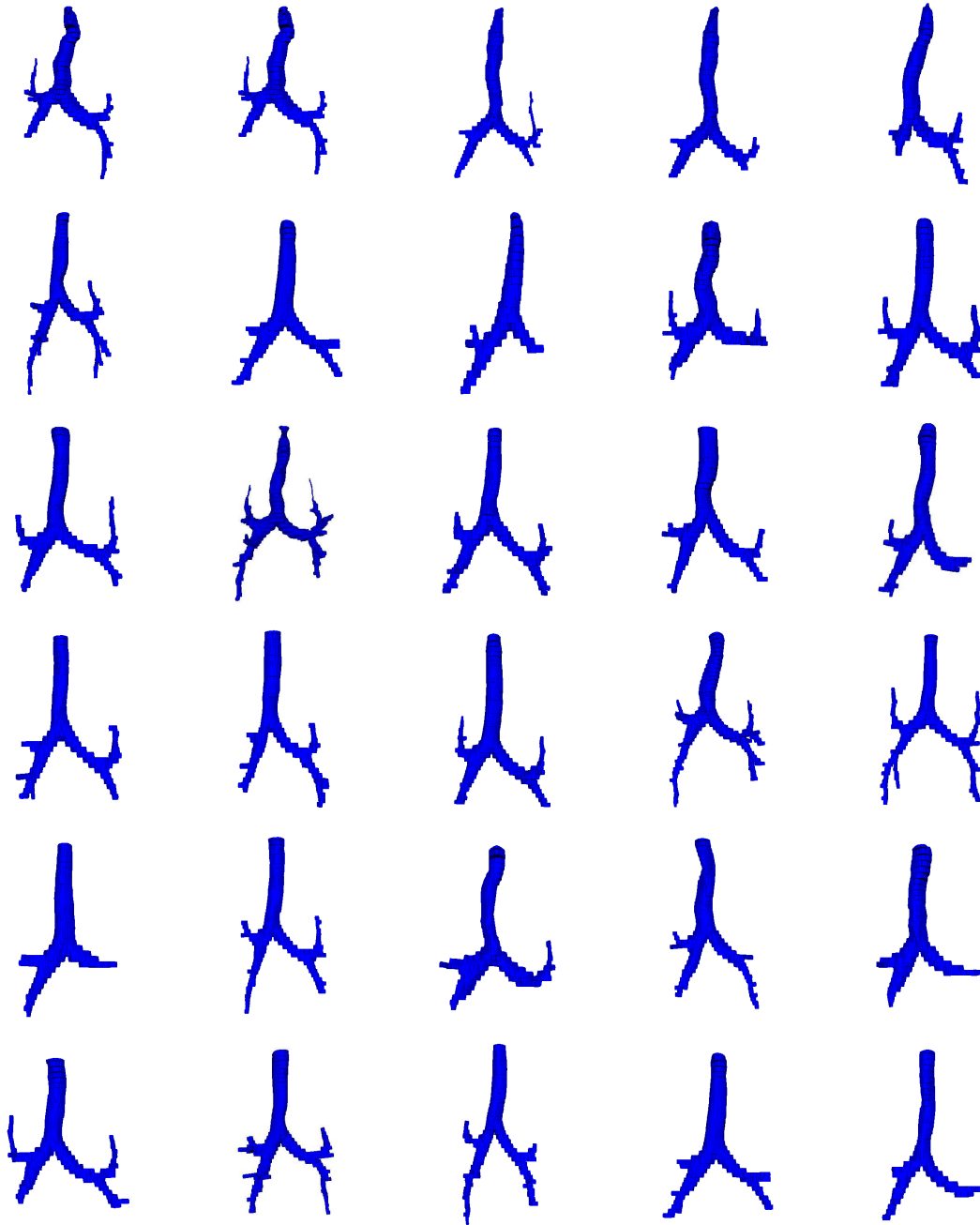


Figure C.1: Large airways segmentation results (surface rendering). The results are shown for all 30 CT images of a private database (HPH). Qualitative evaluation was used to select the best and worst segmentation outputs shown in Figure 5.17.

Appendix D

RADIOLOGICAL DENSITY FROM DIGITAL PLANAR RADIOGRAPH

In this Appendix, the relationship expressed by Eq. 6.25 is deduced. The radiological density $\mathbf{R}_{\text{xray}}$ and the gray level of a digital planar radiograph $\mathbf{X}$ are related to each other by considering the point source geometry of Figure 2.9. We assume that the X-ray source $\mathbf{s}$ is located at position $(0, 0, d)$. The optical transmission at point $\mathbf{p}_d = (x_d, y_d)^T$ of the digital image measured at the pixel detector plane OXY is given by

$$\mathbf{T}(x_d, y_d) = c_1 \mathbf{X}(x_d, y_d) + c_2, \quad (\text{D.1})$$

where c_1 and c_2 are constants related to the process of digitalization. Since the optical density $D = \log[1/T]$ is related to the imparted energy through Eq. 2.29, $D = \eta_1 \log[\eta_2 E_p]$,

$$\log \left[\frac{1}{c_1 \mathbf{X}(x_d, y_d) + c_2} \right] = \eta_1 \log [\eta_2 E_p(x_d, y_d, E_0)], \quad (\text{D.2})$$

and, from Eq. 2.27 and Eq. 2.28,

$$\begin{aligned} \log \left[\frac{1}{c_1 \mathbf{X}(x_d, y_d) + c_2} \right] = \\ \eta_1 \log \left\{ \eta_2 E_{pi}(x_d, y_d, E_0) \exp \left[- \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r} \right] \right\}. \end{aligned} \quad (\text{D.3})$$

Equivalently,

$$\log \left[\frac{1}{c_1 \mathbf{X}(x_d, y_d) + c_2} \right] = c_3 + c_4 \log \left\{ \exp \left[- \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r} \right] \right\}, \quad (\text{D.4})$$

where the constants c_3 and c_4 are defined as

$$\begin{aligned} c_3 &= \eta_1 \log [\eta_2 E_{pi}(x_d, y_d, E_0)], \\ c_4 &= \eta_1. \end{aligned} \quad (D.5)$$

Since $\log(x) = c_3 + c_4 \log(y) \Leftrightarrow x = 10^{c_3} y^{c_4}$, Eq. D.4 is rewritten as

$$\frac{1}{c_1 \mathbf{X}(x_d, y_d) + c_2} = 10^{c_3} \left\{ \exp \left[-c_4 \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r} \right] \right\}, \quad (D.6)$$

and

$$\frac{1}{\mathbf{X}(x_d, y_d) + k_1} = c_1 10^{c_3} \exp \left[-c_4 \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r} \right], \quad (D.7)$$

where the constant $k_1 = c_2/c_1$ has been introduced. The above relation is equivalent to

$$\ln [\mathbf{X}(x_d, y_d) + k_1] = -\ln(c_1 10^{c_3}) + c_4 \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r}. \quad (D.8)$$

At point (x_d, y_d) in the detector plane, the final relationship between the radiologic density $\mathbf{R}_{\text{xray}}$,

$$\mathbf{R}_{\text{xray}}(x_d, y_d) = \int_{\mathbf{s}}^{\mathbf{p}_d} \mu(x, y, z, E_0) d\mathbf{r}, \quad (D.9)$$

and the pixel gray level of the digital planar radiograph $\mathbf{X}$ is obtained for the monochromatic case:

$$\mathbf{R}_{\text{xray}}(x_d, y_d) = k_3 \{ \ln [\mathbf{X}(x_d, y_d) + k_1] + k_2 \}, \quad (D.10)$$

where the constants k_1 , k_2 and k_3 can be computed as

$$\begin{aligned} k_1 &= c_2/c_1, \\ k_2 &= \ln(c_1 10^{c_3}), \\ k_3 &= 1/c_4. \end{aligned} \quad (D.11)$$

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