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An Environment for the Objective Comparison of MRA and DSA Images

by

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Biomedical Engineering

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A Thesis submitted to the Faculty of Graduate
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requirements for the degree of
Master of Engineering.

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Abstract

This thesis describes an environment in which two angiographic methods, Digital Subtraction Angiography (DSA) and Magnetic Resonance Angiography (MRA), can be objectively compared and analyzed.

Such an environment requires that both angiographic projections be displayed from the same view-point and with the same projection geometry. The two angiograms are displayed side by side and several points on the vascular structure are identified in both modalities. These points are used to estimate, using a Least Squares Minimization, the Homogeneous Transformation Matrix (HTM) characterizing the projection of the DSA image. The resulting HTM is used to generate a corresponding Maximum Intensity Projection (MIP) of the MRA dataset. The number and location of the required homologous point-pairs are determined empirically.

Other alternatives to MIP are presented as well, and their performance relative to DSA is discussed. Images from each modality are displayed stereoscopically to reflect the three dimensional nature of the vascular tree.

Résumé

Cette thèse décrit un environnement qui permet de comparer et analyser objectivement deux méthodes d'angiographies, l'Angiographie par Soustraction Digitale (ASD) et l'Angiographie par Résonance Magnétique (ARM).

Cet environnement exige la présentation des deux angiogrammes vues du même point de vue et sous les mêmes conditions de projection. On démontre les deux angiogrammes un à côté de l'autre et plusieurs points sont identifiés, sur les vaisseaux sanguins. Ces points sont utilisés pour la calcul de la Matrice de Transformations Homogènes (MTH), qui définit la projection de l'image ASD, par une minimization de la somme des carrés. Cette MTH est utilisée pour la génération d'une Projection d'Intensité Maximale (PIM) du volume ARM qui correspond à l'ASD. Le nombre et la location des points homologues sont déterminés par des expériences.

D'autres alternatives pour la PIM sont introduits et on étudie leurs performance par rapport à l'ASD. Les images de chaque modalité sont présentées en stéréo pour démontrer la nature tri-dimensionnelle de l'arbre vasculaire.

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Preface

The aim of this thesis was to develop a system that would help the surgeon to compare images from two angiographic imaging modalities, and use this set of two images in the planning and guidance of neurosurgical procedures. This has been accomplished through the simultaneous stereoscopic display of both angiograms viewed with the same projection geometry.

Image guidance in neurosurgery relies on the knowledge the Image Guided Neurosurgery (IGN) system acquires about the internal cerebral structure -anatomical and vascular. This knowledge is enhanced through the combination of several imaging modalities together in order to provide a broader perspective of the internal structure [58, 68, 61].

At the Montreal Neurological Institute and Hospital (MNI/H), Stereoscopic Digital Subtraction Angiography (DSA) projections are used in the planning of neurosurgical procedures [64]. Computerized Tomography (CT) and Magnetic Resonance Imaging (MRI) are also employed as volumetric datasets describing internal anatomical structures, increasing the accuracy of stereotactic neurosurgery [15]. Since these volumetric datasets lack the ability to show vasculature, which might lead to planning paths that intercept vessels causing complications during the procedure, DSA images are correlated with MRI and CT to increase the reliability of Image Guided Neurosurgery (IGN) [62, 60].

Due to its *projection* nature, a single DSA image provides little information about the depth of the vessel being viewed or its location in 3D space. This limitation on

DSA images is compensated for by producing stereoscopic image pairs of the vascular structure in the head and present them in a way as to reflect the volumetric nature of the head. Several techniques are used in the stereoscopic display of DSA images. These include crossing the eyes to produce a third virtual 3D image in front the stereo pair, using the “*Wheatstone*” stereoscope to help the observer fuse the stereoscopic pairs or by means of a computerized system as described in chapter 3 [33, 61, 16].

This work addresses the display of both DSA and MRA datasets. The former is typically a 2D projection of the structure being imaged, while the latter is a 3D volume representation of the object.

DSA images are presented to the user stereoscopically to compensate for the lack of structure depth. Potential distortions of DSA images are presented. “*Pincushion*” distortion is discussed in detail in chapter 4. Such distortion is due to the curving of Image-Intensifiers (II) and is corrected for by generating a displacement map and then applying a set of transformations that correct for this distortion on a pixel-by-pixel basis.

The display of volumetric MRA datasets, on a flat 2D screen is also addressed here. The most popular technique that is used in generating projection angiograms from 3D MRA datasets is called Maximum Intensity Projection (MIP). A simplified algorithm for the rapid generation of good quality MIPs is presented in chapter 4. When a 3-D dataset is presented on a 2-D screen, much of the volumetric information is lost. The 3D nature of the volume may nevertheless be preserved using a stereoscopic display of the projected datasets [36, 35, 32], or by distance coding of the projection [90].

To improve the quality of MRA projections, some pre-processing is performed on the volumetric dataset, to clean the volume of residual background noise that might add ambiguity to the identification of blood vessels [2]. Techniques in automatic and semi-automatic segmentation are presented in chapter 4, including *edge detection*, and *boundary extraction* algorithms [3].

This thesis is organized as follows:

The role of angiography in image-guided neurosurgery is presented in chapter 1. The theory behind image acquisition of both DSA and MRA and the techniques used in producing these images are discussed in chapter 2. The working environment and the software and hardware setup used in the development of this comparison system are introduced in chapter 3 along with a discussion of some image correlation techniques. The techniques for displaying projection angiograms of both DSA and MRA as well as a new and fast technique for generating an MIP are presented in chapter 4. In chapter 5 the correlation algorithm is then applied to simulated and real datasets.

Original contributions to research in this area are:

- the development and implementation of a computerized system for the objective comparison of the two angiographic imaging techniques, DSA and MRA.
- implementing a correlation algorithm to match DSA and MRA projections reliably in the same space.
- the design and implementation of a new and fast technique for the production of MIPs from MRA datasets.
- the stereoscopic display of a correlated set of MRA/DSA angiographic images.

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Chapter 1

Introduction

1.1 Angiography in Neurosurgery

For the last 10 years the surgical team at the Montreal Neurological Institute and Hospital (MNI/H) has been performing stereotactic surgery with the aid of direct image guidance. The rationale for using Image-Guidance is that having accurate information about the position of blood vessels and other major structures in the head allows the neurosurgeon to plan a trajectory that does not cross any major blood vessel or important brain structures. This information is most useful if it specifies the exact 3D location of the vessel lumina and their location relative to other vessels. Within the Image-Guided Neurosurgical (IGN) environment several imaging techniques provide this information, but with different levels of accuracy and detail. Initially, this involved the use of Computerized Tomography (CT) only, but with the introduction of Digital Subtraction Angiography (DSA) and Magnetic Resonance Imaging (MRI) into neurosurgical planning, these modalities were employed as well. The most important imaging modalities for visualizing blood vessels in the head are DSA and Magnetic Resonance Angiography (MRA). In addition, Computerized Tomographic Angiography (CTA) is sometimes used but will not be discussed in this thesis. MRA images are acquired as a volume data-set and provide 3D information about the lo-

cation of the vessel tree in the brain, whereas DSA images provide projections of the vascular system and are normally obtained and displayed stereoscopically in order to portray information about the depth and the 3D nature of the blood vessels.

The discrepancies between the two above mentioned image modalities are due to the differences in the mechanism of acquisition. MRA images are acquired from excitation of spins in the volume to be imaged and quantitatively describe the magnetization difference between moving and stationary spins, and thus a 3D volume representing the locations and size of the blood vessel is obtained. MRA is visualized using a Maximum Intensity Projection (MIP) [43], where a ray is projected through the volume onto a 2D grid picking up the voxel with the highest intensity. Usually an MIP image is generated using parallel ray-casting to save on computation time. On the other hand, DSA images are projected onto the 2D grid from an X-ray point source, with the rays leaving the source and traversing the object summing the electron densities along the way. These rays diverge to envelop the whole volume, so objects that are farther from the X-ray source appear smaller on the projection.

While DSA has become the standard means of visualizing the blood vessel tree in the head, and an important tool in neurosurgical planning, it would be more convenient if the same information could be acquired using MRA alone. Not only would this eliminate the radiation dose to the patient from X-rays, but the MRA procedure could be scheduled concurrently with an MRI study.

In order for the surgeon to objectively compare the different blood vessel imaging modalities, they both need to be visualized in the same space or in corresponding spaces, so that a point in one image modality will have a homologue in the other. From the above description of the nature of the images one can appreciate the difficulty of integrating different images from different modalities in the same space, and the accommodation an experienced neurosurgeon will have to make to correlate the two data sets while planning the neurosurgical procedure.

Unfortunately, since DSA is a projection image of the 3D structures of the blood

vessels in the head onto a 2D plane, most of the 3D information about the vessels position is lost. A solution to this problem is to acquire the DSA images stereoscopically (by taking two images of the same object using two different views). This solution requires that the observer cross his/her eyes, or view the images on a stereoscopic workstation, in order to merge the two images and perceive a three dimensional image of the object.

MRA is a technique that can potentially provide a more accurate 3D representation of the internal vascular structure of the head. The images are acquired by measuring the signal emanating from points in the volume, so a quantitative image representing the location of the blood vessels is possible. The technology for MRA is relatively new and still has many shortcomings, in particular a poorer resolution compared to DSA, as well as potential distortions introduced by patient motion, non-homogeneity of the static magnetic field and irregular flow patterns in the head [49, 57, 89].

1.2 Stereoscopy and Stereotactic Space

“Stereo” is a Greek word meaning solid object, and in the context of vision, stereo vision is the ability to fully visualize a three dimensional object. Stereoscopy is used extensively in image-guided neurosurgery because it enables the surgeon to have to a realistic feeling for the physical nature of the structure being examined, and allows only qualitative 3D information to be derived from pairs of 2D views. To obtain more quantitative information much work is needed to correlate the two views and perform the triangulation, as described later in this chapter.

1.2.1 Stereo Imaging

For the past 60 years, neurosurgeons at the MNI/H have used stereo X-ray images for planning neurosurgical procedures. All images are acquired as stereo pairs giving

projection images relatively close to the geometry of the images obtained by the human eye. Usually one image is acquired in a particular direction followed by a second taken after rotating the axis of the X-ray tube Image Intensifier (II) combination by 5-7 degrees, simulating the separation between the eyes [71, 72], (see figure 1.1).

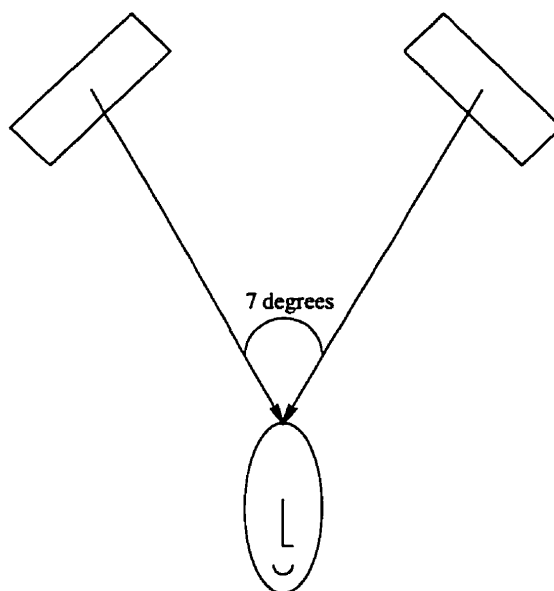


Figure 1.1: Scheme for stereo image acquisition

In order to obtain depth information using a stereoscopic display, two slightly different images of the scene need to be generated. If the exact location of the same structure is determined in each of the two images, then the depth of the object in question can be determined by performing triangulation [24]. The human brain is capable of qualitatively visualizing the 3D object if a stereoscopic pair of views is available. With the use of a computer, quantitative depth information is attainable from a stereo pair, by matching similar objects in the two images on a pixel-by-pixel basis. For each matched pair, a ray from the focal point of each image traversing the particular point is drawn, and the point of intersection of the two rays is the actual physical location of this object point. This procedure can be seen in figure 1.2, where the depth of the object and thus the third dimension of the image can be measured directly, after accurately determining the location of the object in the

two images. The problem of object matching in stereo images is by itself an open problem in computer vision and the solution is not trivial [4, 18]. The usual method of viewing stereo images is by showing the left image to the left eye and the right to the right eye. This is done by either using the “crossed-eye” technique favoured by many radiologists and surgeons, or by providing a computerized display that directs the different images to their respective eyes ¹.

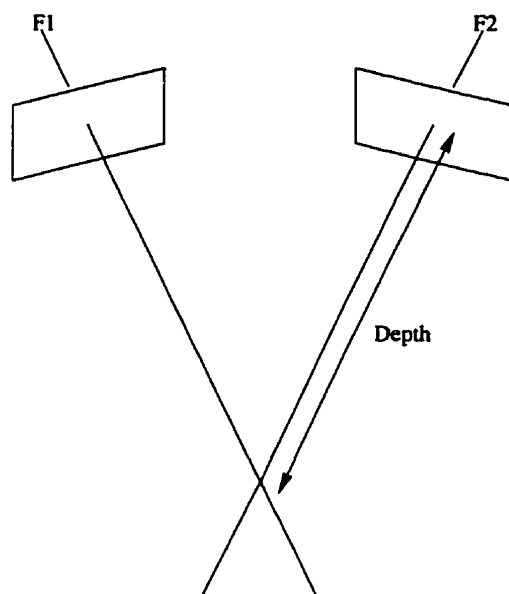


Figure 1.2: Obtaining depth information from a pair of stereo images

1.2.2 Stereotactic Space and the Stereotactic Frame

In order to perform neurosurgical procedures reliably, the surgeon needs to be able to locate structures in the head accurately and precisely. Stereotactic space is the tool used by the neurosurgeon for locating structures in 3D, and provides the coordinate system in which structures are correctly identified and accurately located. This approach allows the surgeon to accurately and unambiguously locate any point in the head, and to plan a minimally invasive path through delicate and vital structures

¹See section 3.2.2

in the head. The surgeon performs all the planning and preparation in stereotactic space, where 3D images of brain structures are visualized and manipulated, without the risk of removing healthy tissues or causing any damage to other brain structures. The instrument that establishes the coordinate system of stereotactic space is the stereotactic frame. This device is clamped onto the patient's head, during imaging and surgery, and defines an origin for the coordinate system that describes the location of objects in stereotactic space. Numerous frames, all of which have basically the same design, exist in the neurosurgical community. They typically consist of a cubical box that holds the patient's head in position and provides support for mounting surgical equipment [45, 46, 29, 54, 56]. Added plates on each side of the frame introduce landmark points that may be visualized in the image. These points help orient the frame in 3D space for CT and MRI and determine the projection geometry in DSA [36, 56].

The transition from the image position to the real position of the structure is achieved via linear transformations which relate stereotactic space with the patient space (the space within which the patient head and brain structures exist [36]). The IGN environment presents to the surgeon all the available information about the position and size of structures in the head, acquired from different imaging modalities (MRI, CT, DSA, MRA, Ultrasound). These images are displayed and organized in the same reference space defined by a single coordinate system in such a way that all manipulations performed on the imaged structures faithfully represent the changes that affect the real structures.

1.3 Aim and Objectives

The concept of using different imaging modalities is not new to Image-Guided Neurosurgery, and several modalities are often integrated together, to assist in the planning of a neurosurgical procedure [67, 69, 59, 66]. The reason for using several modalities

at the same time, is that there is no single imaging modality that gives the surgeon all the needed details (anatomical, vasculature and functional), in order to perform safe neurosurgical procedures. The first two modalities to be introduced into the same space were CT and DSA which provide anatomical and vascular descriptions of the head [15, 34], followed by DSA and MRI, helping surgical guidance by introducing vascular tree location [12, 65, 63, 11, 35]. Then came MRI and Positron Emission Tomography (PET) which provide anatomical and functional descriptions of brain structures [77, 78, 13, 16],

The above mentioned systems rely on the identification of specific points, called fiducial markers, clearly visible on the different imaging modalities being integrated. These fiducial points are permanent markers glued onto, or drilled into the plates of the stereotactic frame, and provide accurate and reliable reference points that can be identified in the different imaging modalities being integrated. Based on these matched points, the transformation from one image modality to the another is possible [12]. The elements of these linear transformations are described by a matrix called the *Homogeneous Transformation Matrix* (HTM). Although these transformations do not account for non-rigid deformations, they are a fast and effective means of correlating different image modalities used in neurosurgical planning at the MNI/H. A major drawback of such a system is the requirement that the patient be wearing the stereotactic frame during imaging and surgery, which is often a cause of pain and discomfort.

The aim here is to develop an environment that will allow the objective comparison of the two important vascular imaging modalities of DSA and MRA. In order for this comparison to be as faithful as possible, the two imaging modalities should be in the same coordinate system and reflect the same view of the vessel tree. The two images must describe the same view of the head, providing similar representations of the vessel tree. If a blood vessel is visualized in the DSA image from a certain view-point, then the same blood vessel should be present in the MRA image with the same

orientation and geometry of the view-point. In order to achieve this, one first needs to generate an MRA projection image using the same viewing parameters as the DSA image. This is obtained by applying a set of linear transformations that reflect the projection geometry of the DSA image, on the MRA data volume. A correspondence between similar structures in the two images is thus established.

This thesis describes the development and the evaluation of an environment in which these two imaging modalities can be objectively compared. It also describes how this environment is used in measuring the performance of each of those two image modalities in frameless stereotactic neurosurgery along with their integration into the Image-Guided Neurosurgical (IGN) environment. The ultimate goal is to substitute DSA images with MRA images in the planning and guidance of neurosurgical procedures, but this will not be possible before an exhaustive evaluation of the two modalities is achieved using an environment such as that described here.

Chapter 2

Angiographic Imaging Techniques

This chapter presents the different methods of angiographic image acquisition employed at the MNI, and briefly discusses the constraints imposed by these acquisition techniques. The technique that is used to correlate two images in the IGNS environment is described below and its limitations discussed. Finally the manner in which these images are displayed to the surgeon is analyzed.

2.1 Digital Subtraction Angiography

When an X-ray beam traverses an object it interacts with its atoms, transferring energy to the molecules, fractionally reducing the intensity of the emanating X-ray beam. The amount of transferred energy is dependent on the medium being traversed: the higher the atomic number, the more energy is transferred. The resulting X-ray intensity is governed by the following relationship (Beers Law):

$$I = I_0 \exp \left[- \int \mu(x, y, z, E) dz \right], \quad (2.1)$$

where I_0 is the initial beam intensity, and I is the output beam intensity after it traverses the imaged body. $\mu(x, y, z, E)$ is the attenuation coefficient specific to the

medium being irradiated. This coefficient relates the number of stopped photons per unit distance compared to the number of incident photons. The attenuation coefficient is dependent on the nature of the medium and is a function of the energy E of the incident X-ray beam [42].

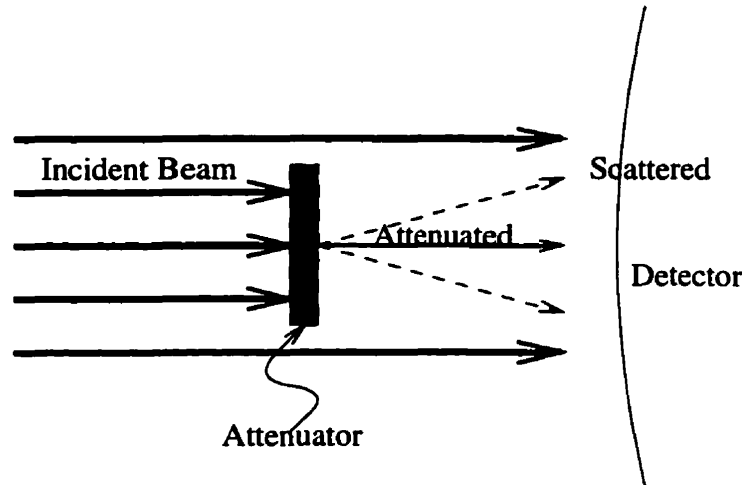


Figure 2.1: The attenuation of X-ray energy as it traverses an object

X-ray contrast agents are non-toxic compounds, based on Iodine ¹, that possess relatively high attenuation coefficients, much larger than the attenuation coefficient of human tissues. These compounds are introduced into the circulation to increase the contrast of the resulting image. Another reason for the use of Iodine compounds is that at 33.2 keV, Iodine absorption of X-ray beam increases abruptly and becomes 10 times larger than bone. This is due to a phenomenon called the K-shell effect, where electrons from the K level act like an additional shield for X-rays [14, 75].

Blood vessels do not show clearly in X-ray images because vessel walls have similar chemical composition to surrounding soft tissues, and thus have a similar X-ray attenuation coefficient. Likewise, because the attenuation coefficient of blood and surrounding tissues are similar, it is equally difficult to distinguish them on the basis of an X-ray projection. In order to view blood vessels clearly, contrast agents, as ex-

¹The contrast agent used at the MNI is *Iothalamate meglumine*, an Iodine based agent with 28.2% or 282 mg/ml chemically bound Iodine.

plained earlier, are introduced into the imaged vessels in order to enhance the signal difference between the blood and surrounding structures. The injection of contrast agent increases the invasiveness of the imaging technique, and augments the level of risk and discomfort associated with it. The contrast of the resulting image is directly dependent on the concentration of the contrast agent in the blood.

In order to produce an image with a given signal-to-noise ratio, the exposure N , to which an imaged body is subjected, depends on: the contrast agent concentration c , in g/cm^3 , the vessel size or the length of the contrast material traversed by the X-ray beam d , in mm , and the resolution p in lines per millimeter required of such an image. These variables satisfy the Rose model equation [44]:

$$N \propto \frac{1}{p^2 c^2 d^2} \quad (2.2)$$

In order to have the correct concentration of contrast agent at the imaged site the amount of injected contrast agent is thus determined by the size of the imaged vessels and the resolution required.

Subtraction radiography is based on the following principle. If the effect of stationary tissues on the attenuation of X-rays can be eliminated, then an image with enhanced blood vessels is attainable with less contrast agent than needed otherwise. This is achieved by obtaining a regular X-ray image obtained without any contrast agent and another with contrast filled blood vessels, taking the natural logarithm of each image (see below), then subtracting them from each other [44].

Subtraction angiography depends very much on the patient remaining motionless during the different exposures. This condition guarantees that the stationary structures will appear in the same place in the images taken at different times. By acquiring several images of the head with and without the presence of contrast agent, a resulting subtracted image of only the blood vessels is obtained.

Traditional subtraction angiograms are obtained by taking an image of the head before the introduction of the contrast agent in the local circulation. This image is

called the *mask* film and is the projection of all the soft tissue and bone structures in the head including blood. The scout film is reversed in polarity and a new image is obtained called the *subtracted-mask* film. A set of images of the head is then taken, this time after the injection of contrast agent in the blood. Several exposures are made in order to obtain several images at different phases of the contrast agent movement in the local circulation. The subtracted-mask and the contrast enhanced images are then added to each other and an image of only the blood vessels is obtained. In fact, subtracted angiograms represent the blood inside the vessels, but because the vessel walls are very thin the acquired images are a fair approximation of the vessel lumina, with an error margin of about 0.3 mm [10].

The subtraction should be performed after taking the logarithm² of the two images because the image intensity I , is proportional to the exponential of the line integral of the attenuation coefficient of the structures being traversed by the X-ray beam (see equation 2.1). If $\mu_t(x, y, z)$ is the attenuation coefficient of the structures being imaged, and $\mu_c(x, y, z)$ is that of the contrast agent, then the intensities of the two images (the subtracted-mask and the angiogram) are defined by:

$$I_1 = I_0 \exp \left[- \int \mu_t(x, y, z) dz \right] \quad (2.3)$$

$$I_2 = I_0 \exp \left[- \int (\mu_t(x, y, z) + \mu_c(x, y, z)) dz \right] \quad (2.4)$$

Taking the logarithm of the two images and subtracting them we obtain:

$$\log \frac{I_0}{I_2} - \log \frac{I_0}{I_1} = \int \mu_c(x, y, z) dz \quad (2.5)$$

which describes a projection through the contrast distribution in the blood vessels [6].

Digital Subtraction Angiography evolved as the natural evolution of X-Ray film

²When film subtraction is performed, the angiograms and the subtracted-mask are aligned and a new film is made of the two together [6].

subtraction techniques after the introduction of computers into the field of medical imaging [6]. In digital radiography, the X-ray beam, (after passing through the patient) impinges on an Image Intensifier (II). The output of the II is a light signal that is captured by a video camera, whose signal is subsequently converted to a digitized image, with the use of an Analogue to Digital Converter (ADC) (figure 2.2). In this process the signal producing the final image has changed several times, from X-ray beam detected by the II, transformed to optical signal at the input of the video camera, and then converted to electrical signal to be sampled and digitized.

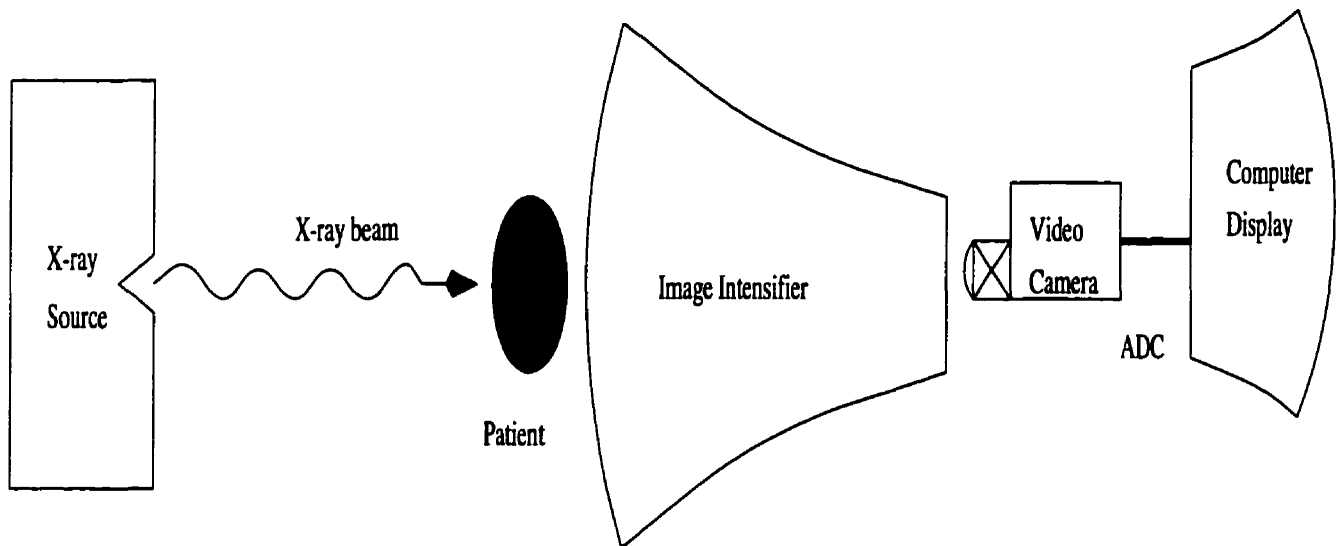


Figure 2.2: Scheme of a digital radiology system

While the image contrast is proportional to the product of the concentration of the contrast agent and the vessel thickness, the upper limit is determined by the maximum patient tolerance for such an intrusion.

Because contrast cannot be injected at the imaged site, special techniques are required in order that the concentration at the region being radiated satisfies equation 2.2. The two methods of introducing the contrast agent via veins (intra-venous) or via arteries (intra-arterial) are discussed below.

2.1.1 Intravenous DSA

In intravenous (IV) DSA, the contrast agent is injected into a vein, and after passing through the heart and the pulmonary circulation it finally arrives at the imaging site. During this mini-circulation its concentration changes due to dilution, temporal spread and the physiological filtering action of the lungs [87]. Images with IV injection therefore tend to have low contrast.

The concentration c of the contrast agent once it leaves the left ventricle, is similar to its concentration at the imaging site, and is given by the following equation [44]:

$$c = \frac{c_i \times R \times T}{V} \quad (2.6)$$

where c_i is the initial concentration of the contrast agent, R the rate of injection, T the injection duration, and V the blood volume that passes through the heart during this time. For typical values of R , T and V of 20 ml/sec, 2 sec and 800 ml, the final concentration of the contrast agent is given by:

$$c = c_i \times \frac{20 \times 2}{800} = \frac{c_i}{20}. \quad (2.7)$$

Hence, the concentration of the contrast agent is reduced approximately 20-fold when using IV injection.

2.1.2 Intra-arterial DSA

With the advent of improved and more secure mechanics of injection, intra-arterial (IA) injection became favourable. The main advantage of the IA injection technique is that the blood carrying the contrast agent travels directly to the imaging site, without passing through the pulmonary circulation. As a result, the decrease in contrast agent concentration is less than in the IV case. Images showing small vessel details and requiring small amounts of exposure become possible using the IA injection

technique. The injection of the dye is performed closer to the artery to be imaged thus allowing for more selective images than in the IV case.

IV DSA was the method used in the early 1980s because of its lower invasiveness compared to the higher risk involved with intra-arterial injection of contrast agent [44]. Another motivation for the use of IV over IA injection is the ability of injecting large amounts of contrast agent into the non-elastic veins in a short time, without causing major hemorrhage.

2.2 Magnetic Resonance Angiography

As is the case with X-ray images, it is difficult to distinguish between blood and neighbouring soft tissues because both have similar relaxation times. Clear visualization of blood vessels is not possible using regular Magnetic Resonance Imaging. Magnetic Resonance Angiography uses the fact that moving spins have different (larger, smaller or out of phase) magnetization than stationary spins. If the signal from stationary spins can be suppressed while the signal from circulating spins enhanced, a 3D map of the vessel tree can be produced.

By identifying moving magnetized spins one can obtain an image where the moving objects emit a larger signal relative to stationary tissues. This technique is called “*Time-Of-Flight*” MRA. Another way to obtain an MRA image is by subtracting an image quantitatively representing the flow velocity of blood from a regular MRI, thus obtaining an image representing the moving blood only. The technique that uses complex subtraction is called “*Phase Contrast*” imaging. Complex subtraction is used because the velocity information is encoded in the phase of the transverse magnetization of the spins.

Before discussing the method of MRA image acquisition, it is worthwhile looking briefly at the physics of blood flow in the human body.

2.2.1 Mechanisms of Blood Flow

The simplest form of fluid flow is constant flow in a rigid, straight, smooth-walled lumen. Although the vascular system is neither rigid, straight, nor smooth-walled, such basic flow can be easily analyzed and provides a language for discussion of the other more complicated forms of *in vivo* flow [49].

The no-slip condition on a fluid flowing on a plate results in the velocity of the fluid at the plate boundary being zero. This causes a velocity gradient to exist near the boundary, resulting in a shear force that acts to decelerate the fluid.

A parameter which characterizes the forces acting on the fluid is the Reynolds number Re , which can be thought of as the ratio of inertial to viscous forces acting on the fluid [57]:

$$Re = \frac{\rho U d}{\mu}. \quad (2.8)$$

Here, ρ is the fluid density, U is the mean velocity of the fluid, d is the diameter of the tube and μ is the viscosity of the fluid. Typical Reynolds numbers range from 1×10^{-2} in the arterioles to 5×10^3 in large arteries [57]. Based on these numbers the flow in the microcirculation is dominated by the effects of viscosity, while inertial forces are dominant in large vessels.

Steady flow

When fluid first enters into a tubular body its flow is described as a single disk with uniform velocity. As it advances in the tube, the tube walls drag the neighbouring fluid causing it to slow down. The fluid at this point flows in concentric rings of constant velocity. In steady flow the streamline rings do not mix or cross, and the flow satisfies the boundary conditions that its velocity must be zero at the walls of the tube [57]. The resulting flow profile is a variation on the “plug” flow where the velocity profile follows a parabolic shape as a function of the radius. This flow is called “laminar” flow, (figure 2.3), where the flow profile depends very strongly on

the viscosity of the fluid, on its density and on the radius of the tube. In addition, the first two factors usually decrease with temperature.

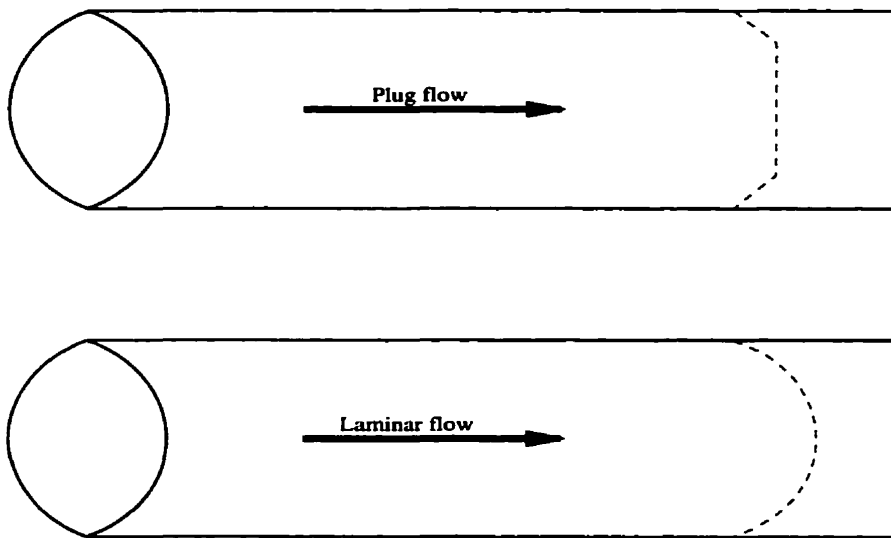


Figure 2.3: Plug flow and Laminar flow in a long straight tube

At higher velocities, a laminar flow profile is not maintained and a new component of the fluid flow shows up with a rapidly fluctuating velocity. This component is characterized by turbulence in the fluid flow that is typical of large arteries near the heart with high arterial pressure. As the flow rate increases, the flow becomes less orderly and more turbulence occurs. This is particularly evident in constrictions in the lumen diameter where the fluid velocity increases abruptly at the constriction and slows down afterwards. This is called “jet” flow (figure 2.4).

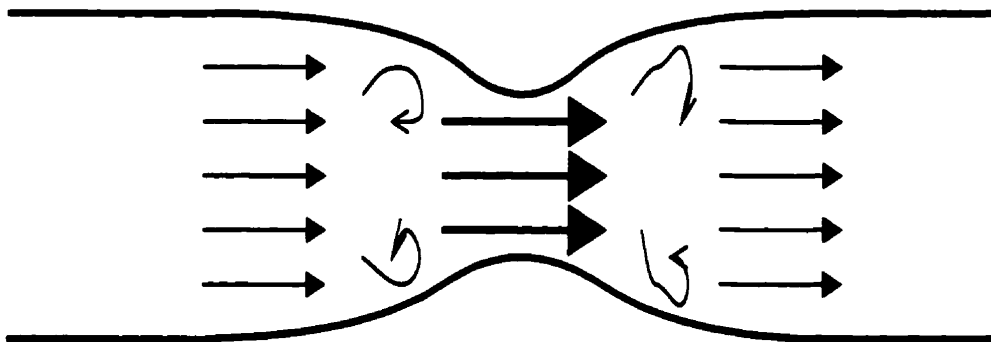


Figure 2.4: Jet flow in a constriction

Flow in curved tubes and bifurcations

When fluid flows in curved tubes, the flow near the inside wall of the tube is faster than the flow near the outside wall. In order to maintain steady flow a pressure gradient exists across the tube, resulting in an acceleration in the direction of the curvature. This gradient affects the velocity of the fluid which loses its pure axial nature and develops a velocity component directed toward the inner wall of the curved tube [57]. The resulting velocity profile has a superimposed cross-sectional velocity field that causes a shift in the peak velocity from the centre of the tube towards its outer wall (away from the bending), as demonstrated in figure 2.5.

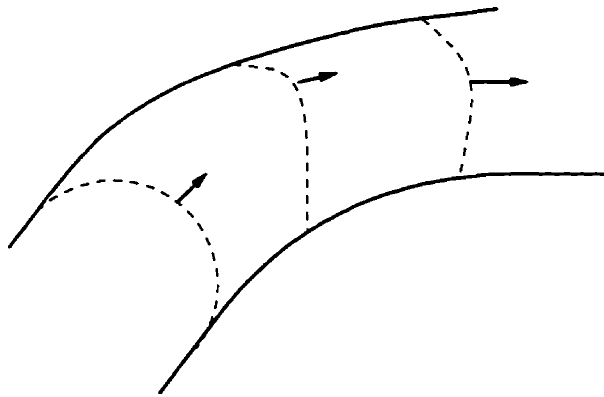


Figure 2.5: Flow in a curved tube and its corresponding velocity profile

This phenomenon is more pronounced in large and highly curved blood vessels and helps explain the flow behaviour in bifurcations. As the flow enters a bifurcation it divides into two, not necessarily equal, parts. As the fraction of the fluid with the highest velocity component (usually in the centre) comes into contact with the wall of one of the secondary vessels in the bifurcation, it must satisfy the boundary condition and thus slows down. The velocity of the flow near the other wall of the parent vessel is already at the desired value of zero. The two sides of the flow in the bifurcation experience different decelerations, which results in an asymmetric velocity profile, where the peak velocity is not at the centre of the vessel but more toward the inner side of the bifurcation. As the flow moves on in the child vessel it develops into

a laminar flow downstream from the bifurcation, (figure 2.6).

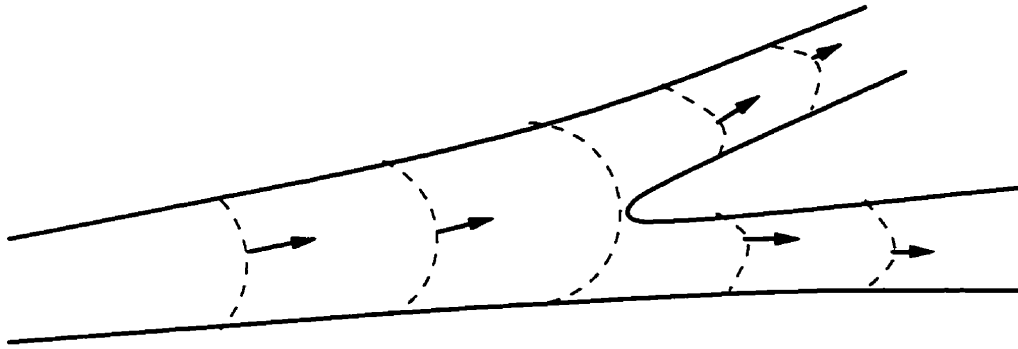


Figure 2.6: Flow in a vessel bifurcation

Pulsatile flow

One of the major complications of blood flow *in vivo* is its pulsatile nature. While this problem is more pronounced in large arteries near the heart, it is less evident in more distant vessels, where the flow is nearly steady. When the arterial pressure is well above 80 *mm Hg* the velocity increases, the flow becomes more turbulent and jet flow results. As the pressure is decreased in veins and distant arteries the fluid velocity decreases and the blood flow becomes laminar.

Another problem that might arise in large arteries is the reversal of the direction of flow and the displacement of the whole vessel as high pressure blood is pushed into it. This effect is seen as artifacts in MR images of large arteries with high pulsatile flow, and is explained further when the mechanism of MR imaging is explained later in this chapter.

2.2.2 Time-Of-Flight MRA

Time-Of-Flight (TOF) MRA techniques rely on the concept of spin *tagging*, where spins outside the region of interest are magnetically tagged and this tag is detected as the spins traverse the imaged region. Spin tagging can be achieved in several ways: inversion of longitudinal magnetization, presaturation, or inflow of fully magnetized

spins [70, 74]. Stationary spins that remain in the imaged volume for a long time receive multiple excitations in the form of spatially selective radio frequency (RF) pulses. They become magnetically saturated and the magnitude of their longitudinal magnetization diminishes considerably. On the other hand, moving spins entering the imaging volume between pulses bring in freshly magnetized spins, which in turn produce a high output signal. Unlike X-ray angiograms where the image intensity depends solely on the density of the contrast material, TOF and other MRA techniques rely on the nature of the flow pattern present in the vascular structure [43].

Different flow patterns exist in the human vascular system depending on the area of the body being imaged. In the steady flow case, blood in the middle of the tube always brings new unsaturated spins with full strength magnetization and induces a bright signal while the blood near the vessel walls elicits a signal whose strength is similar to that of neighbouring structures and the blood vessel walls themselves. Recirculating flow occurs at regions of vessel curvature, and in particular at vessel bifurcations³. The longitudinal magnetization of the spins in this type of blood flow becomes saturated because of its long stay in the excited region.

Pulsatile flow affects TOF MRA because slowly flowing blood results in a suppressed signal due to its long stay in the excited region and thus induces a lower contrast, compared to fast and strong flow that travels further in the region and is not saturated, resulting in a brighter signal. Due to the pulsatile nature of the flow, the magnetization strength varies from one read-out time to another, and is manifested as ghost artifacts along the phase-encoding direction in MRA images [43].

2.2.3 Phase Contrast MRA

While Time-Of-Flight (TOF) MRA imaging relies on the change in the longitudinal magnetization due to the movement of magnetized spins, Phase Contrast (PC) MRA uses the change in the phase of the RF signal generated by the transverse magnetiza-

³See section 2.2.1

tion as the blood moves in the presence of a magnetic field gradient. Since the phase of the transverse magnetization is very sensitive to motion along the directions of the applied magnetic field gradient, spins that are a fraction of a millimeter apart may exhibit significant transverse magnetization phase differences [20].

Phase accumulation in Flow

Hydrogen nuclei precess at the “Larmor” frequency ⁴ in the presence of an applied magnetic field. When a magnetic field gradient is applied, the precessing frequencies of different nuclei depend on their relative positions in the modified field. During their time in the imaged field, the spins develop a relative phase shift, based on their position within the gradients and their displacement velocities.

The phase of the magnetization (flowing or stationary) is a result of the application of the flow encoding gradient. The effects of this gradient can be undone by the application of a second gradient pulse of equal duration but with opposite polarity [70], (both pulses together are referred to as a bipolar gradient pulse), see figure 2.7. First the *spoiler* gradient acts to cancel the effect of any previous pulse and dephase any phase accumulation in the transverse magnetization. The slice selection gradient specifies the plane, with a finite thickness, that is excited by the RF pulse. The flow encoding gradient acts then as described above. The readout, or frequency encoding, gradient allows the magnetization of the spins with different frequencies to be detected by their frequency, according to their location in the slice along this gradient. At the same time the phase encoding gradient encodes the spins in the slice along the other direction with different phases. This is a typical MRI pulse sequence used to generate anatomical images, with the addition of a flow encoding gradient. This gradient causes all stationary nuclei to spin with uniform phase. For flowing nuclei, however, phase differences are directly proportional to the distance they have

⁴A precessing frequency related to the static magnetic field applied B_0 is given by: $f = \gamma B_0$, where γ is the gyromagnetic constant and is equal to 42 MHz/Tesla, for protons.

travelled along the gradient direction during the period of the application of the bipolar pulse. Hence the MR image that describes the flow in the imaged region is the result of the subtraction of phase encoded image P from a regular no-flow compensation sequence image D :

$$I = D - P, \quad (2.9)$$

where I is the intensity of the resulting image.

The above analysis is applicable for the ideal case where flow is constant in a long linear tube, which is not the case for blood flow in the head. This requires the application of more complex gradient pulses that cancel flow velocity and perhaps also higher order terms of motion.

3D Phase Contrast MRA imaging

The phase of the transverse magnetization after the application of a flow-encoding gradient pulse describes the flow in the direction of the applied magnetic field gradient. This is only useful for the component of blood flowing in the direction of the flow encoding gradient. For more complicated flow patterns this gradient encoding pulse is applied in the three principal directions. Three images are generated, each describing the flow along one phase encoding direction. The final image, representing the total flow along all directions at each voxel, is calculated using the Pythagorean relationship:

$$I = \sqrt{(D - A)^2 + (D - B)^2 + (D - C)^2}, \quad (2.10)$$

where I is the intensity of the final 3D image, A , B and C are the intensities of the three principal flow encoded images, and D is the non-flow encoded image. A typical Phase Contrast (PC) MRA with flow compensation along the XYZ directions is shown in figure 2.8. A very high quality anatomical image can be computed using the four generated images, thus reducing the negative effect of blood motion on the

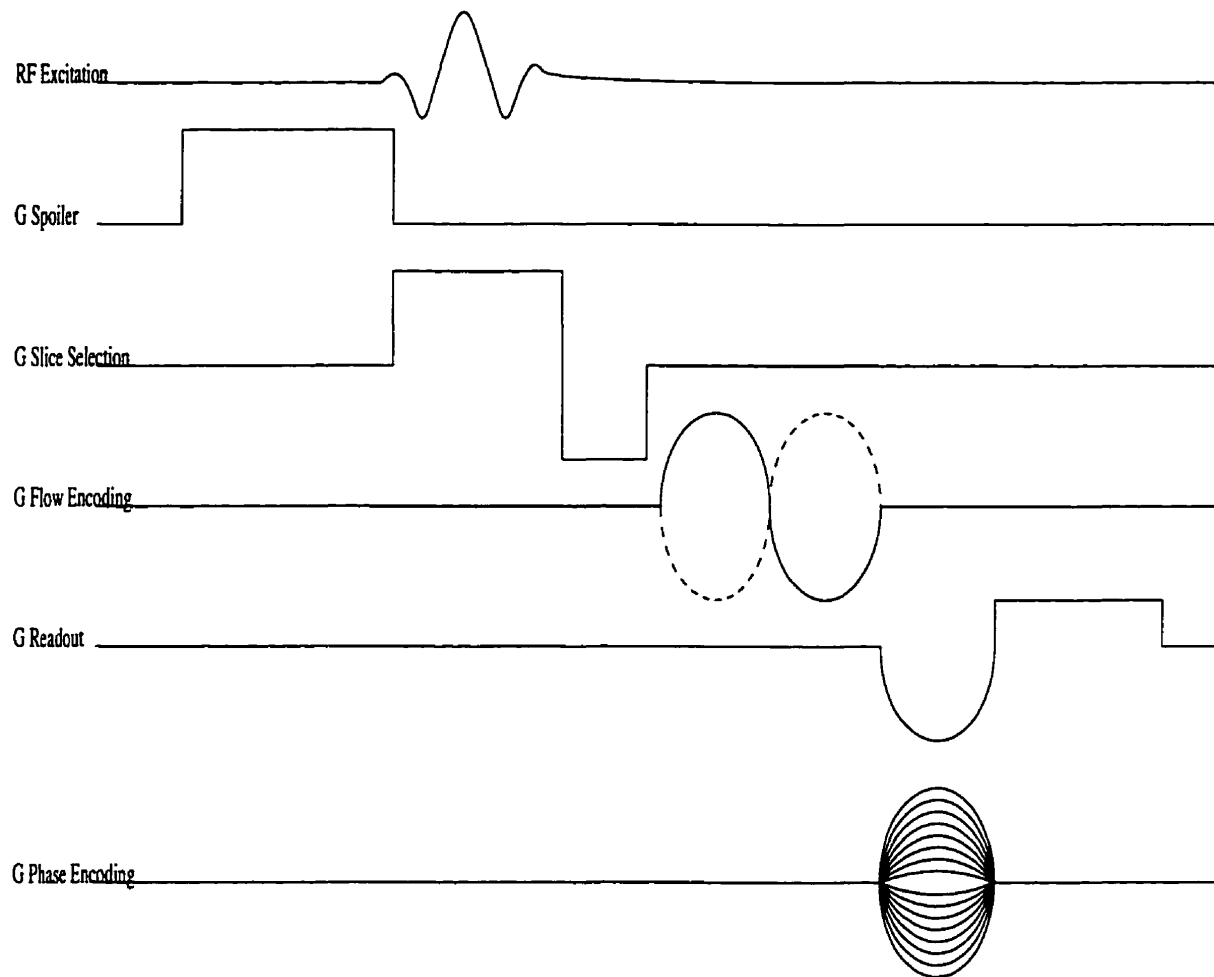


Figure 2.7: Pulse sequence for a typical Phase Contrast MRA

final image:

$$I = \sqrt{A^2 + B^2 + C^2 + D^2} \quad (2.11)$$

2.2.4 Displaying MRA Data

Although MRA is naturally a 3D data set, a 2D raster display must be generated, in order for the user to be able to view the vessel tree representation on a computer screen or on film. This transition from 3D to 2D causes some loss in the volumetric information inherent to an MRA data set.

The most common means of displaying MRA images is by traversing the volume in

“rays”, picking up the voxel with the highest intensity and recording its value on the display raster. This technique is called Maximum Intensity Projection (MIP) (figure 2.8). This projection technique is usually applied through a parallel ray tracing method, which works well for display purposes and qualitative analysis. A major drawback of standard MIP projection is its parallel ray projection nature, resulting in no depth effect on the size of the image of the projected vessel.

Optical “rays” coming to the human eye from an object converge at the pupil. This convergence results in an additional depth cue where objects that are closer to the eye appear larger than distant objects. There is a significant difference in visualization of vessels, between regular parallel ray MIP and DSA images. The latter are effectively projected from a point source, simulating the action of obtaining an image on the eye’s retina.

Some other techniques that have been proposed to view MRA images include segmenting the vessels and using volume rendering algorithms to display this 3D data on a raster. The problem with this approach is that until now, the segmentation stage is still manual and time-consuming. Perspective projection of the first encountered blood vessels⁵ results in great savings in computation time. This technique also generates higher quality angiograms than conventional MIP with more depth information encoded in the projected image of vessel tree [90].

2.3 Image Acquisition

In order for angiographic images to be useful as guidance tools in neurosurgery, they must have:

- A relatively high resolution, of the order of less than .5 mm. Both small and large blood vessels must be clearly distinguishable.

⁵This technique is described later in section 4.5



Figure 2.8: Magnetic Resonance Angiogram projected using parallel ray MIP

- A good contrast to noise ratio. The surgeon should not have to guess whether a particular image segment is a part of a blood vessel or just background noise.

These conditions can be obtained by fine tuning the acquisition parameters, such as kVp, mA, exposure time and field-of-view for DSA, and the gradient pulses and echo and repetition times T_E and T_R for MRA.

2.3.1 DSA images

DSA images in the MNI/H are obtained using a *Siemens*⁶ *Polytron Plus* DSA system. Images are acquired in different orientations depending on the vessels to be imaged: lateral images, where the X-ray source is to the left or the right of the patient's head; anterior posterior (AP) images are taken with the X-ray tube in front of the patient's head; and posterior anterior (PA) images are projected with the tube behind the patient's head. Different image orientations are used to give the radiologist and the surgeon a sense of the three dimensional aspect of the vessel tree. The surgeon or the radiologist is able to correlate these different views to more accurately locate the imaged vessels in the head. Most images are acquired 880 by 880 pixels in size, each pixel being described by 12 bits (pixel depth) allowing for positive and negative intensity values in the subtracted image, ranging from -2048 to 2047. A field of view of 270 mm for lateral images is used, giving rise to a .3 mm pixel size and 170 mm field of view for AP/PA images allowing a .2 mm pixel size.

Sources of Distortion in DSA

If distortion is present in a DSA image, it leads to its misinterpretation and errors in the planning of the neurosurgical procedure. By distortion we refer to any kind of image imperfection that might lead to any uncertainty in the classification of the vessel in the image. Distortions may be due to random noise caused by the X-ray scatter effect, detector imperfection, the Poisson distribution associated with the emission of photons, any fluctuation of the beam before it hits the II or additive noise at the video camera entry. Patient movement induces another distortion on the image causing non perfect subtraction and degradation of image quality. In addition, quantization noise during the digitization process, may also cause distortion in the image. In the following section various aspects of DSA image distortion are discussed

⁶Siemens Medical Systems.

and several possible improvements are presented.

Pincushion Effect This phenomenon is due to the convex nature of the Image Intensifier input window, built this way to support the high vacuum pressure inside, and to optimize electron optics. The resulting output image is distorted in a manner that reflects the convex nature of the detecting surface. The lines of an imaged rectangular grid appear to be curved progressively as a function of distance from the centre of the image. This phenomenon also results in the loss of resolution on the periphery of the image, with the lines appearing more blurred than near the centre. The curved lines can be corrected by taking an X-ray image of a grid, registering this image onto an equivalent digitally generated grid, and then calculating the displacement map for each pixel. Such a map describes the direction and the length of displacement each point has to make in order to correspond to the non-distorted grid. The resulting displacement map can be used to correct for the pincushioning effect induced on other X-ray images. A derivation of this method is given in section 4.2.1.

Poisson noise X-ray production is a stochastic process that follows Poisson statistics. In this sense, the number of photons incident on an object changes from one exposure to another, with the fluctuation being governed by the standard deviation of this random process;

$$\sigma = \sqrt{N} \quad (2.12)$$

where N is the number of incident photons per elemental area.

This effect is seen when the mask and angiogram images are subtracted. The same structure has a different number of detected photons in each of the two images. Thus, perfect cancellation of stationary tissues is not possible. As can be seen from equation 2.12, this effect can be reduced and the difference in object contrast in the different images is reduced, with increased exposure; however, patient exposure is limited by the maximum recommended X-ray dose for each procedure [6, 42].

Patient Motion As can be seen from the description of DSA image acquisition in section 2.1, subtraction angiography is very sensitive to noise and small amounts of patient motion. If the patient moves between different exposures, the resulting mask image and the contrast image may not correspond. Because of this misalignment image subtraction does not result in the removal of stationary tissues, and blood vessels in the final image might appear to be larger or smaller than they actually are. This motion artifact can be reduced if the images are taken in a short time, reducing the chances of patient motion. Sometimes breath holding is required from the patient in order to minimize such motion, although even with all these precautions taken, motion artifacts might still appear due to involuntary movements. This can be corrected by identifying similar structures, usually the skull bones, in both the subtracted-scout and the angiogram images. The technician may interactively displace one image with respect to the other to maximize the subtraction of unwanted tissues [55, 23].

2.3.2 MRA images

MRA images are obtained via a *Philips⁷ ACS 2 Gyroscan* MRI system in both 2D and 3D formats. The volumes are stored as a collection of slices in any of the basic three directions: axial slices, where the acquired slices are perpendicular to the vertical line through the head; coronal slices, covering the head from front to back; and, sagittal slices, which go from one side of the head to the other, perpendicular to the line joining the ears. A typical magnetic field gradient pulse sequence for obtaining a PC MRA is shown in figure 2.7, typically with a T_R of 40 – 47 ms, $T_E = 6.67$ ms, and flip angle $\alpha = 15^\circ$. The resulting images are usually stored in approximately 150 sagittal slices of 256 by 256 pixels each, giving rise to a $1 \times 1 \times 1$ mm³ voxel size. The images are stored in “short” format allowing a 16 bit pixel depth, and a dynamic range from 0 to 65535 or from –32768 to 32767.

⁷Philips Medical Systems.

Sources of Distortion in MRA

Although MR imaging provides a very detailed description of the imaged object, it lacks the geometric robustness of CT images. Different objects in the MR scanner require different acquisition parameters and are subject to different imaging artifacts. This is due to the inherent nature of MR image acquisition, which relies on the presence of a magnetic field. When an object is placed inside the scanner it changes the state of the static magnetic field, causing image structures sometimes not to correspond to their actual locations in the object (Shifts up to several millimeters). Regions of varying magnetic susceptibility cause small local variations in the magnetic field experienced by the nuclei. Major artifacts in MRI are usually caused by moving structure inside the imaged object, or by patient movement in the magnetic field. The first effect is used to advantage in MR angiography, while the second causes image degradation and requires some postprocessing of the data, for example through the use of field maps [17, 79]. Distortion may also be caused by an inhomogeneity in the static B_0 magnetic field, causing incorrect correspondences between the precession frequency and the location of the nuclei.

Patient Motion During MR image acquisition, patient motion degrades the image considerably and causes imaged structures to be misinterpreted and mislocated. Several remedies for motion correction have been proposed by Wood *et al* [89]. Physically restraining the patient's head with straps and pads reduces the effect of the patient's motion but is still limited and causes patient discomfort. Another solution is rapid image acquisition. If the image is acquired in a fraction of a second per slice, then the chances of the patient moving during this time are slim and thus blurring is reduced. The main problem with this approach is the motion during the time between the acquisition of different slices. Post-processing the data or image restoration is another valid option, although image restoration relies on the availability of some information about the displacement of the imaged object during image acquisition, and uses com-

puter vision techniques to correct for the displacement effect. Techniques to obtain information about the motion during image acquisition are under development and might increase the chances of successful image correction [89].

Inhomogeneity in the B_0 Magnetic Field Obtaining a uniform static magnetic field throughout the whole field-of-view (FOV) is technically impossible. This inhomogeneity is caused by the imperfection of the magnet, and the introduction of materials of different susceptibility in the field. Field discrepancies always exist between different points in the field, and this causes the spins to precess at Larmor frequencies different from what is expected at specific locations, giving rise to error in determining the location of these spins. A common technique for reducing the effect of this non-homogeneity is to generate an inhomogeneity map of the field of view, by acquiring a field-mapping scan of a water phantom, or the actual patient brain, and determining the exact magnetic field value at each point in the FOV. This map helps correct the acquired images by determining the actual value of the B_0 field at each location and then correcting the magnetization accordingly [83, 82, 17].

Effect of Pulsatile Flow Due to the pulsatile nature of blood flow in the head, MR measurements acquired at different times will have varied intensities, depending on the strength of the flow. This leads to MR signal discrepancies in the same blood vessel if it spans more than one slice. The pulsatile blood flow in the human body is periodic and follows the electrical signal measured on the heart muscle and recorded by the *electrocardiogram* (ECG) [87]. A proposed solution in MRA image acquisition is the triggering of the repetition time of the MR acquisition sequence (TR) to the heart beat via the QRS complex on the ECG [89, 87]. Taking images at the same point on the cardiac cycle allows for the same flow condition to exist throughout the whole segment of the circulation system. This results in a homogeneous image acquisition condition, but substantially increases the acquisition time and also the effect of patient movement and other sources of MRA distortion.

2.4 General Comparison of DSA and MRA images

Although the two angiographic image acquisition methods try to visualize the same vessel tree structure, they do not reflect the same physical or physiological properties of the blood vessels. One method subtracts the static image of blood from surrounding tissues, and the other takes advantage of the effect of the motion of the blood on the resulting signal.

DSA is a direct representation of the concentration of the bolus inside the blood vessel. The pixel intensity is characterized by a decaying exponential proportional to the line integral of the attenuation coefficient of the dye traversed by the X-ray beam [6]:

$$I = I_0 \exp \int \mu_c(x, y, z) dz \quad (2.13)$$

On the other hand, MRA is a description of the displacement of spins and flow inside the region of interest. The signal intensity of a voxel in the MRA volume is related to the motion of this segment [43, 20]. In the case of TOF MRA ⁸, the voxel intensity is a representation of the displacement of spins perpendicular to the imaged slice. Under some simple assumptions of repetitive excitation by 90° RF pulses and plug flow, the signal is given by [88]:

$$S \propto \frac{T_R}{d} + \left(1 - v \frac{T_R}{d}\right) \left(1 - e^{-\frac{T_R}{T_1}}\right), \quad (2.14)$$

where d is the slice thickness and v is the velocity of the spins. The term $v \frac{T_R}{d}$ represents the fraction of spins remaining in the slice between subsequent excitations. This equation is valid only for flow velocities $0 < v < \frac{d}{T_R}$. If the spins leave the slice completely then the signal reaches a maximum, which is independent of their velocity and T_1 [88]. When more complex flow patterns exist, the corresponding velocity function is used in equation 2.14.

⁸See section 2.2.2

In PC MRA ⁹ the signal at a particular point is related to the phase accumulated in this vessel segment, from the application of the velocity encoding gradient up to the time of the readout gradient. For a simple flow model that includes the first two terms of motion, velocity and acceleration: $x(t) = x(0) + v(0)t + \frac{1}{2}a(0)t^2$, the accumulated phase is given by the following equation [88]:

$$\phi(T_E) = \gamma x(0)M^0 + \gamma v(0)M^1 + \gamma a(0)M^2, \quad (2.15)$$

where M^0 , M^1 and M^2 are the first three gradient moments defined as:

$$\begin{aligned} M^0 &= \int_0^{T_E} G(t)dt \\ M^1 &= \int_0^{T_E} G(t)t dt \\ M^2 &= \int_0^{T_E} G(t)t^2 dt \end{aligned} \quad (2.16)$$

From the above discussion it is clear that the resulting images do not represent the same physical properties of the vascular tree, and the MRA image will in general demonstrate a wider range of vessels than a DSA image.

⁹See section 2.2.3

Chapter 3

Development of Analysis System

3.1 Introduction

This chapter introduces the methodology used in this thesis for the development of the angiography comparison and analysis system. The working environment in which the images are post-processed and manipulated is first described. It includes the software packages used in the development of the comparison system, and all the programming tools that help build the application. Also described are the different computational algorithms that are used to manipulate the images and obtain correlation information. The image display methods along with the software and hardware involved are also described, in particular the manner in which stereo images are presented to the surgeon. The basic principles of image matching are then presented and analyzed, and their application to this particular project is discussed. The concept of image registration through the use of matrix algebra and the *homogeneous transformation matrix* is illustrated. The previous uses of this technique for multi-modality image registrations, and their integration into the IGN environment are discussed. The manner in which the HTM can be used for the registration of DSA and MRA is also introduced. Finally the limitations imposed by the nature of the images involved and the computations needed for the development of such a system are discussed.

3.2 The Working Environment

The process of comparing images from different modalities requires the setup of a computerized system capable of providing the user with all the necessary information to make this comparison as objective as possible. The system should be organized in such a manner as to display both images with their respective views being taken from the same viewpoint and perspective. In addition, any point in one angiogram should have a corresponding point describing the same vessel segment in the other angiogram.

The working environment at the *Image-Guided NeuroSurgery* laboratory is the set of available tools that are used to build the imaging application. These tools include the libraries with the routines responsible for image manipulation, the graphic interface which takes care of displaying the resulting raster, and the programming languages that are used to organize these tools in a structured manner as well as to set up the user-interface. Also discussed is the specialized hardware required to provide the specific environment for the stereo display of stereo-acquired image pairs.

3.2.1 Software Description

The main programming languages employed in the *IGNS* laboratory are *C* and *C++*. While the *C* programming language provides an easy and straightforward syntax, the *object-oriented* nature of *C++* allows for more structured programming and facilitates the creation of large applications. The programmer can partition the application into small manageable pieces by defining new application-specific types, based on previously defined types called classes. This is called *data abstraction*, where the information takes precedence over the functions. Instead of data being what the functions use, functions are what the data perform [81]. A specialized software package *IAP*¹ (Imaging Applications Platform) is used in the IGNS laboratory to

¹ISG Technologies

build and manage imaging applications.

The Image Application Platform

IAP relies on the concept of *client-server* architecture in processing the data (figure 3.1). This is used to split major pieces of work of an application between processes. The client requests a set of tasks from the server which performs and manages these tasks in a manner transparent to the server. Unlike the traditional libraries concept, this architecture is responsible not only for performing the task but also the logistics and all the overhead associated with these tasks.

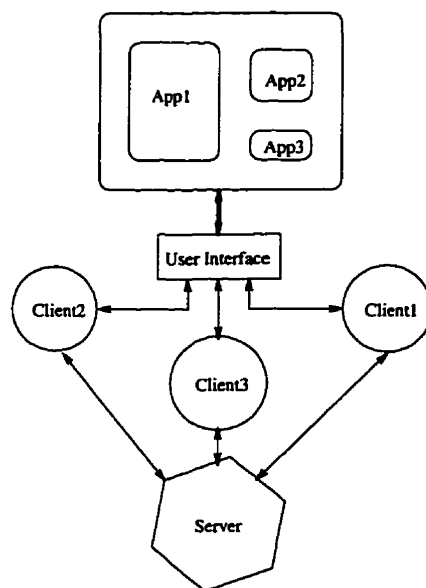


Figure 3.1: Client-Server interaction in the IAP environment

Before describing how an application runs, the basic tools used by the server to process a certain client's requests should be described. IAP is organized as a collection of *objects* each performing a specific task on the images. An object is some set of functions packaged in such a way that interaction with these functions is simplified [40]. The client gives the server a detailed description of the task at hand, by specifying the objects used and their interactions with each other. The components of each task are such objects and their ordering is referred to as object

connection. An application starts first by setting up a pipeline where different objects are connected, describing the ordered tasks to be performed on an image. A typical application pipeline is shown in figure 3.2. From the application programmer's point of view, objects exist in the client and are created, connected and destroyed, using client functions supplied in IAP *toolkit* libraries. In reality the objects created in the client are images of existing objects in the server which execute the requests of the client. A single copy, or "instance", of the object exists in the server at any time but several "handles" to that object may be present simultaneously, in different clients.

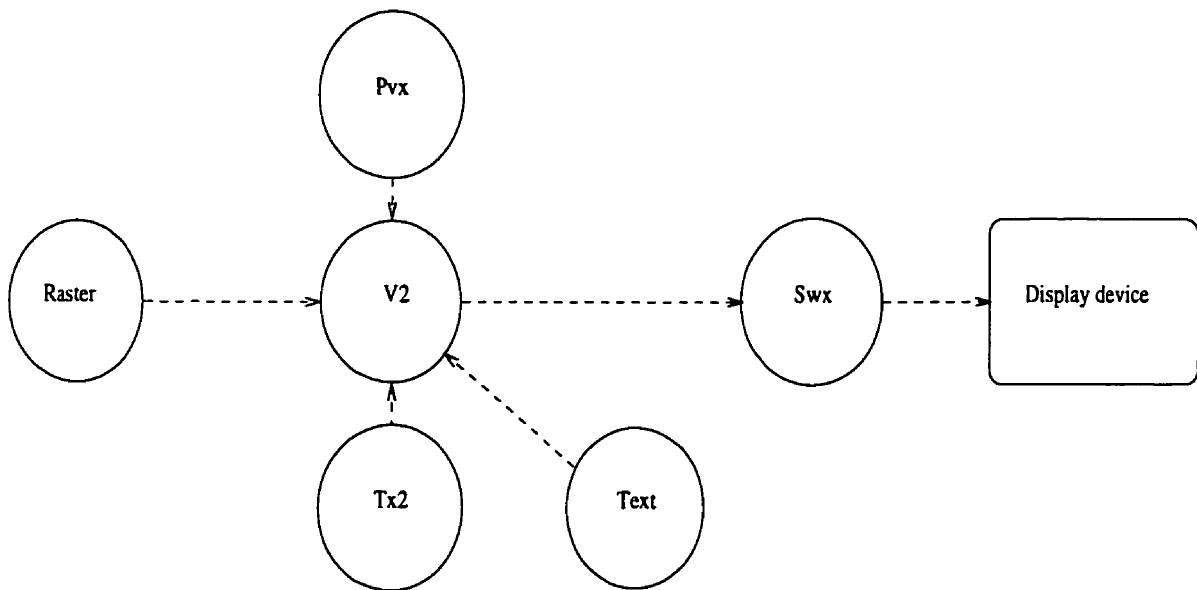


Figure 3.2: Simple application pipeline: A "raster" is connected to a "V2" object where the image is manipulated by "Pvx" and "Tx2" objects, and the "Swx" object is the display sink for this simple application

Client-server information exchange occurs in an asynchronous manner, but can also be specifically set to a synchronous communications mode. Asynchronous information transfer speeds up execution time and improves performance, since the application does not have to wait for a response from the server after receiving or executing a request. This asynchronous nature of inter-process communication requires the applications to be *event-driven*. This means that a task is performed upon the completion of a certain event instead of just executing a pre-ordered sequence

of actions. This imposes the restriction on the programmer that the application be written in *callback* format, where the user asks for a task to be performed and the processor waits for the necessary information to be present and then performs the required procedure.

There are several servers in IAP: Processing server, Database server and Hardcopy server. Each is responsible for a special set of tasks. Although these servers can interact with each other, they run in a mutually independent fashion. The number of clients accessing each server simultaneously is limited by the capabilities of the computing facility, although the clients can run on different processors.

Processing server

The processing server manages active displayable objects and performs all needed computations on these objects. All processing server implementations are similar, differing only in their method of performing low-level processing tasks. A specific image processing task is achieved by utilizing the run-time configurability of the server. The server internally arbitrates the computation requests of the active objects.

Different types of objects are present in each server. In the processing server, which is the only server used in this project, several objects act on the 2D and 3D data sets to generate binary, grayscale and colour images. These objects include the "Ras" object responsible for generating a display raster from a raw 2D data set. Other objects like "Cprog" and "Rf" take care of 3D datasets and generate a raster using either projection or surface rendering. Objects like "Tx2" and "Tx3" are responsible for geometric manipulation of the images.

3.2.2 Stereo Display

As described in section 1.2.1, stereo viewing of angiograms is favored by surgeons and radiologists for its realism, and for allowing depth perception. The manner in which stereo images are often displayed to the user is by presenting the image taken with

the left eye perspective to the left eye and the image with the right eye perspective to the right eye. This can be achieved by placing the two images side by side in reverse order (the left image on the right side and the right image on the left side), and crossing the eyes while focusing on the third “virtual” image appearing in front of the two images. This is an efficient technique used extensively here at the MNI/H, but it requires extra concentration on the part of the user and is not convenient to use while performing neurosurgical procedures.

Stereoscopic Display Devices and Hardware

A computerized technique for displaying these images is provided on SGI² work stations, with the help of additional hardware consisting of Crystal Eyes³ glasses.

Stereoscopic display is achieved by switching the display screen into a special mode where the images are displayed on alternate frames, at 140 Hz (70 Hz for each eye). The screen is synchronized with active shutter eye-ware, via an infrared signal, closing the right lens when the left image is displayed on the screen and closing the left lens when the right image is displayed. In this mode the vertical resolution of the screen is reduced from 1024 to 512 lines, while the horizontal resolution is maintained at 1280 points per line. Each image of the stereo pair alternates on the screen at 140 Hz, $\frac{1}{140}$ second for each view of the pair.

3.3 Image Matching

Image matching is the process of identifying and labeling the corresponding points of the same structure as visualized in different images. This procedure is not easily performed when matching different modalities, because the resulting images do not necessarily reflect the same view of the object nor do they have the same level of

²TM Silicon Graphics Inc.

³TM Stereo Graphics.

detail. To some extent one image may lack some structures present in the other (i.e., very small vessels present in the DSA image may not appear in the corresponding MRA image).

When determining point-to-point correspondences between images, it is assumed that for every point in one image there is a corresponding point in the other. A corresponding point is one that lies on the same structure, i.e., the same blood vessel, and has the same geometric properties as the initial point. This correlation is possible if, for each point in the image, one can establish a feature vector describing the image properties of this particular point. Points with the closest feature vectors correspond to each other, where closeness is determined by the discrepancy between the two vectors. The feature vector is the collection of all relevant geometrical and analytic properties of a particular point or set of points. For example, the curvature of the surface of the structure at a particular point may represent by a feature vector.

If a point p_i in image A has a feature vector V_i and point q_j in image B has a feature vector V_j then these two points correspond to each other if their respective feature vectors have a minimum *Euclidean* distance D , between them⁴.

$$D = \sqrt{V_i^2 - V_j^2} \quad (3.1)$$

If the vector describes more than one feature of the point then $V_i = [v_{i1} \cdots v_{in}]^T$; $V_j = [v_{j1} \cdots v_{jn}]^T$, and the *Euclidian* distance is:

$$D = \sqrt{(v_{i1}^2 - v_{j1}^2) + \cdots + (v_{in}^2 - v_{jn}^2)} \quad (3.2)$$

This feature vector representation allows for robust and reliable matching algorithms to be used in image correspondence. The concept of “Feature Space” is introduced, a space which is the set of the feature vectors belonging to every point in

⁴This is one method for determining the correspondence between the two images, but there are several techniques based on different measures other than *Euclidian* distance.

the image. Each point in the feature space represents a feature vector, and image points with the closest feature space points correspond to each other [52]. The process of matching is achieved then by associating each image point with a corresponding point in the feature space, with nearby points in the feature space corresponding to correlated image points.

Perfect correlation between the two images is achieved if a single match from image *A* is found for every point in image *B*. For a typical image of 256 lines by 256 columns, this requires that the user identify 65536 point pairs, determine their respective feature vectors and calculate the *Euclidian* distance between each pair of vectors. Since the amount of time needed for such a procedure is excessive and computationally expensive, for reliable matching, the number of features and their nature should be optimized. Another drawback for point-by-point matching is that when the two images are acquired using different imaging modalities, some structures appear in one image and not in the other. Finding a match in image *B* for every point in image *A* then becomes an impossible task, because the feature vectors can not represent the same characteristics for points in the two images. Also the existence of a corresponding point-pair in both images is not assured.

3.4 Multi-Modality Image Registration

Because of the high level of complexity of neurological images, a point-to-point correspondence is not realizable nor necessary. A global approach to this matching problem is suggested by *Peters et al* with the use of a stereotactic frame fixed to the head of the patient [59, 66]. The two images are mapped into the same space and registered together, with the corresponding structures coupled. This is possible through the use of linear transformations applied to the images at hand. Instead of finding a match for every point in the image, the coordinate system in which the object is described is transformed into the other coordinate system characterizing the target object.

3.4.1 Linear Transformations and Linear Operators

Linear transformations act on vectors in one space $\mathcal{U}$ and transform them into another space $\mathcal{V}$. A mapping $\mathcal{F}$ defines the set of all linear transformations that are applied to one vector in space $\mathcal{U}$ in order to map it to a vector in the other space $\mathcal{V}$. A linear operator is a mapping that preserves the two basic operations of vector addition and scalar multiplication.

Definition 1 A mapping $\mathcal{F} : \mathcal{U} \mapsto \mathcal{V}$ is linear iff:

$$\forall u, w \in \mathcal{U}, \mathcal{F}(au + bw) = a\mathcal{F}(u) + b\mathcal{F}(w).$$

If all possible linear transformations are applied to object A in a structured manner, then at a certain time the manipulated object will correspond to object B . If such a set of linear transformations exists then one can apply them to one image in order for it to match the other mask image. In simpler terms, these transformations manipulate every point in one space so as to map them to corresponding points in the other space.

If the linear operator is invertible then transformations between the two sets can go in both directions. This is the case if the mapping is *onto* and *one-to-one*.

Definition 2 A mapping $\mathcal{F} : \mathcal{U} \mapsto \mathcal{V}$ is onto iff:

$$\forall v \in \mathcal{V}, \exists u \in \mathcal{U} \text{ such that } \mathcal{F}(u) = v$$

Definition 3 A mapping $\mathcal{F} : \mathcal{U} \mapsto \mathcal{V}$ is one-to-one iff:

$$u_1 \neq u_2 \Rightarrow \mathcal{F}(u_1) \neq \mathcal{F}(u_2)$$

Onto means that for every point in the target set, there is at least one element in the starting set that has this point as an image. *One-to-one* means that if an image point exists then this point is unique. A linear transformation is invertible if for every point in the first system there exists *one and only one* image point in the target system [28].

3.4.2 The Homogeneous Transformation Matrix

The application of linear transformations is characterized by a special matrix called the *Homogeneous Transformation Matrix* (HTM), that acts on the image [84, 80]. This matrix describes all sets of rotation, translation, and scaling that are applied to the coordinate system of the image of interest, to map it to the corresponding coordinate system of the target image. These operations are conveniently described using matrix notation.

The elements of the HTM describe the rotations of the coordinate system around the major three axes: θ defines the rotation around the Z axis, ϕ defines the rotation around the X axis and ψ defines the rotation around the Y axis (see figure 3.3). The other transformations are translation, scaling and cropping along the three principal directions. When perspective viewing is desired, another term is added to these transformations reflecting the perspective nature of the projection. The HTM characterizes the projection geometry of the image, and describes the manner in which this particular view of the object is obtained.

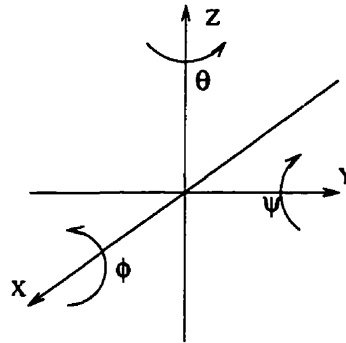


Figure 3.3: The three angles describing rotation, roll and elevation of an object around its three major axis

For ease of understanding, the HTM is decomposed into three ⁵ matrices T , R and S , each representing a set of linear transformations of the same type. The HTM can then be written as $M = TRS$. The T matrix corresponds to shifting the origin by

⁵Perspective projection is not accounted for here, and will be presented later.

$[X_c, Y_c, Z_c]^T$ in the three main directions. In the homogeneous system it is represented as a 4×4 matrix [26]:

$$T = \begin{pmatrix} 1 & 0 & 0 & -X_c \\ 0 & 1 & 0 & -Y_c \\ 0 & 0 & 1 & -Z_c \\ 0 & 0 & 0 & 1 \end{pmatrix} \quad (3.3)$$

The rotation matrix R is itself decomposed into three rotation matrices corresponding to the rotations around three axes; $R = R_\theta R_\phi R_\psi$. The first matrix rotates by θ degrees the XY plane around the Z axis, the second rotates the YZ plane around the X axis by ϕ degrees and the third rotates the ZX plane around the Y axis by ψ degrees.

$$R_\theta = \begin{pmatrix} \cos(\theta) & \sin(\theta) & 0 & 0 \\ -\sin(\theta) & \cos(\theta) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \quad (3.4)$$

$$R_\phi = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos(\phi) & \sin(\phi) & 0 \\ 0 & -\sin(\phi) & \cos(\phi) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \quad (3.5)$$

$$R_\psi = \begin{pmatrix} \cos(\psi) & 0 & -\sin(\psi) & 0 \\ 0 & 1 & 0 & 0 \\ \sin(\psi) & 0 & \cos(\psi) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \quad (3.6)$$

The matrix R enjoys two special properties that ease the mathematics involved in its implementation. First, the rotation matrix is a proper orthonormal *Hermitian* matrix, which means that $R^{-1} = R^T$. Second, the determinant of R is unity, which is evident from the decomposition of the rotation matrix in equations 3.4, 3.5 and 3.6.

The scaling matrix S describes the amount of magnification that is to affect the

coordinate system in the three directions S_x , S_y and S_z .

$$S = \begin{pmatrix} S_x & 0 & 0 & 0 \\ 0 & S_y & 0 & 0 \\ 0 & 0 & S_z & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \quad (3.7)$$

Because each of these matrices represents a linear operator which performs a specific transformation on the coordinate system, the application of these linear operators is equivalent to multiplying the compound matrices together.

When perspective projection is used, i.e., projecting a 3D scene onto a 2D plane in a manner similar to the generation of an image in the eye, an extra matrix P is multiplied by the resulting HTM. This additional matrix has dimensions 3×4 and preserves the relative depth of the object and introduces perspective magnification into the resulting projection, depending on the focal length f of the projection geometry.

$$P = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & -\frac{1}{f} \end{pmatrix} \quad (3.8)$$

When pre-multiplying the original HTM by the perspective projection matrix, the resulting matrix has dimension 3×4 , with the z component missing. The *HTM* in this case is the product $PTRS$. This matrix acts to project its input vector into the 2D plane according to a specific projection geometry. In order to determine the coordinates of the 2D projection, one needs to divide the resulting triplet by its last component α , defined in section 3.4.3 below.

3.4.3 The Application of the HTM for Image Registration

The HTM describes the manner in which each vector in the first coordinate system is transformed to the corresponding vector in the target coordinate system. This is best

described in the following equation, where X is a vector in the starting coordinate system and Y is the corresponding vector in the target system.

$$Y = M X \quad (3.9)$$

In medical imaging, an object is described by a set of points each having a particular intensity value, in 3D imaging space. Every point in the 3D space is described as a triplet $[x, y, z]^T$, while points in a plane are described by an ordered pair $[u, v]^T$. When homogeneous coordinates are used, an extra component is added and the vector is multiplied by a scalar which is called the homogeneous coordinate. A point in 3D is then defined as $X = [\alpha x, \alpha y, \alpha z, \alpha]^T$ and a point in 2D becomes $U = [\alpha u, \alpha v, \alpha]^T$. The α multiplying factor is a constant used for two reasons. First, to make the transformation possible by adding a dimension to input vector. Second, to show that the transformation is not unique, and that several input points can satisfy the equality [80]. The exact location of the point is obtained by dividing the vector by its last element. Homogeneous coordinate systems are used so all linear transformations on the vector are treated similarly [25]. This representation is useful in obtaining perspective transformations that are used in generating the MIPs for MRA data sets employed in this project.

The object in one image modality is transformed to its corresponding location with the correct size in the other image, through the application of the linear operator that describes the linear transformation. This is achieved by multiplying every point in object space (the space in which the volume data exists) by the HTM to obtain the corresponding point in target or image space (equation 3.10).

$$\begin{bmatrix} \alpha u \\ \alpha v \\ \alpha w \\ \alpha \end{bmatrix} = \begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ m_{41} & m_{42} & m_{43} & m_{44} \end{pmatrix} \begin{bmatrix} x \\ y \\ z \\ 1 \end{bmatrix} \quad (3.10)$$

The elements of the HTM are the result of multiplying out the rotation, translation and scaling matrices described in section 3.4.2.

If the transformation is from a 3-dimensional space to a 2-dimensional space then the resulting vector and the original input vector do not have the same dimensions and the HTM is a 3×4 matrix instead.

$$\begin{bmatrix} \alpha u \\ \alpha v \\ \alpha \end{bmatrix} = \begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \end{pmatrix} \begin{bmatrix} x \\ y \\ z \\ 1 \end{bmatrix} \quad (3.11)$$

3.5 Existing Correspondences in the IGN System

Several image modalities have already been integrated together into the IGN environment. CT and MRI are correlated together in the stereotactic space and are both displayed in the IGN system [59, 60, 37, 48]. The correspondence between the two sets of images is obtained through the determination of a linear operator that transformed the coordinate system of one data set to the other. This operator is calculated by taking corresponding sample points in the two volumes and solving for this linear operator, as described in equation 3.9. The number of points depends on the dimension of the homogeneous matrix representing the linear operator. For a transformation from a 3D MRI data set to a 3D CT data set the operator is a 4×4 homogeneous matrix, and requires eight corresponding point pairs. When the stereotactic frame is present in image acquisition, the corresponding point pairs in the two images are the markers on the stereotactic plates. These points provide an accurate localization of the eight points required to determine the HTM.

DSA provides the surgeons with additional information about blood vessels which is not available with CT or MRI [65, 12, 34, 31]. Because of the 2D projection nature of DSA it is only possible to transform from MRI to DSA space, since all the points in the

3D volume along a particular ray project to the same 2D point. The linear operator is not one-to-one and therefore cannot be inverted. The fiducial markers on the stereotactic plates are again used to calculate the homogeneous transformation matrix that relates the images of both modalities. In this case, the matrix has dimensions 4×3 and thus requires the identification of six pairs of corresponding points to solve the system of equations. Usually more than six pairs are identified, an overdetermined system is produced and a least squares solution is implemented to determine the HTM [65].

3.6 Algorithms for Matching DSA with MRA images

A DSA image is an X-ray projection of the imaged vessel tree, as described in section 2.1. If the DSA projection geometry is determined, then a corresponding MRA image can be generated using MIP with the calculated parameters of the X-ray projection. When the projection parameters are determined a transformation between the two spaces, the 2D DSA space and the 3D MRA space, is possible. This transformation is performed by projecting each point in MRA space onto a point in DSA space. Traversing the volume data with rays that describe the projection geometry, the point of intersection between the ray, and the 2D projection plane, corresponds to the 2D image point. This projection is a many-to-one transformation because many points in the 3D space lie on the same ray and project to the same point in the 2D plane. Based on the discussion in section 3.4.1, the projection is an irreversible transformation, meaning that a point in the 2D space cannot be projected back to its corresponding 3D points.

A point in 3D space is transformed into its corresponding 2D image point by the projection operator M . This operator is best characterized by the HTM describing the projection geometry (section 3.4.2). Every point in the MRA volume can then be

projected into a display raster in the same manner that the X-ray beam projects an object onto film.

The first task is to obtain the geometry of the X-ray projection system. This is achieved by identifying the 2D coordinates of points on some particular vessel structures in the DSA image along with the corresponding points on the same structures in the 3D MRA volume set. These two sets of points are related by the HTM, based on equation 3.11. If the homologous points are $U = [\alpha u_i, \alpha v_i, \alpha]^T$ and $[x_i, y_i, z_i, 1]^T$, then multiplying out equation 3.11 results in:

$$\begin{aligned}\alpha u_i &= m_{11}x_i + m_{12}y_i + m_{13}z_i + m_{14} \\ \alpha v_i &= m_{21}x_i + m_{22}y_i + m_{23}z_i + m_{24} \\ \alpha &= m_{31}x_i + m_{32}y_i + m_{33}z_i + m_{34}\end{aligned}\tag{3.12}$$

Substituting back the value for α in the first two equations one obtains the two equations for u_i and v_i , the real 2D coordinates of the projection image, as a function of the 3D coordinates x_i, y_i and z_i and the twelve elements of the HTM.

$$(m_{11} - u_i m_{31})x_i + (m_{12} - u_i m_{32})y_i + (m_{13} - u_i m_{33})z_i + (m_{14} - u_i m_{34}) = 0\tag{3.13}$$

$$(m_{21} - v_i m_{31})x_i + (m_{22} - v_i m_{32})y_i + (m_{23} - v_i m_{33})z_i + (m_{24} - v_i m_{34}) = 0$$

To solve this system for the twelve unknown elements of the HTM, one needs at least twelve equations. If each pair of points results in two equations, then six points are sufficient to describe the system. Because of the properties of the pure rotation matrix R , not all the element of the HTM are independent, and in fact one element can be described as a linear combination of all the others. Thus when calculating the elements of the HTM, the last element can be set arbitrarily to unity without affecting the determination of the HTM, and once one element is set there are only

eleven unknowns to be found. The resulting system is over-determined with six points, and may be solved numerically using the least squares minimization technique.

In practice the observer identifies several points in the DSA image and tries to correctly identify the same set of points in the MRA volume. Usually these points are vessel intersections, curvatures or some visible structures common to both images. The corresponding coordinates of the two sets of points are fed into the program which uses a singular value decomposition algorithm to solve the overdetermined system of linear equations and obtain the elements of the HTM. This same calculated HTM is then used to obtain the MIP projection of the MRA data as described in section 4.4.

3.7 Summary

In this chapter, the methods and the techniques that are needed to develop the DSA/MRA comparison system are introduced. The tools that are used to display the final product to the surgeons are described, namely the programming environment, along with the IAP tools and the display hardware that generate the stereo images. The general concept of image correlation and matching is outlined, and the technique that is used for registering multi-modality medical images is discussed. The mathematics needed for the application of this technique are presented and the concept of the *Homogeneous Transformation Matrix* is fully described.

A brief survey of the existing multi-modality image registrations in the IGN system is presented and examples of these registrations are given. Also the manner in which the HTM registration technique can be modified in order to facilitate the correct registration of DSA and MRA in the same system is analyzed.

Chapter 4

Data Postprocessing

4.1 Introduction

This chapter discusses the different image processing techniques that are applied to the datasets, in order to render the visualization of the vessel tree more realistic. The subtracted digital angiographic images are manipulated to reduce the motion and pincushion artifacts in the final image. MRA post-processing is slightly more involved: the volume needs to be projected onto a 2D array, the display raster; blood vessels have to be identified; and depth of visualized structures must be outlined.

4.2 DSA Data

Digital angiography images are obtained as a set of 2D rasters containing the mask and the angiographic data. The mask is then subtracted from the angiograms after taking the logarithm of both images ¹, and a DSA image is obtained. The alignment of the two images (mask and angiogram) is very important because it affects the subtraction of stationary structures in the image. Techniques that address the determination of blood vessel lumina and the enhancement of the vascular tree in DSA images, using

¹See section 2.1

multiple radiographic projections of the vascular structure in the head, are discussed in [30]. It is also possible to display both arteries and veins on the same image, if instead of subtracting the mask from the arterial or venous phase, the venous phase is subtracted from the arterial phase. The resulting image shows arteries and veins in different colours, with dark veins and bright arteries.

Misregistration between the mask and the contrast image may occur due to several factors ². This can be corrected for, manually or automatically, by selecting similar points on both images and determining the set of transformations that match one image to the other. Another algorithm uses a flexible local registration of the mask with the live image that minimizes distortions caused by the complex motion of the blood vessels due to changes in the flow strength, which sometimes leads to vessel displacement. Then, these transformation are applied to the angiogram before carrying on with the subtraction. Near perfect alignment, in the case of small motion, with a precision on the order of .1 pixel is achievable [19, 86].

4.2.1 Correction for Pincushion Effect in DSA Images

As discussed in section 2.3.1, pincushion effects act on the final image in such a way that straight peripheral lines appear curved, reflecting the convex geometry of the Image Intensifier (figure 4.1).

This can be corrected for by manually superimposing a non-distorted, computer-generated grid image on the X-ray image. This computer-generated grid is obtained by displaying pixels lying on straight lines which correspond to the lines on the actual physical grid. By matching every point on the distorted image with its corresponding exact location in the other image a relationship between the two grids can be obtained. The displacement at each point is determined by calculating the number of pixels that each point has to move, in both x and y directions, in order to correspond to its location on the computer-generated grid. Thus, a displacement map of the image

²See section 2.3.1

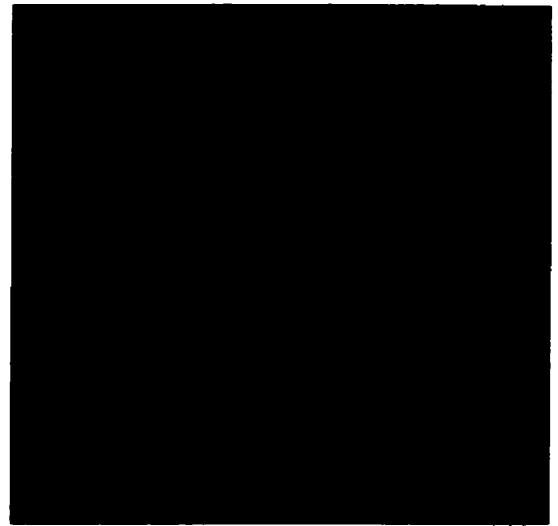
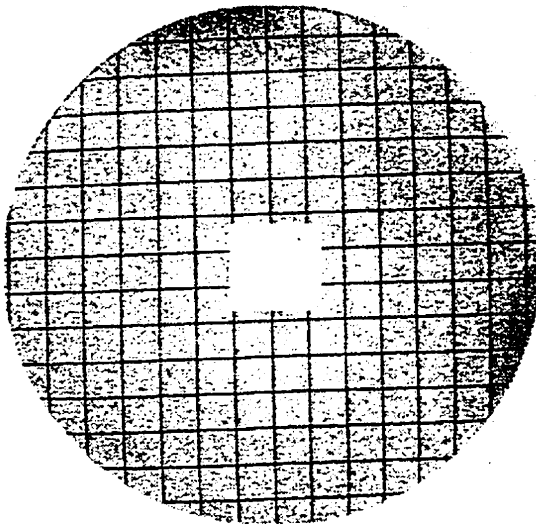


Figure 4.1: X-ray image of a rectangular grid, with 1 *cm* rectangles, demonstrating the pincushion effect (left), and a corresponding computer-generated one (right).

can be generated. This procedure is performed using MATLAB ³, where two images are first manually superimposed. The alignment is performed in such a way that the centre sections of the two grids are perfectly matched, since they experience less distortion than the peripheries. Because finding a match for every point in the two images is an exhaustive task, only points at the intersection of the grid lines are matched. The displacement map for the whole image is calculated by interpolating the sparse data to the complete set of sample points. Note that the quality of the images taken with this machine (Siemens Polytron) is highly superior to images taken with some other DSA machines, and the curving of the lines is hardly noticeable. A displacement map is generated for each view of the Xray because of the effect of the earth magnetic field on the electrons in the Image Intensifier. Depending on the location of the II its electrons will experience a different magnetic field and the deviation will differ from view to view. This is the reason why the displacement map in figure 4.3 is not symmetric.

We used a 15 by 15 cm square grid for these measurements. From figure 4.1

³The MathWorks Inc

one can see that the lines of the grid are perfectly straight and parallel when they are close to the centre, and tend to curve toward the outside the further they are from the centre. The curving of the lines, in this case, is fairly small because of the flatness of the II screen. Nevertheless, this curving might affect the final image when quantitative measurements are needed to determine vessel locations or when planning depth electrode implantation trajectories. The result of matching the two grids is shown in figure 4.2. The arrows show the direction of the displacement of each point, and their magnitude represents the amount of displacement. As expected the arrows near the centre of the image are small or negligible in magnitude, reflecting only minimal distortion, while their magnitudes increase towards the periphery. A magnified segment of the displacement map is shown in figure 4.3, this corresponds to the centre left section of the image. The number of samples in this image is reduced to clarify the display. The maximum resulting distortion is less than 4 mm. The same technique is applied to left and right lateral X-ray projections of the grid, and the results are similar to the Anterior-Posterior case presented below.

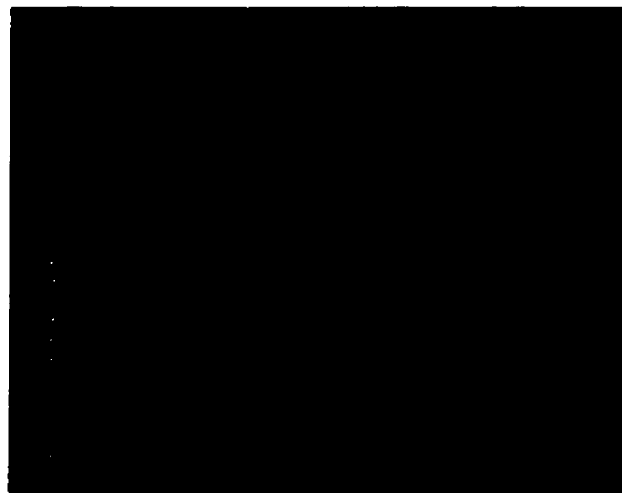


Figure 4.2: Displacement Map corresponding to the matching of a distorted grid to a computer-generated one

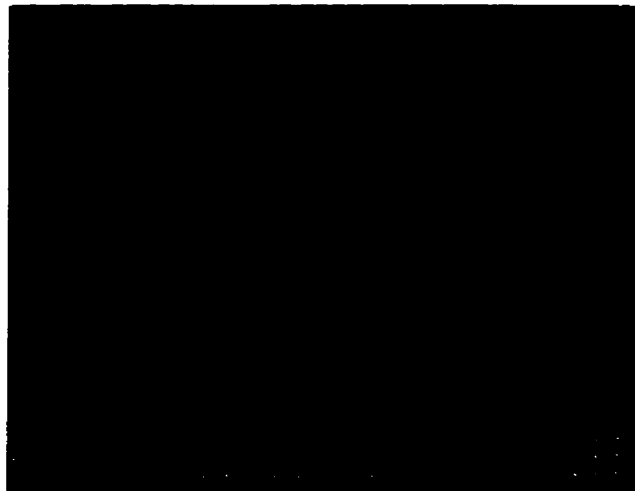


Figure 4.3: Magnified (5×5 cm) section of the displacement map of figure 4.2. The maximum distortion in the lower right corner is 1.9 mm

4.3 MRA Data Sets

In MRA, image intensity is affected by the size of the vessel, the pulse sequence, spin saturation in TOF and the nature of blood flow in PC pulse sequences. A Magnetic Resonance Angiogram is a 3D description of the flow intensity pattern in the region being imaged. The data are gathered as voxels in 3-D space, the size of the voxel is determined by the desired resolution of the final image and the resulting signal-to-noise ratio (SNR). There is a trade off between the degree of detail that MRA can provide and the required SNR, which decreases with voxel size. This imposes a restriction on the size of the voxel volumes. A typical voxel size in a regular PC MRA of the head, is $1mm \times 1mm \times 1mm$.

The MRA volume cannot be visualized on a computer screen unless it is regenerated in 2D format. Viewing a single 2D MRA slice is not very useful for the planning of neurosurgical procedures, since it does not give any information related to connectivity and 3D spatial relationships. See figure 4.4.

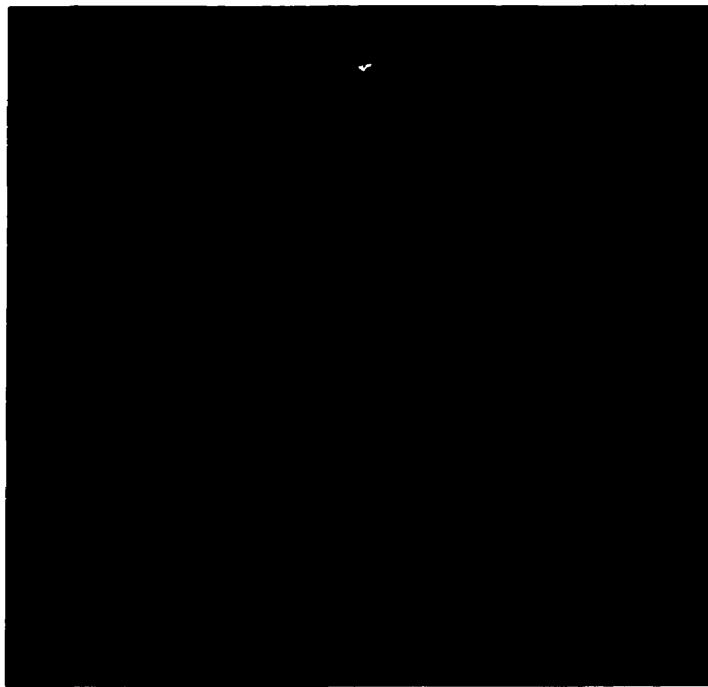


Figure 4.4: Single slice of a 3D MRA volume set

The whole volume must be transformed into a 2D raster that can be displayed on the viewing screen. The process of transforming a 3D data set to a 2D raster is called *projection*, and employs a set of straight lines called *projectors* emanating from a single point, the *centre of projection*, traversing the volume and intersecting a plane called the projection plane. If the centre of projection is at a finite distance from the projection plane then the projection is called *perspective* and realistically represents the images obtained on the retina and in a photographic system. If the centre of projection is at an infinite distance from the projection plane, then the projection is called *parallel* or *orthographic*. In perspective projection the size of the projected object is inversely related to its distance from the centre of projection. Thus, accurate measurement of the exact shape of the object is not possible using perspective projection [25]. When using stereo views relative depth and object size can qualitatively be obtained when the two images are fused together to form a third 3D image 1.2.1.

The process of projecting the volume into a 2D raster induces a loss in the volumetric information present in MRA data sets. When projecting into a plane, some objects might occlude others. In addition, all the available information about the depth of any projected structure is lost in the process. This is true in the case of parallel projection but its effect is less noticeable in perspective projection, where some depth information is embedded in the differential magnification of various structures. This loss of volumetric information should be compensated for by the ability of the projection algorithm to generate several views of the volume taken from different view-points.

MRA images are used for neurosurgical planning and must be able to provide the surgeon with detailed 3D information about the vessel tree in the head. The algorithm used for projecting MRA images onto a display raster should be fast and efficient, in order to generate several accurate views of the data in a short time. In this manner, the surgeon can get a sense of the 3D nature of the imaged object. The

most popular algorithm used for projecting MRA data, called Maximum Intensity Projection (MIP), is a very simple yet effective projection technique which uses the fact that MRA voxel intensity values are closely tied to the nature of blood flow. High intensity values represent areas of fast and steady flow, typical of the centre of the vessel. Picking up the highest value along of the ray results in a good qualitative projection of the 3D volume. The algorithm is described in detail below.

4.4 Maximum Intensity Projection

Maximum Intensity Projection is achieved by traversing the volume dataset with a set of parallel rays, and recording the maximum intensity value intercepted along the path of each ray onto a 2D array. Due to the parallel nature of the rays, objects near and far from the projection plane appear with the same magnification, leading to optical illusions.

To determine the value of the pixel encountered when the ray does not traverse the centre of a voxel, one of several rules may be employed: nearest neighbour, where the closest voxel is chosen as the value of the sample, and interpolation between the eight voxels values G_{ijk} , using tri-linear or higher order functions. A scheme for tri-linear interpolation is shown below (figure 4.5), and the resulting sample value G is calculated as follows:

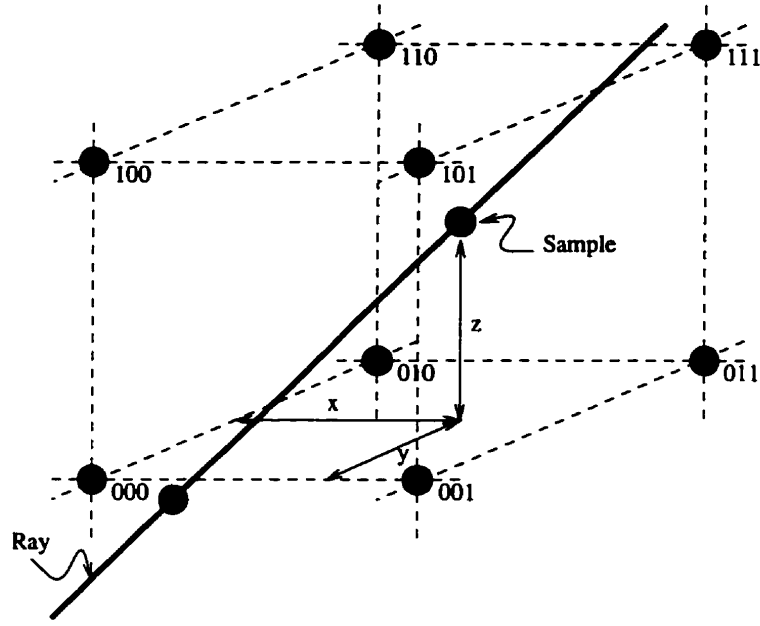


Figure 4.5: Sample point position in a three dimensional grid used for tri-linear interpolation

$$\begin{aligned}
 G(x, y, z) = & (1-x)(1-y)(1-z)G_{000} \\
 & + x(1-y)(1-z)G_{001} \\
 & + (1-x)y(1-z)G_{010} \\
 & + xy(1-z)G_{011} \\
 & + (1-x)(1-y)zG_{100} \\
 & + x(1-y)zG_{101} \\
 & + (1-x)yzG_{110} \\
 & + xyzG_{111}
 \end{aligned} \tag{4.1}$$

where x, y and z are the fractional parts of the sample point coordinates. This operation is computationally expensive, and requires fourteen multiplications and seven additions, even after optimization of the algorithm [90].

Although MIPs provide no depth information, they generate excellent qualitative representations of the vessel tree. Figure 4.6 shows a regular MIP using parallel rays caster, whereas figure 4.7 uses diverging rays for the projection. The technique used

to generate these figures is described in section 4.4.1. In the diverging ray projection it is easier to tell which vessel is in the front and which is in the back than in the parallel ray projection. The parallel rays MIP algorithm is extremely fast and can generate a projection of a volume consisting of 170 slices each of 256×256 pixels in real time.

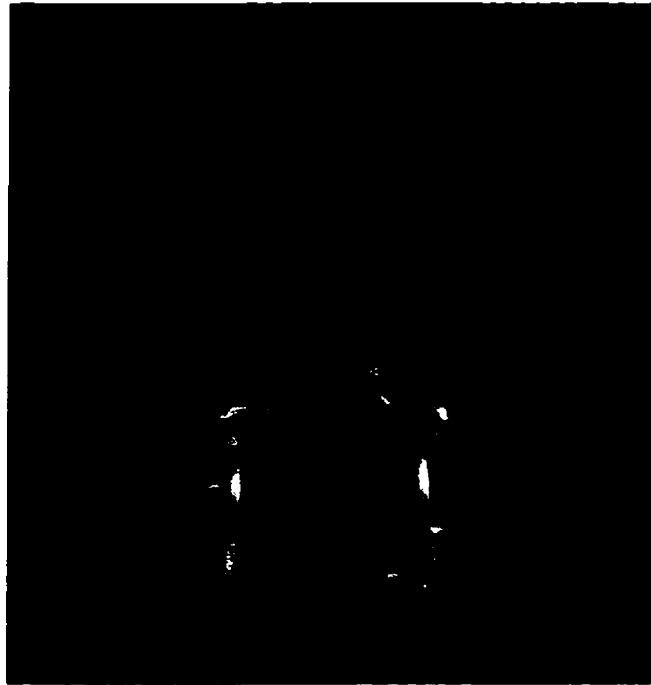


Figure 4.6: Maximum Intensity Projection (MIP) using parallel rays

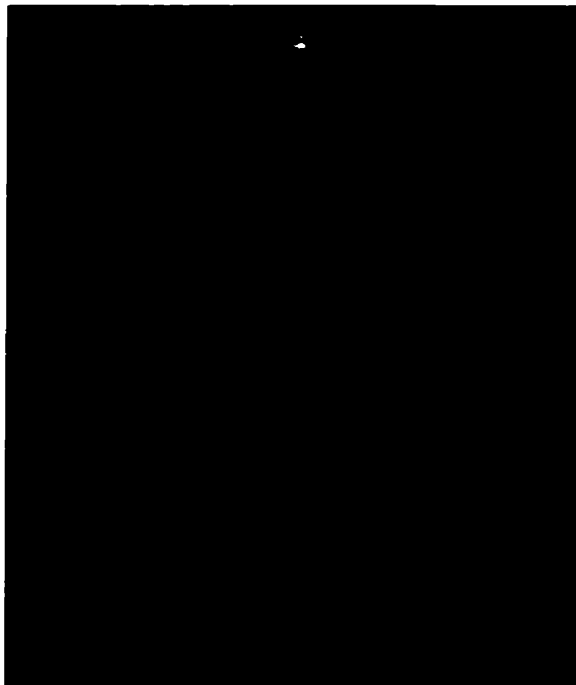


Figure 4.7: Maximum Intensity Projection (MIP) using diverging rays

4.4.1 Modified MIP Implementation

The main problem with regular ray tracing is the need to calculate the sample points along each ray. The ray emanates from the centre of projection and intersects the projection plane at the grid sampling points. The projection process can be accelerated if, instead of determining each ray going out from each point in the projection plane and calculating the samples points along its path, the volume is traversed in a sequential manner. The projection point for each voxel is then determined through the multiplication of each voxel's homogeneous coordinates with the projection HTM, according to equation 3.11⁴. The last stored intensity value in the calculated location is then compared to the new value, and the largest of the two is chosen. The calculated projection points will not always lie exactly on the sample points in the projection plane, and a linear interpolation process is needed to determine the fraction of the voxel that is projected into each of the four neighboring pixels on the projection plane.

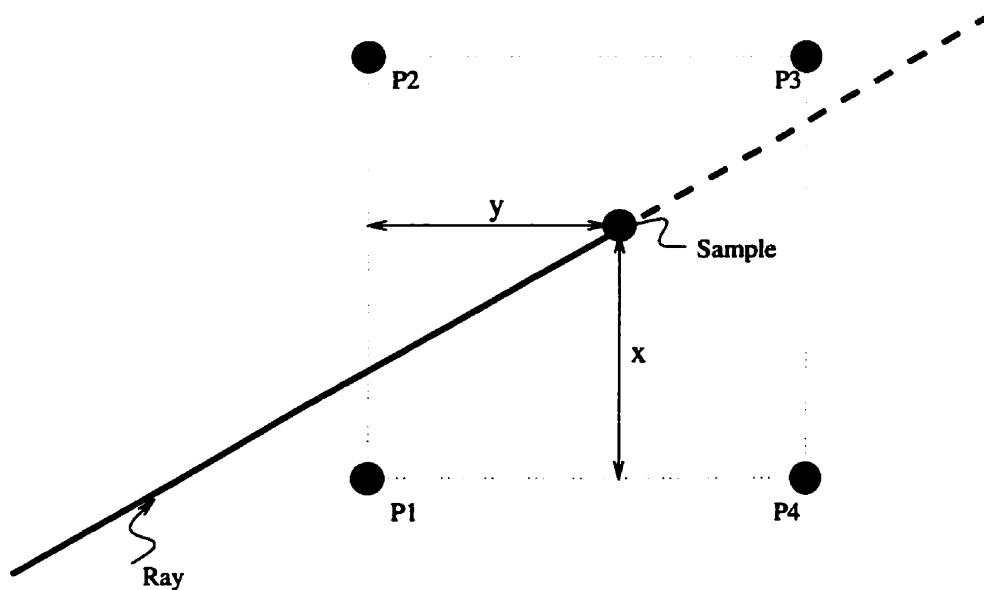


Figure 4.8: Projection point that lies between four sample points on the projection plane

⁴See section 3.4.2

From figure 4.8 each of the four points p_1, p_2, p_3 and p_4 receives a fraction of the intensity value of the projected voxel V according to equation 4.2

$$\begin{aligned}
 p_1 &= V \times x \times y \\
 p_2 &= V \times (1 - x) \times y \\
 p_3 &= V \times (1 - x) \times (1 - y) \\
 p_4 &= V \times x \times (1 - y)
 \end{aligned}
 \tag{4.2}$$

This modified technique results in a saving in memory access as well as computation time, because instead of interpolating between eight neighboring points when ray casting, the interpolation is carried out between the four planar points. The speed of this algorithm is evident when diverging ray projection is used, a volume of 256×256 pixels $\times$ 150 slices takes less than 5 seconds to be projected on a 256×256 pixels raster (See figure 4.7), rather than 3040 seconds using the traditional method.

4.5 Other Projection Algorithms

Although maximum intensity projection provides good quality angiographic images, it suffers from several shortcomings inherent to the non-linear nature of the algorithm, which affect the quantitative analysis of the data [21, 74]:

- Loss of small, low-contrast vessels [51, 53]
- Reduction in vessel diameters
- Lack of depth-cue

Small vessels with relatively slow flow tend to have an intensity value close to the neighbouring stationary tissues (background noise in MRA). This may result in a projection ray picking up background noise instead of a vessel segment, in areas where such vessels are present. This effect results in a reduced signal-to-noise ratio in the

final image, where small low contrast vessels are painted over by noise. As described earlier in section 2.2.1, the value of the voxels in MRA datasets represents the flow in that location. Different flow patterns, such as turbulence and flow direction reversal, affect the resulting voxel value and cause the edges of the vessel to be less intense than the centre. When projecting these parts of the volume the vessels will appear to be smaller than they are, because the edges will be obscured by background noise.

Several methods have been proposed to improve MIP techniques. A method that uses colour coding for distance characterization attempts to include depth information in the colour intensity value of the projected image [21]. Another method just projects the first encountered voxel that belongs to a vessel [90]. This technique shows the relative depth of the vessels by occluding background vessels even if they are brighter, a point not taken into account in regular MIP. Postprocessing of the MRA dataset before applying the projection algorithm is implemented by Moshfeghi *et al.* [51], where the volume is thresholded first, an algorithm for background signal suppression is applied, and the voxels are labeled according to their relative distances from each other. These labels are used to determine the projected pixel value and colour parameters (hue, saturation and intensity).

In X-ray imaging the pixel's intensity represents the line integration of the attenuation coefficient of the structures that an X-ray traverses before encountering the Image Intensifier, see section 2.1. This projection can be simulated using MRA data by implementing a technique similar to MIP. Instead of projecting the voxel with the maximum intensity along each ray, the intensities of the traversed voxels are added.⁵ This technique results in an MRA projection very similar in nature to DSA images and a better blood vessel lumen representation compared to regular MIP. A projection using the summation technique, of the same data used throughout this chapter, is presented in figure 4.9.

⁵The integration becomes a summation in the discrete case.



Figure 4.9: A simulated DSA projection, obtained from the MRA dataset using a summation projection as described in section 4.5

4.6 Blood Vessel Segmentation

The common approach to building a computer vision system is to generate intermediate descriptions of images corresponding to increasing complexity levels leading to a final goal. Segmentation is usually the first stage of such a task [3]. Vessel segmentation cleans up the data in the sense that any residual noise is discarded and all the vessels are clearly labeled. When the vessels are segmented, less data are required to represent the vessel tree. Thus, less storage space is needed, facilitating the fast manipulation of the volume data.

The first attempt to quantitatively determine the blood vessel lumina was performed on DSA images by Fencil et al [23] and Clough et al [10]. Stereoscopic imaging was used to obtain visual representation of the vessel tree; however, several problems are associated with this approach. Determining the depth of the structure requires the availability of complete point-to-point correspondence between the two stereo

views, which is not a trivial obstacle to overcome. Another encountered problem is the algorithm's inability to distinguish blood vessel pixels from background noise, thus determining blood vessel boundaries.

With the introduction of MRA imaging for blood vessels, the two previously mentioned problems associated with vessel segmentation in DSA became irrelevant. MRA images are acquired as a 3D volume dataset with relatively high contrast-to-background ratio, depending on the employed acquisition sequence. On the other hand MRA does not enjoy the high resolution of DSA nor its detailed visualization of small blood vessels.

In practice, several techniques are used to obtain the vessels boundaries [38, 53, 9, 19, 27, 41, 39]. Some are manual, requiring an experienced user to identify all the pixels belonging to a specific blood vessel lumen. Automatic techniques are also possible, where some physiological properties measurable from the volume data are specified to identify vessel lumina. The accuracy of the automatic segmentation method depends on the criteria that are used in decision making.

4.6.1 Manual Segmentation

In this technique the user determines which pixel or set of pixels belong to the particular vessel body. This procedure is repeated in each slice of the original MRA volume. The boundaries of the vessels in such slice are identified and connected to the contour of the same vessel in subsequent slices. Each contour represents the walls of the vessel when it traverses its corresponding slice. The boundary of the whole vessel is determined by stacking the contours on top of each other and then applying a smoothing algorithm, in a direction perpendicular to the slices, for the connectivity and the continuity of the vessel lumen.

This procedure can be semi-automated by introducing the concept of seed growing. The resulting closed boundary from a previous slice is kept in memory and a threshold detector is applied to the current slice to determine whether this contour has to expand

or shrink to envelope all the pixels that belong to the blood vessel segment. The initial contour is determined either by the user or by a computerized region growing algorithm. At each slice, the user has the capability of overriding the machine decision regarding the size and location of each pixel on the boundary, thus monitoring the process of segmentation and correcting any errors.

This technique is time consuming, tedious, and extremely operator dependent. Different users often arrive at different segmented volumes of the same vessel tree. Another disadvantage of this method is that the boundary is affected by the pixel size, since a pixel is either inside the contour or not, and there are no fractions of pixels used in the segmentation process, although this situation can, in principle, be ameliorated by sub-sampling the volume data. The quality of the final segmented image depends also on the accuracy of the pointing device used to outline these contours and the resolution of the display screen. An MRA dataset manually segmented in this way, is shown in figure 4.10.



Figure 4.10: Manually segmented MRA image

4.6.2 Automatic Boundary Extraction Techniques

The goal of any segmentation algorithm is to classify structures of interest, i.e., blood vessels, by extracting features from the dataset that characterize these particular structures. Typical features that are used in the classification of objects in images are edges or regions of interest. *Edge detection* routines search the local neighbourhood for discontinuities in the gray-level function of the volume dataset. *Region extraction* routines apply a decision making algorithm to group together homogeneous areas in the data. While the latter is an efficient method of segmenting some medical data, it is somewhat impractical for MRA data. Edge detection provides a fast and efficient method for the extraction of blood vessel boundaries.

Region extraction begins by implanting seeds in regions of interest in the data set, and then applying some region-growing techniques to obtain complete regions. These techniques work to iteratively merge sets of connected points to form larger regions, according to some homogeneity criteria. Spatial and geometric properties of the image are used for the decision making [5, 2].

In the mathematical sense the boundaries of a certain region correspond to the local gradient extrema, where the gradient is taken along the major three directions X , Y and Z , or to the zero crossing of the Laplacian of the three-dimensional gray-level function. The problem with this representation is that the gradient or the Laplacian calculation involves the differentiation of an n -dimensional noisy signal, which leads to edges occurring in the wrong location, depending on the noise level. In order to overcome this problem, the differential operator is defined with some performance criteria, including characterization of the edges and the noise. These operators are $n \times n$ convolution masks that are applied to the image⁶, to compute the gradient components in the different orthogonal directions [76]. The size of the convolution mask is a very important parameter that largely affects the final segmentation process. Very large convolution masks cannot be implemented because they are computationally

⁶In the 3-D case the mask is $n \times n \times n$.

expensive when the size and the dimensionality of the data increase. On the other hand small masks are very sensitive to noise [3].

A popular mask model for efficient edge detection was introduced by Canny [7]. He defines a comprehensive set of goals for effective edge detection while making minimal assumptions about the form of the solution. An additional criterion ensures that one edge induces one response. The final mathematical form of the detector is obtained through the optimization of the response of the above mentioned functionals [8]. The operator uses the first derivative of a n -dimensional Gaussian function whose performance is superior to other popular operators.

After calculating the gradient for the image, the edge points are determined by thresholding; all points above a certain gradient intensity are marked as boundary points. The problem with this approach is that there is no single threshold value that allows for the selection of all the correct edge points. The gradient value varies strongly within the image. A solution is achieved by first extracting the local extrema of the gradient, in the three directions X, Y and Z , and obtaining a thin one pixel wide edge. A connectivity operator and hysteresis thresholding are then applied to eliminate spurious points while maintaining strong connectivity between the edge points. With this procedure a single pixel, highly connected edge is obtained.

4.6.3 Segmented MRA Images and the Comparison System

A manually segmented MRA image is generated, using the Allegro⁷ segmentation tool in the MNI. The final image is a collection of contours that define the actual vessel tree lumina. This dataset is used in the comparison system and is manually aligned with its DSA counterpart to provide another means of comparing the two image modalities. This correlation between the two image sets increases the amount of information presented to the surgeon during the neurosurgical planning.

As discussed earlier, segmented MRA images enjoy a low level of background

⁷ISG technologies

noise, and allow for a more accurate and precise blood vessel identification. Also, the cleaning up and smoothing of the vessel boundaries during segmentation decreases the probability of selecting a background point with high intensity value outside the blood vessel lumen.

A major drawback to this approach is the loss of small capillaries, that might appear in a regular MIP, in the process of segmentation. This loss is due to the choice of a large threshold value, convolution mask size or operator error.

4.7 Summary

This chapter describes the mathematics used to display the final angiographic images as well as enhancing them and reducing noise and distortion. The linear transformation applied to DSA images to correct for the *pin-cushion* distortion as well as the alignment of the DSA image itself are first introduced. Techniques to improve the quality and speed of Maximum Intensity Projections for MRA datasets, of which several are used in this work, are also discussed. Finally, the segmentation of MRA images along with its usefulness in improving the reliability of the IGN system and reducing potential localization errors are presented.

Chapter 5

Experimental Results and Observations

5.1 Introduction

This chapter presents the different experiments performed to compare the two datasets, DSA and MRA, using the prototype of the comparison system introduced in previous chapters. First, parameters representing the contrast of each image are calculated and compared to determine which angiographic method results in a higher contrast-to-noise ratio. The two angiograms are then superimposed in the same space to give a realistic sense of the introduced correspondence between the two images, allowing the surgeon or radiologist to objectively compare the two modalities. The number of blood vessels present in each image and the size of the smallest visible blood vessel are important measures of the efficiency of each angiographic imaging method.

The mathematics involved in the estimation of the HTM describing the projection geometry of the DSA images are also outlined. The estimated HTM is then used to generate a projection of the MRA dataset corresponding to the acquisition geometry of the DSA image.

5.2 Contrast Measurement in DSA and MRA

Contrast in an image is a parameter that describes the difference between the intensity of objects of interest and the background signal. Hence, contrast is used to compare images acquired using the two angiographic techniques DSA and MRA. While there is no unique rule for the calculation of the contrast characterizing the image, the simplest and most straightforward method is to measure the intensity S of a point on a clearly visible blood vessel, and the intensity of a neighbouring point in the background B . The contrast is then calculated as the ratio of the difference in intensity between the two points to the background signal intensity ¹.

$$Contrast = \frac{S - B}{B} \times 100\%, \quad (5.1)$$

This specific implementation is neither reliable nor robust in characterizing the image contrast, since it depends on the choice of points measured to calculate contrast. A more robust approach is to take the mean value of the intensities inside a region-of-interest (ROI) on the blood vessel and another ROI in the background. In order to compare the two angiographic modalities of the same patient objectively, the ROIs are chosen as 10×10 pixels: one on the brightest blood vessel, and another in a neighbouring vessel-free region. The DSA image is displayed after subtraction of the mask from the angiogram. The MRA dataset is displayed after projection using a regular parallel ray MIP image. The resulting contrast for typical DSA and MRA images of the same patient is found in table 5.1.

Another means of obtaining intensity measurements is by segmenting the vessels and measuring the average intensity value inside the segmented vessels and comparing it to the average intensity of the pixels outside (background pixels). This is time consuming and is prone to errors during the segmentation process. It is also very

¹Special care should be taken to ensure that the background signal is not zero [50], especially in the MIP case.

dependent on the number and size of blood vessels visualized in the image, which vary significantly between MRA and DSA images.

Contrast measurement	DSA contrast	MRA contrast
One point measurement	$58 \pm 2\%$	$84 \pm 2\%$
ROI measurement	$40 \pm 1\%$	$67 \pm 1\%$
Segmented image measurement	$6 \pm .2\%$	$11 \pm .2\%$

Table 5.1: Image contrast calculation for a DSA and an MRA dataset, using the three techniques introduced in section 5.2

Several problems are associated with contrast as a means of comparing two types of angiogram. First, the background signal is highly suppressed when using MIP to display MRA datasets, which leads to extremely high contrast values or an undefined contrast value if the background signal is zero. Second, the range of the intensity values is different for both modalities. MRA datasets tend to have a larger dynamic range than DSA datasets. Third, the two datasets do not necessarily show the same vascular structure even if they have been geometrically manipulated to correspond to the same view. MRA images may not show the small vessels and capillaries that are a trademark of DSA images, and may exhibit no signal in the presence of turbulent blood flow (The differences between the visualized vascular structure are discussed later in the chapter). Finally, DSA tends to be selective, i.e., only a single major vessel along with its capillaries is visualized. MRA images are global and show all the major vessels in the imaged region², but lack the detail of the small capillaries that are present in the DSA images.

5.3 Registration of MRA and DSA datasets

In order that the two imaging modalities may be compared objectively, the different angiograms must be displayed in the same space, i.e., projected onto the display

²This is true only if PC sequences are used, otherwise only vessels along the direction of the tag are visualized.

plane from the same viewpoint with the same scale and magnification. DSA images are already in raster format and their viewing geometry is fixed by the relationship of the X-ray tube and the Image Intensifier to the patient. Therefore, in order to display both datasets in the same space it is necessary to map the projection of the MRA dataset to the X-ray projection. By identifying clearly visible points in both images, the *Homogeneous Transformation Matrix* which describes the projection geometry of the DSA image can be determined (see section 3.4.3). The HTM is then used to generate the corresponding projection of the MRA volume, as discussed in section 4.4.1. Since the two projections are related through the HTM, any point in the MRA image can be projected to its corresponding location in the DSA image. Note however that the reverse transformation is not possible since each point in the DSA image is the projection of an entire line.

The calculation of the HTM from the set of homologous points is achieved through the application of a least squares minimization technique discussed in the following section.

5.3.1 Least Squares Minimization

The *Homogeneous Transformation Matrix* describing the linear transformations that relate the coordinates of the two angiograms is presented in section 3.4.2. The elements of this matrix are obtained via a least squares formulation aimed at minimizing the squared error between the actual point positions and their calculated projections.

Each homologous point-pair results in two linear equations 3.13 relating the projection points, 3D volume points and the elements of the HTM. At least six landmark points need to be identified in each image, giving rise to the 12 simultaneous linear equations used to solve the system of 12 unknowns ³. The steps of the algorithm are as follows:

First each landmark point with coordinates $[x_i, y_i, z_i, 1]^T$ in 3D and $[\alpha u_i, \alpha v_i, \alpha]^T$

³In fact, there are only 11 unknowns because one element can be set arbitrarily to unity [36].

is written as a function of the transformation elements, by expanding equation 3.11, resulting in the set of equations 3.12. Then the value for α is substituted back in the first two equations of the set 3.12, and the following are obtained:

$$u_i m_{34} = x_i m_{11} + y_i m_{12} + z_i m_{13} + m_{14} - u_i x_i m_{31} - u_i y_i m_{32} - u_i z_i m_{33} \quad (5.2)$$

$$v_i m_{34} = x_i m_{21} + y_i m_{22} + z_i m_{23} + m_{24} - v_i x_i m_{31} - v_i y_i m_{32} - v_i z_i m_{33} \quad (5.3)$$

By setting m_{34} to unity, one may rewrite equations 5.2 and 5.3 in matrix form as:

$$\begin{pmatrix} u_i \\ v_i \end{pmatrix} = \begin{bmatrix} x_i & y_i & z_i & 1 & 0 & 0 & 0 & 0 & -u_i x_i & -u_i y_i & -u_i z_i \\ 0 & 0 & 0 & 0 & x_i & y_i & z_i & 1 & -v_i x_i & -v_i y_i & -v_i z_i \end{bmatrix} \times \begin{pmatrix} m_{11} \\ m_{12} \\ m_{13} \\ m_{14} \\ m_{21} \\ m_{22} \\ m_{23} \\ m_{24} \\ m_{31} \\ m_{32} \\ m_{33} \end{pmatrix} \quad (5.4)$$

When picking at least six landmark points in each image, the resulting 12 equations can be written in matrix notation, and specify an overdetermined linear system:

$$A = BM \quad (5.5)$$

Solving for this system the following expression for the matrix M is obtained [36]:

$$M = (B^T B)^{-1} B^T A \quad (5.6)$$

This matrix is solved numerically using the Singular Value Decomposition (SVD) algorithm [73].

5.3.2 Fiducial Point Selection

The selection of fiducial points must be performed carefully. In order for the matrix equation (5.5) to be solved, the raw rank of the B matrix should be at least eleven. At least six points must be identified in each image, and their choice should result in at least eleven independent rows in the B matrix. In order to achieve this, no more than four selected points should be coplanar [1].

There are two criteria that affect the determination of the HTM: the number of homologous points, and their location in the 3D space. A digital 3D phantom, a $256 \times 256 \times 256$ pixel volume with a predefined structure, was generated for testing purposes. The phantom structure was projected into a 2D raster, using a known HTM, to simulate DSA imaging. The two images, the projection and the MIP of the volume, were then displayed side-by-side and several points were identified and labeled. These points were used to obtain an estimate of the HTM using the procedure outlined in section 5.3.1. The error in the estimation of the HTM was calculated by projecting some randomly generated points using the original, and the estimated HTM, and then calculating the *euclidian* distance between the two projections, the same as in Root Mean Squared (RMS) error calculations.

The accuracy of the match improves as the number of selected points increases, because more redundant information is introduced into the system, and small errors in the localization of the homologous point-pairs become relatively less significant. The error associated with the estimation of the HTM decreases with the addition of corresponding pairs, and reaches a minimum when a certain number of point-pairs are identified. Typically, this limit is reached when twelve to eighteen homologous point-pairs have been selected [22] (see figure 5.1).

The robustness of the estimation of the HTM was tested also: eight point pairs

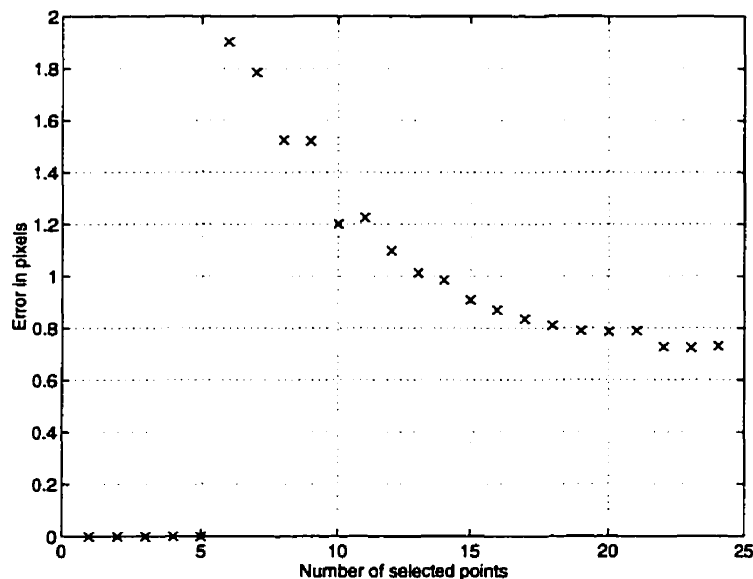


Figure 5.1: Pixel error in the estimation of the HTM as a function of the number of identified homologous points

were identified between the two images, the corresponding HTM was calculated, and the error was computed as previously described ⁴. The results can be seen in figure 5.2. Even at displacements of more than five pixels, the difference between the two projected sets of points is less than one pixel (less than 1 mm), which is typical for the accuracy of the IGN system.

5.3.3 Matching of Angiographic Data

The matching algorithm was applied to real data derived from neurosurgery patients at the MNH. In order to begin with two datasets known to contain exactly the same information, a “DSA projection” was simulated by projecting rays through the MRA 3-D volume [47], so that it is known *a priori* that all the vessels are present in the MRA and simulated DSA images. As with the digital phantom experiment, several point-pairs were identified in both images, and the corresponding HTM calculated.

⁴The error is the *Euclidian* distance between the projected points obtained using the initial HTM and the projected points obtained using the estimated one.

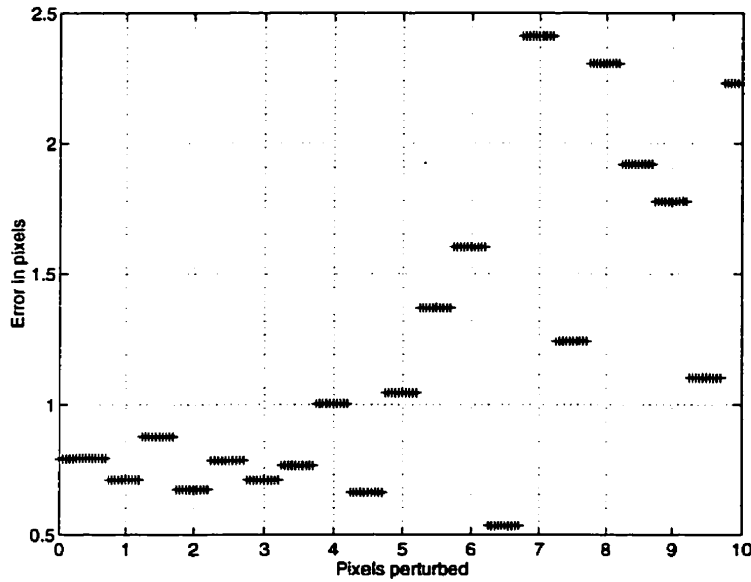


Figure 5.2: Error in the estimation of the HTM, from the digital phantom dataset, as a function of small perturbations in the identified homologous point pairs

The same HTM was then used to reproject the MRA volume using diverging ray MIP and displayed next to the simulated DSA projection (see figure 5.3). The accuracy of the match is shown in figure 5.4, as a function of the number of identified homologous pairs. It can be seen from the graph that the error in the estimation decreases with the number of point-pairs, and saturates after 15 point-pairs have been identified.

If only seven or eight homologous points are selected, the accuracy of the estimate is extremely low, and the error in the reprojection is on the order of twenty pixels. These points are not plotted in figure 5.4. The reason for this high error is the large inaccuracy associated with the selection of the homologous points, especially in the MRA image (see section 4.4). Two factors act to increase the failure rate of this algorithm [85]. First, the vessel intensity may be low due to partial volume effects, slow blood velocity or spin saturation. Second, background signal intensity may be higher than the intensity value of some vessel segments due to poor stationary spin suppression. If one of the identified homologous points is a background voxel⁵, it

⁵This happens when the background point has an intensity value higher than vessel points.

will have coordinates that do not correspond to its DSA counterpart, leading to mis-registration. This problem can be solved in two ways, either by identifying more homologous points and reducing the effect of selecting incorrect points, or by displaying the MRA dataset in stereo and determining the location of the chosen points using the coordinates of the stereoscopic cursor [36]. A discussion of the stereoscopic display of the registered datasets is presented below in section 5.3.4.

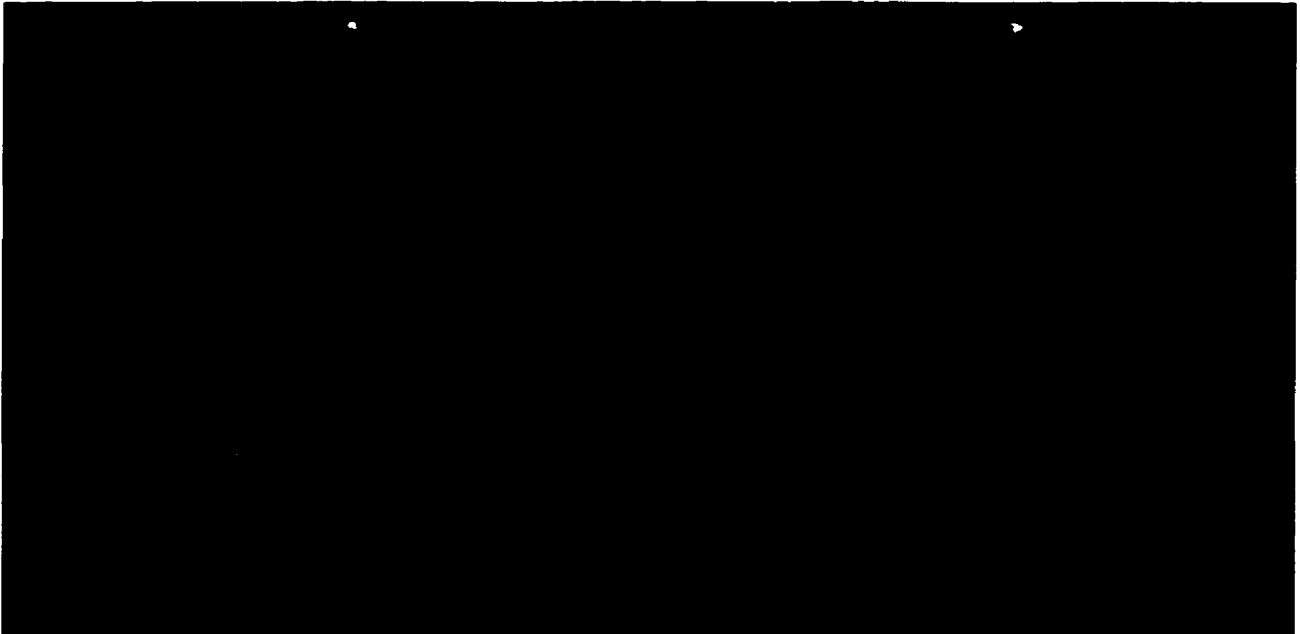


Figure 5.3: Registered MRA to an artificially generated DSA, derived from the original MRA. The MRA is projected using diverging ray MIP while the DSA is generated using a summation projection

When matching MRA volumes to real DSA images the procedure is not as simple as described above. DSA images describe the line integral of the contrast enhanced structure along the projection rays⁶, generally they display only a single major vessel along with its corresponding capillaries. On the other hand MRA datasets capture most of the major vessels in the vascular tree structure and MIP, which is used to project these datasets, describes only the highest intensity points along the path of

⁶See section 2.1

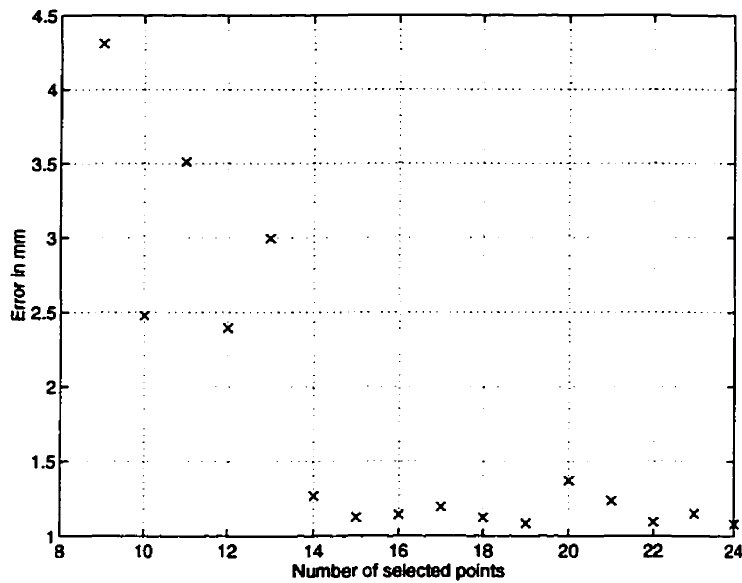


Figure 5.4: Error in the estimation of the HTM from the MRA dataset, as a function of small perturbations in the identified homologous point pairs

the projection rays⁷. Therefore, there may be only minimal overlap between the data-space of the two images, even if the physical spaces are coincident.

The discrepancy between the two angiographic image acquisition methods and the effect on the resulting angiogram, as discussed earlier in section 5.2, increases the ambiguity of the choice of the homologous point-pairs. Therefore, a very experienced user (radiologist or surgeon) familiar with DSA and MRA image should identify these points, using anatomical and vascular information to justify their selection.

In the tests performed here to validate the system, nine point-pairs were identified in the MIP and DSA images. The HTM was then calculated based on these nine points. The resulting MIP was obtained by using the estimated HTM to define the projection parameters, and is shown in figure 5.5 along with the corresponding DSA image. The segments containing the internal carotid artery and its corresponding capillaries, in both images are shown in figure 5.6. As expected, the match was not perfect because there is only one major artery represented in the DSA image along

⁷see section 4.4

with a large number of small vessels. On the other hand the MIP shows most of the major vessels, arteries and veins, but almost none of the small capillaries clearly present in the DSA image. The magnification, due to the X-ray beam emanating from an almost point source, is visible when comparing parallel ray MIPs to the DSA image (see figure 5.7). The magnification is evident as the size of the carotid artery changes, where vessel segments close to the X-ray source appear larger than segments the same size but further away from the source.



Figure 5.5: MRA volume registered to the corresponding real DSA. Note the high density of capillaries present in the DSA image (local details), and the large number of veins and arteries available in the MRA image (global details).

5.3.4 Stereoscopic Image Registration

DSA images for neurosurgery are generated stereoscopically as described in section 1.2.1. Stereoscopic MIP image pairs can be generated from the MRA dataset by

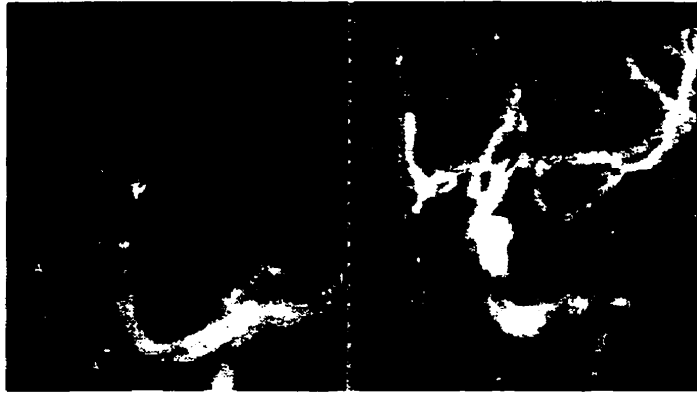


Figure 5.6: Region of correspondence of the two registered MRA and DSA images. The *A* labeled arrows point to structure present in the MRA image only, *B* labeled arrows point to structures present in the DSA image only and the *C* labeled arrows point to common structures to both.

projecting along diverging rays simulating the acquisition geometry of the two DSA images (typically 5-7 degrees apart). Thus stereo datasets from both modalities may be displayed side-by-side on the display monitor, enabling them to be readily compared.

Although the the image pairs are still two dimensional, when put together in a stereoscopic display context as discussed in section 3.2.2, the third virtual image allows the experienced user access to a useful qualitative representation of the three dimensional vessel tree structure in the head. Problems with stereoscopic image analysis such as perceived distortion are discussed in detail by Henri [36]. A registered MRA/DSA stereoscopic pair is shown in figure 5.8.

In order to locate structures in this stereoscopic image a *Stereoscopic* 3D cursor was employed. This cursor is composed of two 2D cursors, one for each of the stereo image pairs. The depth movement of the stereoscopic cursor is simulated by changing the relative horizontal displacement of the left-and-right eye cursors. Because the images are digitized, the depth position of the cursor varies only in discrete steps, limited by the size of the pixels. This limitation reduces the accuracy in determining the position of the selected points used in the image registration mechanism [36].



Figure 5.7: Regular Posterior-Anterior (PA) diverging ray MIP of the MRA volume used in the MRA/DSA registration of figure 5.5

5.3.5 Registration of Segmented MRA with DSA

As discussed in section 4.6.3, several advantages are derived from the use of segmented MRA images in the comparison system. This practice also increases the accuracy of the neurosurgical planning.

A manually segmented MRA image is generated⁸ and this volume dataset can be manipulated to correspond to the DSA image. This is performed using the basic transformations discussed in section 3.4.2.

The use of segmented MRA datasets eases the comparison process and increases its accuracy but some details are lost from the volume. Small capillaries are lost in the thresholding and smoothing stages of the segmentation process. In addition,

⁸See section 4.6.3, and figure 4.10.

the developed comparison system is not optimized to manipulate such a volumetric dataset, and real time manipulation is thus compromised.

5.4 Summary

Although the two angiographic imaging methods visualize the same vessel tree structure in the head, they do not reflect the same physical or physiological properties of the blood vessels. The comparison system registers images from the two different acquisition methods, thus allowing for the objective comparison of these methods. In addition, this system presents the observer with additional information that cannot be obtained using only one angiographic imaging method.

The system presented in this thesis will help surgeons decide on the dataset to rely on in the planning and guidance of the neurosurgical procedure. It will assist them in comparing the two angiograms under the same projection geometry conditions and in the same viewing space. In addition it will increase the information contained in an image, or in a stereo pair of images, from one modality by using additional information available in a different imaging modality. The added image may describe poorly represented or non-existent vascular structures in the first image set. Thus, the overall system will encompass more details of the vascular tree structure.

A general comparison of the different properties between the two methods is presented below in table 5.2. The table summarizes the differences between the two modalities with respect to the visualization of the cerebral vasculature.



Figure 5.8: Registered stereoscopic DSA and MRA pairs, presented for cross-eyes viewing.

Property	DSA	MRA
SUBJECT CONTRAST	Uniform low subject contrast over all the vascular tree.	Regions with a high flow rate have a high subject contrast (on the order of 40-60% depending on whether a PC or TOF MRA sequence is used); turbulence and reversal of flow direction cause a sharp decrease in the contrast
3D VISUALIZATION	A two dimensional projection of the vascular tree, but a three dimensional view can be obtained by generating a pair of stereo images of the head.	Originally acquired as a volumetric dataset that can be projected and viewed from any angle and orientation, allowing one to take full advantage of the three dimensionality of the visualized structure.
FLOW EFFECTS	DSA images do not describe the flow inside the vessels and capillaries. Reversal of flow direction does not show clearly on the final image; only severe constrictions or blocked vessels have an impact on the resulting vessel visualization.	MRA is a description of the flow in the vascular tree, so small changes in the nature of flow affect the resulting image considerably, see section 2.2.1
RESOLUTION	Enjoys a high resolution; where small capillaries with thickness on the order of 1 mm are clearly shown.	The resolution of MRA is limited due to the limits on the size of the voxels. Small vessels are hard to visualize because slow flow typical of small vessels induces a low signal that is comparable to background noise.
VESSEL VISUALIZATION	Only a single artery along with most of the small capillaries associated with it and the draining vein can be visualized.	Most of the large arteries and veins in the head are present in a single MRA dataset. This is true for PC MRA only. TOF MRA shows vessels with blood flowing along a particular direction depending on the pulse sequence used.

Table 5.2: Comparison of DSA and MRA images.

Chapter 6

6.1 Conclusion

This thesis discusses the development of a new environment for the objective comparison of two blood vessel imaging modalities, namely Magnetic Resonance Angiography (MRA) and Digital Subtraction Angiography (DSA). In order for the comparison to be as faithful as possible the two images should be viewed and manipulated in the same manner. This is accurately achieved if the images are set and displayed in the same space and under the same viewing geometry.

The acquisition techniques of the two angiograms are very different, and each image describes different physical or magnetic characteristics of the blood and the vessels themselves. DSA images represent the projection of contrast filled blood vessels. Because X-rays emanating from a small, almost point-like source, diverge and traverse the imaged body like a fan beam, the result is a perspective projection. MRA, on the other hand, is a volumetric representation of the flow in the vessels: the resulting signal is related to the flow pattern and its velocity (See section 2.2).

In addition to being a two-dimensional perspective projection of the vessel tree in the head, DSA suffers from a low contrast-to-noise ratio. The difference in intensity between pixels belonging to blood vessels and background pixels is smaller than that present in MRA. However, as shown in chapter 4, contrast is not a very efficient method for comparing the two angiograms because of the small number of vessels

present in MRA and the background noise cleaning effect introduced by MIP. On the other hand the abundance of small vessels imaged by DSA compensates for its low contrast-to-noise ratio and its two-dimensional nature. As a result, the number of vessels that are present in both images, and thus possible homologous points, is small, reducing the number of corresponding point-pairs that may be chosen in the image matching procedure.

The two angiograms are obtained in as standard a manner as possible, and presented to the observer side by side. In order to be able to display the two datasets with the same viewing geometry, they have to be registered to each other and projected in the same manner and with the same projection parameters described by the Homogeneous Transformation Matrix (HTM). The two images are correlated to each other by means of linear transformations which relate points in the 3D MRA volume to the 2D DSA projection. These transformation are estimated through a minimization process that attempts to register a set of identified points between the two datasets. The selected fiducial points are usually points on some distinct sections of vessel lumina or of vessel intersections.

The display of DSA images is quite straightforward: after subtraction of the angiogram from the mask, or the venous phase from the arterial phase, a bitmap is created and displayed, with each pixel having a grayscale value. Several techniques exist for the display of MRA images; namely, Maximum Intensity Projection (MIP) with parallel and diverging rays, first encountered vessel projection, and surface rendering of the segmented vessel, as discussed in chapter 4.

The identification of vessel boundaries is not a very accurate procedure in either of the two angiographic modalities. In DSA the low contrast-to-noise ratio decreases the chances of correctly labeling the lumen of the vessel, while the low resolution and the nature of image acquisition in MRA increases the uncertainty in the vessel wall location. The latter effect is the result of the different flow patterns that exist in the

body ¹. Blood in contact with vessel lumina is almost stationary and results in an almost zero signal.

When the two image modalities are registered together, a resulting accuracy on the order of 1 *mm* is achievable for digitally generated phantoms. The mean squared error between the estimated HTM and the original HTM, used to generate the digital radiograph gives rise to a displacement error of about 1.3 *mm* ².

In the process of comparing the two angiographic modalities, the advantages and disadvantages of each may be explored, and their effect on neurosurgical planning may be seen. MRA can help improve the volumetric and 3D representation of the vessel tree. According to neurosurgeons and radiologists at the MNI, however, MRA cannot universally replace DSA in guidance and planning, at least with its current low resolution and poor visualization of small vessels.

6.2 Future Work

This work can be extended to include other angiographic modalities in the comparison environment, such as CTA or Power Doppler Ultrasound (US), thus providing the surgeon with the extra vascular information needed to increase the safety of neurosurgical procedures. The addition of US gives the advantage of acquiring the images in real time during surgery. This image acquisition method allows the acquisition to be performed on site in the operating room.

The display of MRA data is still in the embryonic stage, and is a field in need of much research. The automatic segmentation of the vessel tree is one aspect that requires further study, and improvement of accuracy. Inherently, MIP provides very little information about the vessel lumina and their relative positions in 3D space, while a segmented dataset demonstrates this information, and allows it to be more

¹See section 2.2.1

²This error is obtained when at least 20 homologous points are selected

easily manipulated than traditional MIP. Another means of improving the visualization of the MRA datasets is by fitting deformable models to the vessels [39].

The registration procedure can be automated or made semi-automatic by searching for some geometric properties of the blood vessels, defining a feature vector based on these found properties, and then applying a least distance algorithm that minimizes the difference in registration between the two images. Such a matching process could then be applied to the whole image or just some segments of the datasets. This represents a more global approach to the registration compared to the local technique used in this thesis.

Glossary

- **α Flip Angle:** the angle by which the magnetization vector is moved from the Z axis, by the application of Radio Frequency (RF) pulses. This angle is the integration of these pulses over the repetition time T_R .
- **B_0 Magnetic Field:** the static magnetic field that is applied to establish the fundamental Larmor frequency of the imaged body. Typical values of this field range between 0.5 and
- **CTA:** Computerized Tomographic Angiography.
- **DSA:** Digital Subtraction Angiography.
- **Focal length:** the distance between the X-Ray source and the image plane, or the distance between the focal point of the camera and the projection plane.
- **Image or projection plane:** the planar surface on which the projected image is recorded.
- **KVp:** The peak voltage amplitude used in the generation of the X-Ray beam in kilovolts.
- **Laplacian:** The partial second derivative of an n -dimensional function f , it is denoted as: $\nabla^2 f = \frac{\partial^2 f}{\partial x y z \dots}$.
- **Larmor Frequency:** the precession frequency of a spin under the influence of a magnetic field. This frequency is related to the applied field by the *Gyromagnetic* ratio: $F = \gamma \times B_0$. This ratio is, for the Hydrogen atom, 42 MHz/Tesla.
- **MIP:** Maximum Intensity Projection used to project MR volume into a 2D plane, using parallel or diverging ray tracing.
- **MRA:** Magnetic Resonance Angiography.
- **MRI:** Magnetic Resonance Imaging.
- **Orthographic:** a parallel ray projection, such that the viewing point is located at infinity.

- **Perspective:** the differential magnification which causes an object to diminish in size as it recedes from the observer.
- T_1 : MR time constant of the relaxation of the longitudinal magnetization back to thermal equilibrium following rotation away from the positive Z axis by the RF pulse.
- T_2 : MR time constant of the decay of the transverse magnetization, where $T_2 \leq T_1$ in all cases.
- T_R **Repetition Time:** the interval between two consecutive RF pulses in an MR image sequence.
- T_E : the time interval between the application of the RF pulse and the read out of the gradient in an MR image sequence.
- **Triangulation:** the process whereby an object's 3D coordinates are determined from at least two different 2D views.
- **US:** Ultrasound.
- **Voxel:** three dimensional pixel: a unit cube or a parallelepiped from which the sampling volume is constructed.

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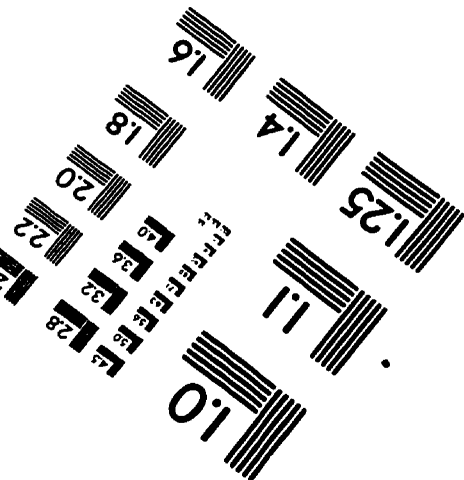
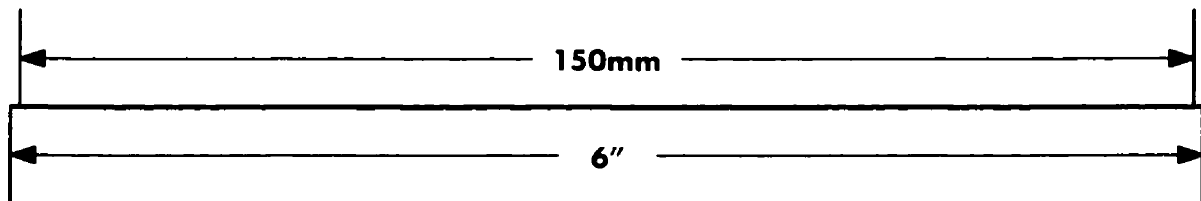
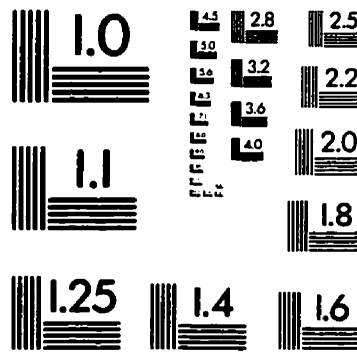
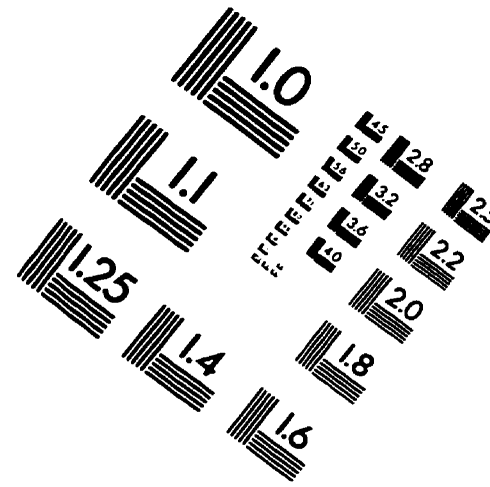
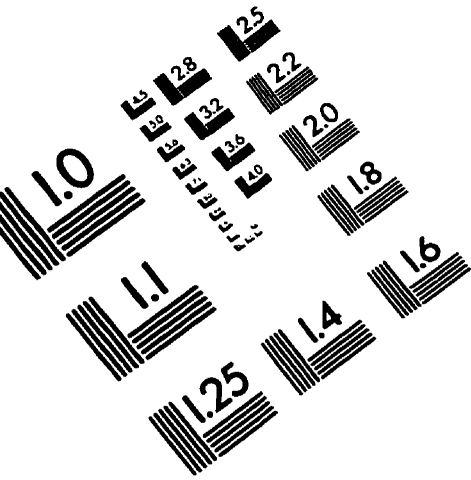
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IMAGE EVALUATION TEST TARGET (QA-3)



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