3D Reconstruction of Magnetic Resonance Imaging using Largely Spaced Slices

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Abstract

This paper presents a full process of reconstruction of magnetic resonance images. The first step is to bring the acquired data from the frequency domain, using a Fast Fourier Transform algorithm. After, a Tomographic Image Interpolation is used to transform a sequence of tomographic slices in an isotropic volume data set, a process also called 3D Reconstruction. This work describes a method whose interpolation stage is based on a previous matching stage that uses Delaunay Triangulation.

1. Introduction

Magnetic Resonance Imaging (MRI) and Computer Tomography (CT) usually deliver cross-sectional images of the human body. The sampling is done in a set of coplanar slices with adjustable distance and thickness. If sequences of adjacent images are put together, it results in a 3D volume representation of the human's body part under consideration. To reconstruct an isotropic 3D volume, the interslice distance needs to be close to the interpixel distance. The distance between consecutive slices is usually larger than the distance between consecutive pixels within a slice, so an interpolation must be done to obtain the pixels between the slices. This is a powerful tool to aid surgery and medical diagnosis [Udupa_91]. An isotropic volume reconstructed like that can be manipulated as the original body, without any risk for it. Nevertheless, two distinct steps are necessary to reconstruct a 3D volume: the 2D Reconstruction of each slice and the 3D Volume Reconstruction.

2. Methodology of Development

The first step in magnetic resonance imaging (MRI) reconstruction is the 2D Reconstruction, which is done through a Fast Fourier Transform (FFT) [Bri_88], producing slices in gray-level, typically matrices, from the

frequency domain data. We have been using data acquired from MR Tomograph of Physics Institute of Sao Carlos of the University of Sao Paulo, where are being developed a low cost, Low Field MR Tomograph. The second step is the 3D Volume Reconstruction using these 2D slices already reconstructed [Bueno_93].

The slices acquired from MRI are usually highly spaced, due to time and equipment restrictions. The sampling rate in the 2D dimension (actually at 256x256 pixels) generates an inter-pixel distance higher then the distance between the slices, resulting in a non isotropic volume. We are seeking an isotropic volume, i.e., the distances in all dimensions must be equal, because it really produces a virtual data from the analyzed data, and the manipulation can be more accurate. This implies the need of to interpolate between 2D slices, to obtain new slides that conducts to an isotropic 3D volume.

The raw data typically are sequences of 256x256x32 or 256x256x64 with 256 gray levels. This work focuses on images with distance between image planes ranging from 6mm to 12mm.

3. Tridimensional reconstruction

Usually 3D reconstruction is made by trilinear interpolation, that is, a simple linear interpolation in X, Y and Z directions. This method is fast, but produces discrepancies in the interpolated images. That discrepancies occur, because the tissues can shrink or expand between two consecutive slices. When that fact happens, a staircase effect disturbs the image. This paper describes a new method, which produces better results.

We are using two phases to generate the images between each pair of original slices: the first phase is the matching, based on correspondences of image points and linear density interpolation. The second phase uses the correspondence obtained on the first phase, and performs an interpolation, limited by the disparities obtained from the matching phase [Gos-92]. The matching phase must define associations between points of same tissue, which have similar characteristics. The border tissue points have high gradient values and can be used to do the matching. Therefore, we make the matching phase into two stages - matching based on high gradient points and matching based on low gradient points.

3.1 Matching based on high gradient points

The points of the tissue contour are characteristic points in the images, which usually have high gradient values. Using a search process, we can establish the correspondence between points in two adjacent images, based on the differences of gradient, density level and geometric position. This is the kernel of the first stage of matching.

We can do the correspondence between two points in two adjacent images using vertical (axis y) and horizontal (axis x) disparity, i. e., a high gradient point must matchs with another high gradient point in the next image. Nevertheless, the second high gradient point can be in a different geometric position from the first high gradient point, then it is necessary to search this point in the region near that geometric position. This search region is established by horizontal and vertical disparity. The horizontal and vertical disparity establish a search window, where the method looks for the higher point gradient in the target image. The figure 1 shows this idea. To determine the correspondences of points in the first stage of matching, we have used the intensities and

gradients of the points, as well as geometric position (disparity) between them. To accomplish this, we have used a vector costs function based on definition presented in [Gostashb92]. The function is defined matching a point (x, y) in the target image to a point (x', y') in the reference image by:

$$\begin{aligned} C(x,y,x',y') = {} & w_1 \cdot |I(x,y) - I'(x',y')| . i + \\ & w_2 \cdot |M(x,y) - M'(x',y')| . j + \\ & w_3 \cdot |\Theta(x,y) - \Theta'(x',y')| . k + \\ & w_4 \cdot Distance[(x,y),(x',y')] . l \end{aligned}$$

where I(x, y), M(x, y), Θ(x, y) are, respectively, the intensity, the gradient magnitude, and the gradient direction of the point (x, y) in the target image; and I'(x', y'), M'(x', y'), Θ'(x', y') are, respectively, the intensity, the gradient magnitude and the gradient direction of the point (x', y') in the reference image; the distance corresponds to the Euclidian distance between (x, y) and (x', y'). The values w_1, w_2, w_3 and w_4 can weight the contribution of each of this. In this work we are using the same contribution for each $w_i = 1$.

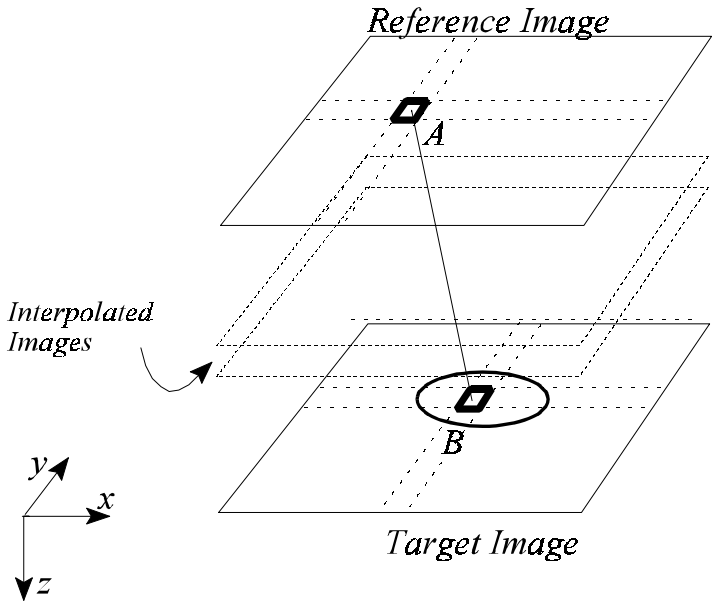


Figure 1 - Defining the search window on target image, where the method searches the high gradient point B, corresponding to high gradient point A in reference image.

The point B found in the target image by this procedure is the best match for point A in the reference image. This approach may not establish only one high gradient point B in the target image for each high gradient level point A in the reference image. Then, to reduce this problem, we invert the reference and target image and execute again the matching phase. Therefore, only the points that match in both ways are marked as real high gradient level points and only they will be used in the second phase of the interpolation method.

3.2 Matching of low gradient points

Low gradient points belong to homogeneous regions of the images. For points with low gradient, we cannot use the same criterium used for the points of high gradients, because such points have similar density level and gradients. Then, using the correspondences established in the first stage of the matching process, we can do an interpolation based on that relationship. Therefore, the adopted approach is:

- First, build a Delaunay triangulation [Aure-91], where the vertexes are the high gradient points with correspondences established in the first phase of matching. The triangulation describes the convex hull for that set of points, and will be used as a guide to perform the interpolation.
- Second, to define disparities for points in homogeneous regions, inside the convex hull, through a procedure of linear interpolation inside triangles.
- Third, to define disparities for points in homogeneous regions, outside the convex hull of the Delaunay triangulation, we are using a procedure of extrapolation. In human images obtained from MR tomographs, the points outside the convex hull are usually background points, then applying an expensive method over them is not necessary. The extrapolation consists in to define a belt limiting the convex hull, where the disparities become progressively linear. This special treatment for the boundary is needed, because only the frontiers of the interesting objects are usually diffuse.

A triangulation is well suited for interpolation if its triangles are nearly equilateral. The Delaunay triangulation produces this type of triangle [Sibs-77]. The interpolation inside triangles is made by linear combination of disparities of vertex triangles. The aim of the extrapolation procedure is to yield a smooth transition between the edge's disparities of the tissues in the images, and the disparities of background images. The extrapolation procedure also can smooth the staircase effect in the borders of objects into the reconstructed volume.

Finishing the matching phase, the linear interpolation can be made, using all the correspondences established. Figure 2 shows two slices interpolated: (a) by linear interpolation; (b) by matching interpolation. Those images

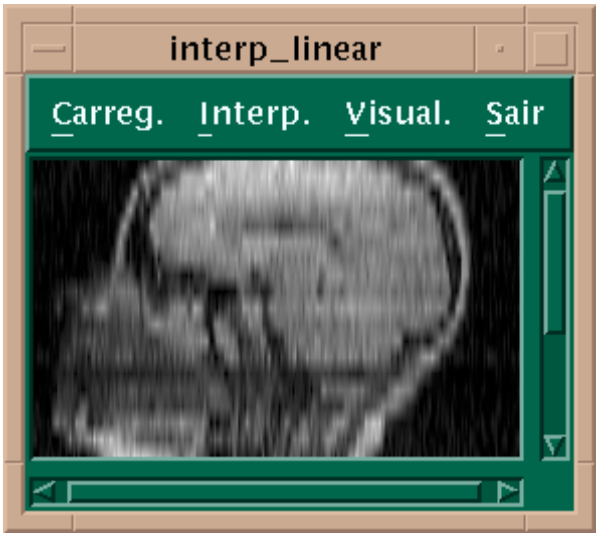
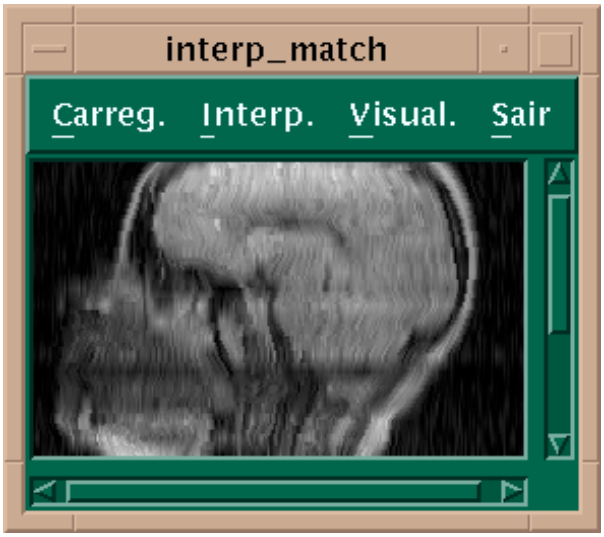


Figure 2 (a) - Sagittal slice generated by linear interpolation.



(b) - Sagittal slice generated by matching interpolation.

are reconstructed from a sequence of 22 transversal images, each separated 8 mm from each other.

4. Results

To evaluate the method proposed here, we used qualitative and quantitative analysis. We utilized RM images of brain and test phantoms to rehearsal the method. The qualitative analysis was made interpolating intermediary slices between serial slices. Using sequences of three images, the method works with the first and the third. The interpolated slice is compared with the second slice, which is in fact a collected slice, computing the root mean square (RMS) error. This determines the medium error on pixels between the collected and the interpolated images. Another measure used is the number of points where a wrong point is selected (number of points in fail - NPF). Images of phantoms used to illustrate the method can be seen in figures 3 and 4. Using the phantom of figure 3 with 30 original slices, we estimated the slices 5, 15 and 25 and they were

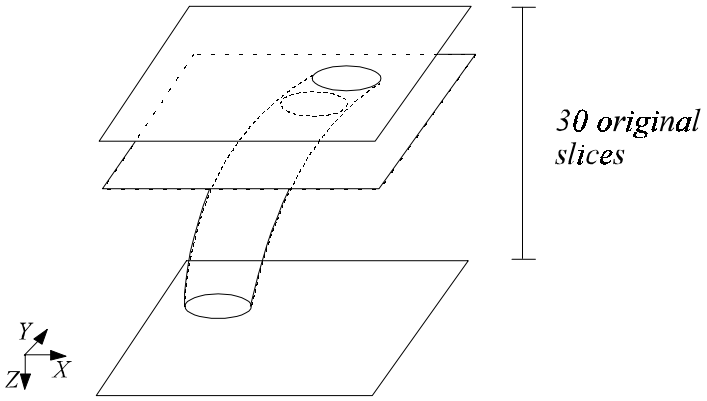


Figure 3 - Phanton of a bending structure.

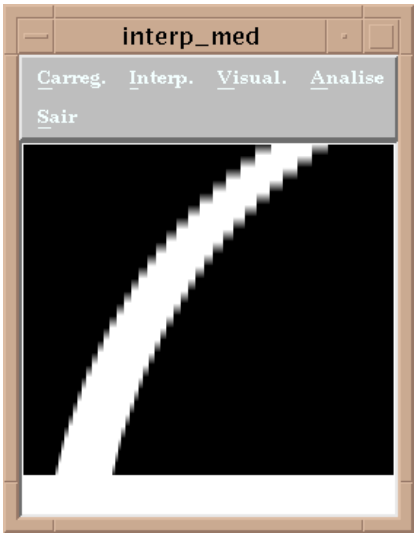
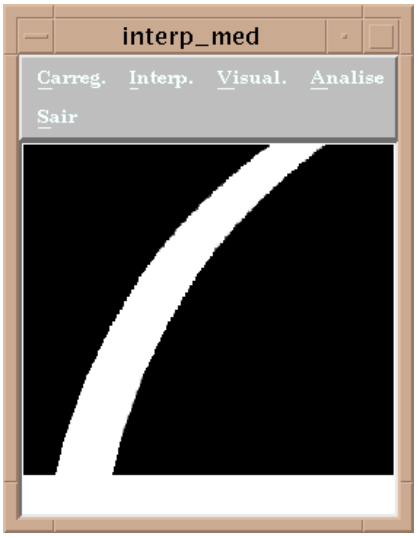


Figura 4 (a) - Phanton slice in yz plane, produced by linear interpolation.



(b) - Phanton slice in yz plane, produced by linear interpolation.

compared with the original slices. The diameter of the phantom is 50 pixels. The quantitative analysis is presented in table 1. Looking at table 1, figure 2 and figure 4, is evident the advantage of matching interpolation over trilinear interpolation.

The results show that in sets of slices with distance between two or 3 mm is better to use linear interpolation, i.e., the image depreciation is very low and the computational costs not so high. Nevertheless, in sets of slices

with greater space between them, the results of the matching interpolation are better.

Estimated image	reference and target image	Quantitative Analisys					
		RMS error			NPF		
		linear	match.	%	linear	match.	%
5	4 and 6	0.6023	0.0994	83.5	612	72	88.2
15	14 and 16	1.0039	0.1365	86.4	1020	101	90.1
25	24 and 26	1.9077	0.3118	83.7	1918	315	83.6
Average		1.1713	0.1825	84.4	1183	163	86.2

Table 1 - Quantitative analisys performed on phanton data.

5. Conclusion

This approach is a modification of that introduced in [Gosh-92]. The matching phase on low gradient points described here uses the Delaunay triangulation, as well as interpolation and extrapolation algorithms. The already obtained results show a better approximation of the volume in an isotropic representation, and are encouraging new refinements [Prado]. This method needs more power from the computational equipment, because the matching interpolation may be up to ten times more demanding than linear interpolation. The great part of computational cost of this method is in the matching phase. However, the 3D reconstruction is made only once, and the volume can be manipulated as needed.

6. Bibliography

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