DISPARITY ANALYSIS AND ITS APPLICATION TO THREE-DIMENSIONAL RECONSTRUCTION OF MEDICAL IMAGES

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Abstract

A novel approach to image alignment or registration for three-dimensional (3D) reconstruction of medical images is introduced in this paper. The scheme is based on recent advances in computer vision. A point-to-point disparity analysis is used in the alignment algorithm. We assume that a sequence of images to be aligned is related by a linear affine transformation. Based on this model, a disparity function is defined by considering the image shape structure or the image intensity changes. The function parameters are estimated simultaneously from the computation of shape or intensity disparity. The decomposition of the disparity function parameters reveals the object rotation, deformation, scaling and translation individually in a 3D space. These parameters provide enough information for image alignment as well as image matching. Experiments on 3D reconstruction of autoradiographic images demonstrate the effectiveness of the disparity analysis method. Under the same framework, the method can also be applied to other medical imaging systems.

Introduction

Sequential medical images contain a great deal of potentially useful 3D information. With advanced digital image processing techniques, it is feasible to reconstruct a 3D object from serial 2D sectional images. It then becomes possible digitally to re-section the object in any standard plane or to associate image data with standardized atlas structure. This will allow researchers to perform extensive and sophisticated analysis that are not feasible with individual 2D sectional images.

A fundamental problem associated with physically sectioned images in 3D reconstruction is that the consecutive 2D images are randomly aligned and registered. Some medical imaging systems can utilize external landmarks to provide additional information for alignment. However, in other imaging systems, for example, autoradiography, it is difficult to adopt external landmarks. Hibbard et al [1,2] applied the principal axes method to the alignment and registration of autoradiographic images. The principal axes are basically the eigenvectors of a 2 × 2 matrix computed from the pixel values. Alignment consisted of a translation that places the image centroid on the origin and a 2D rotation in the image plane to align the principal axes with the x- and y-axes of a reference coordinate system. The principal axes method worked well for most coronal sections. The authors noted [1], however, that...
if the image nearly round (principal axes about equal) or if the bilateral symmetry of the
image is lacking (for example, in damaged or asymmetric sections) the principal axes align-
ment may be unsatisfactory. Correlation is perhaps the most popular approach to medical
image alignment or matching. Cross-correlation is a measure of similarity of two images
in terms of spatial distributions of gray-level values (image intensities), and hence does
not require well defined boundaries. Local correlation is typically computed in the spatial
domain, and it can be used to match regions of interest [3,4]. For global correlation, fast
Fourier transform (FFT) can be used to speed up computation [5]. A major difficulty with
Fourier analysis lies in the fact that translation, rotation and scaling are coupled in the
Fourier domain, and cannot be determined simultaneously. Object shape information can
also be used for image alignment. With shape analysis, the first step is to detect edges or
boundaries, and the analysis is based on the shapes of the boundaries or the binary im-
ages formed from detected boundaries [6,7]. There exist in the image-processing literature
[8,9] numerous algorithms for shape matching; it should be noted, however, most of these
algorithms were designed for shape recognition, instead of shape alignment.

In this paper, we develop a new method for image alignment that will overcome most of the
difficulties experienced by the principal axes method and the cross-correlation method. The
new method is based on a linear affine model to analyze point-to-point disparities in two
images. It is a direct method that estimates scaling, translation and rotation parameters
simultaneously without transformation. The disparity approach is computationally fast,
and it takes into consideration shape differences of sectional images. It is a general and
flexible method that utilizes the same basic principle to deal with different situations such
as damaged or asymmetric sections. The method is applied to autoradiographic images
and is also adaptable to other medical images.

Disparity Analysis

Fig.1 (a) and (b) are autoradiographic images showing two adjacent coronal sections from
a rat brain. With the well-defined section boundaries, let \((x, y)\) be a point on the boundary
of the first coronal section and \((x', y')\) be the corresponding point in the second image. We
assume a linear relationship between the two points.

\[
x' = Ax + c + \varepsilon(x), \tag{1}
\]

where \(A\) is a \(2 \times 2\) linear affine matrix, \(c\) is a \(2 \times 1\) vector and \(\varepsilon\) is a \(2 \times 1\) error vector
due to noise and/or minor local differences of the two boundaries. \(x\) is defined in terms
of its transpose \(x^T = (x, y)\); the vectors \(x', c\) and \(\varepsilon\) are defined in a similar manner. The
disparity vector \(d(x)\) is simply

\[
d(x) = x' - x = Bx + c + \varepsilon(x), \tag{2}
\]

where \(B = A - I\) and \(I\) is the \(2 \times 2\) identity matrix.

The physical meaning of this linear affine model is as follows: 2D translation is represented
by the vector \(c\), and 2D rotation can be represented by a rotation matrix \(A\), which is a
special case of the more general \(A\). With \(A\) and \(c\) computed from two images, alignment
can be easily accomplished by 2D rotation and translation in opposite directions.
We choose the more general affine matrix $A$ to deal with some of the situations that cannot be handled by the principal axes method or cross-correlation method. For example, sectional images may have shape changes other than $x$, $y$ directions. Indeed, the affine matrix $A$ can be uniquely decomposed into 2D rotation, 2D angular deformation (shearing), and high and width changes:

$$A = A_1A_2A_3$$

$$= \begin{pmatrix} l_x & 0 \\ 0 & l_y \end{pmatrix} \begin{pmatrix} \cos \alpha & \sin \alpha \\ -\sin \alpha & \cos \alpha \end{pmatrix} \begin{pmatrix} \cos \theta & -\sin \theta \\ \sin \theta & \cos \theta \end{pmatrix}.$$  \hspace{1cm} (3)

In other words, for a given $A$, the 2D rotation angle $\theta$, the deformation angle $\alpha$, and the height and width changes (scale factors), $l_x$ and $l_y$ can be computed uniquely from the the matrix elements [10].

Consider $N$ points on the boundary of a coronal section $x_i$, $i = 1, 2, \ldots, N$. If the corresponding boundary points $x_i'$, $i = 1, 2, \ldots, N$, in the next image were known, the point-to-point matching problem would be solved. In fact, a polynomial method that includes quadratic terms for motion correction in cine angiograms has been studied, with a human operator selecting the corresponding points in two images [11]. For alignment of autoradiographic images, it is extremely difficult to find accurately the corresponding points by an operator. Furthermore, it is obviously desirable to automate the computation procedure instead of manual selection of corresponding points.

The image point $x_i$ differs from its corresponding point $x_i'$ by a disparity vector, $d_i = x_i' - x_i$. Thus, disparity analysis is an automated method to locate a large number of pairs of corresponding points. The 2D vector $d_i$ can be decomposed into a component tangent to the boundary in the first image and a perpendicular component. The tangent component cannot be measured without knowing $d_i$. For the perpendicular component, let us superimpose the second boundary on the first one and draw a perpendicular line from the boundary point $x_i$ until it intersects the other boundary. The difference between the intersection point and $x_i$ is then the measured perpendicular component. Let $n_i$ be the normal vector in the direction of the perpendicular component and $\nu_i$ be the magnitude of the component. Then,

$$\nu_i = n_i^T d_i.$$  \hspace{1cm} (4)

Substituting (2) into (4), we can directly get a linear function with six unknowns. For an object with $N$-point boundary, the result is a non-iterative, close-form solution in terms of the elements of $B$ and $c$, and the mathematical details are omitted here [12].

If neither boundary of the consecutive 2D sections can be detected with accuracy, image alignment and matching must utilize information contained in image intensities (gray levels). Fig.2 (a) and (b) show such two adjacent coronal sections. Disparity analysis can also be applied to point-to-point matching of image intensities. Consider a point $(x(k), y(k))$ on the $k$-th coronal section and the image intensity $f(x(k), y(k))$. A key concept or assumption is that as we look at the corresponding points in different serial sections, the image intensities at those points are preserved [13]. Thus,

$$\frac{\partial}{\partial k} f(x(k), y(k)) = 0.$$  \hspace{1cm} (5)
Using the chain rule of differentiation, we obtain the fundamental equation,

$$\frac{\partial f}{\partial x} \frac{\partial x}{\partial t} + \frac{\partial f}{\partial y} \frac{\partial y}{\partial t} + \frac{\partial f}{\partial k} \frac{\partial k}{\partial t} = 0.$$  \hspace{1cm} (6)

Let us define $\mathbf{d}^T = (\frac{\partial x}{\partial t}, \frac{\partial y}{\partial t})$, $\mathbf{g}^T = (\frac{\partial f}{\partial x}, \frac{\partial f}{\partial y})$, $\gamma = \frac{\partial f}{\partial k}$. (6) becomes, in matrix notation,

$$\mathbf{g}^T \mathbf{d} + \gamma = 0.$$  \hspace{1cm} (7)

Note that (7) plays the similar functions as (4) and also the vector $\mathbf{d}_i = d(x_i)$ indeed is the disparity vector in disparity analysis. A basic algorithm is summarized as follows:

Step 1. Preprocess: measure the perpendicular component $\nu_i, i = 1, 2, \cdots N$, or calculate partial differentiations $g$ and $\gamma$;
Step 2. Computation of $H$ and $C$: solve a set of linear equations with 6 unknowns, $A = H + L$;
Step 3. Image matching: $\mathbf{x} = A^{-1}(\mathbf{x}' - \mathbf{c})$;
Step 4. Image alignment: $A = A_S A_A A_R, \mathbf{z} = A_R^{-1}(\mathbf{x}' - \mathbf{c})$.

The disparity analysis method can also deal with simple asymmetry of coronal sections automatically. For a damaged section, it will be necessary to detect the damaged portion of the boundary. We used the piecewise disparity analysis scheme, which is to divide the boundary into several segments and to compute the disparities separately for each segment. A linear affine transformation will be obtained for each segment. The parameters of the transformations, i.e., elements of $c$ and $A$, will be approximately the same for undamaged segments, and they will be significantly different if the segment in one of the two images is damaged. Thus, the damaged segment can be detected by using simple cluster analysis techniques [14] in a six-dimensional parameter space. Finally, disparities computed from the damaged segment will be disregarded, and alignment of the two sections will be based on disparities of the undamaged sections only.

**Experimental Results**

Fig.3 (a) is the superimposed two coronal section boundaries before alignment. We note that the two boundaries differ not only at gravity centroids but also at orientation of their principal axes. Fig.3 (b) shows the result of superimposed two boundaries after applying designed alignment algorithm. The accuracy of alignment is within 200 microns in both x-axis and y-axis. Fig.4 (a) and (b) are the slanted reconstructed 3D brain images of glucose metabolism in two different views. Consequently, this reconstructed brain is ready dissected digitally in any orientations. Fig.5 (a) and (b) are reconstructed horizontal sections that are obtained by digitally slicing the reconstructed 3D image parallel to the xz-plane.

**Conclusions**

Disparity analysis for image registration and matching is a general approach that allows us to deal with symmetric or asymmetric and damaged or undamaged 2D sections in a unified manner. In addition, it also yields information on shape differences of coronal sections that
are not available with simple principal axes method or cross-correlation method. The disparity analysis is based on linear operations; its explicit implementation nature will greatly benefit the reconstruction system. The algorithm is initially based on measured boundary information and intensity changes. Since the system utilizes all available information and the parameters of the affine transformation are estimated by a least square error criterion, the system is relatively insensitive to noise. The flexibility is another major advantage in applying disparity analysis. Modifications on disparity analysis will allow one handling alignment and matching problem under the same framework.


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Fig. 1 Adjacent coronal sections with well-defined boundaries.

Fig. 2 Adjacent coronal sections with blurred boundaries.

Fig. 3 Superimposed adjacent coronal sections before and after alignment.
Fig. 4 Slanted 3D brain images in two different views.

Fig. 5 Reconstructed horizontal sections.