Integration of Multimodal Data based on Surface Registration

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Abstract

The paper proposes and evaluates a strategy for the alignment of anatomical and functional data of the brain. The method takes as an input two different sets of images of a same patient: MR data and SPECT. It proceeds in four steps: first, it constructs two voxel models from the two image sets; next, it extracts from the two voxel models the surfaces of regions of interest; in the third step, the surfaces are interactively aligned by corresponding pairs; finally a unique volume model is constructed by selectively applying the geometrical transformations associated to the regions and weighting their contributions. The main advantages of this strategy are (i) that it can be applied retrospectively, (ii) that it is tri-dimensional, and (iii) that it is local. Its main disadvantage with regard to previously published methods it that it requires the extraction of surfaces. However, this step is often required for other stages of the multimodal analysis such as the visualization and therefore its cost can be accounted in the global cost of the process.

Keywords Volume Modeling and Visualization - Multimodal Registration of Data - Brain images-

1 Introduction

The integral study of the anatomy and the activity of the brain is one the major challenges of the present-day medicine. The new registration devices facilitate this study. Thereby, Magnetic Resonance images (MR) provide brain anatomy data, whereas Angiographies (MRA) show the vascular system. Functional Magnetic Resonance (MRf) and Nuclear Medicine devices such as SPECT and PET give information on the cerebral activity. The analysis of these data separately fails at giving a global view of the structures. The integration of the anatomy and the activity makes easier the detection of tumours or injuries, and it allows better predictions to be done about the scope of these lesions and of their secondary effects on the health and the behaviour of the patients. This is why, in the last years, the integration of multimodal data has become a very active research area in hardware as well as in software. New technologies are currently being designed, able to sample simultaneously various types of data [1]. In addition, new methods for the alignment and joint processing of different image sets are being developed [2]. This paper focuses on the software registration methods. It first reviews the current methods and next it describes and evaluates a new strategy.

2 Previous work

The image and volume registration methods can be classified according to several criteria [3]. A key difference between them is if they use external references (extrinsic methods) or they don't (intrinsic methods). Extrinsic methods are applied whenever the need for a multimodal analysis is known a priori. They consist of identifying the markers on the images [4] and of aligning the image sets in order to match the corresponding marks. The external references (stereotactic frames, fiducials markers...) make the alignment easier but they can be inconvenient for the patients. In the opposite side, intrinsic methods, although more complex, present the advantage of being harmless and applicable retrospectively.

The intrinsic strategy is divided into three main groups: (i) the pixel/voxel based methods (ii) the methods based on feature points and, (iii) the methods based on binary segmented regions. The first approach embraces various strategies based on image processing and pattern recognition algorithms, such as the computation of gravity centers and main axes, the global correlation along with the minimization of gradient variances and intensities [5], [6]. Up to now, because of their high cost, these methods are mainly applied in 2D, to image pairs, rather than in 3D. The identification of feature points is probably the most used strategy. It may require the intervention of a specialist who marks the points, either anatomical characteristics or image singularities [7]. The alignment consists of matching the pairs of feature points, by applying a least-squares fit algorithm. The major advantages of this method are its speed and its versatility, since it is applicable to any image set. In contrast, it is mostly suitable for global and rigid alignments.

Finally, the methods based on segmented binary regions look for a matching function between corresponding regions and next, they apply the function to the whole data sets. Borgefors [8] has proposed to directly align the segmented regions using the chamfer distance metrics. The *head and hat* method [9], extracts sets of contours from the images. It has been applied to the skin in MR, CT and PET data. Hill [10] extends the method to the alignment of no identical but equivalent regions, specifically the brain and the skull. Later works focus on the automatic segmentation of the regions. The main drawback of this approach is the extra cost of the segmentation and even more of the contour tracking. However, it should be noted that the segmentation is often necessary in other steps of the data analysis, for instance, in the visualization and in the volumetric computations. Thus, its cost should be attributable to the whole process rather than to the registration only.

A problem of the segmented regions registration is that it only allows global transformations to be computed. It does not take into account local distortions of the data and thus it does not guarantee that the alignment is equally correct in all the volume set. The *snakes* technique [11] performs local and elastic deformations of two equivalent contours in 2D. The extension of this method has been proposed in [12]. The *snakes* are suitable for the registration of images of the same modality but with little similarity such as real images with an atlas [13]. However, their use is often too complex and computationally expensive for the alignment of multimodal images of the same patient, where a global registration is aproximatively correct and it requires only local adjustments.

In this paper, a new methodology for the integration of MR and SPECT data of the same patient is proposed and evaluated. It is based on the registration of pairs of segmented regions. It admits different levels of precision in the alignment and it can be applied locally. It is mainly suitable when the registration function is not completely homogeneous in the images.

3 Surface registration

3.1 General Scheme

Fig. 1 shows an overview of surface registration. Starting from two different sets of images, the corresponding volume data of each modality are constructed. The models are segmented and each voxel is labeled according to the region to which it belongs. The following stage of the registration consists of computing in each modality the boundary surface representation of the interest regions. Next, an interactive application allows the matching function between pairs of corresponding surfaces to be computed. Finally, an integrated model is obtained by assigning to each voxel the corresponding set of properties and weighting them. In this step, the geometrical transformations are locally applied to each region.

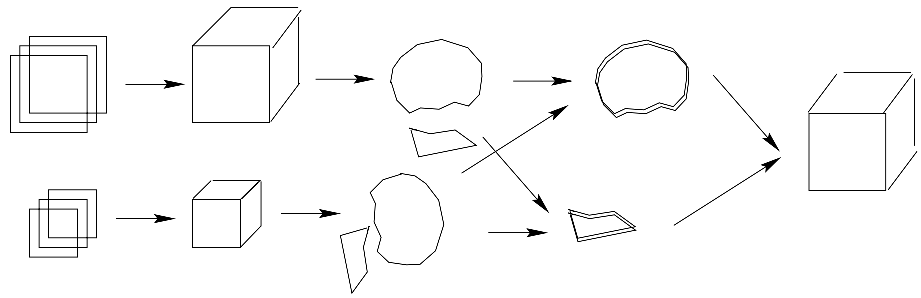

Figure 1. Description of the general scheme.

Region segmentation

The integration of the information acquired with different techniques is difficult, because of the complementary nature of the contents of the images and due to the differences in resolution, position and orientation of the scanned volumes. As an example, the initial images used in the simulations described in Section 3.3 are 512x512x33 and 64x64x64 respectively and they have been captured with completely different orientations. The strategy based on binary discrete regions [8] mentioned in the previous section, is not valid at that such different resolutions. The strategy based on searching for the boundary of corresponding structures in both volumes removes in a natural way the problem of the different sampling rates: the surfaces have the same proportions, although, obviously, the level of detail of the meshes is different and it depends on the initial data sampling.

By opposite to previous references [9], who obtain the polygonal mesh from parallel contours, in this work, the boundary surface is extracted with the Marching Cubes algorithm [14]. This technique avoids the typical surface aspect of polygons ribbons, that gives a artificial orientation and thus may produce a higher matching error. Furthermore, according to the needs, the surfaces can be computed at different levels of resolution in the original data. Even more, different levels of detail can be given to each surface, depending on the degree of interest of the different areas.

Matching procedure

Once a set of points defining a concrete structure has been defined, the next step consists of calculating the geometrical transformation to apply to each dataset. The matching procedure is interactive. The user establishes the correspondences between pairs of surfaces by directly selecting them. Next, two alignment strategies are available: a totally interactive one, and a semiautomatic one. In the fully manual method, the user moves and rotates one surface to make it match the other one. In the semiautomatic method, the user selects at least 3 characteristic pairs of points and a rigid geometrical transformation is computed by using a least-squares fit. Although it fails off the scope of the application, an automatic location of moments and principal axes in the original datasets could also be applied.

Reconstruction

After the matching step, a unique integrated model is constructed. This step is not strictly necessary, if specific algorithm able to process simultaneously the two models and to apply on line the geometrical transformation pairs are designed. However, as the purpose of this work is to perform many operations on the integrated data, it is better to construct the model once, in a pre-process, rather than applying the transformations for each operation. However, the transformation process explained below is basically the same that would be applied on-line.

In this work, the coordinate system of the integrated model is the same as the larger initial model (referenced from now, as *static* model). Therefore, the geometrical transformations that must be applied are those that match the smaller model (referenced as *dynamic* model) over the static model. Currently, the two properties are both kept in all the voxels of the final model. A more efficient representation scheme is under study.

If the transformation between the two data sets is unique, the reconstruction consists simply of revoxelizing the dynamic model. This can be performed by applying the three step affine transformations method [15]. The main problem that must be solved with the proposed approach is how to deal with several rigid transformations.

The method scans through the static model and, for each voxel, it distinguishes three cases: (i) when the voxel does not belong to any of the segmented regions, (ii) when it is interior to one region, and (iii) when it is at the boundary of two or more regions. In the first case, the value is not relevant and thus no geometrical transformation is applied. This is an area of the model where a lot of compression could be done. In the second case, as the classification of the voxel is unique, there is no ambiguity and thus, the geometrical transformation corresponding to the region is directly applied.

Finally, in the third case two or more geometrical transformations can be applied, those corresponding to the boundary regions inside the voxel. In this case, first, the proportion of volume occupied by each region in the voxel is computed. This is done either by aproximatively evaluating the ratio of volume clipped by the extracted surface in the voxel or, by applying a classification function as proposed in [16] and [17]. Next, the geometrical transformations who correspond to the different regions that share the voxel are applied, and the different values obtained are weighted according to the occupancy ratios computed before.

3.2 Matching a phantom

In order to evaluate the proposed strategy, the process has been applied to the phantom model depicted in Figure 2. The original model represented in Figure 2.a is composed of two surfaces L-shaped with different size and orientation.

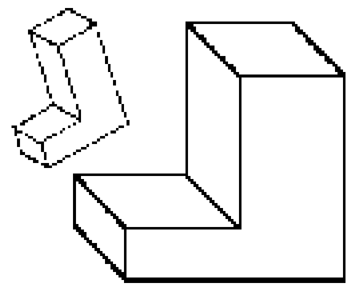

Figure 2a. Surfaces in the original model.

The model is voxelided with two different orientations by applying a rotation to the original model. The resulting voxel models have the same resolution of 128x128x128 (2.b). These models represent the multimodal images that should be aligned.

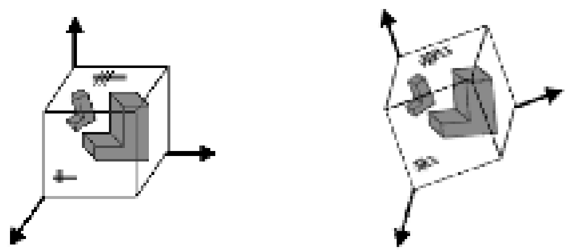

Figure 2b Data models to be aligned.

The boundaries of the two "L" surfaces are extracted from the two voxel models (4 surfaces) using the Marching Cubes algorithm at full resolution. Color Plate 2c shows the surfaces along with their bounding boxes. The four surfaces altogether have a total size of 75.591 polygons. In the next table the different cases are analyzed.

Model	Resolution	Nber. polygons	Processing Time
Two L	128x128x128	23.220	15 seconds
Two Rotated L	128x128x128	52.371	18 seconds

Table 1. Surfaces extraction results.

Next, the two pairs of surfaces have been aligned interactively and the integrated model shown in Color Plate 2.d has been computed. The numerical results are summarized in the next table.

Model	Nro. voxels inside
Two L	44.321
Two Rotated L	78.126
Reconstructed	45.414

Table 2. Registration results.

The final model has a little larger number of voxels inside the region than the original model. Analyzing the images, it can be seen that most of the discrepancy is at a side of the object. This is due to the fact that the original model is binary, thus as the property value is not interpolated, a discretization error occurs at the boundary.

3.3 Matching of cerebral images models

The described method has been applied to MR and SPECT-HMPAO images from the same patient. The MR images have a resolution of 512x512x33 and the SPECT have a resolution of 64x64x64. Figure 3 shows an example of each one.

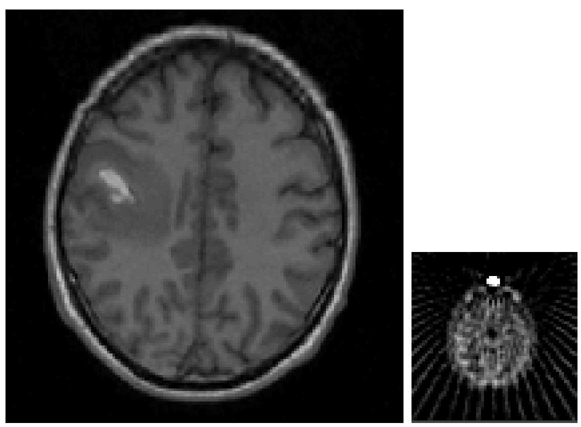

Figure 3 MR and SPECT images.

It can be seen that the MR images are cleaner than the SPECT which are very noisy and present the typical hair-like features around the images. This is why MR images are easier to be segmented than the SPECT ones. However, the regions obtained are more complex in the MR than in the SPECT because of the anatomical structure of the brain. As a consequence, the marching cubes surfaces extracted from MR images are more complex, made of a lot of polygons. Their memory occupancy is very large and they are not easily simplificable.

Specifically, the occupation of the brain surface in the different models, measured as number of polygons is:

Model	Resolution	Polygon number	Time process
MRI	512x512x33	379.769	8 min.
MRI	256x256x33	109.672	43 sg.
SPECT	64x64x64	19.843	9 sg.

Table 3. Surface extraction results.

Color plate 4 shows a rendering of these surfaces.

The registration process takes as input data two pairs of surfaces: the brain and a tumor. The interactive alignment step takes as a dynamic model the SPECT surfaces, which are smaller. The integrated model is computed by applying the local matching and averaging. The numerical results are summarized in the next table. The matching results are good, as it can be seen from the differences in the number of inside voxels which are very little and in all the cases don't arrive at 5

The value in brackets corresponds to the value that would have been computed if a unique global transformation would have been applied. As expected, the results are worse than those of the local transformations. Although, the differences are not very large, they are significant enough to make it necessary to apply local transformations.

Model	Resolution	Nro. voxels inside
Brain MRI	256x256x33	247.196
Brain SPECT	64x64x64	11.130
Reconstructed Brain	256x256x33	236.460
Tumor MRI	256x256x33	2.617
Tumor SPECT	64x64x64	88
Reconstructed Tumor	256x256x33	2.407 (2.113)

Table 4. Data obtained in the brain registration.

The final integrated model is shown in Color Plate 4, too. MR data are rendered in blue and SPECT in red. The colors are simply summed, as the research for multimodal rendering methods giving clues of both data types ([18], [19] falls, by now, out of the scope of this work. The local matching between the two models is visually good. The occupancy of the final model is twice the original one.

4 Conclusions

A new process for the alignment of multimodal data has been proposed. It has been proved on MR and SPECT cerebral images, giving good matching results. The main advantages of the method are that it is local and that it allows different pairs of registration functions being computed and applied simultaneously.

This work has two main future research lines: the investigation of an integrated model that would keep information on the original data at different resolution levels, while minimizing the cost of the data access [20]; the proposal of new integrated visualization strategies able to give as much information as possible of the two data sets in a single image [18].

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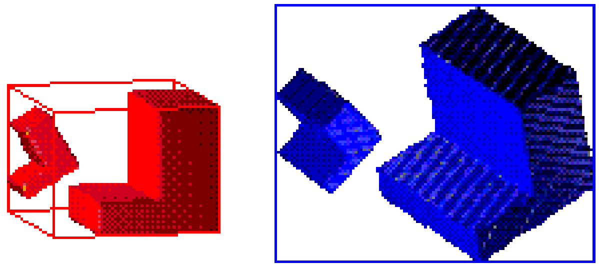
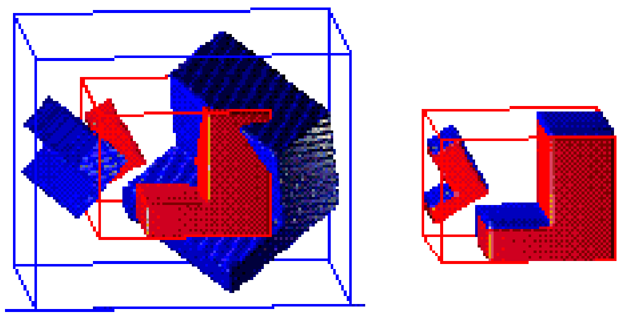
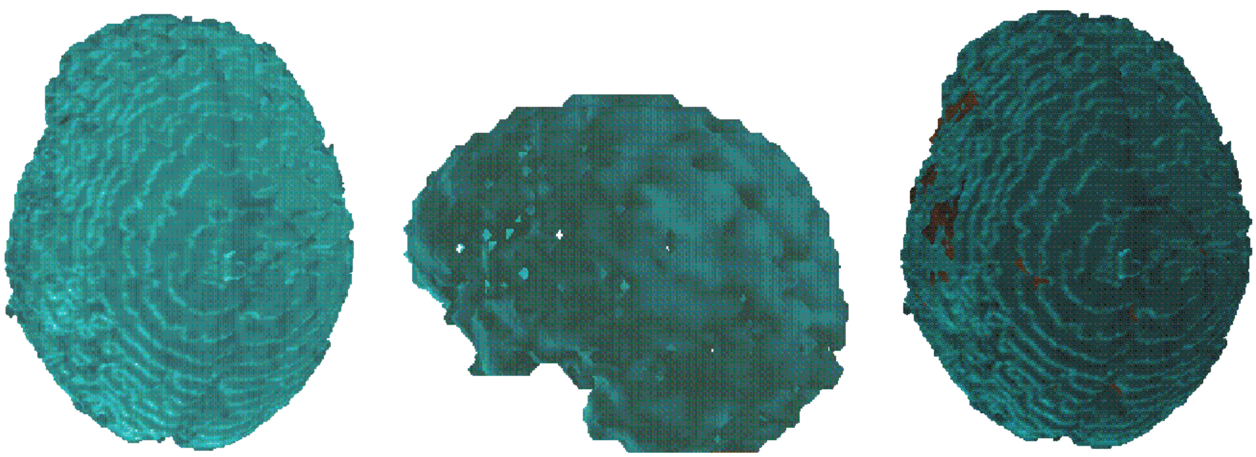


Color Plate 2c Surfaces to be aligned and their bounding boxes.



Color Plate 2d Surfaces before and after the alignment.



Color Plate 4 MR, SPECT and integrated surfaces.