TWO-STAGE MULTIMODALITY MEDICAL VOLUME REGISTRATION

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ABSTRACT

A semi-automatic, two-stage multimodality medical volume registration is described. This registration hinges on surface matching by using 3D chamfer matching algorithm first and on global-information-based matching afterwards. Two stages are applied, because information contents of registered volumes are different and no single registration method works satisfactorily so far. This approach is applied to MRI (Magnetic Resonance Imaging), CT (Computed Tomography) and SPECT (Single Photon Emission Computed Tomography) data volumes. Pilot experiments prove satisfactory results.

Keywords: multimodality volume registration, feature-based registration, 3-D chamfer matching, global-information-based registration, mutual information

1 INTRODUCTION

Registration of volume data of different modalities and the consecutive fusion of registered data are the basic prerequisites for data visualisation and comparison of medical volumes. Registration represents the finding of parameters of geometrical transformation that brings depicted objects into geometric alignment.

A number of medical volume registration methods was published until now. A comprehensive review of these methods has been presented e.g. in [Maint98]. The registration methods can be divided into two main categories: feature-based (FB) and global-information-based (GIB) methods.

FB methods require segmentation of some significant features that are present within both registered volumes. These features can be represented by landmarks (either extrinsic or intrinsic), curves or surfaces, etc. A drawback of FB methods is that registration accuracy depends on segmentation error. The FB methods are commonly automated except for the segmentation step, which is performed semi-automatically most of the time. On the other hand, the methods are advantageous if depicted objects differ by their internal structure but their outlines or surfaces (as is often the case of multimodality data sets).

GIB methods rely on the whole information content of volumes, without prior data reduction by segmentation. These methods require a suitable criterion function evaluating the data similarity. Since dependencies between multimodality volumes may be non-linear, thus the criterion function has to be suited to this fact. A group of non-linear criterion functions includes e.g. Woods's algorithm [Woods93] or mutual information [Maes97]. The criterion function is optimised over a chosen parametric space by using a suitable optimisation strategy. The main drawbacks of the GIB methods are higher computational cost when compared with FB methods and unreliability if geometry of objects is deformed and more complex data dependencies than non-linear are present.

2 DATA

Volume data sets of a human head of three different modalities are registered: MRI (Magnetic Resonance Imaging), CT (X-Ray Computed Tomography) that both depict patient morphology (anatomy) primarily, and SPECT (Single Photon Emission Computed Tomography) that depicts information on the metabolism of the underlying anatomy.

MRI does not represent significant load for patients, therefore, it is possible to perform more detailed measurements and obtain MRI data sets with high resolution along all x, y and z axes. Our MRI sets have 256 × 256 pixels per slice typically and up to 200 slices.

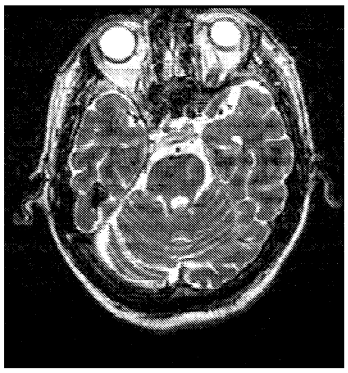

Fig. 1: MRI slice.

On the contrary, CT represents a health risk. Therefore, scan time is minimised, which leads to low resolution in z axe, thus, CT volumes have usually 10-13 slices, each of 256 × 256 pixels. It is possible to obtain CT scans with two options – "bone oriented" (Fig. 2) presenting bones, and "inner structure oriented" (Fig. 3) presenting soft tissues, i.e. somehow similar to MRI data sets.

SPECT volumes carry information about brain metabolic activity. Thus, the part representing anatomical subsets of above-mentioned data volumes is captured (i.e. no slices corresponding to e.g. jaw bone are presented). SPECT data sets have from 30 to 64 slices, each having 128 × 128 pixels, thus SPECT sets are of lower resolution in xy plane when compared with MRI and CT (Fig. 4).

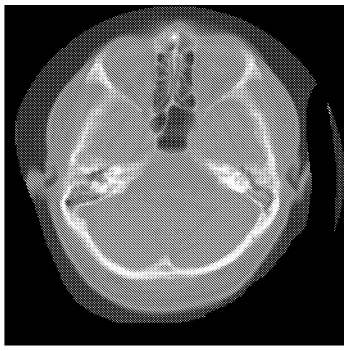

Fig. 2: "Bone oriented" CT slice.

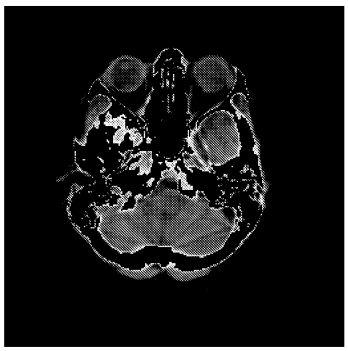

Fig. 3: "Inner structure oriented" CT slice.

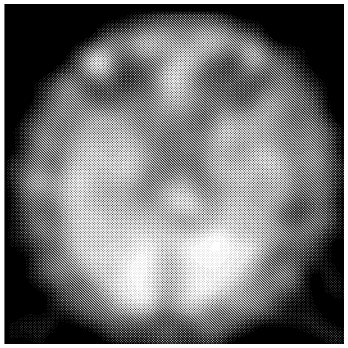

Fig. 4: SPECT slice.

3 METHODS

Both approaches – FB and GIB – are combined in this work, because no single method provides reliable registration in the case of multimodality medical data.

3.1 FB approach

Surfaces of objects are employed as features. Their segmentation is done semi-automatically by user-controlled thresholding of volumes. After obtaining

binary volumes, the surfaces of objects are extracted by using methods of mathematical morphology (closing & dilation & subtraction of binary volumes) [Serra82] (Fig. 5).

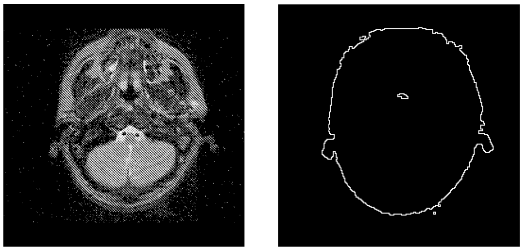

Fig. 5: MRI slice and its extracted 2-D surface.

Surfaces of both volumes are matched by 3-D chamfer matching algorithm [Borge88]. It transforms the floating volume (i.e. undergoing transformations) into "distance volume" the voxels of which take values approximating their Euclidean distances from the nearest surface voxels (darker values are closer to the surface, lighter values are more distant from it – see Fig. 6).

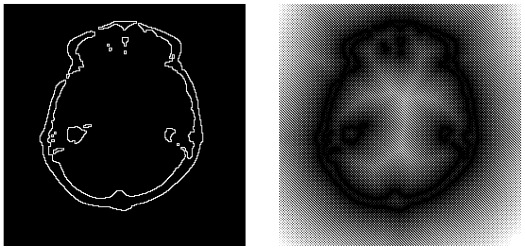

Fig. 6: CT 2-D surface and its distance transformation image.

The distance between a reference surface volume and a floating distance volume, expressed by the root mean square average, is minimised over a parametric space of geometrical transformations by using a suitable optimisation strategy (see below).

3.2 GIB approach

Reliable GIB registration requires a criterion function evaluating data similarity that is smooth, robust regarding noise, changes of photometry of the data sets, and has minimum number of local extremes over a parametric space.

We have investigated a number of criterion functions, including the stochastic sign change criterion (SSC), the sum of absolute valued differences (SAVD), normalised correlation coefficient (NCC), Woods's algorithm and a variety of algorithms of mutual information (MI) evaluation. These functions were evaluated regarding their smoothness, robustness and behaviour in the vicinity of global extreme.

Our results [Čapek99] confirm that the optimal criterion function for medical volume registration is MI computed according to [Maes97]. This function has low computation demands, is smooth, has no local extremes in the vicinity of global one (see Fig. 7) and is robust regarding noise, and linear and non-linear grey-scale transfer function shifts. Moreover, the computation time of this function, in contrast to other above-mentioned ones, is practically independent on the size of data sets, which is advantageous especially in case of large data volumes.

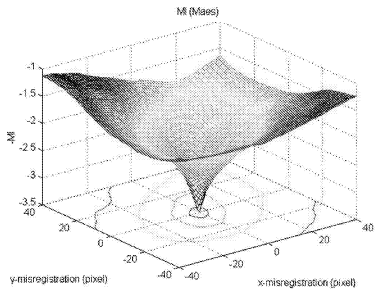

Fig. 7: Behaviour of MI in the vicinity of its global extreme (x, y mutual shifts of ±40 pixels of NMR volumes).

The criterion function has to be optimised over a parametric space, and an optimisation strategy should be fast and converging to global extreme with high probability even in case of non-linear parametric space and in the presence of local extremes in the vicinity of the global one.

A number of optimisation strategies (full-search, genetic algorithm, downhill simplex method, Powell's method, simulated annealing) were tested in order to select the most optimal one [Čapek99]. The best results gave multiply restarted adaptive simulated annealing (ASA) [Ingber]. It provides the highest probability of finding the global extreme in the parametric space and requires low number of evaluations of the criterion function during the optimisation process.

3.3 Implementation issues

The largest amount of computational time required by GIB registration is consumed by geometrical transformations of the floating volume during optimisation. This is due to necessity of evaluation of the volume for every co-ordinate of the parametric space. Selecting a sub-volume, e.g. brain, i.e. eliminating the information void background, shortens the computation time. The sub-volume is determined by thresholding during the segmentation step.

To diminish further the computational load, the criterion function [Pokra96] is evaluated over an evenly distributed random sample of voxels, and a pyramidal set-up is applied. We start with just a few voxels with high number of ASA restarts, and with increasing quality of registration the number of voxels is increased and the number of ASA restarts is decreased. This approach does not need any re-sampling of volumes, therefore, data are not changed during registration.

4 RESULTS

We began our experiments with NMR-NMR registration of the same volume set (consisting of 256×256×23 voxels) in order to evaluate accuracy of the proposed method. The floating volume was randomly misregistered in extents of [-20, 20] voxels for translations and of [-10°, 10°] for rotation using trilinear interpolation.

Registration was done in three levels with growing accuracy and computation time. FB approach was applied first to accomplish coarse registration by using only 10% of all surface voxels to speed-up the computation. Then GIB registration was used in two levels. On the first level (GIB1), 10 re-starts of ASA by using only 1% of voxels (cca 16 000) of the sub-volume mentioned in the chapter 3.3 starting from the registration position given by the FB approach were applied. The GIB1 was followed by GIB2 – 10 ASA re-starts by using 3% of voxels (cca 48 000) of the sub-volume. This set-up kept the computational load low, even when a common PC (Intel Celeron 450 MHz) was exploited, without significant lost of accuracy. Table 1 gives absolute valued errors (dx, dy, dz, dα, dβ, dγ) of geometrical transformation parameters obtained during registration on the individual levels (including time of computation t [s] when the above-mentioned PC was used). Zero registration errors were not obtained due to application of tri-linear interpolation.

	dx	dy	dz	dα	dβ	dγ	t [s]
FB	0.677	0.189	0.137	0.698	1.299	0.689	59
GIB1	0.031	0.183	0.806	0.303	0.208	0.129	458
GIB2	0.032	0.067	0.085	0.246	0.052	0.072	1222

Table 1: Registration errors of identical NMR-NMR data sets for the individual registration levels (see text) and the computation time.

Figures 8-10 represent multimodality registrations. In these cases, without some markers, exact evaluation of registration errors is practically impossible. Therefore, evaluation of registration quality is done by visual comparison of fused slices of different modalities before and after registration.

For all following figures it is valid that the floating volume is in the left half of images, the reference one is in the right half. Left column of images represents volumes before and right column after registration.

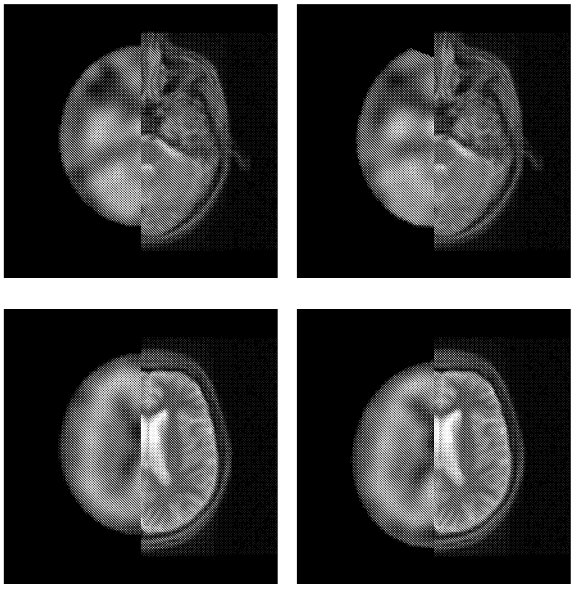

Fig. 8: Fusion of SPECT (128×128×64) – NMR (256×256×23) volumes registered by using the two-stage approach (upper raw = 7th NMR slice, bottom raw = 15th NMR slice). The resulted registration parameters were x=-2.057, y=-5.219, z=-5.081 (SPECT voxels), α=11.990°, β=3.174°, γ=-6.290°.

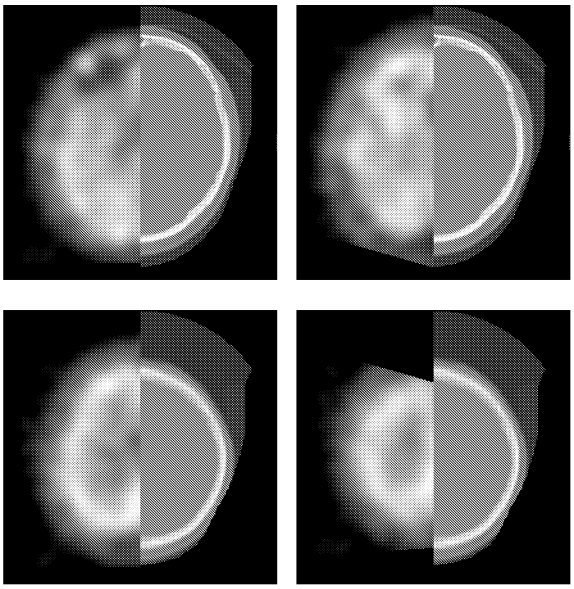

Fig. 9: Fusion of SPECT (128×128×35) – CT (256×256×13, "bone oriented" with manual removal of a bed) volumes registered by using FB approach only – brain to bone surface registration (upper raw = 5th CT slice, bottom raw = 9th CT slice). The resulted registration parameters were x=-0.735, y=16.582, z=11.992 (SPECT voxels), α=-28.070°, β=8.479°, γ=-0.481°.

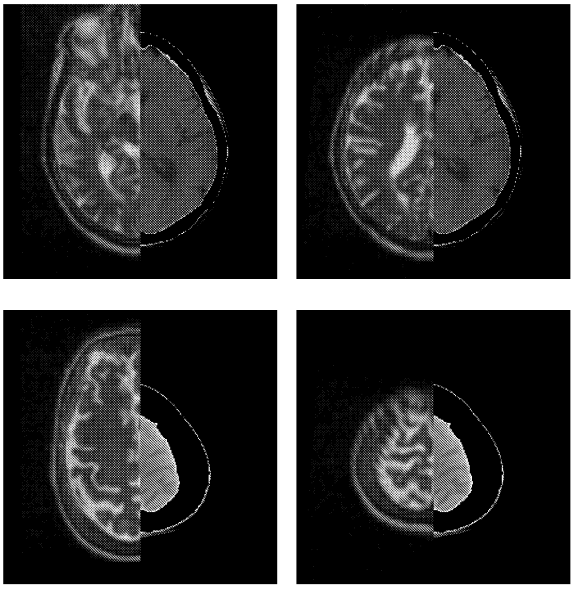

Fig. 10: Fusion of NMR (128×128×40) – CT (256×256×12, "inner structure oriented") volumes registered by using GIB approach only (upper raw = 6th CT slice, bottom raw = 11th CT slice). The resulted registration parameters were x=3.962, y=12.987, z=29.450 (NMR voxels), α=**-40.802**°, β=-3.445°, γ=-4.356°.

5 CONCLUSION

A two-stage, semi-automated multimodality medical volume registration is presented. It was chosen, because multimodality registration is difficult and no single method gives good results when dealing with NMR, CT and SPECT data sets.

Registration of data volumes of the same modality is an easy task, and our method gives satisfactory results with even a low computational burden.

SPECT-NMR registration is more difficult. To avoid local extremes FB registration based on surfaces is applied first. Surfaces of brain from SPECT data are matched with surfaces of skin from NMR data. This procedure result in some translation error in z direction that has to be compensated and results further refined by registration based on a GIB method by using mutual information.

SPECT-CT ("bone oriented") registration can be accomplished by FB approach, because these CT data sets do not show any of inner structures, however, some similarity can be seen in surfaces. Therefore, surfaces of brain from SPECT data are matched with surfaces of bones from CT data. Again, this introduces some translation error in z direction, which, however, is difficult to correct. Moreover, these CT data always contain a bed, on which a patient lies, and this bed has to be removed by-hand before registration, otherwise it would affect the registration.

NMR-CT ("inner structure oriented") registration can be performed by GIB approach. In this case there is no use for FB approach, because data contain a lot of objects (see Fig. 3), which produce undesirable surfaces. Registration of different modality volumes with CT volumes is made more difficult by their sparse sampling in z direction (other modality volumes are sampled with higher density) and by great mutual sagittal inclination of heads (see Fig. 10). These facts result in a great parametrical space that has to be examined and a lot of local minima in this space that make the registration time-consuming or even impossible.

It is obvious that the weakest part of FB registration is segmentation of surfaces, which is done semi-automatically by thresholding. Therefore, it is not possible to segment only brain in NMR data or inner parts of bones in CT data and register them with brain in SPECT data, which would improve registration results. Accordingly, better segmentation of studied objects will be a goal of our future studies.

The next problem dealing with multimodality registration is evaluation of registration quality. We

shall evaluate the described method by joining "The Retrospective Registration Evaluation Project" sponsored by Vanderbilt University in Nashville, TN (USA). This project provides multimodality data which will be registered by us and results will be evaluated by the project.

6 ACKNOWLEDGEMENTS

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