

# MEDICAL IMAGE REGISTRATION BASED ON RANDOM LINE SAMPLING

A. Bardera, M. Feixas, I. Boada, and M. Sbert

Institut d'Informàtica i Aplicacions, Universitat de Girona, 17071-Girona, Spain  
{anton.bardera,miquel.feixas,imma.boada,mateu.sbert}@udg.es

## ABSTRACT

One of the key aspects in 3D-image registration is the computation of the joint intensity histogram. We propose a new approach to compute this histogram using uniformly distributed random lines to sample stochastically the overlapping volume between two 3D-images. The intensity values are captured from the lines at evenly spaced positions, taking an initial random offset different for each line. This method provides us with an accurate, robust and fast mutual information-based registration. The interpolation effects are drastically reduced, due to the stochastic nature of the line generation, and the alignment process is also accelerated. The results obtained show a better performance of the introduced method than the classic computation of the joint histogram.

## 1. INTRODUCTION

Recently, multimodal image registration has played an increasingly important role in medical imaging. Its objective is to find a transformation that maps two or more images, acquired using different imaging modalities, by optimizing a certain similarity measure. Among the different similarity measures that have been proposed, mutual information (MI)[2, 9] and normalized mutual information (NMI)[6] are the most commonly used since they produce satisfactory results in terms of accuracy, robustness and reliability. However, MI-based methods are very sensitive to implementation decisions [3]. In particular, the way of estimating the probability distributions and the choice of the interpolator have a great influence in the accuracy and robustness of the registration results.

The computation of the joint histogram, as proposed in [2], is usually done by taking all the points of the reference image and the corresponding values of the transformed floating image. In general, an interpolation scheme

is needed to estimate these transformed values at non-grid positions. This interpolation provokes undesirable artifacts when the voxel grids have coinciding periodicities [7], reducing the robustness and accuracy of the MI-based methods. Moreover, to accelerate the matching process, different multiresolution and multisampling schemes have been proposed. In particular, downsampling techniques are used to speed up the registration process [3].

In this paper, we introduce a new approach to compute MI-based similarity measures by using uniformly distributed random lines. This method accelerates the alignment and almost suppresses the interpolation artifacts due to the stochastic nature of the process. Several experiments show clearly the suitability of our approach to speed up the registration process and to improve its accuracy and robustness.

This paper is organized as follows. In Section 2, we briefly describe MI-based registration techniques and the main difficulties related to its implementation. In Section 3, a new method to compute the intensity histogram based on random lines is introduced. In Section 4, the registration results obtained with different multimodal images are analyzed. Finally, our conclusions are presented in Section 5.

## 2. MEDICAL IMAGE REGISTRATION

In this section we review some basic notions on MI-based registration methods and the principal difficulties related to their implementation.

MI is a basic concept in information theory, which is usually used to measure the statistical dependence between two random variables  $A$  and  $B$ , and is defined by

$$I(A, B) = \sum \sum p_{AB}(a, b) \log \frac{p_{AB}(a, b)}{p_A(a)p_B(b)},$$

where  $p_{AB}(a, b)$  is the joint probability density function (pdf) and  $p_A(a)$  and  $p_B(b)$  are the marginal pdf's. In the context of image registration, the random variables  $A$  and  $B$  correspond to the reference and floating images, respectively, and registration is achieved by maximizing the MI. The normalization of MI, defined by  $NMI(A, B) = 1 + I(A, B)/H(A, B)$ , is more robust than MI due to its greater independence of the overlap area [6].

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The most successful automatic image registration methods are based on MI, which is a measure of the dependence between two images. All these methods are based on the same four steps: the superposition of the reference and floating images, the computation of the pdf's, the computation of the similarity metric and the optimization of the metric by reorientating the images. Since the differences between them are in the implementation of these steps we are going to review some of the most important implementation aspects.

The key point of the implementation of an MI-based registration technique is the estimation of the marginal and the joint pdf's. To compute them, two different methods are usually applied: the Parzen window method [9] and the joint intensity histogram method [2]. We focus on the latter. The joint intensity histogram is obtained by binning the intensity pairs  $(A, T(B))$  of the overlapping parts of the reference image  $A$  and the transformed image  $T(B)$ . Since generally the grid points of  $T(B)$  do not coincide with the grid points of image  $A$ , the application of this method requires the selection of an interpolator. Although there are different interpolators, all of them introduce artifacts that will deteriorate the accuracy and reliability of the registration. Therefore, the implementation of the interpolator also requires a strategy to reduce interpolation artifacts [7].

Several interpolation schemes have been introduced: linear interpolation (the intensity of a point is obtained from the weighted combination of the intensities of its neighbors), nearest neighbor (NN) interpolation, and partial volume interpolation (the weights of linear interpolation are used to update the histogram, without introducing new intensity values), amongst the most commonly used. Tsao [7] has shown that jittered sampling is extremely beneficial to the robustness and accuracy of registration, reducing considerably the interpolation artifacts. Stochastic sampling has also been proposed to reduce the grid effects which come from sampling the images on a regular grid [8].

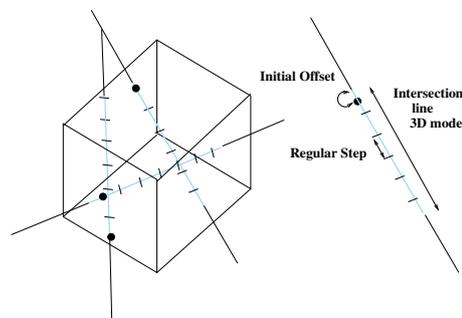
To speed up the registration, multiresolution and multi-sampling techniques have been introduced. The objective is to reduce the computational cost by means of coarse-to-fine hierarchical strategies which start with the reference and floating images on a coarser resolution. Then they gradually improve the estimates of the correspondence or parameters of the mapping functions while going up to the finer resolutions [3].

### 3. UNIFORMLY DISTRIBUTED GLOBAL LINES

In this section, we introduce a new method based on the use of random lines to compute the joint intensity histogram in 3D-image registration, which is the most demanding step in the similarity measure computation. The overlapping volume between two 3D-images is stochastically sampled us-

ing a uniform distribution of lines in the sense of integral geometry, i.e., invariant to translations and rotations [4]. Points chosen on each line provide us with the intensities to calculate the probability distributions. This line density was first used in computer graphics to compute the illumination in a scene. The lines generated using this density were called *global lines* [5].

Two alternatives to generate a global line density can be used. As a first alternative, a global line can be generated taking two random points on a sphere circumscribing the object or the scene [5]. This is only valid for a sphere, that is, taking pairs of points on the surface of any convex body does not result in a uniform density. As a second alternative, a global line can also be generated from the walls of a convex bounding box containing the object or the scene [1]. This can be done taking a random point on the surface of the convex bounding box and a cosine distributed random direction.

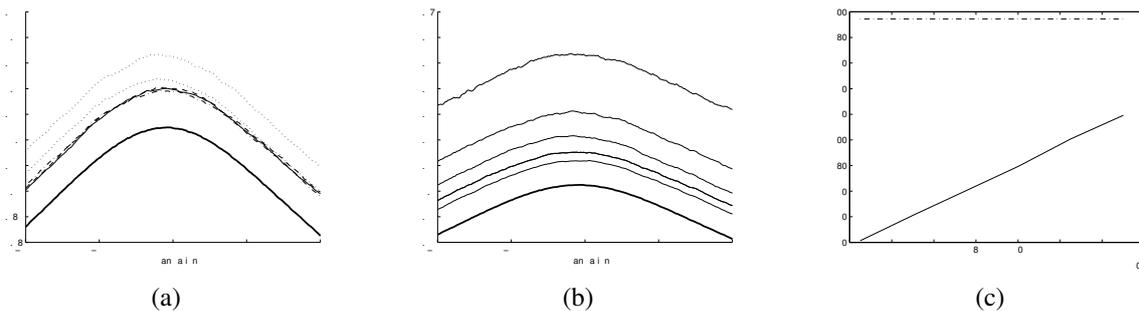


**Fig. 1.** Global lines are cast from the walls of the bounding box.

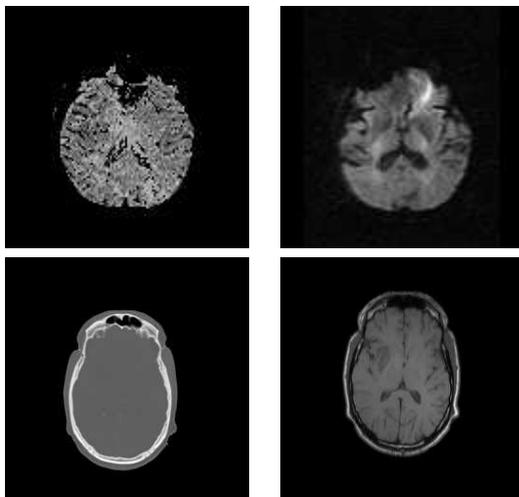
For our registration intentions, we adopt this second alternative, taking the reference image as the bounding box (see Figure 1). The intensity values are captured from the lines at evenly spaced positions, taking an initial random offset different for each line. The random offset ranges from 0 to the step size. The regular grid sampling is thus substituted by sampling with random lines in our method. Although we skip with regular steps, the use of a random offset ensures the stochasticity of the process. The cost of the histogram computation depends on both the number of lines cast and the number of points taken for each line, which is inversely proportional to the step size.

### 4. HISTOGRAM ESTIMATION USING GLOBAL LINES

To evaluate the global line method, different registration experiments were carried out. The data sets used in our tests (see Figure 2) are a diffusion-weighted imaging (DWI) and perfusion weighted imaging (PWI), from the Josep Trueta



**Fig. 3.** (a) NMI using the global line method with 150000 sampling points vs. the slice translation on the X-axis. The step size increases from top to bottom (1, 2, 4, 6 and 8 mm.). The classical NMI curve in bold. (b) NMI using the global line method with a step size of 5 mm. vs. the slice translation on the X-axis. The number of sampled points increases from top to bottom (50000, 75000, 100000, 125000 and 150000 points). The classical NMI curve in bold. (c) Computational cost of the global line method (continuous line) vs. the value obtained with the classical NMI method (dash-dotted line). The horizontal axis represents the number of sampled points and the vertical axis the time units.



**Fig. 2.** PWI-DWI and CT-MR test image pairs.

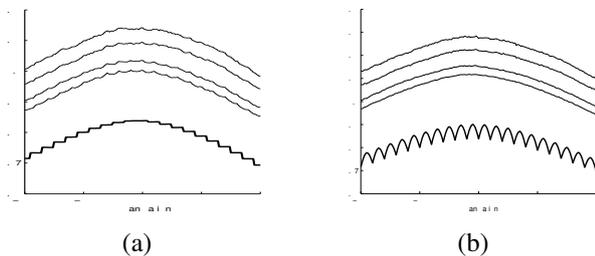
Hospital, and a CT and an MR images, from the Vanderbilt data base. The DWI and PWI sets have a resolution of  $256 \times 256 \times 20$  and  $128 \times 128 \times 12$ . The voxel size is  $0.977 \times 0.977 \times 7.0 \text{ mm}^3$  for the DWI and  $1.797 \times 1.797 \times 10.0 \text{ mm}^3$  for the PWI. The CT image has a resolution of  $512 \times 512 \times 28$  and a voxel size of  $0.654 \times 0.654 \times 4 \text{ mm}^3$ . The resolution of the MR image is  $256 \times 256 \times 26$  and the voxel size is  $1.25 \times 1.25 \times 4 \text{ mm}^3$ . Our results have been compared with the classical NMI method proposed by Studholme et al. [6] which has been represented in all the plots as the bold bottom curve. The first and second experiments aim to analyze the influence on the method of the step size and the number of lines cast. The behaviour of the NMI has been analyzed moving the floating image through the X axis from  $-10 \text{ mm}$  to  $10 \text{ mm}$  around the origin. In these experiments, the PWI-DWI images have been used as

the testing set.

In the first experiment, we have fixed the number of sampled points to 150000, which corresponds to 11% of the original model. Figure 3(a) shows the obtained results considering different step sizes of 1, 2, 4, 6 and 8 mm, from top to bottom. It is important to note that the step size determines the number of cast lines, i.e., a small step size implies a small number of lines, and viceversa. Mainly two facts have to be noted. First, the curves corresponding to the step sizes of 1 and 2 mm give undesired results, as the maxima of these curves do not correspond to the perfect registration. This is a consequence of supersampling, since in general a lower step size can produce several consecutive sampling points into the same voxel. For step sizes greater than 4 mm, the differences between the NMI curves are minimal and there are only small stochastic fluctuations. Second, a reduced number of lines cast do not ensure that the model has been probed in a sufficient number of directions. Thus, taking into account that the computational cost of the method increases with the step size, since more lines have to be generated, the optimization process (minimum cost) is a trade-off between the number of lines and the step size.

In the second experiment, the step size has been fixed to 5 mm and a different number of lines has been considered. The obtained results are represented in Figure 3(b), where, from top to down, the plotted curves correspond to the NMI measure computed using 50, 75, 100, 125 and 150 thousand points. Observe that the NMI value decreases when the number of points taken increases, converging to the NMI value measured in the classical way. This behavior is due to the fact that the joint entropy increases with the number of points [8]. In Figure 3(c) the cost of the classical (dash-dotted line) and the global line (solid line) methods are compared. Note that for our method the time increases

linearly with the number of points. Therefore, using random lines the time can be outstandingly reduced. For example, an acceptable estimation is obtained with 50000 points and a processing time almost five times lower (see Figure 3(b) and 3(c)).



**Fig. 4.** NMI values using (a) the nearest neighbor and (b) the linear interpolator schemes.

In the last experiment, interpolation artifacts are studied. As these especially occur when the voxel grids of the images have coinciding periodicities, the CT-MR pair has been properly rescaled in order to maximize these periodicities. The NMI values have been determined as a function of translation along the X-axis in the range of  $\pm 10$  voxels. Figures 4(a) and (b) show the curves of the NMI values obtained with the global line method using the nearest neighbor and the linear interpolator schemes, respectively. We have considered different number of sampled points, from top to down: 75000, 100000, 150000 and 200000. In both plots, the bottom curve corresponds to the NMI value computed in the classical way. Note that both exhibit interpolation artifacts, in a stairs like mode for the NN scheme and as a set of local minima at every integer-voxel step for the linear scheme [7]. Observe in Figure 4(a) that the curves obtained with the global line method by using the NN scheme also present small artifacts, but not in a stair like mode since in our case the grid alignment causes local maxima. Interestingly, the NN behavior coincides with the one of the partial volume method [3] as our method tends to the partial volume scheme when the number of points is high enough and there is no rotation. Figure 4(b) illustrates the results of the global line method using the linear interpolation scheme. It can be seen that interpolation artifacts have completely disappeared. This is due to the fact that the grid effects have been eliminated by the stochastic sampling and the interpolator has a blurring effect that avoids the artifacts appeared in the previous case.

All the experiments presented reveal a trade-off between accuracy and computational cost. Future work will be addressed to analyze it.

## 5. CONCLUSIONS

In this paper, a new stochastic approach for 3D-image registration based on sampling the images with uniformly distributed random lines has been proposed. The advantages of this method can be summarized as follows. Firstly, similar to the jittered sampling [7], the global line sampling reduces considerably the interpolation artifacts, almost suppressing the periodicities of the voxel grids. Secondly, the registration accuracy is preserved with a high reduction of sampled points, accelerating the computation.

Future work will be addressed towards studying the precise interplay between the step size and the number of lines required for a given accuracy. Our global line method could also be applied within a multiresolution framework. Moreover, we will make use of further coherence provided by bundles of parallel lines, which would allow a hardware implementation by using a z-buffer algorithm.

## 6. REFERENCES

- [1] F. Castro and M. Sbert. Application of quasi-monte carlo sampling to the multipath method for radiosity. In *Proceedings of 3rd International Conference on Monte Carlo and Quasi-Monte Carlo methods in Scientific Computing*, Claremont (CA), USA, June 1998.
- [2] F. Maes, A. Collignon, D. Vandermeulen, G. Marchal, and P. Suetens. Multimodality image registration by maximization of mutual information. *IEEE Trans. on Medical Imaging*, 16(2):187–198, 1997.
- [3] J. P. Pluim, J. Maintz, and M. Viergever. Mutual-information-based registration of medical images: a survey. *IEEE Trans. on Medical Imaging*, 22:986–1004, 2003.
- [4] L. Santaló. *Integral Geometry and Geometric Probability*. Addison-Wesley, Reading (MA), USA, 1976.
- [5] M. Sbert. An integral geometry based method for fast form-factor computation. *Computer Graphics Forum*, 12(3):409–420, 1993.
- [6] C. Studholme. *Measures of 3D Medical Image Alignment*. PhD thesis, University of London, UK, 1997.
- [7] J. Tsao. Interpolation artifacts in multimodal image registration based on maximization of mutual information. *IEEE Trans. on Medical Imaging*, 22:854–864, 2003.
- [8] M. Unser and P. Thévenaz. Stochastic sampling for computing the mutual information of two images. In *Proceedings of SampTA'03*, pages 102–109, May 2003.
- [9] P. A. Viola. *Alignment by Maximization of Mutual Information*. PhD thesis, MIT, USA, 1995.