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Nonrigid Registration Using Regularized Matching Weighted by Local Structure

Eduardo Suárez[1], Carl-Fredrik Westin[2],
Eduardo Rovaris[1], and Juan Ruiz-Alzola[1,2]

[1] Medical Technology Center, Univ. Las Palmas of GC &
Gran Canaria *Dr. Negrín Hospital*, Spain
[2] Laboratory of Mathematics in Imaging, Brigham and Women's Hospital and
Harvard Medical School, USA

Abstract. We present a novel approach to nonrigid registration of volumetric multimodal medical data. We propose a new regularized template matching scheme, where arbitrary similarity measures can be embedded and the regularization imposes spatial coherence taking into account the quality of the matching according to an estimation of the local structure. We propose to use an efficient variation of weighted least squares termed *normalized convolution* as a mathematically coherent framework for the whole approach. Results show that our method is fast as accurate.

1 Introduction

Nonrigid registration is a crucial operation for image guided medicine. Image registration consists of putting into correspondence two or more datasets, possibly obtained with different imaging modalities. Its applications range from pathology follow-up, through a series of clinical studies, to image guided surgery, by registering pre-operative images onto intra-operative ones [1]. Moreover, nonrigid registration is also necessary in order to embed *a priori* anatomic knowledge into medical image processing algorithms and, specially, into segmentation schemes. In this case, a canonical atlas is usually registered onto patient specific information to help classifiers know what the possible classes are for every voxel [2].

Datasets to be registered can therefore correspond to the same or to different patients (or even to an atlas) and can also be from the same or from different imaging modalities. Putting into correspondence two anatomies that can be topologically different (for example, in the case of pathology) and where the voxel intensities measure different physical magnitudes (multimodality) poses a serious challenge that has sparked intensive research over the last years [3].

A review of alternatives is beyond the scope of this paper, and a good one can be found elsewhere [3] with a complete taxonomy of registration methods. Just to focus this work, we will mention that voxel-based registration methods, i.e. those using directly the full content of the image and not simplifying it to a set of features to steer the registration, usually correspond to one of two important families: template matching and variational. The former was popular years

ago due to its conceptual simplicity [4]. Nevertheless, in its conventional formulation, it is not powerful enough to address the challenging needs of medical image registration. Variational methods rely on the minimization of a functional (energy) that is usually formulated as the addition of two terms: data coupling and regularization, the former forcing the similarity between both datasets (target, and source deformed with the estimated field) to be high while the later forcing the estimated field to fulfill some constraint (usually enforcing spatial coherence-smoothness). As opposed to variational methods, template matching do not impose any constraint on the resulting fields which, moreover, due to the discrete movement of the template are discrete fields. These facts have led to an increasing popularity of variational methods for registration while template matching has been loosing its place in this arena.

In this paper we present a novel registration approach using template matching, where its major drawbacks have been explicitly addressed. The resulting method is reliable and fast and it can be a feasible alternative to computationally expensive variational approaches. First any similarity measure can be easily incorporated into the neighborhoods comparison. Then spatial regularization is imposed after template matching, by locally projecting the estimated field onto a vector space. Moreover, the quality of the matching is considered when doing the projection by means of the estimation of local structure. A very efficient variation of weighted least squares termed *normalized convolution* [5,6], provides a natural framework to our regularized matching approach.

The structure of the paper is as follows: Section 2 presents the local structure estimation procedure. Section 3 describes the proposed nonrigid registration algorithm. Results are shown in Section 4 and conclusions in Section 5.

2   Local Structure

Our approach to nonrigid registration relies on template matching. Local structure measures the quantity of discriminant spatial information on every point of an image and it is crucial for template matching performance: the higher the local structure, the better the result obtained on that region with template matching.

In order to quantify local structure, a structure tensor is defined as $\mathbf{T}(\mathbf{x}) = (\nabla I(\mathbf{x}) \cdot \nabla I(\mathbf{x})^t)_\sigma$, where the subscript σ indicates a local smoothing. The structure tensor consists of a symmetric positive-semidefinite 3×3 matrix that can be associated to ellipsoids, i.e., eigenvectors and eigenvalues correspond to the ellipsoids axes directions and lengths respectively. A scalar measure of the local structure can be obtained as [7,8,9,10]

$$structure(\mathbf{x}) = \frac{\det \mathbf{T}(\mathbf{x})}{\operatorname{trace} \mathbf{T}(\mathbf{x})}. \tag{1}$$

Figure 1 shows an MRI T1-weighted axial slice of the brain and the estimated structure tensors overlaid as ellipsoids. Small eigenvalues indicate lack of gradient variation along the associated principal direction and, therefore, high structure
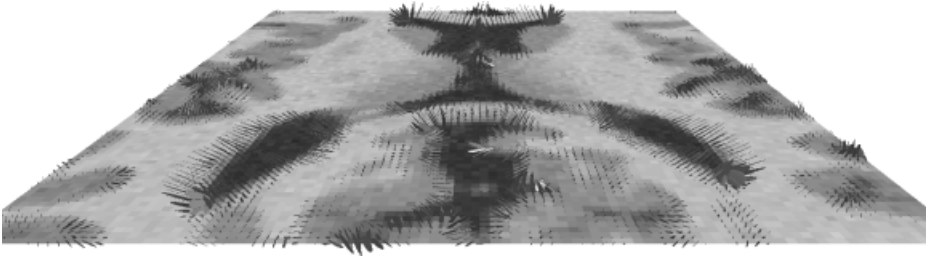
Fig. 1. MRI T1-weighted axial slice of human brain and its structure tensors. The brighter the gray level of the ellipsoids the higher the structure.
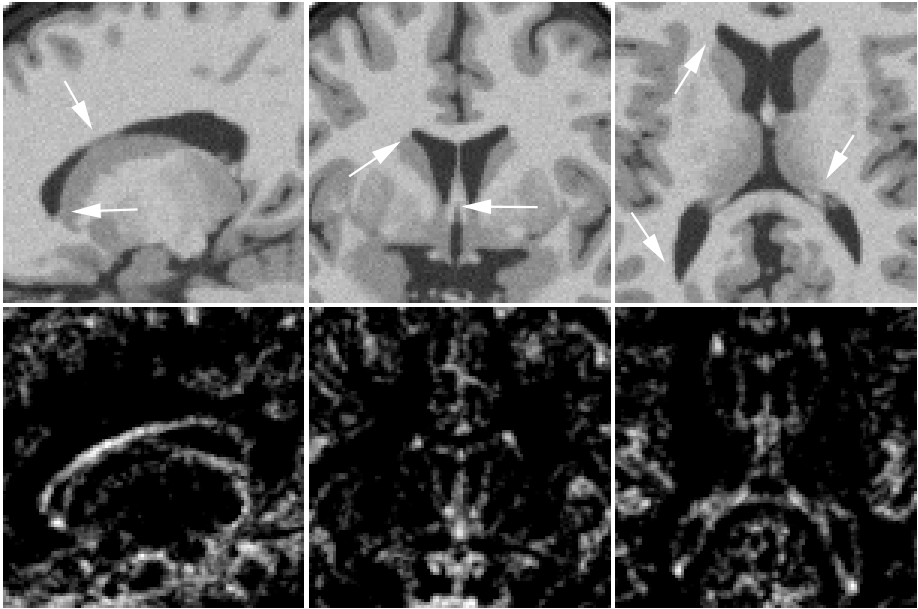

Fig. 2. *Top*: MRI T1-weight cross-sections; *Bottom*: Local structure measure. Arrows point at higher structure regions.

is indicated by big (large eigenvalues), round (no eigenvalue is small) ellipsoids. The gray level coding represents the scalar structure measure, with brighter gray levels indicating higher structure.

Figure 2 shows cross-sections of a T1-weighted MRI dataset of a human brain (top row) and the scalar measure of local structure obtained from them, represented with a logarithmic histogram correction (bottom row). Note how anatomical landmarks have the highest measure of local structure, corresponding to the points indicated by the arrows on the top row. Curves are detected with lower intensity than points and surfaces have even lower intensity. Homogeneous areas have almost no structure.
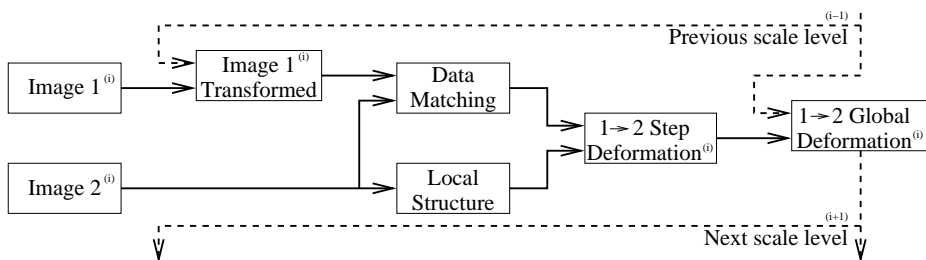
Fig. 3. Algorithm pipeline for pyramidal level (i).

3   The Registration Algorithm

3.1   Algorithm and Multiresolution Pyramid

The algorithm works similar to Kovačič and Bajcsy elastic warping [11], in which images are decomposed on Gaussian multiresolution pyramids. On the highest level, the deformation field is estimated by regularized template matching steered by local structure (details in sections below). On the next level, the source dataset is deformed with a deformation field obtained by spatial interpolation of the one obtained on the first level. The deformed source and the target datasets on the current level are then registered to obtain the deformation field corresponding to the current level of resolution. This process is iterated on every level. The algorithm implementation is summarized in figure 3.

3.2   Template Matching

Template matching finds the displacement for every voxel in a source image by minimizing a local cost measure, obtained from a small neighborhood of the source image and a set of potential correspondent neighborhoods in a target image. The main disadvantage of template matching is that it estimates the displacement field independently in every voxel and no spatial coherence is imposed to the solution. Another disadvantage of template matching is that it needs to test several discrete displacements to find a minimum.

There exists some optimization-based template matching solutions that provide a real solution for every voxel, though they are slow [12]. Therefore, most template matching approaches render discrete displacement fields. Another problem associated to template matching is commonly denoted as the *aperture problem* in the computer vision literature [13]. This essentially consists of the inability of making a good match when no discriminant structure is available, such as in homogeneous regions, surfaces and edges. When this fact is not taken into account the matching process is steered by noise and not by the local structure, since it is not available.

Our approach to nonrigid registration keeps the simplicity of template matching while it addresses its drawbacks. Indeed the algorithm presented here consists

of a weighted regularization of the template matching solution, where weights are obtained from the local structure, in order to render spatially coherent real deformation fields. Thanks to the multiscale nature of our approach only displacements of one voxel are necessary when matching the local neighborhoods.

3.3   Spatial Regularization

The objective in image registration is to find a one-to-one spatial mapping between points of two images. Template matching provides a discrete deformation field where no spatial coherence constraints have been imposed. In this subsection this field is regularized so as to obtain a mathematically consistent continuous mapping. We will consider the deformation field to be a diffeomorphism, i.e. an invertible continuously differentiable mapping. In order to be invertible, the jacobian of the deformation field must be positive. On every scale level, the displacement is small enough to guarantee such condition. For every level of the pyramid the mapping is obtained by composing the transformation on the higher level with the one on the current level, so that the positive jacobian condition is preserved.

Spatial regularization is achieved by locally projecting the deformation field provided by template matching on an appropriate signal subspace, and simultaneously taking into account the quality of the matching as indicated by the scalar measure of local structure. We propose here to use *Normalized Convolution* [6,5], a popular refinement of weighted-least squares that explicitly deals with the so-called signal/certainty philosophy. Essentially the scalar measure of structure is incorporated as a weighting function in a least squares fashion. The field obtained from template matching is then projected onto a vector space described by a non-orthogonal basis, i.e., the dot products between the field and every element of the basis provide covariant components that must be converted into contravariant by an appropriate metric tensor. Normalized convolution provides a simple implementation of this operation. Moreover, an applicability function is enforced on the basis elements in order to guarantee a proper localization and avoid high frequency artifacts. This essentially corresponds to weight each basis element with a Gaussian window.

The desired transformation $\mathbf{y}(\mathbf{x})$ is related to the deformation field $\mathbf{d}(\mathbf{x})$ by the simple relation

$$\mathbf{y}(\mathbf{x}) = \mathbf{d}(\mathbf{x}) + \mathbf{x} \tag{2}$$

where $\mathbf{x}$ and $\mathbf{y}$ denotes coordinates in every dataset.

Since the transformation is differentiable, we can write the function in different orders of approximation.

$$\mathbf{y}(\mathbf{x}) \simeq \mathbf{y}(\mathbf{x}_0), \tag{3}$$

$$\mathbf{y}(\mathbf{x}) \simeq \mathbf{y}(\mathbf{x}_0) + \mathbf{J}(\mathbf{x}_0) \cdot [\mathbf{x} - \mathbf{x}_0]. \tag{4}$$

Equations 3 and 4 consist of linear decompositions of bases of size 3 and 12 basis elements, respectively. We have not found relevant experimental improvement of the registration algorithm by using the linear approximation instead of
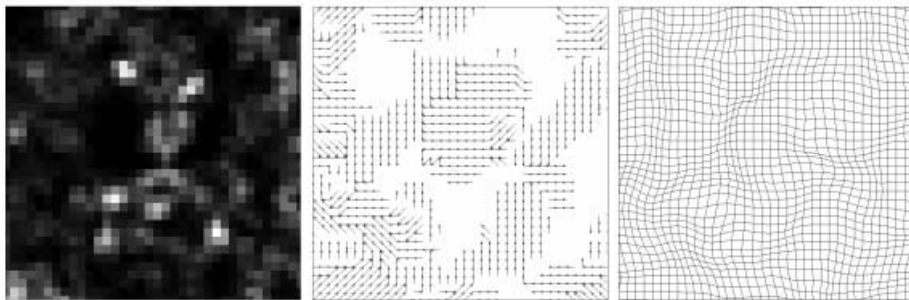
Fig. 4. *Left*: certainty; *Center*: discrete matching deformation; *Right*: weight filtered deformation.

the zero-order one, probably due to the local nature of the algorithm. The basis set used is then:

$$\mathbf{b}_1 \begin{cases} y_1(\mathbf{x}) = 1 \\ y_2(\mathbf{x}) = 0 \\ y_3(\mathbf{x}) = 0 \end{cases} \mathbf{b}_2 \begin{cases} y_1(\mathbf{x}) = 0 \\ y_2(\mathbf{x}) = 1 \\ y_3(\mathbf{x}) = 0 \end{cases} \mathbf{b}_3 \begin{cases} y_1(\mathbf{x}) = 0 \\ y_2(\mathbf{x}) = 0 \\ y_3(\mathbf{x}) = 1 \end{cases} \tag{5}$$

Figure 4 shows a 2-d discrete deformation field that has been regularized using the certainty on the left side and a 2-d Gaussian applicability function with $\sigma = 0.8$.

3.4   Implementation

The algorithm has been written in *Matlab* interfacing some external C libraries. In order to run faster the matching process, the whole dataset has been split and has been parallelized using *Parallel Matlab* [14].

4   Results

In order to illustrate quantitatively the performance of our registration approach, a T1-weighted MRI, size $160 \times 192 \times 160$ with 12 bits depth and with isotropic voxel size of 1 mm, has been deformed using a set of synthetic deformation fields with a spatial bandwidth of 1 cm^{-1} and variable amplitudes. The original and the deformed datasets have been registered with the SSD similarity measure (Sum of Squared Differences) and a Gaussian applicability function with $\sigma = 1.5$. The Root Mean Square (RMS) errors before and after registration is shown in figure 5 in 18 experiments with different maximum displacements. Notice how the difference (RMS error) between both datasets is decreased after registration. The gain is obviously lower when the maximum displacement is bigger. Figure 6 shows from left to right the same sagittal slice of the original, synthetically deformed (maximum amplitude of 15 mm) and the original after the deformation field has been estimated an applied. The registration was done in 7 minutes (volumetric
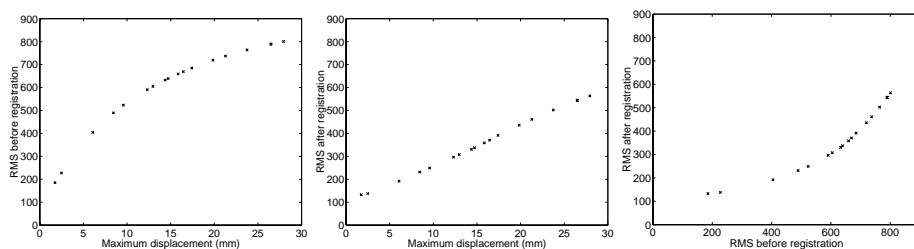
Fig. 5. RMS before and after registration of a 12 bits per voxel T1-weighted MRI $160 \times 192 \times 160$ dataset with a synthetic deformation field of variable amplitude.
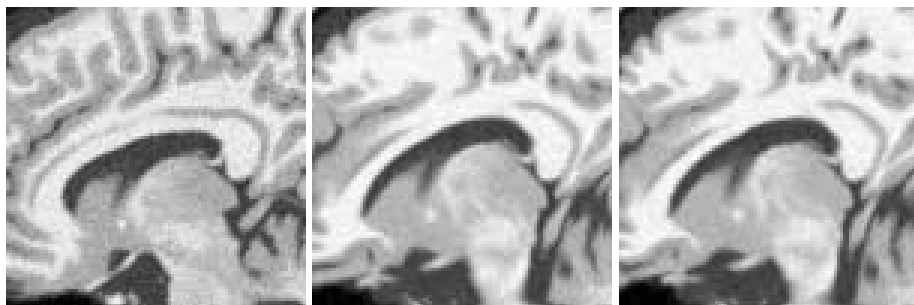

Fig. 6. *Left*: T1W MRI sagittal cross-section; *Center*: T1W MRI sagittal cross-section of the same dataset deformed with a synthetic field of 1 cm^{-1} of spatial bandwidth and 15 mm of maximum displacement; *Right*: T1W MRI sagittal cross-section of the registered dataset.

datasets) on a cluster of eight workstations (hybrid Pentium III and UltraSPARC II).

In order to illustrate qualitatively the performance of our approach for multimodal registration, two volumetric datasets of identical sizes to the previous ones, corresponding to a T1-weighted simulated brain image [15] and a T2-weighted patient image, have been registered using the correlation coefficient as similarity measure, and a Gaussian applicability function with $\sigma = 1.5$. Both datasets were rigidly registered prior to the application of our algorithm. Figure 7 shows, from left to right, T1-weighted, T2-weighted and the T1-weighted dataset deformed onto the T2-weighted one after the field was estimated. Notice, for example, how well the corpus callosum is deformed.

5   Conclusions and Future Work

We have presented a novel nonrigid registration scheme based on template matching, where arbitrary similarity measures can be considered and a deformation field regularization is also carried out. According to our experiments our approach can be a feasible alternative to computationally more expensive
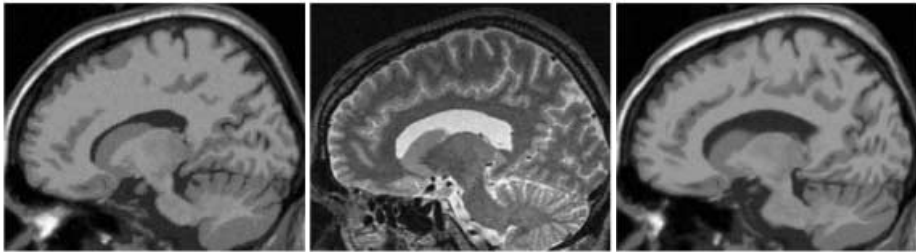
Fig. 7. *Left*: T1W MRI sagittal cross-section from brainweb; *Center*: T2W MRI sagittal cross-section of a clinical patient; *Right*: T1W MRI sagittal cross-section of the registered dataset.

variational methods, yet rendering high accuracy in the registration even in multimodal cases. Our current implementation makes full registrations of volumetric MRI data in seven minutes using a cluster of eight conventional workstations.

Nevertheless yet some improvement can be obtained by doing a full C implementation (currently we are using Matlab and some external libraries). Moreover, other structure detectors as the Harris corner detector [9] and quadrature filter based structure tensors [16] should also be tested.

Acknowledgment

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