Automatic 3D Image Registration for Medical Change Detection Applications

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Abstract

We are developing an automated 3D change detection system which accurately registers medical imagery (e.g., MRI or CT) of the same patient from different times for diagnosing pathologies, monitoring treatment, and tracking tissue changes. The system employs a combination of energy-minimization registration techniques to achieve accurate and robust alignment of 3D data sets. The bases for the registration are 3D surfaces extracted from the 3D imagery. Resultant changes in the data are identified by differencing registered normalized intensity images or comparing measurements of the same segmented tissue over time. The contributions of this work are (1) automation of the registration process, (2) high registration accuracy, and (3) registration stability in the presence of noise, outliers, and data deviations. We have applied this system to a rigid registration problem, namely head registration for multiple sclerosis change detection, and are exploring other rigid and flexible registration applications.

Change Detection Problem

A growing use of clinical imagery is the identification of medically-significant tissue changes over time. In studying conventional single images, medical professionals can locate possibly anomalous structures based on their knowledge of anatomy and pathology. But by *comparing current images against baseline or previous images*, clinicians may also be able to estimate the rate of change in the progression of a disease or as a reaction to a treatment. These improvements should facilitate earlier and more accurate diagnosis. The availability of relatively high resolution 3D raster data sets from diagnostic scanners and the growing emphasis on prevention and early detection of disease combine to underscore the need for accurate change detection technology.

One of the main issues with solving such change detection problems is accurate registration of the imagery over time. In order to achieve this goal we are exploring the application of a series of matching techniques for first coarsely aligning the two data sets and then refining the match using energy-minimization techniques over both interpolated data and finely sampled data.

We have applied our change detection system to the problem of registering magnetic resonance imagery (MRI) of multiple sclerosis (MS) patients over time for the purpose of tracking changes in the MS brain lesions[3]. These lesions, possibly numbering in the hundreds, are small patches of diseased tissue in the brain's white matter. The size and structure of these lesions change over time and indicate the state and severity of the disease. Tracking changes in the lesions can thus provide critical information in understanding the progression of the disease and monitoring treatment. Initial analysis of this data, without temporal registration, included collection of only global statistics over time, such as the changes in the total volume of MS lesions in the brain. But the accurate registration of the MRI data sets over time, described in this report, is facilitating tracking of the individual lesions and allowing study of local changes.

3D Registration Algorithm

For this change detection problem we applied a registration approach which we initially developed for image guided surgery applications [3, 5, 6]. This registration system currently searches for the best *rigid body transformation*. Of course, some medical registration problems will require more flexible registration, but for the head registration described here, rigid transformations appear to suffice. The inputs to the registration process consist of two data sets, represented as sets of 3D points, each in its own coordinate system. The points are assumed to lie on the same structural surface, although the coverages of the points do not need to exactly overlap and outliers may be present. Our problem is to determine a transformation that will map one data set into the other in a consistent manner.

We match the two data sets using the steps outlined in Figure 1. (These are described in more detail in [3, 5].) The input data sets for the MS study consist of the intra-cranial cavity (ICC) surfaces, which are routinely segmented as part of the study. For the Initial Match we use an axis alignment technique if complete data
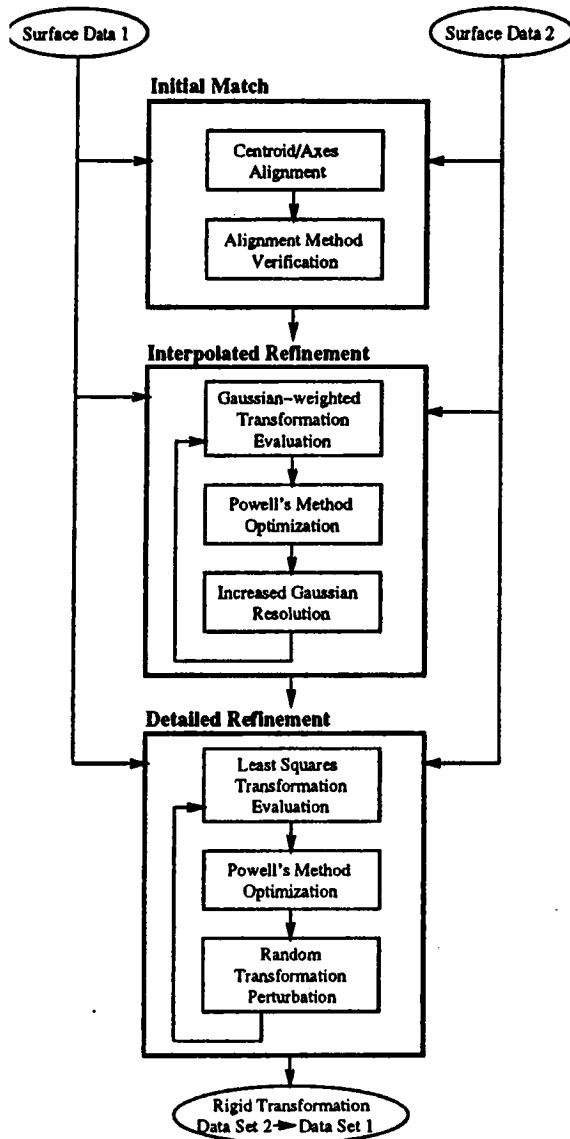
Figure 1: 3D registration algorithm.

vailable (such as in our MRI head registration), or ɔint-based alignment technique if only partial data vailable. Axis alignment is based on aligning the nvectors of the inertia matrix of each of the data . Point-based alignment uses Interpretation Tree rch [4] to match a small set of sampled data points ɔoints in the reference data set and the Alignment .hod [9] to verify possible matches.

˙the RMS errors of the initial matches are high, we ɔrm an Interpolated Refinement aimed at guiding registration in the general direction of the global er-minimum. To perform this refinement we evaluate current pose by summing, for all transformed data ɪts, a term that is itself a sum of the distances from transformed point to all nearby reference surface ɪts, where the distance is weighted by a Gaussian ribution [17]. If ℓ_i is a vector representing a data

point, m_j is a vector representing a reference point, and $\mathcal{T}$ is a coordinate frame transformation, then the evaluation function for a particular pose (or transformation) is $E_1(\mathcal{T}) = -\sum_i \sum_j e^{-\frac{|\mathcal{T}\ell_i - m_j|^2}{2\sigma^2}}$. This objective function is a method for roughly interpolating between sampled reference points. It is generally quite smooth, and thus facilitates "pulling in" solutions from moderately removed locations in parameter space. The evaluation function is iteratively minimized using Powell's method [15].

Based on the resulting pose of the interpolated refinement, we perform a Detailed Refinement using a rectified least squares distance measure. Each pose is evaluated by measuring the distance from each transformed data point to the nearest reference surface point, (with a cutoff at some predefined maximum distance to guard against outliers or missing data). The pose evaluation is the sum of the squared distances of each point. Powell's method is again used to find the least-squares pose solution. Here the evaluation function is $E_2(\mathcal{T}) = \sum_i \min\left\{d_{max}^2, \min_j |\mathcal{T}\ell_i - m_j|^2\right\}$. where d_{max} is some preset maximum distance. This objective function acts much like a robust chamfer matching scheme, similar to that used by [10]. The expectation is that this second objective function is more accurate locally, since it is composed of saturated quadratic forms, but it is also prone to getting stuck in local minima.

In order to avoid such local minima, we randomly perturb the solution and repeat the least squares refinement. We continue this perturbation and refinement process, keeping the new pose if its associated RMS error is better than our current best. We terminate this process when the number of such trials that have passed since the RMS value was last improved becomes larger than some threshold. The final result is a pose, and a measure of the residual deviation of the fit to the reference surface.

Several other groups have reported registration methods similar to ours. Pelizzari and colleagues [12, 13, 14] have developed a method that matches retrospective data sets, such as MRI or CT or PET, using a least squares minimization of distances between data sets, but without automated techniques to avoid potential local minima. Lavallee, Szeliski, and colleagues [2, 16] also perform a least-squares minimization of a distance function to match data sets. They iteratively remove outliers to attempt to avoid local minima. They have also extended their algorithm to deformable tissues by using 3D splines to refine matches. Ayache, Gueziec, and colleagues [1, 7, 8] perform automatic rigid registration of 3D surfaces by matching ridge lines which track points of maximum curvature along the surface. Bajcsy et al [11] use moments of inertia to align two data sets, similar to our initial match, followed by an elastic matching between the aligned data sets to handle small remaining variations.

Change Detection Results

We ran the registration system on 21 double echo MRI data sets of the same patient collected over a period
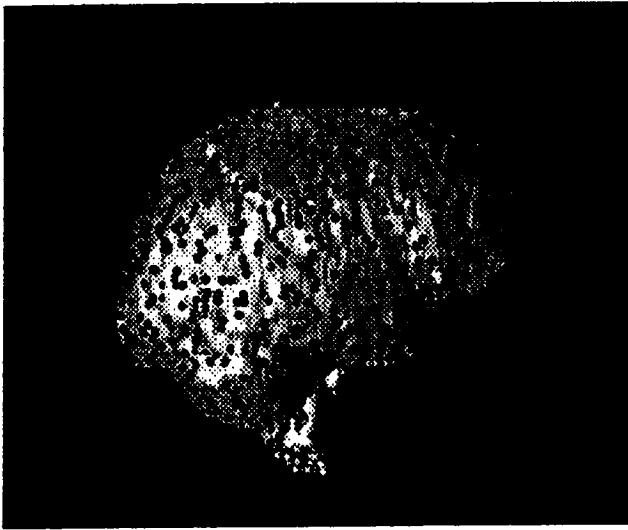
Figure 2: Side view of registered points from one data set overlaid on surface of the other data set. Dot brightness varies from black ($0mm$ distance error) to white ($5mm+$ distance error).

of one year. One of the data sets was selected as the standard and the other 20 were registered to it in order to generate a fixed coordinate frame in which to evaluate changes. The resolution of all the data sets was $0.9375mm$ x $0.9375mm$ x $3.0mm$. Sampling of the data sets for registration resulted in an average of 7060 points in the reference data set (sampling factor of 4) and 1415 points in the transformed data set (sampling factor of 20).

The registration results for one data set pair are shown in Figure 2 which overlays the transformed ICC surface points from one data set onto the surface of the other ICC. Most of the points appear to have been registered well. The principal error sources arise from the brain stem, where one scan included fewer slices, and from the top of the ICC, where the tangency of the surface to the slicing plane leads to partial voluming artifacts and sparser data. The RMS error for this run was $1.96m$, with a median residual distance error of $1.57mm$. These values are close to the expected limits as dictated by the sampled resolution of the data.

Figure 3 shows the results of image differencing an image slice at the same position in the reference and transformed data sets. The intensity images are resliced using trilinear interpolation while the segmented images are resliced using nearest values. Note that the main source of change inside the brain is MS lesion growth.

For the 20 test runs the average final RMS error was $1.92mm$. The average RMS after initial alignment was $2.38mm$. For these runs the gaussian interpolated refinement was not performed since the relatively close initial alignment and the high density of the data resulted in highly accurate registrations with just the detailed RMS minimization refinement[4]. Al-

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[4]Our experience with other data sets, in which the data is much more sparse, indicates that such interpolated refine-

though the initial inertia axis alignment provided close enough starting points for registration refinement, it was generally not sufficient as a final result.

Conclusion

The registration algorithm outlined in this report has been shown to achieve accurate rigid registration results for change detection in MRI imagery of the head. In addition to brain studies, potential domains of application (with extensions to flexible registration) include orthopedics, mammography, and craniofacial surgery. The registration technique incorporates the following goals:

- **Stability in the presense of input data errors.**
  Our registration technique combines matching contributions across all the available data, but limits the impact of data deviations by placing a limit on any one data point's contribution to the alignment evaluation. The resultant truncated least-squares approach is designed to achieve accurate registration in the presence of surface extraction deviations (e.g., data segmentation errors), data outliers (e.g., non-overlapping surfaces), clutter points, and imaging distortions.

- **Minimum dependence on initial alignment.**
  By incorporating techniques to automatically generate initial alignments and then refine them using both interpolation and fine sampling techniques, we are able to register data sets independently of any input alignments. If known, such initial alignments can be exploited to accelerate the registration process, but are not required.

- **Avoidance of local minima.**
  Since we are using energy-minimization optimization techniques on a complex underlying evaluation function, a key issue is reaching the global minimum without getting trapped into local minima. We have incorporated two techniques to treat this problem: interpolation of the evaluation function and random perturbation of resultant transformations.

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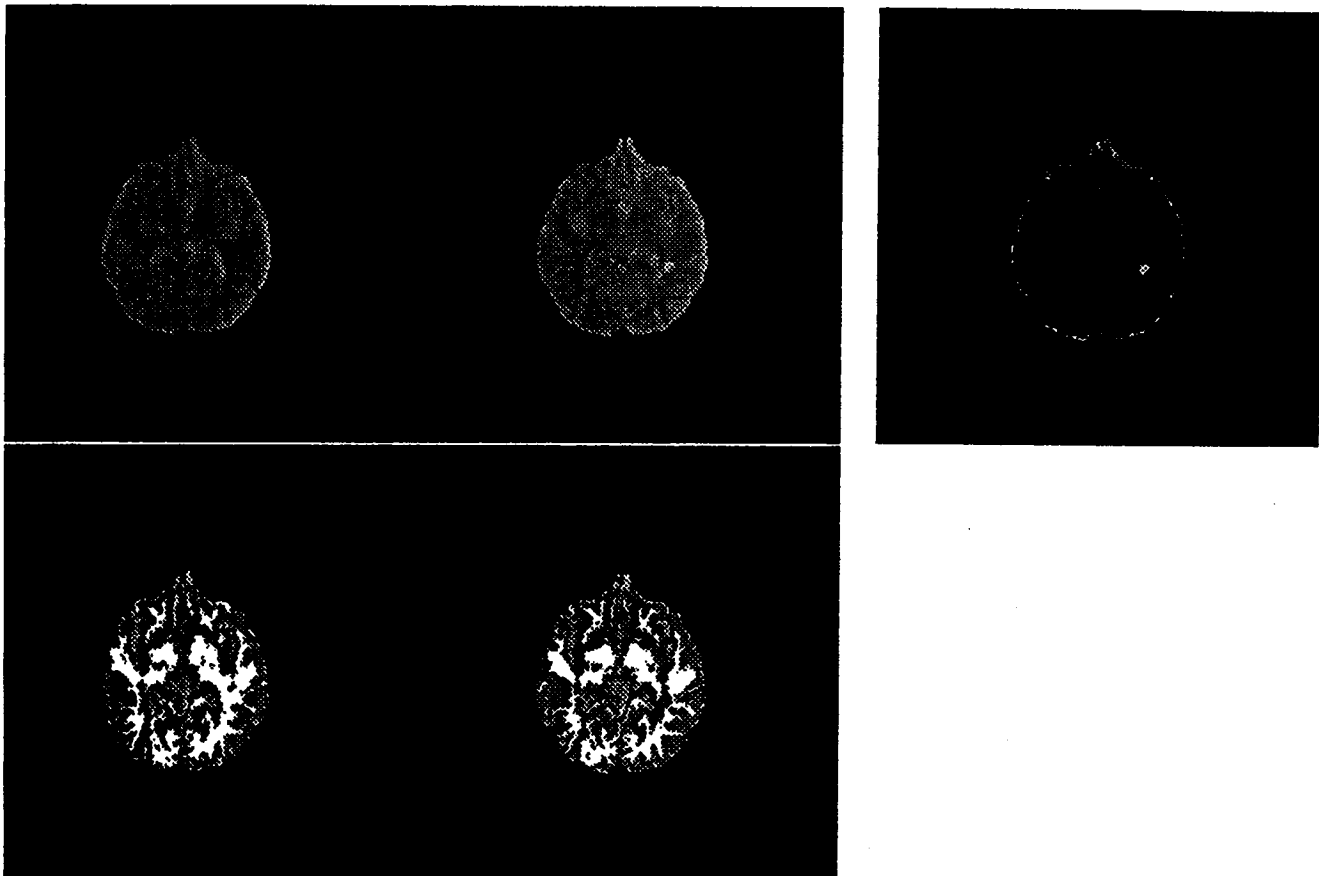
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ment can be a powerful tool in avoiding local minima.

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ure 3: Changes in the same slice position. First column is transformed data which was registered to second column. gery in second column was taken eight months later. Top row is normalized intensity imagery from one of the two MR ᴀ echos used in the study, along with the absolute difference between the two. Bottom row is the segmented imagery: dark ' = grey matter, white = white matter, light grey = CSF, and black = lesions.

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