Histogram Transformation for Inter-Modality Image Registration

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***Abstract*—This paper describes an efficient image transformation method based on histogram information and some prior knowledge of tissue expression in different modalities for registration of images from different image aquisition methods, such as CT and MRI. The metric defined in this paper represents a computationally efficient alternative to traditional, mutual information based methods. The optimization step in the registration algorithm can be carried out either by using a normalized cross-correlation function or as a simple image subtraction, which makes it suitable for hardware implementations.**

I. Introduction

Arising from the clinical need for multimodal imaging, this article describes a set of algorithms that form an integrated system for automated large-scale image processing, multimodal image registration and multi-source volume rendering. The system has been developed to enable simultaneous processing and rendering of image data from multiple medical imaging sources. The algorithms described here satisfy real-time data processing constraints, as required for clinical deployment.

This article is structured as follows. Section II describes the difference between intermodal and intramodal registration and provides examples of both techniques. Section III explains how intramodality techniques can be used for intermodality image registration. Section IV describes the pre-processing step of segmenting the images in each modality and correlating the scalar values for each cluster. Section V outlines the registration process using cross-correlation as a similarity measure, and section V shows the results obtained using this method. Section VI summarizes the findings and outlines future research goals and potential directions.

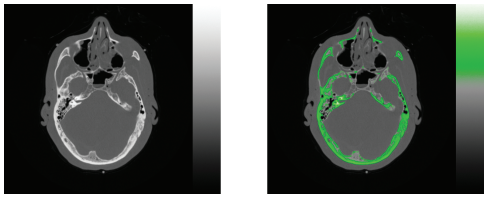

Fig. 1. Bone tissue highlighted (green) in a CT scan.

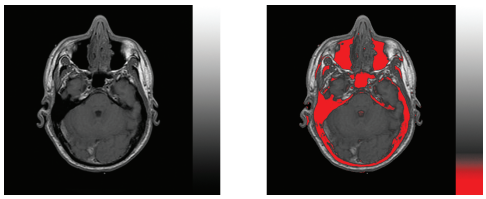

Fig. 2. Bone tissue highlighted (red) in an MRI scan.

II. Previous Work

A. Registration of Different Modalities

This section addresses the problem of automated, intermodal registration, such as the registration of CT and MR images. In contrast to intramodal registration, intermodal registration is a non-trivial task due to the fact that a given tissue type is represented differently in the two modalities. Furthermore, the histogram ranges associated with each tissue type may appear in a different order. This means that a tissue that is expressed as a high value (bright gray level) due to a high degree of X-ray absorption (CT scan), may be represented by a low value (dark gray level) due to low proton density (MRI scan). The difference in the gray level representation comes from the fact that different physical quantities are being measured. For example, bone is visually represented as bright white (high X-ray absorption) in CT scans (figure 1), and as a black band (low proton density) in MRI scans (figure 2). Hence, the correlation between corresponding pixels in each scan is not linear (figure 3). This makes the task of aligning them, without the use of stereotactic frames or markers, difficult.

As an alternative approach to intermodality registration, a method that uses feature segmentation based on intensity histograms [Gon02] of the two images is proposed here. The idea is that if one of the scans is transformed to match the gray value distribution of the other scan, then the similarity measures used in *intramodality* registration techniques can be used for *intermodality* registration. Section IV outlines techniques to achieve a reasonable segmentation of the various tissue types and correlation of the same to achieve a robust registration. The fact that the algorithm in the current implementation uses several different tissue types to control the alignment process and the correlation computations adds

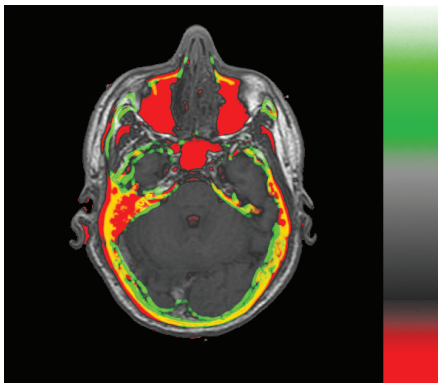

Fig. 3. Bone tissue highlighted (red) in an MRI scan (same as in fi gure 2). CT representation of bone (same es in fi gure 1) superimposed (green). Common areas are represented in yellow.

additional robustness to the approach.

Combining multiple scans of the same specimen into a single image or volume has numerous advantages in diagnostics, pre-surgical planning and radiation therapy planning, especially when multiple modalities depicting various physical properties of the scanned sample are involved. Some tissue types may be better visible in one type of scan, others may only appear in another scan.

Similar scans (e.g. multiple CT scans) can be registered by using a simple differential function as a similarity measure (*intramodal registration*). Combining images taken from different modalities (*intermodal registration*) is a much harder problem. The main reason is the fact that the various tissue types that occur in the images are represented in different ways in different modalities and may appear in a permutated order in the gray level spectrum. For example, a linear transfer function maps the high X-ray absorption values of bone to an intensity value that is visually represented as a bright white, whereas the same linear transfer function would produce a black pixel for the same location in an MRI scan due to the low proton density of bone matter. Hence, the correlation between corresponding pixels in each scan is not linear over the entire range of values. Moreover, the intensity ranges associated with a particular tissue type do not appear in the same order in a histogram. This makes the task of aligning two images from different modalities difficult.

B. Other Registration Methods

Three different, classical registration methods with different prerequisites and application areas are presented here. The *Global Difference* method is based on the assumption that intensities in the two participating images are linearly correlated. This assumption makes the method not suitable for intermodal registration, because absolute values, the spacing between these values in an intensity histogram, and the order of clusters in such a histogram vary due to the difference in the way material properties and the physical quantities measured by a particular scanning method differ.

The second method is called *Geometric Features*. It compares outlines of objects, which can be identified by extracting intensity gradients using a Laplacian or high-pass filter. This method is based on the assumption that tissue gradients are expressed similarly in both images. Unfortunately, this is not the case for the same reason as for the absolute values, i.e., because of the differences in the physical quantities being measured by the two incompatible image acquisition devices.

A third method is known as *Mutual Information*. This technique computes the statistical dependence or information redundancy between image intensities of corresponding pixels in both images. No specific assumptions about feature expression are being made. This method is suitable for intermodal registration and has been widely studied in the literature [Mae97].

Mutual information (MI) works for different modalities that contain the same information, but expressed differently. It is typically computed as a summation of the product of the mutual histogram for all intensities and the logarithm of the ratio between the mutual histogram and the individual histograms [Mae97]. The goal is to maximize MI.

Numerous attempts to accelerate the alignment process, ranging from manual to semi-automatic to fully automatic methods [Els94], [Els95], [Stu96], [Pen98], [Hil01], [Jen02], [LoC03], have been proposed in the literature. These methods include histogram matching [Hua98], texture matching [Ash95], intensity cross-correlation [Mai98], kernel-based classification methods [Cri00], information divergence minimization [Sto98] and optical flow matching [Lef01]. A good survey can be found in [Bro92].

More recently developed fully automated methods essentially revolve around entropy [Mey97], [But01], [Zhu02] and mutual information (MI) [Vio95], [Wel96], [Plu03], [Wel96]. Even though they are more convenient than manual or semi-automatic techniques, they are still time consuming and computationally expensive. The general consensus on MI-based techniques is that they provide the best results in terms of alignment precision and are generally consistent with manual, expert-based alignment procedures. However, the loss of spatial coherence during the registration, which is due to the different physical quantities being measured and the resulting variations in the feature boundaries and gradients, is a potential cause of inaccurate registration.

The idea of the method presented in this paper is that methods suitable only for *intramodal registration* (same imaging device type) can be adapted to work also for *intermodal registration* (different imaging device types). The method can be efficiently implemented using a look-up table and, depending on the implementation of the intramodal registration algorithm, is therefore potentially faster than the computationally expensive MI method.

III. Using Intramodality Techniques for Intermodality Registration

As described before, we propose an alternate method for registering CT and MRI scans, usually requiring *intermodality* techniques. The method described here employs *intramodality*

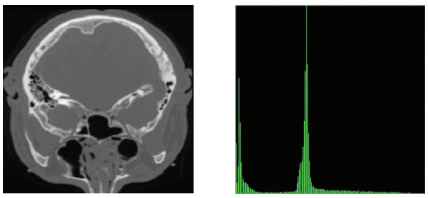

Fig. 4. CT scan and intensity histogram.

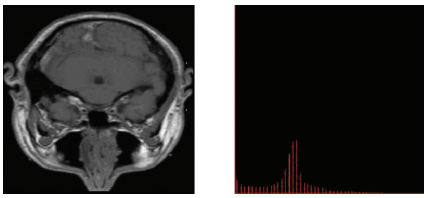

Fig. 5. MRI scan and intensity histogram.

methods to accomplish the alignment task. Our approach is rather intuitive and inexpensive. We hypothesize that if we convert one of the scans (e.g. MRI) to match the other (e.g. CT) in terms of the scalar value representation of various tissue types that occur in the images, then by applying a similarity measure based on the correlation between corresponding features and globally optimizing this parameter, we can achieve alignment of the two different modalities at a relatively cheaper cost, providing results comparable in quality to those of intermodality registration techniques.

The task of converting the representation of the various tissue types present in one scan into the representation given by another scanning technology or modality involves the use of feature segmentation followed by histogram matching [Hua98]. By sorting the intensities of each image into clusters corresponding to the intensity ranges of characteristic features, we can approximately segment the scans into the various compounds or tissue types. These individual segmentation clusters can then be mapped onto relevant bins from the second scan. A histogram matching of these segmented images, which includes a permutation and adaptation of the bin widths in the histogram, generates a transfer function that defines a mapping between the original scan and the alternate scan.

IV. Segmentation Using Histogram Permutation

In order to correlate the individual representations of the various anatomical structures in each scan, we use intensity histograms. Figure 4 shows the intensity profile of a CT scan (data specification: 512 x 512 grayscale image). Figure 5 shows the intensity profile of an MRI scan (data specification: T1-weighted, 256 x 256 grayscale image) of a human head. All images and histograms were stored in an 8-bit format (value range [0...255]).

Histogram permutation is an approximation technique based on known expressions of particular tissue types in various modalities. Depending on the number of expected distinct features (i.e. tissue types), we create bins of intensity clusters. For example, we have one bin to store all the high intensity pixels in a CT image which are characteristic of skull bone (high X-ray absorption). This would map onto the bin containing the low intensities from the skull in the MRI scan (low hydrogen proton concentration in bone). Similarly, the gray matter, white matter and cerebral spinal fluid (CSF) can be stored in one bin corresponding to the uniform gray region of brain matter in the CT.

The bins thus correspond to a partitioning of the image into characteristic tissue expressions. Initial bins were obtained and refined using user interaction, and a table of mapping values was generated (table I).

TABLE I
Mapping of MRI intensities to corresponding CT intensities for each feature space.

CT intensity	MR intensity	Feature
0 – 9	0 – 1	Background
10 – 60	175 – 255	Adipose
61 – 140	56 – 119	Soft tissue
141 – 255	2 – 55	Bone

Having thus created the desired bins, we then generate a transfer function to carry out the mapping between each segment (bin) of the MRI and the CT scan based on table I, using the principles of histogram matching [Hua98]. This process of selective histogram matching ensures a good approximation.

Figure 6 shows a graphical representation of the bins and a typical permutation. It becomes obvious that bone, for instance, is represented differently in different modalities, and that the width of the bins varies. Therefore, the mapping is not linear. A piece-wise linear transfer function is designed to perform the permutation and scaling of the histogram bins.

After applying the transfer function, the MRI image now contains intensity values that correspond to those found in the CT scan. This means that the various tissue types are now represented by a similar intensity value. Figure 7 shows the original superimposed histograms of the CT and the MRI scan before application of the transfer function. The image shows that there is minimal overlap, which makes

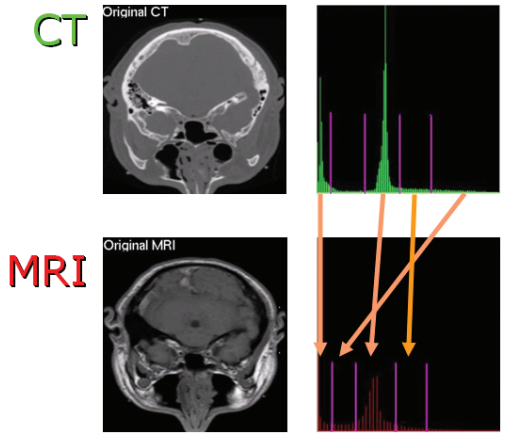

Fig. 6. Mapping of CT histogram (green) onto MRI histogram (red). Bin boundaries are shown in purple color.

image registration of features that are expressed differently difficult. Figure 8 shows the superimposed histograms of the CT and the transformed MRI scan. Obviously, there is a much better match in the overall shape of the histogram, indicating that the two images, even though generated by two different modalities, will yield a much better registration of individual features. Figures 9(a) and (b) show the corresponding images, i.e., the original MRI image, and the new MRI image after application of the transfer function. Figure 9(b) is now similar to the original CT image, which is shown in figure 9(c) for comparison.

The quality of the transformation can be evaluated by subtracting either the histograms or the images. Using a low-pass filter on the images or a quantization on the histogram is necessary to obtain a reasonable measure of the quality, because due to the difference in the image acquisition process, the individual pixels or bin distributions will still be very different, but the average distribution is similar.

Our registration algorithm takes as input a file that contains the segmentation information, i.e., the number of clusters or bins followed by the intensity range for each cluster. The algorithm then optimizes a global similarity measure based on correlation, as described in the following section.

V. Cross-Correlation and Image Registration

The registration was done using an intensity-based similarity measure. Optimization of a normalized cross-correlation (NCC) function using Powell's multi-dimensional line maximization [Jac77] formed the basis of the similarity measure.

$$R = \frac{\sum_{k=0}^{n}[(r(k) - \mu(r)) - (f(k) - \mu(f))]}{\sqrt{\sum_{k=0}^{n}(r(k) - \mu(r))^2 - \sum_{k=0}^{n}((f(k) - \mu(f))^2}} \quad (1)$$

Equation 1 shows the NCC function. Here r and f represent the reference and the floating image, respectively. $\mu(r)$ and $\mu(f)$ represent the mean intensity values of the reference and the floating image. In our case, the CT scan is the reference image and the transformed MRI is the floating image. R represents the metric used to determine the similarity between the CT and the transformed MR image. $R = 1$ implies maximum correlation, $R = 0$ implies no correlation, and $R = -1$ implies an opposing relation between the intensities from the two modalities. Powell's multi-dimensional line maximization algorithm, which employs Brent's one-dimensional optimization algorithm, was used to determine the optimum value for R in the X-Y plane.

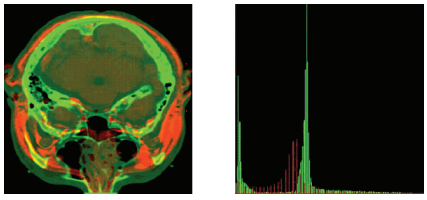

Fig. 7. Overlap of CT (green) and MRI (red) scans and intensity profiles before permutation and histogram matching.

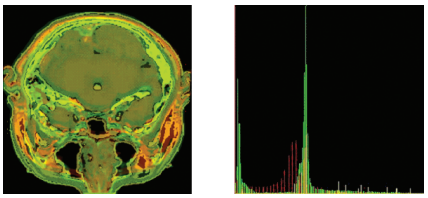

Fig. 8. Overlap of CT (green) and transformed MRI (yellow) scans and intensity profiles after histogram permutation and matching. Red indicates the original MRI image and profile. The yellow intensity profile (transformed MRI) is a better match than the red intensity profile (original MRI) to the green one (CT scan).

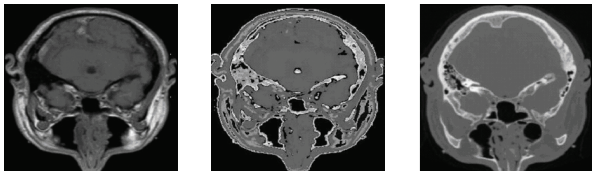

Fig. 9. (a) Original MRI image. (b) Transformed MRI image. (c) Original CT image. The transformed MRI (center) matches the geometry of the original MRI (left) and the intensity profile of the CT scan (right).

A "sum of squared differences" technique may also be used for the registration process, since specific optimization algorithms work very efficiently for the same. However, the choice of NCC as a similarity measure was dictated by the fact that tissue-type-based clustering is not an exact science due to large variations in individual tissue expressions across patients. In addition, noise, if not removed prior to the transformation, is also transformed by the histogram matching process, has a strong effect on the "sum of squared differences" method and interferes with the registration, especially when the noise is not uniformly distributed or Gaussian. The NCC function together with a low-pass filter ensure the robustness of the algorithm.

VI. Results

Figure 10(a) shows the superimposed images of the CT and the original MRI scans in their initial, unregistered position. Note that the bone (bright red or bright cyan) is not aligned (white, composition of red and cyan). Figure 10(b) shows the registered set, again with no good match (few white pixels). The hollow space (transparent) in the MRI is completely filled by the skull (cyan) from CT. This means that the bone is hardly visible in the given MRI scan.

Figure 11(a) shows the same results for a transformed MRI image. Note that the bone (white, composition of cyan and red) is much better visible now. Especially after registration (figure 11(b)), the bone appears mostly white. This means that it is visible in both images (CT and transformed MRI). This property is most obvious for tissues that appear bright in the current representation (bone), but it also applies to other tissue types, as is shown in the following images. The assignment of intensity ranges (histogram bin mapping) is arbitrary and typically chosen to match one of the two modalities, in this case the CT scan.

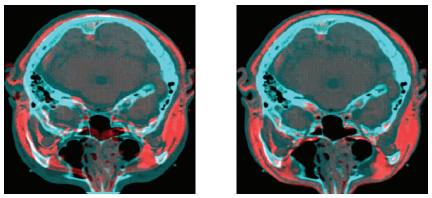

Fig. 10. CT (cyan) and original MRI (red). (a) unregistered, (b) registered.

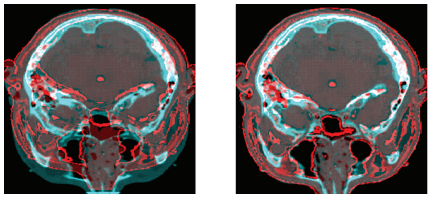

Fig. 11. CT (cyan) and transformed MRI (red). (a) unregistered, (b) registered. White regions indicate matched bone regions expressed similarly in the CT and the transformed MRI scan.

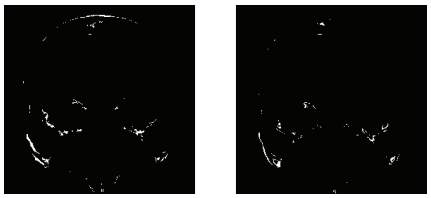

Fig. 12. CT and original MRI. (a) unregistered, (b) registered. (Bone only.)

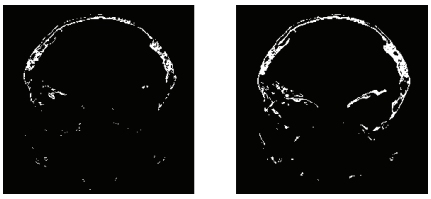

Fig. 13. CT and transformed MRI. (a) unregistered, (b) registered. (Bone only.) White regions indicate matched bone regions expressed similarly in the CT and the transformed MRI scan.

Figures 12 and 13 were created using thresholding of the pixels that indicate the highest structural similarity (bone only). As stated before, not only the pixels with the highest values (typically bone) can be used for a correspondence analysis. Other tissue types can be used as well, as shown in figures 14 and 15 (all tissue types).

The last image in each series (figures 13(b) and 15(b)) shows the largest number of pixels usable for correspondence analyses. An analysis of the pixel count indicates that the transformation using transfer functions and histogram permutation increases the number of pixels that can be used for correspondence analyses, therefore increasing the accuracy and robustness of the method.

The algorithm can be very efficiently implemented using look-up tables so that it was possible to run it on a laptop computer. In comparison to other intensity-based techniques for intermodality registrations that use entropy or MI calculations, NCC computations are less expensive. The pre-processing step is also inexpensive and is independent of the alignment routine. Performance data of the various algorithms is difficult to compare due to large variations in the implementations and applications. Therefore, absolute timing measurements were taken, which may serve as a guideline for similar implementations.

The computation of the transformation of the original MRI to its CT-look-alike took approximately 10 milliseconds, and the alignment algorithm took 3.25 seconds for a single slice (approx. 6 minutes for a typical data set of 113 slices) on an IBM R40 Thinkpad with 256MB RAM and 1.4 GHz PentiumM processor. The graphics card is an ATI Mobility Radeon with 16MB memory.

VII. Summary and Future Work

This paper explained how histogram information of a grayscale image can be adapted based on another image using previous knowledge about the bins of the reference image histogram. By transforming one image into the value range of the reference image using a non-linear mapping, *intramodal* registration techniques, as opposed to computationally more expensive *intermodal* techniques, can be used to align the images. Optimization of a normalized cross-correlation function (NCC) is an efficient way to implement an intramodal image registration algorithm.

As a simpler alternative to the NCC method, the correlation between the images can be carried out by subtracting one image from the other after applying an affine transformation. The minimum sum of the differences woudl indicates optimal correlation. The simplicity of the two steps, affine transformation and subtraction, make this method very suitable for an implementation in hardware. Future work will include an OpenGL-based implementation of these two steps using GPU programming, where the two images will be loaded into

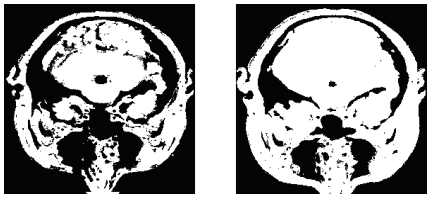

Fig. 14. CT and original MRI. (a) unregistered, (b) registered. (All tissue types.)

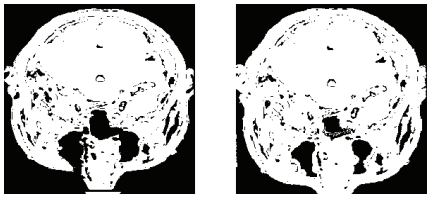

Fig. 15. CT and transformed MRI. (a) unregistered, (b) registered. (All tissue types.) White regions indicate matched regions of all tissue types expressed similarly in the CT and the transformed MRI scan. The right image shows an almost perfect match (all tissue types).

texture memory, the histogram transformation will be carried out on one of the images, and then, after applying different affine transformations, the two images will be subtracted. Since the graphics processing unit (GPU) can carry out all of these operations, a significant speed-up in determining the optimal affine transformation for image registration is expected.

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