Image registration of diffusion weighted and conventional breast MRI

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ABSTRACT

Compared to traditional magnetic resonance imaging, which provides anatomical information with high contrast, diffusion weighted imaging (DWI) can add functional information for a more precise detection and localization of breast cancer. However, DWI may suffer from artifacts due to off-resonance effects, including geometric distortions. This hinders combined view, e.g. by image fusion. In this work, we investigate a distortion correction of DWI based on a nonlinear image registration with a T2 weighted image. Our method consists of three steps: a data cleaning step in which differences in image sections and resolution are compensated, an edge detection step which extracts the outline and inner structures of the breast in both DWI and T2 weight image, and finally a non-rigid registration step using the demons algorithm. We use two clinical datasets with a total of seven patients for evaluation. Manual annotations of landmarks in 227 slices serve as basis to calculate the registration error. Our method reduces the target registration error based on the center of gravity of annotations from in average 5.5 mm to 3.1 mm and is most effective in cases with large initial deformation. Compared to the other methods tested in this study the proposed method shows the lowest error. The method may contribute to a better combined diagnosis and e.g. facilitate computer aided detection and diagnosis by enabling combination of spatially well-aligned information.

Keywords: Magnetic Resonance Imaging, Diffusion weighted imaging, Image registration, Distortion correction, Image fusion

1. INTRODUCTION

Magnet resonance imaging (MRI) is a powerful tool for sensitive breast cancer diagnosis. While providing anatomical information with high contrast using traditional MRI sequences, functional information may be added for diagnosis by acquiring diffusion weighted images (DWI). Due to cancer tissue showing high cellular density and intact cells membranes, it can be distinguished from healthy tissue using DWI.[1] Yet, images derived from diffusion tend to have low contrast and lack anatomical information. It is important to combine the functional information of DWI and the anatomical information in conventional MRI sequences for better visualization and localization of breast cancer. However, due to the need for low scanning time to capture the water diffusion, DWI makes use of echo-planar imaging, which frequently introduces artifacts due to off-resonance effects, including geometric distortions.[2] This hinders combined view, e.g. by image fusion.

Currently distortion correction approaches usually make use of additional data such as reverse phase-encoding scans or field-maps.[3,4] However, the additional data acquisition required for this is not always included in the scanning protocol as it may increase the scanning time and thereby the risk of patient motion. Thus, image registration has been tested to compensate the geometric deformation. Due to the non-linearity of the distortions, free form deformation registration techniques such as B-spline grid based methods[5] or the demons algorithm[6] can be used. A registration-free approach was also introduced, which trains a neural network on synthesizing an undistorted image using T1 weighted images and distorted diffusion weighted images as an input.[7] So far, most of theses approaches were only used on brain images and can not be directly translated to breast image

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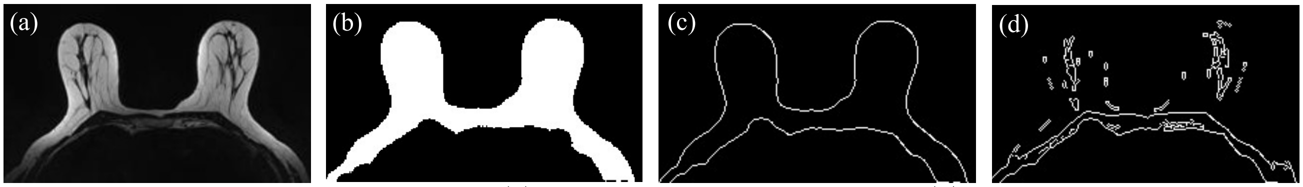


Figure 1: Processing of reference image: (a) Initial T2 weighted MR image, (b) binary mask separating the breast from the background, (c) detected outline of the breast, (d) detected outlines of inner structures of the breast.

data. Especially, a neural network would need a large dataset for training, even consisting of undistorted images. Hence, a registration based approach is beneficial to perform a distortion correction without the need for additional scans.

In this work we investigate the distortion correction of DWI based on a nonlinear image registration using the demons algorithm similar to Takatsu et al.,[6] while extending their methods, testing the method on clinical datasets of two different devices and protocols and comparing the method to other image based registration methods.

2. METHODS

2.1 Proposed image registration method

Our goal is to register the DWI image (moving image) with a T2 weighted image (reference image). The b0 DWI, b0 being the applied magnetic field strength, has been chosen as the moving image since it is acquired without any diffusion sensitization and thereby provides structural information comparable to the reference image. Our method consists of three steps: data cleaning, edge detection and non-rigid registration using the demons algorithm.

In the data cleaning step, we select the common image volume covered by both images using the meta data given in the DICOM header. We then resample the image with higher resolution (typically T2 weighted image) to the one with lower resolution (typically DWI). Finally we compensate the potentially different spacing between slices in both images by a resampling with a Lanczos kernel to obtain a stack of 2D slices which are then at the same geometric position in the MRI coordinate system, and at the same resolution.

The following process is performed on slice basis. The edge detection step is split into the breast outline detection and the detection of inner structures. In the first edge detection step we use a threshold to binarize the T2 weighted image, followed by morphological operations to close inner holes (Figure 1 (b)) before selecting the outline of the binary object as breast outline (Figure 1 (c)).

To overcome misdetections of the breast outline in DWI by ghosting artifacts, which are common in DWI, we make use of the breast mask computed based on the T2 weighted image (Figure 1 (b)): a probability map was created using repeated morphological dilation and smoothing of the breast mask (Figure 2 (b)). Assuming that the breast outline closest to the one in the T2 weighted image is more probably the correct one, the probability map is multiplied with the DWI image. Another typical problem in DWI is that the breast outline is not very distinct, i.e. mostly inner structures are represented with high contrast. To tackle this problem in the outline detection, we initially binarize the DWI with a threshold. This so-called skeleton may contain holes in the outline of the breast due to low contrast to the background (Figure 2 (c)). To compensate this problem we subsequently use the binary mask based on the T2 weighted image and deform it to match the visible outlines of the skeleton using Demons algorithm with a strong regularization for smoothness of the surface (Figure 2 (d)) before then extracting the breast contour for the DWI image (Figure 2 (e)).

In the second edge detection step we extract the outline of inner structures such as fibroglandular tissue, connective tissue or tumors which show a contrast in both images. In the T2 weighted image the inner structures were detected using thresholding inside the already computed breast mask ((Figure 1 (d))). To obtain the presumably same structures in the DWI, we again make use of the location of these structures in the T2 weighted image, assuming a distortion of the DWI in a certain range, e.g. $< 10\,mm$. For this purpose, we dilate

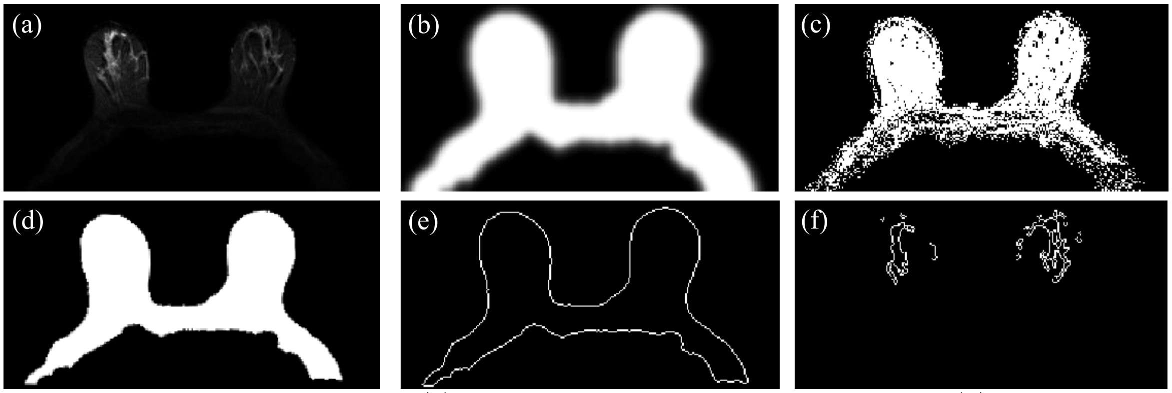


Figure 2: Processing of moving image: (a) Initial b0 diffusion weighted MR image, (b) probability map for outline detection based on the binary mask of the T2 weighted MRI, (c) initial binary mask of DWI, (d) binary mask of DWI processed by registering the binary mask of the T2 weighted image to the initial binary mask of DWI with strong regularization, (e) detected outline of the breast, (f) detected outlines of inner structures of the breast.

Figure 3: Comparison of the manual annotation before (left) and after (middle) applying image matting. Overlay of contours for visual comparison (right).

the edges found in the T2 weighted image. Within this dilated area we search for an optimal threshold which obtains edges that have the most similarity (considering mutual information as image similarity metric) when registered to the T2 weighted inner structures by the Demons algorithm (Figure 2 (f)).

The detected breast outlines and edges of inner structures in both the moving and reference image are combined in a binary mask which is then used for final non-linear registration. In this final step, the demons algorithm is applied with a multi-resolution strategy.

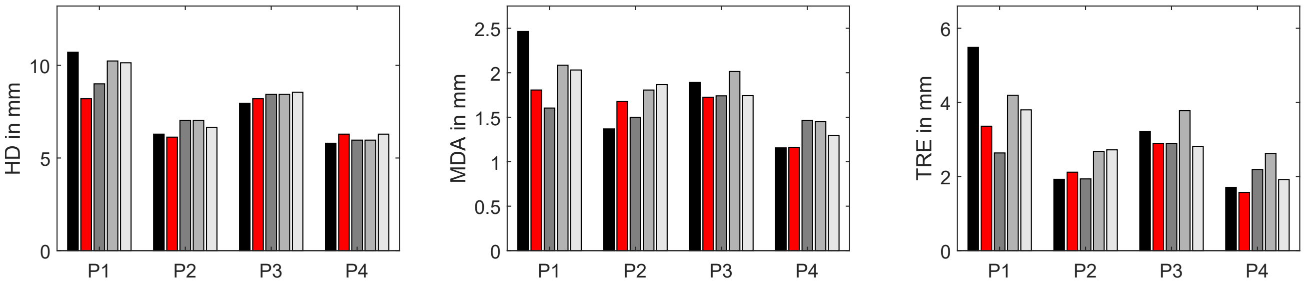
2.2 Evaluation methods

For evaluation we used two datasets: one from clinical routine at University Medicine Vienna containing four patients, and one from the Reference Image Database to Evaluate Therapy Response (RIDER),[8] which is publicly available, containing three patients. To assess the accuracy of the image registration, annotations of anatomical structures, e.g. connective tissue, outlines of tumors or outlines of fibroglandular compartments, were acquired from experts using a custom graphical user interface with a freehand tool. To reduce subjectivity of the annotation we applied image matting.[9] In total 227 slices in the seven available patients have been annotated. An exemplary annotation before and after applying image matting is shown in Figure 3. To quantify the registration accuracy we calculated the target registration error (TRE) defined by the euclidean distance between the center of gravity of annotations, the Hausdorff distance (HD)[10] and mean distance to agreement (MDA)[11] of the annotations.

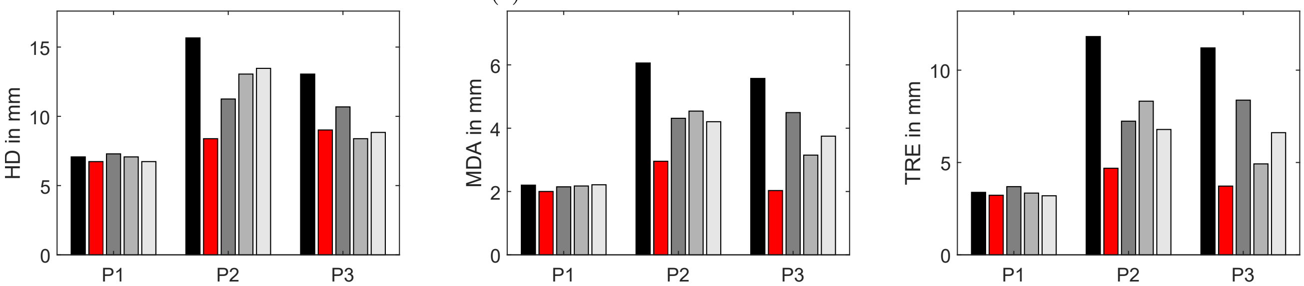
We furthermore compare our method to (1) a registration based on Demons algorithm with the breast outline only, (2) a registration based on Demons algorithm with DWI and T2 weighted gray scale images and (3) with an affine transformation.

3. RESULTS

Figure 4 shows a comparison of the median values for HD, MDA, and TRE before (black) and after the registration with the proposed method (red) has been applied. Averaged for all patients of the Vienna dataset the HD is reduced from $7.7\,mm$ to $7.2\,mm$, MDA is reduced from $1.7\,mm$ to $1.6\,mm$, and TRE is reduced from $3.1\,mm$ to



(a) Results for Vienna dataset



(b) Results for RIDER dataset

Figure 4: Median HD, MDA and TRE for individual patients in both datasets. The black bars indicate the errors before the registration was applied. Red bars represent the result when the proposed method is applied. The three gray bars indicate the result when (from left to right) the registration based on demons algorithm with the breast outline only, (2) a registration based on demons algorithm with the gray scale images and (3) with an affine transformation is applied.

	HD in mm	**MDA in** mm	**TRE in** mm
Before registration	9.5	2.9	5.5
Our method	7.6	1.9	3.1
Demons with outline only	8.5	2.5	4.1
Demons intensity-based	8.6	2.5	4.3
Affine	8.7	2.4	4.0

Table 1: Average errors across all patients in both datasets. The Hausdorff distance (HD), the mean distance to agreement (MDA) and the target registration error (TRE) is given before registration and after applying the different described methods.

$2.5\,mm$ using our method. For the RIDER dataset the average HD is reduced from $11.9\,mm$ to $8.0\,mm$, MDA from $4.6\,mm$ to $2.3\,mm$, and TRE from $8.8\,mm$ to $3.9\,mm$. For the individual patients it can be recognized that the deformation before the registration is of quite different magnitude. Patients with larger initial error profit more from the registration than patients in which the initial error is already low. For those cases with low initial error, the applied method however also does not degrade the results, which can be interpreted as having reached a local or the global minimum for the particular case. The remaining differences may also be based on uncertainties in the annotation process and therefore represent the baseline for the accuracy that can be reached. This becomes also obvious comparing the results of the Vienna dataset and the RIDER dataset: for both the TRE after registration is for all patients approximately in the same range between $2\,mm$ and $4\,mm$, nearly independently of the initial error.

Compared to the other methods (1-3) described in section 2.2 our method shows the lowest error for nearly all patients and all metrics: across both datasets and all patients the average HD, MDA and TRE are given in Table 1.

Figure 5 shows exemplary results of an image fusion between DWI (color-coded) and T2 weighted image (intensity background) performed before and after our proposed registration method has been applied.

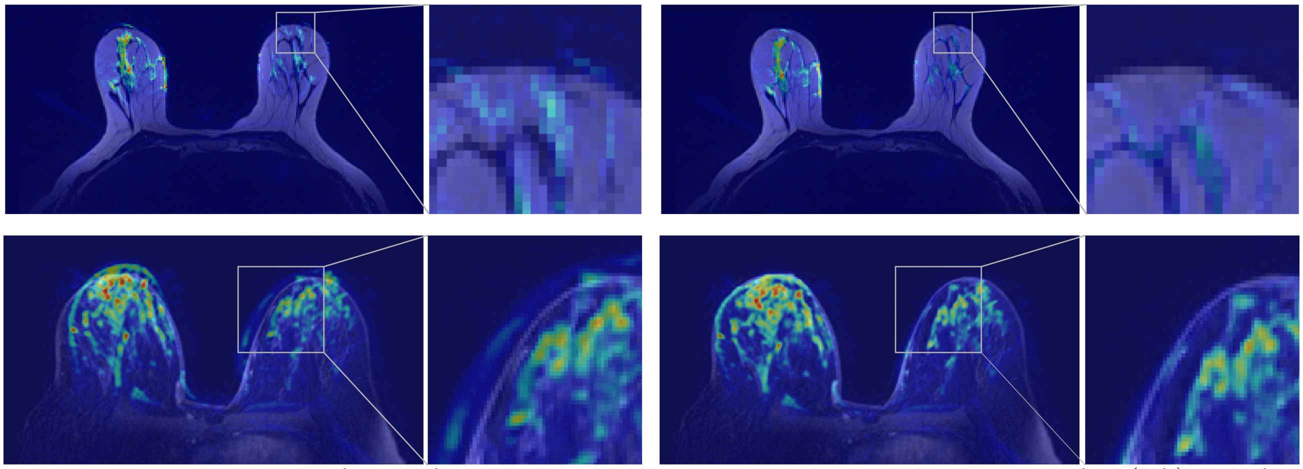


Figure 5: Exemplary result of image fusion between b0 DW image and T2 weighted image before (left) and after (right) applying our proposed image registration. The DW image is color-coded using a jet colormap. The top row shows the result for a slice of patient 1 from the Vienna dataset, the bottom row shows the result for a slice of patient 2 from the RIDER dataset.

4. DISCUSSION AND CONCLUSION

We presented a novel approach for aligning T2 weighted and DW MRI, which extends previous methods such as[6] by robust identification of the breast outline in the presence of artifacts and adding inner structures as features for an registration of binarized images. We subsequently apply the widely used Demon's algorithm to estimate the non-linear deformation field. The method was evaluated with two different datasets with a total of seven patients and a large number of annotated landmarks. Though the total number of patients in both datasets is limited, the initial results are promising and lead to a considerable better aligned image fusion of DW images and T2 weighted MR images. The use of two datasets with different imaging protocols shows that the proposed methods seems to work robustly.

While the methods we compared our approach to use similar core algorithms (registration by Demon's algorithm) or simple deformation models (affine transformation), the comparison showed that a non-linear deformation model, the registration of outlines and the extraction of inner structures are essential steps which improve the results of the matching. In future we will work on extension of the evaluation with a larger number of clinical cases. Depending on those results, the method may - if necessary - be extended with more sophisticated image segmentation algorithms to extract the outline of the breast and inner structures.

The proposed method especially works well in cases with large initial errors (see e.g. Figure 5 bottom row), while cases which are already aligned well are not distorted. The method may contribute to a better combined diagnosis and e.g. facilitate computer aided detection and diagnosis by enabling combination of spatially well-aligned information.

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