Automatic Correspondence Detection in Mammogram and Breast Tomosynthesis Images

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ABSTRACT

Two-dimensional mammography is the major imaging modality in breast cancer detection. A disadvantage of mammography is the projective nature of this imaging technique. Tomosynthesis is an attractive modality with the potential to combine the high contrast and high resolution of digital mammography with the advantages of 3D imaging. In order to facilitate diagnostics and treatment in the current clinical work-flow, correspondences between tomosynthesis images and previous mammographic exams of the same women have to be determined.

In this paper, we propose a method to detect correspondences in 2D mammograms and 3D tomosynthesis images automatically. In general, this 2D/3D correspondence problem is ill-posed, because a point in the 2D mammogram corresponds to a line in the 3D tomosynthesis image. The goal of our method is to detect the "most probable" 3D position in the tomosynthesis images corresponding to a selected point in the 2D mammogram. We present two alternative approaches to solve this 2D/3D correspondence problem: a 2D/3D registration method and a 2D/2D mapping between mammogram and tomosynthesis projection images with a following back projection. The advantages and limitations of both approaches are discussed and the performance of the methods is evaluated qualitatively and quantitatively using a software phantom and clinical breast image data.

Although the proposed 2D/3D registration method can compensate for moderate breast deformations caused by different breast compressions, this approach is not suitable for clinical tomosynthesis data due to the limited resolution and blurring effects perpendicular to the direction of projection. The quantitative results show that the proposed 2D/2D mapping method is capable of detecting corresponding positions in mammograms and tomosynthesis images automatically for 61 out of 65 landmarks. The proposed method can facilitate diagnosis, visual inspection and comparison of 2D mammograms and 3D tomosynthesis images for the physician.

Keywords: mammography, tomosynthesis, 2D/3D registration, template matching

1. PURPOSE

Two-dimensional mammography is the major imaging modality in breast cancer detection. A disadvantage of mammography is the projective nature of this imaging technique. Tomosynthesis is an attractive modality with the potential to combine the high contrast and high resolution of digital mammography with the advantages of 3D imaging. Despite these advantages of tomosynthesis, in the current clinical work-flow digital mammographic imaging is used routinely because of the increased irradiation doses of tomosynthesis (approx. 1.5 times to twice the doses of digital mammography) and the better signal-to-noise ratio in the mammographic images. Additional tomosynthesis images are generated in case of suspicious findings or to localize suspicious tissue in 3D prior to a biopsy or surgery. In these cases, corresponding positions in the mammograms and tomosynthesis images have to be determined. This 2D/3D correspondence problem is ill-posed, because a point in the 2D mammogram corresponds to a line in the 3D tomosynthesis image. Typically, the compression of the breast is not identical during the two image acquisitions, and algorithms have to deal with (small) deformations of breast tissue.

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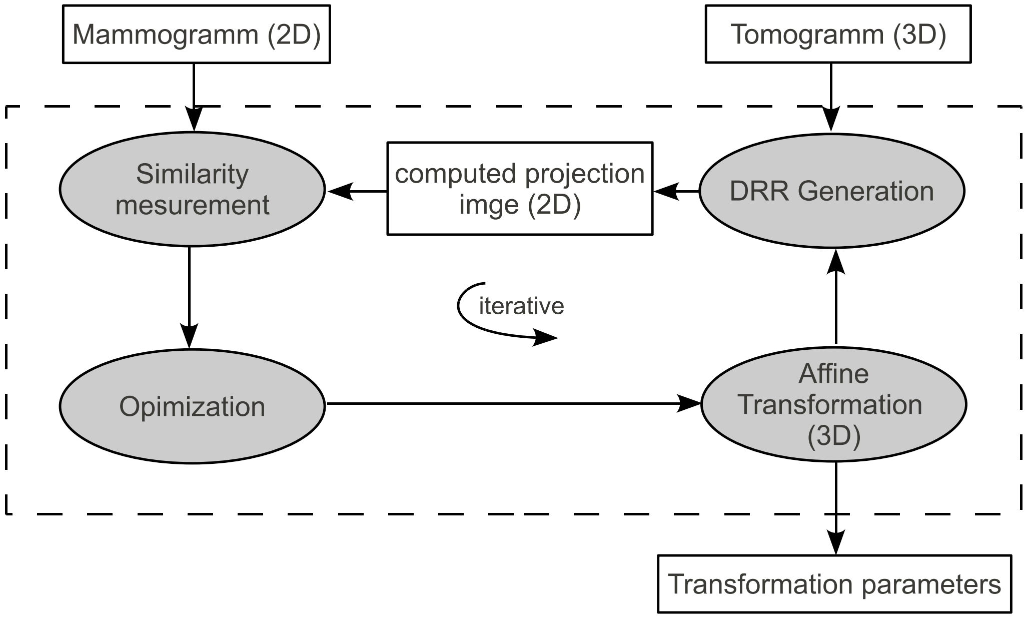


Figure 1. Iterative procedure of 2D/3D registration of mammogram and tomosynthesis image.

There are a few reported articles about the fusion of mammographic and tomosynthesis images, only. Some approaches were developed for the 2D/2D registration of mammograms in follow-up studies.[1] 2D/3D registration is used for the fusion of breast MR and mammographic images.[2] First approaches for the registration of mammographic images and tomosynthesis images are restricted to a 2D/2D registration.[3]

In this paper, we present two alternative approaches to solve this 2D/3D correspondence problem in order to facilitate the clinical work-flow. The goal of the method is to suggest a probable 3D position in the tomosynthesis image to a given 2D position in the mammogram. In the first approach, a 2D/3D registration method is used to match the 3D tomosynthesis image with the digital mammogram. The second approach combines 2D/2D registration steps and template matching techniques to find corresponding positions in the mammogram and in the tomographic projection images. The 3D localization is determined by back projecting the detected positions in the tomographic projection images.

We present first results of the correspondence detection and we discuss the advantages and limitations of these approaches. The performance of the methods is evaluated qualitatively and quantitatively using a software phantom and clinical breast image data (e.g. anonymized human breast image data acquired in clinical routine exams).

2. METHODS

Due to different compressions of the breast during the acquisition of the mammographic and tomosynthesis images, the correspondence between the two images is not given by a simple rigid transformation. Though, we assume identical directions of projection (CC, ML or MLO) for both images so that the deformations of the breast can be considered as "small".

In a first approach, a 2D/3D registration method is applied to map the two-dimensional mammograms and three-dimensional tomograms directly. In this approach, breast deformations can be simulated by deforming the 3D tomosynthesis image.

2.1 2D/3D registration of digital mammography and tomosynthesis images

The iterative intensity-based 2D/3D registration method is summarized in Figure 1. To generate a digitally reconstructed radiograph (DRR) from the 3D tomosynthesis image, an X-ray projection is simulated by using a perspective projection algorithm and ray casting.[4] An affine transformation of the tomosynthesis image is

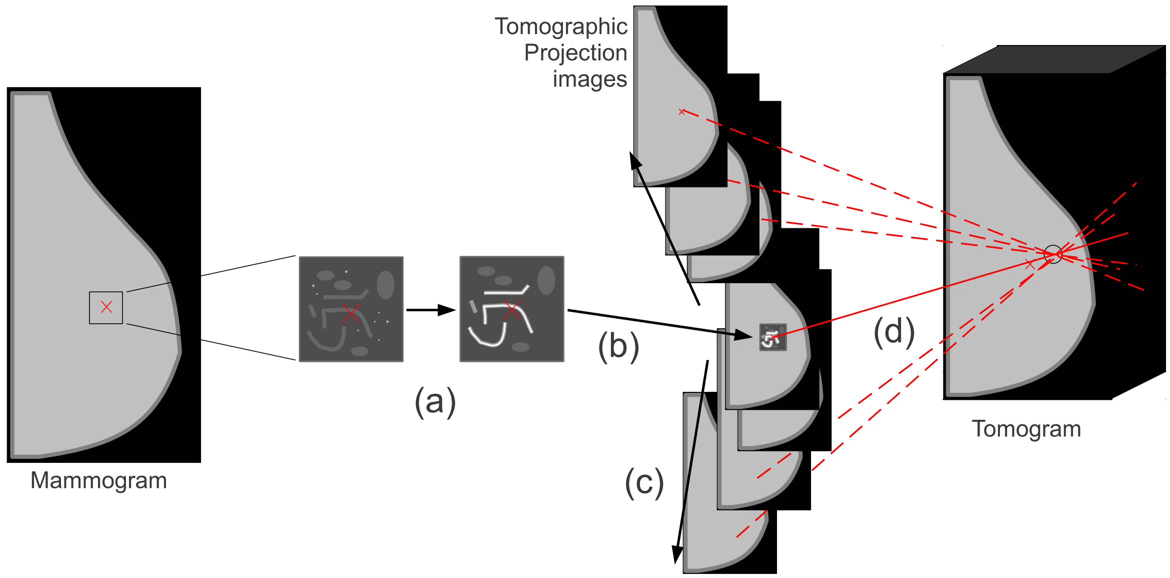


Figure 2. Procedure of 2D/2D mapping: preprocessing of mammogram and projection images (a); mapping between mammogram and central projection image (b); transfer of corresponding point between central projection image and all other projection images (c); reconstruction of 3D localization by back projection (d).

supposed to compensate the different breast positions and deformations. The deformation of the breast related to different compressions during image acquisition are approximated by applying a shear in x- and y-direction. Sum of squared intensity differences are used to compare the generated DRR and the mammogram. To match the tomosynthesis image $I_{3D} : \Omega_1 \subset \mathbb{R}^3 \to \mathbb{R}$ and mammogram $I_{2D} : \Omega_2 \subset \mathbb{R}^2 \to \mathbb{R}$ with respect to the transformation $\boldsymbol{\varphi} : \mathbb{R}^3 \to \mathbb{R}^3$ the following energy functional is minimized:

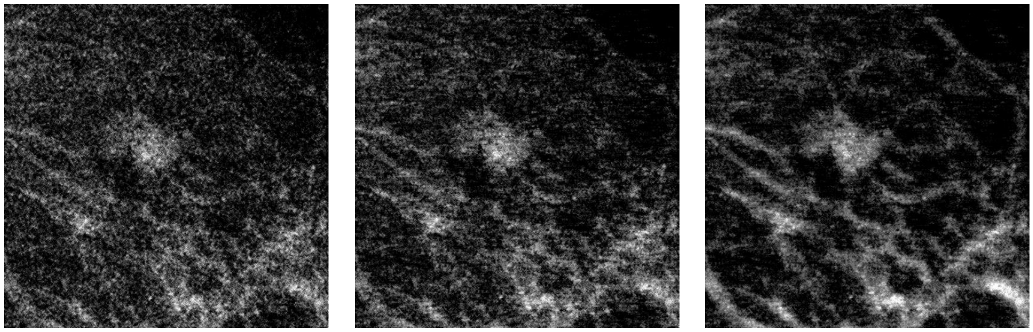
$$\mathcal{J}[I_{2D}, I_{3D}; \boldsymbol{\varphi}] = \int_{\Omega_2} \left(I_{2D}(\boldsymbol{x}) - \mathcal{H}\left(\int_0^1 (I_{3D} \circ \boldsymbol{\varphi})(\boldsymbol{s}(\boldsymbol{x}, t)\ dt) \right) \right)^2 d\boldsymbol{x}. \tag{1}$$

Here, a simplified ray casting is applied to speed-up the computation. $\boldsymbol{s} : \mathbb{R}^2 \times \mathbb{R} \to \mathbb{R}^3$ computes the 3D positions along the projection beam starting from the X-ray source and passing through the point $\boldsymbol{x}$ in the mammogram. An intensity correction is applied by the function $\mathcal{H}$ computed using histogram matching. The affine transformation $\boldsymbol{\varphi}$ is composed of a translation in x- and y-direction, a 3D rotation and a shear in x- and y-direction, where the z-axis of the tomosynthesis image is perpendicular to the detector plate. In general, more complex transformations can be used to account for soft tissue deformations, however a regularization will be necessary in eq. (1) in this case. We decided to use a simple transformation model with a small number of degrees of freedom due to the limited z-resolution of tomosynthesis images. This will be discussed in section 3.

2.2 2D/2D mapping between digital mammography and tomographic projection images

In the second approach, the tomographic projection images are used to map digital mammography and tomosynthesis data. The tomographic projection images are used to reconstruct the 3D data. The used tomosynthesis device (Siemens Mammomat Inspiration) acquires 25 projection images in an angular range of ±25 degree in a craniocaudal (CC) (or mediolateral oblique (MLO)) view. Bakic et al.[3] perform a non-linear registration between mammogram and central projection image. However, the deformation of the breast related to the different compressions can not be compensated in the projection images. Therefore, we concentrate on finding points that have been marked by an expert using a pre-registration and template matching.

Figure 2 illustrates the main idea of this approach: preprocess the mammogram and all projection images (a); determine the point of interest (marked in the mammogram) in the central projection that provides the same view angle as the mammogram (b); find that point in as many projections as possible (c) and reconstruct the three-dimensional point from the found two-dimensional points (d). These steps are detailed below.



(a) projection image (b) denoised image (c) vessel enhanced image

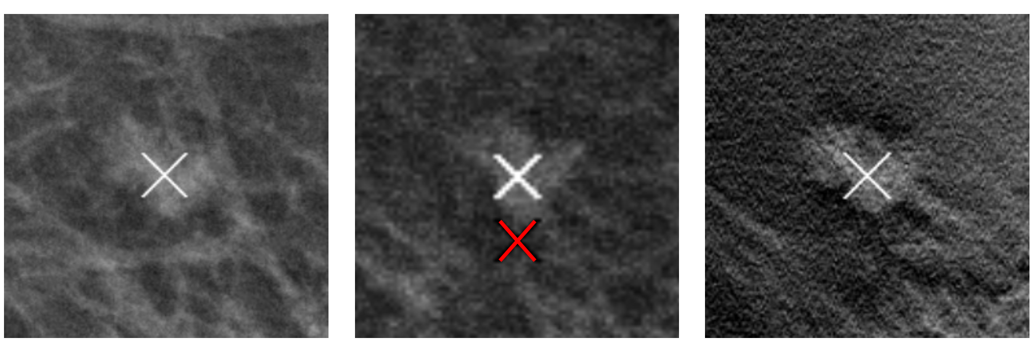
Figure 3. Preprocessing of the projection images.

Preprocessing: The projection images are denoised by a morphologic filter.[5] The mammogram and the tomographic projection images are enhanced by combining the gray value information with a multi-scale vesselness measurement.[6] Figure 3 shows the result of the preprocessing of a projection image. Furthermore, breast contours and mammilla are segmented automatically in the mammogram and in the 25 projection images.

Mapping between mammogram and projection image: To map the point of interest from the mammogram to the central projection image, the breast contours and mammilla in the images are registered using the iterative closest point (ICP) algorithm.[7] The approximate resulting position of the point of interest in the projection image is improved by using template matching to find the best matching position in a neighborhood (template size: 1×1 cm, search size: 2×2 cm).

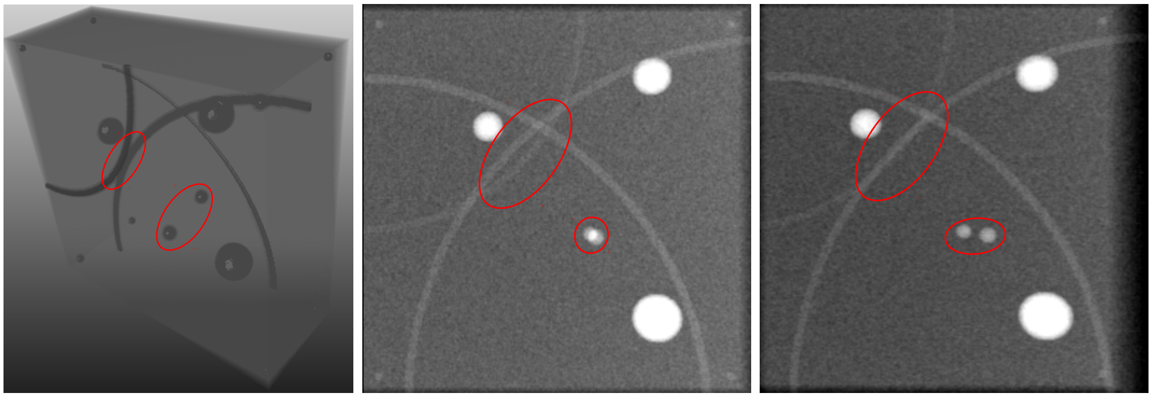
Mapping between the projection images: The marked point in the central projection image has to be transferred to the other projection images. Therefore, we use a non-linear registration between adjacent projection images. First, the ICP algorithm is applied to the breast contours to compensate the translation caused by the different view positions (X-ray source positions). A non-linear registration method accounts for the perspective changes between the projection images. In general, structures may appear or disappear and the topology may change between different projection images and a registration of such images will fail. Here, we assume that the changes between adjacent images are small and therefore a non-linear registration of adjacent images may produce valid results. We use an adapted demon algorithm[8] with deformations restricted to the y-direction, because the X-ray source only moves in that direction. The marked point in the central projection image is transferred to the other images by a concatenation of the computed transformations.

Rejection of invalid transferred points: The non-linear registration is error-prone and a well-defined correspondence does not exist between all projection images. Therefore, some of the transferred points may be invalid. A correlation-based measure is used to reject invalid transferred points in the projection images.



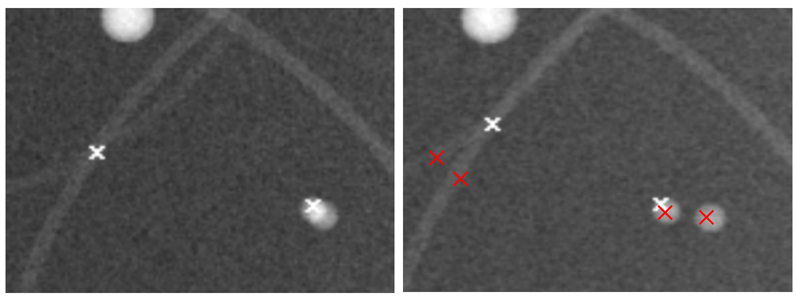
(a) mammogram (b) central projection image (c) 3D tomosynthesis slice

Figure 4. Correspondences between mammographic and tomosynthesis images: (a) user-defined point, (b) point after rigid registration (red) and template matching (white) and (c) corresponding point in the determined tomosynthesis slice.



(a) 3D software phantom (b) simulated mammogram (c) simulated central projection

Figure 5. Software phantom consisting of a 3D image with vessel- and lesion-like structures (a), the simulated mammogram is generated using a DRR algorithm (b) and the simulated central projection image generated after a deformation of the 3D volume (c). Comparing the mammogram and the resulting central projection image, superpositions of structures are visible (marked in red).



(a) simulated mammogram (b) simulated central projection

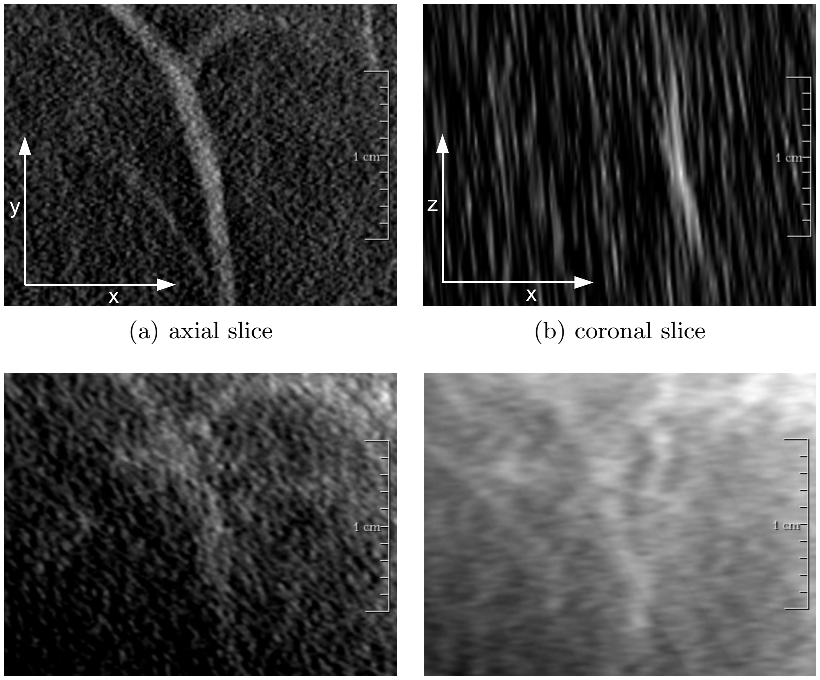
Figure 6. Results of the template matching applied to the software phantom: Two points are selected in the simulated mammogram (a). Due to the superposition of different structures in the mammogram, there is no "correct" corresponding point in the central projection image (b). Possible correspondences are marked with red crosses. The corresponding points detected using template matching are shown as white crosses. User interaction is needed to handle this intrinsic limitation of the 2D/2D mapping approach.

3D reconstruction: The remaining valid points are projected into the three-dimensional tomosynthesis data. The 3D point is located on the projection beam from the central point, because the direction of projection between mammogram and central projection image are identical. To determine the corresponding z-coordinate, the distance between the central projection beam and the back projected beams of the other projection images is computed for every slice in the 3D volume. The slice with the minimum sum of squared differences is selected as approximated z-coordinate.

3. RESULTS AND DISCUSSION

Phantom-based evaluation: For a first qualitative evaluation, a software phantom was generated consisting of a 3D image with vessel- and lesion-like structures (fig. 5). In a first step, a simulated mammogram was generated using a DRR algorithm. Then, the software phantom was deformed by applying shear transformations in x- and y-directions, simulating breast deformations in the tomosynthesis images. Comparing the mammogram and the resulting central projection image, superpositions of structures are visible (fig. 5(b) and (c)).

The 2D/3D registration approach presented in section 2.1 succeeded in matching the simulated mammogram and tomosynthesis images. This shows the capability of the algorithm to compensate moderate breast deformations. In contrast, the template matching approach (sec. 2.2) is not able to dissolve ambiguities which arise from superpositions in the deformed image (see fig. 6). This is an intrinsic limitation of this approach and we



(a) axial slice (b) coronal slice

(c) DRR projection in z-direction (d) projection after transformation

Figure 7. Limited z-resolution in tomosynthesis images. A vessel structure is visualized in axial direction (parallel to the detector plate) with high contrast and resolution (a). Due to the limited angular range for image acquisition this structure is blurred over several slices in z-direction (perpendicular to the detector plate) in the image (b). Projection image generated from tomosynthesis data using a DRR algorithm (c). Structures appear blurred in a simulated projection image after applying a shear transformation to the tomosynthesis data (d).

added the possibility of an interactive correction of the mapping between mammogram and central projection image to handle such cases. Here the user shall define the structure of interest. However, we assume small differences in the breast deformations in mammogram and tomosynthesis images, and therefore these cases should be rare. Furthermore, the template matching will fail in low-contrast regions and the user can correct interactively mis-detected points in the central projection image.

Quantitative evaluation with clinical data: Five patient data sets are used to evaluate the two approaches. Each patient data set consists of one digital mammogram (size: 2800×3518 pixel and spacing: 0.085×0.085 mm^2), one 3D tomosynthesis image (size approx. $2000 \times 3000 \times 50 - 72$ voxel, spacing: $0.085 \times 0.085 \times 1.000$ mm^3) and 25 projection images acquired in the angular range of ± 25 degree. Mammogram and tomosynthesis images were acquired using the same device (Siemens Mammomat Inspiration) and view position (CC or MLO). Information needed for the DRR algorithm, e.g. focal position, view position and tube-detector distance, were extracted from the DICOM header.

Tomosynthesis images suffer from a limited z-resolution and a reduced signal-to-noise ratio, due to limited angular range and reduced dose exposure during image acquisition. Because of the limited z-resolution, small structures and vessels are blurred in the simulated projection images when applying a shear or rotation (see fig. 7). In consequence, a 2D/3D registration does not lead to results of sufficient accuracy, because of missing details in the DRR of the transformed tomosynthesis image. Therefore the approach proves to be not suitable for presently available clinical data, although this approach is favorable from a theoretical point of view in regards to the breast deformations.

A quantitative evaluation was performed for the 2D/2D mapping approach. Two sets of corresponding landmarks were defined in the 2D mammogram and the 3D tomosynthesis image for each patient. Set 1 contains landmarks located at well-defined structures, e.g. vessel bifurcations or small lesions. Set 2 contains landmarks at clinical relevant positions, i.e. near suspicious tissue. Two different measures are used for the quantitative evaluation: point-to-line distance and point-to-point distance. Point-to-line distance computes the distance between the projection beam from the point automatically detected in the central projection image and the user-defined 3D landmark position in the tomosynthesis image. A medical expert defined a deviation of $< 5\ mm$ as sufficient for clinical use. The point-to-point distance is measured between user-defined 3D landmark position and the automatically detected 3D point found by back projection. Due to the blurring of the tomosynthesis images in z-direction a correct identification of the 3D landmark position is impossible. Therefore, differences up to 3 mm (3 slices) in z-direction are accepted as "correct". The results are summarized in table 1 and 2. The table shows that the requirements of a maximum deviation of 5 mm are fulfilled for 61 out of 65 landmark points. 51 landmarks were detected with a point-to-line distance less than 2 mm. The average point-to-line distance is 1.92 mm for set 1 and 1.71 mm for set 2. An interactive correction was necessary in 4 cases. After the interactive correction of the corresponding point in the central projection image, the back projection has detected the correct slice ($\pm$ 3 slices) in 62 cases. This result indicates a robust transfer of the corresponding point in the central projection image to the adjacent projection images and a robust rejection of invalid transferred points. In average, 12 points in the tomosynthesis projection images are used for back projection (min: 4 points, max: 18 points).

		point-to-line distance				point-to-point distance
	Set 1 #	$< 2\ mm$	$< 5\ mm$	mean distance	manual corrected	correct slice (distance $\leq$ 3 slices)
Pat. 1	9	6	8	2.58	1	9
Pat. 2	5	4	5	1.72	0	5
Pat. 3	6	3	6	2.23	0	6
Pat. 4	5	5	5	0.40	0	5
overall	25	18	24	1.92	1	25

Table 1. Quantitative evaluation of the 2D/2D mapping approach; results for landmark set 1.

		point-to-line distance				point-to-point distance
	Set 2 #	$< 2\ mm$	$< 5\ mm$	mean distance	manual corrected	correct slice (distance $\leq$ 3 slices)
Pat. 1	10	8	9	1.78	1	10
Pat. 2	5	4	5	2.23	0	5
Pat. 3	9	9	9	1.23	0	8
Pat. 4	12	10	10	1.97	2	10
Pat. 5	4	2	4	1.82	0	4
overall	40	33	37	1.71	3	37

Table 2. Quantitative evaluation of the 2D/2D mapping approach; results for landmark set 2.

4. CONCLUSION

We presented two methods for automatic correspondence detection between 2D mammographic images and 3D tomosynthesis images. A goal of this method is to support diagnostics and treatment of breast cancer by automatically selecting appropriate 3D positions in tomosynthesis images for given points of interest in mammograms.

In a first approach, we proposed a 2D/3D registration method which may compensate moderate breast deformations caused by different breast compressions in principle. However, this approach is not suitable for clinical tomosynthesis data due to the limited resolution and blurring effects perpendicular to the direction of projection.

A second approach combines 2D/2D registration, template matching and back projection to compute point correspondences in 2D mammograms and 3D tomosynthesis images. In contrast to the first approach, this method uses the acquired tomographic projection images, only, and is independent of the reconstructed 3D volume. This approach does not compensate breast deformations directly. Furthermore, the template matching will fail in homogeneous image regions. Therefore, we assume that the breast was clamped in similar positions during the image acquisitions, and that suspicious tissue appears in textured regions in the images. This means: the given 2D point shows distinct features and the breast deformation between mammogram and tomosynthesis image is small.

Small breast deformations were present in the test data, and these deformations were compensated by the local search using template matching. The quantitative results show a point-to-line distance less than 5 mm for most landmarks. The correspondence detection fails mostly for small structures with a low contrast, e.g. microcalcifications. Here, an adaptive selection of template size and search radius may improve the results. Another source of error is the non-linear registration of adjacent projection images. A regularization is necessary to ensure robustness of the registration algorithm due to a low signal-to-noise ratio. On the other hand, a strong regularization decreases the influence of small structures in the registration process and leads to an impaired matching of such structures.

In summary, the presented results indicate that the proposed 2D/2D mapping method is capable of detecting corresponding positions in mammographic and tomosynthesis images, automatically. The proposed method may facilitate diagnosis, visual inspection and comparison of 2D mammograms and 3D tomosynthesis images for the reading physician. A major objection of the presented work is the small number of clinical test cases. In future work, we will substantiate our statements about the performance of the proposed correspondence detection by analysing a larger number of data sets.

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