Automatic Point Correspondence and Registration Based on Linear Structures *

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Abstract

A novel method to obtain point correspondence in pairs of images is presented. Our approach is based on automatically establishing correspondence between linear structures which appear in images using robust features such as orientation, width and curvature extracted from those structures. The extracted points can be used to register sets of images. The potential of the developed approach is demonstrated on mammographic images.

Keywords: linear structures, feature matching, image registration, medical imaging.

1 Introduction

Automatic landmark correspondence [1] within two or more views is a well known problem in computer vision and it is present in a large range of applications such as medical imaging [2], remote sensing, stereo-vision and robot navigation. In medical images, and more specifically in mammography, there is no agreement on a definition of robust landmarks when comparing two mammograms of the same patient. This paper presents a novel method to establish image correspondence in mammographic images based on matching their major linear structures (e.g. ducts and vessels) which we believe are reliable landmarks as they appear in both mammograms.

The problem of establishing line correspondence in mammograms involves various steps: 1. to identify linear structures in both mammograms (see section 2), 2. to extract reliable information from those structures (see section 3) and 3. to obtain correspondence between the structures based on the best matching of the information previously extracted (see section 4). Once matching points have been detected, we are able to register both mammograms using a point based method like thin plate splines [3]. The matching algorithm is developed using a multi-scale approach in order to obtain more robust registration (see section 4).

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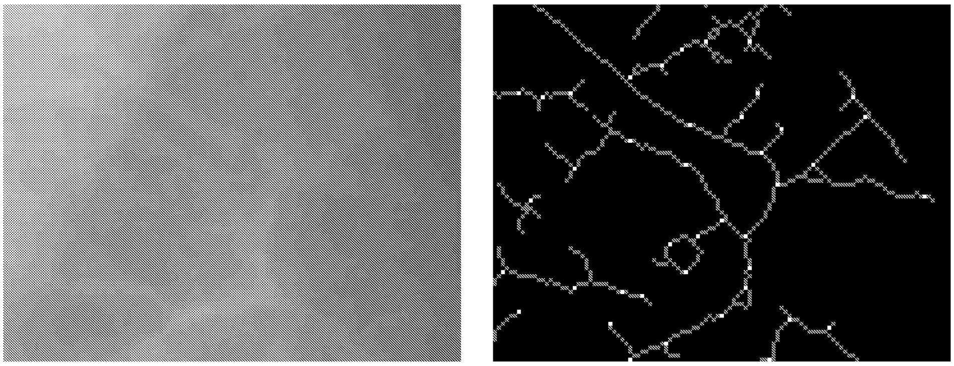
2 Detection of Linear Structures

We use a non-linear line operator [4] to detect linear structures in both mammograms. Once strength, direction and scale information have been obtained we perform different operations to facilitate the feature extraction process. First, we set a conservative threshold on the line strength image in order to remove background noise. Then non-maximum suppression [5] is applied which removes pixels with low intensity values compared to their neighbours along the normal of the linear structure. The line strength image after non-maximum suppression will be used to extract the width of the linear structures in the feature extraction section. Finally a thinning operation will obtain the backbone of the most representative linear structures in the mammograms.

3 Feature Extraction

After obtaining the salient linear structures in both mammograms, feature extraction is needed in order to obtain descriptors of the structures to be used in the matching process. Therefore, registration results will strongly depend on the reliability of the extracted features. Features used in the literature include line strength (contrast) [6], line width [6, 7], line length [7], orientation [6, 7], curvature [8], corners [9], crossing points [8] and end points [6, 7, 8]. Corresponding linear structures in two mammograms can present large differences related to line strength and line continuity (due to different radiation exposure and breast compression) but width and orientation of the line and local curvature and branching points are more likely to be preserved and often are features used by radiologists when comparing mammograms. Therefore, features which take line length, end points and line strength into account turn out to be unreliable features to tackle the correspondence problem. In this paper we use local features such as curvature, width and orientation. The basic idea of our method is to extract characteristic points of linear structures determined by their high global curvature and maximal curvature within a local neighbourhood along the linear structure. An example of such points is shown in figure 1.

Curvature values at each pixel are obtained with a similar approach as used in [8]. Curvature (or directional change) at a pixel p is defined by the scalar product between the normal vector of p and its neighbouring pixels. Position, orientation and width are then extracted from those points and used in the matching process. Orientation is obtained directly from the thinned linear structures. Width is extracted after non-maximum suppression of the line strength images as described in section 2. The width of a linear structure at a point is given by the number of pixels along the normal of the structure until a non-structure pixel is found.



(a) (b)

Figure 1: Curvature points of a linear structure: (a) original mammogram and (b) extracted linear structures (in grey) and curvature points (in white).

4 Matching

The matching process of two sets of feature points needs to consider the following assumptions:

- Non-rigid motion: linear structures in mammograms suffer local distortions, therefore they may move independently and no geometrical relationship is established between neighbouring structures.
- Multiple matches: a linear structure in one mammogram can match more than one structure in the other mammogram, and vice versa.
- Non-bijectivity: a linear structure in one mammogram may not have a corresponding linear structure in the other, and vice versa.
- Localisation: After global breast misalignment is removed, matched linear structures lie in approximately the same area in both mammograms. We will refer to this area as the localisation area M.

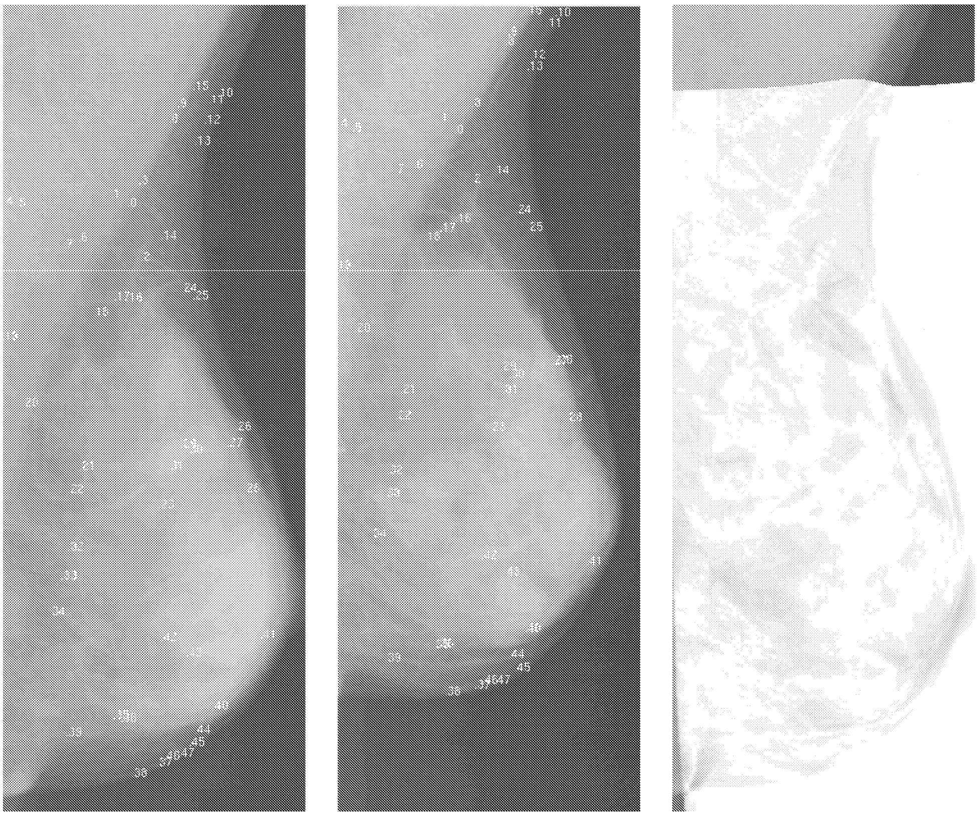
We adopt here a similar but more general approach than the one used in [10]. We denote the set of feature points from both mammograms, as $\{a_i | 1 \leq i \leq N_i\}$ and $\{b_j | 1 \leq j \leq N_j\}$, where N_i and N_j are the number of feature points used, which may not be the same. Subsequently, we build a distance matrix (DM) in which each position $DM(i, j)$ describes the normalised distance between features of points a_i and b_j. Hence, a low value means good matching between points. The use of the distance matrix structure fullfills the first three assumptions: independent motion (matched points a_i, b_j do not imply matching a_{i+1}, b_{j+1}); a point a_i may have multiple matched points b_j; and a point in either mammogram may remain unmatched.

Satisfying the last assumption, localisation, position $DM(i, j)$ will be updated only if points a_i and b_j lie in the same localisation area in both mammograms. This assumption can only be stated if both mammograms are globally aligned, that is, global deformation (i.e. rotation, translation, scale and shear) is removed. Therefore, we initially register mammograms maximising a mutual information measure using an affine transformation [11]. The final normalised distance between two points is obtained by linear combination of various normalised distances: Euclidean distance between points (after performing the global registration mentioned earlier), orientation change and width difference.

A multi-level approach is used here to ensure a spread of control points over the whole image and to improve the accuracy of the registration process. At the first level, we register the full images obtaining the transformation parameters α_1. Subsequently, we move to the second level dividing each mammogram in six rectangular sub-images and again align each sub-image to its corresponding sub-image. Note that transformation parameters are carried through each level, assuming that each sub-image at lower levels would suffer a different transformation but it would be related to the deformation on the higher level. Assuming this, we speed up the optimisation process as well as avoiding local minima situated away from the optimum solution. Once the last level i is reached, transformation parameters α_i in each sub-image on that level establish a correspondence area for structures within each sub-image. In addition, extracting the local best matches in each sub-image assures that a minimum number of matches will be present in each sub-image, having an homogeneous point distribution over the whole mammogram.

5 Results

In this section we present initial results using our described approach applied to mammographic images. Figure 2 shows two mammograms of the same patient taken three years apart where matches between the linear structures are indicated by numbers. Matched points can be used as control points to register mammograms using a point based method such as thin plate splines [3]. Figure 2c shows the subtracted image (where darker areas mean larger misalignment) obtained after automatic registration using the proposed method. Although misregistration can be observed near the breast outline, registration of internal breast regions is comparable to manually placement of control points. Figure 3 shows registration results of temporal (same breast taken at different times) and contralateral (right-left comparison) mammograms. Graphs are obtained measuring normalised mutual information between reference and registered images. A high value denotes high similarity between images, therefore good registration. Graph results show that automatic registration performs equally or slightly better in most cases, although some poor results are also obtained. These are due to specific breast characteristics such as the lack of major linear structures (mammograms 4 and 5 in figure 3a) or large deformation (mammograms 15 and 16 in figure 3b).

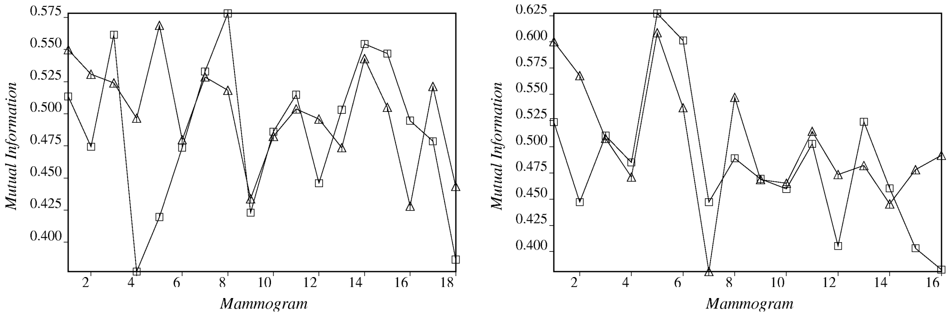


(a) (b) (c)

Figure 2: Correspondence between linear structures in temporal mammograms: (a) reference image (b) warped image (c) difference between registered image and reference.

6 Conclusion

The work presented here describes a novel approach to solve the problem of extraction of reliable features in mammographic images and establishes correspondence between them in pairs of mammograms. We have shown that features extracted from linear structures can provide a robust automatic approach to the generation of control points for image registration. Features based on scale, orientation and position have been used. Initial results based on a temporal and contralateral comparison look promising. But further work will be needed to establish the full benefit of our approach, including testing on a larger mammographic dataset and further evaluation will be needed. In addition, other features could be incorporated such as breast boundary and the position of the nipple.



(a) (b)

Figure 3: Registration results for (a) temporal and (b) contralateral experiments where automatic registration (□) using the proposed method is compared to manual registration (△).

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