Tracking Mammographic Structures Over Time

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Abstract

A method to correspond linear structures in mammographic 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 resulting correspondence is used to track linear structures and regions in mammographic images taken at different times.

1 Introduction

Medical image analysis [1] has been an important research subject in recent years where computer vision techniques have been successfully applied to develop detection and diagnosis systems, enhancement and training tools. The analysis of mammographic images is one of those fields and as such a very challenging one due to the complexity of the images and the subtle nature of the abnormalities.

Detection of abnormal structures or architectural distortions in mammographic images can be performed by analysing different images of the same patient. Various approaches have been adopted which bring images into alignment in order to detect differences which are likely to be due to an abnormality. A large number of those methods are based on automatically corresponding extracted landmarks from mammographic images. Those landmarks include breast boundary [15, 20, 9], pectoral muscle [9], salient regions extracted using wavelets [14], iso-intensity contours [11] or steerable filters [20] and crossing points of horizontal and vertical structures [22].

This work presents an approach to the correspondence in mammographic images based on anatomical features which appear as linear structures in the images. The correspondence is used here to track linear structures in mammograms of the same patient over several years. Tracking of linear structures could be used to assess and model the development of architectural changes and abnormal structures. By being able to track regions back in time the available information will help to improve early detection of subtle abnormalities which are initially missed by radiologists.

The tracking of objects in image sequences is a well-developed area [21]. However, in general this involves rigid objects (like cars [8]) or objects with a predictable behaviour (like humans [10] or animals [18]). Another difference with the current application is the fact that normally tracking is established using sequences of tens to hundreds of images and not only a few.

2 Problem Definition

The problem of tracking linear structures in mammograms involves various steps: 1. to identify linear structures in mammograms (Section 3), 2. to extract reliable information from those structures (Section 4) and 3. to obtain correspondence between the structures (Section 5). Detection of linear structures is performed using a multi-scale non-linear operator [7]. Detected lines are processed to obtain the major linear structures in each mammogram. Subsequently, features such as orientation, width and curvature are extracted and used by a matching process to find correspondence between points. From those points, linear structures are identified and tracked through various images of the same breast taken at various screening years. Figure 1 shows an overview of the proposed method.

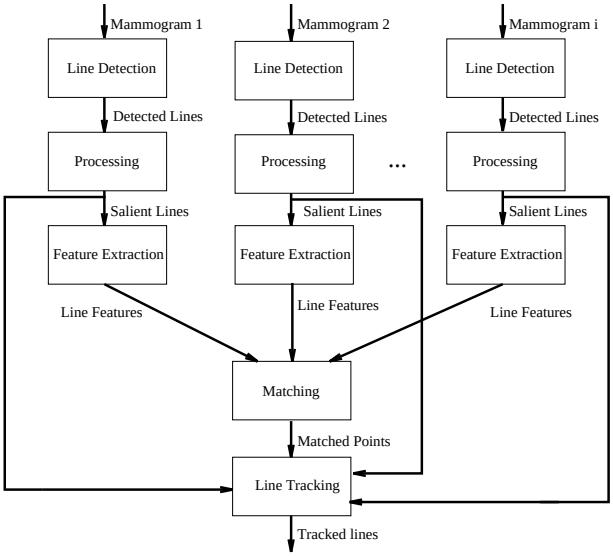


Figure 1: Overview of the proposed method.

3 Detection of Linear Structures

Initially mammograms are segmented in order to extract the breast region where a line detector will be applied as described in [16]. We use a non-linear line operator [7] to detect linear structures. At a given scale, the line operator provides for every pixel a strength and orientation of the linear structure. Then different operations (threshold, non-maximum suppression and thinning) are applied in order to obtain the backbone of the major linear structures. Figure 2 shows an example of the detected major linear structures in a mammogram.

(a) (b)

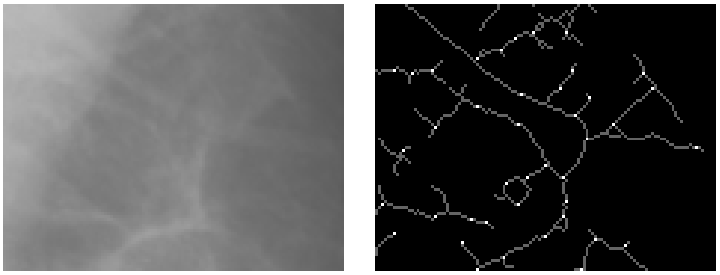
Figure 2: Detection of linear structures: (a) original mammogram and (b) detected major linear structures.

4 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) [17], line width [17, 5, 12], line length [5], orientation [17, 5, 12], curvature [19, 6], corners [4, 13], crossing points [6] and end points [17, 5, 6].

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 features such as orientation and width from points determined by their maximal curvature within a local neighbourhood along the linear structure. Maximum curvature points are likely to be characteristic for a linear structure in terms of local curvature and branching points. Example of such points are shown in Figure 3.

Curvature values at each pixel are obtained with a similar approach as used in [6]. Curvature (or directional change) between two pixels p and q is defined by the scalar product of their normal vectors. Hence, the curvature measure of a given pixel p is obtained by



(a) (b)

Figure 3: Curvature points of a linear structure: (a) original mammogram and (b) extracted linear structures (in grey) and curvature points (in white).

computing the scalar product between p and its neighbouring pixels.

$$C_p = \frac{1}{N} \sum_{i=1}^{N} \exp(-d_{ip}^2)(1 - \cos(\phi_p - \phi_i)) \quad (1)$$

where ϕ_i is the angle of the normal at each pixel i. As we will be extracting curvature from binary thinned images, we assume unit vectors. N is the number of points in a local neighbourhood and d_{ip} is the Euclidean distance between points i and p. The distance factor is used here to weight the curvature of each point i, in order to incorporate a bias for points closer to p.

5 Matching

Matching two sets of feature points is a common problem in computer vision. To minimise computation time different approaches have been used such as chamfer matching [3], iterative closest point [2] and relaxation based approaches [17, 5]. However all the above methods make assumptions which are not applicable to our matching problem (i.e. rigid movement and geometric relationship between structures).

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; the localisation area M.

We adopt here a similar but more general approach than the one used in [22]. 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.

5.1 Feature Distances

Satisfying the last assumption, localisation, position $DM(i,j)$ will only have a finite value if points a_i and b_j are 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.

The normalised distance between feature points (a_i, b_j) is determined by three components: The first distance is the Euclidean distance (D_E) between point coordinates normalised using the diameter of the localisation area (M). Coordinates of one of the points are transformed (T_α) using the parameters obtained from the global alignment mentioned earlier. The second distance is the orientation difference between two points (D_ϕ), similar to the curvature definition in Equation 1. The third distance is the width difference between two points (D_w) normalised using the maximum width of all the linear structures (W). The normalised distance is given by

$$\begin{aligned} DM(i,j) &= D_E + D_\phi + D_w \\ &= \frac{|T_\alpha(a_i) - b_j)|}{M} + \frac{1 - \cos(\phi_i - \phi_j)}{2} + \frac{|w_i - w_j|}{W}. \end{aligned} \tag{2}$$

6 Tracking

Matched points obtained in the process described in the last section are used to identify and track linear structures in sequences of images. Corresponding linear structures are those structures which contain common matched points as shown in Figure 4. For example, control points 12, 13 and 21 match the same linear structure, although broken in (a), but not in (b). Linear structures in grey do not contain any control points, therefore remain unmatched (note that these are likely to be small structures).

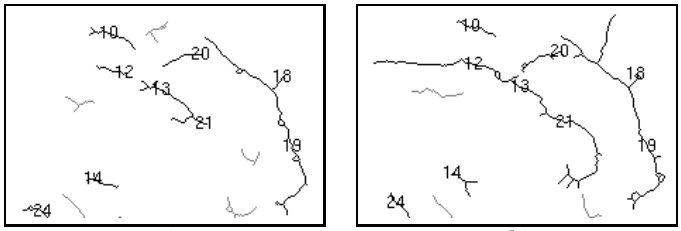
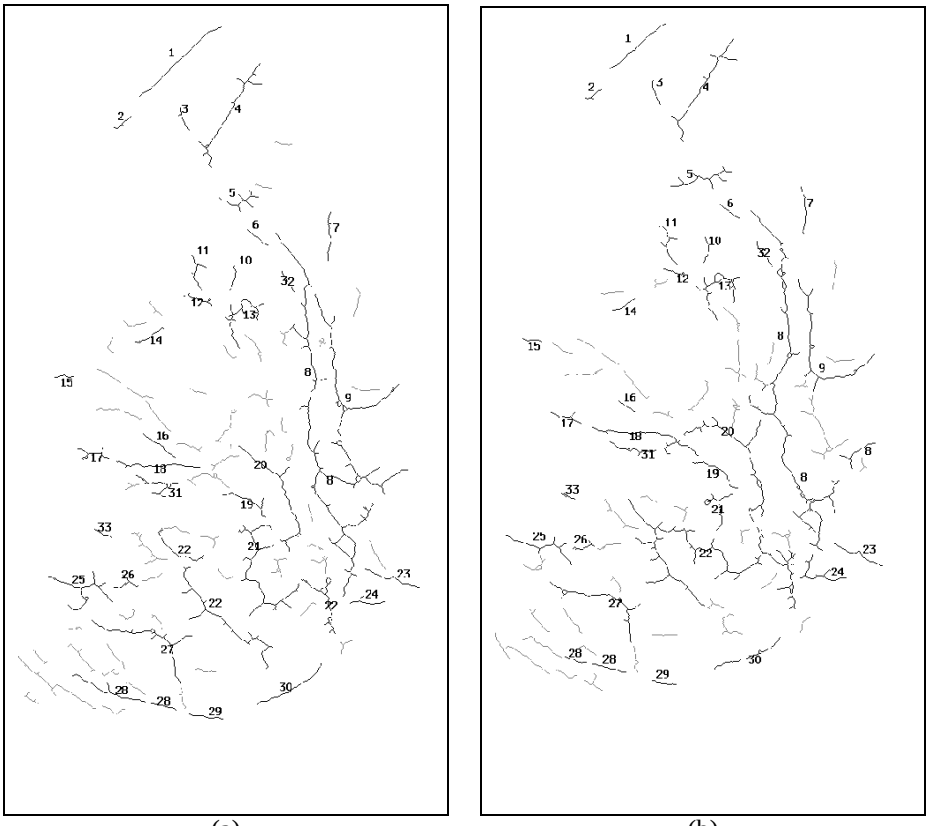


Figure 4: Tracking of linear structures: Matched points (numbers) and matched linear structures in two mammograms.

The proposed tracking method is tested using mammographic images. Figure 5 shows tracking between the mammogram of Figure 2 and a deformed version of it (the defor-

mation has a local nature and is based on registration between screening rounds), where numbers depict corresponding linear structures. This indicates the local movement of the linear structures. Due to line fragmentation, linear structures in one image may correspond to more than one linear structure in the other. This explains the repeated numbers in Figure 5. It can be seen that major linear structures have been successfully identified and tracked.



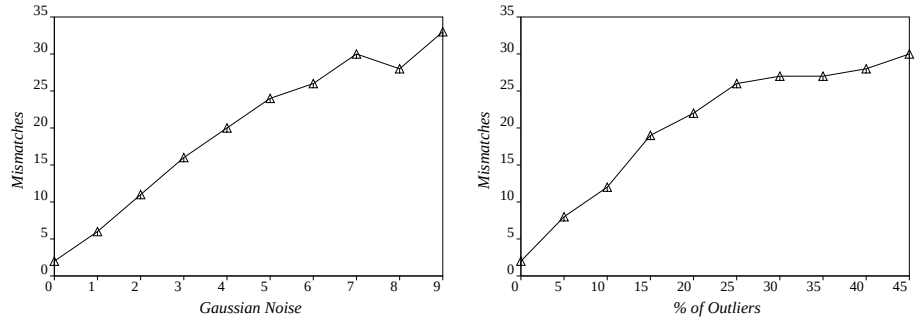
(a) (b)

Figure 5: Tracking of linear structures: (a) original and (b) deformed mammogram.

Using the example of Figure 5, we test the robustness of the tracking algorithm in the presence of noise and outliers. Evaluation has been carried out counting the number of matching errors found in the images. It should be noted that a matching error does not mean that both corresponding structures are completely mismatched, as we are matching linear structures, not only points. Therefore the number of matching errors and the number of matches are not related.

Figure 6a shows the number of matching errors found in the images when different amounts of Gaussian noise ($N(\mu, \sigma)$) are added to the feature points. At each plotted point in Figure 6a noise is affecting all features: position with $N(0, 20)$, orientation with $N(0, \pi/6)$ and width with $N(0, 10)$. It should be noted that noise for each point is added to the previous noise level and the graph presents a linear behaviour which denotes the

robustness of the method. Another test has been performed to determine the dependence of the method on the presence of outliers. Outliers are defined here as matched points which are not related to major mammographic linear structures, most of the time these are due to noise, image artifacts or spurious structures. Outliers have been generated using the following method: A number of initially extracted feature points have been randomly removed and replaced by the same number of randomly generated points. Figure 6b plots the number of matching errors as a function of the percentage of those outliers. Again, the response presents a linear behaviour even with a large percentage of outliers.

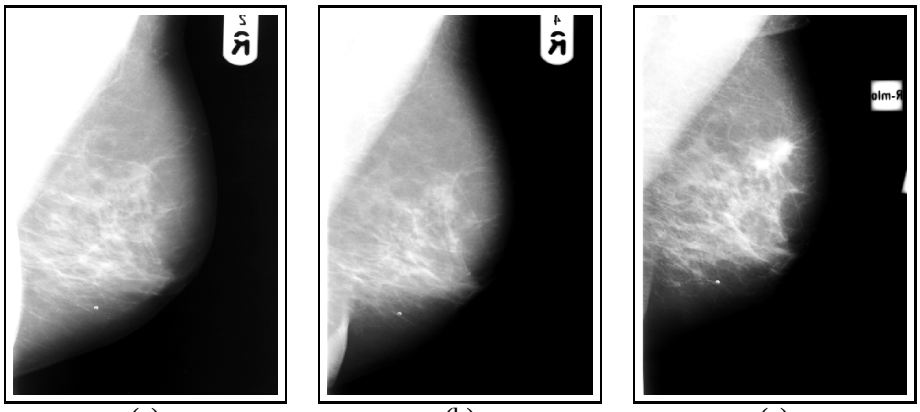


(a) (b)

Figure 6: Evaluation of the tracking of linear structures: (a) Gaussian noise added to feature points and (b) presence of outliers.

7 Results

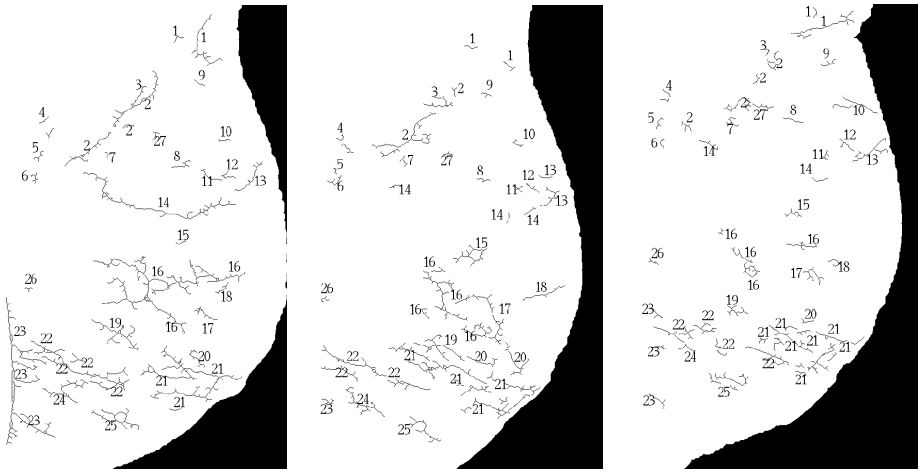
This section presents initial tracking results. Figure 7 shows three mammograms taken at different screening rounds (with approximately three years time between each one) where an abnormality has been diagnosed in the last screening round.



(a) (b) (c)

Figure 7: Mammograms from various screening years: (a) 1992, (b) 1995 and (c) 2000.

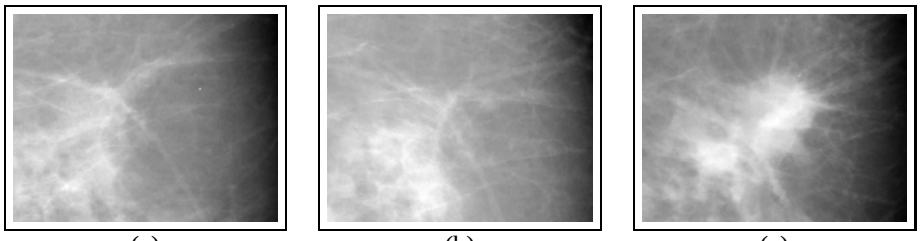
Figure 8 shows the tracking of linear structures in the mammograms of the Figure 7. It can be seen that tracking results are not as good as in the test image in Figure 5, but major linear structures are still being tracked. It should be noted that the abnormality occurs in an area which does not contain a large number of mammographic linear structures.



(a) (b) (c)

Figure 8: Tracking of linear structures in mammograms from various screening years: (a) 1992, (b) 1995 and (c) 2000.

In addition, using tracking results from the linear structures, regions of interest can also be tracked over time. Correspondence between linear structures is used here to align mammograms in order to track a region of interest, in this case the abnormal region. Alignment is further described in [16]. In Figure 9 a small region containing the abnormal structure within the mammographic sequence is shown. This shows that the abnormality is only present in the final year with no mammographic evidence in earlier screening rounds.



(a) (b) (c)

Figure 9: Tracking of an abnormal region in mammograms from various screening years: (a) 1992, (b) 1995 and (c) 2000.

8 Discussion

Tracking results depend on a satisfactory line and feature detection, which is not straightforward to achieve due to different and uncontralable imaging conditions (breast compression, radiation exposure, patient movement). Other line detection methods and also image normalisation approaches could be investigated. Linear structures appear to be non-uniformly fragmented over the images. Line linking algorithms could be applied, but special care has to be taken in choosing the linking criterion due to complex geometry of the linear structures. Statistical modelling of the tracked abnormal regions over time can be used to assess the subtle presence of abnormalities in early screenings.

9 Conclusion

The work presented here describes an approach to solve the problem of extraction of reliable features in mammographic images and establishes correspondence between them in sequences of mammograms. Local features based on scale, orientation and position have been used. Results show that tracking of linear structures over time in mammographic images is feasible and can provide valuable information regarding changes in the breast structure and can be used to asses the development of structural abnormalities. Future work will be focused to further assess the proposed method using various datasets and to apply it to detect and track abnormalities over time using the information extracted from the linear structures. In addition, it is our aim to incorporate information from other modalities and extend the method to 3D data.

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