ORIGINAL RESEARCH

Shape localization, quantification and correspondence using Region Matching Algorithm

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ABSTRACT

We propose a method for local, region-based matching of planar shapes, especially as those shapes that change over time. This is a problem fundamental to medical imaging, specifically the comparison over time of mammograms. The method is based on the non-emergence and non-enhancement of maxima, as well as the causality principle of integral invariant scale space. The core idea of our Region Matching Algorithm (RMA) is to divide a shape into a number of "salient" regions and then to compare all such regions for local similarity in order to quantitatively identify new growths or partial/complete occlusions. The algorithm has several advantages over commonly used methods for shape comparison of segmented regions. First, it provides improved key-point alignment for optimal shape correspondence. Second, it identifies localized changes such as new growths as well as complete/partial occlusion in corresponding regions by dividing the segmented region into sub-regions based upon the extrema that persist over a sufficient range of scales. Third, the algorithm does not depend upon the spatial locations of mammographic features and eliminates the need for registration to identify salient changes over time. Finally, the algorithm is fast to compute and requires no human intervention. We apply the method to temporal pairs of mammograms in order to detect potentially important differences between them.

Key Words: Region matching, Shape matching, Occluded shapes, Aligning shapes, Temporal changes, Mammograms

1. INTRODUCTION

Shape matching is a key issue and an established area of research in computer vision. In our previous work we have noted that shape description using Integral Invariants (II) yields signatures that are invariant to articulations and bending, and which are robust to noise. Geometric invariants, which are invariant under affine, Euclidean, or similarity transformations, may be used to describe shapes. Shape matching is a particularly challenging problem in medical image analysis, most often for pairs of images of the same patient taken at different times. Such image pairs may show differences that are the result of illness, response to therapy, or, more prosaically differences in the imaging conditions. Projective invariants may help with many small changes; but cannot deal with complete or partial occlusion of articulations of the shape which are frequently diagnostically important to take into account. For example, irregular change in the sizes of nuclei in Fine Needle Aspiration (FNA) may suggest the presence of malignancy. Image registration techniques have previously been used to address this issue.[1,2] Registration techniques, both rigid and non-rigid, yield a dense warp map that establishes correspondences between all pixels inside a shape and focuses on shape retrieval and matching instead of quantifying regions at a local level. Other tech-

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niques require a "shape space", which depend on training data to enable comparisons.[3] These approaches aside, there appears to have been little or no research aimed at identifying and quantifying new growths and partial occlusions by comparing two planar shapes regardless of scale, spatial variations, and orientation. This is the problem that we address.

The first step in comparing two shapes is to align them by identifying key points. The alignment of curves and matching of shapes is discussed in Ref.[4] based on local curvature information, and often produces good results. However, curvature, being a second derivative, is intrinsically susceptible to noise. Our algorithm imposes a metric based on circular II[5] on a shape, which, in combination with a scale space analysis,[6] enables us to obtain descriptive information and key points, then divides the shape into a number of regions based on those key points. II are used for shape matching in Ref.[5] In that work, dynamic programing and Fast Marching Algorithms are used to match shapes and to establish point-wise correspondences between them. Those studies neither detect nor quantify changes in shapes. This paper presents a method that does not depend upon a (computationally expensive) optimization algorithm. Instead, we compare shapes as closed planar contours with no self-interactions between them. We use circular II to describe the shapes. II are descriptors that robustly define edges, corners and peaks, thus delineating salient regions in the shapes that we use to subdivide them, again using II scale space.

Background

We assume that a shape describes a single entity in the form of a closed contour.[3–9] Shape description defines an anatomical structure at several scales of observations. A comprehensive overview of shape representation with respect to application categories is given in Refs.[6,9] A brief list is recalled in Figure 1.

Contour-based shape descriptions are reported extensively in Refs.[4,5] For example, B-splines have been used to represent shapes and to match them.[10–15] Chain codes are an effective shape representation, especially for coding;[16] however, as they are sensitive to discretization errors in rotation and scale, they are rarely used to match shapes. The most widely used methods to describe shapes are based on curvature.[17,18] This can work well and also has an extensive basis in mathematics.[9,19,20] In practice, the main disadvantage of using curvature, which is a differential invariant, is that its measurement is highly sensitive to noise. II, which are fundamentally related to differential invariants, can be used effectively for shape representation[21] and reconstruction,[22] and are robust to noise.[21,23,24] Al-Kadi *et al*. also measured feature robustness under noise presence in medical images and is reported in Refs.[25–27] II outperform differential invariants[28,29] for invariance to small perturbations in shapes. Circular II is a structural approach that describes a shape in a unique way,[30] as do conic II.[22] Structural invariants are known to deal with partial occlusions and partial matching of shapes, which further emphasizes their importance in medical imaging.

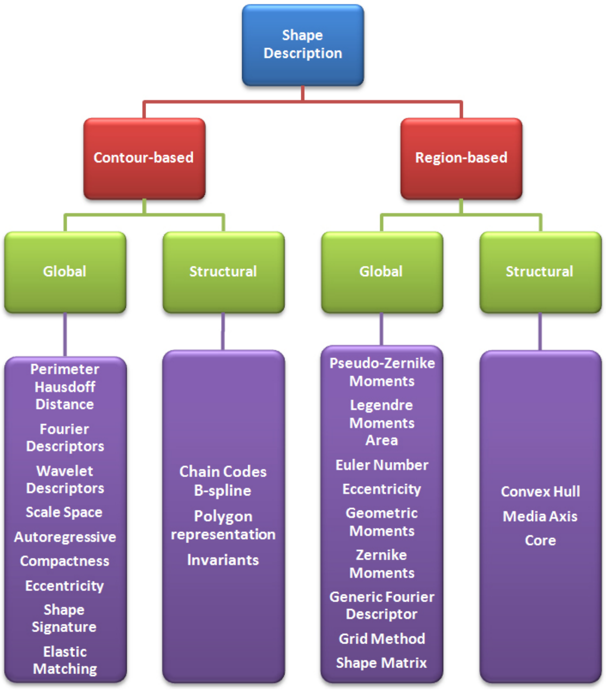

Figure 1. A list of the most popular shape analysis methods proposed to date, together with their classification (mostly described in Ref.[6])

2. METHODS

Various methods are discussed briefly to cover the breath of the subject, which relates to a huge body of literature that further amounts to variety applications. As mentioned earlier our method is based on the II scale space, which is inspired from Ref.[24] and eventually provides the basis for the RMA that we develop.

2.1 Approaches to match shapes

Typically, point-wise correspondences are established to match shapes based on intrinsic statistical properties found by anatomical modelling or by computing a matching cost for the points on the boundary.[31,32] Landmarks are generally identified in two shapes using a certain descriptor,[33] for example with genetic algorithms,[34] Eccentricity transformations,[35] phase congruency,[36,37] differential methods[17,18,38] or II. Descriptors that represent a shape as a transformation, such as Fourier components,[39] highlight salient features in a shape at the cost of suppressing deformation and ignoring translation or rotation.[35] Techniques[36,40–44] that establish a dense correspondence between shapes by embedding 2D or 3D shapes in a canonical domain usually fail to deal effectively with shape articulations. Indeed, the fact that they preserve geodesic distances,[45–47] phase angles and other structural features, makes it difficult to cope with isometric deformations, such as bending.[48,49] Other techniques involve shape appearance in descriptions, such as shape skeletons,[50] graph matching,[51–54] contour flexibility,[55] Laplace spectra,[56] partial differential equations[57,58] and the rolling penetrate descriptor.[58] Histogram geometry[56] has also been evaluated to subdivide shapes into parts using topographic features and then to register them.

Sebastian[59,82] presented an alignment criterion which compares one curve to another, one of which is considered to be the model curve. Dijkstra's algorithm was used with encouraging results to correspond points on the two shapes.[18] Other studies[60,61] confirmed its efficiency in matching visual parts and shape contexts. However, the method suffers from the "city block" problem and sub-pixel accuracy, which has subsequently been improved[62] using the Fast Marching Algorithm.[63–65] Other effective methods to match shapes include: Eccentricity transforms,[35,66–68] Skeletonization,[69,70] dynamic programing,[32] Fast Sweeping Algorithm,[71,72] Ant Colony Optimization,[73] Bee Colony optimization,[74–76] and Bending invariants.[77,78] Comprehensive surveys of shape matching techniques with respect to local correspondence can be found in Refs.[79–81]

A descriptor is called an invariant if it can accommodate a certain shape transformation class.[82] A projective transformation, from the set of transformations known as the projective group, is widely used in computer vision. Transformation groups or group actions are tools to generate application-specific invariants[36,83–91] and are central to invariant theory.[9,92] Invariants can be algebraic;[82,93–95] geometrical[83,96] combinations of coplanar points or planes;[94,95,97–103] differential[20,36,104–110] or Integral.[21,29,111,112] Since algebraic and geometric invariants are defined for the whole shape rather than boundary, and since differential invariants are very sensitive to boundary noise, we use circular II that are relatively robust to boundary noise. In this paper, we refer to circular II simply as II. At first glance, II are similar to the SUSAN feature detector,[113] which has been used in a variety of applications[114–120] and reproduced with various enhancements.[120–123] However, the fundamental limitation of SUSAN, which renders it far less relevant in our application, is the assumption of homogeneity in a circular region. Medical images, especially mammograms, are at best piecewise homogeneous. Various shape signatures have been proposed;[21,30,93,112,124,125] however, none of them quantify changes in regions while matching shapes. This is what distinguishes our method.

2.2 Circular II

Many *et al.*[24] applied circular II for shape matching. They showed that it can robustly handle occluded shapes. Despite its simplicity, it gives a unique shape description, which we have previously exploited for region matching and shape correspondence. It has properties of non-emergence and non-enhancement of extrema in a linear fashion. It has also been used for image enhancement and noise suppression.[126] II is similar to Gaussian smoothing in terms of implementation, though it has very different diffusion and related properties.

II is defined[24] by considering a disc B_r(p) of radius r applied to every point p of a closed contour γ, parameterized to n points. The representative function that evaluates the intersection of the disc B_r(p) and the contour γ is as follows:

$$\chi(B_r(p),C)(x)=\begin{cases}1 & if \quad x\epsilon\,\{B_r(p)\cap\bar{\gamma}\}\\ 0 & \quad otherwise\end{cases} \tag{1}$$

Where $\bar{\gamma}$ is the interior of the curve. The local integral area $I_r(\gamma)$ of the curve is given by the function I^r_γ(p) at every point p ϵ $\bar{\gamma}$ with integral kernel χ as follows:

$$I^r_\gamma(p)=\int_{B_r(p)\cap\bar{\gamma}}^{n}dx \tag{2}$$

The range of I^r_γ(p), is a positive real and spans the interval from zero to the area of the curve bounded by the disc.

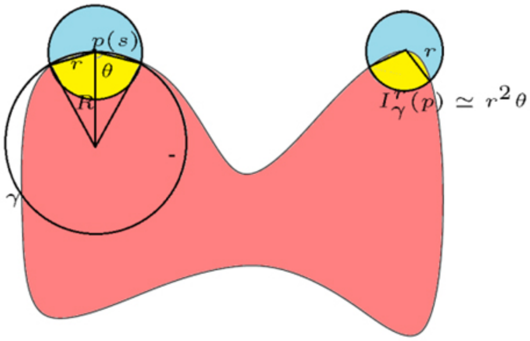

Figure 2. Integral Invariant defined in Eq-2 and explained in Ref.[24]

In the above equation Ω is the domain of the curve C. Figure 2 illustrates II as discussed in Ref.[21] and given by Equation 2. Changing the size of the II kernel creates a scale space, and which does not amplify noise. Rather it suppresses noise; however, at the cost of image details, which is an inevitable consequence of smoothing. In Figure 3, the value of the II for shape description occurs when the circle is centered not on a point along the curve but near to it, so that the circle overlaps the pink region. II have a strong and unique expression for encoding shapes and is closely related to curvature functions. In one sense, it is a weighted reciprocal of curvature, where the II shape description is almost a vertically flipped version of the graph generated by curvature. However, curvature is based on differential derivatives which are sensitive to noise,[128] though there is also a less popular way to compute II from differentiating area invariants.[12] A comprehensive mathematical evaluation of projective curvature and II is explained in Ref.[129] and with applications in Ref.[130] Circular II are referred to as II throughout this paper.

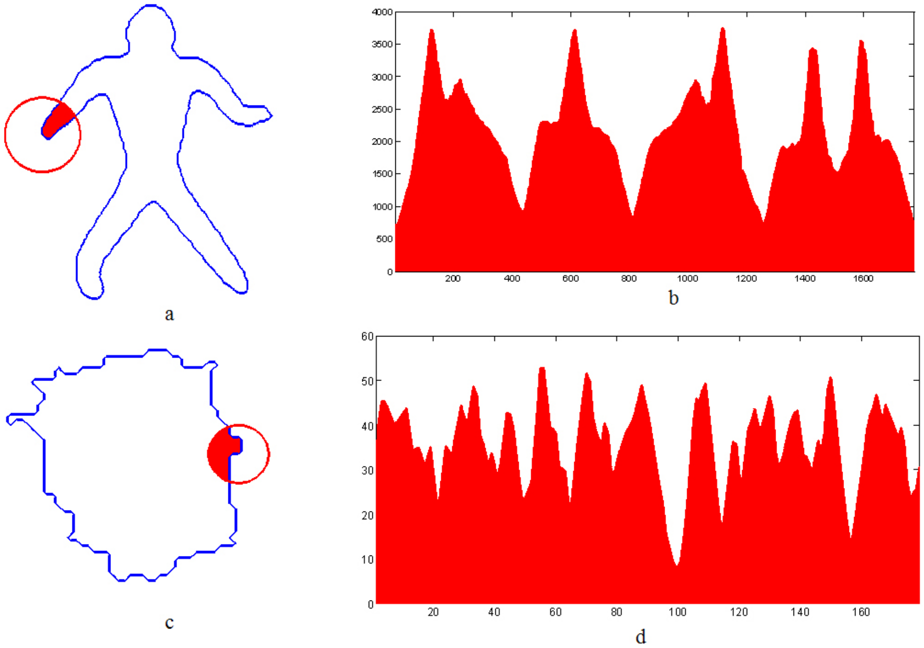

Figure 3. (a) and (c) are two examples of closed polygons with integration kernels imposed on them and highlight the integration area in red; (b) and (d) are the corresponding Integral Invariant for the complete curves. (c) is the outline of a segmented tumour mass from the Mini-MIAS mammographic database[127]

2.3 Region Matching Algorithm (RMA)

This section explains the RMA that we have developed to divide shapes into regions based on the causality of II scale space and then quantifies those regions to estimate articulations and new growth. Though RMA does not require initial alignment for region matching, it can be used to find points of initial alignment that are then used to establish point-wise correspondences of shapes. Currently, regions are matched simply on the basis of a least sum of squared differences, which we have found works well in our application. If the two shapes being compared are not expected to differ substantially, then the normalized difference of centroids of regions can also be used as an additional feature for finding similarity. The variation between two regions can be presented in terms of the number of pixels and percentage difference. The areas of regions might be useful in applications where most of the regions in corresponding shapes are likely to be the similar in size. Other factors such as texture and gradient measures as well as additional shape features can be used with the existing shape descriptor to meet the requirements of a specific application.[127]

The core issue in scale space is scale selection. In our case, the maximum scale is selected in accordance with the size of the shape and the size of the II kernel; and is application dependent. The scale space of the kernel should range from being able to identify localized changes in shapes to describing the overall structure; that is, moving from a fine to a coarse scale. At a coarse scale, shape description is less sensitive to small perturbations and noise.

To divide a shape into regions, we first need to set the maximum or coarsest scale. The coarsest scale may be determined automatically by taking the mean value of the shape-to-integration kernel ratio (SIR) of the two shapes. Let r_{max} be the maximum scale indicator (this equates to the radius of the circular II disc at the maximum scale). Then comparing shapes (S_1, S_2) for region matching where the area of SIR can be adjusted depending upon the size and variability of the shapes.

$$r_{max} = \lceil mean(r_{S_{1max}}, r_{S_{2max}}) \rceil \tag{3}$$

Where $r_{S_{imax}} = \sqrt{\frac{Area of S_i}{SIR*\pi}}$, i = [1, 2].

3. RESULTS

First, we illustrate the application of RMA to the pair of shapes shown in Figure 4. Figure 5 shows the II signature at the coarsest scale. This illustrates the effectiveness of RMA for initial alignment of two shapes. It finds the best region with the minimum matching cost and designates its starting point as a point of initial alignment. A second example is given in Figure 6, where a new growth has been identified (which corresponds, in fact, to the rabbit's tail). Other examples are given in Figures 7 and 8. The accuracy of initial alignment for shapes with locally distinct geometry is high, as is evident from Table 1.

We have applied RMA to a range of shapes from the Kimia database, and assessed its performance for within-group similarity. The accuracy of region matching is assessed manually as a surrogate for ground truth. Experiments were carried out on 146 dissimilar shapes from four similar object groups of the Kimia database. Region matching for each pair of shapes was assigned a score from 1-6, whereas the accuracy of new growth and occluded regions was assessed qualitatively and assigned a grade from 1-4. The results are summarized in Table 1.

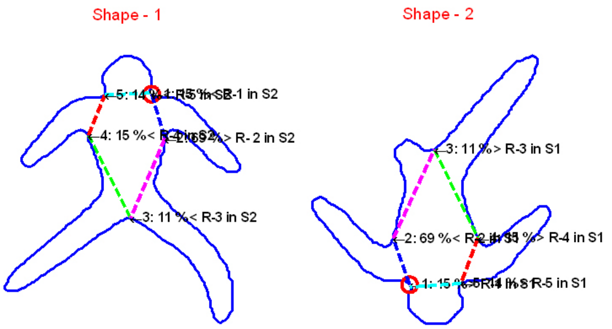

Figure 4. RMA applied to two shapes of "dude" category from Kimia database for local region matching. Regions are identified accurately in this example while quantifying regional change in each part. The regions are identified correctly because of the prior initial alignment, which is basically to align shape signatures to start from the most similar points.

The relatively poor results of RMA on hand shapes stem from the fact that the inner left, right and center fingers of each hand have very similar structures. Similarly, the symmetry of kite shapes is also a misleading factor in identifying regions correctly. In machine vision, matching asymmetry is generally accepted and may not be counted as an error, in which case the results improve dramatically. Incorporating translational and reflection symmetries into our framework, while enabling the detection of new growths and occlusions; is the subject of current work.

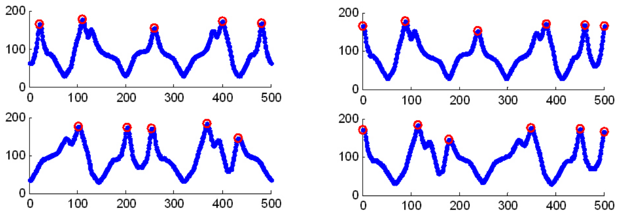

Figure 5. Integral invariant signature at the coarsest scale with causal peaks of two shapes in Figure 4, for shape-1 on the top and shape-2 in the bottom row. Left: the signatures are shown without initial alignment. Right: after initial alignment; the causal peaks at the coarsest scale are highlighted in red. Plots of $I^r_\gamma(p)$, against the parameterization of the shape at every point p.

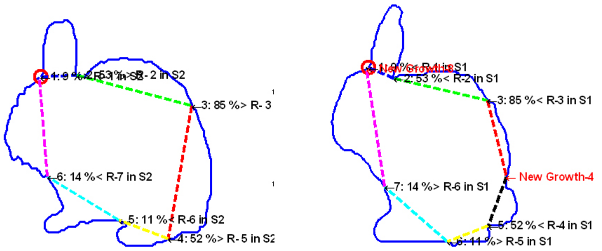

Figure 6. RMA applied to two shapes of "bunny" category from Kimia database for local region matching. Shape on the right is been identified with a new growth in comparison with the shape on the left.

The temporal mammograms that were used in this study were made available to us by Matakina Technologies. We begin by applying a variation of the hierarchical algorithm based on iso-contours.[131] The reason for using this algorithm here is that it is computationally very efficient, and indeed it can be the basis of a real time system, even without resorting to a GPU implementation. The algorithm segments the complete internal topography of the breast in a structured way that can subsequently be used to establish correspondences between mammograms. The algorithm has worked well of mammograms we have processed to date.

Table 1. Results of applying RMA to variable and occluded shapes from the Kimia database. Note that matching asymmetry is considered to be an error (we have mammograms in mind), though in machine vision applications it may be deemed acceptable, which would further improve the results.

Criteria	"bunny"/Rabbits	"dude"/Man	"fgen"/Alien	"kk"/Kite	"hand"
Initial Alignment	91.7	100	91.67	77.78	55.56
Detection of new growth	98.05	None	90	91.38	53.34
Regional Correspondence	98.33	100	86.11	91.61	78.05

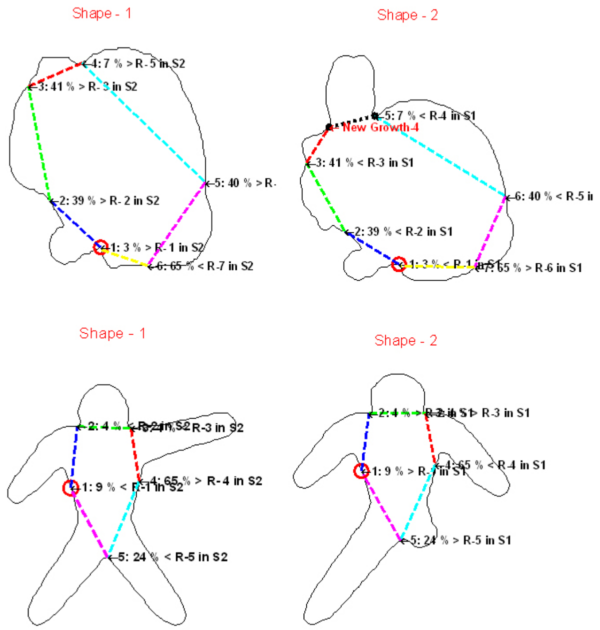

Figure 7. Continued to the next page for caption

An example of alignment for a segmentation of nested regions is shown in Figure 9. RMA matches regions in shapes irrespective of their sequence. However, in this particular case the accuracy of matching is obvious by comparing the II signatures of both mammograms after initial key-point alignment.

Shape correspondence using RMA has been applied to the regions segmented in this way, as illustrated in Figure 10. The mammograms are de-noised using a Perona-Malik anisotropic diffusion filter. The lesions from pairs of temporal mammograms are put into regional correspondences. In some cases the algorithm identifies the segments (and associated sub-regions) that correspond to new growth, while at the same time calculating the percentage change in other sub-regions. It may be noted that the number of regions in both shapes may not be equal. Some obvious mismatches can also be seen where the regional differences are substantial or the non-corresponding regions are very similar. The correspondence of regions does not currently depend upon the texture or gradient information enclosed in them. Detailed examples of RMA applied to regions segmented and matched from temporal mammograms are given in Figure 11.

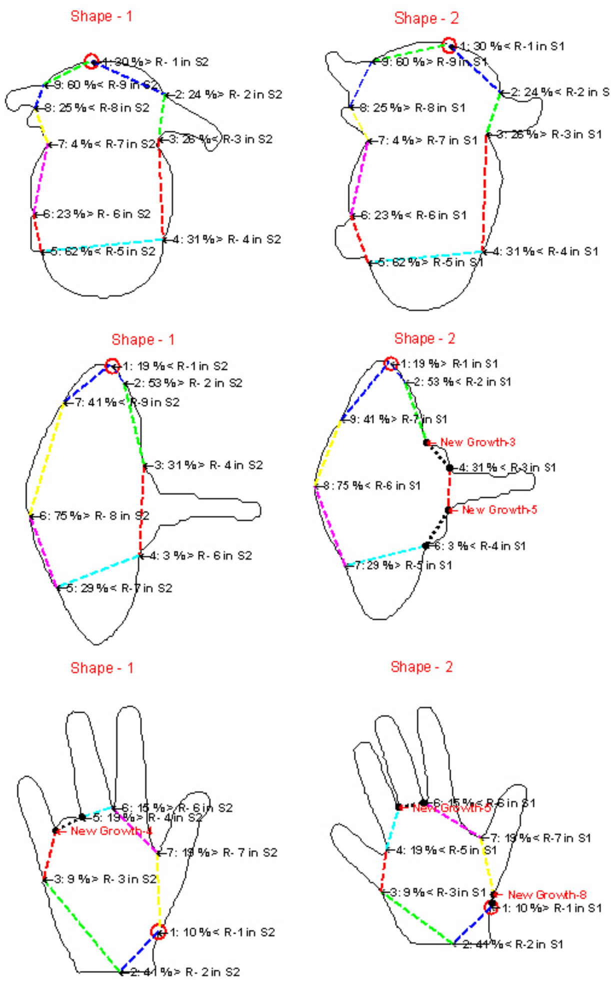

Figure 8. Examples of RMA application on 2D planar shapes of varying spatial scale. Some mismatches can also be seen as the algorithm is similarity driven, independent of spatial information.

4. CONCLUSION

This paper has introduced a novel local RMA using II scale space. Shape matching and correspondence algorithms usually match and establish point-wise correspondences between two shapes and may even handle partial occlusion. However, they typically do not quantify partial occlusions nor identify complete occlusions or new growth. It is important to measure regional differences quantitatively within each shape and establish correspondences based upon region matching. For masses, it is vital to analyze their growth and notice the emergence or disappearance of any region. This can be helpful in detecting new growths and identifying their orientation. Following region of interest segmentation, we have introduced a method of local shape correspondence and region matching using II scale space. II are calculated for segmented shapes from mammograms at all scales. The algorithm identifies causal peaks of this scale space as key points and breaks the shape into sub-regions based upon them. The best matching region is selected as a point of initial alignment and regions are corresponded based on a similarity measure. RMA gives encouraging results in detecting tumor growths and its aggressiveness with respect to shape.

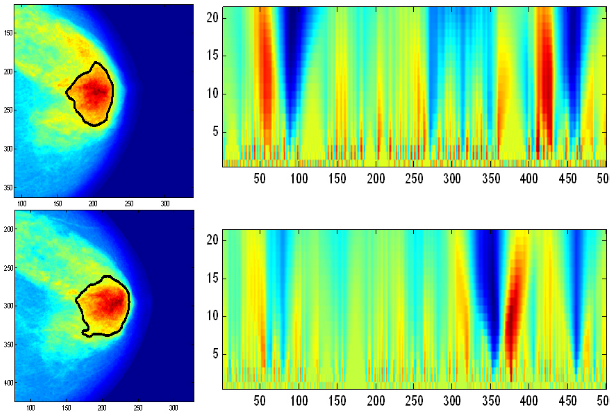

Figure 9. Segmented regions from temporal mammograms on the left while their corresponding scale spaces is given on the right hand side

The fundamental limitation of this approach is that it does not know the spatial layout of the regions it is matching, which of course has to be spatially invariant. This has resulted in the mismatching in Figures 7, 8 and 12, and will not improve existing models if this framework is extended to the point-wise corresponding. Transformations to incorporate information from inside of the shape can be applied prior to applying RMA, which will add value to the shape signature and reduce correspondence error. Some of the examples of such shape transformations are bending invariants, eccentricity transform and interpolation of medial axis within the shape.

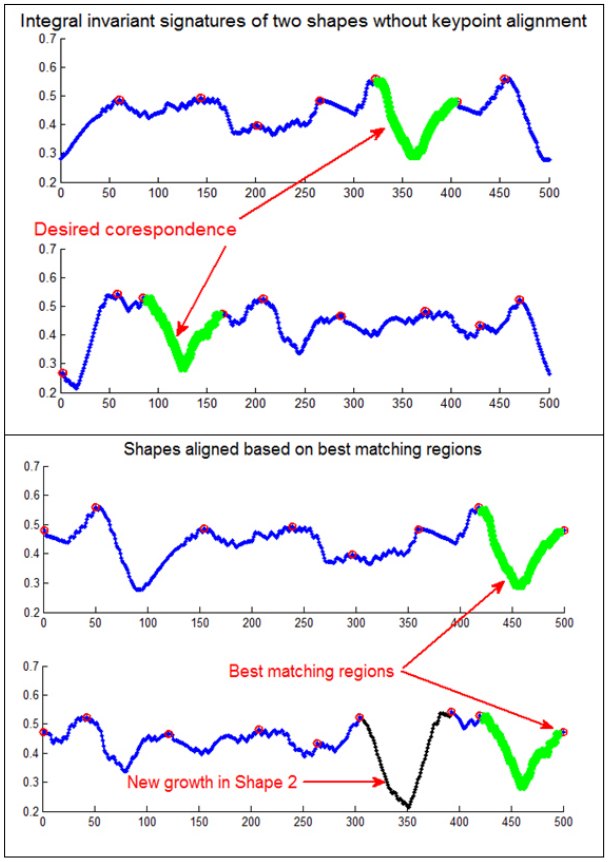

Figure 10. Above is the scale space signature of two corresponding shapes in Figure 8 at the coarsest scale. On the left, the signatures are unaligned whereas on the right side they are aligned using RMA.

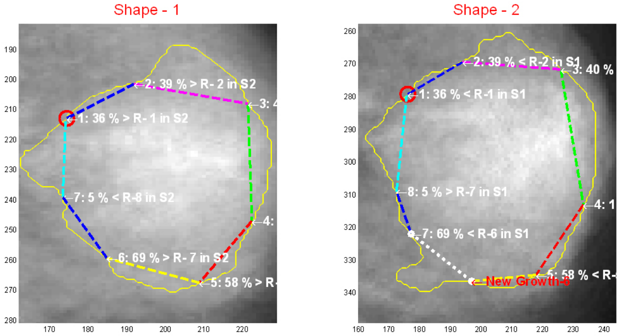

Figure 11. Final RMA results of the regions segmented in Figure 9 and aligned for a match in Figure 10. Detailed examples are given in Figure 12.

CONFLICTS OF INTEREST DISCLOSURE

The authors declare that they have no competing interests.

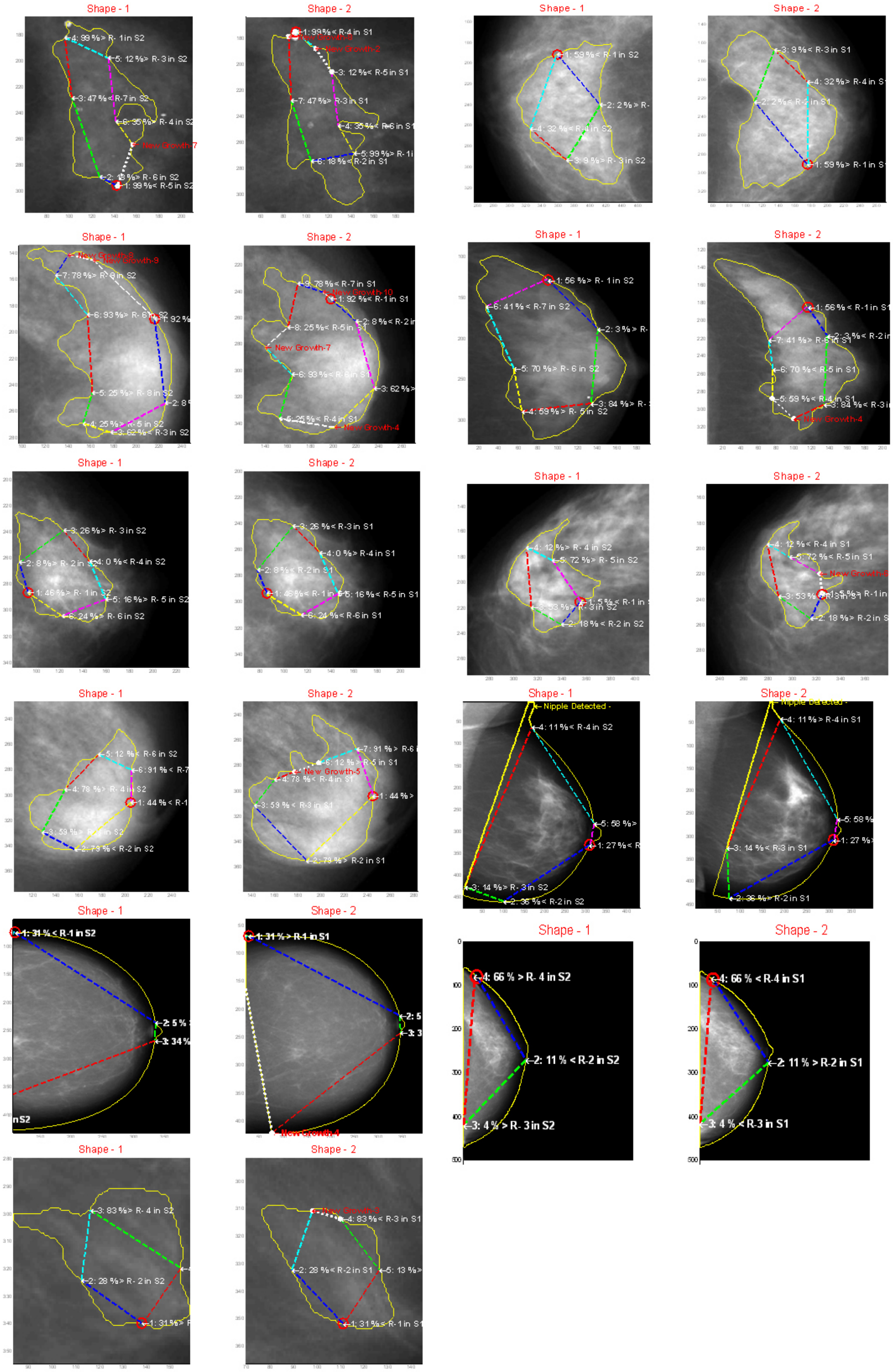

Figure 12. Region matching of corresponding contours on the temporal mammograms. The red circles in the shapes identify points of initial alignment. Regions are color-coded and show both good and bad examples of regional correspondences.

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