

An Adaptive Approach for Image Subtraction

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Abstract—Image subtraction is widely used in angiography as a means of highlighting differences induced by contrast agents. New knowledge of previously unsuspected causes of disease, in particular, secondhand smoke exposure, spurs interest in pushing the limits of early accurate diagnosis. Simple image subtraction induces artifacts causing problems for ensuing measurements and 3D reconstruction. Image registration techniques have been used to partially solve this problem. However, a complete registration is slow, and misregistration often occurs in images where bones are surrounded by vessels with similar image characteristics. In this paper, we propose an approach based on the idea of global match followed by local refinements. In the global match, an image pair is aligned using a similarity measure so as to reduce overall difference. In the local refinements, localized displacements and deformations of tissue are handled by a combination of techniques: image registration, region growing, erosion, and dilation. This approach is fast compared to registration based image subtraction and it can find vessels abutting a bone. It is designed to be especially suitable for large cross-section image stacks. With additional vessel connectivity analysis between adjacent slices, the algorithm provides a good foundation for 3D vessel reconstruction.

Keywords—Image subtraction, image registration, region growing, erosion, dilation, similarity measure, scattergram

non-vessel tissues as a basis for comparison.

Let I_c , I_m and I_s be the contrast, mask and subtraction images respectively. A simple image subtraction would be $I_s(i,j) = |I_c(i,j) - I_m(i,j)|$. This assumes tissues do not change in position (relative to the scanner) or intensity between scans. In practice, patient motion occurs frequently, and there are physiological motions (breath, heartbeat), which cause the subtraction images to show motion artifacts. Fig. 1 (c) shows an example of such artifacts: the outer border of a bone remains after subtraction (pointed to by an arrow). Though there are artifacts caused by other factors, the predominant one is motion artifact. In this paper, we deal with motion artifacts only.

We develop an adaptive image subtraction approach based on the idea of global match followed by local refinements. In the global match, an image pair is aligned using a similarity measure so as to reduce overall difference. In the local refinement, localized displacements and deformations of tissue are handled by a combination of techniques: image registration, region growing, erosion, and dilation. This approach is fast compared to registration based image subtraction and it can find vessels abutting a bone. It is designed to be especially suitable for large cross-section image stacks.

I. INTRODUCTION

Image subtraction is a way to discover differences between images. It has many applications in medical image processing, especially in angiography: in this application, one image taken after injection of a contrast agent (referred to as a contrast image or contrast) highlights vessels and some non-vessel tissues, such as bone, in relation to their background, and a previously obtained image (referred to as mask image or mask) of the same area provides only

II. RELATED WORK

Several motion correction techniques that require expensive devices have been developed for digital subtraction angiography (DSA). However, they have never been used on a large scale in clinical practices [1].

Research in motion correction has focused on an image processing technique: mapping the pixels in the mask to the contrast, i.e. doing an *image registration*. After image registration, subtraction is straight forward.

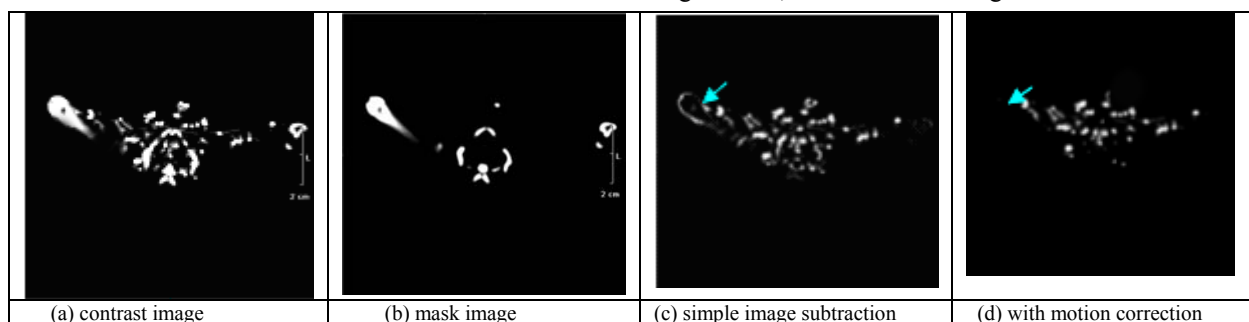


Fig.1 CT images for an angiography study using a rat hindlimb ischemia model. Panel (a) shows the contrast image (highlighting both vessels and bones), while (b) shows mask image (highlighting bones). Panel (c) is the result of simple image subtraction after a global registration. We can see some outer borders of bones were left as artifacts (arrow). Panel (d) shows image subtraction with artifact correction using our approach. There is no artifact at the arrow, but a nearby vessel close to the bone remains.

Quite a few image registration techniques have been developed [3]: phase correlation [2] (based on the translation property of the Fourier transform), control points (landmark) mapping [1], and elastic model based matching [4]. More specifically, image registration techniques dedicated to DSA have been studied in [1, 5, 6] and can be summarized as follows:

1. Find control points (on the borders of tissues [1] or on a regular grid [5, 6]) in the mask automatically.
2. Map control points to corresponding points in the contrast image (using an optical flow approach [8] or template matching [7]).
3. Interpolate other points (linear, spline).

The above approach has worked acceptably for projection images as [1] shows but it is not optimized for large cross-section image stacks. Also Fig. 1 (a) illustrates a problem: cross-sections through bones may have neighboring vessel segments of similar intensity and shape. In such conditions the automated control points might not register accurately. Further more, methods acceptable for one pair of projection images typically are not fast enough for efficiently clinical use on stacks of 100 or more slices.

III. METHOD

Our approach considers the characteristics of stacks of cross-section images:

1. Warping of tissues in the mask is not common (we should tolerate a small scale warping though we don't use a deformable model to model it).
2. Motion of the subject is predominantly global.
3. Physiological motions include localized and regionally independent elastic displacement (again we will not apply an explicit model; in this case we instead rely on morphological erosion/dilation).

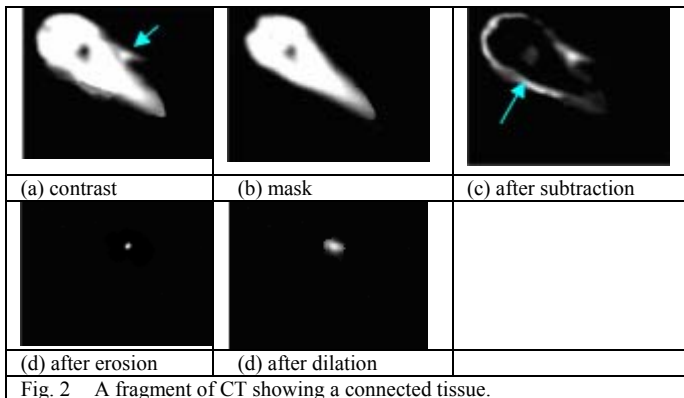


Fig. 2 A fragment of CT showing a connected tissue.

To address global motion, we apply a global motion correction step to match the mask and contrast by shift/rotation using the similarity measure discussed in section IV below.

In addition local elastic deformations require local elastic corrections as refinements of the global alignment. For local refinements, we do not require registering every pixel in the mask. Instead we need only register one pixel in a connected tissue to find the corresponding tissue in the contrast.

Fig. 2 (a) shows a connected background tissue (a bone section) that needs local refinement. The contrast contains a vessel cross-section that abuts the background object (arrow). The contrast is scanned in a slightly different plane (caused by motion) which causes the bone in Fig. 2 (a) to be bigger than the bone in Fig. 2 (b). This results in the vessel cross-section being combined with a rim artifact from the larger bone in the contrast if we do a simple subtraction as Fig. 2 (c) shows.

Assuming that the local motion (after correction for global motion) is sufficiently small, an inner pixel of the bone in Fig. 2 (b) can be registered to a pixel of the corresponding bone in Fig. 2 (a). We can region grow from the registered pixel in Fig. 2 (a) to get the corresponding connected segment in the contrast. If we remove such a connected segment from the contrast, we would lose a vessel which is connected to the bone. Hence we do a simple subtraction of Fig. 2 (a) and Fig. 2 (b) to get Fig. 2 (c). Then we erode Fig. 2 (c) to get Fig. 2 (d). We use the remaining high intensity pixel in Fig. 2 (c) as a seed for morphological dilation with the condition that only high intensity pixels in Fig. 2 (c) can be dilated. By applying this condition we can restore the seed to a shape similar to that of the vessel in Fig 2 (a).

These local refinements are applied sequentially to each connected patch; each time, the algorithm tries to remove one connected bone out of the contrast image. Since the number of connected bones is typically not large and the operations above are relatively simple, this approach is quite fast.

The algorithm is as follows:

1. Conduct global motion correction by scattergram based similarity measure (discussed in section IV).
2. For each connected bone mass with area M in *mask*, find an inner point P belonging to that mass. Finding an inner point can be done by eroding that mass multiple times until a core of that mass can be found.
3. Find the corresponding point P' (of P) in the *contrast* that maximizes the similarity measure under the condition that
 - a) P' has a high intensity (this means P' belongs to some tissue).
 - b) the area C of region growing of P' should not be conspicuously less than A .
4. If there are two or more such C s that overlap, we get a case where two or more originally separated bone masses get connected by vessels. We detect this and treat the original two or more C s as a whole.
5. Do a simple image subtraction of M and C to get S .
6. Erode S k times to get S' .

7. Dilate S' k times to get S'' with the condition that the only new pixels added should previously exist in S .
8. Replace C with S'' .

The above algorithm uses a parameter k which is determined by M (larger values of M lead to larger k). The two conditions in step 3 will ensure a tissue pixel is picked and the corresponding tissue is not a conspicuously smaller vessel. By these conditions alone, there is still a possibility that the chosen pixel belongs to an abutting larger vessel. However, since the motion of the subject is predominantly global (we corrected it in the first step), since we used a similarity measure to find the best match in the local refinements, and since we used an inner pixel for the match, with a high probability we will get the right pixel in step 3.

IV. SIMILARITY MEASURE

An *image similarity measure* is a function that when given an image pair as input produces a value indicating the degree of correspondence between their corresponding pixels. Using an image similarity measure, we can compare similarity values as rotation and scaling occur to identify the configuration leading to the best match.

Among the several similarity measures for image registration developed, normalized correlation is perhaps the most obvious; however, Buzug [7] pointed out that correlation could fail to reflect the true similarity if one of the images is gray-level distorted.

We adopt a scattergram-based similarity measure. Given a contrast and mask, let Sg denote the scattergram. $Sg(i,j)$ is the number of intensity value pairs in the contrast, mask image pair matching intensity value pair (i,j) . A scattergram is a 2D analogy to a histogram that shows the joint distribution of pixel pairs. Based on the meaning of the scattergram, we know two images are similar if the points (values) in the scattergram are clustered. This is true even if the gray level is distorted. More strictly, the similarity function for a scattergram should meet two requirements:

1. If the values are distributed in only one spot, the function should get one extreme value.
2. If the total values are evenly distributed, the function should get the other extreme value.

An entropy-based function:

$$\sum_i \sum_j p(Sg(i,j)) \log p(Sg(i,j))$$

where $p(Sg(i,j))$ denote the normalized fraction of pixel pairs with gray value (i,j) , satisfies above requirements.

V. DISCUSSION AND CONCLUSION

Previous work in motion artifact correction of image subtraction is mostly dedicated to DSA. In those studies, DSA is mainly used to show a projection image instead of a cross-section image. A projection can show a whole vessel tree, while a cross-section can only show a slice of the tree. In this sense, cross-sections are less complicated in structure making recognizing a connected tissue relatively easy.

Our algorithm utilizes the fact above. Unlike previous work, it is not image registration based (though it registers a few pixels). It uses a combination of techniques: similarity measure, image registration, region growing, erosion, and dilation. By this combination, the algorithm can correct most motion artifacts. It doesn't use deformable models to identify deformation, yet it can tolerate minor deformations. As an additional advantage over previous work, it works well for images where bones have nearby vessels with similar image characteristics. Also it runs fast so that a typical stack of 100 images or more can be processed very efficiently.

With additional vessel connectivity analysis between two adjacent slices, the algorithm provides a good foundation for 3D reconstruction of vessels.

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