

# **Semiautomated ROI Analysis in Dynamic MRI-Studies: Part I: Image Analysis Tools for Automatic Correction of Organ Displacements**

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**Short title:**

Automatic correction of organ displacements

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## Abstract

The most important problem in the analysis of time-sequences is the compensation for artefactual motion. Due to motion, medical images of the abdominal region do not represent organs with fixed configuration. Analysis of organ function with dynamic contrast media studies using regions of interest (ROI) is thus not readily accomplished. Images of the organ of interest need to be registered and corrected prior to a detailed local analysis.

We have developed an image analysis scheme which allows the automatic detection of the organ contours, the extraction of the motion parameters per frame and the registration of images. The complete procedure requires only minimal user interaction and results in a readjusted image sequence, where organs of interest remain fixed.

Both, a visual analysis of the dynamic behavior of functional properties, such as a quantitative statistical analysis of signal intensity versus time within local regions-of-interest, is considerably facilitated using the corrected series.

**Keywords:** Medical image analysis, motion compensation, object recognition, MRI dynamic sequence, ROI analysis

## Introduction

Interpretation of radiological images requires much a priori knowledge which partly has to be made accessible for computer vision processes. At present we are far away from building a computer vision system that is able to recognize and understand visual information in entire radiological images, but it is possible to demonstrate the usefulness and effectiveness of computer-assisted interpretation in some limited applications.

There is growing interest in the development of powerful methods for the automated analysis of medical images, as the image data acquired by new imaging techniques are of improved quality and the acquisition times have been decreased significantly, which leads to the acquisition of larger number of slices. The discrete representation of medical image data allows the qualitative and quantitative exploration of the image data using computer vision methods. In fact, by applying a variety of image processing methods, much more information can be explicitly extracted than obtained by the usual visual analysis of sections represented on a console or as hardcopies.

The present paper addresses the important topic of analyzing time series of medical image data. Such time series are acquired to study either the movement of an anatomical part (e.g. beating heart) or the dynamic behavior of signal intensity of specific areas within anatomical parts, especially after injection of contrast media with the aim to extract functional information. It has been shown that regional renal glomerular filtration can be studied using gradient echo imaging techniques (MRI) coupled with a bolus injection of Gadolinium-DTPA [1], [2]. If region-of-interest based function curves are generated over a time-sequence of several tens of images, the renal contours have to be *exactly superimposable* from scan to scan, which is not the case even using breath holding techniques, because the end-inspiratory position varies.

## Problem of artefactual motion

To observe human organ function it is common place in Nuclear Medicine to inject tracers and to measure the temporal change of radioactivity by acquiring a time series of images. For the automated analysis of local regions it must be assumed that organs or regions thereof remain fixed during the overall acquisition time, a prerequisite which due to poor spatial resolution is often met in Nuclear Medicine, but hard to fulfill when high resolution methods such as MR-studies are analyzed. Even when imaging techniques can overcome the problem of movements during one acquisition cycle (fast imaging under breath hold, triggering, gating) and generate sharp images without motion artefacts, the motion of organs between scans (above all in the abdominal region due to variable inspiration depths) will remain. An example is given in figure 1, where the motion of the kidney positions in 4 subsequent scans taken under breath hold conditions is clearly visible (see [4] for a detailed description of kidney displacements during breathing). The renal outlines which have been interactively defined in one typical frame are shown as black curves.

The displacements of organs represent a big problem for an automated computerized analysis of an image sequence, because it must be assumed that corresponding anatomical structures in subsequent frames remain fixed for the analysis of ROI's to generate time-signal intensity curves. Due to the considerable movement and rotation of the kidneys between image frames the ROI's would have to be redrawn tediously from frame to frame.

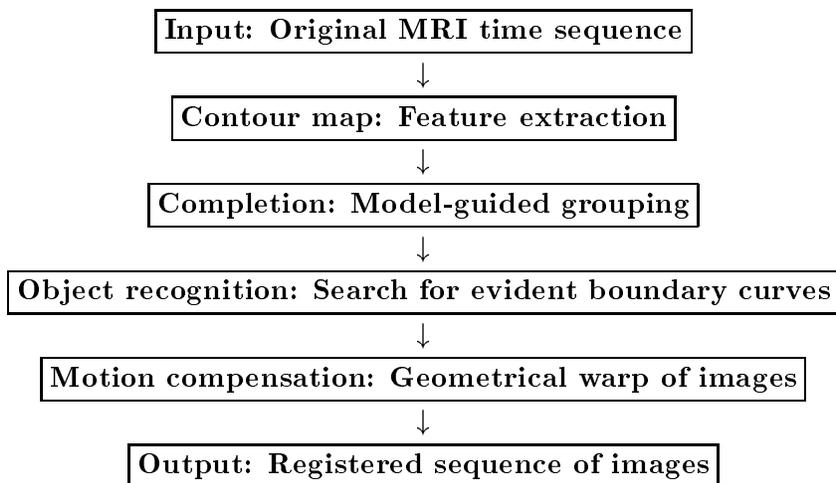
To efficiently detect changes in large time series of images we have to develop highly automated methods which require only minimal user interaction. We therefore propose a processing scheme to automatically recognize movable parts, to quantify their relative new position and to superimpose them using image registration methods. The procedure stages of the proposed system are illustrated

by the example of motion compensation in dynamic gradient echo imaging of the kidneys after bolus injection of MR contrast media [3].

## Image processing methods

To facilitate the understanding of processing steps in image analysis our description is guided by the example of renal boundary detection.

It is convenient to divide the image analysis up into two principle stages: In a first stage, the digital image is simplified by explicitly extracting image intensity discontinuities as candidates for object contours. This processing step is known as *feature detection*. A next processing stage recognizes desired object contours by combining partly defined boundaries (feature elements) to complete global contours. This linking procedure needs a priori information about the objects of interest, which is introduced by an appropriate model description (in the present work by drawing the kidney contours). This second stage will be called *model-guided grouping*. The complete processing scheme is illustrated below, the processing steps will be described in detail in the following sections.



### Extraction of boundary features

Important cues in images are the contours of objects. They are represented as discontinuities in image brightness, either as sharp intensity changes or curve-like light or dark line-structures surrounding the objects. The images used were gradient echo "opposed phase" images which exhibit a dark rim between renal parenchyma and retroperitoneal fat (TE is chosen such that the signal from voxels containing a mixture of fatty tissue and kidney cortex was cancelled). This dark rim can be defined as the key feature of the renal contour and will be enhanced in a feature extraction process, transforming the original image frame (figure 2a) into a so-called contour map (figure 2b). We have developed a valley/ridge-detection algorithm which is based on regularization and differentiation of the original image data. The process results in a limited set of characteristic image points representing objects by their contours, which is a much simpler curve-like description of important image structures in terms of their boundaries. The *contour-map* obtained in this first processing stage (figure 2b) does not only contain the desired left and right renal contours, but

represents a set of boundary fragments of the entire image contents. For a human observer it is easy to detect the desired contours, as the biological visual system is highly specialized to recognize objects in line- drawings by combining curve elements to meaningful object contours. A computer has no *higher knowledge* about the objects to be detected. We have to tell the computer what we are looking for in an appropriate way. This incorporation of anatomical knowledge enables the linking of boundary fragments to complete object contours.

## Model-guided global grouping: Hough transform

A simple idea of knowledge representation is to feed an image processing routine with the information about the contour of interest. The user displays a typical frame of the study on a screen and draws the object outlines by interactive means (cursor, lightpen), thus generating *model-curves*. If we assume to deal with rigid, nondeformable objects, these model-curves (representing the outlines of the sought anatomical objects) remain valid for each frame of the sequence. The models of the left and right renal contours are shown in figure 2c. Intuitively it should be possible to move a model-curve over the image and to mark locations where sets of boundary points in the contour-map match best with the model. A degree of match can be expressed by the accumulated number of contour points which completely overlap with the model curve at each specific position. This method is known as template matching or, with respect to curve-like contours, as a Hough Transform, a concept proposed by P.V.C. Hough in 1962 [5] and applied to object recognition tasks by Duda and Hart [6]. Extensions are found in [7], [8] and [9].

The matching process is a correlation of a template curve with the image resulting in a *correlation image*. The degree of correlation at a specific position of the model curve is obtained by accumulating the pixel intensities of the contour-map image 2b which are superposed by the model curve 2c. The model curve is shifted from pixel to pixel in a scan-wise order, and the accumulation is repeatedly done (see appendix for the algorithmic description of the procedure). This processing scheme results in accumulation votes at each position of the model curve relative to the contour-map image. The complete set of votes forms an accumulator image (or correlation image) 2d, where the horizontal and vertical coordinates code the shift coordinates of the model curve relative to the contour-map image, and the pixel intensities express the correlation degree (proportional to the number of contour points covered by the model curve). A high correlation degree (dark spots in figure 2d) expresses a high evidence for a curve of predefined shape in the contour-map at the specific location, which means that at this position a most likely curve could be detected. The left and right model curves are matched individually with the left respectively right half of the contour-map image, which is splitted along the vertical centerline.

The Hough transform converts the global pattern detection problem of finding a curve of predefined shape into a local problem, i.e. finding local maxima in a correlation image, which is equivalent to assigning best matching (curve-) templates to sets of contour points in image space.

Until now only positionally displaced curves were mentioned. To extend the search to objects with arbitrary rotation and scaling, correlations with rotated and scaled versions of the original model-curve can be carried out. For each correlation with a thereby modified model-curve a new correlation image is generated. Generalizing this idea it directly follows that each new parameter represents an additional dimension of the correlation "image", more appropriately called *correlation space*. The problem of maintaining a high dimensional correlation space has been solved by proposing a new optimization technique. This algorithmic problem is not a matter of the present paper and has been analyzed elsewhere [10],[11], [12], but the result is important: For an arbitrary number of parameters (position, rotation, scaling) the problem can be reduced to the analysis of a two-dimensional correlation image. In our kidney-detection scheme the scaling has been kept fixed,

whereas the orientation varies between -4 to 4 degrees in 1 degree steps. The correlation process is done individually for each rotation, resulting in 9 correlation images. Using the assumption that only one correlation is optimal at each shift position of the model curve (which is obviously suitable since we are looking for one object only), the information of the 9 correlation images can be condensed to one plane by applying a projection strategy. Two planes, one containing accumulated evidence and the other the corresponding parameter (here: rotation) replace a higher dimensional accumulator space and allow more efficient storage and retrieval of evidence information.

Grouping techniques are known to be computationally expensive, especially if curves of varying size and rotation have to be detected. Although Hough techniques for image processing applications have been known for more than fifteen years, the problems of great computational expense and of multidimensional maxima detection have hindered their general use in the past. To overcome limitations on computation we have implemented the transformation in parallel (see [13] and appendix). The usage of specific a priori knowledge about anatomical facts (maximum rotation of kidneys) helps to significantly reduce the overall computational expense by limiting the range of the rotation parameter. The new projection and update technique reduces a high dimensional correlation space to only two dimensions [10],[11], resulting in a further significant decrease of the computational expense. The computation time and the hardware needed to run such a complex segmentation scheme are very important criteria if we think of applications in clinical routine practice.

Finally, the object detection is reduced to a search for maximum votes in the sharpened correlation space, a simple search process which can be performed very efficient. The sharp maxima in correlation space corresponds to centers of most evident curves. Once a maximum has been found, it contains the full information about the global curve in image space. The coordinates represent the horizontal and vertical positions, and the maxima themselves the number of contour points combined to form a curve in image space, the information about rotation and eventual scaling is kept as an additional attribute to each correlation maxima.

## Registering and statistical analysis

The displacement and rotation parameters of the objects are determined by the location and orientation information obtained from the evaluation of the correlation maxima. We use a linear geometric transformation to register the objects in each frame to the position of the model curve, to speed up the procedure a special hardware for geometric transformations has been used. After registration, the object boundaries of the geometrically corrected frames coincide exactly with the model curve and therefore among each other. Figure 3 illustrates a scan before (left) and after (right) geometric correction, the model-curve is overlaid in black. A bicubic interpolation assures an optimal registration of original image pixels to subpixel positions calculated by the affine transformation (see smoothed transformation result Fig. 3 right). Again, separate warps of the left and the right image parts are performed, because the correlation between the movements of the left and right kidneys is only weak.

The sequence of corrected frames opens up the possibility to a simple ROI analysis of the time varying information, because local regions of the objects of interest stay fixed in each frame of the sequence. We can analyze the functional behavior qualitatively by generating a movie-sequence, the fixed object position gives the visual impression of varying local information. To explore quantitative information within local regions, the user has to define regions of interest only *once* in one typical frame. The registered sequence gives access to exactly the same object subarea (and its brightness statistics) in each frame of the sequence. The ROI analysis then results in intensity vs. time information, which can be represented as functional curves.

## Results

The only interactive step in the image processing scheme is the definition of the renal contours, the rest of the procedure is fully automatic. After extraction of the boundary features the Hough transform runs twice on each frame of a study, once for the detection of the left and a second time for the right renal contour. Each resulting correlation image contains information about the spatial motion of the kidneys, which is used to register the study frame by frame.

The procedure runs on a VAX11/780 with a Gould-Deanza Image Processing System (IP8500). The Hough transform is implemented on the digital video processor (DVP) of the Deanza System, which supports quasi parallel image processing operations by its pipeline architecture. The memory size of 512 by 512 allows a simultaneous processing of 4 image frames. A special hardware warping device performs geometric transformations with bycubic interpolation in real time. Typical processing times including feature extraction (dark lines), contour recognition by the Hough transform (rotations from -4 to 4 degrees in 1 degree steps) and geometric correction range between 2 and 3 CPU minutes for a set of 4 image frames, depending on the size of the model curve. The overall time for the analysis of a typical series of 64 frames divides into time needed for the interactive definition of the model curves and the ROI's (about 10 minutes by a trained expert) and the CPU time (30-50 minutes) for the automatic registering of the whole series (a batch job running in the background). In comparison to the automated technique, an interactive definition of 5-10 anatomically identical ROI's in each of the 64 image frames would require several hours of tedious work.

The algorithm for motion compensation has been applied to more than 20 patient studies. The assesment of the regional kidney function is significantly simplified as the ROI analysis could be performed on motion-corrected series of image frames, reducing the effort needed by the physician to about 10-15 minutes. The success of the feature extraction and Hough transform decisively depends on the image quality of the MR scans. The example guiding our explanations clearly demonstrates the quality that has to be achieved. A poor image contrast or missing dark rims along the renal boundaries impede a successful recognition of the renal outlines.

If a suboptimal image occurs during a series (i.e. when the patient inadvertently moves or breathes), the detection of the kidney contour may be severely impeded. In such cases, a sharp maximum in the correlation image is missing, and a false correlation maximum (with low evidence) could be found to represent a possible kidney contour position. To overcome this problem we define a minimum correlation vote required by the procedure to assign a vote to a possible contour position. In our applications, the lower limit is set to 50% of the maximally achievable vote, thereby defining that at least 50% of the kidney contour has to be detected. If necessary, a further control of the result of the automatic procedure is possible at the end of the image processing. The geometrically corrected series of images is analyzed visually by displaying it as a movie. Falsely corrected frames are marked and the ROI statistics of such frames are removed from the function curves.

A detailed description of the patient studies and the quantitative evaluation of the local renal function can be found in the companion Part II paper.

The proposed processing scheme represents a step towards robust image analysis not only working on single carefully selected frames but on large series of images taken under different imaging conditions.

## Conclusions

We faced the problem of spatially registering time series of MR images of the kidneys. An image processing system is presented which uses model-based segmentation to find the contours of anatomical parts (the kidneys) in each frame of a time series of images. It is assumed that the

parts can be modelled as rigid bodies, but are displaced between scans. We allow translational and rotational movements. After contour detection, each frame of the study is geometrically corrected using the resulting transformation parameters. The anatomical parts in the resulting series of images are positionally readjusted and do exactly match. A simple region of interest analysis on multiple images thus becomes possible, because the definition of a region in one frame gives access to the signal intensities of exactly the same anatomic region in each frame of the sequence.

The improved feature extraction methods and the augmented Hough technique proposed here proved to be a powerful image processing tool to detect dislocated objects and to perform an automatic registration of objects in a series of image scans. The application to MRI sequences clearly shows the need of robust techniques for the automation of recognition and analysis tasks, as it is nearly impossible to analyze large series of images in clinical practice by interactive means, due to constraints in time and manpower. In the companion paper (Part II) our experience with the use of these procedures on a total of over 20 MRI time-sequence studies (each up to 100 scenes) is presented. The accuracy and the error-rate of the geometric corrections are discussed in detail.

A further extension to detect even nonrigid objects has been developed [14], first tests on the recognition of deformed renal contours (up to  $\pm 10\%$  in size) have been run successfully. The promising results clearly show that our extended Hough technique overcomes the basic limitations not only to computational complexity, but also to the application to real problems, where objects very often undergo a certain kind of deformation.

The computer processing applied to two-dimensional image data corrects in-plane translation and rotation. Renal motions in the third dimension (in/out-plane) are minimized by choosing an optimal slice orientation for the acquisition of the images. With the availability of multiple slice data the procedure can be extended to the compensation of three-dimensional translation and rotation, using a three-dimensional contour model (contour surface). The increase of computation time will be proportional to the increase of the size of the contour model and the number of motion parameters.

A transportable implementation of the complex correction scheme runs even on small workstations. Workstations are more and more used as additional consoles for the image analysis and manipulation together with MR-scanners, thus providing a transfer of our method to clinical routine practice in the near future.

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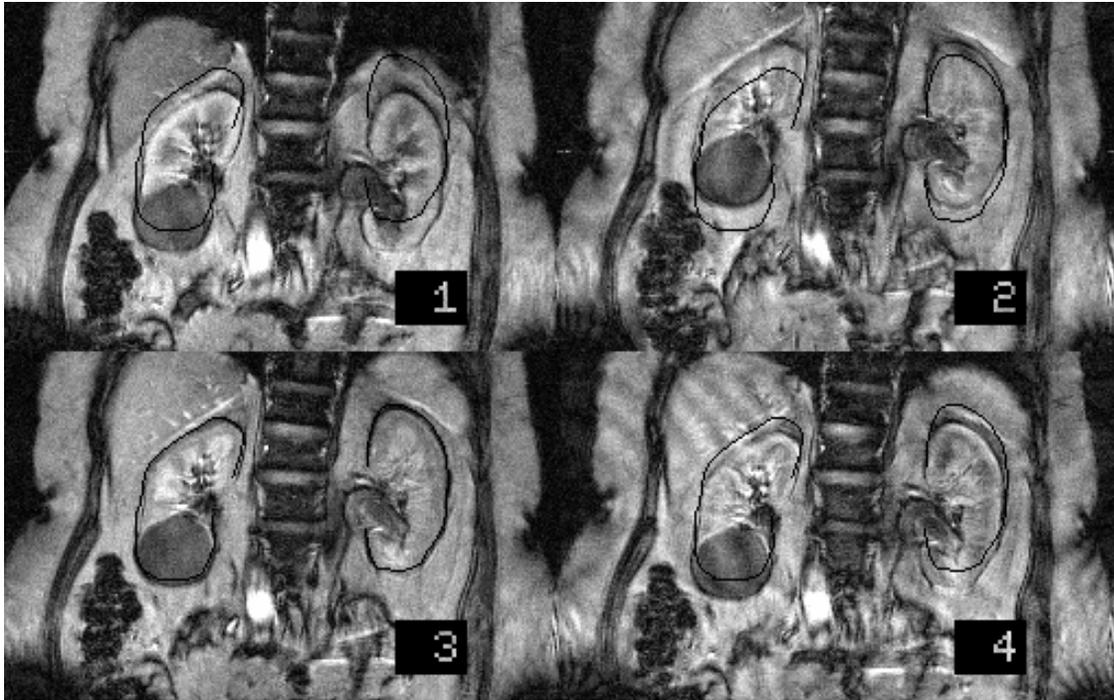


Figure 1: Original sequence of MRI scans (4 out of 64, gradient echo, TE 16.5ms, TR 30ms, flip angle 40 deg, FOV 400mm, slice thickness 10mm)

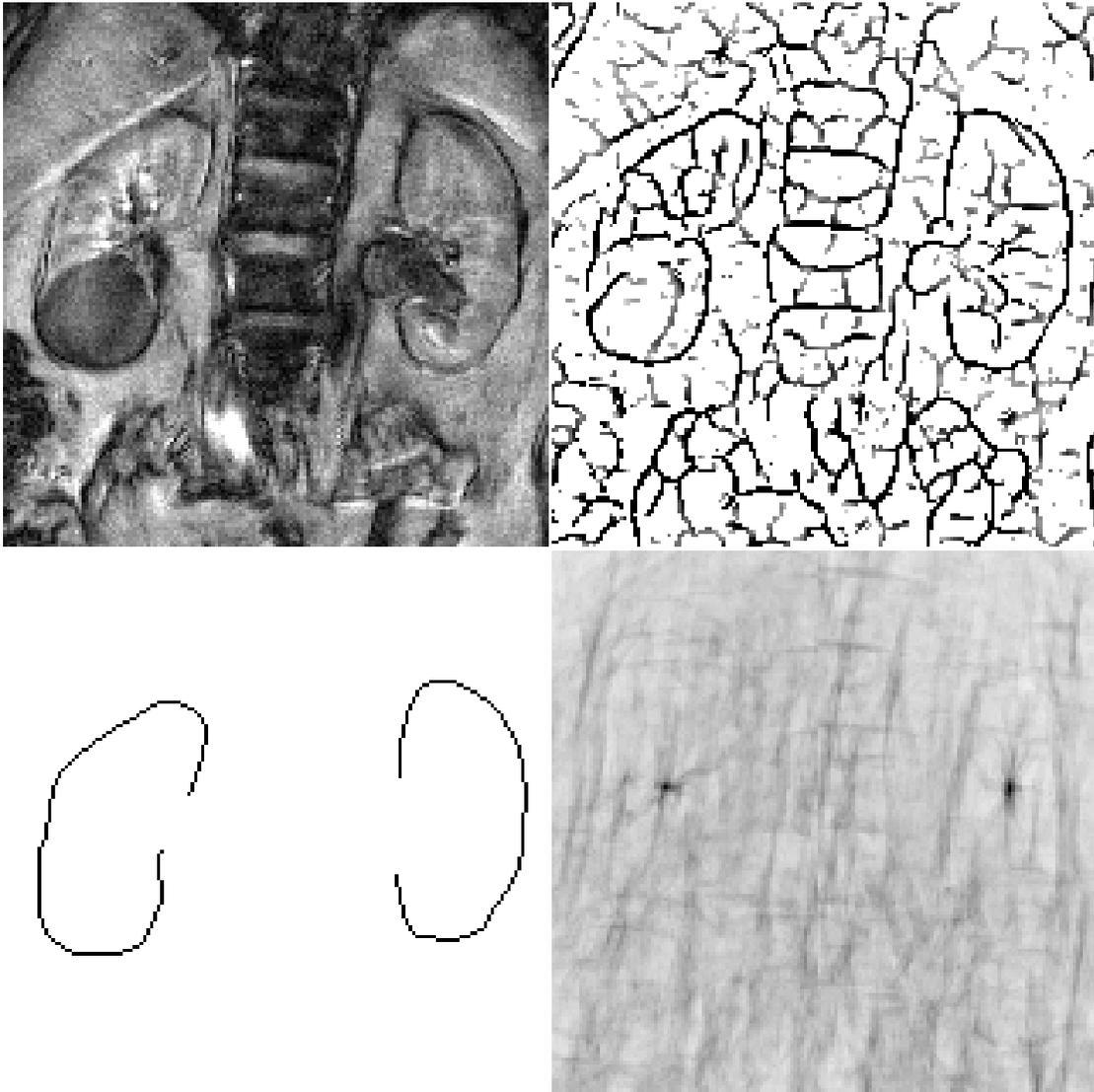


Figure 2: **a**: Original image / **b**: Contour-map image after feature extraction / **c**: Model curves / **d**: Correlation image, representing the degree of correlation between the model curves and the contour-map for each shift position. Dark spots (arrows) express the highest evidence for a contour, its coordinates define the position of the detected contours. The left and right model curves are matched individually.

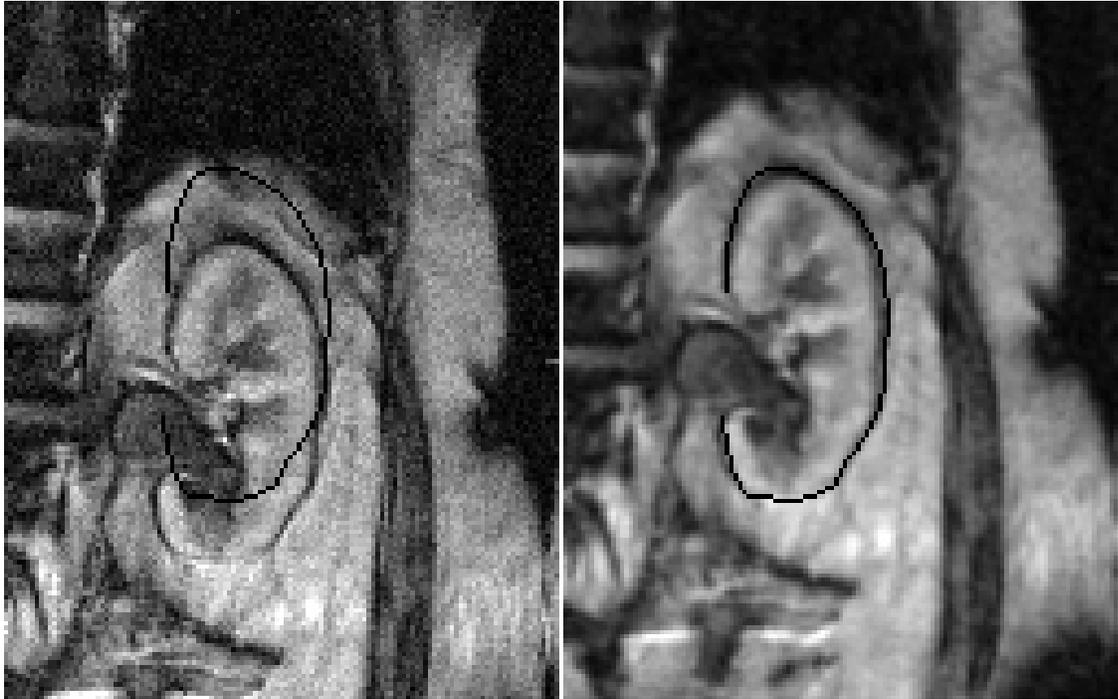


Figure 3: Readjustement of image to cover the model-curve (warp and bicubic fit)