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Improved Edge Detection Scheme for Segmentation in MRI Kidney Image Registration

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Abstract— The Kidney disease detection mainly depends upon the GFR value of MRI kidney image. The existing system kidney image requires proper motion correction and it produce less accuracy and loss of reproducibility. It is not available in clinical modeling due to loss of reliability. The proposed method is to attain accuracy and to efficiently detect kidney disease using DCE-MRI kidney image from the MRI moving kidneys and edge detection algorithm are used to detect edges from MRI kidney image. The combined registration and segmentation is to improve the accuracy of kidney defect detection in efficiently. The GFR value can be calculated as quantity of the volume of the filtered fluid per unit time from the blood pool in the glomerular capillaries to the tubular space in the Bowman’s capsule. The GFR value can be calculated by combined model and compared with physiological parameters like age, weight, height, blood pressure. The proposed system is experimentally evaluated using real time input image from MRI moving kidneys and it is very useful to analyze doctors to know patients prostate disease and related treatments. Keywords— Glomerular Filtration Rate, segmentation, magnetic resonance imaging

I. INTRODUCTION

Image processing has great potential for exploring the meaningful and detecting diseases in medical domain. Discovery of kidney diseases through MRI kidney images is critical to evaluate and diagnosis. Advanced medical image processing is efficient and useful to detect diseases and suggest related treatment. Image processing includes the process of registration, segmentation, extraction, feature detection, edge detection, correction, preprocessing, and normalization. Emphasis in this research work is analysis of medical data. Medical profiles such as patient name, age, sex, height, weight, GFR value, time, date, etc., can be used to analysis kidney disease of patients.

The Glomerular Filtration Rate (GFR) is an important parameter in the assessment of kidney dysfunction and disease. It is a measure of the volume of filtered fluid per unit time from the blood pool in the glomerular capillaries to the tubular space in Bowman’s capsule. Low values of GFR are associated with kidney dysfunction and renal disease. Serum creatinine is the most used measure for GFR. Other and more accurate filtration markers are Iohexol (serum clearance) and Inulin (urinary clearance) for the total kidney GFR estimation.

In this respect, dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is an in vivo imaging method for measurement of physiological parameters like perfusion, transfer rates, permeability-surface products, and capillary leakage in normal and abnormal tissue in a wide range of organs and disease processes. In practice, however, voxels based measurements are corrupted by lack of reliability in at least three major processing steps: (I) registration (motion correction of organ motion), (ii) segmentation (identification of tissue compartments), and (iii) the establishment of a pharmacokinetic model. First to combine the registration and segmentation and finally detect the kidney disease from the MRI image

II. RELATED WORK

First to select the kidney image datasets which is collected from the video sequence of MRI and also have to gather the patient detail of the considered kidney image. Dataset has to be selected and inserted into the database after loading the image has to get the patient detail from the gathered information. Preprocess the image and also the data by considering the images which are loaded into the database and collect the left and right side kidney volume based on that have to apply the affine registration. Apply the preprocessing on the patient data for removing the unwanted data. Eliminate the unwanted symbols or converted into null symbols in the dataset. Apply the normalization process into the preprocessed image. Normalization process called as the sifting of the pixel position of the considered image which is loaded into the process. Increase the accuracy of the analyzing process. Crop the kidney image into two as the left and right side kidney. The segmentation process takes place on the cropped image one by one. Then considered process is takes place and shown with the help of the RGB colors. The affected portions are obtained and shown in the color wise manner.

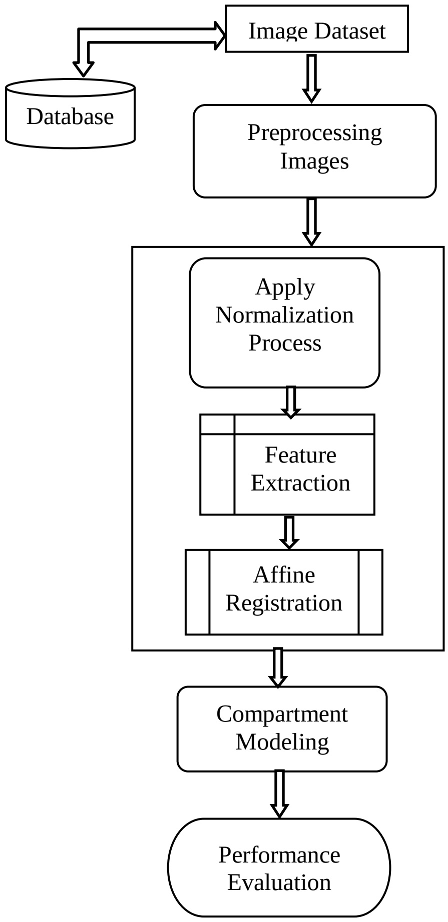

Figure 1 system architecture

This segmentation process called fuzzy means clustering process which is called as the iteration process. Evaluate the GFR value based on the other parameters like the age, mass, etc. of the patients and also based on the serum clearance value.

The gradient term not only seeks to align locations of high gradient magnitude, but also aims for a similar orientation of the gradients at these locations. Mutual information itself does not contain the spatial information (except in the interpolation of grey values). Setting aside interpolation, a random reshuffling of the image voxels (identical for both images) yields the same mutual information value as for the original images. Combine mutual information with a gradient measure to provide spatial information. The accuracy of the combined measures was shown to be similar to that of standard and normalized mutual information [24]. Registration using the combined measures is likely to be more robust because of the better defined registration functions. No distinct differences were found between combined measures based on standard or normalized mutual information.

Registration of Dynamic Contrast-Enhanced Magnetic Resonance Images (DCE-MRI) is difficult. Contrast enhancement introduces new information into images of a dynamic series so registration cost-functions that depend on information content are compromised, leading to erroneous registrations. Cost functions that seek similarity between structures in two images are confounded by the appearance of both new structure and artificial boundaries generated and enhanced by the dynamic intensity shifts induced by a contrast agent. A principal components analysis of the current best-registered time-series data PCA on a time-series of N images results in a set of N principal components. Images are created for the next step. The PPCR [20] repeats adding an additional principal component at each stage. The process ends once N-1 principal components are included. The aim is a dataset that has had random motion artefacts eliminated but long-term contrast-enhancement implicitly preserved.

A kidney segmentation approach from DCE-MRI introduces a new shape-based segmentation approach based on level sets. Training shapes are collected from different real data sets to represent the shape variations. Signed distance functions are used to represent these shapes. The methodology incorporates image and shape prior information in a variation framework. The shape registration is considered the backbone of the approach where more general transformations can be used to handle the process. It did not use the classification approach. It did not differentiate between normal and acute rejection patients. It provides efficiency in their proposed technique. After segmentation, the ultimate goal of the proposed algorithms is to successfully construct a renogram (mean intensity signal curves) from the DCE-MRI sequences, showing the behaviour of the kidney as the contrast agent perfuse [1] into the transplant. In acute rejection patients, the DCEMRI images show a delayed perfusion pattern and a reduced cortical enhancement.

The prevalence of chronic kidney disease (CKD) is increasing worldwide. CKD is associated with serious, reduced life expectancy, and high economic costs; hence, early detection and adequate treatment of kidney disease are important in kidney volume assessment by MRI is desirable and feasible. Methods for volume estimation have just recently been introduced in the clinics and are still under development, and a close collaboration between clinicians and image-processing researchers is needed in the process, as well as carefully designed studies to validate the accuracy of volumetry by these new MRI techniques. The goal is to obtain faster and more accurate volumetric procedures for the quantitative assessment and clinical follow-up of patients with progressive kidney diseases. Thresholding [28] methods have been used to segment the cortex from the medulla or cysts. The threshold is obtained by analysing the histogram of pixel intensities of an ROI. Region-based approaches aggregate pixels according to their local neighbourhood properties.

Motion correction of DCE-MRI time series is crucial for a reliable tracer modelling and estimation of pharmacokinetic parameters such as GFR. Without a proper motion correction of the non-linear displacement of the kidney during imaging time series, assessment of voxels wise kidney parameters is not possible or the estimation becomes highly corrupted. The better performance of NGF is also supported by subjective inspection of the data sets. The small, but observable discrepancy between NGF and MI for co-registration of kidney DCE-MRI time courses can possibly be explained by the non uniform change of signal intensities upon bolus arrival which creates a more dispersed joint histogram.

III. SCOPE OF THE PAPER

This work focuses on detect kidney disease in mri kidney imaging. Chronic renal let downiest accumulative problematic in world-wide up to 5% of the world's population may in the near future agonize from end-stage renal disease(ESRD), with dialysis or kidney relocation as the expensive the paretic replacements. Also, Reno vascular disease appears to be a separate risk issue for cardio vascular disease. Therefore it is important for patients and society that methods are developed to monitor renal function precisely, thus enhancing the assessment of disease progression, the prognosis, and follow-up therapy. At present, diagnosis of renal dysfunction is based on such measurements as urea, and electrolytes. In addition, these clinical chemistry measurement scan not detect local differences in the kidneys and cannot distinguish between left and right kidney.

To overcome these limitations, dynamic contrast-enhanced MR imaging (DCE MRI) has emerged as a technique that can be used furthermore accurate assessment of regional renal function. With thetechnique, signal intensity evolution can be measured and visualized as images that reflect the passage of an injected tracer or contrast agent through the organ. Dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) of the kidneys requires proper motion correction and segmentation to enable an estimation of glomerular filtration rate. A validation of the combined registration and segmentation approach is presented and demonstrates that the simultaneous solution of both problems.

An important obstacle to these dynamic measurement techniques that complicates further analysis is the movement of the organ of interest during image acquisitions, when the individual voxels undergo complex displacements due to respiratory motion and pulsation. Such movements are often overlooked in studies of renal function.

IV. EXPERIMENTAL EVALUATION

The proposed algorithm is evaluated in several experiments to simulate scenarios, involving different types of changes. In the following sections.

A. Registration

Proper registration is a critical step in the processing chain, as uncorrected voxel displacements will corrupt the voxel time courses. The motion artefacts are caused by respiratory motion, intestinal peristalsis, cardiac pulsations,or patient movement during data collection through GFR estimates can become strongly biased or even invalidated. To perform motion correction, affine registration can also be used as an initialization step to a supplementary deformable registration. Clearly, due to respiration there is a significant local affine motion component directed along the head-to-feat axis, as modelled in and also observed in our experiments (cf. Section IV-E.3). Still, there is also a deformable motion component due to the elastic properties of the kidney, deforming along with local geometric restrictions in the proximate surroundings. The model presented in this work is rather general and the choice of data terms is basically open and not a topic for discussion here. Still, an optimal data term is necessary in order to obtain the best possible registration. In the literature, deformable image registration of DCE-MRI time series for estimation of GFR has mainly been accomplished using (normalized) mutual information (N)MI which is regarded as a method-of-choice in multi modal registration. Normalized mutual information or mutual information has also been applied in several recent methodological papers for co-registration of DCE-MRI time series , although an optimal method has not yet been settled . Normally, the images contain durable edge information between various tissue types, and also within the kidney after the arrival of contrast agent. This phenomenon favours the use of a gradient dependent cost functional for registration. A normalized gradient field (NGF) was a viable alternative to MI for the registration of DCE-MRI images.

B. Segmentation

The task of *segmenting* the kidney in DCE-MRI recordings has taken several approaches Manual delineation performed by an expert is potentially accurate, but also highly subjective and time consuming in contrast to automated methods . Automated segmentation methods employing *k*-means clustering and *k*-nearest neighbour classification have been proposed. For these methods the signal intensities in time are used as a high-dimensional feature vector in each voxel. The advantage of these approaches is that the classification of a tissue voxel is based on the actual tissue response to the bolus wash-in and wash-out. Alternatively, active contours and related methods employing region and boundary properties in combination with shape constraints have been used. In this work, we apply the temporal tissue response and minimal boundary length as shape information for the segmentation.

C. Compartment Modeling

Renal filtration, mainly taking place in the renal cortex, can be estimated using compartment models within a defined segmentation of the kidney. The compartment time series are then fed into the chosen pharmacokinetic model, producing voxelwise parameters that best match the data. Compartment wise parameters can be obtained summing up the voxel-wise contributions over the whole compartment. A valid estimation of GFR thus depends on a successful registration and segmentation, which are the critical steps in the processing chain.

D. Combined Registation and Segmentation

A significant portion of the disagreements between DCE-MRI estimated and iohexol-estimated GFR can originate from at least three of the above mentioned processing steps that are executed separately: registration, segmentation, and compartment modeling. Errors occurring in one step are propagated to the next, not being adjusted or compensated for since the steps are essentially uncoupled. This is the major motivation for our proposed method, a combined registration and segmentation where the segmentation has a feedback term in the registration, thus assisting towards a more consistent alignment of time points. Several works in other research areas report that a combined segmentation and registration improves the overall performance compared to a sequential processing . Segmentations of the input and target image combined with a joint affine registration were used to improve both the registration and segmentation accuracy of 2D images. Their method was not suited to incorporate non-affine deformations in the registration part due to the linearity. Inital segmentation is assumed, and this prior information is used to guide a combined registration and segmentation of either the input or the reference image, depending on the application. Thereby, the input and reference images are matched along the curve enclosing the segmented region and the rest of the image is deformed according to the regularization of the deformation field. In some of these publications an additional image similarity measure was applied, usually the sum-of-squared differences (SSD)

E. *Experimental setup*

The experimental part was executed using five different experimental setups:
(a) Unprocessed images.
(b) Affine registration using FSL's MCFLIRT.

(c) An initial registration ($\beta = 0$) with NGF as cost functional followed by a plain segmentation ($\beta = 10$) discarding *D(u), R(u)*. This setup represents a traditional, sequential approach for analyzing DCE-MRI images, here referred to as the *Sequential model*.
(d) Our suggested model with combined registration and segmentation, using $\beta = 10$ and NGF as cost function in *D(u)*. This approach is referred to as *RegSeg*.
(e) Only the segmentation functional and the linear elasticity terms, thus excluding *D(u)* in. By this approach to demonstrate that the squared Mahalanobis distance in has the potential to act as an independent cost function for co-registration of time series.

V. CONCLUSION

Main novel contribution is to detect kidney diseases in MRI kidney images. The problem of registration of MRI kidney image requires proper motion correction for combined registration and segmentation, applicable to 4D DCE-MRI acquisitions of the moving human kidney images. The segmentation term affects the registration by enforcing time course similarity of voxels inside and outside the kidney. We conclude that our segmentation driven registration approach has a great potential for further development into a full-blown pharmacokinetic GFR model driven segmentation of the kidneys and its useful method to detect kidney diseases in medical image processing.

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