Automatic Arterial Input Function Detection for Prostate Dynamic Contrast Enhanced MRI

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Introduction

Dynamic Contrast Enhanced MRI (DCEMRI) has shown promise in non-invasive assessment of tumor vascular properties with application in prostate cancer staging and treatment monitoring. Accurate quantification from DCEMRI however, depends on the robust determination of the arterial input function (AIF) – concentration of contrast agent in feeding vasculature. AIF determination in prostate DCEMRI is challenging because of extreme significant intensity non-uniformity due to the use of an endo-rectal coil. Therefore existing methods in the literature do not perform well. In this work, we use both the temporal and spatial information of the dataset to determine the AIF for DCEMRI of the prostate. In order to address the problem of intensity non-uniformity in prostate datasets, we develop a Gamma variate function (GVF) fitting algorithm to find the pixels which have candidate shapes of AIF curves in time domain. The candidate pixels are then further refined using spatial information from the images to eliminate spurious pixels. We validate our method by clinical results and compare our automated AIF approach with expert traced manual AIFs.

Methods

Acquisition: 8 patients with known prostate cancer were scanned on a 3T Signa HDX MRI scanner (GE Healthcare, Waukesha, WI) under IRB approved protocols, using a 3D SPGR sequence (TR/TE 3.8/1.3ms, FA 15°, BW ±31 kHz, FOV 26 cm, matrix 256 x 160 x 16, thickness 3 mm). In each study 50-65 volumes were obtained in 4-5 mins (~4.5 sec/volume). 0.1 mmol/kg Gd-DTPA was injected i.v at 0.3 cc/sec for 100 seconds (Figure 1a).

Manual AIF Selection: DICOM data was processed using a pharmacokinetic analysis package (Cinetool, GE Healthcare) custom built in IDL. Following inspection of the time series data, a small ROI was placed within the left femoral artery to generate the manual AIF. A central slice location was selected to minimize inflow effects. The generated signal-intensity curve was converted into [Gd] concentration estimates using a blood T1 value of 1.6s at 3T. The AIF curve was then scaled to peak concentration of 2.3 mM based on published data from model based AIFs to make it robust to B1 inhomogeneity errors. Automatic delay correction was performed to shift the AIF so that the arrival of contrast matched that in the tumor for model-fitting.

Automatic AIF Estimation: In our method, we use GVF as a reference to detect the pixels which have characteristic shape of AIF using a fitting algorithm. After GVF fitting, the candidate pixels are further refined by applying spatial constraints using a message passing algorithm to only select arterial pixels in close proximity so that they lie in a large vessel, for final result. The flowchart of our method are shown in Fig. 1.

1. Derive theoretical bounds on GVF parameters that describe good AIF curves.
2. Determine bolus arrival time and peak time from the curvature of the SI-time curves.
3. Generate a GVF for each pixel by fitting the GVF to the time series of each voxel.
4. Select pixels whose GVF parameters are within the upper and lower bounds determined by our analytical methods.
5. Apply spatial information by using a message passing algorithm to find N pixels which have good fits with the GVF and minimize the distance to other candidate pixels.
6. Determine AIF by calculating the average signal curve from these N pixels. This automatic AIF is scaled and delay-corrected similar to the manual AIF above.
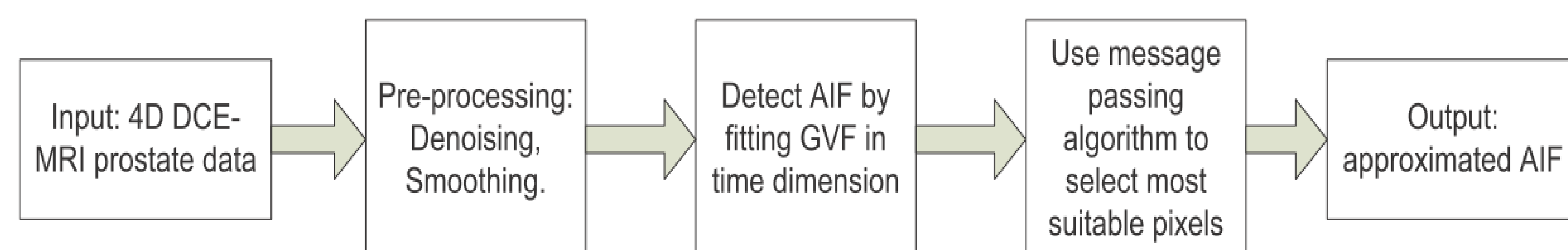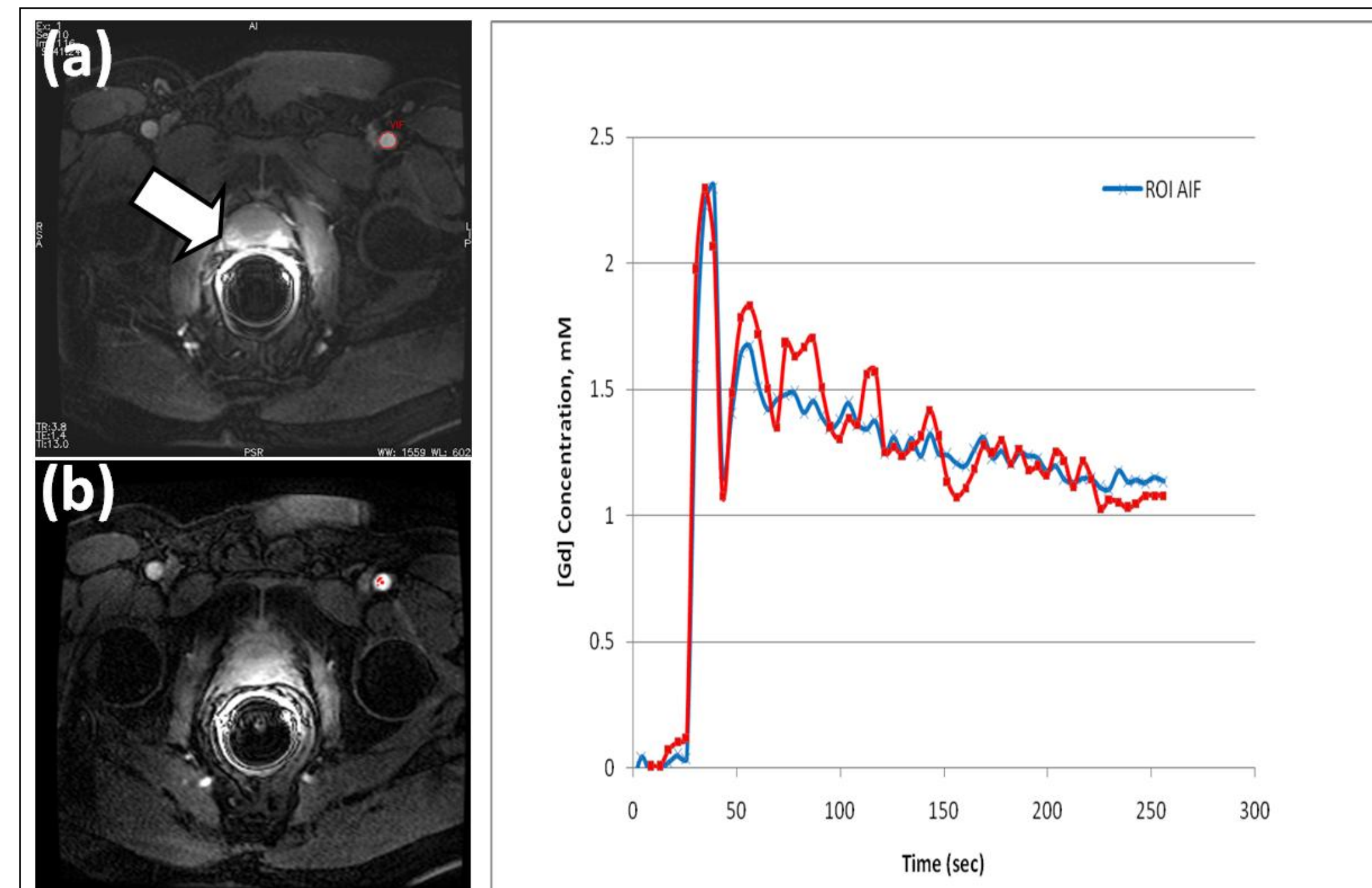

Fig. 1: Flowchart of our method.

Fig. 2: (a), Example DCEMRI image with manually selected AIF region (b), Image of (a) with AIF region selected by our method.
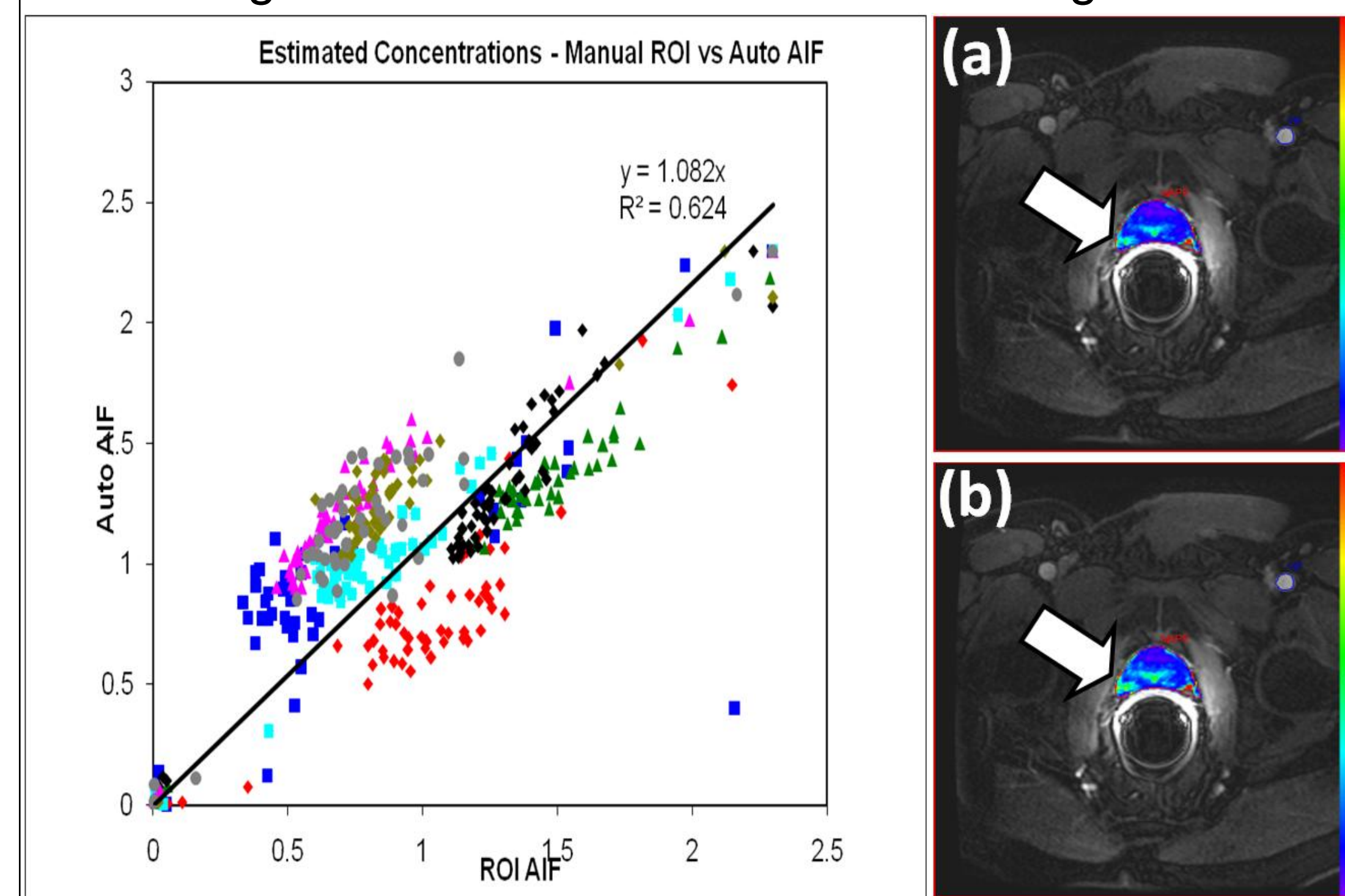Fig. 3: AIF curves obtained by manual (red) and our method (blue).

Fig. 4: Point-wise scatter plot of manual AIF and automatic AIF.
Fig. 5: (a), K^{trans} parametric map obtained by using the manual AIF. (b), K^{trans} parametric. map obtained by using the manual AIF.

Results and Conclusions

Our method was tested on 8 clinical DCEMRI datasets. The figures above show our results comparing the automatic AIF method to manual AIF. The effect of using the automated AIF versus manual AIF on the estimation of pharmacokinetic maps using the general kinetic model was also analyzed. No significant difference was observed in all calculated PK maps. Sample K^{trans} parametric map from one dataset by using the manual AIF and the automatic AIF are shown in Figures. 5(a) and (b) respectively. The tumor in the right peripheral gland is clearly visualized in both cases (shown by arrow).

In conslusion, we have developed a fully automatic method to determine the AIF for prostate DCEMRI, and validated our method using clinical data. Although our method is demonstrated for prostate DCEMRI, it is directly applicable to other body dynamic data.

References

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