Assessment of Renal Function using MR Renography without Aortic Input Information

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Dynamic contrast-enhanced MR renography (MRR) has been shown to be a valuable approach for the non-invasive assessment of renal function. Most current tracer-kinetic models to analyze MRR data require an input concentration versus time curve [1,2], which is usually measured from an aortic region of interest (ROI). However, aortic concentration versus time curve obtained from MR images suffers from several measurement errors, such as partial volume problem, flow effects, intravoxel dephasing, T2* effects, and others. Such errors in aortic curve may be propagated into the estimated renal parameters, such as glomerular filtration rate (GFR). In this study, we explored a new modeling approach which obviates input function measurements and estimates GFR based only on renal cortex and medulla enhancement curves.

Theory

In the kidney, plasma with tracer transits through intra-renal arteries and veins, and a fraction of it is filtered and goes in renal tubules and then collecting ducts. Tracer retention in renal medulla can be generally divided into 2 parts: tracer that transits fast in vascular pathway; and tracer that transits relatively slowly in tubules and collecting ducts. We proposed to express the medullary tracer retention as follows,

$$V_{Med} \cdot [Med] = V_{Med} \cdot f \cdot [Cx] + \Gamma \cdot [Cx] * R \,, \qquad (1)$$

where [Cx] and [Med] are the cortical and medullary concentration versus time curves, and V_{Med} is the volume of renal medulla. The first component in the right side of Eq. (1) approximates the vascular and early tubular tracer retention in medulla by using [Cx] and *f*, which accounts for the difference of tissue compartmental volume fraction between cortex and medulla. The second component expresses the tracer retention in later tubules and collecting ducts by a convolution of [Cx] as input with a retention function, R. The impulse retention function (IRF) (Fig. 1) contains three free parameters that reflecting the tracer's transit delay, minimum retention, and its dispersion.

Method

Nine patients with suspected renovascular disease underwent DCE-MRI at 1.5 T system (Avanto, Siemens) using a coronal 3D FLASH (TR/TE/flip angle=2.84/1.05/12°, 1.7x1.7x2.5 mm^3 voxel, 3s acquisition) after a 4 ml bolus of Gd-DTPA and 20 ml saline flush both at 2 ml/s. Following image registration and segmentation [3] and conversion of signal intensity to Gd concentration [4], measured cortical and medullary concentration curves were fed into Eq. (1), and the parameters (including Γ) in the right side were adjusted to minimize the residual difference between the two sides of Eq.(1).

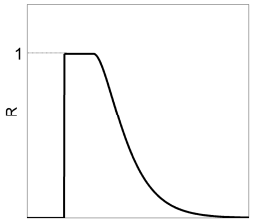

Fig.1

For every patient, ^{99m}Tc-DTPA renal scintigraphy was done in the same morning as MRI. Total GFR was estimated by plasma clearance method, and was split into left and right GFR according to renal uptake on gamma camera images at 2-3 min. One kidney was excluded due to multiple cysts. The single-kidney GFR and the fitted Γ for the patients were compared by correlation plot and regression line.

Monte Carlo simulation was performed to evaluate the precision and accuracy of the model-fitted Γ in the presence of noise. Two kidney cases from patient data were chosen to represent normal (GFR = 80.1 ml/min) and dysfunctional kidneys (GFR = 17.2 ml/min). For each case, the cortical and the medullary concentration versus time curves were first interpolated to 1s intervals, and then every 3 points were averaged to obtain smoothed 3s-interval data. To these curves 5% noise was added, and then the curves were re-sampled to the same time intervals as in actual data. The noised data were fitted by the proposed model fitting as described above. One thousand trials were run, and the coefficient of variance (CV) of the Γ estimates was computed to indicate the precision of the estimates. Model fitting of the noise-free curve provided Γ value that could be regarded as true value. Relative deviation of the Γ estimates from the true Γ was calculated as an indicator of accuracy.

Results and discussion

Model-fits for [Med] according to Eq.(1) for two representative patients are shown in Fig.2 (a) and (b). For all 19 kidneys (GFR range = 3.5 – 80.1 ml/min), the root mean square errors for fitting [Med] averaged 0.016 ± 0.006 mM. There was excellent correlation (R = 0.95) between parameter Γ and the scintigraphy GFR measurements (Fig. 3, y = 1.00x – 1.62).

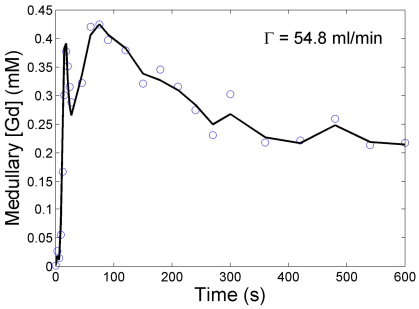

Fig. 2 (a)

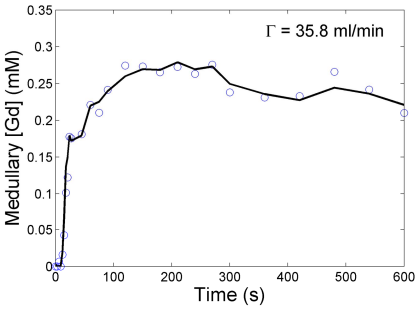

Fig. 2 (b)

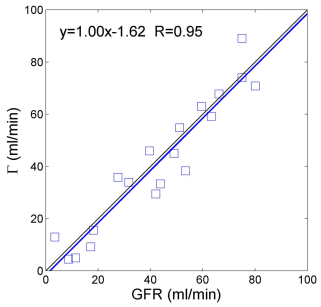

Fig.3

In Monte Carlo simulation, estimates of Γ for the normal kidney averaged 60.6±4.9 ml/min, for a CV of 8.0% and deviated from its true value (64.9 ml/min) by 5.1%. For the dysfunctional case, Γ estimates were 8.2±1.4 ml/min, whose CV was 16.7% and relative deviation from its true value (8.2 ml/min) was 0%. This simulation indicated that Γ could be estimated with high precision and accuracy under typical levels of noise.

Conclusion

The proposed method does not require the aortic input for assessment of renal function, and may prove a useful alternative approach for patient data in which an aortic input is hard to define. However, further study is needed to validate the use of parameter Γ to represent renal filtration under pathological conditions and to explore the utility of other parameters obtained by fitting the new model to MRR data.

[1] Annet L et al. J Magn Reson Imaging 2004;20:843-849. [2] Hackstein N et al. J Magn Reson Imaging 2005;22:406-414.
[3] Rusinek H et al. Magn Reson Med 2007; 57: 1159-1167. [4] Bokacheva L et al. Magn Reson Med 2006;55:1186-1190.