Estimating GFR from early (uptake) portion of DCE MRI renal data, using a 3-compartment model, improves reproducibility and may eliminate need for cortical segmentation.

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Hypotheses: 1) analysing the uptake-only (i.e. early) portion of Dynamic Contrast Enhanced (DCE) MRI kidney data will have benefits, since efflux is absent. 2) Larger Regions of Interest (ROI’s), over-including the cortex and parenchyma, will estimate total slice GFR, with reduced dependence on ROI boundary.

Introduction: A 3-compartment model fits DCE data up to 3 minutes1,2; however there are two practical difficulties. (1) the stationary compartmental model includes efflux from tubules, however physiologically this cannot happen for at least 50-90s, and there is MRI evidence to support this3. (2) Defining a cortical ROI is an intricate operation, requiring significant prior knowledge, and with potentially large between-observer variation.

Methods: MRI: 10 normal subjects were imaged before and after injection of 0.05 mmole/kg of Gd-DTPA, on a Siemens 1.5T Avanto imager, using a TIM 32 channel body phased array coil. A spoilt gradient echo 3D sequence had TR=1.6ms, TE=0.6ms, FA=17°. 18 contiguous 7.5mm slices were collected every 2.5s, with in-plane resolution 3.1 x 3.1mm, covering both kidneys. Subjects were imaged a week later, giving a total of 40 normal kidney curves.

Compartmental Modelling: The simple 3-compartment model for renal uptake has the following features.

\[
C_p(t) = C_{p_{aorta}}(t) \otimes g(t) = \int_0^t C_{p_{aorta}}(t-\tau) g(\tau) d\tau
\]

\[
\frac{dC_d}{dt} = F_1 - F_2 = K_{trans} C_{glomerulus} - K_{efflux} C_d
\]

\[
v_d C_d(t) = K_{trans} C_{glomerulus}(t) \otimes \exp(-K_{efflux} t/v_d)
\]

\[
C_i(t) = v_b (1-Hct) C_{glomerulus} + v_d C_d(t)
\]

Compartmental Modelling assumptions:

- Compartmental parameters were the time-dependent concentrations in \( v_a \), aortic plasma, glomerular plasma, and kidney tissue respectively. \( v_a \), \( v_b \), and \( v_d \) are the fractional volumes of glomerular plasma, glomerular blood and the distribution space for tracer extracted from the blood (principally the tubules). The delay and dispersion4 features are the delay of plasma-borne tracer travelling from the aorta to the glomeruli are described the Glomerular Impulse Response Function (GIRF) g(t). \( F_i \) is the tracer extraction rate per unit volume (m mole min \(^{-1} \)) from the glomerular plasma by the kidney; \( K_{trans} \) is the transfer constant from glomerular plasma to kidney (GFR per unit volume of tissue); \( K_{efflux} \) is the efflux (or on ward flux) from the kidney voxel, which in the model can be turned off; \( K_{trans} \) describes stationary efflux proportional the renal concentration. The symbol \( \otimes \) denotes convolution. \( v_p(1-Hct) \), v_a, where Hct is the hematocrit.

MRI modelling: Fitting was carried out in a Microsoft Excel spreadsheet. There were 6 free parameters: the pre-Gd tissue signal, \( v_b \), \( K_{trans} \), \( K_{efflux} \) (which could be turned off), and delay and dispersion parameters. The GIRF was interpolated to a resolution of 0.2s before convolution.

MRI analysis: ROI’s were placed on the descending aorta. In a central slice in each kidney, seven ROI’s were generated, ranging from a small piece of cortex to one that over-included the whole kidney (whilst excluding adjacent organs such as liver and spleen). Datasets with duration 50-100s after initial tracer arrival at the aorta were analysed. Total GFR for a ROI (\( \text{GFR}_{ROI} = K_{trans} V_{ROI} \)), where \( V_{ROI} \) was area of ROI x slice thickness, was calculated.

Results: Rms signal residual (n=40) was <2% of peak kidney value, gaussian GIRF’s fitted best, and fitting took <5s. Parenchymal data co plotted on Fig 1 and Fig 2.

Discussion and Conclusions:

1. Fitting the uptake-only portion gives reliable estimates of \( K_{trans} \), using the simplified model with efflux turned off, and \( K_{trans} \) reproducibility is improved.
2. The onset of trace efflux can be seen by monitoring the residuals from the ‘efflux-off’ fit (Fig 1). With efflux, signal is below that predicted by the model.
3. Slice GFR is approximately independent of ROI size, if the ROI over-includes all parenchyma, as expected from Object Strength studies of partial volume2.
4. RBF and transit time estimates are available from the GIRF estimate, in spite of the limited temporal resolution of the data (2.5s).

References:
1. Tofts ISMRM 2008; 454
2. Tofts ESMRMB 2008; 36
4. Annet JMRI 2004; 20:843
5. Tofts JMRI 1999; 10:223