Single Kidney GFR Measurements Derived from a Multicompartmental Model Analysis of 3D MR Renography

V. S. Lee[1], A. J. Huang[1], M. Kaur[1], H. Rusinek[1], C. A. Nazzaro[1], E. L. Kramer[1], E. Leonard[2]

[1]Department of Radiology, New York University School of Medicine, New York, NY, United States, [2]Department of Chemical Engineering, Columbia University, New York, NY, United States

Introduction

Gadolinium chelates such as Gd-DTPA are freely filtered at the glomerulus without tubular secretion or resorption and therefore their tracer kinetics can be used to determine physiologic parameters such as glomerular filtration rate (GFR) (1). With high temporal resolution 3D imaging, the passage of Gd chelates can be visualized in near-real time through intrarenal regions. Low doses of contrast material ensures that T2* effects of concentrated Gd are avoided and make MR renography compatible with routine clinical contrast-enhanced imaging of the kidneys and renal arteries (2). Several qualitative and quantitative methods have been proposed to to derive GFR values from MR renography (2-5, for example). We propose an approach based on a multicompartmental model that recapitulates nephron physiology and test the method against GFR measurements derived from ^{99m}Tc-DTPA clearance.

Model

The model, schematically represented in Fig 1, divides the vascular-nephron unit into 7 physiologically and anatomically-defined compartments: the aorta (Ao), which serves as the input function, the intrarenal arteries and glomerular vessels (A), the vasa recta and veins (V), the proximal convoluted tubule (P), the loop of Henle (L), the distal collecting tubule (D), and the collecting system and ureter (U). [Ao] is measured, the others are fitted. The regional concentrations, cortex (Cx) and medulla (Med) are linear combinations of these compartmental concentrations, weighted based on the volume fractions of each compartment within that region. The general model contains 13 parameters: renal plasma flow (RPF), glomerular filtration rate (GFR), the fractional weights each compartment contributes to the cortex and medulla (wA_{Cx}, wP_{Cx}, wD_{Cx}, wV_{Cx}, wA_{Med}, wL_{Med}, wD_{Med}, wV_{Med}), and the flow rates at which the filtrate in the various compartments is resorbed back into the veins (F_P, F_L, F_D, which represent fractions of the GFR). The total volumes of the cortex, medulla, and collecting system are derived from segmented image sets.

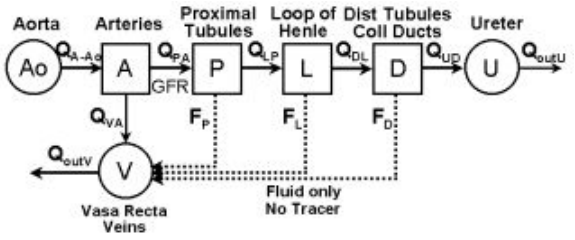


Figure 1. Multicompartmental Model of Kidney

Rather than solving the system of differential equations for all 6 compartments and 3 regions simultaneously, the problem can be divided into separate steps solved sequentially. First, the transit of tracer from Aorta (Ao) to Cortex (A,P) is modeled (Eqns 1), and the measured cortical Gd-time curve used to derive estimates of RPF, V_A, f_P, as well as GFR, where wP_{Cx} is approximated to be 0.3 (6,7). Then the transit from Cortex (A,P) to Medulla (A,L) is modeled (Eqns 1 and 2), and the medullary Gd-time curve fit to obtain more robust measurements of GFR, as well as estimates of wA_{Med} and f_P, where values for wA_{Cx}, RPF, and f_P are derived from fits in the first step, and wL_{Med} is assumed to equal 0.5 (6,7). The model was implemented using JSIM (National Simulation Resource, Univ of Washington).

$$\frac{d[A]}{dt} = \frac{RPF}{V_A}\left(\frac{[Ao]}{(1-Hct)} - [A]\right) = \frac{RPF}{wA_{Cx}V_{Cx}}\left(\frac{[Ao]}{(1-Hct)} - [A]\right)$$

$$\frac{d[P]}{dt} = \frac{GFR}{V_P}\left([A] - (1-f_P)[P]\right) = \frac{GFR}{wP_{Cx}V_{Cx}}\left([A] - (1-f_P)[P]\right)$$

$$[Cx] = \frac{V_A}{V_{Cx}}[A] + \frac{V_P}{V_{Cx}}[P]$$

Eqns 1

$$\frac{d[L]}{dt} = \frac{GFR}{V_L}\left((1-f_P)[P] - (1-f_P-f_L)[L]\right) = \frac{GFR}{wL_{Med}V_{Med}}\left((1-f_P)[P] - (1-f_P-f_L)[L]\right)$$

$$[Med] = \frac{V_{A,Med}}{V_{Med}}[A] + \frac{V_L}{V_{Med}}[L] = (wA_{Med})[A] + (wL_{Med})[L]$$

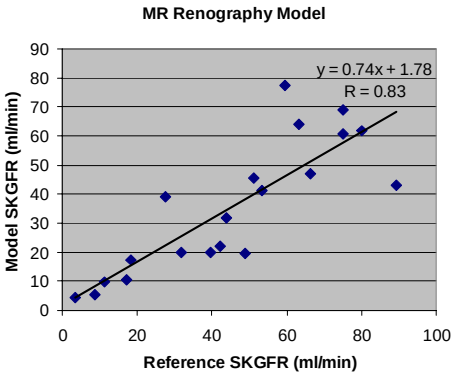
Eqns 2

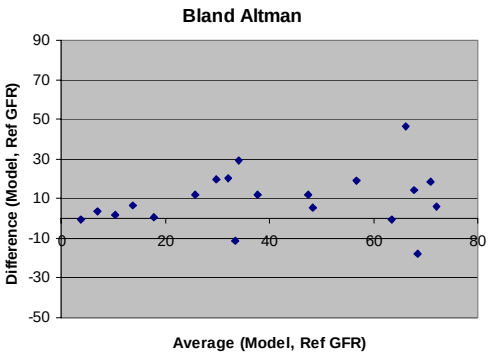
Methods

We examined 10 patients referred for suspected renovascular disease. MR renography was performed on a 1.5T system (Avanto, Siemens) using a coronal interpolated 3D spoiled GRE (2.84/1.05/12°, 20 interpolated to 40 partitions, voxel size 1.6 x 1.6 x 2.5 mm, with parallel factor 3, acquisition time 3 sec). Acquisitions were repeated continuously for 30 sec and then at multiple time points up to 10 – 20 min following intravenous injection of 4 ml Gd-DTPA. Following semi-automated registration and segmentation of the datasets, aortic, cortical, and medullary time-intensity curves were converted to Gd concentration curves based on an empirically derived relative signal intensity conversion. All subjects also underwent same day ^{99m}Tc-DTPA blood clearance measurements based on 1 and 3 hr blood draws to estimate total GFR. Split renal function based on gamma camera imaging of renal uptake was used to calculate individual kidney GFR.

Results

Among the ten patients, single kidney GFRs derived from scintigraphic studies ranged from 3.5 to 89.4 ml/min. Multicompartmental model-derived values ranged from 4.3 to 77.3 ml/min. The correlation between model-based SKGFR and reference values was high (r = 0.83, p<0.001, Fig 2). Bland Altman analysis is shown in Fig 3.





Conclusion

A nephron-based multicompartmental model can be used to derive single kidney GFR from low dose MR renography.

References

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