

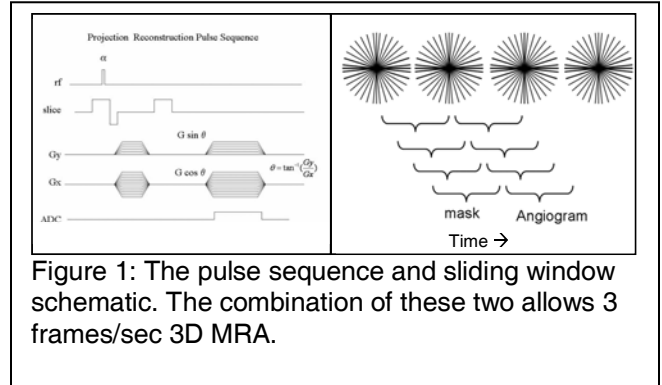
Pulse Sequence for Comprehensive Evaluation of Renal Artery Stenosis

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Introduction:

Angiography of the renal arteries has become a mainstay in the diagnosis of renal artery stenosis (RAS). Renal perfusion, less commonly evaluated, has information regarding viability, function, or the hemodynamic significance of a single kidney. MRA and perfusion scans are normally performed as separate acquisitions, requiring a separate contrast injection and breath-hold. An acquisition which combines anatomic and functional information would be desirable, since it would require less time and contrast agent than two separate scans. We have developed a 3D radial sequence reconstructed to 3 frames/s time resolution, which was used to obtain perfusion maps of the renal parenchyma, in addition to the dynamic angiograms of the renal system. This sequence is based on a radial acquisition, using bit-reversed angular sampling and sliding window view-sharing scheme which allows 3D frame rates as high as 3 frames/sec (Figure 1).



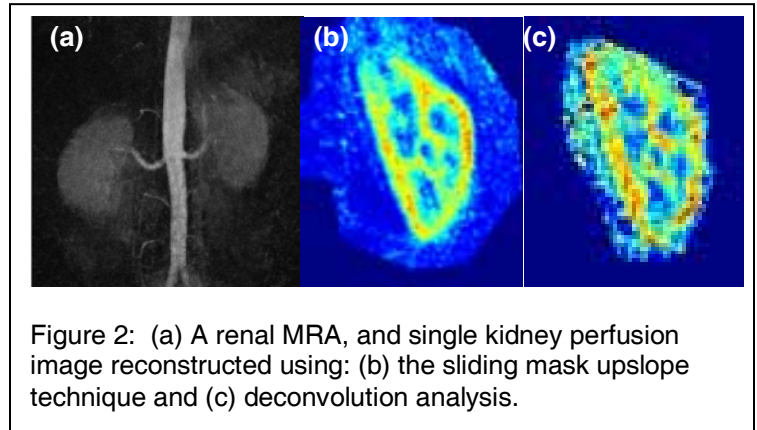
Materials and Methods:

3 healthy volunteers were recruited for the Siemens 3T scanner. 4-channel body coil was used to image the abdominal areas. A 3D FLASH sequence with radial in-plane trajectories ($N_p=128$, $N_{RO}=192$, $FOV=220\text{mm}$, $TR=3.05\text{ms}$, $TE=1.08$) was used. The data was reconstructed with sliding window technique. Renal MRA benefits from radial trajectories since the center of k-space is sampled on every TR. For angiography, the images were subtracted using a sliding mask, where the mask is not the first frame but some set number of frames behind the current image[1].

For perfusion analysis, the arterial input function (AIF) was first determined by selecting an ROI in the aorta. Calculation of blood flow was done using two different methods, 1) the upslope method[2] and 2) the deconvolution method[3].

For the upslope method, relative renal blood flow (rRBF) was calculated by dividing the maximum slope of renal [Gd] vs. time curve by the maximum value of the AIF. Since the sliding mask subtraction is effectively the derivative of unsubtracted images, the maximum value of the subtracted images was taken to be the maximum slope.

For the deconvolution method, the renal [Gd] curve was deconvolved with the AIF using singular value decomposition to obtain the impulse response function (IRF). Then the rRBF of each voxel was calculated by taking the maximum value of IRF. The upslope method is much faster than the deconvolution method, but the deconvolution method calculates the IRF, which gives a complete characterization of the system.



Results/Discussion:

High spatial and temporal resolution 3D MRA images with 3 frames/sec were obtained using this method, as well as perfusion maps of the entire kidney in a single scan. Figure 2 shows representative images acquired from one scan. The two methods of perfusion analysis were compared, but did not correlate well. The deconvolution seemed to suffer too much from errors. Furthermore, the computation time for deconvolution using SVD was too lengthy to be practical. On the other hand, using the upslope method, an angiogram and a perfusion map can potentially be obtained instantly from the scanner.

References:

[1] Cashen, T.A., et al., ISMRM 2006. [2] Vallee, J.P., et al., Eur Radiol, 2000. [3] Dujardin, M., et al., MRM 2005.