

## Comparison of Different Models for Analysis of Renal Diffusion Imaging

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**Introduction:** Compared to the standard mono-exponential approach to analyze diffusion weighted MRI data, the application of more complex models can result in valuable additional insight into pathological processes. This work compares results from mono-exponential, stretched-exponential, diffusional kurtosis and bi-exponential models, which were applied to analyze renal diffusion imaging data sets. In a first step, reference data for each model was obtained from 5 healthy subjects. The reference model parameters were then compared to results from renal pathologies.

**Methods:** Studies were performed on a 1.5T whole body system (Magnetom Avanto, Siemens, Germany). The kidneys of 5 healthy subjects and 2 patients with focal kidney lesions (Patient 1: benign cortical cyst; Patient 2: Multifocal papillary renal cell carcinoma (RCC)) were investigated during free breathing with a single-shot EPI DWI sequence with 8 b-values of 0, 10, 40, 70, 120, 250, 450, and 700s/mm<sup>2</sup>. Other imaging parameters were: matrix:156x192, voxel size:2.4x2.2x6.0 mm<sup>3</sup>, TR=3700ms, TE=65ms, 4 averages. Acquisition time was 5 min 38 s using parallel imaging with an acceleration factor of 2 and partial Fourier acquisition. Four different models were fitted to the data on a pixel by pixel basis using MatLab (Mathworks, Natick, Mass). Eq.1 describes the mono-exponential diffusion model (1) with the apparent diffusion coefficient as parameter of interest. The stretched exponential model (2) including the stretching parameter  $\alpha$ , that defines the deviation of the signal decay from a mono-exponential and the distributed diffusion coefficient DDC is given by eq.2. The Kurtosis model (3) described by eq.3 results in an apparent diffusion coefficient  $D_{app}$  and the diffusional kurtosis  $K_{app}$ . The bi-exponential model (4) as given by eq.4 consists of the perfusion fraction f, the diffusion coefficient  $D_1$  and the pseudo-diffusion coefficient  $D_2$ .  $S(b)$  is the signal measured at a given b-value,  $S_0$  is the signal amplitude in the absence of diffusion weighting.

**Results and Discussion:** Fig 1-3 show the pixel wise fit results from the kidneys of one healthy volunteer and the two patients. Fig 4 presents the average values of the fit results of the five healthy subjects, as well as ROI-based values from the focal pathologies present in patient 1 and 2. Both the stretched exponential model and the kurtosis model provided solid fit results for the parameters  $\alpha$  and  $K_{app}$ , respectively. While the cyst is characterized by an  $\alpha$ -value close to 1, the two RCC lesions show a clear deviation from mono-exponential behavior with  $\alpha$ -values around 0.5. This deviation from Gaussian diffusion is even more pronounced in the kurtosis maps, where both RCC-lesions can be clearly differentiated from healthy parenchyma by their higher  $K_{app}$ , which is consistent with reduced diffusivity in the tumor due to high cellular density. Compared to the other approaches the application of a bi-exponential model to our data resulted in a very high variability of the resulting parameters and in addition did not allow for a clear discrimination of tissues.

### Conclusion:

Quantification of renal DWI data by stretched exponential and diffusion kurtosis models result in additional parameters that may facilitate the better characterization of different tissue types like RCCs.

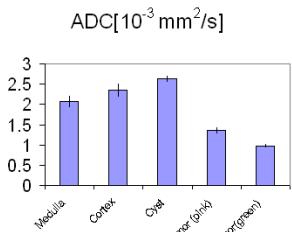
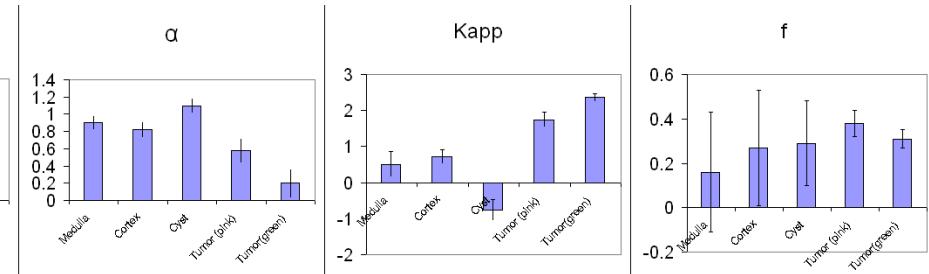


Fig. 4: Fit results of the average values of five healthy volunteers, one cyst, and two RCC lesions



**Acknowledgements:** The authors acknowledge support by the Chinese Scholarship Council

**References:** (1) Le Bihan et al. , *Radiology* 161(1986), (2) Bennett et al. , *MRM* 50(2003), (3) Jensen JH et al. , *MRM* 53(2005), (4) Le Bihan et al. , *Radiology* 168(1988),