Fractal Analysis of Real-Time BOLD Data from Healthy Kidneys

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Introduction: BOLD kidney MRI thus far has been acquired during breath holding to reduce motion related artifacts in T2* and R2* maps **[1]**. Because breath holding may not be feasible for elderly or diseased subjects, it is beneficial to explore novel techniques for BOLD kidney analysis that allow for quiet breathing during image acquisition. Fractal analysis on real-time BOLD data has been used to study microvascular organization in rectal carcinoma **[2]**. In this study, real-time BOLD data from healthy kidneys was analyzed to determine whether signal variations are fractal, and if so whether they can be characterized as fractional Gaussian noise (fGn) or fractional Brownian motion (fBm).

Materials and Methods: In a study approved by our research ethics board, the kidneys of healthy subjects (n=5) were imaged using a T2* weighted (BOLD) GRE EPI sequence (TR/TE=250/35ms, flip=70^o, FOV=30cm 96x96 matrix, 3 slices 5mm thick, 0mm skip, oblique-coronal plane, 2400 temporal points, 10 minutes total time). The acquisition plane was prescribed from a sagittal multiphase FIESTA to select along the longitudinal axis of the right kidney, which is the direction of motion during breathing. All scans were done using a GE Healthcare 3T HD Signa MRI and 8 channel torso phased array coil. During BOLD scanning, subjects were instructed to breathe normally. After data collection, the images were processed with a template matching algorithm previously used for kidney analysis **[3]**. Regions of interest (ROI) were selected for the renal medulla and renal cortex using AFNI **[4]**, and this data was exported to MATAB (The Mathworks, Natick MA)**.** Data was analyzed in MATLAB using an in-house developed algorithm based on the work done by Eke *et al.* [**5**] to calculate the fractal dimension and Hurst coefficient of data within each ROI.

Results: In both the renal medulla and cortex, the data was found to be fractal, both having a majority of voxels being fGn (**Table 1**). The mean Hurst coefficients (H) and fractal dimension (D) are shown in (**Table 1**). Mean ± standard deviation of Hurst coefficient in the cortex and medulla were 0.7140 ± 0.1657 and 0.7448 ± 0.1494 respectively. Voxels with fBm were excluded from the calculation of these means as their H values differ greatly from fGn and they represent fewer voxels.

Subject	Ratio of fGn/fBm (cortex)	Fractal Dimension (cortex)	Hurst Coefficient (cortex)	Ratio of fGn/fBm (medulla)	Fractal Dimension (medulla)	Hurst Coefficient (medulla)
1	Inf	1.38	0.62	Inf	1.37	0.63
2	4.56	1.01	0.99	23.50	1.04	0.96
3	Inf	1.39	0.61	Inf	1.37	0.63
4	5.29	1.18	0.82	9	1.16	0.84
5	Inf	1.46	0.54	Inf	1.40	0.60
6	7.13	1.28	0.72	4.44	1.19	0.81

Table 1: Ratio of number of voxels where data was characterized as fractional Gaussian noise (fGn) to number characterized as fractional Brownian motion (fBm) and mean of fractal dimension and Hurst coefficient for each ROI, using only fGn voxels.

Conclusion: Rapidly acquired BOLD data from both kidney cortex and medulla behave fractally, where the majority of the data is characterized as fGn. This approach to BOLD signal assessment could be of use during renal challenge and may be useful in differentiating disease processes.

References:

[1] Notohamiprodjo M, *et al*. (2010) *Eur J Radiol*. 76:337-347. **[2]** Wardlaw G, *et al.* (2008) *Physica Medica* 24:87-91. **[3]** Boyd BJ and Noseworthy MD. (2009) *ESMRMB* 26:678. **[4]** Cox RW. (1996) *Comp Biomed Res.* 29:162-173. [**5**] Eke A, *et al.* (2000) *Eur J Physiol*, 439:403-415.