Sensitivity and specificity of prostate tumor discrimination by IVIM approximation

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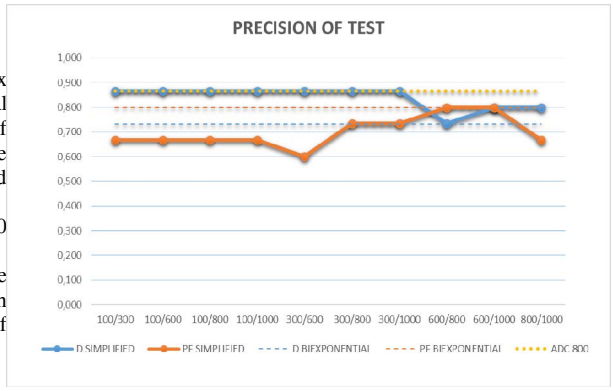
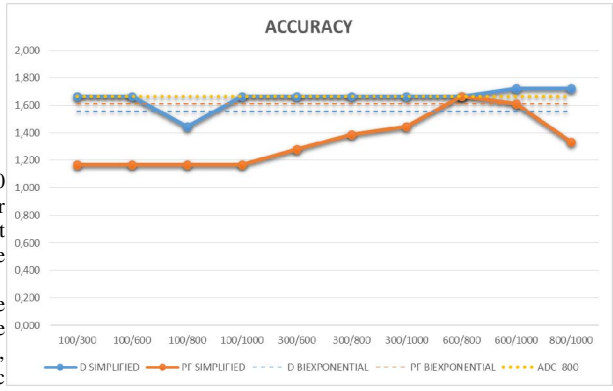
Purpose: There is growing interest in the IVIM analysis of diffusion-weighted imaging (DWI) of prostate cancer. The bi-exponential model has been shown to explain experimental data better than the pure diffusivity mono-exponential model [1]. However, the bi-exponential analysis of data needs a multi b-values set of images leading to long acquisition time. In this regard, a simplified analysis of IVIM parameters, based on the model presented in [2], has been proposed in order to reduce time of acquisition [3].This simplified analysis allows one to estimate the diffusion coefficient (D) and pseudo-diffusion fraction (pf) from only two images acquired at high b-values. This method is based on the approximation that the pseudo-diffusion term is negligible when the b-value is sufficiently high. Although the IVIM parameters calculated in this way are not good estimates of the corresponding values obtained by the bi-exponential fit [4], their value is statistically different in pathological and healthy tissues. Moreover, in the literature there is no agreement on the acquisition parameters to use.
The aim of this work is to investigate the ability of the IVIM parameters, obtained using the simplified method applied to DWI acquired at various b-values, to differentiate prostate tumor from normal tissues.
Methods: Ten patients with a diagnosis of prostate cancer were considered in this study. DWI images were acquired using 6 different b-values (10, 100, 300, 600, 800, 1000 sec/mm2). Malignant and healthy tissues of prostate were delineated by 3D contouring on a T2-weighted image, then registered to DWI volumes. A correction for patient and organ motion and for eddy currents distortions were performed on DWI images.
ADC was evaluated for each b-value in every voxel according to

$$ADC_b = \frac{1}{b} ln \frac{S(b)}{S(0)}$$

The values for pf and D were obtained by a bi-exponential fit in every voxel of the prostate. Six non-diffusion weighted images were used to build a standard deviation map used as statistical weight in the non-linear fit. The goodness of the fit was evaluated by the coefficient of determination R2. Only voxels with R2>0.99 were considered in subsequent analysis. The simplified method was applied for each pair of b-values greater than 100 sec/mm2 to obtain pf and D in all prostate voxels.
In order to test the quality of the scanner, a phantom was imaged using b-values from 0 to 2000 sec/mm2 at steps of 10 and the goodness of the fit was evaluated.
ROC analysis were used to extract the optimum cut-off for ADC, pf and D in order to reduce the number of false negatives (FN) and of false positives (FP), prioritizing FN. The cut-off was chosen to maximize the accuracy (specificity + sensitivity) of test. Specificity, sensitivity and precision of test were calculated for each pair of b-values and for bi-exponential fit.





Results: We found cut-off value to zero FN for
- ADC: using b-values greater than 300 sec/mm2;
- D: using intermediate b-values pair (100-800 to 300-1000 sec/mm2);
- pf: using low b-values pair (100-300 to 100-1000 sec/mm2).

Better precision and accuracy were observed in:
- ADC: using b-values greater than 300 sec/mm2;
- D: using pair of low b-values (100-300 to 300-1000 sec/mm2)
- pf: using intermediate pair of b-values (300-800 to 600-1000 sec/mm2).

Discussion: The bi-exponential fit presents poorer accuracy and precision than ADC (for b>300 sec/mm2) and pf is a better discriminant than D. Furthermore, the simplified model exhibits better behavior when differentiating tumors, with respect to the bi-exponential model when using D but not when using pf. The best accuracy and precision was reached when using D evaluated by the simplified model acquiring intermediate b-values (from 100-1000 to 300-1000 sec/mm2).
Conclusion: Even if IVIM parameters calculated using the simplified model are not accurate estimates of the corresponding ones derived with the bi-exponential fit, we found that the simplified model discriminates prostate tumor from healthy tissues in a accurate way. Therefore, this simplified technique allows to reduce the acquisition time and preserve a good diagnostic accuracy.

References:

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