PRECISION AND ACCURACY OF INTRAVOXEL INCOHERENT MOTION (IVIM) MRI: APPLICABILITY IN WELL-PERFUSED TISSUES

Mie Kee Lam[1], Clemens Bos[1], Chrit T W Moonen[1], Max A Viergever[1], and Lambertus W Bartels[1]
[1]*Image Sciences Institute, UMC Utrecht, Utrecht, Utrecht, Netherlands*

Purpose

Intravoxel incoherent motion (IVIM) MRI is a method to extract perfusion and diffusion information from diffusion weighted MR data using a bi-exponential fit[1]. The ability of the method to estimate IVIM parameters precisely was investigated by Pekar et al. for the relatively low perfusion fraction typical of the brain (5%)[2]. They showed that an SNR of 400 was required to achieve a relative precision of 20% in the perfusion fraction f_p. In the past years, the interest in IVIM MRI has increased for the purpose of detecting lesions in well-perfused organs[3-5]. A recent study showed that IVIM parameters are sensitive to signal from vascular components, by comparing the IVIM parameters with and without applying blood suppression in well-perfused organs[6]. The purpose of this study was to investigate the performance of IVIM MRI by Monte Carlo simulations, including high perfusion fractions typical of tumors and well-perfused organs.

Methods

For IVIM MRI parameter extraction there are two commonly used fit methods: the direct fit[3,6] and the segmented fit[4,5]. With the direct fit, the bi-exponential function[1]: $S(b) = S_0(f_p\, e^{-bD_p} + (1 - f_p)\, e^{-bD_t})$ is directly fitted to data points representing the signal intensity for a number of *b*-values, S_0 is the initial signal amplitude, f_p is the perfusion fraction, D_p is the pseudo-diffusion coefficient originating from vascular components and D_t is the true diffusion coefficient. In this direct fit S_0, f_p, D_p and D_t are the fit parameters. The segmented fit uses a mono-exponential fit first on higher *b*-values ($b \geq b_{cut\text{-}off}$) to extract D_t and f_p. Then the bi-exponential function defined above is fitted to the measured signal at all available *b*-values while keeping D_t and f_p fixed to the estimated values from the first step, leaving S_0 and D_p as fit parameters[4,5].

To investigate the accuracy and precision that can be achieved in IVIM parameter estimation with IVIM MRI, Monte Carlo simulations were performed in Matlab (2013b, Mathworks, Natick, MA). The IVIM signal was simulated using the bi-exponential function defined above, where the signal was normalized: $S_{0,true} = 1$ and the true values of the other parameters were adapted from literature: $D_{p,true} = 15{\cdot}10^{-3}$ mm^2/s [4,5], $D_{t,true} = 1{\cdot}10^{-3}$ mm^2/s [2-5], $f_{p,true} = 0.05$, 0.15 and 0.25; perfusion fractions from the brain[2], tumors[4] and well-perfused organs[3,6]. The *b*-values at which the signal was sampled were comparable to those used in other studies[3-5]: b = 0, 25, 50, 75, 100, 150, 200, 400, 600 and 800 s/mm^2. Gaussian noise was added to the signal for SNR values based on $S(b{=}0)$ of 10, 20, 30, 40, 50, 100, 150, 200, 250, and 500.

The simulated signals were fitted with an iterative non-linear least squares fit (Matlab 2013b, Mathworks, Natick, MA) with the following starting values and lower and upper boundaries: $f_{p,start} = 0.15$, $f_{p,low} = 0$, $f_{p,upp} = 1$, $D_{p,start} = 15{\cdot}10^{-3}$ mm^2/s, $D_{p,low} = 0$ mm^2/s, $D_{p,upp} = 0.1$ mm^2/s, $D_{t,start} = 1{\cdot}10^{-3}$ mm^2/s, $D_{t,low} = 0$ mm^2/s, $D_{t,upp} = 0.1$ mm^2/s. N = 1000 trials were performed for a simulation of the direct fit and for simulations of the segmented fit using the following $b_{cut\text{-}off}$ values: 150, 200 and 400 s/mm^2. The relative estimation precision (estimation variation over all trials) and accuracy (mean absolute estimated error over all trials) of the fit parameters f_p and D_p were used for analysis as percentage of $f_{p,true}$ and $D_{p,true}$.

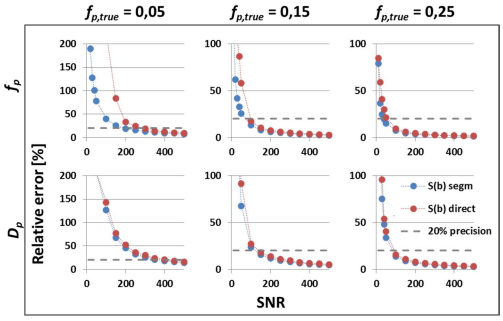

Figure 1 Relative estimation precision of f_p and D_p for different $f_{p,true}$ values, with $b_{cut\text{-}off}$ = 200 for the segmented fit. The grey dashed line indicates the acceptable relative precision of 20%.

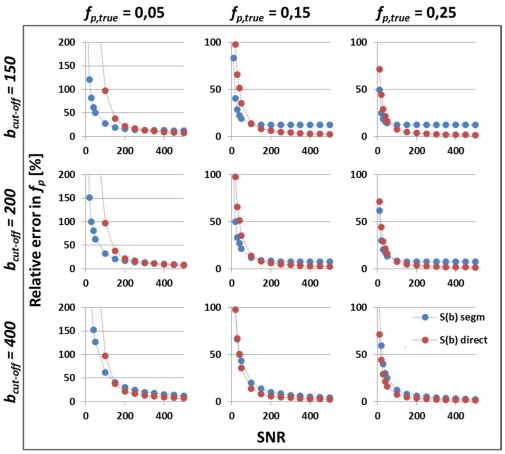

Figure 2 Relative estimation accuracy of f_p for different $f_{p,true}$ values using different $b_{cut\text{-}off}$ for the segmented fit.

Results

Figure 1 shows the relative estimation precision of f_p and D_p for the direct fit and the segmented fit using $b_{cut\text{-}off}$ = 200 s/mm^2. The acceptable relative precision in f_p of 20% defined by Pekar et al.[2] is indicated by a dashed line. To achieve this precision with $f_{p,true} = 0.05$ it requires an SNR of about 300 with the direct method. With increasing f_p the required SNR decreases for both fit methods: SNR = 100 suffices for $f_{p,true} = 0.15$ for both methods, for $f_{p,true} = 0.25$ an SNR of 50 suffices for the direct fit and an SNR of 40 for the segmented fit. For $f_{p,true} = 0.25$ at SNR = 75, D_p can be estimated with 20% relative precision using the segmented fit. Figure 2 shows the relative estimation accuracy of f_p for the direct fit and the segmented fit using all $b_{cut\text{-}off}$ values. The estimation accuracy increases with increasing $f_{p,true}$ for both fit methods, but the segmented fit shows a bias (systematic error) at higher f_p which is highest for lower $b_{cut\text{-}off}$.

Discussion & conclusion

The simulations confirm that a high SNR of 300 is required to achieve a relative estimation precision of 20% in f_p with the direct fit method at a perfusion fraction typical of the brain ($f_{p,true} = 0.05$), similar to the SNR of 400 reported by Pekar et al., where $D_{p,true}$, = $10{\cdot}10^{-3}$ mm^2/s was used[2]. However, our results show that at a perfusion fraction expected in well-perfused organs ($f_{p,true} = 0.25$) an SNR of 50 suffices with the direct fit and an SNR of 40 suffices with the segmented fit. The segmented fit method shows systematic accuracy errors that persist at high SNRs (Fig.2), specifically at higher $f_{p,true}$. The bias reduces when using higher $b_{cut\text{-}off}$ values, suggesting the influence of residual signal from the perfusion component in the mono-exponential step of the segmented fit. Our results suggest that it is feasible to retrieve perfusion parameters at realistic SNRs with acceptable accuracy and precision using IVIM MRI for perfusion fractions typical of tumors and well-perfused organs. Especially at the high perfusion fractions found in these tissues, care should be taken when choosing $b_{cut\text{-}off}$ in relation to D_p with the segmented fit method to avoid systematic errors caused by residual perfusion signal.

THIS RESEARCH WAS SUPPORTED BY THE CENTER FOR TRANSLATIONAL MOLECULAR MEDICINE (HIFU-CHEM)

References: (1) LeBihan et al., Radiology, 1988, 168: 497-505. (2) Pekar et al., MRM, 1992, 23: 122-129. (3) Lemke et al., Inv Rad, 2009, 44(12): 769-775. (4) Sigmund et al., MRM, 2011, 65: 1437-1447. (5) Chandarana et al., Inv Rad, 2011, 46(5): 258-291. (6) Lemke et al., MRM, 2010, 64: 1580-1585.