What is a good sampling rate for DSC-MRI brain perfusion measurements?

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Purpose

Perfusion weighted imaging is an important tool in acute stroke and other cerebro-vascular diseases. For proper diagnosis and treatment planning the absolute values of perfusion parameters as flow (CBF), volume (CBV) and mean transit time (MTT) are crucial. Estimation of quantitative perfusion parameters requires deconvolution to reconstruct the impulse response function (IRF) [1] in brain tissue. In the deconvolution process regularization is added in the deconvolution process to remove noise-dominated components which otherwise lead to physically implausible results. Generally the regularization removes all components whose power is comparable to the noise level. Because typical arterial input function (AIF) and tissue signals in human brain have monotonically decreasing spectra, regularization attends to be strong low-pass filtering, effectively removing noise-dominated high frequency components of the IRF (Fig. 1). Since high frequencies are not used for determination of the IRF, one can speculate whether or not they need to be sampled and if a lower temporal resolution might be adequate. The use of longer repetition times (TR) might be advantageous in DSC-MRI because less T1w effects could be anticipated as well as a larger number of slices could be interleaved within one TR. The objective of this study was therefore to determine whether or not there is an optimal sampling rate for DSC-MRI perfusion measurements if deconvolution with regularization is applied.

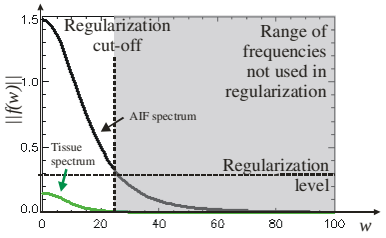

Fig. 1: Frequency components removed in regularization

Methods

Deconvolution can be seen as providing the system's dynamic characteristics to an impulsive perturbation by comparing the frequency spectra of input and output signals. Mathematically, it can be implemented using e.g. Singular Value Decomposition (SVD) or Fourier Transform (FT). For ease of explanation the FT approach was used here. Recently it was shown that deconvolution is equivalent in time and frequency domain [2]. While the regularization threshold is related to the noise level, it is often simply set to a fixed value relative to the input signal spectrum (truncated SVD) or obtained by evaluating the properties of the computed IRF (Tikhonov regularization, Wiener filtering). Only those spectral components whose power is significantly higher than of the noise power or regularization level are used to reconstruct IRF. Therefore, to determine an optimal sampling resolution for DSC-MRI the shape of the AIF and tissue signals, and the contrast-to-noise ratio (CNR) of the PWI acquisition must be considered together. We propose to determine the ideal sampling rate as follows: (1) determine the regularization cut-off frequency f_c. (2) derive the sampling rate under consideration that a prolonged TR in DSC-MRI will cause aliasing of the signal spectra (Fig. 2). Hence, sampling at TR related to f_c will cause undesired change in the power of the sampled spectral components. To avoid this unwanted effect, the signal will be sampled at a higher sampling frequency f_s such that the effect of spectral aliasing in the deconvolution operation is lower or equal than the noise-variation. If we define f_n as the frequency where the power of the AIF spectra falls under the power of the noise, then $f_s = (f_c + f_n)/2$. To verify this approach we first performed numerical simulations using typical DSC-MRI signals measured in human brain. The AIF signal was modeled by a gamma-variate function ($y = A(t-t_0)^{\alpha}\exp(-(t-t_0)/\beta)$, *A=20, α=3.51, β=1.0, t_0=10.0,* constituting AIF with a peak level of 50.0 [a.u.] and a FWHM = 4.6s) and the impulse response function by a half-Gaussian profile (simulating a typical human brain IRF) with a MTT=6s and CBF=70ml/min/100g. The tissue response curve was obtained by numerical convolution of AIF and modeled IRF (using Δt = 0.1s). Recovered IRF were obtained by FT deconvolution with fixed regularization thresholds of 10, 15, 20 and 25% of the component with maximum power, where the effect of varying TR was evaluated. The IRF was reconstructed at an artificial sampling rate of 1.0s by zero-padding in frequency domain to suppress sampling errors. Secondly, we processed a brain perfusion dataset (PERMEATE sequence [3], multi-shot, multi-echo GRE-EPI, TE_i = 13/32/51ms, 96x96, 15 slices) at original TR_1=1.225s and also at TR_2=2.45s (obtained by leaving out every second sample) with sinc-interpolation applied as well.

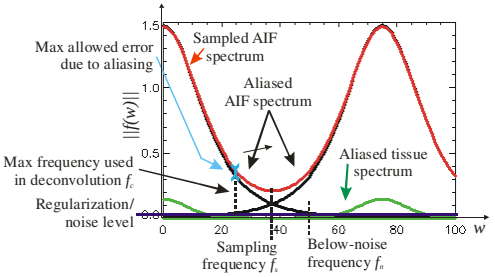

Fig. 2: Longer TR causes spectra aliasing. Therefore, signals should not be sampled at regularization cut-off frequency f_c, but at higher frequency f_s.

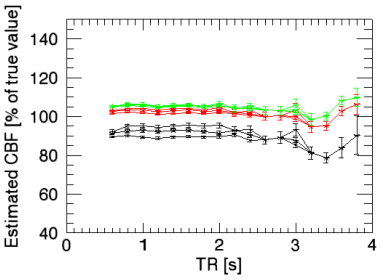

Fig. 3: Numerical simulations showing independence of CBF estimates on sampling rate for different IRF MTTs: 5s (black), 10s (red), 15s (green). Multiple results for each MTT are FT-thresholds 10, 15, 20%.

Results

For typical AIF and gray-matter tissue signal profiles in human brain with injection of 0.5-molar gadolinium tracer at 0.1mM/kg, SNR=30 and FT-threshold 20%, the computed TR for DSC-MRI was 2.1s. For threshold of 15%, the computed good TR was 1.9s. As shown on Fig. 3, the influence of TR variation is negligible for TR <= 2.0s, independent of MTT and regularization level. This is also demonstrated on Fig. 4, where a dataset was processed at TR_1=1.225s and at TR_2=2.45s, the CBF estimates are very similar (for FT-threshold 20%). The typical difference is less than 10%, while the most significant difference was found only in areas with very low DSC-MRI signal, i.e. mostly noise. The TR of 2.45s is longer than calculated as optimal, but was used due to the underlying TR of the data.

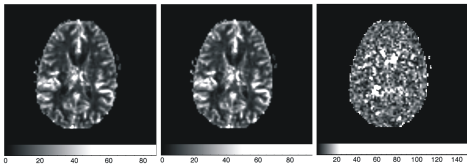

Fig. 4: Comparison of quantitative CBF maps for data sampled at TR_1=1.225s (a) and TR_2=2.45s (b). (c) shows relative difference between the maps.

Conclusion

As shown for current DSC-MRI acquisitions with SNR~30, 0.5-molar gadolinium tracer concentrations and typical dynamics of brain parenchyma, it might be not advantageous to sample with sampling rates faster than 1.9s. A longer TR would afford larger slice coverage and less T1 sensitivity during contrast passage and subsequent steady state. Spectra of IRF recovered at optimized and shorter-then-optimized TRs might be very similar. However, for good results the sinc interpolation of the IRF might be needed to alleviate sampling errors in IRF reconstruction. Short TRs might be useful only if better CNR and/or narrower AIF/tissue signals are obtained. The findings of this study might also have considerable implications for CT perfusion (CTP) also as CTP is challenged by keeping the radiation dose low and slow table movements (e.g. toggle mode). Since in CTP data acquisition is continuous over TR the spectral aliasing is less severe thus CTP might allow for even longer TRs.

References

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[3] Newbould RD et al, Magn Reson Med. 2007 Jul;58(1):70-81

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