Detection of dispersion from bolus-tracking MRI improves cerebral blood flow quantification: a simulation study

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Introduction. Cerebral blood flow (CBF) can be estimated from bolus-tracking MRI images by deconvolution from arterial input function, AIF(t), and tissue concentration, C(t): $C(t) = CBF \cdot [AIF(t) \otimes R'(t)]$ (eq. 1), where R'(t) is the "effective" residue function affected by bolus dispersion [1]. R'(t) can be described as $R'(t) = R(t) \otimes d(t)$ (eq. 2), with R(t) the non dispersed residue function and d(t) a term accounting for vascular dispersion. Usually, CBF is estimated from the maximum of the deconvolved R'(t) instead from R(t) at time t=0. This leads to underestimation of CBF. Thus, a deconvolution method able to detect the non dispersed R(t) is needed to improve CBF quantification. In [2,3], a nonlinear stochastic regularization method (NSR) was proposed to account for smoothness and non-negativity of R'(t). Here, we show NSR ability to resolving non dispersed residue function on simulated data.

Material and Methods.

Simulation. Data were simulated as in [3,4,5] with a gamma-variate AIF(t), two fixed CBF values typically found in normal (n) and pathological (p) grey matter (GM), and four models for of residue function, an exponential (type 1) and a lorentzian (type 2) function for the absence of dispersion, a gamma-variate (type 3) and a dispersed exponential (type 4) for presence of dispersion. The tissue noise-free curves were obtained from eq. 1 and MRI S(t) signals were generated according to $S(t) = S_0 \cdot \exp(-k \cdot C(t) \cdot TE)$ (eq. 3) with S_0=100, TE=80 ms, k selected to achieve a peak signal drop of 40%. Gaussian noise with four signal-to-noise ratio (SNR=500-50-10-5) was then added to data. Simulations were repeated 100 times for each residue function type and two sampling times (TR=1 s, TR=0.3 s).

NSR NSR [2,3,6] is a Bayesian method which incorporates a model of the unknown R'(t) that prevents negative values. NSR considers CBF·R'(t) as the convolution of the exponential of a Brownian motion with a deterministic exponential function: $CBF \cdot R'(t) = d(t) \otimes CBF \cdot e^{R_1(t)}$ (eq. 4) where $d(t) = 1/\theta_1 \exp(-t/\theta_1)$ (eq. 5) and $R_1(t) = \alpha + \theta_2 \beta(t)$ (eq. 6) with $\beta(t)$ Brownian motion and θ_1, θ_2, α unknown scalars plus a parameter θ_3 related to the amplitude of the noise level.

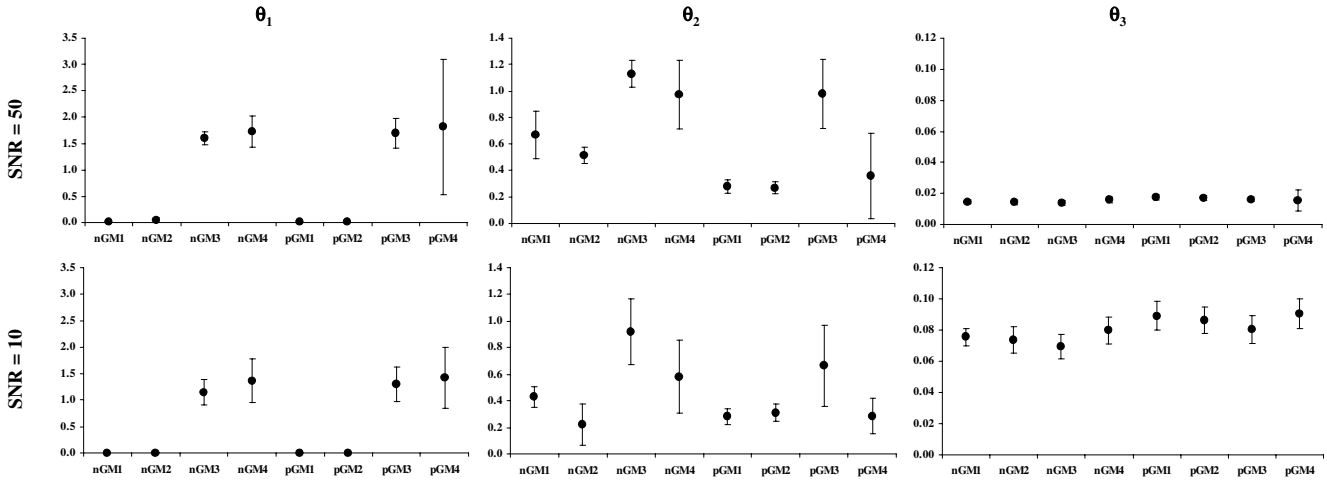

Figure: θ_1, θ_2, and θ_3 estimates; n=normal, p=pathological, GM= grey matter; #1,2,3 &4 = type of residue function

Results. Figure shows the mean ± SD of θ_1, θ_2, and θ_3 obtained with SNR=50 and SNR=10, TR=1 s, for the four simulated R'(t) with normal (nGM1, nGM2, nGM3, nGM4) and pathological CBF (pGM1, pGM2, pGM3, pGM4) respectively. θ_1 takes into account the level of dispersion. It is virtually zero in absence of dispersion (nGM1, pGM1 and nGM2, pGM2) and increases in presence of dispersion (nGM3, pGM3 and nGM4, pGM4). Consequently, θ_1 estimate agrees with the simulated level of dispersion, i.e. θ_1 of GM4>θ_1 of GM3. θ_2 describes the non dispersed R(t) from its maximum value CBF can be estimated. Variability of θ_2 takes into account the various simulated residue functions. θ_3 stands for the noise level present in the data: it is relatively costant among the different tissue types, depending only on the noise level and increasing with noise. α results are not shown since it is a constant value not describing the dynamics of R(t). Our results with TR=0.3 s and SNR=500-5 (not shown) show that NSR parameters are independent on the sampling frequency and noise level.

Discussion. NSR has been shown in [3] to estimate with good accuracy the physiological shape of R'(t) both in presence and absence of dispersion. Here we have shown that NSR also quantifies the level of dispersion present in the estimated dispersed R'(t) thus assessing the bias affecting CBF estimates when obtained from the maximum of the deconvolved curve R'(t).

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