A Log-normal dispersion model for parametric deconvolution of DSC-MRI images: assessment on simulated data

F. Zanderigo[1], A. Bertoldo[1], and C. Cobelli[1]
[1]Department of Information Engineering, University of Padova, Padova, Italy

Introduction. Dynamic Susceptibility Contrast – Magnetic Resonance Imaging (DSC-MRI) allows to quantify Cerebral Blood Flow (CBF), Volume (CBV) and Mean Transit Time (MTT) by deconvolution from Arterial Input Function AIF(t) and tissue concentration C(t) time curves: $C(t) = CBF \cdot [AIF(t) \otimes R(t)]$ (eq.1), where R(t) is the tissue Residue function. The most used approach is to assume R(t) unknown and perform nonparametric deconvolution via Singular Value Decomposition (SVD) [1]. An alternative is to assume known the structure of R(t) and perform parametric deconvolution. Up to now, only a few attempts have been made along this direction [2,3,4]. Here, a new Log-normal dispersion model is proposed and validated on simulated data. The new approach is compared to the two commonly used SVD [1] and block-circulant SVD (cSVD) [5] and to our recently proposed Nonlinear Stochastic Regularization (NSR) [6] nonparametric deconvolution methods.

Material and Methods.
Simulated Data Set. Data were simulated as in [1,6] with a gamma-variate AIF(t), two fixed CBF values typically found in normal and pathological grey matter and four models for R(t): Exponential and Lorentzian in absence and Gamma-variate and Dispersed Exponential in presence of dispersion. Gaussian noise with four Signal-to-Noise Ratios (SNR=500-50-10-5) was added to data. Simulations were repeated 100 times for each R(t) with sampling times TR=1 s.
Log-normal Dispersion Model (LDM). We considered the model proposed in [3] and differently characterized three of its structural components: feeding artery and capillary transport functions, and flow Probability Density Function (PDF). **Artery.** In Multiple Indicator Dilution (MID) theory, a stochastic model is assumed for distribution within organs with the assumption of concurrent convective (pseudo-diffusive) movements in the direction of flow [7]; the flow velocities within capillary bed are replaced by a single average velocity, modified by a diffusion-like process to add randomness to blood elements movement. Considering closed (open) boundary condition at the inflow (outflow), the solution of the convection-diffusion equation represents the random walk distribution, which has proved to be particularly suitable for investigation of substances not leaving the vasculature. Here the model is applied to interpret the feeding artery transport function. The convolution with a deterministic dispersive term is considered to take into account high levels of dispersion. **Capillary.** We model each of the 20 capillary paths of [3] using a transport function description equivalent to that of the artery. **PDF.** In [8], the density function of myocardial blood flow transit times, h(t), is expressed as the weighted sum of individual $h_i(t)$ describing regional pathways. A suitable expression for $h_i(t)$s was found to be the Log-normal distribution, which can be applied to DSC-MRI data as the global PDF assigning appropriate flows and weights to the 20 parallel vascular paths. LDM estimates 10 parameters by means of nonlinear least-squares.
Assessment Criteria. R(t) shape and CBF estimation by LDM were assessed by measuring the difference between true and estimated by Root Mean Square Error $RMSE_{curve}$ and $RMSE_{peak}$. Results were compared to those obtained by SVD, cSVD, and NSR.

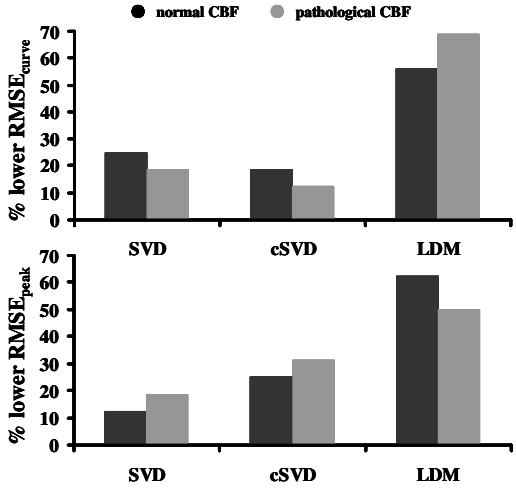

Figure 1: percentage of lower $RMSE_{curve}$ (upper panel) and $RMSE_{peak}$ (lower panel) obtained by SVD, cSVD and LDM.

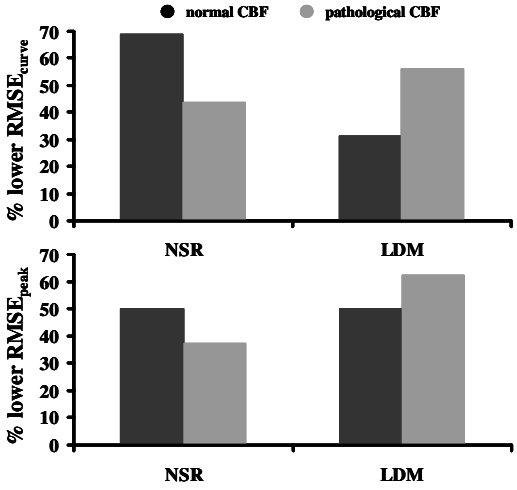

Figure 2: percentage of lower $RMSE_{curve}$ (upper panel) and $RMSE_{peak}$ (lower panel) obtained by NSR and LDM.

Results. LDM is sensitive to noise level only for SNR=5 and performs better as dispersion increases, especially with pathological CBF. The comparison vs nonparametric deconvolution methods shows promising results (Fig.1): LDM provides lower $RMSE_{curve}$ indexes in 56% (69%) of the cases for normal (pathological) state respectively, SVD in 25% (19%) and cSVD in 19% (12%); considering $RMSE_{peak}$, LDM shows lower values in 63% (50%) of the cases for normal (pathological) state respectively, SVD in 12% (19%) and cSVD in 25% (31%) of the cases. LDM results are also comparable to those obtained by NSR (Fig.2): LDM provides lower $RMSE_{curve}$ indexes in 31% (56%) while NSR in 69% (44%) of the cases for normal (pathological) state respectively; considering $RMSE_{peak}$, LDM shows lower values in 50% (63%) while NSR in 50% (37%) of the cases. Of note is that LDM performs better than NSR when pathological CBF and SNR≤20 are considered. Mean Coefficients of Variation of LDM parameters are in the range 2%-140%, which is acceptable considering that estimation is made on a pixel-by-pixel basis.

Discussion. We have previously shown that NSR characterizes R(t) and CBF better than commonly used SVD and cSVD [6]. LDM represents a faster approach, including physiological considerations, alternative to NSR which, as every nonparametric deconvolution method, suffers for ill-posedness and ill-conditioning problem. Furthermore, as NSR does [9], LDM provides not only CBF, MTT and CBV, but also the dispersion term, which can be used as an alternative indicator of pathological tissue state. Anyway, further work is necessary to improve LDM performance. The precision obtained in the estimation of the parameters is acceptable, but it can be improved since there is room for model parameters reduction. A comparison to other parametric techniques may further clarify the reliability of LDM.

[1] Østergaard et al., Magn Reson Med. 36: 715-725, 1996; [2] Larson et al., J. of Theor. Biol. 170: 1-14 , 1994; [3] Østergaard et al., J. of Cereb. Blood Flow and Metab. 19: 690-699, 1999; [4] Mouridsen et al., NeuroImage 33: 570-579, 2006; [5] Wu et al., Magn Reson Med. 50: 164-174, 2003; [6] Zanderigo et al., 13th ISMRM Intern. Congr. & Exhibit., Miami Beach, Florida, USA, May 2005; [7] Schwab et al., J. of Pharmacok. and Biopharm. 26(2): 163-181, 1998; [8] Bassingthwaighte et al., In Myocardial Blood Flow in Man: Methods and Significance in Coronary Disease, A.Maseri, Torino, Italy. Minerva Medica, p. 197-205, 1972; [9] Zanderigo et al., 14th ISMRM Intern. Congr. & Exhibit., Seattle, Washington, USA, May 2006.