Improved Vascular Transport Function Characterization in DSC-MRI via Deconvolution with Dispersion-Compliant Bases

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Synopsis. Bolus dispersion phenomena affect the residue function computed via deconvolution of DSC-MRI data. Indeed the obtained effective residue function can be expressed as the convolution of the true one with a Vascular Transport Function (VTF) that characterizes the dispersion. The state-of-the-art technique CPI+VTF allows to estimate the actual residue function by assuming a model for the VTF. We propose to perform deconvolution representing the effective residue function with Dispersion-Compliant Bases (DCB) without assumptions on the VTF, and then apply the CPI+VTF on DCB results. We show that DCB improve robustness to noise and allow to better characterize the VTF.

Purpose. To improve robustness of dispersion kernel characterization in DSC-MRI by means of Dispersion-Compliant Bases.

Introduction. The residual amount of tracer, i.e. the residue function $R(t)$ computed from deconvolution of the measured arterial $C_a(t)$ and tissular $C_{ts}(t)$ concentrations, characterizes the tissue perfusion. However the actual arterial concentration may undergo dispersion. This causes the effective residue function to reflect additional vascular properties mathematically described by the convolution $R^*(t) = R(t) \otimes VTF(t)$ where VTF is the Vascular Transport Function [1, 2]. This severely affects the estimation of hemodynamic parameters such as the blood flow CBF, corresponding to the peak of $R(t)$, and the mean transit time $MTT = BV/CBF$ with BV the blood volume. Indeed only effective parameters CBF^* (peak of R^* and MTT^* are computed. A recent state-of-the-art technique [3] based on control point interpolation, CPI+VTF, allows to recover the actual $R(t)$ assuming it is convolved with a VTF described by a Gamma Dispersion Kernel (GDK)

$$VTF(t,s,p) = GDK(t,s,p) = \frac{s^{1+sp}}{\Gamma(1+sp)} t^{sp} e^{-st} \tag{1}$$

where s, p are unknown. This allows the estimation of the actual CBF [3]. The estimation of s, p, CBF is not an easy task and requires a non-linear optimization routine which results are sensitive to noise. We propose to improve robustness and precision of some of the estimates by performing deconvolution with Dispersion-Compliant Bases [4] (DCB), and subesquently fit the CPI+VTF [3] model to the obtianied effective residue function.

Methods. We perform DCB deconvolution representing $R^*(t)$ on a sampling grid $t_1, t_2, .., t_M$ as5

$$R_{DCB}(t) = \Theta(t-\tau) \sum_{n=1}^{N} [a_n + b_n(t-\tau)] e^{-\alpha_n (t-\tau)} \tag{2}$$

with order N ($N = 6$ here), τ, a_n, b_n unknown an α_n predefined5. The solution was constrained via quadratic programming to $R(t_m) \geq 0 \forall t_m \in [t_1, t_{M-1}]$ and $R(t_M) = 0$.

The CPI+VTF deconvolution technique was implemented as in literature [3] with 12 control points and initial parameters p, s for the optimization routine $log2 \pm 2$ ($mean \pm SD$). In order to decouple the influence of the estimation framework from the model the estimation was performed non-linearly bounding parameters to $mean \pm 3 * SD$. The CPI+VTF model was also fitted on the effective residue function computed with DCB by minimizing $||R_{DCB}(t) - CPI + VTF_{model}||^2$ over the control points, time instant separations, and parameters CBF, s, p [3].

We perform synthetic experiments generating $C_a(t)$ in $[0:1:90]s$ as a gamma-variate function as in literature [1, 4] for $SNR = 50$ [3].The tissular concntration $C_{ts}(t)$ was generated as $C_{ts}(t) = C_a \otimes [R \otimes VTF(t)](t)$ with bi-exponential5 $R(t)$. Three ground-truth VTF models were used [3]: gamma (GDK), exponetial and log-normal. For each, three dispersion levels were tested: low, medium, high [3]. Number 100 repetitions were generated for each combination of dispersion kernel, level, $CBF \in [5:10:65] ml/100g/min$, $MTT \in [2:4:18]s$, and $delay \in [0,5]s$ [3] with noise added [4] with $SNR = 50$ [3]. For each repetition DCB and CPI+VTF deconvolutions were performed, as well as the fitting of the CPI+VTF model on $R_{DCB}(t)$, henceforth DCB+VTF.

We then proceed with the following experiments: 1. we compare DCB5, CPI+VTF and oSVD [5] deconvolutions and calculate the relative errors of the recovered effective parameters CBF^* (Fig. 1), $MTT^* = BV/CBF^*$ (Fig. 2), and time-to-maximum t_{max} of the R^* (Fig. 3); comparisons are performed on all the ground-truth dispersion kernels (left images) and just on the GDK (right images); 2. we compare estimates of p, s, CBF obtained with CPI+VTF and DCB+VTF in case of GDK (Fig. 4); 3. we apply DCB+VTF on stroke MRI data and show maps of p, s, CBF (Fig.5).

Results. Results in Fig. 1,2,3-left show that DCB-based estimates of CBF^*, MTT^*, t_{max} have sensibily lower relative error than those obtained with CPI+VTF and oSVD. When the gound-truth kernel is GDK (right columns) CPI+VTF sensibly improve but still DCB perform comparably or better. DCB generally reduce errors and their variability. In addition DCB results appears more stable than with CPI+VTF when changing to the GDK kernel. Results in Fig. 4 show that CPI+VTF and DCB+VTF render equally good results for CBF, p but estimation of s dramatically improves with DCB+VTF. Maps in Fig. 5 well depict the infarcted area specially highlighted in the p-map.

Discussion. The use of DCB deconvolution renders a better estimation of the effective hemodynamic parameters. The DCB do not assume any model for the dispersion kernel (VTF) and can handle the exponential and log-normal kernels better than CPI+VTF. The use of these functional bases improves robustness to noise and reduces variability in the results (Figs. 1-3). This leads to a graet improvement also when the CPI+VTF technique is applied directly on the DCB results (DCB+VTF) , particularly in the estimation of the s parameter of the gamma kernel (Fig. 4). The quality of the estimation with DCB+VTF in a real case is shown in Fig. 5.

Conclusion. Perfusion deconvolution of DSC-MRI data by means of Dispersion-Compliant Bases (DCB) provides more robust results in quantifying the effective residue function and improves subsequent VTF assessments.

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Figures

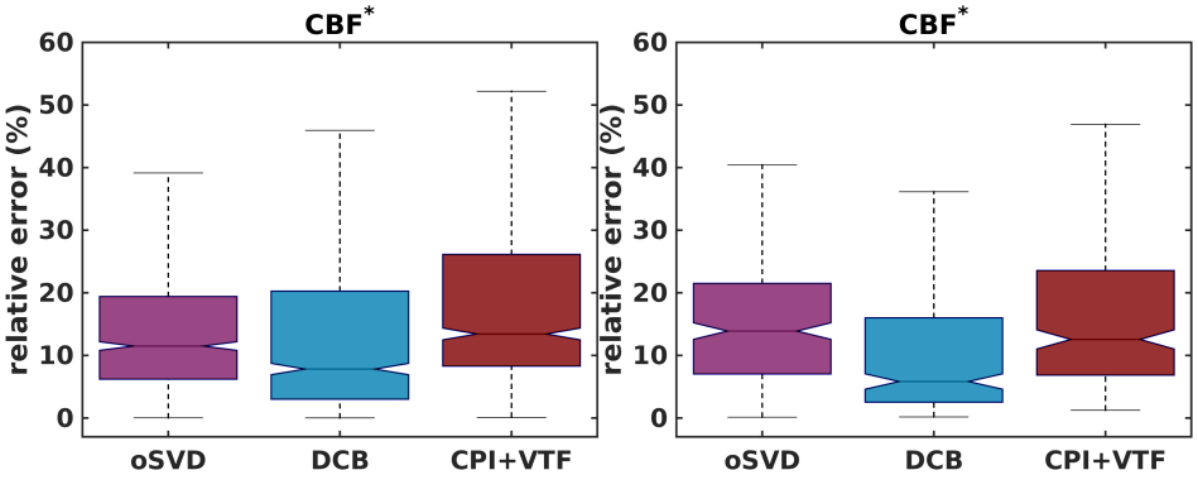

Figure 1

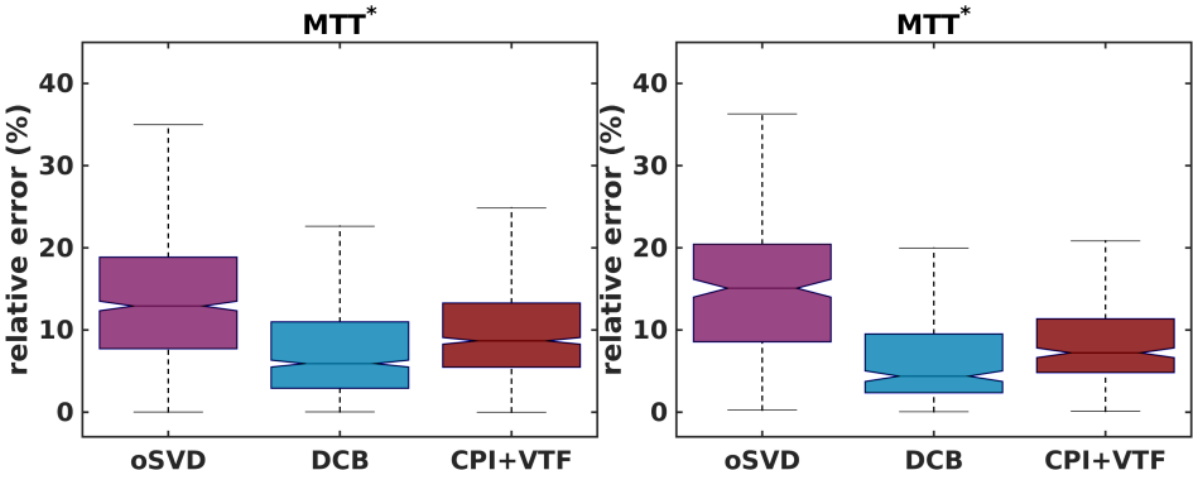

Figure 2

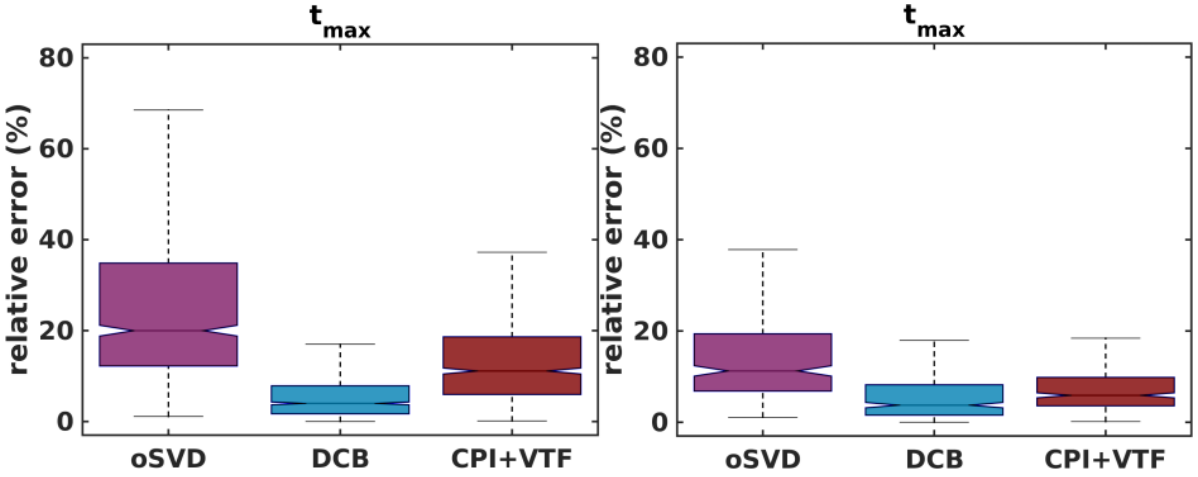

Figure 3

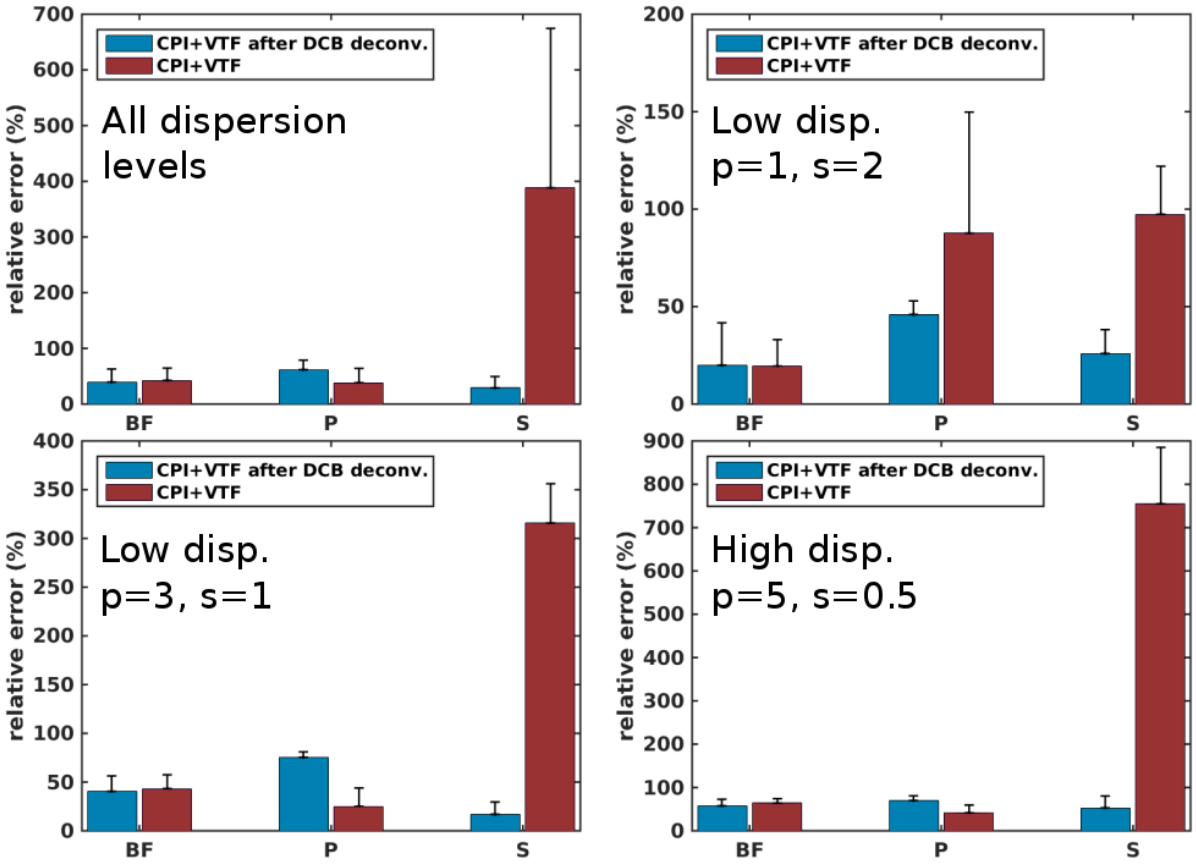

Figure 4

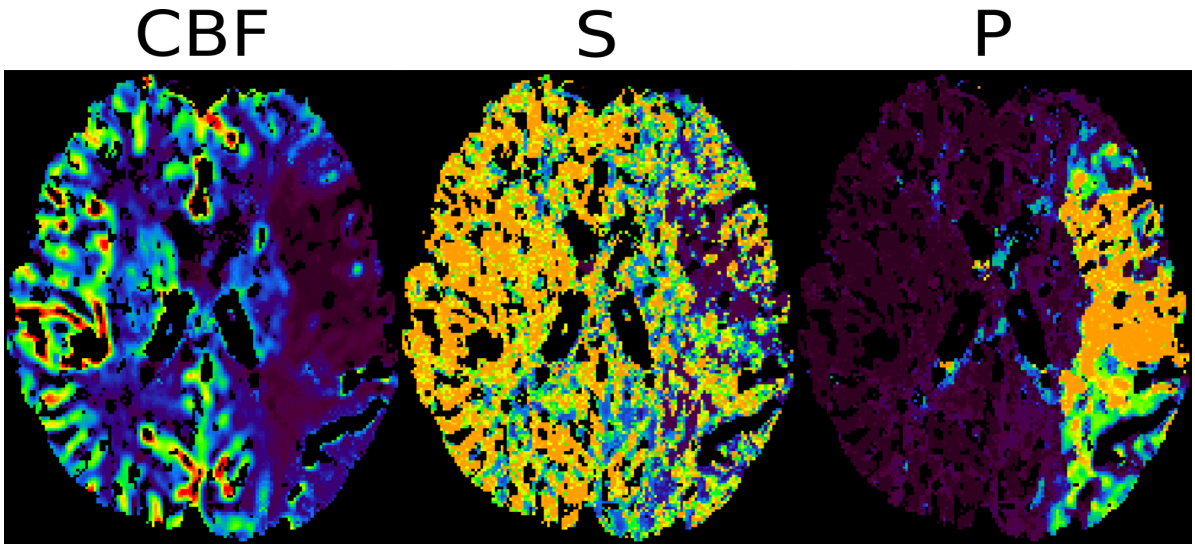

Figure 5