Improved Vascular Transport Function Characterization in DSC-MRI via Deconvolution with Dispersion-Compliant Bases Marco Pizzolato^{1†}, Rutger Fick¹, Timothé Boutelier², Rachid Deriche¹

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 obtained effective residue function.

Methods. We perform DCB deconvolution representing $R^*(t)$ on a sampling grid $t_1, t_2, ..., t_M$ as 5

$$R_{DCB}(t) = \Theta(t-\tau) \sum_{n=1}^{N} [a_n + b_n(t-\tau)] e^{-\alpha_n(t-\tau)}$$
(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 $R(t_m) \ge 0 \forall t_m \in [t_1, t_{M-1}]$ 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 concurration $C_{ts}(t)$ was generated as $C_{ts}(t) = C_a \otimes [R \otimes VTF(t)](t)$ with bi-exponentials R(t). Three ground-truth VTF models were used [3]: gamma (GDK), exponential 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.

Acknowledgments. We thank Olea Medical and to the PACA Regional Council for providing grant and support.

Reference to the original publication. In ISMRM 24th Annual Meeting. Proc. Int. Soc. Mag. Reson. Med. 24 (2016).

References

- Calamante et al., Delay and dispersion effects in dynamic susceptibility contrast mri: simulations using singular value decomposition, Magn Reson Med, vol. 44(3), pp. 466–473, 2000
- [2] Calamante et al., Estimation of bolus dispersion effects in perfusion mri using image-based computational fluid dynamics, NeuroImage, vol. 19, pp. 341–353, 2003.
- [3] Mehndiratta et al., Modeling and correction of bolus dispersion effects in dynamic susceptibility contrast mri: Dispersion correction with cpi in dsc-mri, Magn Reson Med, vol. 72, pp. 17621774, 2013.

¹Université Côte d'Azur, Inria, France; [†] expresses his thanks to Olea Medical and to the Provence-Alpes-Côte d'Azur Regional Council for providing support. ²Olea Medical, La Ciotat, France

- [4] Pizzolato et al., Perfusion mri deconvolution with delay estimation and non-negativity constraints, in 12th International Symposium on Biomedical Imaging (ISBI). IEEE, 2015, pp. 1073–1076.
- [5] Wu et al., Tracer arrival timinginsensitive technique for estimating flow in mr perfusionweighted imaging using singular value decomposition with a blockcirculant deconvolution matrix, Magn Reson Med, vol. 50(1), pp. 164–174, 2003.



Figure 3





Figure 5