A Novel Nonparametric Population Deconvolution for DSC-MRI Quantification: Assessment on Simulated Data

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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 residue function. The most used approach exploits singular value decomposition (SVD) [1], but bears some limitations: nonphysiological oscillations and negative values in R(t), estimated CBF dependence on selected threshold, delay/dispersion in AIF [2]. Here, we propose a novel nonparametric population deconvolution algorithm (PD). In particular, this method allows to simultaneously estimate the residue functions taking advantage of the entire collection of measures obtained from a population of pixels.

MATERIALS AND METHODS: The simulated data set was generated by using an AIF modelled as in [1] and an exponential residue function R'(t)=CBF·R(t)=CBF·exp(-t/MTT) [3]. Relative CBF and MTT values are assumed to be Gaussian (CBF: 0.02±0.003 mean±SD; MTT: 6±1 mean±SD) and a population of 100 different noise-free realizations, i.e. pixels, were generated. Finally white Gaussian noise was added to generate the population composed by 100 noisy pixels. In particular, four different signal-to-noise ratios (SNR) were exploited (SNR=5, 10, 50, 500). Then, the simulation has been repeated using different description of R(t), i.e. lorentzian, gamma-variate and dispersed exponential [3]. In summary, 16 different pixel populations were considered.

The problem is the estimation of the realization of the stochastic process $C(t) = AIF(t) \otimes R'(t)$ that describes the measured data as in [4], from which the minimum variance estimate of the residue function can then be obtained. Following [5], R'(t) is the sum of an average curve, common to all the pixels, and an additional curve that explain the individual shift from the average curve. Both these curves are modelled as two-fold integration of white noise, with unknown variance estimated from data. The entire estimation process, i.e. variance estimation and residue function computation, requires inversion of a sequence of matrices whose size is small, thus yielding a fast numerical procedure.

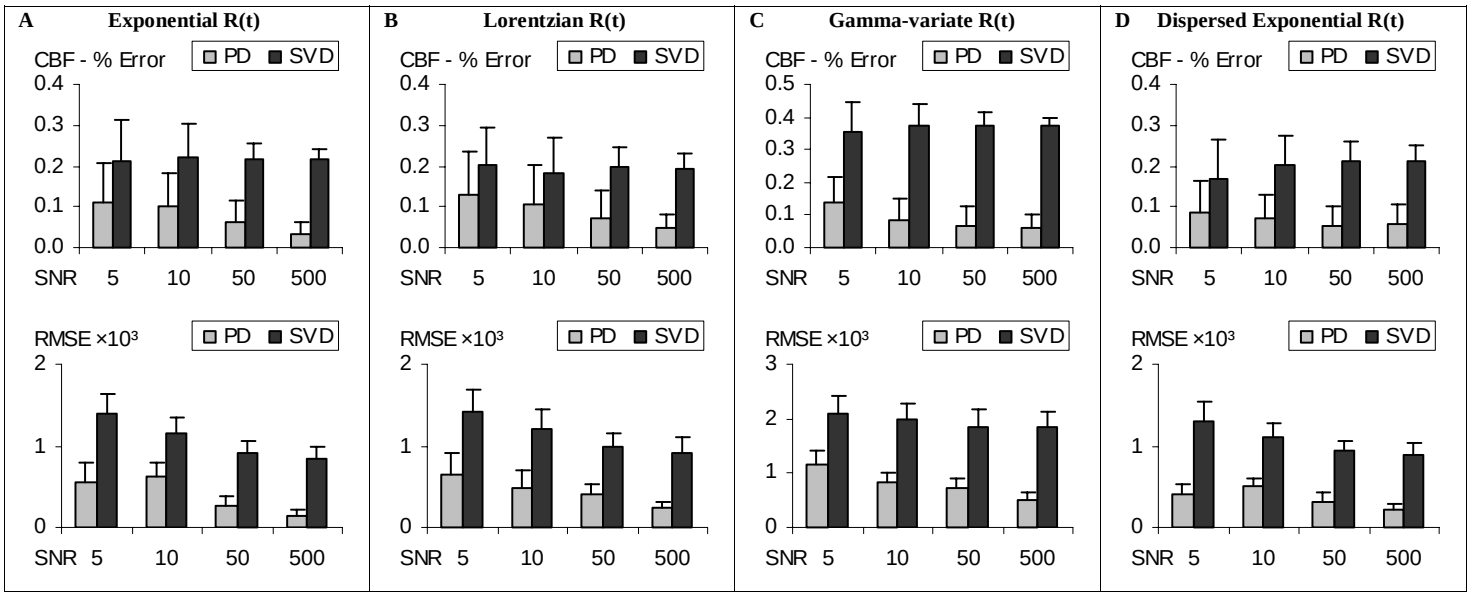

Fig 1: Error in CBF estimates obtained with PD and SVD methods (upper panel) and mean distance from true residue function expressed as root mean square error, RMSE (lower panel).

RESULTS: Comparison between PD and SVD [1] results are shown in Fig. 1. PD provides more accurate estimates of CBF values than SVD, especially in presence of dispersed R(t) (panels C D). R(t) obtained by PD are very regular and without unphysiological oscillations (results not shown). Moreover, they are closer to true R(t) than those obtained by SVD (Fig.1, lower panels).

DISCUSSION: A nonparametric deconvolution method based on a pixel population approach has been proposed and validated on a simulated data set. PD provides more accurate and more physiological estimates of R(t) than SVD when a population having a variability close to that assumed for our simulations is considered. PD was also applied on a simulated pixel population having a bimodal CBF distribution, providing closer estimates of R(t) than SVD, but less accurate CBF values. This suggests that a pre clustering operation on the data before deconvolution operation is recommended. PD is not computationally expensive, the estimated computation time of a 128x128 slice, using matlab© non optimized software on an Intel dual core Pentium® 2.0 GHz, is about 5 minutes.

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