Reducing the tissue specific MTT-biases in Quantitative Cerebral Blood Flow Measurements

M. Salluzzi[1], R. Frayne[2,3], M. R. Smith[1,3]

[1]Electrical and Computer Engineering, University of Calgary, Calgary, Alberta, Canada, [2]Seaman Family MR Research Centre, Foothills Medical Centre, Calgary, Alberta, Canada, [3]Radiology, University of Calgary, Calgary, Alberta, Canada

INTRODUCTION

In magnetic resonance dynamic susceptibility contrast (DSC) perfusion studies, the cerebral blood flow (CBF) parameter is estimated from the peak of the scaled residue function obtained from deconvolving the tissue concentration curve by the arterial concentration curve [1]. Deconvolution enhances the high frequency noise components, compromising algorithm stability. The noise reduction techniques necessary to ensure stability remove both noise and signal components of the residue function, distorting the estimate of the residue function and leading to incorrect CBF estimates [2]. CBF estimates using singular value decomposition (SVD) and Fourier transform (FT) deconvolution approaches show high sensitivity to the tissue mean transit time (MTT), giving higher biased CBF estimates for short MTT values. Adaptive noise filter thresholds [3] and direct gamma-variate modeling [4] of the concentration signals have been suggested as means of reducing these CBF biases. Frequency-domain modeling techniques that characterize the spectral components of the residue function have also been suggested [5, 6] for removing deconvolution artefacts. We propose the use of the transient error reconstruction algorithm (TERA) [7] to provide estimates of the residue function that are less distorted by the filtering techniques. The aim is to improve deconvolution accuracy and stability by recovering spectral components of the residue function that were removed during filtering. The ability of the TERA algorithm to characterize the spectral components of the residue function obtained from DSC-MR studies and reintroduce the missing residue function frequency components is assessed.

METHOD

The vascular bed was modeled as a single, well-mixed compartment [1]. The arterial input function was modeled by a gamma-variate function [1]. Tissue signal samples were analytically generated at times $t = n\,\Delta T_{EXPT}$, $0 \le n < N$, where the sample interval ΔT_{EXPT} is equal to the pulse repetition time of DSC-MR images. TERA is based on an auto-regressive moving-average (ARMA) model [7]. The ARMA order was adaptively selected by minimizing the prediction error between the known residue function spectral components and those of the model using filter parameters determined using the Steiglitz-McBride algorithm [8]. CBF values were calculated from the peak value of the residue function reconstructed from the ARMA parameters. The rSVD [9] algorithm with a singular values threshold parameter, P_{SVD}, set to 0.2 was used to provide CBF estimates to compare against those generated using TERA results.

RESULTS

The TERA-based residue function is narrower and less distorted than that calculated using rSVD, with a sharper leading edge (Fig 1A). The oscillations in the rSVD residue function, evidence of the truncation of the high-frequency residue function spectral components, are absent with TERA (Fig 1A). This demonstrates that the TERA algorithm had the ability to at least partially recover the frequency components removed by noise-related filtering. In simulation studies both TERA and rSVD approaches underestimate the CBF (Fig 1B), but with a smaller MTT sensitivity observed for the TERA algorithm. In clinical applications the white matter MR CBF estimates are cross-calibrated to those found in PET studies [10]. The use of this white matter calibration factor across tissues with differing MTT values is only valid if there is minimal MTT sensitivity of the CBF estimates as with the TERA algorithm. Figs 2A and 2B show the rSVD and TERA images independently calibrated to match the PET CBF estimates for normal white matter. Fig 2C shows the difference image (rSVD - TERA). In this image the infarct tissue appears bright, indicating that the rSVD CBF estimates are larger than the TERA estimates as predicted from the simulation study.

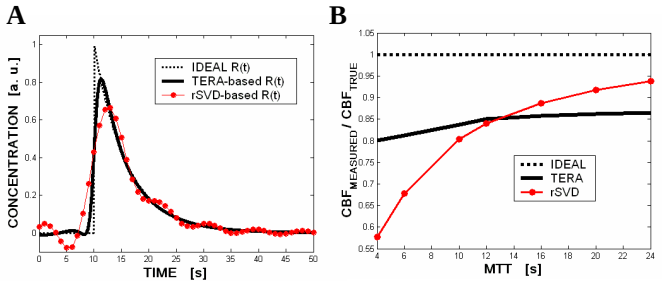

Fig 1 (A) The TERA residue functions estimate is improved compared to the rSVD estimate. (B) The TERA CBF estimates in noise free simulations are less MTT sensitive than those from rSVD; an advantage when cross-calibrating MR and PET CBF studies.

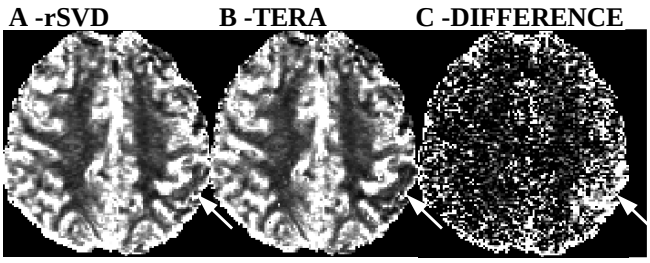

Fig. 2 Cross-calibrated CBF maps for the (A)rSVD and (B)TERA. The difference image (C) indicates that SVD over estimates CBF (hyper-perfusion) for infracted tissue as expected from the simulation study.

CONCLUSION

Noise filtering techniques are required to ensure algorithmic stability when using deconvolution to determine quantitative CBF estimates from DSC-MR studies. Based on the results of simulations, this filtering yields incorrect CBF estimates that are sensitive to mean transit time (MTT). The frequency-domain modeling transit error reconstruction algorithm (TERA) was used to re-introduce the residue function spectral components removed by filtering. TERA was shown to give CBF estimates that were less sensitive to MTT than the estimates obtained using SVD. After cross-calibration of clinical DSC-MR with PET studies, infarcted tissue appears hyper-perfused with higher CBF values from the SVD compared to TERA algorithm.

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