A new approach using the distribution of transit times (DTT) to determine improved absolute CBF values in patients with ischemic stroke

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INTRODUCTION

A positive patient outcome after ischemic stroke depends on an accurate diagnosis. Absolute cerebral blood flow (CBF) values can be obtained from magnetic resonance (MR) dynamic susceptibility contrast (DSC) perfusion studies after cross-calibrating with PET studies [1]. Chen *et al*. [2] indicate that using a single scaling factor to obtain absolute CBF values is not appropriate with FT and SVD deconvolution since the accuracy of the CBF estimate varies with tissue mean transit time (MTT); a consequence of distortions introduced when ensuring algorithm stability. We propose re-examination of the use of the distribution of transit times (DTT) [3] to determine if this little-used approach can provide less systematically biased absolute CBF estimates.

METHOD

The arterial and tissue signals were analytically generated based on a single compartment (exponential) residue function as per [4]. CBF_{rSVD} estimates were obtained from the peak of the residue function $R(t)$ recovered using the delay-insensitive rSVD algorithm [5]. An important limitation in determining the distribution of transit times ($h(t) = -dR(t)/dt$) [3] is the necessity of differentiating the sparsely sampled residue functions ($TR \approx 1$ s to 2 s). In the proposed interpolated distribution of transit time technique (iDTT), Fourier-domain interpolation is first applied to the residue function estimates [6] to determine the DTT function from the continuous residue function that underlies the sampled values. CBF_{iDTT} estimates are then calculated via the central volume principle [7]; CBF = CBV / MTT. The cerebral blood flow volume (CBV) is determined from the zero moment of the concentration curves [1] and MTT values calculated using a modified first moment equation, $MTT = \int_{ATD}^{\infty} (\tau - ATD)\ h(\tau - ATD)d\tau \Big/ \int_{ATD}^{\infty} h(\tau - ATD)d\tau$, to consider the presence of arterial tissue delay (ATD). Both the maximum slope [6] and peak of the residue function were used as ATD estimates.

RESULTS

The differentiation of the sparsely sampled residue function (Fig. 1A) will lead to estimates of the distribution of transit times ($h(t)$) that vary depending whether the peak of the residue function is, or is not, sampled within the DSC image sequence (a random event). Estimating $h(t)$ by differentiating the Fourier interpolated residue function [6] permits a more accurate DTT estimate (Fig. 1B). Accurate absolute CBF values after MR-PET calibration depend on the availability of a single cross-calibration scaling value valid across all tissue types. This is only appropriate when $\Delta(CBF_{MEASURED}/\ CBF_{TRUE}) / \Delta MTT$ is small. It was found that the iDTT algorithm, using an ATD value based on the peak of the residue function, provides significantly more accurate, tissue type (MTT) independent, absolute CBF estimates (Fig. 2) than the rSVD algorithm, and by implication FT and other SVD variants [8].

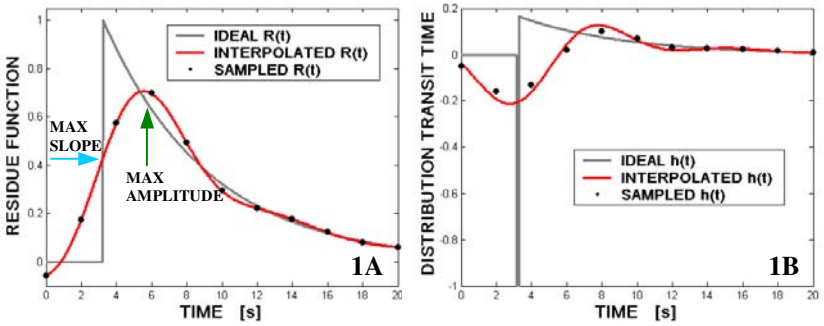

Fig. 1. Estimates of the distribution of transit times are obtained by differentiating the residue function estimates (A) Both the maximum slope (cyan arrow) and peak (green arrow) of the residue function were used as ATD estimates. Estimates of DTT are best obtained (B) from the Fourier interpolated (red line) than directly from the sparsely sampled (dots) residue function.

CONCLUSION

Simulation studies indicate that iDTT-based CBF estimates have a lower dependency on mean transit time than those CBF estimates from conventional deconvolution algorithms. This is an advantage when MR- PET cross-calibration is performed, leading to better (less systematically biased) characterization of the perfusion level (absolute CBF value) in brain tissue. Theoretically the MTT estimates should be derived using ATD estimates based on the maximum slope of the residue function rather than, as was found experimentally, its peak. This discrepancy implies the need to move beyond the standard relationship between the residue and the DTT functions ($R(t) = 1 - \int_0^t h(\tau)d\tau$ [3]), to take into account the fact that the bolus arrival is not instantaneous.

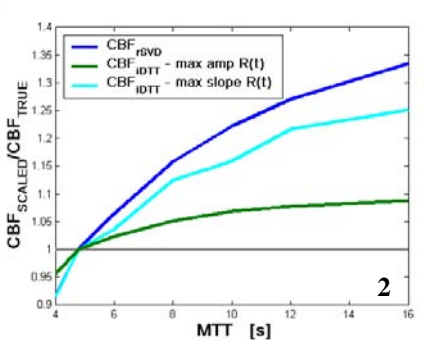

Fig. 2. The small $\Delta(CBF_{MEASURED}/\ CBF_{TRUE})/\Delta MTT$ for the iDTT algorithm implies that is more appropriate to use a MTT-independent MR-PET cross-calibration factor with this algorithm than other SVD and FT deconvolution approaches.

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