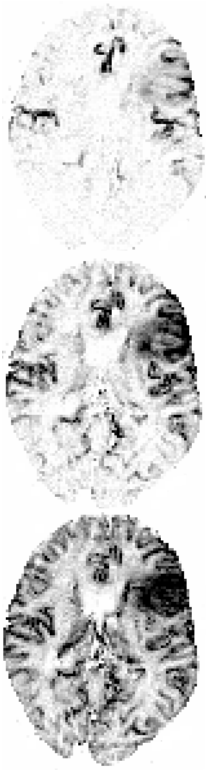
Single Voxel Iterative Blind Deconvolution of Brain Perfusion Images

R. Grüner[1,2], T. Taxt[1,2]

[1]University of Bergen, Bergen, Norway, [2]Haukeland University Hospital, Bergen, Norway

To find the regional tissue specific hemodynamic parameters in magnetic resonance perfusion images, the observed contrast signals have to be deconvolved using voxel specific arterial input functions. Only arterial input functions local to each voxel tissue eliminate effects of delay and dispersion of the contrast from the peripheral venous injection. Iterative blind deconvolution, using the algorithm of Richardson-Lucy ([1]-[5]), achieves this. Before applying the iterative algorithm, the first pass is identified by removing additional signal contributions from recirculation and contrast leakage. These additive terms are estimated using Pickard iterations and simple properties of the contrast signal in Fourier domain.



MATERIALS AND METHODS

Acquisition:

Patient data, from a male adult with tumor in the left frontal lobe of the cerebrum, were acquired using vendor provided gradient-echo echo-planar imaging (Siemens Vision 1.5T, TR/TE=1442/60.82 ms, FoV=230 mm, Matrix =128x128, Time point measurements = 50) and the contrast agent Gadovist (Schering) which was administered automatically.

Analysis:

The additive terms of the contrast signal due to recirculation and leakage were removed first using standard models for leakage and recirculation [5]. The first pass contrast concentration function, $c_i(t) = v_i(t) * u_i(t)$, in an image voxel i, was defined by the convolution between arterial input function $v_i(t)$, and the tissue residue function $u_i(t) = F_i\, r_i(t)$ scaled by flow F_i. Including additional terms describing leakage and recirculation gave a more complex expression for each voxel i, $c_i(t) = v_i(t) * u_i(t) + m\,(v_i(t+T_i) * v_o(t) * u_i(t)) + \kappa_i \int v_i(\tau) * u_i(\tau) d\tau + \kappa_i \int u_i(\tau) * v(\tau) * v_i(\tau+T_i) d\tau + \eta_i(t)$, where κ_i represented the leakage constant, m the recirculated fraction of the contrast, $v_o(t)$ the additional arterial input function due to recirculation of the contrast once through the circulation system (assumed commen for all voxels, for simplicity modeled as a Gaussian distribution), T_i the recirculation time specific for each voxel and $\eta_i(t)$ the noise signal. For reduced computation time, m was set to a fixed value of 0.05, while T_i and κ_i were optimized using a simple Picard relaxation algorithm with 5 iterations. After removing the additive terms, only the first pass contrast concentration functions remained. The Richardson-Lucy algorithm ([1]-[4]), which originates from the fields of optics and astronomy, was used to iteratively estimate the arterial input function and the tissue residue function on a voxel-by-voxel basis. In short, the algorithm started with non-zeros initial values (vectors with value one) for the two unknown functions $v_i(t)$ and $u_i(t)$. Then, Richardson-Lucy iterations gave the next estimate of $v^k_i(t)$ based on $u^{k-1}_i(t)$, followed by Richardson-Lucy iterations to find $u^k_i(t)$ given $v^k_i(t)$ and so forth.

RESULTS

Different arterial input functions were estimated in different regions of the brain (Fig.1), allowing informative visualization of the patient blood supply system. The time to peak values showed better time differentiation compared to the standard approach where the contrast concentration in one major artery was used in the deconvolution (Fig. 2). The estimated κ_i image showed anatomical structures (Fig. 3), though was not immediately comparable to static T1 contrast images. This is because only an apparent leakage image was created, as T1 effects were not accounted for.

DISCUSSION/CONCLUSION

Correction of leakage and recirculation combined with the refinement of the voxel specific arterial input function estimates and tissue residue function estimates by iterative chain deconvolution reduced the variance of the tissue specific hemodynamic volume and time parameters. Further clinical evaluation of the proposed method is currently under progress.

REFERENCES

[1] Richardson WH, J Opt Soc Am 1972;62:55-59
[2] Lucy LB, Astron J 1972;79:745-765
[3] Holmes TJ, et al., J Opt Soc Am A 1992;9:1052-1061
[4] Fish DA et al., J Opt Soc Am A 1995;12:58-65
[5] Vonken EPA et al., Magn Reson Med 2000;26:820-827

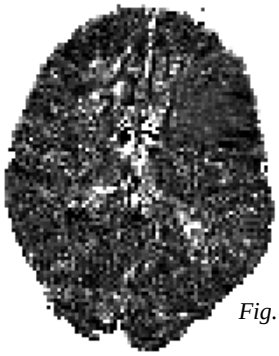


Fig. 3 Leakage image

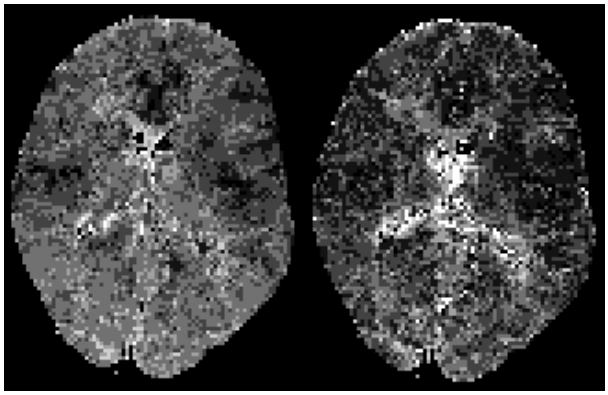


Fig. 2 Time to peak image using Richardson-Lucy algorithm (left) and conventional artery deconvolution (right)

Fig. 1. Time course of arterial input function. Frame time difference 1.5s