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Poster 7

Reconstruction of Collateral Flow Map in MR Perfusion and its Application

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Purpose

To calculate the relative collateral blood flow and recirculation from the total rCBV map using gamma-variate fitting of the concentration-time curve.

Introduction

The quantitative analysis of the brain perfusion MRI can explain the disease process involving alteration of microscopic flow including hemodynamics. The gamma-variate function has been used to fit the measured concentration-time curves to eliminate effects of tracer recirculation.[1] The concentration curve may also contain both the direct flow from the arteries and the indirect blood supplies (collateral flow) from other surroundings vessels, such as for MOYAMOYA.

The aim of this study was to separate the direct first pass CBV from the total CBV for the recostruction of the difference image, which may reflect the indirect flow.

Methods

The signal-time curve was converted into transverse relaxivity (DR_2^*)-time according to the formula $DR_2^* = 1/T_2^* = -\{\ln (S(t) /S(0))\}/TE$, where S(t) is the signal intensity at time t during contrast agent passage through the vascular network, S(0) pre-contrast signal intensity, TE the echo time. The change in transverse relaxivity is proportional to the concentration of contrast agent remaining in the tissue[1].

The dynamic perfusion series were processed on a pixel-by-pixel basis by the home-made program under the commercial image analysis software IDL (Interactive Data Language, Research System Inc., CO, USA).

The first part of dynamic curve was fitted to the gamma-variate function, $DR_2^*(t) = DR_2^*(0)\ t^a e^{-bt}$. For non-linear gamma-fitting, we used about 20 phase data in the initial of the DR_2^* curve through the least square algorithm non-linear fitting [2] and then obtained the values of a and b, for the fitted first pass volume to be generated.

The total rCBV map was constructed by direct summation of the curve. The maximum relaxivity was searched for the TTP (Time-To-Peak) map.

MR images used in this abstract (Figure 1 and 2) were obtained at a 1.5 T clinical MRI system quipped with EPI capability (Siemens Vision, Erlangen, Germany), with the scan parameters of TR/TE 1200/42 msec.

Results

The relaxivitytime curves in Figure 1 are, (a) raw data and (b) gamma-variate fitted curve for the first pass. The reconstructed images in Figure 2 are, (a) the total CBV, (b) a gamma-variate fitted map gCBV, and (c) the difference of the two images (a) and (b), and (d) the time to peak map (TTP).

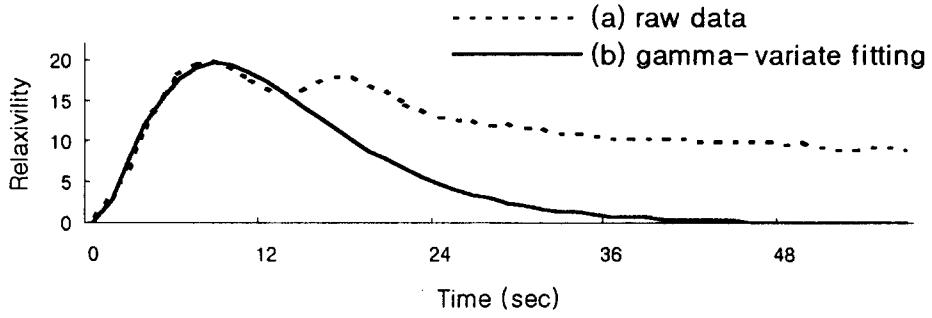

Figure 1. The fitted curve plot of gamma-variat function of concentration-time image data. The second peak may be due to collateral.

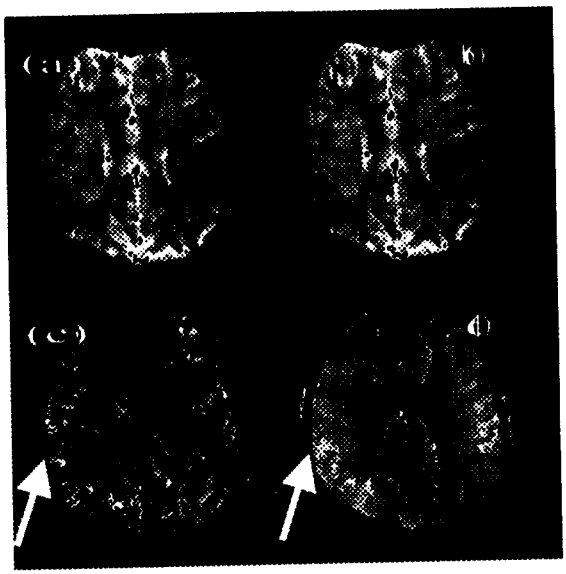

Figure 2. Blood volume maps: total cerebral blood volum (CBV) , the first pass cerebral blood volum (gCBV) map, difference volume map, reconstructed by subtracting (b) from (a), andTTP map. TTP was the time from a starting of dynamic change to the peak of DR_2^*

Discussion

Elimination of the 1st pass blood volume from the total CBV results in the recirculatory volume, which may be in general proportional to the fitst pass volume. For the region with extra indirect blood supply with time lag such as the patient with moyamoya disease, the information about the secondary flow by this study may be important for the understanding of the hemodynamics. TTP map in Figure 2 (d) clearly showed time-lagging at the region with lots of collateral flow.

References

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