# A Correlation Method of MR Contrast Perfusion Quantification Base on SVD Deconvolution

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**Introduction**

In quantifying cerebral perfusion with dynamic magnetic resonance contrast perfusion weighted image (MR-PWI), the accuracy of quantitative results is critical, including Cerebral Blood Flow (CBF), Cerebral Blood Value (CBV), and Mean Transit Time (MTT). A number of factors can affect the quantitation results [1], including second-pass, non-measurable coefficients, deconvolution methods, Artery Input Function (AIF), and S/N ratio of image. Conventionally, manual operation was used to remove the second pass in a fixed time delay region using whole brain average time intensity curve (TIC). Among the several available methods, singular value decomposition (SVD) deconvolution has been used due to its accuracy. However, it overvalues in the region of the tissue around brain artery or vein, or undervalues in the region of diseased tissue. During SVD deconvolution, a filter is used to decrease noise. This filter applies a fixed parameter to all of the voxels [2]. Since the vascular model is sensitive to data noise for different cerebral tissue (white matter, gray matter and diseased tissue), the filter parameter needed to be changed depending on data noise. We developed a fully automatic method for detecting the first-pass region voxel-by-voxel for decreasing the data noise as a pre-processing. And we proposed to detect the filter parameter voxel-by-voxel for SVD deconvolution. MR-PWI map was compared with PET CBF as the gold standard on the same subject. The results show that the new method has a higher significance correlation with PET CBF mapping. The new method can detect the disease region effectively in MTT mapping.

**Method**

CBF can be found in equation 1.

$$CBF = \frac{CBV}{MTT} \qquad \text{[eq.1]}$$

The concentration of indicator within tissue, $C_{tissue}(t)$, is given by convolution of AIF, $C_{aif}(t)$, with the tissue impulse residue function $R(t)$.

$$C_{tissue}(t) = CBF \int_0^t C_{aif}(\tau) R(t-\tau) dt \qquad \text{[eq.2]}$$

$C_{tissue}(t)$ and $C_{aif}(t)$ can be measured discretely by MR system. So eq.2 can be rewritten as eq.3, and for brevity, also can be rewritten as eq.4

$$\begin{pmatrix} Ctissue(t_0) \\ Ctissue(t_1) \\ \dots \\ Ctissue(t_N) \end{pmatrix} = \Delta t \cdot \begin{pmatrix} Caif(t_0) & 0 & \dots & 0 \\ Caif(t_1) & Caif(t_0) & \dots & 0 \\ \dots & \dots & \dots & \dots \\ Caif(t_N) & Caif(t_{N-1}) & \dots & Caif(t_0) \end{pmatrix} \cdot \begin{pmatrix} R(t_0) \\ R(t_1) \\ \\ R(t_N) \end{pmatrix} \qquad \text{[eq.3]}$$

$$\vec{C}_{tissue} = A \cdot \vec{R} \qquad \text{[eq.4]}$$

where $A$ is a matrix created by AIF, and $C_{tissue}$ is a vector. $R$ can be corresponded by

$$\vec{R} = A^{-1} \cdot \vec{C}_{tissue} \qquad \text{[eq.5]}, \quad \text{where} \quad A^{-1} = U \cdot S^{-1} \cdot V^T \qquad \text{[eq.6]}$$

$V$ and $U$ are two orthogonal matrixes, and $S$ is a diagonal matrix. In the current status, for decreasing data noise, SVD deconvolution filters noise by $p = 20\%$ to reduce elements of $S$ matrix to level of $p \cdot S_1$ for all of the voxels. However, data noise in each voxel TIC is different. $p$ should be optimized for each voxel. In this work, we define a new parameter $p$ for noise trace as:

$$p = 1 - average(s) / max(s) \qquad \text{[eq.7]}$$

Each voxel TIC should be processed by full automatic first pass detection.

**Result and Discussion**

The new method was applied to three normal volunteers to compare the CBF map of PET. Fig.1 shows the MR-PWI resulted from CBF and PET. Fig.2 shows the correlation of 13 ROIs on the same subject.

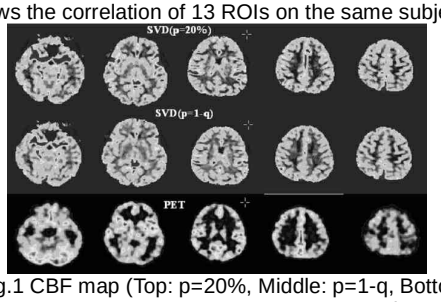


Fig.1 CBF map (Top: p=20%, Middle: p=1-q, Bottom: PET)

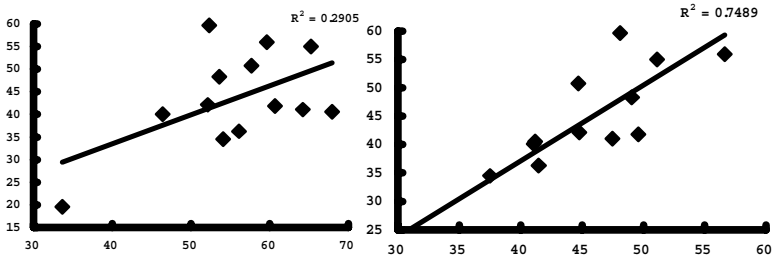


Fig.2 Correlation of CBF map, Left: p=20%, Right: p =1-q

Tab.1 Correlations of PET-CBF and MR-PWI-CBF with different p

| p value | Volunteer 1 | Volunteer 2 | Volunteer 3 |
|---|---|---|---|
| p = 20 | 0.2905 | 0.3951 | 0.2730 |
| p = 1-q | 0.7489 | 0.5258 | 0.9051 |

Tab.1 lists the correlation of the three subjects. It shows the new method has a higher correlation with the PET-CBF gold standard.

In this work, the effect on quantitative result of MR-PWI was considered from three perspectives: 1) sensitivity to image data noise, 2) different indicator concentration from different tissue, and 3) effect of noise on the result of residue function. We proposed a new method of SVD filtering for SVD deconvolution of MR-PWI quantitative analysis. Filter parameter p is detected voxel-by-voxel, which can fit the feature of each voxel TIC. In verification, data from 3 volunteers were compared with PET-CBF, showing a higher correlation when parameter p was optimized for each voxel and the overvaluation and undervaluation was suppressed. It has also been confirmed by clinical physicians that the MTT map has a high sensitivity in detecting the disease tissue.

**References**

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