Dynamic Susceptibility Contrast Perfusion Quantification using Spread Bases Function

B Rajeswari, P Abdul Khayum

ABSTRACT--- ***Dynamic Susceptibility Contrast (DSC) perfusion Magnetic Resonance (MR) imaging of the brain provides tissue perfusion characterization. This characterization can be done by recovering scalar parameters like cerebral blood volume (CBV), cerebral blood flow (CBF), and mean transit time (MTT) and also tissue impulse response function. Scattering effect of bolus causes not only the information to reflect tissue perfusion and also provide macro vascular properties. The possibilities of obtaining disperse response functions and parameters can be done by performing deconvolution. The proposed method of Spread Bases Function (SBF) used to denote the response function in the presence of scattering for effective parameter estimation. The simulated results show that SBF deconvolution gives better performance than oSVD in the effective estimation of perfusion parameter, irrespective of the occurrence of scattering. Furthermore, the SBF method recovers response functions effectively that carry out with both healthy and pathological conditions, and offers the benefit of making no suspicions about the nature of scattering at different levels of perfusion. The simulated results are implemented on the digital head phantom.***

Key words: Perfusion, Dynamic Susceptibility Contrast, Spread Bases Function

I. INTRODUCTION

Magnetic Resonance Perfusion imaging using Dynamic Susceptibility Contrast (DSC) provide information which is useful in diagnosis of neurological problems, brain tumors grading, characterization of problems, and also about ischemic strokes [1].This related information is provided in determining the disease by using the parameters like parameters of hemodynamics or perfusion parameters or brain maps, like cerebral blood volume (CBV), cerebral blood flow (CBF) and also mean transit time (MTT). The intravenous injection of a tracer gives the result of tissue concentration time-curves and also arterial input. The measured values of tissue concentration time-curve $C_{ts}(t)$, arterial input time-curve $C_a(t)$, the brain maps can be obtained for each voxel. The calculation of CBF and MTT for each voxel are related to the residue function estimation r(t) in measuring the residual amount of tracer which depends on time through deconvolution. The modeling of perfusion is modeled by using a linear system with input and output as $C_a(t)$, $C_{ts}(t)$ respectively. And the impulse response function of the tissue is unknown convolution kernel describes in perfusion and encoded by capillary hemodynamic information[2].The effective response function estimation can be obtained by the deconvolution of the measured values of tissue concentration time-curve $C_{ts}(t)$ and arterial input time-curve $C_a(t)$. The shape of the results gives the estimation of an effective response function and reveals properties of vasculature and also the properties of tissue perfusion. In particular, MTT overestimation and CBF underestimation arises because of the presence of dispersion. Whenever the time delay τ exists between the measured concentrations $C_{ts}(t)$, $C_a(t)$, then it will complicates the scattering characterization and response function. In DSC- MRI, the scattering may occur in the injected bolus of the tracer.

As a result, the shape of the convolution kernel changes in measured values of tissue concentration $C_{ts}(t)$ and arterial $C_a(t)$. The scattering effect and its characterization can be done by a Vascular Transit Function (VTF). This VTF (t) is the probability density function with respective to time. The proposed method is used to carry out deconvolution of perfusion for the estimation of response function and the hemodynamic parameters. This estimation of parameters can be done at different levels of scattering effect. Similarly, the estimation of the time-delay which exists between the measured tissue and arterial concentrations is required for estimation of parameters. Here to attain the effective convolution kernel which is measured between $C_{ts}(t)$ and $C_a(t)$, the proposed method is Spread Bases Function (SBF) as it is a non-parametric representation which depends on the response function . Further characterization of eventual presence and amount of scattering can be done based on the shape. The proposed method performance can be measured at different levels of scattering along with different dispersion kernels. This will gives both quantitative as well as qualitative results on MR data related to stroke data.

II. DYNAMIC SUSCEPTIBILITY CONTRAST MRI

The perfusion theoretical background and the variation in the tissue impulse response function is reiterated when the bolus scattering is present. After that the influence of scattering on the parameters of perfusion are measured, and proposed to characterize the amount with the scattering time and its ensuing presence. The Spread Bases Function (SBF) is used to measure the effective response function even when the effect of scattering is present. The tracer injection of the contrast agent i.e. a paramagnetic is helpful for performing the characterization in perfusion by means of DSC-MRI. The portrayal depends on the tracer energy dependent on the supposition of the tracer is intravascular and the blood cerebrum boundary is flawless. The phase dishomogenization of spins caused because of the allowing

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of the paramagnetic agent in correspondence with the blood vessels or capillaries due to susceptibility effects. The T_2^* in case of Gradient-Echo which is transverse relaxation time shortening and T2 with Spin-Echo leads to decrease in signal intensity. The signal intensity increases as long as the tracer clears out. The measured S(t) which depends on time is connected to the concentration time-curve C(t) via the relation as

$$S(t)=S_0 \cdot e^{-k \cdot C(t) \cdot TE} \quad (1)$$

Here the baseline signal is indicated by S_0 before the arrival of tracer, the echo-time is indicated by TE , and the contrast agent transverse relaxivity indicated by κ. The $C_{ts}(t)$ is the concentration in a tissue voxel is articulated as the convolution between $C_a(t)$ and R(t), arterial and the unknown tissue impulse response function respectively. Based on the indicator-dilution theory R(t) given by R(t) = CBF ·r(t)

$$C_{ts}(t) = \int_0^t C_a(\theta)\, \mathrm{R(t-\theta)d\theta} \quad (2)$$

The ratio between the integrals of the tissue concentration and arterial concentration gives the value of cerebral blood volume (CBV). This is calculated with respect to the arterial reference, the relative tracer amount in the voxel as

$$CBV = \frac{\int_0^t C_{ts}(t)dt}{\int_0^t C_a(t)dt} \quad (3)$$

The amount of average time which takes for a particle of tracer to enter the vascular system, underlying a voxel and to leave it definitely defines as the mean transit time (MTT) [5]. MTT expression can be written as below based on the central volume theorem.

$$MTT = \frac{CBV}{CBF} \quad (4)$$

Hence, the calculation of MTT can be done based on the values of other parameters. So as to compare the performance of the techniques that are tested, the cerebral blood volume can be computed by using central volume theorem as

$$CBV = \int R(t)dt \quad (5)$$

The prime objective of MR perfusion deconvolution is to estimate the parameters of perfusion such as CBV, CBF, MTT and residue function r(t). Those values can be found out depending on the information of R(t) and the above equations (3),(4) and (5). Actually, the estimation of CBF can be done as the maximum value of R(t) is there when scattering is not present. To be sure that when the bolus injection is following, the part of the tracer staying in the tissue underlying the voxel through time specifies the residue function r(t). As a result, for t = 0 function has its theoretical maximum that gives r(0) = 1, which indicates R(0) = CBF. The decrease in residue function causes the tracer clearance in due time. The earlier research work shows the shape of r(t) and the slow and fast flow components of the capillary causes are explored by bi-exponential model. The superiority of perfusion parameters estimation relies upon the recovered R(t) from the measurement of $C_{ts}(t)$ and $C_a(t)$. This ill-posed problem can be solved by deconvolution, given in equation (2).The time delay matters will arise in related with arterial input $C_a(t)$ in physiologically delayed measuring of $C_{ts}(t)$.Due to presence of scattering, the shape of response function will be severely affected.

III. EFFECTIVE RESPONSE FUNCTION

The tissue concentration $C_{ts}(t)$ can be measured at the bolus of tracer, which will undergo scattering at the interested voxel. This procedure is illustrated by convolution between the measured input of the arterial $C_a(t)$ and the VTF(Vascular Transport Function) [7].Thus effective arterial input $C_a^*(t)$ and tissue concentration $C_{ts}(t)$ is formulated as below

$$C_a^*(t) = C_a \otimes V\,T\,F\,(t) \quad (6)$$

$$C_{ts}(t) = CBF \cdot [C_a \otimes V\,T\,F(t)] \otimes r(t)$$

$$= CBF \cdot [C_a \otimes [V\,T\,F \otimes r(t)]$$

$$C_{ts}(t) = C_a \otimes R^*(t) \quad (7)$$

Let R*(t) is the effective dispersed tissue response function when the scattering is not there, i.e. R*(t) = R(t) ⟺ VTF(t) = δ(t). When the scattering is present, VTF (t) will project the probability density function of VTF with unknown vascular dynamics. Different kernel like exponential kernel, lognormal kernel and the gamma kernel are used and given in equation (8).

$$VTF\,(t) = \begin{cases} \mathrm{EDK(t,\beta)} = \beta e^{-\beta t} \\ \mathrm{LNDK(t,\mu,\sigma)} = \frac{1}{t\sigma\sqrt{2\pi}}\, e^{\frac{-(\ln(t)-\mu)^2}{2\sigma^2}} \\ \mathrm{GDK(t,p,s)} = \frac{s^{1+sp}}{\Gamma(1+sp)}\, t^{sp} e^{-st} \end{cases} \quad (8)$$

The shape parameters are where β, σ, μ, s, p. For each kernel a MTT_v, the measurement of $C_a(t)$ for selected voxel can be calculated.

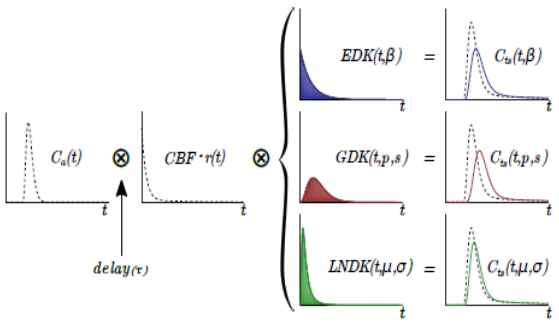

Figure 1: Arterial input and tissue concentration relation.

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Dotted line shown in the figure is related to non-scattered case and the convolution kernel (response function) is represented by the product CBF and r(t). The exponential, gamma and lognormal scattering kernels effect respectively are shown in the figure 3 and defined in eq. (8). The time-delay τ is represented as arrow indication.

IV. DECONVOLUTION WITH SPREAD BASES FUNCTION (SBF)

The effective response function representation can be implemented by using Spread Bases Function with or without scattering effect. The approximate value of $R^*(t)$ is the sum of N bases functions and every basis function is organized as a sum of an exponential and its derivative term with time rate, respectively. The scaling factors are defined as a_n and b_n. The time rates α_n for exponential term and β_n for derivative term are selected to most generalized solution. Any shape can be represented by the sum of these bases ranges between an exponential decay property and differential coefficients. The expression of the bases approximation is given in equation (9)

$$R^*_{DCB} = \Theta(t) \sum_{n=1}^{N} \left(a_n e^{-\alpha_n t} + b_n t e^{-\beta_n t}\right) \quad (9)$$

$\Theta(t) = 1\ \forall t \geq 0$(Heaviside step function). The parameters β_n, α_n, a_n and b_n which are unknown have to be calculated. In the formulation of bases,α_n , β_n are non-linearly in nature with time rates. The τ (time-delay) is a non-linear parameter to be calculated between $C_a(t)$ and response function approximation can be measure using commutative property of convolution given below

$$C_a(t-\tau) \otimes R^*(t) = C_a(t) \otimes R^*(t-\tau) \quad (10)$$

$$R^*_{DCB}(t) = \Theta(t-\tau) \sum_{n=1}^{N} \left(a_n e^{-\alpha_n (t-\tau)} + b_n (t-\tau) e^{-\beta_n (t-\tau)}\right) \quad (11)$$

The convolution problem is discretized in eq. (2) and these can be computed by assuming the tissue concentrations and arterial concentrations i.e $C_{ts}(t)$ and $C_a(t)$ respectively are measured on an equally spaced time grid t_1, t_2, . . . , t_M of length M, with

$$\Delta t = t_{i+1} - t_i$$

$$C_{ts}(t_j) = \Delta t \sum_{n=1}^{\infty} C_a(t_i) R^*(t_j - t_j) \quad (12)$$

The eventual presence of scattering effects for the $R^*(t)$ is underlined. The matrix notation of eq.(12) is represented with $C_{ts} = A_r$, where A is convolution matrix with size M×M along with the arterial input concentration samples of $C_a(t)$, C_{ts} contains the tissue concentration of unknown M samples of the effective response function(r). The M ×1 vector r which is unknown is computed using deconvolution. This intends to compute the set of unknown parameters with defined response function representation. The bases approximation has vectors with linear coefficients $\mathbf{p}_L = [a_1, b_1, a_2, \ldots a_N, b_N]$ and time-rates as non-linearly entering vector $\mathbf{p}_{NL} = [\alpha_1, \beta_1, \alpha_2, \ldots, \alpha_N, \beta_N]$, in size 2N × 1 with 4N ≤ M of unknowns. As a result the response function which can be represented as $R^*(t) = g(t, \mathbf{p}_L, \mathbf{p}_{NL})$. The matrix representation of the convolution problem is given eq. (13)

$$C_{ts} = \mathbf{AG}(\mathbf{p}_{NL})\mathbf{p}_L \quad (13)$$

The design matrix represented by AG ($\mathbf{p}_{NL}$) is depending on $\mathbf{p}_{NL}$. The circular convolution is implemented for oSVD with time-delay τ into consideration [7]. The zero-padding with length L ≥ 2M helps to avoid aliasing effect in computing the arterial and tissue concentration time-curves of length M. The circular convolution matrix A^c has entries with the order of L × L as

$$A^c_{i,j} = \begin{cases} \Delta t \cdot C_a(t_{i-j+1}) \text{ for } j \leq i \\ \Delta t \cdot C_a(t_{L+i-j+1}) \text{ for } j > i \end{cases} \quad (14)$$

Generally, higher order equation like trapezoidal rules or Simpson's integration rules will present better approximations. The convolution equation is reformulated as

$$C_{ts} = A^c G^\tau (p_{NL}) p_L \quad (15)$$

Where $G^\tau (p_{NL})$ is designed with matrix size as L X 2N depending on p_{NL} and $_\tau$ of the circular time sampling grid. The value of τ can be estimated within a range [τmin, τmax] seconds in grid search, with step time $\tau_s \leq \Delta t$. The gradient-descent methods used to obtain the estimated vectors of parameters $\hat{p}_L$, $\hat{p}_{NL}$ will be obtained with estimated delay $\hat{\tau}$ and the minimizing factor is $\|cts - A^c G^\tau (\hat{p}_{NL}) \hat{p}_L\|^2$ among all $\tau \in [\tau_{min}, \tau_{max}]$. The advantage of functional bases in computing the analytic Jacobian matrix will provide the non-linear routine speed in estimation of the parameters.

V. RESULTS AND DISCUSSION

In result analysis create a simulation digital phantom similar to that of real 4D perfusion phantom. The regularization of the data is specific for reproducible computation of reconstruction methods. First time this digital phantom is developed to simulate the deconvolution methods in estimating the parameters. This digital phantom have similar properties like the real brain and all the perfusion relation experiment can be measured. If particular methods are working well with the digital phantom then the same method can be implemented on the MR perfusion data.This digital phantom simulation will help to avoid typical process of perfusion on the subject with different dosage of gadolinium. This simulation will give better estimation results by proper setting of perfusion. The anatomical brain structure is modeled with nonlinear equation. This is used to represent the tissues concentrations built on real physiological data and avoiding sparsity by varying perfusion parameters continuously. To minimize sparsity of the brain phantom the tissue voxels are useful. T1 imaging is more suitable to do analysis of brain stroke in different stages with the available algorithm. The normalized values are assigned to each voxel of T1

weighted image. The values must be in the interval [-1, 1] and statistical properties for each voxel are measured. The mean and variance is calculated for the segmented parts of voxels.

The mean value is calculated by subtracting the values from the MR values and those values are limited to [-2*σ, +2*σ] by setting all values < -2*σ to 2*σ respectively. Finally all the values are divided by 2*σ. The perfusion parameters of each tissue voxel are varied by the relation :

$$PV(x) = P(x) + NMR(x) * DP(X) \quad (16)$$

PV(x) represents the varied perfusion parameter of voxel x.

The T1 weighted image is of 256 x 256 size and a slice is shown below in Figure 2 and in the parameter estimation the skull part is removed. The segmentation of gray matter (GM), white matter (WM) and cerebral semi fluid (CSF) is done. . The segmented part is marked with reduced perfusion and severely reduced perfusion with yellow and red colors and these parts are simulated by the proposed method for parameters quantification as shown in Figure 3.

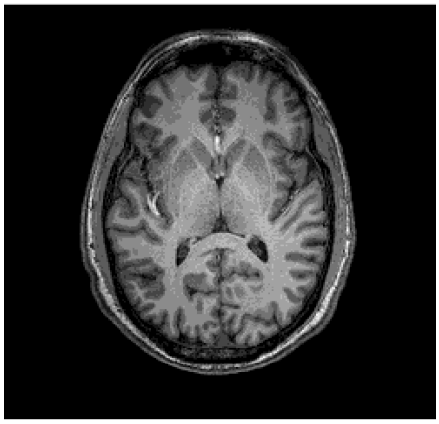

Figure 2. T1 weighted Image

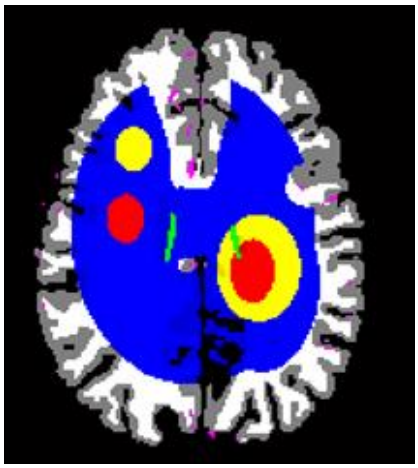

Figure 3. Digital phantom slice

The examination between two non-parametric ways to deal with deconvolution utilizing proposed and oSVD, are figured under the nearness of abnormal amounts of dispersing. To execute this calculation the exponential part changing the MTTv = 1/β in range [1, 10] seconds are taken.

The comparison between two non-parametric approaches such as oSVD and the proposed method to deal with deconvolution are computed under the existence of high levels of scattering. To execute this algorithm the exponential kernel varying the MTTv = 1/β in range [1, 10] seconds are taken. The generated signals will be having step time with reference (Δt = 0) and then the process of a repetition time TR = 1s at down-sampled. The considered and tested delays are 0, 1, 2, 3, 4, 5 seconds and SBF in a broader range [−7, 7] sec with τs = 1s. Some parameters are also tested like MTT ∈ {4, 8, 12, 16}s and CBF ∈ {15,30,45,60} ml/100g/min. The assessment is done by the calculation of mean error and SD over thousand noisy realizations. In figure 4 and 5, the comparative errors for MTT* and CBF* are reported. The absolute error for the maximum time t_{max} of the effective response $R^*(t)$ is presented in figure 6 which provides the absolute error of scattering time, τ_δ.

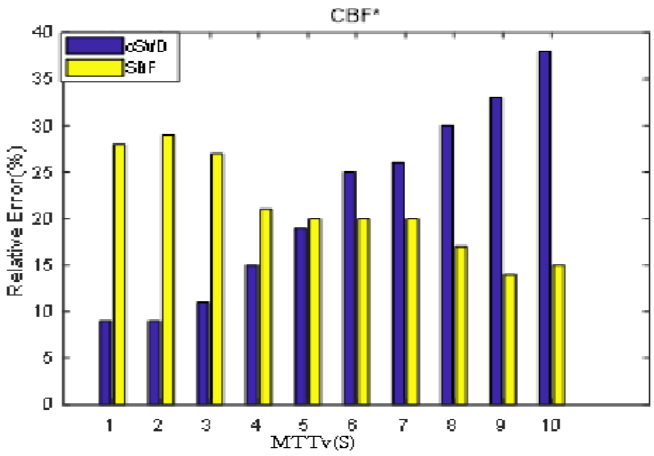

Figure 4. Relative errors for CBF∗

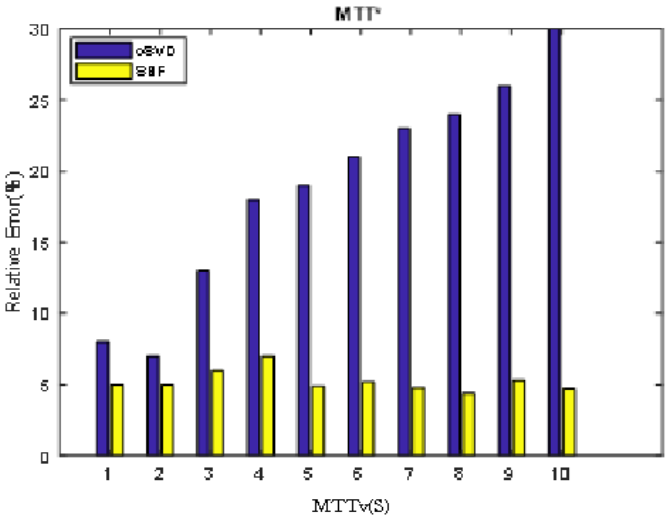

Figure 5. Relative errors for MTT∗

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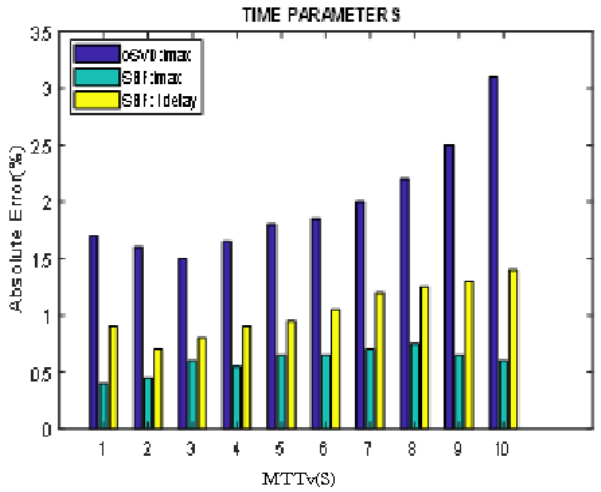

Figure 6. Absolute error for MTT* with Time parameters

In Figure (4) relative estimation errors CBF* is plotted between the proposed method and oSVD and is observed that Figure (5) in MTT*. The absolute errors t_{max} of the effective response function for Spread Bases function can be indicated by using bar plot in the image with respect to the scattering time τ_{δ}. As shown in figure (6), based on scattering response function with exponential scattering kernel(EDK), by varying MTT,CBF and delay τ as specified the synthetic data if created.. During the observation, the SBF gives good values than oSVD. When as scattered level are increased which show that overall estimation is improved for the tested parameters.

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