An Efficient, Bolus-Stage Based Method for Motion Correction in Perfusion Weighted MRI

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Abstract

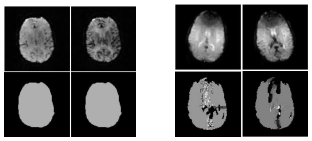
This paper addresses the data corruption that occurs due to patient motion during a scan which is particularly a problem in perfusion weighted MRI due to long scan times. Motion correction is typically the rate-limiting step in processing as each volume has to be registered to a reference volume. This is compounded by the dynamically varying contrast in the volume series due to passage of an injected contrast agent. We propose an efficient two stage motion correction method, consisting of motion detection and a 2-pass registration method for aligning the motion-corrupted volumes. A 2D block-wise phase correlation in central slices is used for the first stage. Alignment employs a strategy which is sensitive to the status of the bolus in the volume and is based on gamma-variate function fitting for intensity correction to handle dynamic contrast in DSC-MRI. Evaluation of the approach shows that it is fast and accurate.

1. Introduction

Perfusion measurements with MRI are widely used for assessing different pathological processes including tumour characterization and progression, determining salvageable tissues post acute ischemic event in brain, inflammation and infectious diseases. Here, an exogenous paramagnetic contrast agent (bolus) is injected into the blood stream and tracked over a region of interest by acquiring a time series of MR volumes (4D data) [3]. Perfusion data are of two types: T2*-weighted dynamic susceptibility contrast(DSC) imaging and T1-weighted dynamic contrast enhancement (DCE) imaging. The tracked information is parametrized on voxel-by-voxel basis by physiological models to derive blood flow characteristics in different tissues. This information forms the basis of disease detection and treatment planning[3].

Perfusion imaging requires acquiring a time series of MR volumes and patient motion is often observed in the final data which can corrupt the measurement of signal intensity change. This in turn affects the derived perfusion indices. Due to constraints imposed by the data acquisition method, motion correction is generally done retrospectively. Therefore, reliable detection and correction of motion is of interest. The main challenge in motion correction is the localised variation in signal intensity in the volume time series (4D data) due to wash-in and wash-out of bolus.

Motion correction of the 4D data can be seen as alignment of motion corrupted volumes to "stationary" volumes. A technique proposed for DSC-MRI data registers each volume in the time series to either a single volume at a specific time or the mean volume of complete time-series data [4]. Inclusion of a model of dynamic contrast in an iterative registration process has been proposed for tumour motion tracking [1]. Aligning volumes to correct for motion can be a time-limiting step ($\sim$90% of processing time) in a PWI analysis pipeline [7]. In this paper we aim to reduce this processing time by identifying the set of volumes corrupted by motion and propose a novel and efficient method to correct for motion in those volumes. Specifically, we propose a 2-pass motion correction approach wherein the time-series is divided into three sets according to the status of the bolus. Motion correction is first carried out in each of these sets independently followed by a final registration step.



(a) no motion (b) with motion

Figure 1. Slice pairs (top row) and their flow maps U_n and V_n (bottom row).

2 Method

In perfusion studies, bolus injected into the bloodstream takes some time to reach the region of interest, pass through and eventually pass out of the region. Hence, the given 4D data set can be divided into 3 distinct sets based on the bolus status: volumes belonging to 1) pre-wash-in, 2) transit and 3) post wash-out sets.

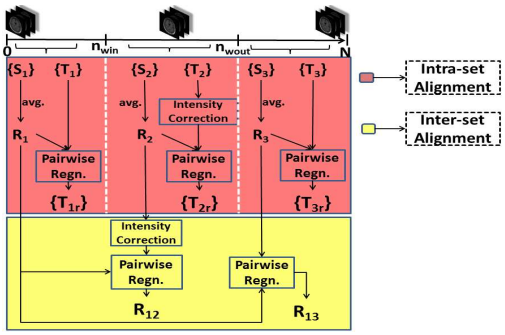


Figure 2. Block diagram for motion correction. $\{.\}$ denotes a set of volumes.

Given a PWI time series, we first identify the volumes corrupted by motion by analysing pairs of adjacent volumes using a phase correlation-based approach. The subset of volumes detected to have motion are then corrected using a bolus status-specific approach. We begin with the description of the motion detection approach.

2.1 Motion Detection

Given a time series, a quick way to detect motion is to consider only the central slices (I_n, I_{n+1}) for every pair of adjacent volumes and compute the motion field (U_n, V_n) between them. In the absence of any motion between the volumes, this field will be uniformly zero. We propose computing this motion field by considering a block of pixels $b(i,j)$ around every pixel at location (i,j) in the slice pair and performing a phase correlation. The inter-slice intensity variation that is characteristic of DSC-MRI is handled by normalising the blocks first by shifting the mean pixel value of every block to zero. Phase correlation is applied to every pair of normalised blocks $(\tilde{b}_n(i,j), \tilde{b}_{n+1}(i,j))$ and the desired flow vector $\vec{r}(i,j) = (u(i,j), v(i,j))$ is found from the locations of maxima of the cross power spectrum $G_{\tilde{b}_n\tilde{b}_{n+1}}$. The flow maps $U_n = [u(i,j)]$ and $V_n = [v(i,j)]$ for motion between I_n and I_{n+1} are given by:

$$(u,v) = argmax_{(i,j)\varepsilon b_{i,j}} \left(\mathfrak{F}^{-1}\left\{G_{\tilde{b}_n\tilde{b}_{n+1}}\right\}\right) \quad (1)$$

where, $\mathfrak{F}^{-1}$ denotes the inverse Fourier transform; $G_{\tilde{b}_n\tilde{b}_{n+1}} = \frac{\tilde{B}_n\tilde{B}^*_{n+1}}{|\tilde{B}_n||\tilde{B}^*_{n+1}|}$ and $\tilde{B} = \mathfrak{F}\{\tilde{b}\}$.

In our implementation, the given slice of size 128×128 was down-sampled by a factor of 4 to obtain a 32×32 slice for computational efficiency and the block size was chosen at 8×8.

The flow maps U_n and V_n describe flow field relating two central slices (I_n and I_{n+1}) of the volumes at time n and $n+1$. Fig.1 show sample slice pairs and the derived flow maps. The slice pair in Fig.1(a) is from a pair of volumes with no motion. It can be noted that despite changes in the signal intensities, the flow maps are almost uniform, indicating that proposed approach is mostly immune to bolus-contrast based signal changes. The slice pair in Fig.1(b) is an example where motion was present. This is seen to be reflected clearly in the flow maps as non-uniform areas (which experience motion). Motion corrupted volumes are identified using the total entropy(found by adding entropies in U_n and V_n) and passed on to the motion correction module presented in the next section.

2.2 Motion Correction

Fig.2 shows the complete block diagram for the proposed motion correction technique. The first step in correction is to divide the given PWI time series into 3 distinct sets based on the status of the bolus in the brain. These sets are identified using the well known gamma-variate function [2] which describes the transverse relaxation rate of magnetization with the passage of the bolus. This function is given as:

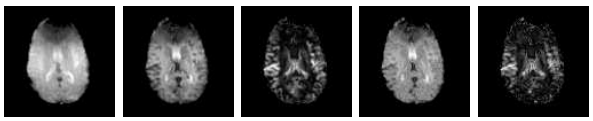
$$\Delta R2^*(t) = A(t-t_0)^\alpha e^{-(t-t_0)/\beta}, t > t_0 \quad (2)$$

where, $\Delta R2^*(t)$ is the transverse relaxation rate, t_0 is the wash-in time-point of bolus, and A, α and β are parameters that decide the shape of function. The mean intensity of each volume is computed to derive a curve $I_a(t)$. The wash-in time-point(t_0) is roughly set at time-point where mean intensity falls abruptly. The above gamma-variate function (GVF) is then fit to $I_a(t)$ to accurately determine the wash-in (n_{win}) and wash-out time points (n_{wout}). These are the time-points of sudden change in signal intensities in the GVF-fit-mean-intensity curve ($G_a(t)$). These points help divide the given 4D dataset into three sets: Set 1 of pre-wash-in, Set 2 of transit and Set 3 of post-washout stage of the bolus passage.

The next step in motion correction is to align the motion-corrupted volumes. A 2-pass process was designed for this purpose with the first pass aimed at intra-set alignment while the second pass aimed at inter-set alignment. All pairwise alignments were done with sum of squared difference (SSD) based rigid registration using limited memory Broyden-Fletcher-Goldfarb-Shanno method(l-BFGS) for optimization. In the construction of reference volume for registration, the fact that the subject motion (during acquisition) is transient in nature, i.e. stationary for a set of contiguous time-points followed by a irregular motion for short period of time can be exploited. Hence, the reference volume R_m for each stage of the bolus (before, during and after the passage) is constructed as:

$$R_m = \frac{\sum_{n=n_1}^{n_2} S_m(n)}{(n_2 - n_1 + 1)}; \quad m\epsilon\{1,2,3\} \quad (3)$$

where $S_m(n)$ is a stationary volume,$(n_2 - n_1)$ is the longest time interval of contiguous stationary volumes



(a)R (b)T (c)$|R-T|$ (d) T^c (e)$|R-T^c|$

Figure 3. Intensity Correction Example

in the m^{th} set. Next, the intra-set alignment procedure is explained.

2.2.1 Intra-set Alignment

As the bolus is not present in the volumes in Sets 1 and 3, hence these volumes do not suffer from the dynamic change in contrast, which is not the case with the volumes in Set 2. Thus, different alignment methods need to be employed for these two cases. For Sets 1 and 3, the procedure is to find the reference volume using eqn.(3) and then do a pairwise registration of every moving volume T with this reference volume. For Set 2, an intensity correction step is required prior to the pairwise registration.

Intensity Correction

In DSC-MRI, there is a signal loss or decrease in the image intensity, only in regions where the bolus is present. This leads to a non-uniform intensity change within the volume. We identify the bolus-affected regions using a Fuzzy c-means clustering method. This aids in segmenting the moving volume (T) into normal (T_a) and bolus affected (T_b) regions. To account for changes in image intensity across time points, we use the above gamma-variate function fitting on the mean-intensity perfusion curve($G_a(t)$), to obtain the intensity change across time points. The intensity correction is then applied to only bolus affected regions. The intensity corrected floating volume $T^c(n)$ is generated by:

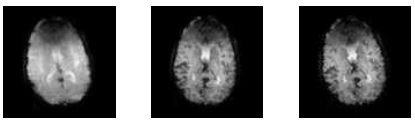
$$T_b^c(n) = T_b \frac{G_a(n_{R2})}{G_a(n)}; \quad T^c(n) = T_a(n) \cup T_b^c(n) \qquad (4)$$

where n_{R2} is the centre of time-points used for constructing reference volume R_2.

Fig.3 shows an example of reduction in intensity difference between images after intensity correction. This results in a reduction of the contribution of bolus in intensity difference and makes the distance measure in registration more accurate. Finally, this intensity-corrected volume $T^c(n)$ is registered to the reference R_2. Next, the inter-set alignment is presented.

2.2.2 Inter-set Alignment

The reference volume R_1 for the first set is taken to be the fixed reference for inter-set alignment. Reference volumes R_2 and R_3 are aligned to this fixed reference. Since Set 2 has dynamic contrast change, an intensity correction step has to precede the pairwise registration of R_2 and R_1. This is done similar to the step described



(a)R_1 (b)R_2 (c)R_{12}

Figure 4. Result of registration of two reference volumes(R_1 and R_2). Only a slice is shown.

in intra-set alignment. R_2^c is generated by:

$$R_{2b}^c = R_{2b} \frac{I_a(n_{R1})}{G_a(n_{R2})}; \quad R_2^c = R_{2a} \cup R_{2b}^c \qquad (5)$$

Here, usage of $I_a(n_{R1})$ instead of $G_a(n_{R1})$ reflects that GVF fitting is applicable only after bolus has washed-in. The generated volume R_2^c is then registered to R_1.

At the end of inter-class alignment we have all required transformations to align the complete time series. Let X_{12} and X_{13} be the transformations relating (R_1,R_2) and (R_1,R_3). These can be used to align the corrupted volumes in Sets 2 and 3 to R_1 as follows:

$$T_{2r} \xrightarrow{X_{12}} T_{12}; \quad T_{3r} \xrightarrow{X_{13}} T_{13} \qquad (6)$$

3 Experiments and Results

A DSC-MRI dataset was acquired from a 1.5T GE MRI scanner with number of volumes = 40(1s/phase), number of slices = 20, slice thickness = 5 mm, matrix size = 128×128. For validating the proposed method, a set of experiments were performed. All the computations were performed on 64-bit Intel(R) Core(TM)2 Duo processors(2.20 GHz) with 2GB RAM and MATLAB v7.12.0.

In our experiments, known amount of 3D rotation were added in the volumes to simulate patient motion during DSC-MRI. Transient nature of motion was reflected by adding motion to volumes at a random interval of time-points. The rotation angles were generated randomly in the range [-20° 20°] in transverse direction(R_z) and [0° 10°] in coronal direction(R_x). The randomness in generation of angles captures the worst case scenario of motion where the subject is highly agitated. Translation motion inside the scanner is found absent in most of the cases. These ranges were chosen on the advise of a neuroradiologist as depicting typical patient motion.

We first present qualitative results of registration with our approach. Fig.4 shows the inter-set registration (R_2 with R_1) with our approach. Despite the changes in contrast, R_2 is correctly registered to R_1 to produce the final registered output (R_{12}). The alignment was quantitatively assessed using the dice coefficient ($DC = 2\frac{A \cap B}{A \cup B}$ for two sets A and B) of segmented brain masks. A DC value of 1 indicates perfect alignment. With R_1 as the reference volume, the DC values are presented in Table 1 for all the registered volumes in the time-series. After registration, the degree of overlap between the volumes increases which is verified by

Table 1. Dice Coefficient(DC) values

Rotation in R_z(degrees)	Rotation in R_x(degrees)	DC before Registration	DC after Registration
[0 10]	[-10 10]	0.88	**0.93**
[0 10]	[-15 15]	0.86	**0.92**
[0 10]	[-20 20]	0.87	**0.93**

Table 2. Evaluation of our approach

Total no. of Volumes	No. of corrupt Volumes	Rotation in R_x (degrees)	Rotation in R_z (degrees)	Registration Method	No. of Corrupt Volumes Detected	Regn. Error (e_{rms})	Time Taken (min)
39	25	[0 10]	[-10 10]	MI based	NA	0.28	26.83
				Our approach	21	**0.22**	**13.64**
39	25	[0 10]	[-15 15]	MI based	NA	0.60	30.17
				Our approach	24	**0.37**	**17.62**
39	25	[0 10]	[-20 20]	MI based	NA	0.54	27.58
				Our approach	22	**0.34**	**14.90**

the DC values before and after registration. A second type of evaluation was done to study the effect of registration on mean-intensity of a manually selected ROI before and after registration. The results are shown in Fig.5. Prior to registration, subject motion causes a shift in ROI and intensity-time curve does not depict a typical behaviour of DSC-MRI. After registration, the ROI remains stationary across time-points and a typical DSC-MRI intensity-time curve is obtained.

The performance of our approach was also compared with traditional registration techniques reported in literature where the whole time-series is registered to a mean volume [4]. The evaluation metric chosen for this purpose was the RMS difference of the residual difference (e_{rms})[6] defined as:

$$e_{rms} = \sqrt{\frac{1}{N}\sum_{\mathbf{x}\epsilon\Omega}(U_a^{-1}(\mathbf{x}) - U_o(\mathbf{x}))^2}; \quad \mathbf{x} = [x, y, z]^T \qquad (7)$$

where, U_a is the applied transformation and U_o is the obtained transformation, N is the number of voxels in object Ω. Table 2 provides a detailed comparison of performance of our approach and an MI based registration method[5] for different degrees of rotation. A number of points can be noted from the tabulated results. Firstly, the motion detection step applied prior to motion correction helps reject the stationary volumes from the time-series. Thus, only a subset of volumes are corrected in our approach as compared to traditional approaches that register all the volumes in the time-series to a mean volume. The success in detecting motion-corrupted volumes was generally found to be lower for small rotation angles. This is primarily due to the block size chosen in the phase correlation. The randomness in generation of rotation angles meant that even for large range of motion([-20° 20°]), the actual angle of rotation added to a volume could be small, thus resulting in a lower number of correct detection. Second, the registration error(e_{rms}) in our approach is consistently lower than that for the MI based approach. An increase in amount of rotation in R_z direction results in an increase in error for both methods but the increase is less for our

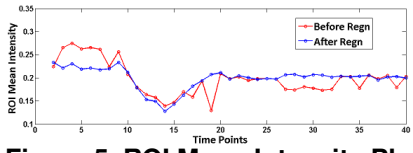


Figure 5. ROI Mean-Intensity Plot

method. Lastly, the time taken for correction of entire time-series with our approach is less. This is both due to MI based methods being computationally intensive and that the number of volumes being corrected is also higher. The time taken (for detection and correction) can be reduced further by using a multicore architecture built in C++.

4 Discussion and Conclusions

We present a novel and efficient two stage motion correction method, consisting of motion detection and 2-pass registration for alignment of motion-corrupt volumes in brain DSC-MRI. The motion detection step helps reject the stationary volumes in the time-series, thus reducing the number of rigid transformations required to estimate. The 2-pass registration divides the time-series into different sets depending upon the status of bolus and uses gamma-variate function fitting for intensity correction in both intra-set and inter-set alignment of volumes. This makes the motion correction process accurate. The method assumes that motion is rigid in nature. The limitations in the approach lie in motion detection where i) the sensitivity to mild motions may be compromised and ii) using the central slice in every volume for motion detection assumes that there is no intra-volume motion.

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