Adaptive spatio-temporal resolution for accelerated (ASTRA) DCEMRI driven by pharmacokinetic modelling

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Introduction: DCE-MRI is a method for imaging the physiology of the microcirculation. The contrast enhancement patterns on DCE-MRI are significantly influenced by tumor angiogenisis. As the tumors grow, the demand for the nutrients increases and microcirculation is disorganised [1]. The pharmacokinetic (PK) analysis can be undertaken to model as to how the CA distributes in the body and how it depends on characteristics of the tumor biology, given the gadolinium concentration as a function of time [2]. The rapid intake of CA is significant in the signal intensity time curve for determination of pharmacokinetic parameters. These curves are fit to different PK models resulting in the determination of the kinetic parameters. The value of K^{trans} indicates the tissue perfusion per unit volume, if the contrast uptake of the tissue is flow limited and indicates the tissue permeability if the uptake is permeability limited [1]. The slope of wash out curve of the signal intensity denotes V_e and larger V_e tumors take longer to reach their peaks [2]. The proposed algorithm exploits **this dependence of K^{trans} on uptake of CA and predominant dependence of V_e on wash-out of CA**.

Methods: This algorithm is an application of sampling strategy involving Compressed Sensing (CS) on DCEMRI. To reduce the image acquisition time

Figure 1: Plot of Signal intensity vs. Number of frames

[3] and obtain better quality of reconstruction, CS is applied to DCEMRI. CS with various under-sampling factors is applied on DCEMRI and the reconstructed results are compared. During uptake, the acquisition in number of frames is varied by using an under-sampling mask. The number of frames acquired depends on the acceleration factor that is used. The data acquisition in case of DCEMRI is divided into 2 regions: 1. Temporal resolution (TR) 2. Spatial resolution (SR). During the uptake of CA, frames are acquired in TR region: whereas during the washout of CA, frames are acquired in SR region. In case of conventional CS, same acceleration factors are used during both the uptake and wash out of CA. In the proposed method, combinations of different acceleration factors are used. No acceleration factor is applied during the acquisition of baseline (Images acquired before injecting CA) images. The wash out of CA represents the SR region which is determined by calculating the maximum k-space difference between two frames. If the difference obtained is negative for three consecutive values, then it is considered to be the beginning of SR region. Reconstruction is performed for 1X,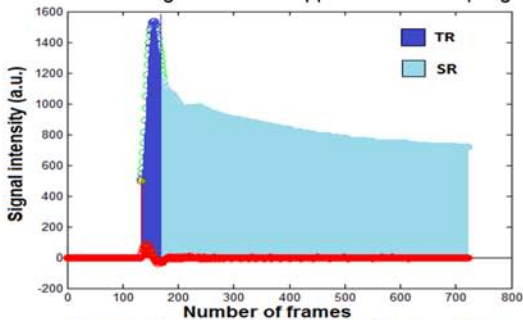 2X, 4X, 6X and 6X/4X accelerations respectively. The reconstructed images are fed into JIM6 software [5] to obtain the parametric maps.

Undersampling strategy: The algorithm uses variable density poisson mask as the under-sampling mask which randomly undersamples the k-space data. On application of this mask, the k-space samples at the centre are sampled more than that at the periphery as in BRISK model which is an extension to keyhole idea [4]. It is generated by taking multiple densities of sampling, with each sampling density containing samples at a fixed distance from each other. Area of these circles is computed based on undersampling factor. Then the points are filled in these circles by linearly increasing the inter-pixel distance as we move away from the centre towards periphery. Centre circular area of fixed radius is completely filled with zero distance and the extreme circle has an inter-pixel distance of three for different accelerations.

Dataset: All experiments were performed using QIBA data set (QIBA_v7_Tofts) of 721 frames with parameters having a flip angle of 30 degrees, repetition time 5 msecs, time interval between the DCE images 1 second, assuming T1 (in tissue) 1000 msecs and T1 (in blood vessel) 1440 msecs. The reconstruction of QIBA data is done using the undersampling mask based on the required acceleration factor. For example case 2 (acceleration factor 2X) data was generated by taking every sixth frame and applying 50% under-sampling mask on it, assuming total acquisition time 12 seconds/frame. Similarly 4X corresponds to every third frame, 6X corresponds to every second frame and so on.

Results and Discussion: The proposed method gives K^{trans} and V_e maps for different acceleration factors (1X,2X,4X,6X and 6X/4X) as shown in Figure 2. We can infer that K^{trans} and V_e value of 6X/4X combination matches with K^{trans} of 6X and V_e of 4X respectively. Hence, determination of K^{trans} is done from TR region and V_e from SR. NRMSE value is calculated for different acceleration factors as depicted in Figure 3.
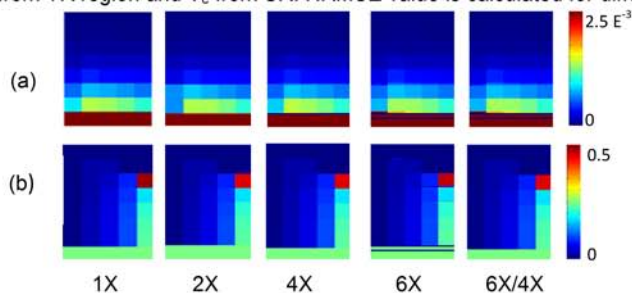

Figure 2: (a) K^{trans} map (b) V_e map for the 5 acceleration factors

Figure 3: Graph showing NRMSE values for 5 acceleration factors

Conclusion and Future work: NRMSE value for the combination 6X/4X lies between that of 6X and 4X as shown in Figure 3, which shows that the combination of two different acceleration factors can yield better pharmacokinetic maps than either of the two (6X/4X K^{trans} is better than 4X K^{trans}, 6X/4X V_e is better than 6X V_e). Future work includes mapping of kspace samples from SR region to TR region to enhance high frequency information in TR region to retain edge information.

Figure 4: Arterial input function (AIF) of reconstructed images

References: [1] Barış Türkbey et al., Diagn Interv Radiol 2010 [2] Paul S et al., Magnetom Flash 3/2010 [3] Lustig M et al., Mag. Res. in Med 2007 [4] Matt A. Bernstein et al., 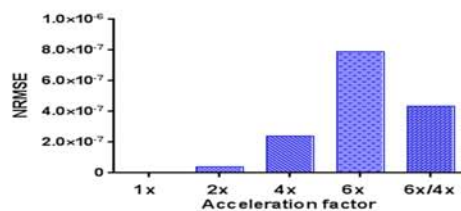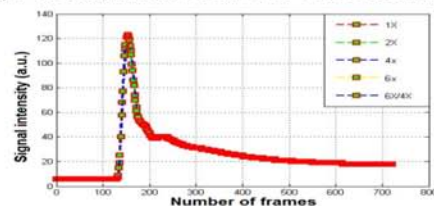Elsevier Inc. 2004 [5] www.xinapse.com/Manual/inde.html