A Cluster-Based Method for Parametric Maps in Dynamic Contrast-Enhanced -MRI

Patrik Brynolfsson[1], Anders Garpebring[1], Thomas Asklund[2], and Tufve Nyholm[1]
[1]*Dept. of Radiation Sciences, Umeå University, Umeå, Sweden,* [2]*Division of Oncology, Dept. of Radiation Sciences, Umeå University, Umeå, Sweden*

Introduction

Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) can estimate pharmacokinetic (PK) parameters that give important information of physiological quantities and has applications in, e.g., oncology [1]. Estimation of the parametric maps require fitting of a PK model to the data which is time consuming and can be unreliable given the inherently noisy data of DCE-MRI. Kimura *et al.* [2] have, in the context of positron emission tomography (PET), proposed clustering of voxels by their dynamic profile for calculation of parametric maps. The spatial resolution is thus maintained while reducing noise, at the expense of parametric discretization. Calculating PK parameters on the clusters rather than on a voxel-by-voxel basis has the potential to significantly reduce computational time and noise. The aim of this work was to investigate if the clustering method can be applied to DCE-MRI for fast PK parameter estimation with the extended Tofts model [3].

Materials and methods

DCE-MRI data from one male patient (age 63) diagnosed with glioblastoma multiforme was used to evaluate the method. A T1 map was acquired using an inversion recovery spin echo sequence with settings TR/TE = 9820/11 ms, TI = [100, 208, 400, 750, 1000, 2000] ms. The DCE-MRI signal was acquired with a 3D spoiled gradient echo (SPGR) sequence with TR/TE = 4/1.79 ms, and flip angle = 20°. The temporal resolution and total duration of the data acquisition of DCE-MRI data was 2.65 s and 424 s, respectively.

All data processing was performed on one slice placed in the center of the tumor. The contrast agent (CA) concentration was calculated by inversion of the SPGR signal equation [4]. The dimensionality of the CA curves was first reduced using principal component analysis (PCA) to four components. Then, k-means clustering was performed on the principal components to yield 100 clusters of similar CA kinetics. PK parameters were evaluated using nonlinear curve-fitting on the cluster medians. Finally, the obtained PK parameters for each cluster were distributed to form parametric maps of K^{trans} v_e, and v_p.

Results

Fig. 1a – c show PK parametric maps calculated using the clustering method, while Fig. 1d – f show PK parametric maps calculated on a voxel-by-voxel basis. A correlation analysis of the two methods are shown in Fig. 1g – i. The computational time of one slice was 11.9 s and 98.2 s for the clustering method and the voxel-by-voxel method, respectively.

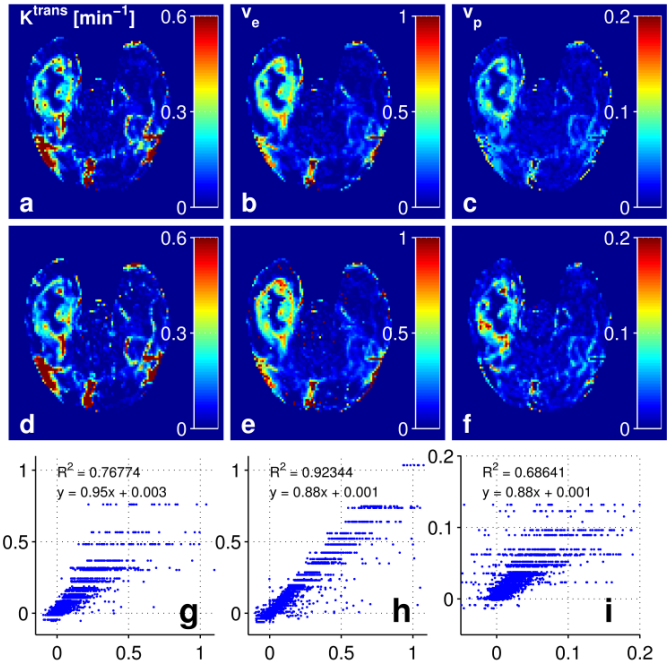

Figure 1*. PK parameters generated by clustering the four largest principal components of the CA conc. curve (a – c) and using voxel-by-voxel PK estimation (d – f). A correlation analysis of the methods are shown in g –*

Conclusion and discussion

The proposed method reduced computational time significantly. However, the method was only applied to a single slice, and for a larger volume it is anticipated that an even larger gain in computational speed can be obtained. On visual inspection the clustering method produced parametric maps similar to the conventional voxel-by-voxel method. However, the correlation analysis revealed that there are discrepancies between the methods. The large spread within each cluster indicates that the clustering criteria should be improved in future studies.

References

[1] Jackson, A., Buckley, D. L., Parker, G. J. M. Contrast-Enhanced Magnetic Resonance Imaging in Oncology; Springer: Berlin, 2005.
[2] Kimura, Y., Hsu, H., Toyama, H., Senda, M., Alpert, N. M. Improved signal-to-noise ratio in parametric images by cluster analysis. NeuroImage 1999, 9, 554-61.
[3] Tofts, P. S. Modeling tracer kinetics in dynamic Gd-DTPA MR imaging. Journal of Magnetic Resonance Imaging 1997, 7, 91-101.
[4] Schabel, M. C., Parker, D. L. Uncertainty and bias in contrast concentration measurements using spoiled gradient echo pulse sequences. Physics in Medicine and Biology 2008, 53, 2345-73.