A New Algorithm for the Fusion of MRSI & MRI on the Brain Tumour Diagnosis

Xin Liu[1], Yuqian Li[1], Yiming Pi[1], Sofie Van Cauter[2], Yi Yao[3,4], and Jiunjie Wang[5]

[1]*School of Electronic Engineering, University of Electronic Science and Technology of China, Chengdu, China,* [2]*Department of Radiology, University Hospitals Leuven, Belgium,* [3]*School of Communication and Information Engineering, University of Electronic Science and Technology of China, Chengdu, China,* [4]*National Key Laboratory of Science and Technology on Communications, China,* [5]*Department of Medical Imaging and Radiological Sciences, ChangGung University, Taiwan*

Target Audience: neuroradiologist for tumour diagnosis, researches interested in image processing on fusion.

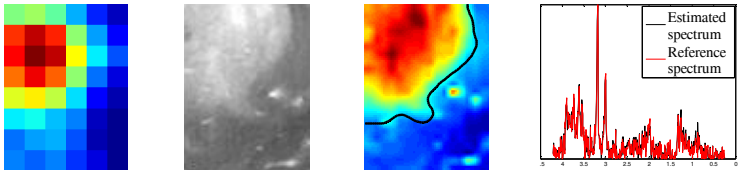
Purpose: to propose an unsupervised multi-modality fusion method for MRSI and MRI data in brain abnormality diagnosis.

Introduction: The potential of MRI is limited because of the variability of tumour visuality. MRSI has shown great potentials for detecting the tumour heterogeneity, however, with much lower resolution. We propose an data fusion method for brain tumor diagnosis taking the advantage of the MRI and MRSI.

Fusion Methods: The observations $\mathbf{X(S,I)}$ can be approximated as linear combination. $\mathbf{X(S,I)} \approx \mathbf{W(S)H(I)} + \mathbf{N}$, $s.t.\ \mathbf{X} \geq 0, \mathbf{S} \geq 0, \mathbf{I} \geq 0.$ $\mathbf{W(S)}$ is the biochemical source and $\mathbf{H(I)}$ is the high resolution spatial distribution. $\mathbf{N}$ represents for the additive noise; $\mathbf{S}$ and $\mathbf{I}$ are the observed information by MRSI and MRI, respectively. This multimodality fusion model can be solved by Hierarchical Alternating Least Squares[3] (HALS) as a nonnegative matrix factorization implementation. The spatial distribution $\mathbf{H}^{(0)}\mathbf{(S)}$ from the MRSI data was used as the initial value. During each iteration, the spatial distribution $\mathbf{H}^{(k)}\mathbf{(S)}$ of the tissue-specific spectral sources can be estimated using the $\mathbf{W}^{(k)}$ from MRSI. Then, $\mathbf{H}^{(k)}\mathbf{(S)}$ is fused with the image features $\mathbf{I}$ obtained from the high resolution MR image using the wavelet components. The fused spatial distribution $\mathbf{H}^{(k)}\mathbf{(I)}$ is subsequently used to update the source spectra $\mathbf{W}^{(k+1)}$. The resolution of the estimated spatial distribution could be gradually improved with the accuracy of sources retained as much as possible. The number of sources was set to two.

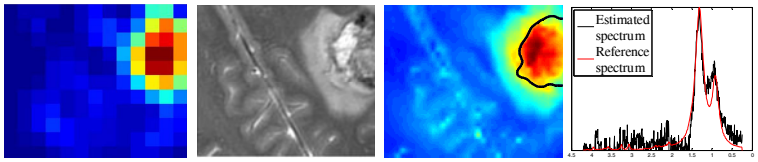
Materials: Both short-TE ^{1}H MRSI and T2-weighted images were acquired from one patients with low grade glioma (patient 1) and glioblastoma multiforme (patient 2). The institutional review board approved this study. Written informed consent was obtained before participation in the study. MRSI data are preprocessed using SPID[5] to remove the residual water components. The negative values from noise were set to zero because of the non-negativity assumption. T2-weighted images are interpolated so that one voxel in MRSI data corresponds to a matrix of 11×11 pixels. Two level wavelet transform was used to extract both the high and low frequencies of the images respectively, which was used as the features for fusion.

Results and Discussion: Fig. 1 a) and Fig. 2 a) showed the abnormal regions (patient 1 for the tumour; patient 2 for the tumour and necrosis) estimated using only MRSI. The tumour edge is not well delineated because of the poor spatial resolution. The corresponding panels in c) – d) demonstrated the fusion result. Well correspondence can be noticed between the estimated tumour boundary and the specialist delineation. The fused spectrum still maintained the biochemical information (d). The fusion method can provide the tissue differentiation while maintain both high spatial distribution and high accuracy.



a) tumour region provided by MRSI | b) T2-weighted MR image | c) **Fusion result**: spatial distribution of tumour with tumour delineation (black) | d) **Fusion result**: estimated tumour spectrum (black) compared with reference spectrum (red)

Figure 1 Patient 1 with low grade glioma



a) abnormal (i.e. tumour and necrosis) region provided by MRSI | b) T2-weighted MR image | c) **Fusion result**: spatial distribution of abnormal with abnormal delineation (black) | d) **Fusion result**: estimated abnormal spectrum (black) compared with reference spectrum (red)

Figure 2 Patient 2 with glioblastoma multiforme

Conclusions: An unsupervised data fusion method based on nonnegative matrix factorization for tumour diagnosis is proposed. The *in vivo* experiments demonstrated successful fusion between MRSI data and MRI in brain tumour.

Acknowledgement: The research is supported by National Postdoctoral Research Fund (2014M552341) and National Natural Science Foundation of China (61401068).

Reference: [1] Y. Li et al. NMR in Biomedicine, vol. 26, no. 3, pp. 307–319, 2013. [2] Y. Li. IEEE BME, vol. 60, no. 6, pp. 1760–1763, 2013. [3] A Cichocki et al. IEICE Trans. Fund. Electron. Comm. Comput. Sci. 2009; 3: 708–721. [4] D. D. Lee et al. Nature, 1999, 401: 778-791. [5] JB Poullet. PhD Thesis, Leuven; 2008