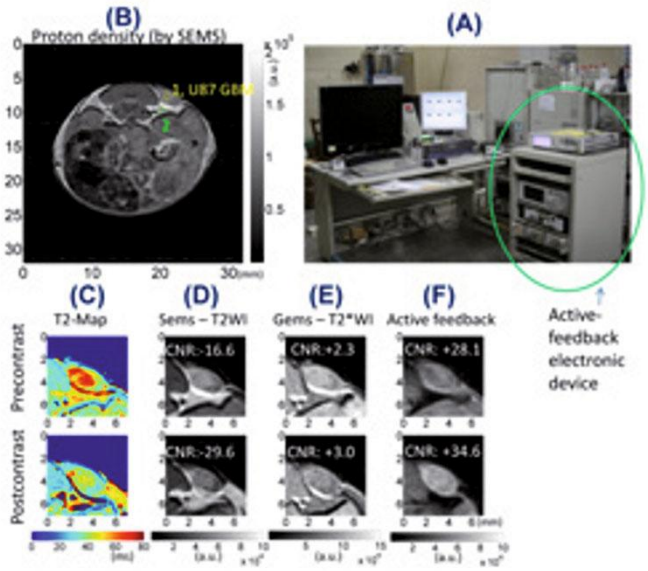
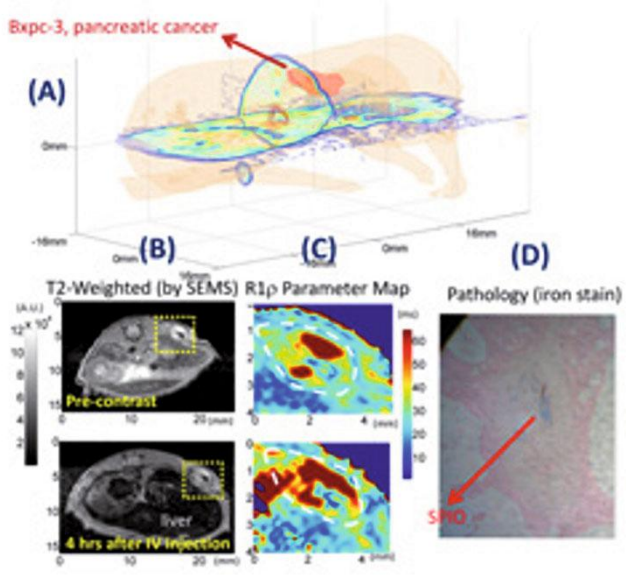




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Tissue type differentiation for brain tumor diagnosis using non-negative matrix factorization on MRSI data

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Purpose/Introduction: Glioblastoma multiforme (GBM) is the most common and aggressive type of brain tumor in adults. Because of the heterogeneity of GBMs, accurate diagnosis is of utmost importance in guiding therapy and determining prognosis. Non-negative matrix factorization (NMF), as a blind source separation technique, is able to solve spectral separation problems. The capability of differentiating brain tumor tissue types using NMF is explored by a simulation study comparing the performance of several NMF algorithms. A hierarchical decomposition approach was applied to *in vivo* magnetic resonance spectroscopy imaging (MRSI) data of GBM patients containing necrotic areas and successfully differentiated the brain tumor tissue into three tissue types: normal tissue, tumor and necrosis.

Subjects and Methods: In order to explain the partial volume effect in each voxel, measured MRSI spectra can be approximated by linear combinations of ideal spectra pertaining to different constituent tissue types.

$$X = WH + N$$

NMF solves the factorization using the mathematical formulation as shown below.

$$\min_{W,H} f(W,H) = \frac{1}{2} \| X - WH \|_F^2$$

$$subject\ to\ \forall ij,\ W_{ij}, H_{ij} \geq 0$$

To differentiate the tissue types using *in vivo* MRSI signals, we proposed a hierarchical framework based on NMF. Firstly, apply NMF to the preprocessed MRSI signals with the number of components chosen to be 2. After finding the normal tissue and abnormal tissue with their corresponding spatial distributions, apply NMF on the abnormal signals. In this way, the third components, necrosis, can be found.

Results: Several recent NMF algorithms were compared with widely used NMF algorithms using simulated MRSI signals. Accelerated hierarchical alternating least squares (**hals**)[1] was chosen to be applied to the *in vivo* MRSI signals of a patient with GBM, to test our proposed hierarchical decomposition approach.

1. Simulated results: Correlation coefficients of spectra and error rate of the corresponding spatial distribution between estimated signals and original signals are calculated to evaluate the performance of each algorithm.

Evaluation of the performance of several NMF algorithms

Algorithms		mu	cjlin	als	hals	amu	ahals
	Normal	0.90	0.91	0.93	0.95	0.91	0.95
R	Tumor	0.87	0.90	0.90	0.89	0.89	0.88
	Necrosis	0.96	0.96	0.97	0.96	0.96	0.96
	Normal	3.0%	2.8%	3.5%	2.0%	3.9%	2.0%
Error Rate	Tumor	42%	34%	25%	24%	31%	16%
	Necrosis	22%	16%	12%	14%	16%	14%
Time per run (s)		1.22	9.30	1.35	3.55	5.31	3.54

R: correlation coefficients between obtained source and true source.

$$\text{Error Rate} = \frac{\sum (h_e - h_r)^2}{\sum h_r^2} \cdot 100\%$$

h_e : spatial distribution of estimated source

h_r : spatial distribution of simulated MRSI signals

2. *In vivo* results: Results show that the proposed hierarchical approach is capable of differentiating *in vivo* brain tumor tissue into 3 tissue types step by step.

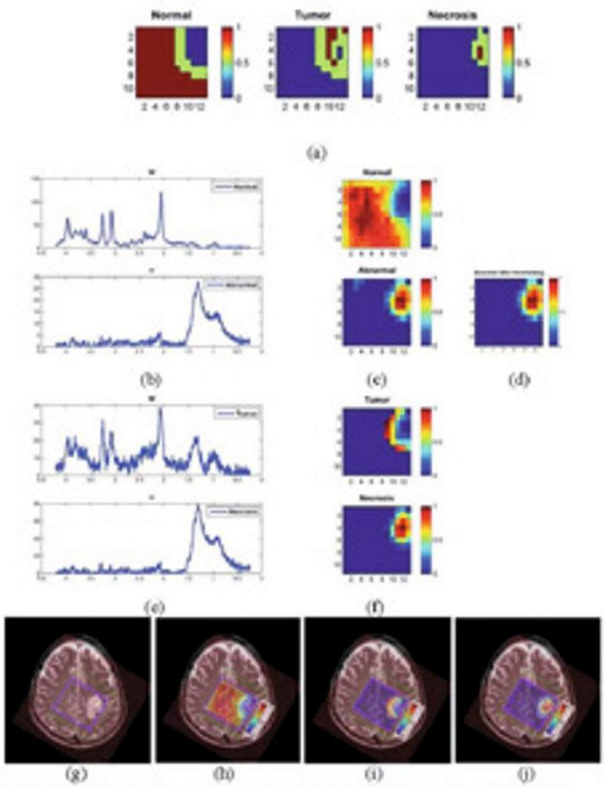


Fig 1: Hierarchical factorization results of MRSI human brain data on patient 1. (a) Expert-based labeling of tissue-specific spatial distribution. (b)-(d): First-level factorization. (b) Recovered spectra of the first-level factorization. (c) Spatial distributions of the corresponding tissue-specific spectral patterns in (b). (d) Distribution of abnormal tissue after thresholding and eliminating outliers. (e)-(f): Second-level factorization. (e) Recovered spectra of the second-level factorization. (f) Spatial distribution of the corresponding tissue-specific spectral patterns in (e). (g) Anatomic image of patient 1. The green box is the PRESS box and the purple box is the selection of voxels overlapped to the T2-weighted MRI of a patient with glioblastoma. (h)-(j): overlap of the distribution map of each tissue type onto the anatomical image (g). (h): normal, (i): tumor, (j): necrosis.

Discussion/Conclusion: The results show that NMF can be used for tissue type differentiation and the proposed method is able to differentiate data from GBM patients into 3 tissue types: normal, tumor and necrosis.

References:

[1] Gillis N, Nonnegative matrix factorization complexity, algorithms and applications, PhD Thesis, Louvain-La-Neuve, Belgium, 2011.

37 Young Investigator Award Finals

2:40 pm - 3:40 pm *Hall 2*

Young Investigator Award Finals

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Correction of susceptibility-induced GRE phase shift for accurate PRFS thermometry proximal to cryoablation iceball

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Purpose/Introduction: Particularly in at-risk structures adjacent to the treated organ/zone it is necessary to monitor temperature changes in real-time during a cryo-ablation procedure. This study demonstrates that susceptibility artifacts in GRE phase images induced by cryotherapy iceball can be corrected in real time, allowing the PRFS method to be used to monitor near-zero temperatures during the intervention.

Subjects and Methods: Susceptibility artifacts were corrected as post-processing in less than 1s per 3D data set. The iceball region was segmented semi-automatically at each time point to approximate the difference in bulk magnetic susceptibility between frozen and non-frozen tissue. This difference in bulk magnetic susceptibility was considered uniform over the iceball volume and was determined from the isothermal principle applied to the phase-transition frontier of compartments. Subsequently, the magnetic perturbation field was calculated in 3D using a Fourier-convolution [1]. Experimental studies were performed in two scenarios: tissue defrosting in water bath and induction of iceball by MR-compatible cryogenic probe (Figure 1).

Results: The susceptibility artifacts yielded PRFS temperature errors as high as 10-12°C proximal to the iceball, positive or negative upon the relative orientation of the position vector from B_0 direction. These effects were fully corrected, down to the measurement noise range. Some exemplarily results of the cooling using the MR-compatible cryogenic probe can be seen in the Figure 2. The susceptibility-corrected PRFS temperature values were consistent with the phase-transition conditions, whatever the local orientation with respect to B_0 direction.

Discussion/Conclusion: By implementing in-line the post processing algorithm, PRFS MRT may be used as safety tool for non-invasive and accurate monitoring of near-zero temperatures during MR-guided clinical cryotherapy.

References:

[1] Salomir et. al. Concepts in Magnetic Resonance. 2003 (part B), vol 19B (1) 26-34