Identification of breast carcinoma in dynamic contrast-enhanced magnetic resonance imaging (DCE MRI) by Independent **Component Analysis (ICA) - Initial Results**

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Introduction:

ICA was originally proposed to solve the blind source separation problem (Bell and Sejnowski 1995), i.e to recover a set of independent source signals from a set of measured signals. Assuming that each measured signal is a linear combination of independent sources, ICA attempts to derive a set of source components that are maximally independent of each other.

Aim:

We aim to determine if ICA can extract tumor component maps from DCE MRI of the breast similar to tumor manually outlined by a radiologist.

Materials and Methods:

The study was approved by the local institutional review board and written informed consent was obtained from 6 patients (all female, age 41-60) who were histopathologically confirmed with breast carcinoma (invasive ductal carcinoma and ductal carcinoma-in-situ) from tru-cut biopsies. MR examinations were performed on a 1.5T MR unit (Signa LX, General Electric Medical Systems, Milwaukee, WI) using breast surface coil. Axial fast T₁weighted, three-dimensional Spoiled Gradient-Recalled echo (3D SPGR) acquisition was planned on the breast with tumor. Scan parameters were: TE = 1.48-1.66ms, TR = 4.4-5.9 ms, flip angle = 20°, 4 slices per slab, temporal resolution = 8 s. Five baseline (pre-contrast) 3D image sets were acquired, before injection of Gadodiamide at a dose of 0.2 mmol/kg, using an automatic injector and at a rate of 3 ml/s, followed by 60 post-contrast acquisitions. Only 2 slices from the central partition was used. A spatial ICA approach, similar to those applied on fMRI images (Mckeown et al 1998), was implemented on the DCE MR images of breast tumors. For a series of T (=60) dynamic MR images, a T-by-M matrix X is constructed, where M (=256×256) is the number of voxels in each image, such that each row in X contains the spatial (image) information sampled at a particular time point. Assuming that X can be expressed in the form of a linear generative model X = AC, where the mixing matrix A (*T*-by-*N*) and the component matrix C (*N*-by-*M*) are unknown, the spatial ICA problem is to arrive at solutions for C = WX, by appropriately selecting the unmixing matrix W, such that the components (rows) in C are mutually (statistically) independent of each other. Each independent component (IC) in C can be reverted back to a spatial image or IC map, and the columns in A (or W¹) give the time courses of activation for the IC maps. We implemented the FastICA algorithm, which minimizes the mutual information of the components by the maximization of a robust approximation of the negentropy, using a fast fixed-point iteration scheme (Hyvärinen 1999). The usual ICA preprocessing steps of centering (i.e subtracting the dataset X by its mean) and whitening (a linear transformation of X such that the resulting components have unit variance and are uncorrelated) were applied before performing FastICA.

Results:

The derived component maps from ICA show typical enhancement patterns previously described for breast carcinoma - rapid enhancement with washout, and rapid enhancement with plateau. The spatial map of areas showing these enhancement characteristics correlated well with tumor outlined by the pathologist and the independent radiologist in all 6 cases. A progressively enhancing pattern correlated with peri-tumoral areas of fibrocystic change and fibrosis (see Case 1). Component maps do not suffer from volume averaging in heterogenous tumors (see Case 2).

References:

1. Bell A J and Sejnowski T J. Neural Comput 7:

Conclusion:

ICA can identify breast carcinoma in DCE MRI breast comparable to tumor outlining by radiologist.



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