Breast Tumor Segmentation and Characterization Using Dynamic Contrast-Enhanced MR Images for Computer Aided Diagnosis

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INTRODUCTION

Parametric maps based on contrast uptake and washout characteristics of tumors measured using dynamic contrast-enhanced MRI (DCE-MRI) provides functional information that may distinguish between benign and malignant lesions [1-7]. Several research groups have developed segmentation algorithms based on the contrast dynamics of breast tumors. Semi-automated techniques using cross-correlation between a reference curve [4,5], or visual inspection of subtraction images derived from uptake and washout [6,7] have been successful for identifying the location and boundaries of suspicious lesions. Furthermore, multi-compartmental perfusion models indicate that malignant lesions demonstrate an increased rate of contrast uptake and washout due to their high vascular volume and permeability [1-3]. This work combines the time-based segmentation and multi-compartmental modeling into an automated computer aided diagnostic (CAD) graphical interface. The two step method consists of a 3D segmentation based on the local variations in contrast uptake and arrival time followed by detailed inspection using multi-compartmental modeling to obtain permeability maps for suspicious lesions.

METHODS

The automated segmentation was developed and tested using a Matlab (Mathworks Inc.) simulation, with tumors of 3 different sizes and 3 known contrast uptake curves. The segmentation was further tested in 6 patients with a total of 8 breast lesions (6 malignant, 2 benign). Patients were scanned on a 1.5 T scanner (Signa LX; GE Medical Systems, Milwaukee, WI) using an SPGR sequence with a temporal resolution of 30 sec. Gd-DTPA (Omniscan, Amersham Health, Princeton NJ) was injected intravenously (0.1 mmol/kg). Major components of the segmentation step are: (a) registration of the dynamic MR image sequence using affine transforms [9] with mutual information measures as a cost-function (package developed by T. Hartkens), (b) calculation of an arrival time map of a volume, (c) calculation of local roughness by convolution of the time-of-arrival map with a standard deviation kernel [8], (d) correlation with step function based on arrival time, and (e) thresholding using the standard deviation and correlation values. Voxels with low local roughness in the time-of-arrival image and high correlation typically represent enhancing lesions while those with high local roughness and low correlation typically represent background voxels. The second step consists of multi-compartmental modeling based on non-linear fitting (Nelder-Meade Simplex) to the Tofts model [1] of contrast-enhancement to generate the permeability map.

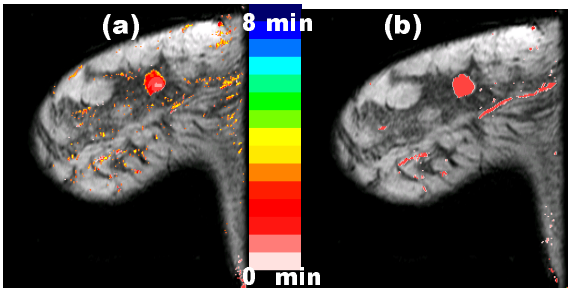

Fig 1 Segmentation results of a 1.1 cm invasive ductal carcinoma : pre registration (a) and post registration (b)

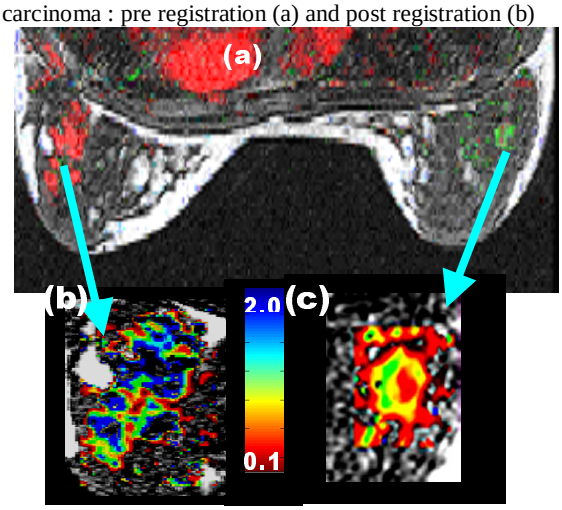

Fig 2 Segmentation results of a 4 cm DCIS in the left breast and a fibro adenoma in the right breast (a). Permeability maps for the malignant tumor (b) and the benign tumor (c)

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RESULTS and DISCUSSION

A graphic user interface was developed to assess the performance of the CAD tools. The automated segmentation step was assessed independently by comparing the result to a supervised segmentation performed by a radiologist. In all cases tumor volume and overlap were calculated with that of the supervised segmentation and used as a metric to assess performance. Image registration reduced motion between time frames (~ 4 mm translation per time frame) and improved segmentation as shown in Fig 1b compared to Fig 1a. Fig 2 demonstrates both the segmentation results (Fig. 2a) and the permeability map (Fig. 2b) for a patient with bilateral lesions. The malignant tumor shows early arrival time (red) and high permeability ($>1.2\ min^{-1}$) whereas the benign tumor shows a later arrival time (green) and lower permeability ($< 0.8 min^{-1}$) The diagnosis for both tumors was confirmed by biopsy.

CONCLUSIONS

The combination of contrast uptake and permeability measures is being investigated in an on-going clinical study to assess the sensitivity and specificity of this computer-aided diagnosis (CAD) technique. The combination of breast MRI and automated segmentation algorithms can improve the consistency of breast cancer diagnosis. The proposed CAD technique may also improve specificity and thus reduce the number of benign surgical biopsies performed annually. We are currently testing the performance on a larger group of 80 patients with known architectural distortions. In parallel we are applying a sequence using PR-TRICKS to improve the temporal and spatial resolution of the data acquisition to exploit the strengths of the time-based segmentation.

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