Statistical Modeling for Differentiation of Clinical Breast Tumors using Multiparametric MRI

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INTRODUCTION

By combining different magnetic resonance imaging (MRI) parameters into a multiparametric dataset, we obtain information that may be useful in differentiating benign from malignant breast lesion in the clinical setting. Objective computerized multiparameter MRI combined with statistical modeling has not been previously employed to identify and classify breast tumors. This study presents a novel model of tissue characterization based upon the angular separation of tissue clusters in multidimensional feature space, and other features common in breast cancer. This model uses an objective (unsupervised) image-segmentation algorithm called the Iterative Self-Organizing Data Analysis Technique (ISODATA) [1], and a statistical discriminant function. We test the utility of this model to classify breast tumors in the clinical setting, and compare the results with histological diagnosis.

METHODS

44 patients with indeterminate morphological features underwent diagnostic and dynamic contrast enhancement (DCE) MR imaging on a GE 1.5T MR scanner using a dedicated phased array breast coil. Diagnostic MR consisted of T1 FSPGR (TR/TE =200/4.4ms, FOV=18x18 cm,256×128, 4mm), fat suppressed T2WI (TR/TE=5700/102ms,FOV=18x18 cm,256×128,4 mm). DCE was performed using a localizer, sagittal 2D T1 FSPGR scan (TR/TE=100/4ms, FOV=18x18cm,256×128, 1.7-2.5mm, temporal resolution=15sec) before and after intravenous administration of gadolinium. Time intensity curves were generated from the most strongly enhancing region of the breast as persistent (Type 1), plateau (Type 2), or washout (Type 3) pattern enhancement [2]. All image analysis was accomplished using Eigentool software [3,4], and lesion areas were defined using the diagnostic MR data into the ISODATA model [1]. ISODATA tissue clusters were tested for similarity using the inner product between tissue-signature vectors and classified as normal or abnormal [1]. This approach permitted mapping of different tissue types based on tissue signatures extracted from ISODATA. To evaluate classification accuracy for angular separation, we implemented a statistical model using discriminant analysis using SPSS statistical software. We started with variables of age, angular separation between fatty tissue, glandular tissue, and lesion, and distances between these features. We employed stepwise discriminant analysis to determine the combination of variables (including interactions) that best predicts histology. In addition, we generated receiver operating characteristic (ROC) curves for each model, and computed the area under the curve (AUC) for each model. Statistical significance was set at p<0.05.

RESULTS

44 patients (age range, 18-80 years; median, 47 yr) with suspicious mammogram finding (BIRADS \geq 4) were studied retrospectively, 22 with benign lesions, and 22 with malignant tumors. Figure 1 demonstrates the ISODATA model and the DCE curve on a 54-year-old patient with invasive carcinoma. The resulting objective discriminant model included 2 variables of significance with the final equation = 0.822 * Angle - 0.574 * Age, that gave the greatest AUC. Similarly, angular separation and age performed well in discriminating benign from malignant lesions. This model correctly predicted 16/22 of benign cases, and 18/22 malignant cases, and is summarized in Table 1.

DISCUSSION

We have developed a objective statistical model, using multiparametric MRI data and the ISODATA method, which can segment and classify malignant breast tissue from normal or benign breast tissue. This statistical model may aid in differentiating benign from malignant tumors. Further predictors, such as hormonal status, may add additional power. If proved feasible in larger studies, this model could be applied to images from patients undergoing therapeutic intervention, to predict response to therapy.

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Table 1. Statistical Results		
Variable	AUC	p-value
Age	0.740	=0.006
Angle	0.833	< 0.001
Angle Distance	0.742	=0.006
Discriminant		
function	0.855	< 0.001

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