DynaMammoAnalyst: Simultaneous Dynamic and Morphologic Analysis Software for MR Mammography

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Introduction

Accurate assessment of breast cancer using contrast enhanced MR Mammography requires high spatial and temporal resolution scanning in which a large volume of image data is produced [1]. Analysis of the data is a time intensive and error-prone process. Recent computerized methods offer improved lesion visualization by color coded maps of various enhancement parameters such as initial contrast uptake and washout rates [2-5]. However, these systems rely on subjective assessments that increase interobserver variability. Here, we present software that may be helpful for quantitative simultaneous dynamic and morphologic evaluations.

Methods

DynaMammoAnalyst, is a special 32-bit software written by the authors in Borland Delphi 7.0 (Borland Software Cooperation, Inc., USA) to explore contrast enhanced breast MR data. It facilitates lesion identification, delineation and quantitative lesion evaluation. For each slice, from pre and post-contrast images, *DynaMammoAnalyst* generates subtraction images, maximum intensity projection and color-coded map of normalized maximum intensity time ratio (nMITR) in HSV format. nMITR values higher than a user selected threshold (default value 0.27 sec^{-1}) are displayed in red while values lower than 0.14 sec^{-1} are shown in blue. The user may interactively adjust this threshold for proper segmentation of an identified lesion from the surrounding vascular tissues that show moderate enhancements. After manual selection of a seed point inside the lesion, region growing is performed to generate irregular whole lesion region of interest (ROI). Several descriptive parameters are calculated next such as lesion location, lesion area, bounding box area, initial and post-initial signal behaviors and mean curve coordinates. Among these, normalized complexity of the ROI is computed to quantify the shape of the lesion while the tissue with the maximum nMITR, inside the ROI is interrogated pixel by pixel to determine the enhancement behavior of the lesion. These two features are the inputs of a maximum likelihood classifier which is embedded into the software. The classifier supplies a decision to help the radiologist.

The software was used to evaluate 30 cases (14 benign and 16 malignant) imaged on a 1.5 Tesla Siemens Symphony MR scanner using T1-weighted 3D fast low angle shot (Flash) sequence with the following parameters: TR/TE 9.80/4.76 msec, flip angle 25°, slice thickness 2.5 mm with no gap and resolution $0.625mm^2$, 1precontrast and 5 postcontrast images per slice. For each case, the slice in which the lesion had the largest diameter was considered for analysis. The significance of features in discrimination of malignancy were evaluated using SPSS 14 (SPSS Inc., USA).The independent samples t-test with either a pooled or separate variance as determined by the Levene's test for equality of variances was performed. Diagnostic accuracies of the features were calculated from the area under the ROC curve (A_z) [6]. The classifier is trained with 16 lesions and is tested with the remaining 16 lesions.

Figure 1. nMITR map of a malignant lesion (on the left breast)

Results

Figure 1 shows an nMITR map for a malignant case. The computed parameters are displayed in the "Zoom" window (Figure 2a) and in the "Dynamic Analysis" window (Figure 2b). The mean enhancement curve is plotted in the latter window. There are significant differences between the benign and malignant lesions for normalized complexity (0.28 ± 0.15 and 0.48 ± 0.23, P <0.05, A_z= 0.73±0.10) and maximum nMITR (1.33 ± 0.76 and 3.11 ± 1.52, P <0.05, A_z= 0.89±0.06). The accuracy of the classifier is 0.87 for the test set.

Conclusion

The simultaneous dynamic and morphologic analysis software developed can be used for evaluations of breast lesions with high accuracy.

References

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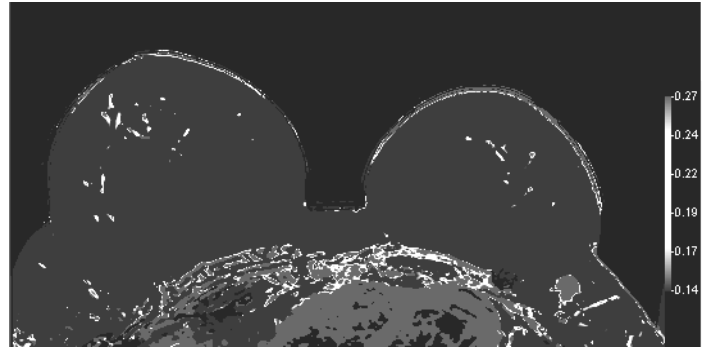5. Parker GJM, et al. RadioGraphics, 1998.18:497-506.
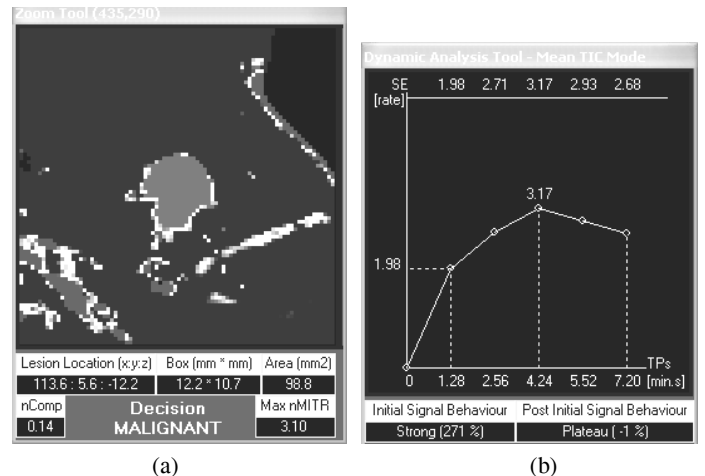
(a)   (b)

Figure 2. Computed parameters displayed in (a) Zoom window and (b) Dynamic Analysis window