

Comparison of Computerized Image Analyses for Digitized Screen-Film Mammograms and Full-Field Digital Mammography Images

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Abstract. We have developed computerized methods for the analysis of mammo-graphic lesions in order to aid in the diagnosis of breast cancer. Our automatic methods include the extraction of the lesion from the breast parenchyma, the characterization of the lesion features in terms of mathematical descriptors, and the merging of these lesion features into an estimate of the probability of malignancy. Our initial development was performed on digitized screen film mammograms. We report our progress here in converting our methods for use with images from full-field digital mammography (FFDM). It is apparent from our initial comparisons on CAD for SFM_D and FFDM that the overall concepts and image analysis techniques are similar, however reoptimization for a particular lesion segmentation or a particular mammo-graphic imaging system are warranted.

1 Introduction

We have developed computerized methods for the analysis of mammographic lesions in order to aid in the diagnosis of breast cancer [1-9]. The automatic methods include the extraction of the lesion from the breast parenchyma, the characterization of the lesion features in terms of mathematical descriptors, and the merging of these lesion features into an estimate of the probability of malignancy. Our initial development was performed on digitized screen film mammograms (SFM_D; 0.1 mm pixel size). We report our progress here in converting our methods for use with images from full-field digital mammography (FFDM).

2 Databases

Our digitized screen/film mammographic (SFM_D) database and our FFDM database currently arise from different cases. Thus, comparison of image analysis results between SFM_D and FFDM is not directly possible. However, conclusions can be drawn by the analysis of trends seen in the data. The SFM_D database includes screen/film mammograms digitized to 0.1 mm pixel size and 10-bit quantization. The FFDM database includes images from a GE Senographe 2000D.

3 Lesion Segmentation

We continue to investigate methods with which to extract the lesion (margin) from the parenchymal background in a mammographic image. These methods have included a region growing technique [1,2], a radial gradient index technique (RGI) [3], and an active contour snake method [9]. In the region growing method, the lesion image undergoes histogram equalization followed by gray level thresholding. By monitoring the size and shape of the evolving contour with each incremented gray level threshold step, a lesion contour is automatically selected at an abrupt transition from high circularity to low circularity, and from small size to larger size. In the RGI method, a Gaussian constraint function is applied to the image data in order to suppress the influence of distant pixels. From a series of potential contours obtained by thresholding, the contour whose margin yields the maximum RGI value is chosen as the one that best delineates the lesion. The RGI value corresponds to the average proportion of the gradients in the radially outward direction. The snake method involves a two-stage segmentation that uses an active contour algorithm to minimize an energy function based on the homogeneities inside and outside of the evolving contour. The minimization algorithm solves, by the level set method, the Euler-Lagrange equation that describes the contour evolution. Prior to the application of the active contour algorithm, the RGI-based segmentation method is applied to yield an initial contour closer to the lesion margin location in a computationally efficient manner. This initial RGI segmentation also estimates an effective background, for subsequent use in the active contour approach, by using the values of the image within a given radius of the initial contour.

Our evaluation of the three methods on SFM_D and FFDM included only images on which human-delineated lesion margins had been obtained. Performance was determined based on an overlap measure [3], where the overlap was calculated by the ratio of the areas within the intersection of the human-delineated margin contour (Rad. A) and the computer-determined margin contour to the union of the two areas. The results are presented in terms of percent of lesion images accurately segmented at a given threshold cutoff (e.g. at a threshold cutoff of 0.4 as shown in Table 1). It is apparent from Table 1 and Figure 1 that, overall, the two-stage active contour snake method is the most promising for both the SFM_D and FFDM databases.

Table 1. Percent of lesion images accurately segmented at an overlap threshold cutoff of 0.4 for the SFM_D and FFDM databases and the three segmentation methods

SFM _D Database	Total Cases	Total Images	Region growing	RGI	Snake
Malignant	55	96	74.0%	66.7%	86.7%
Benign	29	51	76.5%	90.2%	88.2%
Total	84	147	74.8%	74.8%	87.1%
FFDM Database	Total Cases	Total Images	Region growing	RGI	Snake
Malignant	148	412	66.0%	66.7%	75.7%
Benign	139	327	72.5%	81.0%	85.6%
Total	287	739	68.9%	73.1%	80.1%