Comparison of Methods for Classification of Breast Ductal Branching Patterns

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Abstract. Topological properties of the breast ductal network have shown the potential for classifying clinical breast images with and without radiological findings. In this paper, we review three methods for the description and classification of breast ductal topology. The methods are based on ramification matrices and symbolic representation via string encoding signatures. The performance of these methods has been compared using clinical x-ray and MR images of breast ductal networks. We observed the accuracy of the classification between the ductal trees segmented from the x-ray galactograms with radiological findings and normal cases in the range of 0.86-0.91%. The accuracy of the classification of the ductal trees segmented from the MR autogalactograms was observed in the range of 0.5-0.89%.

1 Background

The vast majority of breast cancers originate from the epithelial tissue of breast ducts. Due to low radiographic contrast, ducts are barely visible in mammograms. However, the breast ducts contribute to the complexity of the parenchymal pattern, which has been used in computer algorithms for early cancer detection and cancer risk estimation [1].

Breast ductal branching patterns have been previously analyzed by manually tracing ductal trees from galactograms, 2D x-ray images of contrast-enhanced ducts. That preliminary analysis, performed using ramification matrices (R matrices), was applied to classify galactograms with radiological findings and normal cases (i.e., no radiographic findings) [2]. More recently, the analysis has been extended to include other descriptors of ductal topology [3,4]. This paper compares three methods for describing and classifying breast ductal topology. The performance of these methods is compared using breast ductal networks as visualized in clinical x-ray and MR images.

2 Methods

In this section, we describe methods to acquire clinical images of the ductal network and to extract ductal topology descriptors from clinical images.

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2.1 Data Acquisition

We have traced ductal topology in clinical x-ray galactograms and magnetic resonance (MR) autogalactograms (see Fig. 1). Galactograms are x-ray images of the breast, in which a small amount of contrast material has been injected into a nipple opening leading to a ductal lobe (subtree). The ductal subtrees have been segmented manually.

Autogalactograms refer to breast MR images of women in which portions of their ductal network enhanced due to the presence of protein or blood in the ducts [5]. The enhanced portions of the ductal tree were segmented in MR slices acquired with a 3D GRASS pulse-sequence [5]. A semi-automated region growing algorithm was used for segmentation. The 3D ductal topology was manually reconstructed from the segmented portions in each slice.

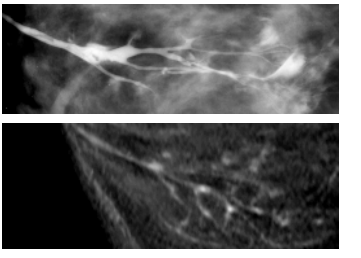

Fig. 1. Breast ductal network visualized in a galactogram (top) or an autogalactogram (bottom)

In this project we analyzed 22 clinical x-ray galactograms obtained retrospectively from 14 women (mean age 49.2 years, range 29–75 years), examined at the Thomas Jefferson University Breast Imaging Center, Philadelphia, PA, during the period of June 1994 through January 2001. Of these, seven women (13 images) had radiological findings corresponding to benign abnormalities, and eight women (12 images) had no findings; no malignant cases were available.

We also analyzed nine clinical autogalactograms obtained retrospectively from eight women (mean age 53.1 years; range 40-72 years), who had their breast MR studies at the Hospital of the University of Pennsylvania between June 2000 and April 2005. The five of eight women had radiological findings (four benign and one malignant; the latter with two identifiable ductal subtrees) and three cases were normal.

2.2 Description of Ductal Topology

R matrices. Elements of R matrices represent probabilities of branching at different levels of a ductal tree, computed following the Strahler labeling of individual ducts (see Fig. 2) [6]. Each R-matrix element $r_{k,j}$ can be expressed as [2]:

$$r_{k,j} = b_{k,j} / a_k , \tag{1}$$

where a_k is the total number of branches at the same level of the tree (those branches are identified by label k) and $b_{k,j}$ is the number of branches with label k, where the child branches are labeled k and j. The lateral branching is identified by labels $j \neq k$, while $j=k$ identifies bifurcation into child branches of the same order. The method for R matrix estimation from ductal trees has been described previously [7]. The R matrices estimated from clinical images have been used to realistically generate synthetic ductal network [8]. In addition, such estimated branching probabilities have been used for classification of galactograms with radiological findings and normal cases [2]. In this paper, we have extended that classification approach to include MR autogalactograms.