Mammalyzer II

A Decision Support System for Early Detection of Breast Cancer in Contrast-Enhanced MRI

Dirk Krechel[1], Felix Hess[1], Ralf Comes[1]
Aldo v.Wangenheim[2], Klaus Blasinger[3]

[1]Arbeitsgruppe Expertensysteme, Universität Kaiserslautern,
Postfach 3049, 67653 Kaiserslautern
Email: {krechel,hess,comes}@informatik.uni-kl.de
[2]Department of Computer Sciences, Universidade Federal de Santa Caterina,
88049-900 Florianpolis - S.C., Brazil
Email: awangenh@inf.ufsc.br
[3]Radiologische Gemeinschaftpraxis Dr. Buddenbrock,Dr. Blasinger Dr.Benz
Kaiserstr. 20, 51116 Mainz

Abstract. We present an integrated system for the automatic analysis of MRI-breast images towards the early detection of breast cancer. The system operates on taken images using the method of dynamic contrast-enhanced MRI. Suspicious breast lesions are automatically marked with colours, thus directing the physician's attention towards the critical regions. The medical support system is based on image-matching algorithms using self organizing maps (SOM) and Monte Carlo methods, which enables the system to work properly even with image sequences that are strongly deformed by the patients breathing movements. The system is tested on real patient data and is now being refined in cooperation with Dr. Buddenbrock, Dr Blasinger, Dr. Benz hospital for Radiology and Nuclear Medicine, Mainz.

Keywords: MR-Mammography, Configuration, Motion Artifacts, Monte Carlo Methods, Tumor Detection

1 Introduction

The MAMMALYZER II presents a diagnosis supporting image processing system which preprocesses dynamic MR-Mammographs (MRM) for easier and less erroneous analyses by the medical practitioner. The breast images are provided by a special MRI sequence which is based on the work of [1], [2]. It uses the property that malignant tumors need a much higher perfusion than healthy tissue. Making use of a contrast-agent such as GDTA, the need for higher perfusion results in a faster accumulation of contrast agent in those areas. A comparison of the observed signal-increase ratios between different MRM-volumes gives an indication on the healthiness of the shown tissue. During the patient's examination several MR volumes of the breast are taken, one of which is a reference volume (native) containing no contrast agent. A cancerous region can then be

defined as an image region showing a significant signal increase, which is a relative increase of more than 90% during the first minute. This threshold is stated according to the publications of both representative authors [1], [2]. An appropriate method for analyzing the signal increase is the Kelcz criterion [6], which is based on a histogram analysis over more time steps (we, however, use 10 steps in our protocol).

For medical practitioners the analysis of MR images is a tiring and errorprone process, since a complete examination with an up-to-date MR scanner creates up to 160 image slices per examination(10 frames with 16 slices). An automation greatly reduces the workload and thus errors of medical staff. When designing a system for achieving this, two main problems occur. On the one hand there were disparities between native and GDTA volumes caused by the patient's breathing and other movements. On the other hand the problem of noisy input images arises. A proper and careful decision procedure is needed to differentiate between increases of signal intensity triggered by noise and tissue dislocations (motion artifacts) and increases that are triggered by an accumulation of contrast agent in the related breast region. Both of them were not adequately addressed in research performed up to present. Related work in the field has been done by [3], who restricted her approach to the analysis of images that do not show any motion artifacts.

2 AI Methods

The first prototype of MAMMALYZER [4] was structured as a pipeline of different image-processing filters controlled by a graphical user interface. This pipeline can be interactively controlled by the physician, who chooses one of two processing pipes. One for fast results and one for a more accurate analysis.

A problem of the first prototype was, that most of the parameters for both matching and marking modules depend on image characteristics such as TE, TR, slice thickness, field of view, and image resolution and also on the extent of motion artifacts. A set of standard parameters was developed that works stable with the standard MRM sequences of the 1.0 T scanner of the former partner hospital in Kaiserslautern. These parameters have to be modified if one uses images from another scanner or images with another acquisition protocol. For this reason, the analysis sequences are modeled under the knowledge-based image analysis system Cyclops [5], developed at the University of Kaiserslautern, that uses AI techniques of configuration and planning to choose optimal image operator sequences and parameter sets for the analysis of given images based on image parameters, coded knowledge and already acquired image analysis results. The aim of modeling the MRM analysis [8] under this expert system is to automatically use the results of a previous calculation of MRM-inter-volume disparities and knowledge about interrelations between image parameters and module parameters for choosing optimal analysis sequences and module parameters. Thus, users do not have to perform the task of choosing between different analysis sequences and lots of parameters, since the sequence is automatically chosen and

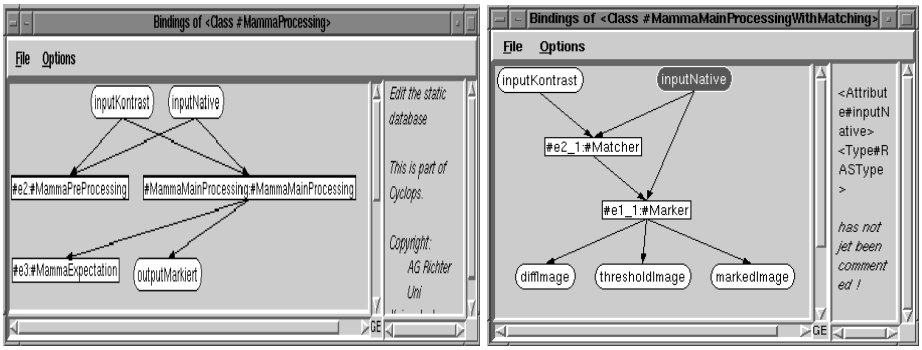

Fig. 1. Complete model of the MR-Mammography analysis process (left), decomposition of the Mamma main process into abstract image operators (right).

parameterized by Cyclops which communicates with MAMMALYZER II.
Figure 1 left shows the complete Mamma analysis process. The system automatically recognizes the type of sequence and chooses appropriate image operators and parameters (right). After execution of the configured pipeline an expectation matching module controls the process results and decides whether they have an acceptable quality or pipeline parts must be changed. With the aid of a TMS-structure only the responsible operators, and those operators using their results, must be refined.

3 Volume Processing Methods

3.1 Suppression of Motion Artifacts

The procedure of applying a redistortion process, i.e. the suppression of motion artifacts by comparing two subsequently measured MR-volumes V_1 and V_2, is to determine the proper voxel correspondance of every voxel $v \in V_1$ in V_2. Without loss of generalization, this process can be broken down to pictures (here volume slices), and therefore will be investigated in the following.
For every pixel $p_{xy} := (x, y)$ of picture $P_1 := \{(x, y) | x \in \mathbb{N}, y \in \mathbb{N}\}$, it is necessary to determine the corresponding pixel $p_{x'y'}$ in picture P_2. As consequence, the set $M := \{D_{xy} = (d_x(x, y), d_y(x, y)) | (x, y) \in P_1\}$, denoted as distortion map, delivers for every pixel $p_{xy} \in P_1$ the disparity D_{xy} towards picture P_2, if $d_x(x, y) = (x - x')$ and $d_y(x, y) = (y - y')$ holds for every corresponding pixel pair $p_{xy} \in P_1$ and $p_{x'y'} \in P_2$.

Speaking of pixel intensities $Int_P(x, y)$ of pixel $p_{xy} \in P$, one can derive a redistorted picture $R = P_1$ out of P_2 for every pixel $p_{xy} \in P_1$ by means of

$$Int_R(x, y) := Int_{P_2}(x + d_x(x, y), y + d_y(x, y)) \ , \ (d_x(x, y), d_y(x, y)) \in M \quad (1)$$

Thus, $Int_R(x,y)$ denotes the proper pixel intensity of pixel $p_{xy} \in P_2$. Now, the correspondence problem reduces to finding the redistortion map M and therefore determining the disparity D_{xy} of every pixel in $P1$.
Our approach makes use of the least square error calculation of picture windows in P_1 and P_2. Given a pixel $p_{xy} \in P_1$ to be further invesigated, the native window in P_1 having a certain scale is centered at p_{xy} while the test window in P_2 of the same scale is moved around p_{xy}. Looking at the square error calculation of both windows (see equation 2), a least square error occurs where both windows fit best with respect to their respective pixel intensities.
In short, given a native window $NW := \{(x',y') | x' \in [x - c_x; x + c_x], y' \in [y - c_y; y + c_y]\}$ and an error window $EW := \{(x',y') | x' \in [-e_x; e_x], y' \in [-e_y; e_y]\}$ with widths and heights c_x,c_y,e_x, and e_y, one can derive the least square error disparity $D_{xy} = (d_x(x,y), d_y(x,y))$ of pixel p_{xy} by

$$D_{xy} = \arg \min_{(x',y') \in CW} \sqrt{\sum_{(x'',y'') \in EW} (Int_{P_1}(x + x'', y + y'') - Int_{P_2}(x' + x'', y' + y''))^2} \tag{2}$$

Due to the large-scale nature of motion artifacts in MR-Mammographies (large tissue structures are moved with slight increases in resulting disparities), it is in terms of computational efforts suitable to apply a Monte-Carlo method for determining M. This means, only a fraction of pixels $p_{xy} \in P_1$ containing tissue information are processed in the above described way, and those left aside gain their disparity D_{xy} by an approximation process.

3.2 Improved Visualization

Due to a better image understanding using three dimensional volume representation methods, we implemented a ray-tracing operator generating pixel intensity based volume visualizations. By applying alpha buffering, breast tissue can be made translucent giving an insight view towards segmentated tumors. Furthermore, the application of stereoscopic imaging using LCD-shutter glasses gives the medical staff a better impression of the localization and topology of suspicious breast regions and tumors (see Fig. 2 right for details).

4 Discussion and Future Work

With the presented knowledge-based expert system MAMMALYZER II it is possible to automatically process different MR acquistions and protocols by means of adapted operator configurations and parameterizations. We introduced a Monte-Carlo based alternative to the SOM-matching with a better calculation performance. MAMMALYZER II reduces workload of medical staff when dealing with the time consuming choice of image processing sequences and supports them with a realistic visualization of suspicious breast regions. In the near future, the system will learn the combination of image parameter and operator sequence choices and shall apply and adapt this knowledge to unknown cases.

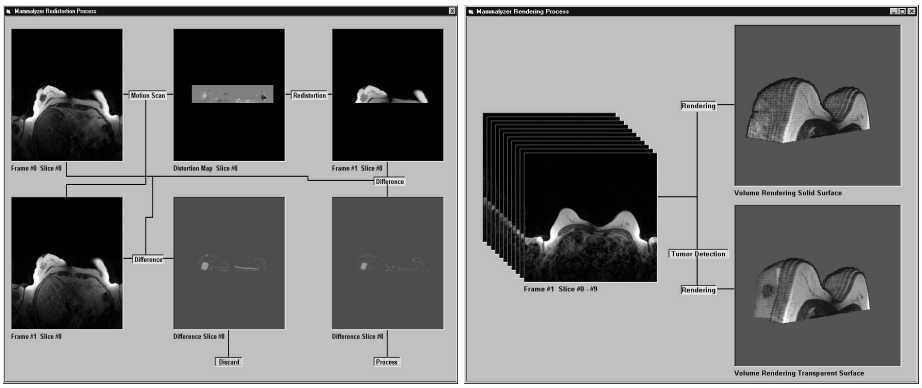

Fig. 2. Redistortion process (left) and improved visualization (right). While a pixelwise calculation of differences between two pictures (upper left and lower left, left figure) leads to a noised signal (lower middle, left), the Monte-Carlo based method creates a better difference picture (lower right, left). Applying a ray tracer using raw MR-volume information helps the physician gain a better understanding of position and type of suspicious breast regions (right figure).

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