Mammalyzer II
A Decision Support System for early Detection of Breast Cancer in Contrast-Enhanced MRI

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Abstract. We present an integrated system for the automatic analysis of MRI-breast images for the early detection of breast cancer. MAMMALYZER II is developed in cooperation with Dr. Buddenbrock, Dr Blasinger, Dr. Benz hospital for Radiology and Nuclear Medicine, Mainz. The system operates on taken images using the method of dynamic contrast-enhanced MRI. Suspicious lesions in the breast are automatically marked with special colors, thus directing the physician's attention towards the critical breast regions. The medical support system is based on a image-matching algorithms using self-organizing maps (SOM) or 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 was tested on real patient data and is now being refined.

Keywords: MR-Mammography, Configuration, Motion Artifacts

1 Introduction

The MAMMALYZER 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].

This MRI-technique of medical breast examination for detecting breast cancer is a relatively new method. 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 on those areas. Comparison of the observed signal-increase-ratios between different MRM-volumes gives an indication of 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 a 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 [2] [1]. Both representative authors for dynamic breast MRI state the same threshold for a suspicious signal increase in the first minute after applying the contrast agent. Another method for analysing the signal increase is the kelcz criterion [**?**], which is based on an histogramm analysis over more time steps(We use 10 Steps in our protocol).

For the medical practitioners the analysis of the images is a tiring and errorprone process, since a complete examination with an uptodate MR-scanner creates in up to 160 image slices per examination(10 frames with 16 slices). Nine conrast images must be compared to the related native slices. An automation greatly reduces the workload and thus errors of medical staff. When designing a system for achieving this, two main problems occurred. 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 arose. 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 disparities. The following sections present an approach for handling real data as found in common hospitals.

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 (Dr.Brandt, Dr.Noegel and Dr. Seybold-Epting). 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 of MAMMALYZER 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 al-

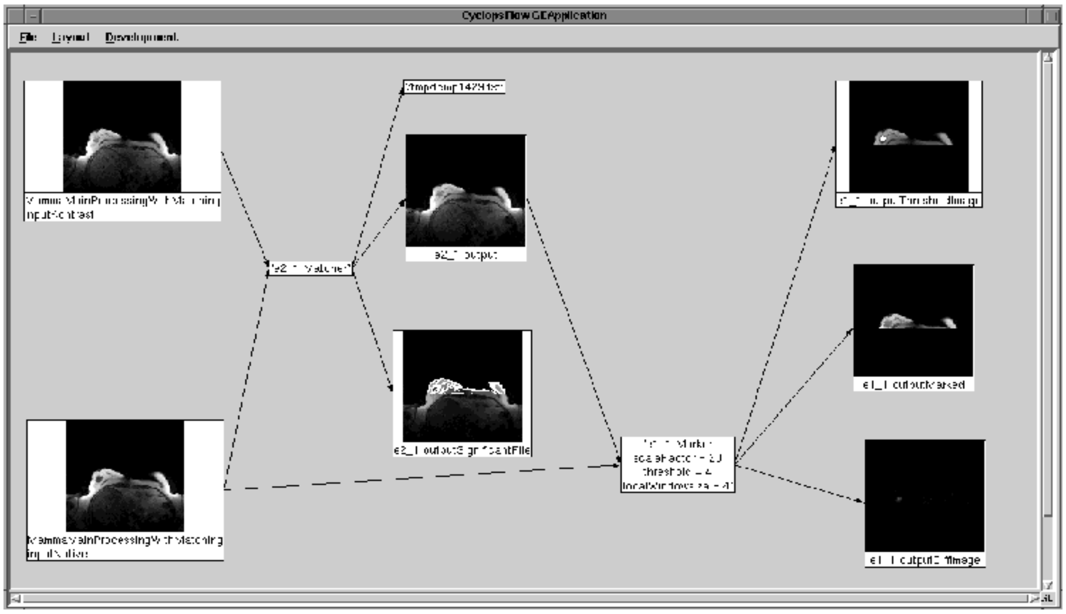

Fig. 1. Part of the configuration

ready 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 to choose between different analysis sequences and lots of parameters, since the sequence is automatically chosen and parameterized by the expert system Cyclops which communicates with the MAMMALYZER II.

Figure 1 shows a small part of the automatically configured mamma processing. The system automatically recognice the typ of sequence and chooses the image operators and parameters, here SOM-Matching and marking with the kaisers threshold criterion. After execution of the configurated pipeline an expactaion matching modul controls the result and decides if the results are good or some parameters must be changed. With the aid of an TMS-strucure only the reponsible operator, and the operators which use the result of it, must be executed with the new parameter sets or new inputs .

2.1 Configuration

2.2 Expectation Matching

2.3 Heuristic Backtracking

3 Vision Methods

3.1 Matching

The problem stated for the matching module can be summarized as trying to locally deform a source image for maximizing the correspondence between the match and the target image. For a detailed discussion of image matching algorithms and methods [9] can be consulted. Certain assumptions can be established on the estimated kind of deformations in dynamic MRM [10]:

- Deformations are of a local nature,
- Deformations are topology-preserving.
- Deformations can be nonlinear.

Furthermore the matching module has to fulfill the following requirements:

- The matcher should find an optimal pixel to pixel-mapping which not only takes some border information of the breasts into account but also considers all subimage information.
- It should be fault-tolerant in order to even find a topology-preserving transformation, in case there are inhomogenous variations of greylevels due to contrast agent or noise.

Suppression of Motion Artefacts The procedure of applying a redistortion process, i.e. the suppression of motion artefacts by comparing two subsequently measured MR-volumens 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 picture element (pixel) $p_{xy} := (x, y)$ of picture $P_1 := \{(x, y)|x \in , y \in \}$, 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 by means of

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

for every pixel $p_{xy} \in P_1$.

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 $P1$.

Out 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

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

Furthermore, in order to decrease the calculation time, a steepest gradient method minimizing the l_2-error between native and test window is implemented, such that the calculation complexity is broken down from $O(n^2)$ to $O(n)$. After that, the redistortion process ends up with processing every volume slice (or, in a more complex way every volume voxel) and by this gaining volume data for a proper tumor detection investigating the increase of contrast agent in Mamma tissue.

3.2 Marker

The marker module computes the pixelwise signal increase between the pixels of two given images. Noise is taken into account by representing the marker basically as a local neighborhood operator. In contrast to the usually employed neighborhood operators in image processing [**?**], the presented one operates on two images simultaneously. For a specified pixel of the GDTA image (x, y) all neighboring pixels of the native image, where the neighborhood is centered at (x, y) are taken into consideration. The best fitting pixel (x_{best}, y_{best}) is chosen for the computation of the signal increase according to the rule (see fig. **??**):

$$\begin{aligned} &\forall (x_i, y_i) \in U_{m \times m}(x, y) : \\ &\quad |I_{gdta}(x, y) - I_{nat}(x_i, y_i)| \geq \\ &\quad |I_{gdta}(x, y) - I_{nat}(x_{best}, y_{best})| \end{aligned} \tag{3}$$

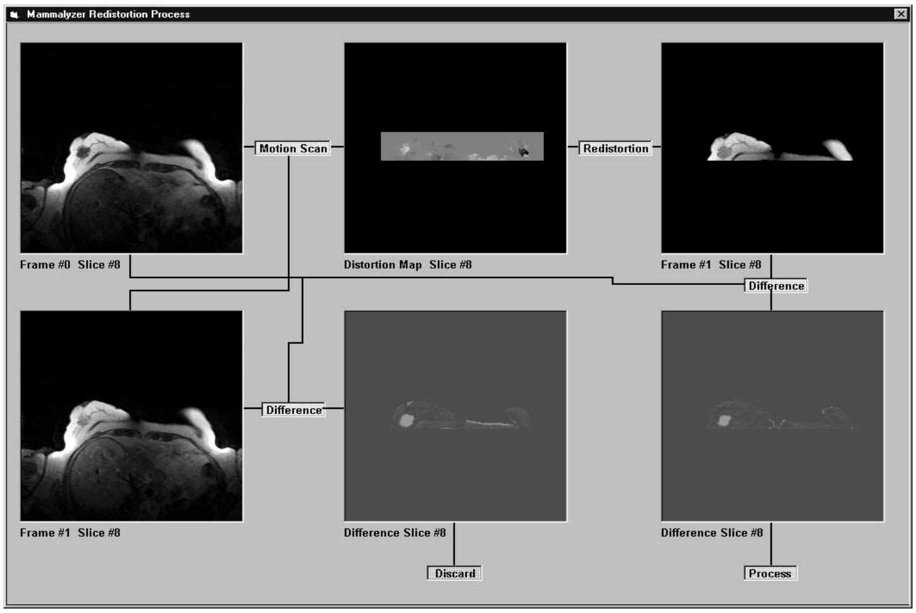

Fig. 2. Matching Result (Monto Carlo Version)

The marker will also be extended with more reliable histogram analysis techniques for better diagnosis support. For this task, the methology of F. Kelcz should be implemented as an improvement of the existing marking algorithm. This methodology can be performed in three steps. The first step is that all lesions which do not appear to enhance differently from surrounding fibroglandular tissue were called benign. The second step in the later phase (¿3 min) of the enhancement profile was used to classify the patients into the categories benign, malignant and interminate by direct examination of the signal intensity (SI) curve. In the third step the intermediate lesions of step 2 were classified by analysing the uptake portion of the SI profile.

3.3 Visualisation

4 Discussion and Future Work

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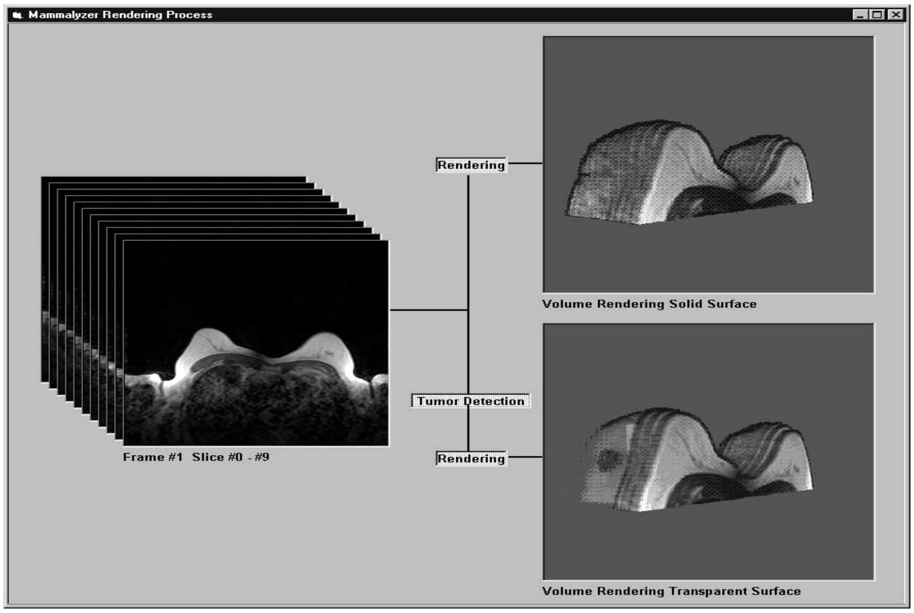

Fig. 3. Visualization of the Results

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