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3D Multi-parametric Breast MRI Segmentation using Hierarchical Support Vector Machine with Coil Sensitivity Correction

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Abstract

Rationale and Objectives—The goal of the study is to develop a technique to achieve accurate volumetric breast tissue segmentation using MRI data. This segmentation can be useful to aid in the diagnosis of breast cancers and to assess breast cancer risk based on breast density. Tissue segmentation is also essential for development of acoustic and thermal models used in magnetic resonance guided high-intensity focused ultrasound treatment of breast lesions.

Materials and Methods—In addition to commonly used T₁-, T₂- and proton density-weighted images, three-point Dixon water- and fat-only images were also included as part of the multi-parametric inputs to a tissue segmentation algorithm using a hierarchical support vector machine (SVM). The effectiveness of a variety of pre-processing schemes was evaluated through two *in vivo* datasets. The performance of the hierarchical SVM was investigated and compared to the conventional classification algorithms—conventional SVM and fuzzy C-mean (FCM).

Results—The need for co-registration, zero filled interpolation, coil sensitivity correction and optimal SNR reconstruction before the final stage classification was demonstrated. The overlap ratios of the hierarchical SVM, conventional SVM and FCM were 93.25%–94.08%, 81.68–92.28%, and 75.96%–91.02% respectively. Classification outputs from *in vivo* experiments showed that the presented methodology is consistent and outperforms other algorithms.

Conclusion—The presented hierarchical SVM-based technique showed promising results in automatically segmenting breast tissues into fat, fibroglandular tissue, skin and lesions. The results provide evidence that both the multi-parametric breast MRI inputs and the pre-processing procedures contribute to the high accuracy of tissue classification.

Keywords

breast MRI segmentation; support vector machine; coil sensitivity correction; multiparametric input

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INTRODUCTION

Breast magnetic resonance (MR) imaging has becoming a very useful imaging modality for breast cancer screening and diagnosis (1). It has been shown that 17–34 % of cancer foci visible on breast MRI are not detected by mammography (2). Not only does breast MRI offer higher sensitivity for detection of breast cancer than x-ray mammography, ultrasound, clinical examination, or any combination of these, it also has a superior ability to delineate fatty and fibroglandular tissue (3).

Although lesions can be detected by visual inspection of breast MRI images, including dynamic contrast enhanced (DCE) studies, there is evidence that quantitative measurements of different structures in the breast with and without contrast can assist not only in the detection of abnormal tissues, but also in the discrimination between fibroadenomas, cysts, and various types of malignancies (1, 4). In an attempt to improve the performance of breast computer-aided diagnosis (CAD) systems that are designed to supplement visual inspection and interpretation of breast MRI, methods for fully- and semi-automatic segmentation of lesion mass based on DCE-MR images have been developed (5-6). Efforts have also been made to discriminate between benign and malignant lesions using quantitative morphological and feature analyses (7-8). In addition to automatic lesion detection and discrimination, breast tissue segmentation could also be used to determine the percentage of fibroglandular tissue present in the breast, which is directly linked to breast parenchymal patterns (9-10), where the parenchymal pattern characterization parameters are taken as risk factors of developing breast cancer (3).

Breast tissue classification is an essential initial step for breast MRI qualitative and quantitative analyses. In addition, segmentation of breast tissue can also be useful in interventional treatments that require accurate knowledge of the internal anatomy of the breast, such as magnetic resonance guided high-intensity focused ultrasound (MRgHIFU) therapy. For this treatment modality, pre-treatment planning, real-time control of treatment, and post-treatment evaluation can be improved with accurate segmentation of fatty tissue, fibroglandular tissue, lesion and skin. A primary motivation for this paper is to improve the accuracy of segmented models that are used to predict ultrasound field distributions in the breast and thus assist in planning focused ultrasound procedures to treat breast lesions. Since the variation of the thermal and acoustic properties between different tissue types affects both the simulated ultrasound beam pattern and the resulting thermal models, it is essential to not only know the distribution of the lesion to be treated, but also the acoustic and thermal properties of the tissue along the proposed ultrasound trajectory. Additionally, segmentation of fatty and glandular tissue is essential for MRI based temperature measurements because phase-based MRI thermometry works in glandular tissue but not in fat (11).

Multi-parametric inputs to tissue segmentation routines have previously included T_1 , T_2 and proton density (PD) weighted images (12-13). T_1 -weighted (T_1 -w) and PD-weighted (PD-w) images generally show clear contrast between fatty and fibroglandular tissue; Fat-suppressed (FS) T_2 -weighted (T_2 -w) images provide good delineation of fluid (water)-containing structures, such as cysts, necrosis and fibroadenomas (14). In our methodology, to emphasize the fatty-fibroglandular tissue contrast, three-point Dixon water-only and fat-only contrasts are also included in the multi-parametric inputs, which are then input into the subsequent pre-processing and segmentation routines. Our hypothesis is that image pixels each represented by a five-element vector in the multi-dimensional feature space composed of T_1 , T_2 , PD, three-point Dixon water-only and fat-only contrasts can be accurately classified using the presented segmentation schemes.

Prior to performing intensity-based tissue classification it may be necessary to correct for intensity inhomogeneity—often times called ‘bias field’—across the imaging field of view (FOV), which is very common in MR imaging because of the non-uniform coil sensitivity distribution, especially when surface coils are used. Meyer (15) estimates that the intensity variation across the image FOV can be as much as 30% of image amplitudes. Although this effect of coil sensitivity on MR images can sometimes be disregarded when viewed by an expert radiologist making qualitative diagnosis, the intensity variation can be especially challenging to computerized MR segmentation (16). The inhomogeneity results in broadening of the signal intensity distribution for each particular tissue type, which results in further ambiguity and inaccuracy when classifying different tissue types. Based on whether the coil sensitivity map is obtained during or after the scan, bias field correction algorithms can be categorized as prospective (17-18) or retrospective (10, 16).

Various algorithms have been applied for breast tissue segmentation in MR images. Fuzzy c-mean (FCM) (19), an iterative algorithm that assigns voxels into groups according to their distance measured in a feature space, has been used in lesion detection (20) and fibroglandular tissue density quantification (9). Iterative self-organizing data (ISODATA) (12), as a derivation from k-mean clustering with additional features of splitting and merging steps to adjust the number of clusters, was investigated for differentiating benign and malignant lesions. A hierarchical k-mean clustering procedure (21) was employed for lesion tissue detection in a murine model. Spectral signature detection approaches (22-23) and conventional SVM (13) have also been studied for the classification of breast tissues.

In this work, we present a hierarchical SVM-based 3D breast tissue classification workflow and evaluate the utility of each pre-processing and final segmentation steps. The importance of incorporating three-point Dixon water-only and fat-only images in the multi-parametric inputs and the implementation of intensity inhomogeneity correction are demonstrated. The performance of the presented hierarchical SVM in segmenting breast tissue into fatty, fibroglandular, lesion and skin components is compared with that of conventional SVM and FCM. A measure of algorithm stability is made by comparing the tissue classification obtained from different orientations of the 3D volumes. Statistical analysis shows that the segmentation performance of the proposed methodology is repeatable and exceeds that of conventional algorithms.

MATERIALS & METHODS

I. Subjects and image acquisition

Imaging was performed on a Siemens MAGNETOM TIM Trio 3T MRI scanner (Siemens, Erlangen, Germany) using a four-channel breast coil. With informed consent obtained from the volunteers, four subjects (three normal subjects and one subject with confirmed fibroadenoma) were examined using the following protocol: unilateral imaging of 88–100 sagittal slices with a FOV=192×192 mm², matrix size = 192×192 and slice thickness = 1 mm, resulting in the 1 mm³ isotropic resolution. T₁-w three-point Dixon was performed using a 3D gradient echo (GRE) sequence with TR/TE1/TE2/TE3=11/4.7/5.75/6.8 ms; T₂-w and PD-w images were acquired using a 2D turbo spin echo (TSE) sequence with bandwidth (BW) = 789 Hz/Px, echo trains per slice = 15, TR/TE = 13s/91ms and 13s/8.2ms respectively. All together, multi-parametric combination of T₁-w, FS T₂-w, PD-w and three-point Dixon water-only and fat-only MR images were obtained.

II. Pre-processing

The multi-stage pre-processing routine is comprised of six steps, including co-registration, zero-filled interpolation (ZFI), three-point Dixon reconstruction, skin extraction, coil

sensitivity estimation, and optimal SNR reconstruction with bias field correction, as detailed in the following descriptions. All the data analyses were performed using Matlab (The MathWorks, Natick, MA, USA).

Co-registration—The total image acquisition time for a subject using the protocol mentioned above is 20–30 minutes. During the course of the data acquisition, motion may occur due to subject movement and other physiological activities, such as respiratory and cardiac movement. Co-registration was therefore performed by manually adjusting the displacement to correct for the misalignment between different scans. All the images from the five MR multi-parametric inputs need to be co-registered, and T_1 -weighted image was selected as the reference sequence. Specifically, since the water-only and fat-only are derived from the T_1 -weighted images, the only registration needed for the Dixon images is to correct for the relative fat-water shift due to the chemical shift. The amount of the shift could be calculated using the readout bandwidth and the 420 Hz frequency shift between fat and water at 3T. Further, T_2 -w and PD-w images are registered to the T_1 sequence, where a single slice from each volumetric data is overlaid on the T_1 -w image with the same slice location. The same amount of adjustment is then applied to the whole image volume.

Zero-filled interpolation—ZFI creates reduced voxel spacing by filling zeros surrounding the original k-space measurements. Even though this processing does not change the spatial resolution of the original data, the denser imaging grid smoothes out the images and alleviates the partial volume effects (24). To study the impact of ZFI on segmentation, a factor of two ZFI was applied and the segmentation performance with ZFI was compared to the performance without ZFI.

Three-point Dixon reconstruction—In three-point Dixon (25), the small frequency difference between the fat and water signal, and the resulting phase difference as a function of TE, make it possible to separate the fat and water signal by acquiring images at different values of TE. In our technique, images were acquired with fat and water in phase at TE = 4.7 and 6.8 ms, and with fat and water 180° out of phase at TE=5.75 ms. The phase difference between the two in-phase images was used to obtain the phase evolution due to other factors, such as the magnetic field inhomogeneity. Furthermore, by averaging the magnitude signal from the two in-phase images, the signal approximates the same effective T_2^* decay as that of the opposed-phase images because of the sequential acquisition of in-phase (TE = 4.7ms), out-of-phase (TE = 5.75ms), and again in-phase (TE = 6.8ms) images (26). Water-only and fat-only images can thus be obtained based on the opposed-phase and averaged in-phase images. To overcome any phase wrap that appeared in the phase images, an unwrapping algorithm based on a solution of the Poisson equation (27) was used. The separated water-only and fat-only images guarantee a clear separation of fibroglandular and fatty tissues. Moreover, three-point Dixon reconstruction provides excellent delineation of skin facilitating skin extraction in the multi-stage preprocessing procedure, as explained below.

Skin extraction—In breast MRI, skin and fibroglandular tissue commonly share similar signal intensities. The impact of skin segmentation on quantitative measurement of breast density was studied by Nie, *et al.* (28). Due to the overlap of the signal intensity from skin and that from fibroglandular tissue in the multi-spectral feature space, we separate out the skin segmentation from the SVM process. Based on three-point Dixon water-only images, where the bright signal of skin is sharply delineated from the surrounding background and breast tissues, a Canny filter (29) was used as an edge detector and pixels in between the boundaries were assigned as skin component.

Coil sensitivity estimation—To correct for the intensity inhomogeneity, the sensitivity for each individual coil was estimated retrospectively using the algorithm developed by P. Vemuri, *et al.* (30). The algorithm does not require an increase in imaging time and eliminates the possible discrepancies between the estimated and true coil sensitivity profiles. Assuming that the sensitivity varies slowly as a function of position, sensitivity magnitude profiles of the individual coil elements were obtained by fitting a lower order polynomial function to the image intensity occupied by a dominant tissue type. In our application, depending on whether fatty or fibroglandular tissue was the dominant tissue in the breast, three-point Dixon fat-only or water-only images were used to determine the pixels for the polynomial fitting.

Optimal SNR reconstruction—With the estimated coil sensitivity map, the optimal SNR images were calculated where each coil was reconstructed separately and combined with weights that are a function of voxel location (31). Mathematically, optimal SNR reconstructed image I_{opt} can be calculated by:

$$I_{opt}(\mathbf{r}) = \frac{\mathbf{R}(\mathbf{r}) \Psi^{-1} \mathbf{S}^T(\mathbf{r})}{\mathbf{S}(\mathbf{r}) \Psi^{-1} \mathbf{S}^T(\mathbf{r})}$$

where $\mathbf{r}$ denotes the position in the image space; $\mathbf{R}(\mathbf{r}) = [R_1(\mathbf{r}), R_2(\mathbf{r}), \dots, R_L(\mathbf{r})]$ is the row vector of coil images; $\mathbf{S}(\mathbf{r}) = [S_1(\mathbf{r}), S_2(\mathbf{r}), \dots, S_L(\mathbf{r})]$ is the row vector of coil sensitivities estimated from above step; Ψ is an L by L matrix which describes the coupling and noise correlations between the coil elements. The noise matrix was assumed to be an identity matrix in the actual calculation for simplicity, and it was shown by Roemer *et al.* (31) that there was only a 10% SNR loss when assuming there is no noise correlation.

III. Tissue segmentation using hierarchical SVM

The supervised learning algorithm, SVM (32-33), uses training data to construct hyper-planes to minimize the margin between classes. The program learns behavior by using a small amount of the input data to train the SVM algorithm and then applies this learned behavior to the rest of the dataset. Instead of segmenting breast tissue into a specified number of target tissues types by applying SVM once as in the conventional manner, the SVM processing was divided into hierarchical stages where in each stage only two tissue types were classified. We decompose the one-time multi-class segmentation into hierarchical binary-class segmentation. Fig. 1 shows the schematic structure of the hierarchical SVM with corresponding multi-parametric inputs and target output tissue types. Different combinations of multi-parametric images were assigned at each level of SVM. In the first stage (level), the entire dataset was classified into background vs. breast tissue using the PD-w images. After excluding the background pixels, the second stage of SVM was applied to the tissue pixels only. T₁-w and three-point Dixon fat-only and water-only images were selected as the input features to segment out fatty tissue from the non-fatty tissues, including fibroglandular tissue, skin and lesion (if present). In the third stage, lesion vs. non-lesion pixels (i.e., fibroglandular tissue and skin) were classified with inputs being T₁-w, T₂-w and PD-w images. In the final step, outputs from all three stages were combined and presented in a final color map with each color representing a single tissue type. The multi-class classification problem was decomposed into multiple binary-class classification problems. Better performance is expected because designing a classifier for separating two classes is easier than designing a classifier to separate multiple classes simultaneously (34). For comparison, we evaluated segmentation using conventional SVM and one of the most widely used unsupervised learning algorithms — fuzzy c-mean clustering with identical

multi-parametric input. All the human volunteer studies were approved by the local institutional review board.

IV. Statistical analysis

The performance of the proposed hierarchical SVM along with conventional SVM and FCM were evaluated by comparing with the manual classification performed by an experienced breast radiologist blinded to the segmentation results. Specifically, about 100 points were selected on each slice in a spatially random manner to which radiologist assigned different tissue types. Even though random sampling results in unbalanced sampling points for different tissue types, complete randomness avoids any potential bias in the interpretation of radiologists who are blinded to the segmentation results. The classification accuracy of the algorithms on the 3D volumetric datasets was evaluated by measuring the overlap ratio of segmentation results with the manual classification as the gold standard. The overlap ratio is defined as the ratio of the points that are correctly classified by the computer program based on radiologist's classification to the total number of pixels that are randomly chosen for radiologist to classify. The impacts of the pre-processing steps, including co-registration, ZFI and coil sensitivity correction, were quantitatively accessed by comparing the overlap ratio from segmentation with and without these procedures. Additionally, consensus reading is attained on one subject by adding a second breast radiologist, to quantify the expected inter-observer variability of manual segmentation. Lastly, a measure of algorithm stability was made by comparing the segmentation obtained using sagittal and axial views of the 3D volumes.

RESULTS

Fig. 2 (a) shows an example slice from a 3D multi-parametric input of a subject with a confirmed fibroadenoma (circled). Image contrasts of T_1 -w, T_2 -w, PD-w, three-point Dixon fat-only and water-only are shown from left to right. In Fig. 2 (b), image intensities from region of interest on fatty tissue, fibroglandular tissue, skin, fibroadenoma and background are plotted in a three-dimensional feature space composed of T_1 , T_2 and PD contrast. It is noticeable in Fig. 2(b) that the signal of skin overlaps with that of the fibroglandular tissue, which makes the classification problem non-separable. Therefore, we take skin extraction as an independent step from the final tissue classification.

To show the range of the datasets included in this study, the central slice of T_1 -w images from each dataset is displayed in Fig. 3. The scaling is included in the figure to indicate the relative size of the breasts. These four datasets represent a wide range of breast volumes, shapes and densities. For the four datasets analyzed in this paper, the registration shift between the T_1 -w and PD-w image volumes was 2, 0.5, 0.5, and 2 mm respectively. The validity of applying the shift to the entire volume of 3D images was verified by visual comparisons of the other slices for all four datasets.

The necessity of co-registration is illustrated in Fig. 4. Due to the motion, PD-w image in the multi-parametric input was off to the right by two pixels relative to the rest of the dataset. After the translational shift was manually corrected, the one-side misclassification at the tissue boundary of the fibroglandular tissue island and the surrounding fatty tissue (see Fig. 4 (a)) is reduced, as shown in Fig. 4 (b).

Fig. 5 (a, b) shows an example sagittal slice of three-point Dixon water-only image and the edge detection results after applying a Canny filter. Pixels between the inner and outer boundary of the skin were assigned as skin component, presented in Fig. 5 (c).

A slice of PD-w images from a healthy subject is displayed in Fig. 6 (a) with clear bias field inhomogeneity across the imaging FOV. The signal intensity varies as the proximity of breast to the phased-array coils changes. Fig. 6 (b) and (c) show the estimated coil sensitivity and the optimal SNR reconstructed image with corrected bias field respectively. The corrected image shows good intensity uniformity, which improves the accuracy of the breast tissue segmentation.

Histograms of breast tissue signal intensity of the example shown in Fig. 6 are plotted in Fig. 7. The narrowing of the histogram after coil sensitivity correction indicates the importance of intensity inhomogeneity correction in computerized tissue segmentation, because the histogram width depends greatly on image intensities.

Lateral projection through the 3D volumetric segmentation output of the hierarchical SVM for the subject with confirmed fibroadenoma is demonstrated in Fig. 8. A slice of segmentation output from hierarchical SVM, conventional SVM and FCM with identical multi-parametric input is displayed in Fig. 9. It is evident that hierarchical SVM outperforms the conventional SVM and FCM in terms of the least misclassification error, referring to the anatomical input shown in Fig. 2 (a). The observation is further confirmed by the statistical analysis performed based on the complete 3D volumes, where the overlap ratios were calculated for each algorithm in comparison to radiologist's manual classification, as listed in Table 1. A bar diagram of the overlap ratios from hierarchical SVM along sagittal and axial directions, conventional SVM, and FCM algorithms are shown in Fig. 10 for the four datasets. Consistently higher overlap ratios from the hierarchical SVM along both directions indicate the superior performance and stability of the hierarchical SVM than other algorithms.

To get more insight into the statistics given in Table 1, the performances of segmentation for each individual tissue type are presented in Tables 2–5. Specifically, for each tissue type that was manually classified by the radiologist, the corresponding classification outputs from the hierarchical SVM are listed. Pixels that were correctly classified, incorrectly classified and the resulting overlap ratios for dataset #1–4 are presented in Tables 2–5 respectively.

To further understand the performance of segmentation from hierarchical SVM along axial and sagittal directions, the tissue specific overlap ratios from the two orientations are calculated based on the combined data from subject #1 and #2, as listed in Table 6.

DISCUSSIONS

A 3D hierarchical SVM-based segmentation algorithm was proposed for breast MRI tissue segmentation, with special emphasis on the inclusion of three-point Dixon images in the multi-parametric MR inputs and coil sensitivity correction as one of the critical pre-processing steps. The segmentation output from hierarchical SVM was compared with other algorithms — conventional SVM and FCM. It was shown that the proposed breast MRI classification workflow segments tissue with the highest accuracy.

In our technique, the binary hierarchical SVM decomposes the four-class classification problem into three sub-problems, each separating two classes, as illustrated in Fig. 1. Since each classifier is simpler, better classification performance is expected, as confirmed by the statistics from Table 1. The average computational time for a complete 3D volume was six minutes on a desktop PC with Intel Core 2 Duo CPU and 2.98GB of RAM.

The primary motivation of the presented methodology is to provide a segmented breast tissue model as input to ultrasound beam simulations in MRgHIFU treatments. However, this technique may also be useful for other purposes such as diagnostic evaluation.

Segmentation of tissue types does not remove information from the images, but rather classifies by tissue type. Segmentation of skin may be helpful for clinical evaluation; a segmented image depicting the skin alone might make abnormal skin thickening more easily visible.

The unsupervised learning algorithm FCM has been used for lesion segmentation on localized areas successfully (20). However, for larger FOV data sets, one tissue type could end up being classified into multiple clusters. When a pre-determined number of tissue types are specified in FCM, as in the presented case, the dominant tissue is likely to be classified into more than one cluster, while a tissue type with fewer pixels could be overlooked in the clustering process. Therefore, while the FCM algorithm is completely data driven, human intervention is required during post-processing to assign the misclassified voxels to the desired target tissue type.

The importance of the three pre-processing steps on the accuracy of segmentation was evaluated as shown in Table 1. Performance degradation is clearly seen when the image intensity inhomogeneity caused by the coil sensitivity is not considered. However, ZFI did not provide significant improvement in the classification output statistically. This may be because, due to the complete randomness used in choosing the sampling points, the calculated overlap ratios may not fully represent the advantage of ZFI, because one would expect the improvement from ZFI to appear mostly on the tissue boundaries. Based on the overlap ratios from classification of the datasets with and without co-registration, co-registration resulted in improved accuracy in dataset #1 and #4, but not dataset #2 and #3. The difference in improvement observed is likely due to the fact that the displacement of datasets #1 (four pixels in y) and #4 (four pixels in y) was greater than datasets #2 (one pixel in both x and y) and #3 (one pixel in y), requiring larger shifts for co-registration between scans.

The statistics for individual tissue type suggest that for certain tissue types, such as skin and lesion, the overlap ratios are lower in comparison to other tissue types, as shown in Tables 2–5. Spatially, the misclassified pixels mostly appear at the tissue boundary. For example, the fibroadenoma in dataset #1 is surrounded by fibroglandular tissue, and the misclassified fibroadenoma pixels were all incorrectly assigned as fibroglandular tissue in Table 2.a. Based on the manual classification from the two radiologists, individual tissue segmentation of dataset #1 was evaluated in Table 2.a and 2.b. A good correlation is found between the two radiologists' segmentation because of a reasonably consistent overlap ratios across various tissue type. The correlation coefficient between the two readers is 90.23%. Detection of lesions and delineation from normal fibroglandular tissue is difficult, and in clinical practice requires administration of intravenous contrast. Therefore, it is not surprising that any method using only non-contrast images, whether automated or manual, is less effective at classifying fibroglandular tissue vs. solid breast lesions. Future work will investigate the potential improvement of tissue classification accuracy with the incorporation of contrast-enhanced scans as an input to the algorithm.

The consistency of the presented results in both the sagittal and axial orientations, shown in Tables 1 and 6, indicates the stability of the proposed segmentation routine and also implies the robustness to the possible variations in the generation of training data. This suggests that the proposed algorithm could be applied in longitudinal follow-up studies to detect changes, e.g., the change of breast density evaluation for risk assessment, and for post-treatment evaluation of neoadjuvant chemotherapy.

Currently, the targeted segmentation tissue types include only fatty tissue, fibroglandular tissue, skin, and lesions. Components such as blood vessels were not considered. Efforts are

being made to visualize blood vessel while suppressing the fibroglandular tissue so that the segmentation could be further improved by incorporating more tissue types. Investigation into this improvement is ongoing and will be evaluated on more subjects, including both normal subjects and those with confirmed breast lesions.

CONCLUSION

Breast tissue classification of MRI data may be useful to aid in the diagnosis of breast cancers and to assess breast cancer risk based on breast density. In this work, a hierarchical SVM algorithm along with a series of pre-processing schemes was presented to automatically segment breast tissues using 3D multi-parametric breast MRI. The importance of multi-parametric MRI contrasts and coil sensitivity correction was investigated. Results show that more accurate breast MRI segmentation can be obtained using the hierarchical SVM with proper pre-processing compared to other available algorithms.

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Fig. 1. Schematic structure of hierarchical SVM process with corresponding input feature and output segmented tissue type.

Fig. 2.

(a) An example sagittal slice from the multi-parametric input of a subject with confirmed fibroadenoma (circled). Contrasts displayed from left to right: T₁, FS T₂, PD, three-point Dixon fat-only and water-only images. (b) Region of interest based image intensities from fatty tissue, fibroglandular tissue, skin, fibroadenoma and background are plotted in a three-dimensional feature space composed of T₁, T₂ and PD contrast.

Fig. 3.

The central slice of T₁-w images from dataset 1–4 is displayed in (a)–(d) respectively. The axes units are in mm. The four datasets in this study represent a wide range of breast volumes, shapes and densities.

Fig. 4. Segmentation output (a) without and (b) with co-registration. Fatty tissue, fibroglandular tissue, skin and fibroadenoma are presented in dark blue, light blue, yellow and red respectively. The misclassification appears on the border of the fibroglandular tissue island (light blue) and the surrounding fatty tissue (dark blue) drops considerably after co-registration, as pointed by the arrow.

Fig. 5. Skin extraction using (a) three-point Dixon water-only image; (b) Canny filtering output; (c) final skin pixels extracted from the water-only image.

Fig. 6. Coil sensitivity correction on an example PD-w sagittal image of a healthy subject. (a) Original image, (b) estimated coil sensitivity, and (c) optimal SNR reconstructed image with coil sensitivity correction.

Fig. 7. Line plot of histograms of image intensity before and after coil sensitivity correction, based on the example from Fig. 6.

Fig. 8. Lateral projection through the 3D volumetric segmentation output of the hierarchical SVM algorithm for the subject with confirmed fibroadenoma. Fatty tissue, fibroglandular tissue, skin and fibroadenoma are presented in blue, green, yellow, and red respectively.

Fig. 9. Segmentation output of (a) hierarchical SVM, (b) conventional SVM, and (c) FCM from the subject with a confirmed fibroadenoma. Fatty tissue, fibroglandular tissue, skin and fibroadenoma are presented in dark blue, light blue, green and red respectively. The corresponding multi-parametric input was shown in Fig. 2.

Fig. 10.

Bar diagram illustration of the overlap ratios from hierarchical SVM along sagittal and axial directions, conventional SVM, and fuzzy c-mean algorithms for four datasets, according to Table 1. The overlap ratios are calculated by comparing the performance of the methods to manual segmentation by radiologist. Consistently higher overlap ratios from the hierarchical SVM along both directions indicate the superior performance and stability of the hierarchical SVM than other algorithms.

Overlap ratios of various algorithms with radiologist's manual classification as ground truth. Hierarchical SVM (h-SVM) offers highest overlap ratio than the conventional SVM (c-SVM) and the FCM algorithm. Three pre-processing steps: coil sensitivity correction (CSC), zero-filled interpolation (ZFI), and co-registration are also evaluated.

Table 1

Overlap Ratio	h-SVM (sagittal)	h-SVM (axial)	c-SVM	FCM	h-SVM w/o CSC	h-SVM w/o ZFI	h-SVM w/o co-registration
dataset #1	90.94%	90.47%	86.97%	75.96%	82.09%	90.69%	88.81%
dataset #2	94.08%	93.92%	90.30%	80.58%	83.42%	94.50%	93.67%
dataset #3	93.90%	93.90%	81.68%	91.02%	95.45%	94.41%	95.38%
dataset #4	93.25%	92.79%	92.28%	80.06%	81.39%	92.76%	81.12%

Individual tissue type analysis of Dataset #1 segmentation: correctly classified, incorrectly classified and overlap ratios of hierarchical SVM for each individual tissue type, comparing to the manual classification from Radiologist #1.

Table 2a

Hierarchical SVM Radiologist	Fat	Fibroglandular	Skin	Lesion	Air	Overlap Ratio
Fat	3877	165	45	4	116	92.16%
Fibroglandular	222	467	17	2	1	65.87%
Skin	8	37	180	2	91	56.60%
Lesion	0	8	0	8	0	50.00%
Air	6	30	14	0	3401	98.55%

Individual tissue type analysis of Dataset #1 segmentation: correctly classified, incorrectly classified and overlap ratios of hierarchical SVM for each individual tissue type, comparing to the manual classification from Radiologist #2.

Table 2.b

Hierarchical SVM Radiologist	Fat	Fibroglandular	Skin	Lesion	Air	Overlap Ratio
Fat	3483	122	22	0	112	93.15%
Fibroglandular	445	467	211	1	0	50.00%
Skin	73	40	200	2	15	46.51%
Lesion	0	1	0	7	0	87.50%
Air	19	33	14	0	3378	98.08%

Table 3

Correctly classified, incorrectly classified and overlap ratios of hierarchical SVM in sagittal orientation for each individual tissue type in dataset #2.

Hierarchical SVM Radiologist	Fat	Fibroglandular	Skin	Air	Overlap Ratio
Fat	3279	180	33	45	92.71%
Fibroglandular	142	632	9	3	80.41%
Skin	6	83	143	56	49.65%
Air	2	7	12	5443	99.62%

Correctly classified, incorrectly classified and overlap ratios of hierarchical SVM in sagittal orientation for each individual tissue type in dataset #3.

Table 4

Hierarchical SVM Radiologist	Fat	Fibroglandular	Skin	Air	Overlap Ratio
Fat	3006	40	0	28	97.79%
Fibroglandular	115	379	0	2	76.41%
Skin	27	85	110	39	42.15%
Air	123	4	2	4046	96.91%

Correctly classified, incorrectly classified and overlap ratios of hierarchical SVM in sagittal orientation for each individual tissue type in dataset #4.

Table 5

Hierarchical SVM Radiologist	Fat	Fibroglandular	Skin	Air	Overlap Ratio
Fat	1223	52	12	180	83.37%
Fibroglandular	26	1340	1	57	94.10%
Skin	9	78	145	38	53.70%
Air	3	22	29	4517	98.82%

Table 6

Overlap ratios of hierarchical SVM at two orientations (sagittal and axial) for each individual tissue type.

Sagittal SVM Axial SVM	Fat	Fibroglandular	Skin	Lesion	Air	Total Points	Overlap Ratio
Fat	4,532,681	156,116	3,926	967	19,280	4,712,970	96.17%
Fibroglandular	50,442	1,027,900	0	1,178	7,192	1,086,712	94.59%
Skin	1,629	0	268,830	252	1,330	272,041	98.82%
Lesion	18	994	110	4,123	18	5,263	78.34%
Air	6,807	8,440	52	0	5,482,907	5,498,206	99.72%