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Breast pectoral muscle segmentation in mammograms using a modified holistically-nested edge detection network

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ABSTRACT

This paper presents a method for automatic breast pectoral muscle segmentation in mediolateral oblique mammograms using a Convolutional Neural Network (CNN) inspired by the Holistically-nested Edge Detection (HED) network. Most of the existing methods in the literature are based on hand-crafted models such as straight-line, curve-based techniques or a combination of both. Unfortunately, such models are insufficient when dealing with complex shape variations of the pectoral muscle boundary and when the boundary is unclear due to overlapping breast tissue. To compensate for these issues, we propose a neural network framework that incorporates multi-scale and multi-level learning, capable of learning complex hierarchical features to resolve spatial ambiguity in estimating the pectoral muscle boundary. For this purpose, we modified the HED network architecture to specifically find 'contour-like' objects in mammograms. The proposed framework produced a probability map that can be used to estimate the initial pectoral muscle boundary. Subsequently, we process these maps by extracting morphological properties to find the actual pectoral muscle boundary. Finally, we developed two different post-processing steps to find the actual pectoral muscle boundary. Quantitative evaluation results show that the proposed method is comparable with alternative state-of-the-art methods producing on average values of $94.8 \pm 8.5\%$ and $97.5 \pm 6.3\%$ for the Jaccard and Dice similarity metrics, respectively, across four different databases.

1. Introduction

Mammography is a standard breast imaging procedure to screen women for early signs of breast cancer. Unfortunately, with relatively small number of radiologists compared to the vast number of mammograms to be analysed, visual inspection is an extremely demanding and time consuming task. The use of computer-aided diagnosis (CAD) is considered crucial to reduce the workload and to help the clinician making decisions in the diagnosis and prognosis of health conditions.

According to Kwok et al. (2004), Gupta and Undrill (1995), Karssemeijer (1998), Saha et al. (2001), Eklund and Cardenosa (1992), Bassett et al. (1993), Heywang-Kobrunner et al. (2001), Shi et al. (2018) and Rampun et al. (2018b), accurate segmentation of the pectoral muscle is important for mammographic analysis because: (a) the pectoral muscle region and the breast region may have similar intensity or texture appearance and including the pectoral muscle region into breast density quantification may lead to inaccurate breast density estimation; and (b) in mammogram-pair registration and comparison the pectoral muscle boundary is one of the crucial landmarks and thus its correct estimation leads to accurate mammogram pair registration. Additionally, from a clinical point of view, a good quality mediolateral oblique (MLO) mammogram should display the pectoral muscle to the level of the nipple detection and its orientation should not be more than

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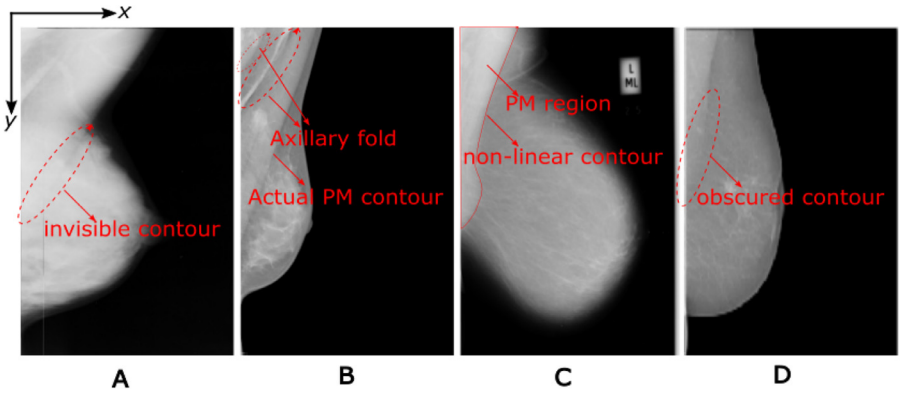

Fig. 1. Different challenges in estimating the pectoral muscle boundary. Invisible pectoral muscle boundary (A), multiple *axillary fold* (B), non-linear (or irregular) shape of the pectoral muscle boundary (C) and the lower part of the pectoral muscle boundary is obscured (D). PM indicates pectoral muscle region.

70◦ from the y-axis of the image (this is not always the case in the dataset used). Hence segmenting the pectoral muscle is essential as a pre-processing step for breast cancer CAD systems.

In breast cancer CAD systems three anatomical landmarks need to be extracted automatically, namely the breast border, the nipple and the pectoral muscle (Chandrasekhar and Attikiouzel, 2000; 1997; Kwok et al., 2001). The majority of mammograms are digital (full field digital mammograms (FFDM)), which makes separating the breast boundary from the air background less complicated. However, nipple and pectoral muscle segmentation remain challenging due to their significant variability. The main challenges are depicted in Fig. 1: (A) the pectoral boundary is invisible due to dense tissues (and the breast and pectoral regions have a similar appearance); (B) the appearance of the *axillary fold* in the pectoral muscle can have a significant effect (false positive) when finding the actual pectoral muscle contour; (C) the curvature of the pectoral muscle boundary can be convex, concave, a straight line or a mixture of these; (D) the majority of the lower part of the pectoral muscle boundary is obscured due to overlapping fibro-glandular tissue. The pectoral muscle region tends to be a 'triangular-shaped' region located in the top left corner of a mammogram as depicted in Fig. 1C.

2. Literature review

Although many methods have been developed for pectoral muscle segmentation, due to a lack of ground truth the majority of studies are evaluated using the Mammographic Image Analysis Society (MIAS) database (Suckling et al., 1994). In early studies, straight-line based methods (Karssemeijer, 1998; Aylward et al., 1998) using the Hough transform in conjunction with a gradient magnitude and a set of threshold values were used to estimate the pectoral muscle boundary. Unfortunately, these studies are unreliable in complex cases when the appearance of the pectoral muscle boundary is non-linear (or irregular), where the Hough transform fails to estimate a straight line. To compensate for the limitations of such methods, Chakraborty et al. (2012) developed a straight-line estimation technique based on texture and morphological features to find the initial boundary, followed by an iterative tuning procedure to produce a smooth curve. Although this approach improved the previous methods, it is sensitive to the pectoral muscle's morphological properties, which can significantly affect the initial detection of the pectoral boundary.

Later, Kwok et al. (2004) and Ferrari et al. (2004) developed methods by combining straight-line and contour-based methods. Kwok et al. (2004) estimated the initial pectoral muscle boundary based on a straight-line approximation technique, followed by a 'cliff detection' method to refine the initial boundary iteratively. Ferrari et al. (2004) proposed an approach based on a multiresolution technique using Gabor wavelet filters, which overcame the limitations of the straight-line based techniques used in Kwok et al. (2004), Karssemeijer (1998), Aylward et al. (1998) and Chakraborty et al. (2012). There were 48 Gabor filters used to enhance the appearance of the edges within the region of interest containing the pectoral muscle. Subsequently, the magnitude value for each pixel was propagated using 'edge-flow' in the direction of the phase. Although both methods showed promising results, only a small number of images were used to evaluate the performance of the methods.

Adaptive thresholding-based methods were proposed by several authors (Czaplicka and Włodarczyk, 2012; Mustra and Grgic, 2013) to directly segment the entire pectoral region. From our own experience, using an adaptive thresholding approach can only work if the majority of the pectoral region appears to have significant variation in intensity or texture appearance. In cases where the pectoral muscle boundary is overlapping with fibro-glandular tissues, the segmentation results are affected significantly. Another alternative solution proposed in the literature is a region-growing based technique (Chen and Zwiggelaar, 2010). However, such an intensity-based technique can be very sensitive to noise and could easily over-segment the muscle when the pectoral muscle and the breast have similar intensities. Another disadvantage of using this technique is that it stopped when there was a sharp intensity change and hence it can lead to under-segmentation when an *axillary fold* was visible in the image.

Curve fitting-based techniques (Mustra and Grgic, 2013; Bora et al., 2016; Vikhe and Thool, 2017; Chen et al., 2015) have also been used as a part of the segmentation or post-processing step to estimate the pectoral muscle curve. Mustra and Grgic (2013) manually selected initial points for polynomial fitting to estimate the actual muscle boundary, which they assumed to be concave or convex. Bora et al. (2016) estimated the initial boundary using the Hough transform technique based on texture gradient. Subsequently, a smooth pectoral boundary was obtained using Euclidean distance regression in conjunction with polynomial modelling. A similar approach was developed by Vikhe and Thool (2017) whose method used curve fitting by the Least Square Error (LSE) to refine the rough initial boundary points estimated via thresholding. Chen et al. (2015) refined the initial boundary determined via shape-based region growing using a cubic polynomial function, whereas Yoon et al. (2016) used quadratic curve fitting using the random sample consensus algorithm. Unfortunately, such techniques require the user to decide the degree of the curve and were limited to boundaries with 'curve-like' shapes only.

Recently, Taghanaki et al. (2017) proposed a geomerty-based method supporting different types of pectoral muscle boundaries.

The initial boundary was first estimated using a straight line based on the detection of a maximum-inscribed circle (MIC) followed by a restricted region growing method to extract the actual boundary. The main limitation of their method was that it assumed each mammogram contained a pectoral muscle, whereas in a real clinical environment there are many cases where the pectoral muscle is absent. A robust pectoral muscle segmentation algorithm must not only be able to find the boundary accurately, but also determine whether it was truly present. To eliminate user interaction, prior knowledge of the existence of pectoral muscle and the limitations of curve-fitting based techniques, Rampun et al. (2017b) proposed a method based on edge features such as length ($\hat{L}$), eccentricity (E_c), orientation (θ), intensity and extent (E_x) to select initial candidates. Subsequently, a majority voting approach was used to select the best edge as the initial pectoral muscle boundary and 'grown' based on the most similar intensity among its neighbouring pixels. However, this method was less accurate in cases where the lower part of the pectoral muscle boundary overlapped with the fibro-glandular tissues or had a convex shape.

The use of deep learning in the field of medical image analysis is becoming a methodology of choice and is one of the most popular topics in pattern recognition and machine learning. The main focus for most computer scientists is designing network architectures to suit their problem domain instead of developing feature extraction methods, which may require specialised knowledge (Litjens et al., 2017; Moeskops et al., 2016). Despite a large number of studies in the literature using deep learning in the medical imaging domain, based on the surveys conducted by Litjens et al. (2017) and Hamidinekoo et al. (2018), there are only two works that focus on pectoral muscle segmentation in mammograms (Dubrovina et al., 2016) and in Magnetic Resonance Imaging (MRI) (Moeskops et al., 2016). Dubrovina et al. (2016) used a CNN not only for pectoral muscle segmentation, but also for tissue classification and nipple segmentation. On the other hand, Moeskops et al. (2016) used a CNN to segment different organs (e.g. breast, brain and heart) in different modalities. In both studies the networks were trained on mini patches extracted from the pectoral muscle region, which means that their networks were modelled based on the structural appearance of the pectoral muscle and did not take the contextual information into account. Although both authors reported satisfactory results, the probability maps generated by their proposed networks contained many false positives.

Despite of the promising results reported in the studies described above, the following limitations have been identified:

1. The majority of the studies (Kwok et al., 2004; Ferrari et al., 2004; Karssemeijer, 1998; Aylward et al., 1998; Chen and Zwiggelaar, 2010; Chakraborty et al., 2012; Rampun et al., 2017b; Taghanaki et al., 2017; Bora et al., 2016; Vikhe and Thool, 2017; Chen et al., 2015; Yoon et al., 2016) tried to manually model the curve structure of the pectoral muscle either using straight-line techniques, curve-based techniques or a combination of these two. In other words, the majority of the existing methods are hand-crafted models that require specific knowledge and were insufficient in dealing with the large variation of pectoral muscle boundaries.
2. The majority of the studies (Kwok et al., 2004; Ferrari et al., 2004; Karssemeijer, 1998; Aylward et al., 1998; Chen and Zwiggelaar, 2010; Chakraborty et al., 2012) used only a small number of images for evaluation and only a small number of them (Taghanaki et al., 2017; Bora et al., 2016) were evaluated across different datasets.
3. None of the methods can automatically identify whether the pectoral muscle is truly present in the image. A fully automated CAD system should be able to recognise cases where the pectoral muscle region is absent.
4. Many studies (Mustra and Grgic, 2013; Chen and Zwiggelaar, 2010; Chakraborty et al., 2012; Bora et al., 2016) required user interaction, such as seed initialisation and setting the degree of the polynomial function.
5. For deep learning-based methods (Dubrovina et al., 2016; Moeskops et al., 2016), networks were trained on patches and based on the information from the region's surface (which increased false positives), whereas our proposed network was trained based on the information along the region's boundary using the whole image.

To overcome these limitations, we have proposed a pectoral muscle segmentation method using a CNN in conjunction with morphological post-processing steps. Our motivation in using a CNN derived from the HED network (Xie and Tu, 2015) was to learn and model the characteristics of the pectoral muscle boundary automatically, without the need to model its complex geometrical appearance variation manually. The original HED network (Xie and Tu, 2015) was designed for edge detection purposes in natural images, which captures fine and coarse geometrical structures (e.g. contours, spots, lines and edges), whereas we were interested in only capturing the main boundary structures in mammograms, as most pectoral boundaries appear as 'contour-like' objects. Although contours can be detected using edge-based approaches such as Canny and Sobel operators, these methods usually fail when the fibro-glandular tissue overlaps with the pectoral muscle (Rampun et al., 2017b). To compensate for this problem, we modified the HED architecture (Xie and Tu, 2015) so that unnecessary details could be ignored and 'contour-like' objects can be found.

Most pectoral muscle boundaries have unique appearances such as having sharp intensity changes, and being morphologically smooth and continuous. Modelling these characteristics manually (as proposed in Rampun et al. (2017b), Dubrovina et al. (2016), Moeskops et al. (2016) and Taghanaki et al. (2017)) was difficult and restricted the model's capability in dealing with the variations of contour appearance; fortunately the HED network (Xie and Tu, 2015) can be used to learn these characteristics automatically, and with few modifications it can be used to learn boundary cues. Furthermore, our motivation for training the proposed network based on contour appearance rather than the structure appearance of the pectoral muscle is two-fold: (a) overlapping structure information in both breast and pectoral muscle regions makes learning the pectoral muscle structure more difficult, yielding a large number of false positives, as visually shown in studies by Dubrovina et al. (2016) and Moeskops et al. (2016), and our own experiment in Section 6.3; (b) usually there are only three types of possible contours in a mammogram: the *auxiliary fold*, pectoral muscle boundary and breast boundary. By learning these cues only, the learning process became simpler because we have narrowed it down to specific problems. Therefore, this contributed to not only generating a small number of false positives, but also simplified the post-processing step.

The contributions of our study are:

1. We have proposed a contour based CNN method that has learned the boundary representation rather than the appearance of the pectoral muscle region (as the current deep learning based methods for pectoral muscle segmentation in the literature have (Dubrovina et al., 2016; Moeskops et al., 2016)). Our approach not only reduced false positives but simplified the subsequent post processing steps.
2. We modify the original HED network by making it shorter (hence faster), having used an element-wise fusing operation instead of concatenation (hence more accurate in locating

Table 1
Summary of the datasets used in this study.

Database	# Images	Image size	Format	# Pectoral
MIAS (Suckling et al., 1994)	322	Various	SFM	321
InBreast (Moreira et al., 2011)	208	2560×3328	FFDM	201
BCDR (Lopez et al., 2012)	100	3328×4048	FFDM	100
CBIS-DDSM (Lee et al., 2017)	457	Various	SFM	457

the pectoral muscle boundary), and we introduced a weighted softmax loss function to deal with data imbalance between classes.

3. We conduct extensive experimental evaluation covering both full field digital mammograms (FFDM) and scanned film mammograms (SFM) using four different datasets (Mammographic Image Analysis Society (MIAS) (Suckling et al., 1994), Breast Cancer Digital Repository (BCDR) (Lopez et al., 2012), InBreast (Moreira et al., 2011), and Curated Breast Imaging Subset of Digital Database for Screening Mammography (CBIS-DDSM) (Lee et al., 2017)), which to the best of our knowledge has been the largest validation study to date.
4. The proposed method has been fully automated and does not need any user intervention (such as seed initialisation, and selection of smoothing and curve parameters) and can recognise cases where the pectoral muscle was absent in the image.

3. Materials

Table 1 provides an overview of the four datasets used in our study, which cover both scanned-film mammograms (SFM) and full field digital mammograms (FFDM), to evaluate the robustness of the proposed method when dealing with different image types. Moreover, the majority of the existing methods in the literature have used the MIAS dataset (SFM), so including this dataset in our study enables us to make quantitative and qualitative comparisons. The following image formats were used: *.png* (MIAS), *.jpeg* (CBIS-DDSM) and *.tiff* (InBreast and BCDR) for view images were used and no additional pre-processing was done. Similar to the existing studies, only MLO view images were used which tend to include the pectoral muscle, whereas in the Craniocaudal (CC) view in most cases the pectoral muscle is absent.

Regarding ground truth generation, for the MIAS (Suckling et al., 1994) dataset, each contour for the pectoral muscle boundary was annotated by a clinician supervised closely by an expert radiologist. For the InBreast (Moreira et al., 2011) dataset annotations were provided by an expert radiologist, and for the BCDR (Lopez et al., 2012) and CBIS-DDSM (Lee et al., 2017) databases, pectoral muscle boundaries were provided by an experienced observer and verified by an expert radiologist.

Regarding the implementation, the proposed CNN was trained, validated and tested on an Intel Xeon E5-1650 v3 processor, using Nvidia Corporation's Deep Learning GPU Training System (DIGITS) based on Caffe, with a Nvidia's Quadro M6000 (12Gb) graphics card. The post-processing methods were developed under the MATLAB environment version 9 (2016a) on a Windows 10 operating system with an Intel CORE i7 vPro processor.

4. Methodology

The first subsection introduces a definition of the contour from a pectoral muscle perspective and we explain how we generate it for CNN training.The technical aspects of the proposed method are explained in the subsequent subsections, which cover two main steps: (1) initial pectoral contour delineation based on a CNN and (2) refinement of this contour using prior knowledge of the boundary shape and whole pectoral muscle segmentation in the post-processing steps.

4.1. Pectoral muscle contour

In this study we refer to a contour as a boundary between two regions of interest (i.e. the pectoral muscle region and the breast region). Let C be a smooth contour containing a set of continuously connected pixels, where c_1 and c_{end} are the starts and end points, respectively. Therefore, the pectoral muscle contour is defined as:

$$C = \{c_1(x,y), \ldots, c_i(x,y), \ldots, c_{end}(x,y)\} \tag{1}$$

where c is a pixel with coordinates (x, y) in a 2D image I (with M (rows) $\times$ N (columns)) and i is the ith pixel on C. Note that the conditions for x and y must be $\mathbb{Z}_x = \{x \in \mathbb{Z} | 0 \leq x \leq M-1\}$ and $\mathbb{Z}_y = \{y \in \mathbb{Z} | 0 \leq y \leq N-1\}$, respectively. In Eq. (1), each pixel $c_i(x, y)$ in C is unique so that the boundary does not intersect itself. Since the pectoral muscle contour always starts at the x-axis and end at the y-axis of the image, we further restrict C to the following conditions:

$$c_1(x,y) = (0, 0 \leq y < N) \tag{2}$$

$$c_{end}(x,y) = (0 \leq x < M, N-1) \tag{3}$$

where $0 \leq y < N$ and $0 \leq x < M$ indicate that C must intersect with the y-axis (at $x = 0$) and with the x-axis (at $y = N-1$), respectively.

Fig. 2 shows a step by step procedure for generating the pectoral muscle contours for training the CNN. Firstly, we applied the Canny edge detection technique to the whole pectoral muscle mask to get the pixels located along the contour. Secondly, in order to enrich contour information with neighbouring pixels, the edge is dilated using a line-shaped structuring element (ϵ) with the following properties: neighbourhood ($\eta = 5$) and orientation ($\theta = 90^\circ$). The 'Edge' (E) sub-image in Fig. 2 is the superimposed red square region in the pectoral muscle mask image. The 'Dilated Edge' (DE) sub-image in Fig. 2 is the dilated edge derived from sub-image E, and the right-most image is the contour and its neighbouring pixels.

For training, we consider pixels with values '1' in the image of the pectoral muscle contour mask (I_{pm}) as objects (e.g. class one) and pixel values equal to '0' as non-objects (e.g. class two) which can be obtained using the following equation

$$I_{tr(+)} = I_{pm} \times I \tag{4}$$

where $I_{tr(+)}$ is the training image containing grey-level pixels located within C_d as its centre pixel and $\times$ is an element wise multiplication. Therefore, our training samples for class one ($\mathcal{T}^+$) which were the objects (or the contours) were defined as

$$\mathcal{T}^+ = \{I^1_{tr(+)}, I^2_{tr(+)}, I^3_{tr(+)} \ldots I^d_{tr(+)}\} \tag{5}$$

where d is the dth $I_{tr(+)}$ in $\mathcal{T}^+$. The training samples for class two ($\mathcal{T}^-$) which were the background (or the non-contour) were defined as

$$I_{tr(-)} = (I_{pm})' \times I \tag{6}$$

$$\mathcal{T}^- = \{I^1_{tr(-)}, I^2_{tr(-)}, I^3_{tr(-)} \ldots I^d_{tr(-)}\} \tag{7}$$

where $(I_{pm})'$ is the binary image complement of I_{pm}.

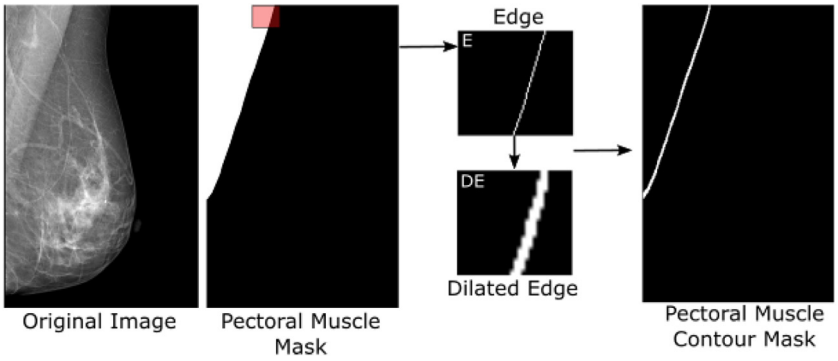

Fig. 2. Contour generation to capture the pectoral muscle boundary and its surrounding neighbourhood pixels.

4.2. Network architecture

The proposed network architecture was inspired by the Holistically-Nested Edge Detection (HED) network presented in Xie and Tu (2015). The HED network automatically learns rich hierarchical image representations that are essential to resolve ambiguities in edge and object boundary detection and allows us to train and make predictions from the whole image end-to-end (holistically), using a per-pixel labeling cost. It incorporates multi-scale and multi-level learning of deep image features using auxiliary cost functions at each convolutional layer, and its multiple stages with different convolutional strides can capture the inherent scales of organ contours (Roth et al., 2018). Hence, HED-based CNN architectures have been successfully employed in medical image analysis for pancreas localization and segmentation (Roth et al., 2018), retinal blood vessel segmentation (Fu et al., 2016), aneurysm segmentation (López-Linares et al., 2017) and pathological lung segmentation (Harrison et al., 2017).

While the HED network aimed to find all possible edges in an image, our network aimed to find 'contour-like' appearances between the breast and the pectoral muscle regions. Our network was composed of a single-stream deep network divided into four blocks of convolution and pooling layers producing a different number of feature maps. Multiple side connections are inserted after the last convolution layer of each block to extract output feature maps at different scale levels. The size of these maps became smaller along the network, and thus deconvolutional layers with larger receptive fields were needed to recover the original image size. To ensure that all the maps had the same size as the original image after deconvolution, a cropping operation was applied. Cropped feature maps were element-wise fused in order to get the final prediction, as shown in Fig. 3. Lastly, to overcome the problem of imbalance between foreground (contour) and background pixels, a weighted softmax loss function was employed, such as in Badrinarayanan et al. (2015).

Therefore, in contrast to the original HED network (Xie and Tu, 2015) our architecture has five main modifications:

1. We have modified the network to have 3 pooling layers and 4 side-output maps. The final layers of the original HED network reduced the resolution of the input image and provided a very coarse feature map. The effect of this resultant coarse map on the final segmentation was undesirable, as the very thick contour loads to a loss of accuracy when detecting the pectoral boundary. With the removal of these layers, we also obtained a faster network.
2. We have reduced the padding introduced in the first convolutional layer. In the original HED network, a large padding was needed as it is a deeper network, whereas our network was shorter.
3. The cropping offset was calculated to have the resulting image centered before fusing and to avoid cropping relevant information.
4. Instead of minimizing multiple loss functions, one per side-output map, and a global fused loss function obtained by concatenating the feature maps at different scales, we compute a unique loss function from the element-wise fusing of side-output feature maps. By applying an element-wise fusing operation, the strongest activations are kept, and the global loss is computed taking into account the information from feature maps at different scales in a combined manner.
5. We introduce a weighted softmax loss function, which accounts for the imbalance between contour and background pixels in the global loss function, whereas in the original HED network it was addressed independently at each side-output loss function.

The combination of feature maps at different detail levels provided the ability to obtain a global object boundary where weak edges were omitted, but whose precision was improved when fusing it with finer-detailed feature maps. Fig. 4 depicts feature maps before and after fusing for two example images.

The proposed network architecture was trained and validated with $\mathcal{T}^+$ and $\mathcal{T}^-$ from three databases (e.g. MIAS, BCDR and CBIS-DDSM) and the network model was used to find each pectoral muscle boundary from each image in the fourth database (e.g. InBreast). Note that each database contains patients collected from different institutions, ensuring no images from the same patient appear in the training and testing datasets. From the training dataset, we randomly split approximately 10% of the images for validation taking into account that both left and right mammograms of the same patient are included in the same set (i.e. train or validation) to avoid a possible bias due to the similarity between both breasts. All images were resized to 256×256 using bilinear interpolation, and data augmentation was applied to the training set in the form of $\theta = 90^\circ$, 180° and 270° rotations. All images (including the augmented ones) that come from the same patient were separated either in the training or validation set to ensure no bias due to similarity between breast/contour structures. The process was repeated in a round robin basis for the other databases. Table 2 summarizes the number of images used for training, testing and validating in each of our experiments.

Following the studies of Xie and Tu (2015), López-Linares et al. (2017) and Roth et al. (2018), the network weights were initialised from the weights of the original HED network trained on natural images, which helped in dealing with overfitting and accelerated convergence. We used the stochastic gradient descent optimizer, with a learning rate of 0.01, step-wise learning rate decay policy and momentum of 0.9. A batch size of 16 images was employed and the network was trained for 100

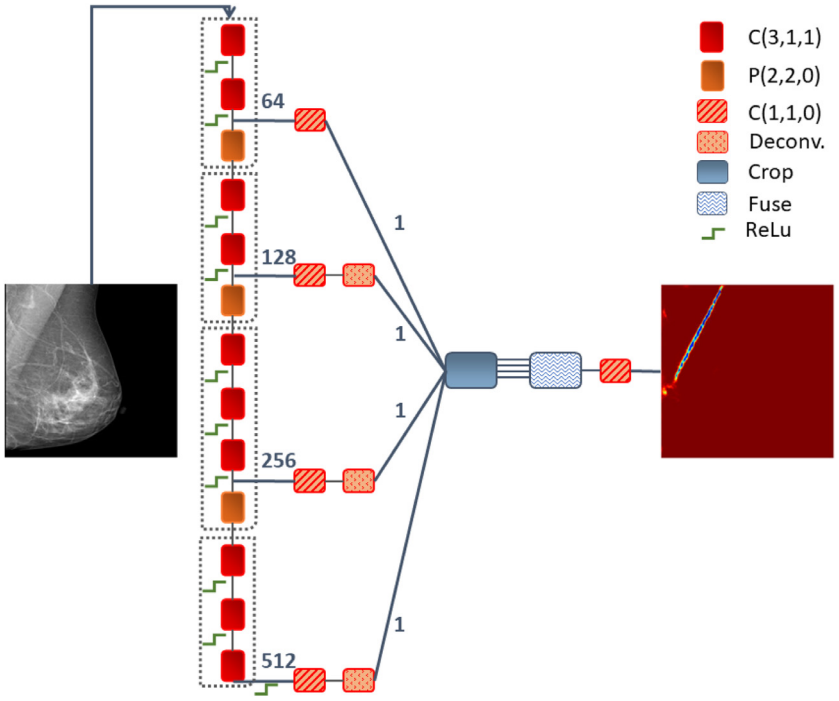

Fig. 3. CNN for pectoral muscle contour segmentation, depicting also the input image and corresponding likelihood map. C: convolutional layer (kernel,stride,padding); P: max-pooling layer (kernel,stride,padding); Deconv: deconvolutional layer; Fuse: element-wise fusing; ReLu: Rectified Linear Unit Activations. The number of feature maps at different stages were included next to the connection lines.

Table 2
Number of training, validation and testing images employed for each of our experiments.

Training/val. DB	Testing DB	# Training	# Validation	# Testing
BCDR+InBreast+(CBIS-DDSM)	MIAS	2729	303	321
BCDR+MIAS+(CBIS-DDSM)	InBreast	3165	351	201
MIAS+InBreast+(CBIS-DDSM)	BCDR	3528	392	100
MIAS+InBreast+BCDR	(CBIS-DDSM)	2243	249	457

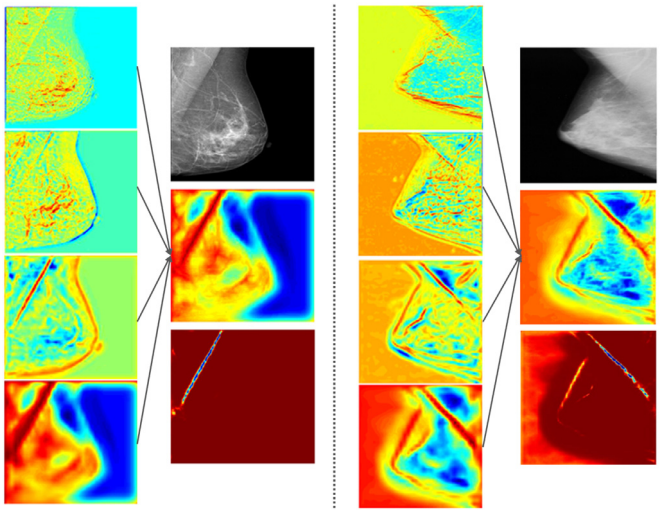

Fig. 4. Side feature maps after deconvolution and cropping obtained for two example images from different datasets: BCDR (right) (Lopez et al., 2012) and MIAS (left) (Suckling et al., 1994). In both examples, the left column represents feature maps from finer to coarser, while the right column shows the input image, the fused response and the final likelihood map.

epochs since otherwise the network started over-fitting due to the small number of pixels labeled as foreground. The function to be minimized was a Softmax function, which provides the probability distribution over classes:

$$L = \frac{1}{N}\sum_{n=1}^{N} -log\left(\frac{e^{f_n}}{\sum_{k=1}^{k=2} e^{f_k}}\right) \quad (8)$$

where f_k denotes the kth element ($k \in [1, K]$, K is the number of classes (i.e. in our case K=2)) of the vector of class scores f, and N is the number of training images.

As explained in Badrinarayanan et al. (2015), when there was large variation in the number of pixels in each class in the training set there was a need to weight the loss based on each class. Thus, a weight was assigned to each class in the loss function; in our case, we set a weight of 10 for the contour and a weight of 1 for the background. These values were selected experimentally considering the reduced number of contour pixels with respect to the background. Setting an even larger weight value produced additional over-fitting, and thus the value was limited to 10.

4.3. Estimating the pectoral muscle boundary

Since the output of the network was a prediction map (or likelihood map), it was necessary to process the map to obtain the estimated pectoral muscle boundary (hence obtaining the pectoral muscle region). The majority of the existing studies (Kwok et al., 2004; Ferrari et al., 2004; Eklund and Cardenosa, 1992; Bassett et al., 1993; Heywang-Kobrunner et al., 2001; Rampun et al., 2017b) developed their post-processing techniques based on the MIAS dataset, and therefore some of the rules were derived

from a smaller training set by the previous authors. We further studied this problem by investigating more datasets and, based on our extensive study, we developed more robust post-processing techniques which are able to handle more cases such as when the contour is disconnected. For this purpose, we developed post-processing techniques based on previous studies (Kwok et al., 2004; Ferrari et al., 2004; Eklund and Cardenosa, 1992; Bassett et al., 1993; Heywang-Kobrunner et al., 2001; Rampun et al., 2017b). The techniques were based on the following hypotheses:

1. The pectoral muscle was located either in the left or right upper corner of the mammogram. However, in this study we always assume that the pectoral muscle is located in the left upper corner of I (after all right breasts in the MLO view mammograms were automatically flipped to the left using a method from Rampun et al. (2017b).
2. After the right breast image was flipped to the left, the orientation (θ) of the pectoral muscle boundary should be in the range of 20° and 90° as suggested in Eklund and Cardenosa (1992), Bassett et al. (1993) and Heywang-Kobrunner et al. (2001).
3. The appearance of the pectoral muscle boundary was called an 'open contour', where the start and end points of the contour must not be the same.
4. In the probability map generated by the proposed network, the pectoral muscle contour tended to have the longest length compared to non-pectoral contours.

Fig. 5 shows an overview of the post-processing approach used to estimate the actual pectoral muscle boundary. Note that these heuristic rules were applied identically across the different datasets. The CNN's prediction map (I_{map}) was dilated using a "line" shaped structuring element with $\eta = 5$ and $\theta = 90°$, resulting in I^{ϵ}_{map}. We set a constant threshold value and applied binary thresholding to segment I_b. To select the best threshold value we tested values over the range $[0.1, \ldots, 0.7]$ at intervals of 0.03 and found that 0.1 and 0.13 produced the best results in terms of Jaccard and Dice metrics (see Section 6.5). If there is no segmented region (e.g. $\sum_{x=1,y=1}^{M,N} I_b(x,y) = 0$) we assumed that the pectoral muscle region is absent in I. Otherwise we searched for the longest region (L_r) in I_b and determined whether L_r intersected at the x and y axes. Finally, if L_r intersected both axes, the first post-processing step was selected, otherwise it defaulted to the second post-processing step. To illustrate this process graphically, Fig. 6 shows a step by step representation for the flow chart in Fig. 5.

As can be observed in Fig. 6, applying $\epsilon^{\eta=5}_{\theta=90°}$ (these values were determined empirically) to I_{map} resulted in a connected and solid contour in the I^{ϵ}_{map}. Image I_b was generated by thresholding I^{ϵ}_{map}. Finally, in I^{Lr}_b we retained the longest region (L_r) with an orientation within $20° \leq \theta \leq 90°$, which was based on the second hypothesis in this study and previous studies (Kwok et al., 2004; Ferrari et al., 2004; Eklund and Cardenosa, 1992; Bassett et al., 1993; Heywang-Kobrunner et al., 2001; Rampun et al., 2017b). The I^{Lr}_b located in the top row in Fig. 6 shows it intersects both x- and y-axes, whereas the I^{Lr}_b located in the bottom row in Fig. 6 shows it intersects only the y-axis. To account for these two options, two post-processing approaches are proposed in the following subsections.

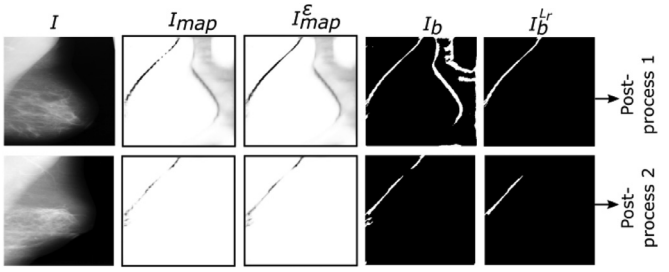

Fig. 6. A graphical representation for the flow chart in Fig. 5. Note that the I^{Lr}_b was an image that contained the longest region with $20° \leq \theta \leq 90°$.

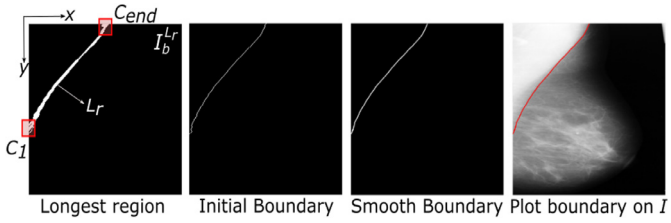

Fig. 7. An overview for post-processing option one. The process starts from left to the right.

4.3.1. Post-processing option one

Fig. 7 shows an overview of the first post-processing option. C_{end} was determined by taking a pixel that has the smallest and largest y and x coordinate values, respectively. C_1 was determined by taking a pixel that has the smallest and largest x and y coordinate values, respectively. The initial boundary (C_b) contains the furthest pixel of each row in L_r from the y-axis. We applied a simple "moving average" on C_b to get the final boundary C_f. Finally, to get the pectoral muscle region, we created a binary mask and filled in the region inside C_f (on the left side) by replacing each pixel with '1'.

4.3.2. Post-processing option two

Fig. 8 shows an overview of the second post-processing option. Firstly, we determined C_1 and C_{end}, then get y_u and y_b by shifting 20 pixels of y_z to the left (y_u) and right (y_b) horizontally to identify associate contour candidates. Next, we removed false positives (yellow circle in image 8.2) by retaining the first connected pixels found in each column of the image and all remaining pixels are

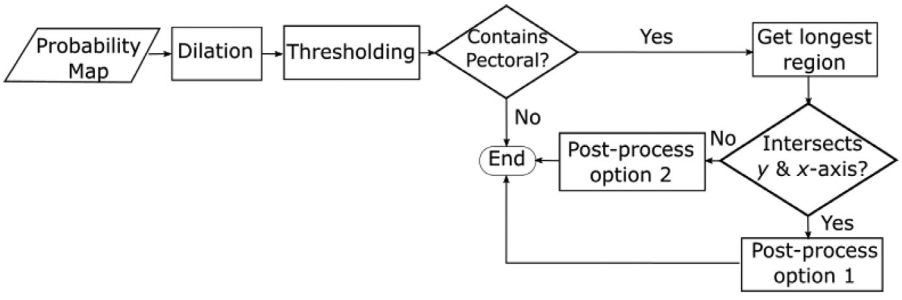

Fig. 5. An overview of the post-processing approach to estimate the actual pectoral muscle boundary.

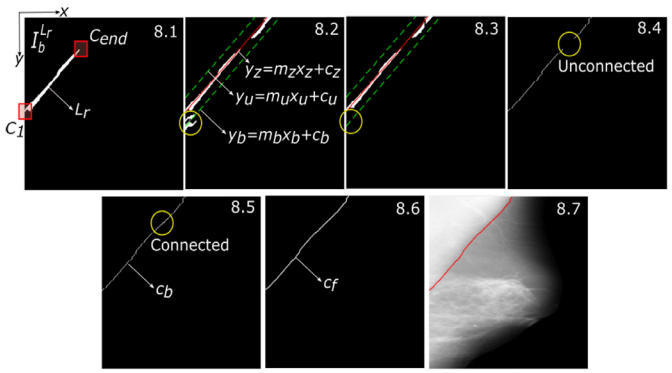

Fig. 8. An overview for post-processing option two.

deleted. Subsequently, we determinded C_b by taking the furthest pixel located within y_u and y_b followed by connecting a gap (or gaps) between contours using the straight line (red line in image 8.3) interpolation technique. We relocated each point based on the highest probability within a small 5×5 neighbourhood in the probability map. Finally, we applied the "moving average" technique on C_b to get C_f (see image 9.6). Similar to the first post-processing step, to segment the pectoral muscle region we created a binary mask and filled in the region on the left side of C_f by replacing each pixel with '1'.

5. Experimental results

The proposed method was evaluated based on 1087 MLO mammograms (of which 1079 mammograms contained a pectoral muscle boundary) from four different datasets: MIAS (Suckling et al., 1994), InBreast (Moreira et al., 2011), BCDR (Lopez et al., 2012) and CBIS-DDSM (Lee et al., 2017). Note that the segmentation evaluation is based on the pectoral muscle region obtained at the end of the post-processing step.

To evaluate the performance of the proposed method we used the following metrics: the Jaccard ($\ddot{J}$) coefficient, which measureed the ratio of the number of overlapping elements to the number of union elements from segmented region (A) of the proposed method and ground truth region (B); the Dice ($\ddot{D}$) coefficient, which measured the ratio of twice the common number of overlapping elements to the total number of elements from both A and B; and accuracy, which measured the ratio of the number of pixels classified correctly to the total number of pixels. Furthermore, we used sensitivity ($\ddot{S}$) and specificity ($\bar{S}$) to measure the proportions of true positives (TP) and true negatives (TN), respectively, and correctness ($\ddot{C}$), which measured the ratio of the number of true positives to the false positives (FP) and true positives. Finally, true positives, true negatives, false negatives and false positives rates are denoted as TPR, TNR, FNR and FPR, respectively. Further details of these metrics can be found in Rampun et al. (2017b).

5.1. Quantitative results

Table 3 shows the average quantitative results for the MIAS, InBreast, BCDR and CBIS-DDSM databases, which indicated that the proposed method yields very good results across the different evaluation metrics. The best results are obtained when estimating the pectoral muscle region in the BCDR database, with $\ddot{J} = 96.9\%$ and $\ddot{D} = 98.8\%$ and a small $FPR = 0.1 \pm 0.8$.

For the MIAS database, we achieve $\ddot{J} = 94.6\%$ and $\ddot{D} = 97.5\%$, whereas for the InBreast database the proposed method produces values of $\ddot{J} = 92.6\%$ and $\ddot{D} = 95.6\%$. On a larger number of images (CBIS-DDSM) the Jaccard and Dice coefficients obtained are

Table 3
Average quantitative results from MIAS, BCDR, InBreast and CBIS-DDSM databases. All metrics are presented as percentages with standard deviation ($\% \pm \sigma$).

Metric	MIAS	InBreast	BCDR	CBIS-DDSM	Mean
$\ddot{J}$	94.6 ± 9.8	92.6 ± 10.6	96.9 ± 4.1	95.1 ± 9.4	94.8 ± 8.5
$\ddot{D}$	97.5 ± 7.5	95.6 ± 8.4	98.8 ± 2.2	98.1 ± 7.1	97.5 ± 6.3
$\ddot{A}$	99.3 ± 1.4	99.6 ± 2.2	99.9 ± 1.1	99.5 ± 1.3	99.6 ± 1.5
$\ddot{S}$	98.2 ± 7.6	95.2 ± 8.6	99.6 ± 1.4	98.3 ± 7.6	97.8 ± 6.3
$\bar{S}$	99.5 ± 1.2	99.8 ± 1.8	99.9 ± 1.0	99.6 ± 1.4	99.7 ± 1.4
$\ddot{C}$	96.5 ± 6.7	96.3 ± 9.2	99.7 ± 1.3	97.2 ± 6.5	97.4 ± 5.9
FPR	0.6 ± 1.8	0.3 ± 2.1	0.1 ± 0.8	0.4 ± 0.6	0.3 ± 1.3
FNR	3.2 ± 2.9	5.7 ± 6.5	1.9 ± 1.3	3.8 ± 2.5	3.6 ± 3.3

$\ddot{J} = 95.1\%$ and $\ddot{D} = 98.1\%$, respectively. Regarding $\ddot{S}$, the method achieves at least 95.2% with an average $\ddot{S} = 97.8\%$ for the four different databases. To summarise the results, on average our approach yields $\ddot{J} > 94\%$, $\ddot{D} > 97\%$, $\ddot{A} > 99\%$, $\ddot{S} > 97\%$, $\bar{S} > 99\%$ and $\ddot{C} > 97\%$ across various datasets, which is comparable with the existing methods. Furthermore, the method also produces small $FPR = 0.3 \pm 1.3$ and $FNR = 3.6 \pm 3.3$, which indicates that the majority of the estimated pectoral muscle regions were very close to the ground truth. Most of the pectoral muscle boundaries in the InBreast database were more complex and obscured than in the other datasets, which was probably the reason of the lower $\ddot{J}$. In contrast, the pectoral muscle contours in the BCDR database were mostly visible and less complex, and thus the evaluation results are higher. Note that the standard deviations for the MIAS, InBreast and CBIS-DDSM datasets were much larger than for the BCDR dataset due to a few cases that are over- or under-segmented. Overall, the experimental results indicated that the proposed CNN model is robust and not limited to features from either SFM or FFDM only. In terms of the ability to generalise across different datasets/images types, Table 3 shows that promising quantitative results were achieved in each individual dataset with very small FPR and FNR when training the network using a mixture of SFM and FFDM images. To further evaluate its generalisation, we conducted an additional experiment by training the proposed CNN based on FFDM images only (e.g. InBreast and BCDR datasets) and tested it on SFM images (e.g. MIAS dataset only). We achieved the following results: $\ddot{J} = 91.1 \pm 10.5$, $\ddot{D} = 95.4 \pm 9.6$, $\ddot{A} = 98.9 \pm 2.2$, $\ddot{S} = 96.5 \pm 8.5$, $\bar{S} = 99.1 \pm 2.1$, $\ddot{C} = 93.5 \pm 10.6$, $FPR = 0.8 \pm 2.1$ and $FNR = 3.8 \pm 3.9$. These results show that the proposed CNN can find a "contour-like" object regardless of the type of images (e.g. FFDM or SFM) which illustrates the ability of the proposed method to generalise across different datasets. The pectoral muscle segmentation pipeline takes approximately 2.5 ± 1.2 s per image.

5.2. Qualitative results

Fig. 9 shows examples of estimated pectoral muscle boundaries from images of the different datasets used in this study.

It can be observed that the proposed method can estimate the pectoral muscle boundary under a variety of different conditions.For example, images 9.3, 9.7, and 9.9 show that the *axillary fold* appeared in the pectoral muscle region, which could lead to incorrect estimation of the pectoral muscle boundary due to more than one estimated contour in the I_{map}. In fact, in image 9.7 and 9.8, the modified HED ignores the *axillary fold* boundary, resulting in one single boundary in the I_{map}. Nevertheless, the proposed method handled the majority of cases based on the hypothesis that the pectoral muscle tends to have the longest length. On the other hand, images 9.2, 9.4 and 9.10 showed that the lower part of the pectoral muscle contour was obscured, but the proposed

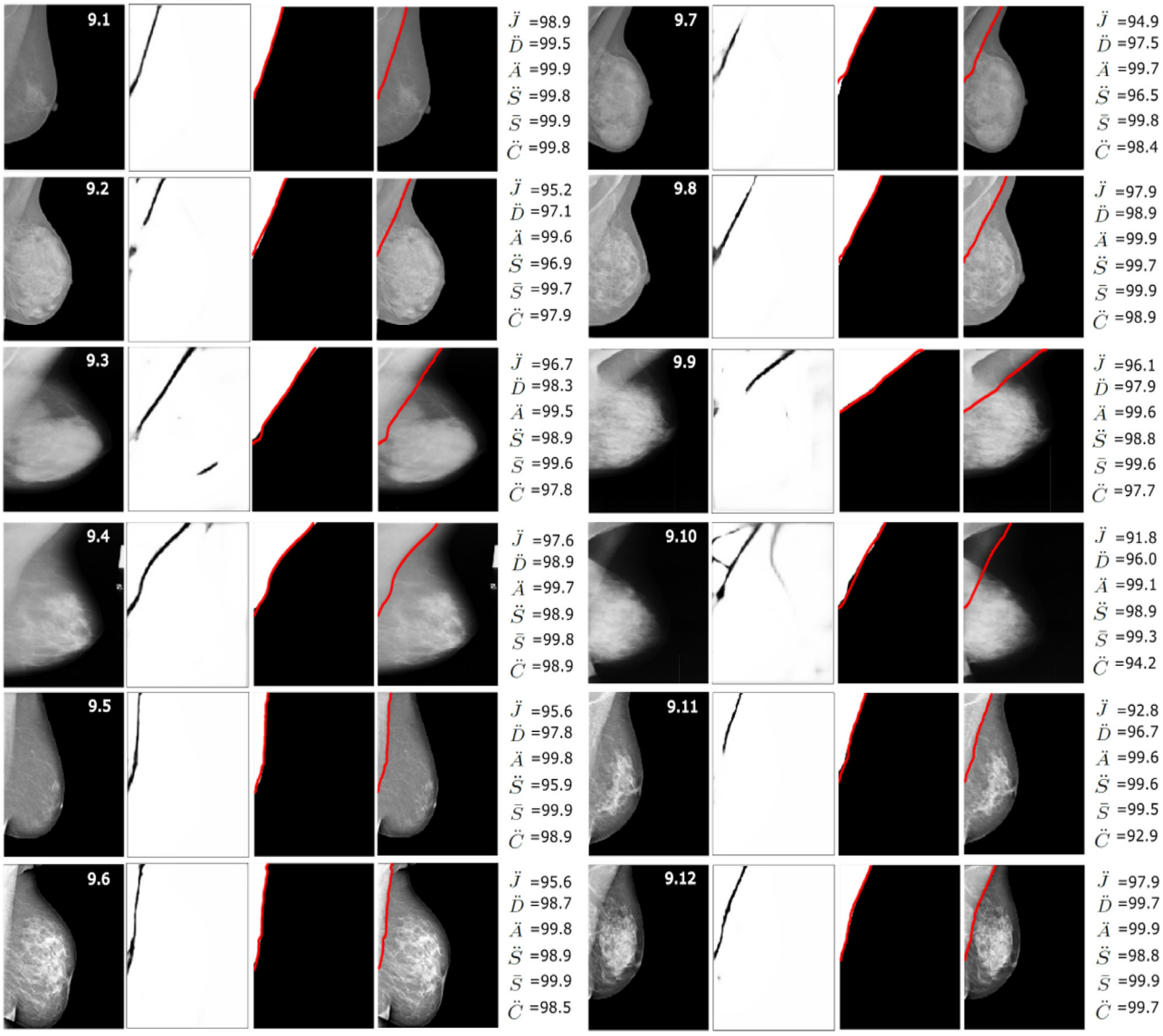

Fig. 9. Examples of segmentation results (red line) with their corresponding ground truth. From left (first and sixth columns) to right this shows the original image, probability map, C_f superimposed on the ground truth image, C_f superimposed on the original image and evaluation results. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

network delineated it as shown in each of their corresponding I_{map}. In image 9.12, the middle part of the pectoral muscle contour was obscured due to the overlapping fibro-glandular tissues from the breast region. However, this part is delineated in I_{map}, resulting in high quantitative results across different evaluation metrics. In cases where a few parts of the estimated contour were disconnected, such as in the I_{map} from images 9.5, 9.6 and 9.11, the post-processing step played an important role in connecting these contours. Many of the cases with clear or obvious pectoral muscle contours, such as in image 9.1, tended to have a well defined contour in the I_{map}.

5.3. Validation accuracy and loss curves

Fig. 10 shows an example of the validation accuracy and loss curves for one of the networks trained on BCDR, InBreast and CBIS-DDSM datasets. It can be observed that constant accuracies were achieved on both background and foreground (pectoral boundary) from the 50th to the 100th iterations, which is similar in this regard to the value of the validation loss function.

6. Discussion

Fig. 11 shows segmentation results for four cases representing the main challenges explained in Section 1 when finding the pectoral muscle boundary: invisible boundary, presence of the *axillary fold*, complex shape and obscured boundary. In image 11.1 the pectoral muscle boundary is invisible due to dense tissue overlapping with the pectoral muscle region. It can be observed that after performing a thresholding operation on I^{ϵ}_{map} and the post-processing step, we found a small region (possible contour) which was invisible in the original image. All candidate contours were connected using the post-processing, resulting in C_f as shown in the fourth (ground truth) and fifth (original image) columns and giving $\ddot{J} = 90.3\%$ and $\ddot{D} = 94.9\%$. For image 11.2 it can be observed that the I^{ϵ}_{map} generated showed an accurate initial estimate for the pectoral muscle contour. The post-processing technique retained the longest contour and connected it with the contour located within y_b and y_z, which produces an accurate estimate with $\ddot{J} = 98.2\%$ and $\ddot{D} = 99.1\%$. In this case the proposed method was not affected by the presence of multiple *axillary folds*. For

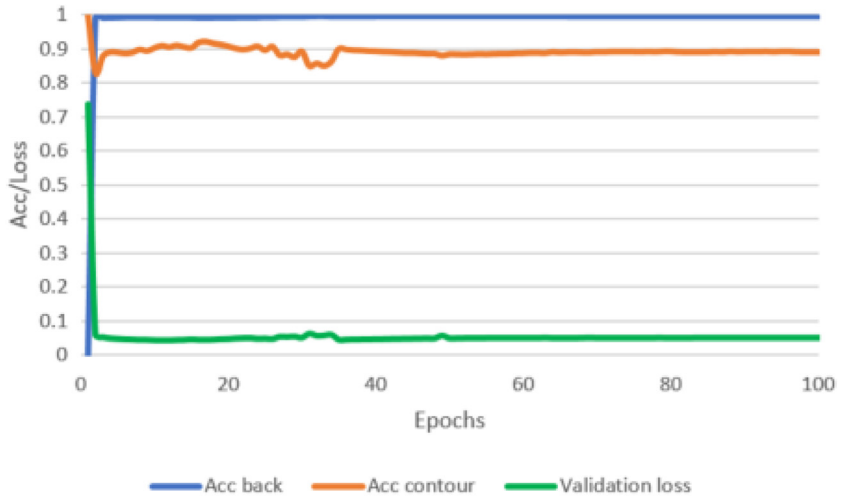

Fig. 10. Validation accuracy and loss curves of the proposed network during training for an example network trained with the BCDR, InBreast and CBIS-DDSM datasets.

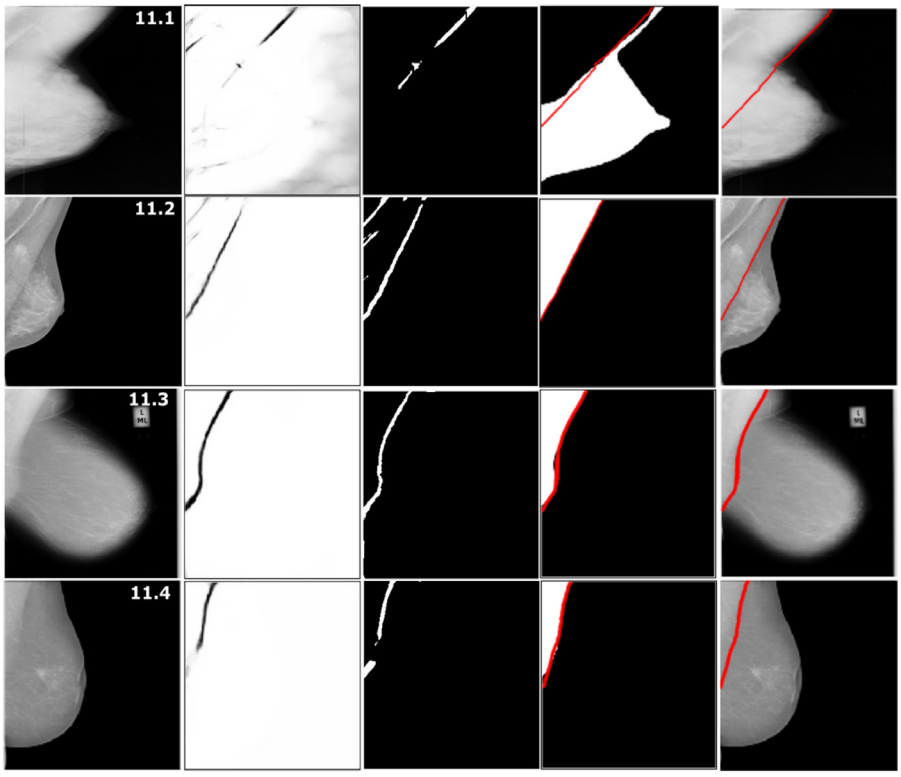

Fig. 11. Segmentation results for cases shown in Fig. 1. The second and the third column are the I^{ϵ}_{map} and I_b, respectively. From left to right this shows the original image, probability map, C_f superimposed on the graound truth image, and C_f superimposed on the original image.

image 11.3, where the shape of the boundary is more complex, a high probability distributed along the contour can be observed; by processing I_b with the simple post-processing step, evaluation results achieve $\dot{J} = 91.2\%$ and $\ddot{D} = 95.3\%$. When the pectoral muscle contour was obscured as shown in image 11.4, the proposed method manages to find the lower and upper parts of the contour. By connecting these contours using the post-processing technique, the estimated C_f has evaluation results of $\dot{J} = 90.6\%$ and $\ddot{D} = 95.1\%$.

6.1. Comparative study

A direct comparison is difficult due to the differences in evaluation techniques and the number of images employed. However, for comparison, we have summarised our results and present some of the existing methods in the literature in Tables 4 and 5. Note that we cover only those studies based on the datasets used in our study. Although there are many methods developed in the literature, the majority of them were evaluated qualitatively by expert radiologists (Kwok et al., 2004; Chen and Zwiggelaar, 2010) or have been evaluated using their own private datasets. It can be observed in Table 4 that our proposed method outperformed our previous method (Rampun et al., 2017b) across three datasets (MIAS, BCDR and InBreast) in all evaluation metrics. The main reason for this was that our previous model considered only intensity and geometry information, whereas the proposed approach in this study took texture (both local and global) and the geometry information into account, hence making it more flexible and robust. Furthermore, like the majority of the methods in the literature our first

Table 4
Jaccard and Dice qualitative comparison. The * indicates that the evaluation metrics were computed based on the number of pixels overlapping with the entire image.

Authors	Dataset (#)	Results	
		Jaccard (%)	Dice (%)
Proposed method	MIAS (All)	94.6	97.5
	InBreast (All)	92.6	95.6
	BCDR (100)	96.9	98.8
	CBIS-DDSM (457)	95.7	98.1
Rampun et al. (2017b)	MIAS (All)	92.1	97.8
	InBreast (All)	84.6	89.6
	BCDR (100)	85.8	91.9
Oliver et al. (2014)	MIAS (149)	–	83
Taghanaki et al. (2017)*	MIAS (298)	97	98
	InBreast (197)	97	98.5
	IRMA (All)	96.6	98.1

Table 5
True positives rate and true negatives rate qualitative comparison.

Authors	Dataset (#)	Results	
		FPR (%)	FNR (%)
Proposed method	MIAS (All)	0.60	3.20
	InBreast (All)	0.30	5.70
	BCDR (100)	0.10	1.90
	CBIS-DDSM (457)	0.40	3.80
Vikhe and Thool (2017)	miniMIAS (All)	0.93	5.07
Chen et al. (2015)	miniMIAS (All)	1.02	5.63
Liu et al. (2014)	miniMIAS (All)	3.34	4.57
Yoon et al. (2016)	miniMIAS (All)	4.51	5.68
Bora et al. (2016)	miniMIAS (200)	1.56	2.83
Ferrari et al. (2004)	miniMIAS (84)	0.58	5.77
Camilus et al. (2010)	MIAS (84)	0.64	5.58

geometry model presented in Rampun et al. (2017b) was developed based on the assumption that the pectoral muscle was either a straight line, concave, convex or a combination of these. Although in general this assumption was correct, the model developed might be restricted to certain shapes. In contrast, deep learning did not make such assumptions, which made the model presented in this work more flexible and robust. Oliver et al. (2014), whose method used an atlas, intensity and texture information in probability functions, achieved much lower results ($\ddot{D} = 83\%$) based on 84 images in the MIAS dataset. Taghanaki et al. (2017) achieved over 96% $\ddot{D}$ and $\ddot{J}$ across three datasets. However, it should be noted that their results were based on the number of pixels overlapping with the entire image. In our case, we calculated both metrics based on the number of pixels overlapping with the pectoral muscle region only. Moreover Taghanaki et al. (2017) did not use all images from the MIAS and InBreast datasets.

In terms of the false negative and false positive rates obtained with the MIAS dataset, our method produced $FNR = 3.2\%$ and $FPR = 0.6\%$, respectively, which indicated that we quantitatively outperform recent studies (Vikhe and Thool, 2017; Chen et al., 2015; Yoon et al., 2016; Liu et al., 2014). Although the studies of Camilus et al. (2010) and Ferrari et al. (2004) reported small false positives, their proposed methods produced large false negatives of 5.58% and 5.77%, respectively. In a qualitative evaluation, Kwok et al. (2004) used a five level assessment scale (exact, optimal, adequate, sub-optimal and inadequate) and reported 83.9% of the segmentations to be adequate or better. Chen and Zwiggelaar (2010), whose method was tested based on 240 mammograms from the EPIC (European Prospective Investigation on Cancer) dataset and used a four level assessment (accurate, nearly accurate, acceptable and unacceptable), reported that 93.5% of their pectoral segmentations are at least acceptable.

6.2. Visual comparison

Fig. 12 shows visual comparisons with some of the existing studies in the literature taken from the MIAS and InBreast datasets. The segmentation results of the other studies were taken from the authors" papers. We have also presented a quantitative comparison for a few cases where numerical results were available from the authors" papers (Kwok et al., 2004; Ferrari et al., 2004; Rampun et al., 2017b). Note that for improved visual representation, we have coloured the estimated pectoral muscle boundaries from the authors' papers. For image *pdb151lx* it can be observed that the proposed method quantitatively outperforms our previous method (Rampun et al., 2017b) by at least 10% for both metrics. For this image the methods developed by Kwok et al. (2004) and Chen et al. (2015) under segmented the lower part of the pectoral muscle region. The method of Kwok et al. (2004) under estimated the boundary and was reported as inadequate by their expert radiologist. Rampun et al. (2017b) under segmented the lower part of the pectoral muscle resulting in $\ddot{J}$ and $\ddot{D} < 10\%$, lower than with our proposed method.

For *pdb065lm*, the estimated pectoral boundary of Kwok et al. (2004) was assessed as 'inadequate' by an expert radiologist. In comparison, quantitative results of Rampun et al. (2017b) reported $\ddot{J} = 86.7\%$ and $\ddot{D} = 92.9\%$, whereas our method produces $\ddot{J} = 90.6\%$ and $\ddot{D} = 95.9\%$. For *pdb112rl, r3* reported $FNR = 16.2\%$ and $FPR = 2.3\%$ and our proposed method yields $FNR = 1.6\%$ and $FPR = 0.5\%$. In fact, our proposed method estimates the pectoral muscle boundary closer to the ground truth ($\ddot{J} = 92.6\%$ and $\ddot{D} = 96.2\%$) than the method in (Rampun et al., 2017b) ($\ddot{J} = 91.0\%$ and $\ddot{D} = 95.3\%$). In contrast, Ferrari et al. (2004) and Rampun et al. (2017b) reported good results for a case where the pectoral muscle contour was well defined, as can be observed in *pdb003ll*. For the case *pdb170ls*, the method of Kwok et al. (2004) failed to find the contour boundary due to dense tissue overlapping with the pectoral muscle boundary. Our proposed method outperforms the results in Rampun et al. (2017b) by at least 7% and 4% for metrics $\ddot{J}$ and $\ddot{D}$, respectively. For *pdb028rl*, where 'blotch like' tissue appeared on the contour, the method proposed in Ferrari et al. (2004) and our approach estimate the pectoral muscle boundary very close to the ground truth, whereas with the technique presented in Rampun et al. (2017b) the upper part of the pectoral muscle boundary is over estimated.

For a comparison with recent studies in the literature, we use images *pdb156rl, pdb183ll, pdb277lm* (MIAS), *InBreast1* and *InBreast2* (InBreast). One of the major limitations of the current methods in the literature (Kwok et al., 2004; Ferrari et al., 2004; Taghanaki et al., 2017; Bora et al., 2016; Vikhe and Thool, 2017; Chen et al., 2015) was their inability to deal with complex curves due to the geometrical architecture of the model. This can be seen in image *InBreast1* where both of the methods of Taghanaki et al. (2017) and Rampun et al. (2017b) failed to estimate the pectoral boundary close to the ground truth, whereas our proposed method achieves $\ddot{J} = 89.8\%$ and $\ddot{D} = 94.6\%$. In a case of multiple layered pectoral muscle (*InBreast2*), the method proposed in this study yields $\ddot{J} = 93.5\%$ and $\ddot{D} = 96.6\%$, which clearly outperforms our previous method (Rampun et al., 2017b), whereas the method of Taghanaki et al. (2017) over-segmented the upper end of the pectoral region. For *pdb277lm* Bora et al. (2016) over-segmented the lower part of the pectoral muscle region and our previous method (Rampun et al., 2017b) outperforms the proposed method in this study (one of the few cases where this happened). For images *pdb183ll* and *pdb156rl*, the method explained in this paper yields more accurate segmentation results than the methods developed by Vikhe and Thool (2017), Chen et al. (2015) and Rampun et al. (2017b).

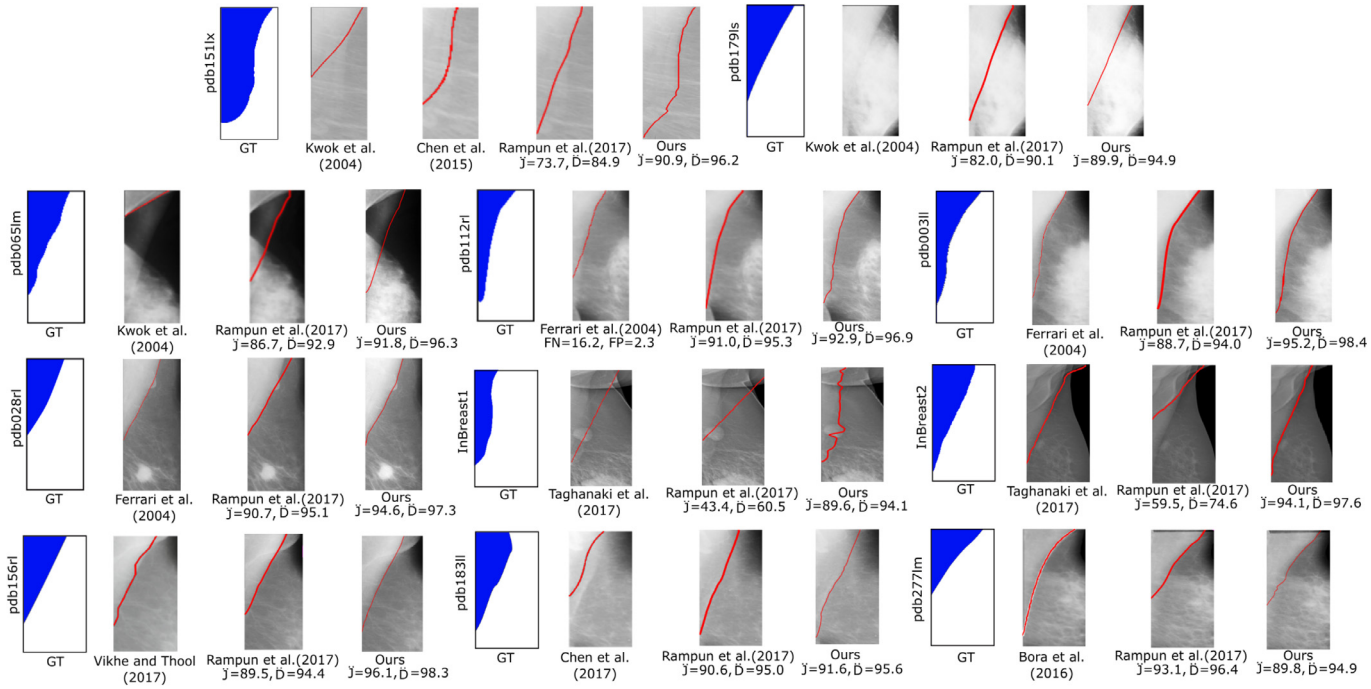

Fig. 12. Qualitative and quantitative comparisons with some of the current studies in the literature. The image with a blue region represents the ground truth (GT) where the blue area is the pectoral muscle region. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

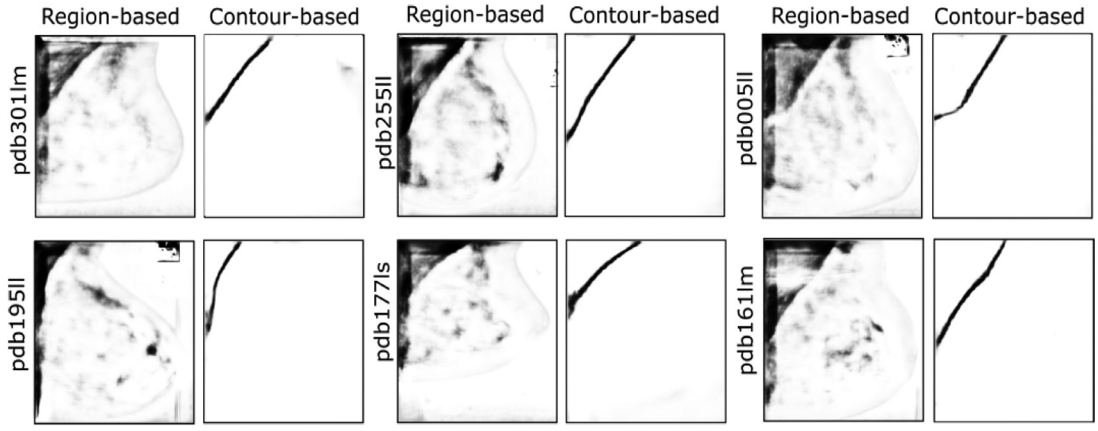

Fig. 13. A visual comparison of the probability maps using region-based versus contour-based approaches taken from the MIAS database.

6.3. Learning region's structure

Fig. 13 shows a comparison of the probability maps obtained when training the proposed CNN with the whole pectoral muscle region versus the maps extracted using the proposed contour-based approach. It can be observed that learning the region's structure tended to produce more false positives. Fig. 14 shows example patches extracted from different regions in the mammogram. We used a 3D mesh to visualise each of the patches. It can be qualitatively assessed that P5, P6 and P7 are dissimilar in comparison to the other patches. Learning directly the region's structure (as performed by the studies of Dubrovina et al. (2016) and Moeskops et al. (2016)) yielded more false positives because some parts of the pectoral muscle were similar to the breast region. For example, P1 (a patch from the pectoral muscle) was similar to P8 (a patch from the breast region). This is also the case for P2 and P4. In contrast, P5, P6 and P7 (patches extracted from the pectoral muscle boundary) were quite distinct, which made our predictive model more accurate in finding the muscle boundary.

6.4. Effects of post-processing

Fig. 15 shows visual comparison of the proposed post-processing method against Canny (Canny, 1986), Prewitt (Parker, 1997) and Sobel (Parker, 1997) operators when applied to the probability map. It can be observed that the post-processing method made a substantial contribution to the final results. The Canny operator (Canny, 1986) tended to capture more details, which could lead to a more complicated post-processing step. Although the Prewitt (Parker, 1997) and Sobel (Parker, 1997) operators captured fewer details of the probability map, further post processing steps were still required to connect and remove unwanted contours.

From the examples shown in Fig. 15, all three operators (Canny, Prewitt and Sobel) were insufficient in finding the actual pectoral muscle boundary and it was essential to use our proposed post-processing steps to: (a) remove false positives (see step three in Section 4.3.2), (b) select the pectoral contour in a case of multiple contours detected in the probability map, (c) recover the missing parts of the contour in the probability map, (d) connect the

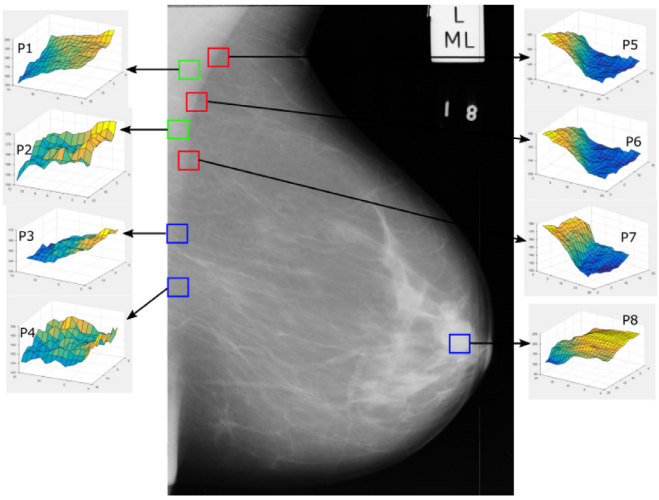

Fig. 14. A 3D mesh visualisation for patches extracted from the breast region (blue boxes), pectoral muscle (green boxes) and boundary regions (red boxes). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

missing lines or pixels of the contour and (e) smooth the final estimated pectoral muscle boundary.

6.5. Effects of threshold values

Fig. 16 shows the performance evaluation of the proposed method using different threshold values when extracting initial candidates from the I_{map}. The metrics $\ddot{J}$ and $\ddot{D}$ were chosen as evaluation metrics for all datasets. The training and testing sets are as described in Table 2 where each database was tested on a round robin basis. For this purpose, we tested 21 different threshold values from 0.1 to 0.7 with an interval 0.03. It can be observed that results for both metrics were consistent from 0.1 to 0.58. The evaluation results across different datasets decreased when using a threshold value larger than 0.58. As can be observed, the performance of the proposed method reduced after a threshold value of 0.58. Choosing a higher threshold value (e.g. 0.8 or 0.9) further deteriorated the performance due to loss of boundary/important cues in the binary image. Selecting a maximum threshold value (e.g. 1) removed all boundaries hence producing an empty binary image. On the other hand, choosing a smaller interval value (e.g. 0.01) did not make a significant difference in terms of performance. This is because the effect of a small interval value is only a small number of pixels resulting in very similar binary images.

6.6. Visual heat-maps comparison

Fig. 17 shows visual likelihood map comparisons between the original HED and the proposed network (modified HED). It can be observed that our network was more precise in locating the boundary of the pectoral muscle, whereas the original HED can only approximately estimate the location. For example, regions with high probability of being a contour (dark red) were larger in the original HED heat-maps than in the modified HED heat-maps, which made it more difficult to estimate the pectoral boundary in the post-processing step. Moreover, this suggested that the number of false positives (the number of pixels with dark red colour) in the heat-maps generated by the original HED is much higher. In contrast, only pixels (and their neighbouring pixels) located along the contour have high probability in the heat-maps generated by our proposed network. This can be explained when the original HED captured more finer and coarser details, yielding a coarser side-output in each convolution layer. As a result, the original HED network generated a blurry/coarser final output when fusing all the side-outputs from each convolution layer.

6.7. HED versus modified HED

This section presents a quantitative comparison between the performance of the original HED and our proposed network. Table 6 shows the experimental results across different metrics used in this study. The resulting probability maps produced by both networks fed into the post-processing pipeline developed in our study. These quantitative results clearly show that our proposed network outperformed the original HED. Note that the standard deviations produced by the original HED are much higher due to cases where the detected boundary was far away from the actual boundary. Fig. 18 shows some examples of probability maps produced by both networks. It can be observed that (i) the

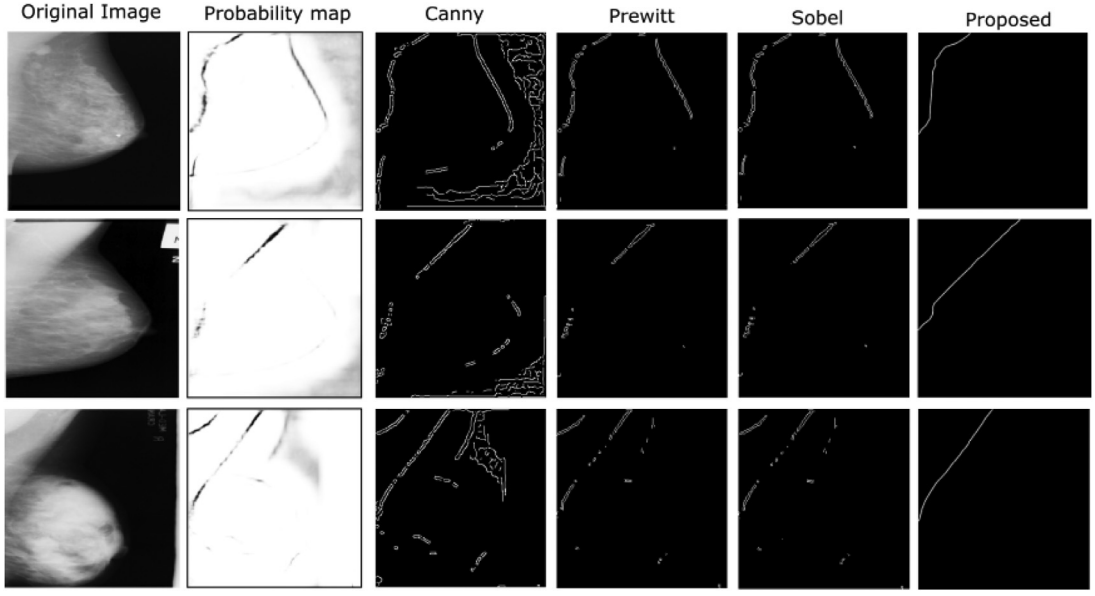

Fig. 15. A visual comparison between contour detection using Canny, Prewitt, Sobel and the proposed post processing method.

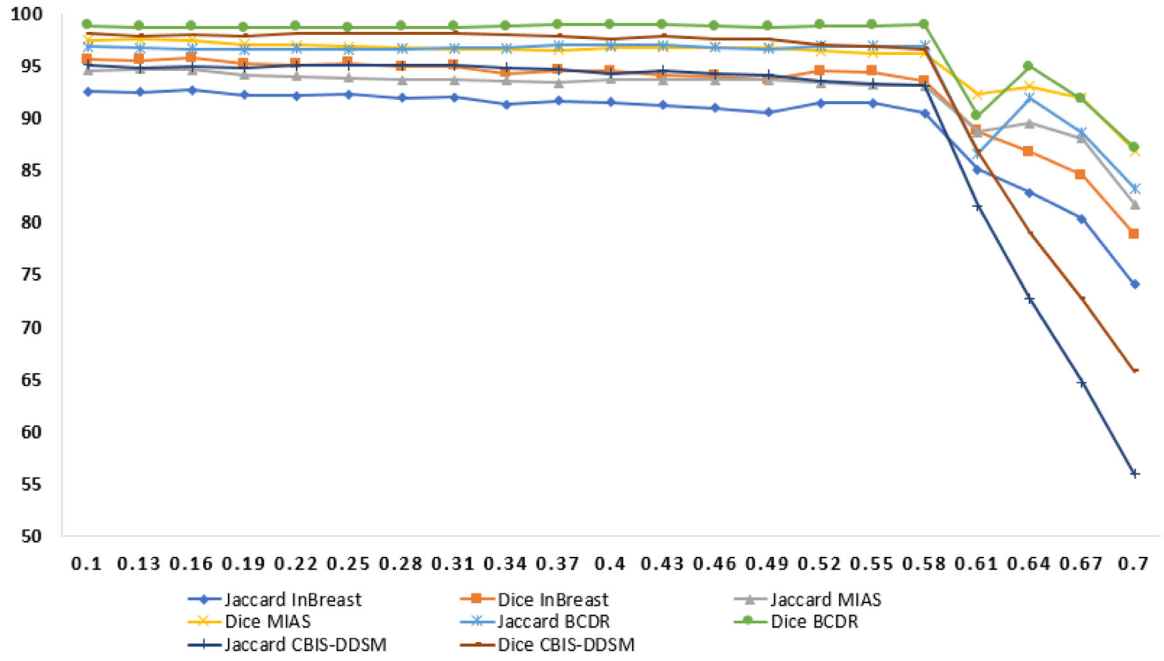

Fig. 16. Performance evaluation using different threshold values for the $\ddot{J}$ and $\ddot{D}$.

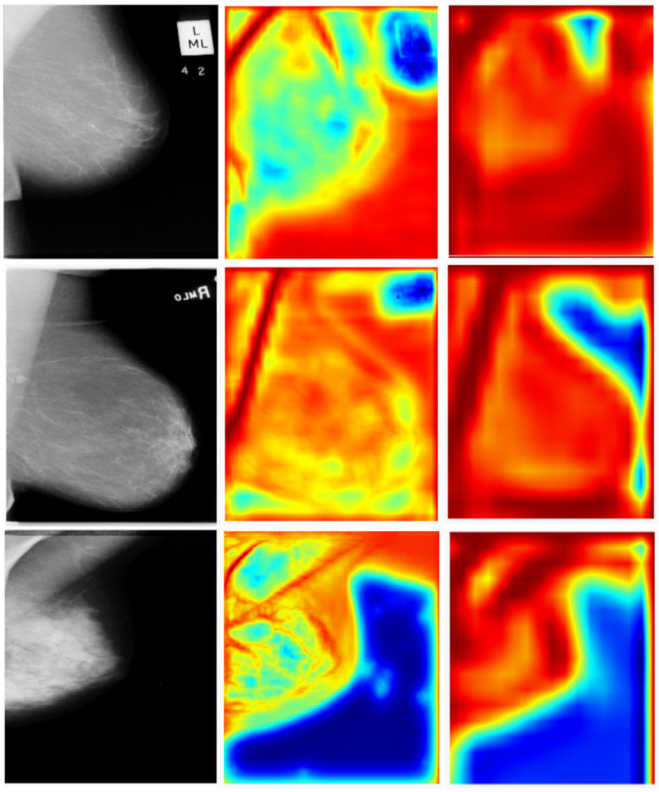

Fig. 17. Visual heat-maps comparison between the modofied HED (second column) and the original HED (third column). Dark red colour indicates higher probability of being an object (e.g. a contour). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

original HED network was unable to find the pectoral boundary when it is obscured (e.g. first and second rows), (ii) the original HED tended to produce a jagged boundary whereas our proposed network produced a smooth boundary (e.g. third and fourth row),

Table 6
Quantitative comparison between the original HED and our proposed network. All metrics are presented as percentages with standard deviation ($\% \pm \sigma$).

Metric	HED (Xie and Tu, 2015)	Proposed network
$\ddot{J}$	79.3 ± 11.5	96.9 ± 4.1
$\ddot{D}$	84.1 ± 9.3	98.8 ± 2.2
$\ddot{A}$	85.5 ± 8.4	99.9 ± 1.1
$\ddot{S}$	86.2 ± 8.6	99.6 ± 1.4
$\bar{S}$	87.9 ± 8.2	99.9 ± 1.0
$\ddot{C}$	86.4 ± 9.3	99.7 ± 1.3
FPR	8.9 ± 9.1	0.1 ± 0.8
FNR	10.9 ± 9.3	1.9 ± 1.3

(iii) the original HED was unable to find accurate location of the pectoral boundary when it overlaps with breast tissue (e.g. sixth row), (iv) the original HED under estimated the locations of the pectoral muscle boundaries in most cases (think boundary), and (v) the proposed network produced more accurate location, clearer probability map and more robust.

6.8. Choice of evaluation metrics

The metrics used to evaluate the performance of our proposed method are standard metrics used in most studies in the literature. We chose these metrics to enable us to make a quantitative comparison with existing studies. Many studies used visual evaluation by a radiologist which is subjective (e.g. perfect, accurate, adequate and poor). Some studies used only *FPR* and *FNR* or $\ddot{D}$ and $\ddot{J}$ or $\ddot{A}$ or $\ddot{S}$. We used as many metrics as possible in our study so that we can compare the performance of our study across different studies available in the literature. The $\ddot{D}$ and $\ddot{J}$ metrics are more sensitive in comparison to the other metrics such as $\ddot{A}$ or $\ddot{S}$. However, these metrics are less sensitive to visual error. Segmentation results of the other studies (e.g. studies of Rampun et al. (2017b) and Taghanaki et al. (2017)) also qualitatively show that these metrics are less sensitive to visual error.

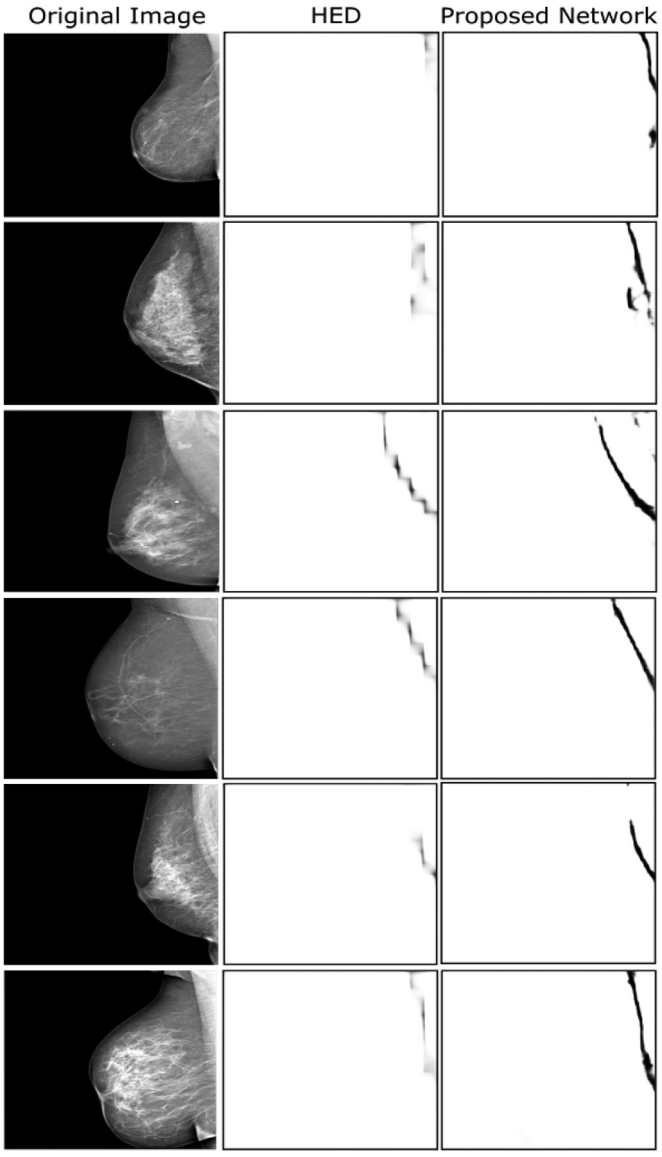

Fig. 18. A visual comparison between probability maps produced by the original HED and our proposed network.

6.9. Cross validation

Quantitative results presented in this paper represent a single training instance. We did not perform a cross-validation exercise during the training and validation phase mainly due to (i) the number of training images is sufficient (in our case over 2200 to 3500), hence cross validation is unnecessary, (ii) cross-validation is extremely time consuming. In our case, a single training instance takes 7 h on an Intel Xeon E5-1650 v3 processor, using Nvidia Corporation's Deep Learning GPU Training System (DIGITS) based on Caffe, with a Nvidia's Quadro M6000 (12Gb) graphics card. Doing cross-validation, for example 3-fold cross validation of 10 runs in each fold, would be $7 \times 30 = 210$ h, which is approximately 9 days. If we repeat this for all four datasets on a round robin basis it will take 36 days and (iii) even without cross-validation we already achieve very promising results across different datasets.

6.10. Up-sampling resulting contour

Once we find the boundary, which is a set of x- and y-coordinates, it can up-sample using an image up-sampling technique. For example, if the original image is down sampled by a factor of 4 then each pectoral boundary coordinate should be up sampled by a factor of 4 so that a close boundary can be projected on the original image (similar to Oliver et al. (2014)). In other words, the coordinates of the resulting contours can be projected on an original space based on the ratio between the original and down sampled resolutions. Obviously, the projection would not be 100% accurate, but this should not affect the breast density estimation greatly as the majority of dense tissue appears within the mamae corpus (or mammary gland) rather than within the pectoral muscle boundary (Rampun et al., 2018a; 2017a). This is similar to other tasks such as microcalcification or lesion detection as they dont usually appear close to the pectoral muscle boundary (Rampun et al., 2018c).

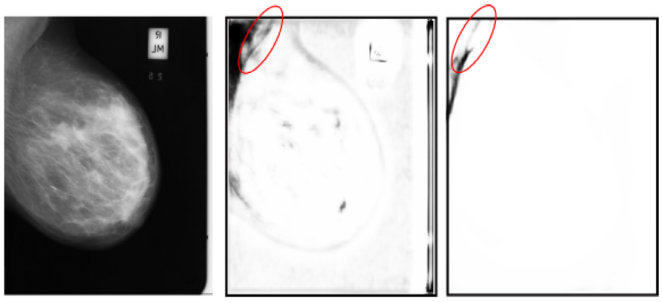

Fig. 19. Illustration of combining probability maps generated by region-based (middle) approach and contour-based approach (right).

6.11. Study limitations and future work

The main limitations of our study are (i) firstly, since all images were down sampled to 256×256, direct quantitative comparison to studies which have used a full image resolution is difficult. However, there are many previous non-CNN methods which have down-sampled the original size of the image and made quantitative evaluation based on the down-sampled image, with several examples are the studies of Mustra and Grgic (2013), Kwok et al. (2004), Oliver et al. (2014) and Rampun et al. (2017b). Secondly (ii) image down sampling may affect the actual representation and accuracy of the pectoral muscle boundary in a full image resolution. However down sampling is necessary to accommodate memory and processing time requirement.

Fig. 19 illustrates a possible future direction of this work. Probability maps generated by the region-based approach may contain additional information and could be used as a 'secondary reference' to find contours which are invisible in the I_{map} generated by the contour-based approach. For example, approximately 50% (red ellipse) of the contour in the right image was invisible. However, this path could be found in the middle image (probability map generated by the region-based approach). Our preliminary observation suggested that region-based approaches tend to generate many false positives, which affects the post-processing step. However, if these could be reduced, it will have the potential to be a secondary source of information when retrieving invisible contour paths in I_{map}. Another possible future direction of our study would be to generalise the network for generic object segmentation purposes in images.

7. Summary and conclusions

In summary, we have presented a contour based approach for breast pectoral muscle segmentation in mammograms inspired

by the Holistically-Nested Edge Detection (HED) network of Xie and Tu (2015), automatically learning rich hierarchical image representations that were essential to resolve ambiguities in edge and object boundary detection. Once the probability map (I_{map}) is generated, we first processed it using a morphological operation to connect any small gaps between contours to generate I^{ϵ}_{map}. Subsequently, we applied a thresholding operation on I^{ϵ}_{map} to obtain a binary image (I_b). Finally, I_b was post-processed based on the axes intersections of the longest region (L_r) in I_b and a simple 'moving average' was employed to smooth the final contour (C_f). The main attractive feature of the proposed method is the fact that we treat the segmentation problem as an object detection task by training our network to recognise 'contour-like' objects in a mammogram rather than training the network to differentiate two regions (e.g. pectoral muscle region versus breast region) which is the more conventional approach in image segmentation. As a result, the proposed method is robust and capable of reducing false positives/negatives resulting in a more accurate segmentation. In comparison to non-CNN methods, our proposed method is fully automated both in terms of its execution (some of the existing methods require user interaction such as seed initialisation and choosing the degree for the polynomial curve) and modelling the appearance of the pectoral muscle. This yields a more robust model which is able to handle variety in appearance/shape of the pectoral boundary including when it is obscured or invisible. Most non-CNN methods require extensive knowledge of the appearance of the pectoral muscle boundary model in a mammogram to successfully develop a robust geometrical-based model. Unfortunately, such models usually fail to deal with obscured and invisible pectoral muscle due to significant difference between the actual model and the actual appearance of the pectoral boundary. For example, some boundaries cannot be represented or modelled geometrically. Furthermore, in a case where the pectoral muscle is unavailable (hence no pectoral muscle) in a mammogram, our method is able to detect this automatically whereas all the non-CNN methods in the literature assume that each mammogram contains a pectoral muscle region. Finally, this study conducted the largest experimental validation in the literature covering four different databases collected from different institutions.

In conclusion, we have proposed a contour-based approach by modifying the original HED network architecture to find the boundary of the pectoral muscle using a single-stream deep network divided into four blocks of convolution and pooling layers which are different from the patch-based approaches and region-based approaches (used by the studies of Dubrovina et al., 2016 and Moeskops et al., 2016). Our network was designed and trained to specifically find 'contour-like' objects in mammograms. Experimental results based on four different datasets covering SFM and FFDM suggested that the proposed network can find 'contour-like' appearances between the breast and the pectoral muscle regions. In conjunction with the post-processing approaches used in this study, the probability maps generated by the proposed network can be enhanced to estimate the pectoral muscle boundary. Quantitative evaluation results showed that our method produced on average Jaccard and Dice values of $94.8 \pm 8.5\%$ and $97.5 \pm 6.3\%$, respectively, from four datasets, namely MIAS, InBreast, BCDR and CBIS-DDSM. The proposed method outperformed some of the previous (Ferrari et al., 2004; Kwok et al., 2004) and current (Bora et al., 2016; Rampun et al., 2017b) methods quantitatively and qualitatively. However, an overall comparison was difficult due to differences in the number of images and evaluation metrics used in different studies. Finally, in the future, we plan to investigate a more robust way to generate a likelihood map by combining all probability maps generated from contour-based and region-based approaches.

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Conflict of interest

None.

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