

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

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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.

Keywords: Breast mammography, Pectoral Muscle Segmentation, Computer Aided Diagnosis, Convolutional Neural Networks, Deep learning

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; 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 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.

25 In breast cancer CAD systems three anatomical landmarks need to be ex-
 26 tracted automatically, namely the breast border, the nipple and the pectoral
 27 muscle (Chandrasekhar and Attikiouzel, 2000, 1997; Kwok et al., 2001).
 28 The majority of mammograms are digital (full field digital mammograms
 29 (FFDM)), which makes separating the breast boundary from the air back-
 30 ground less complicated. However, nipple and pectoral muscle segmentation
 31 remain challenging due to their significant variability. The main challenges
 32 are depicted in Figure 1: A) the pectoral boundary is invisible due to dense
 33 tissues (and the breast and pectoral regions have a similar appearance); B)
 34 the appearance of the *axillary fold* in the pectoral muscle can have a signifi-
 35 cant effect (false positive) when finding the actual pectoral muscle contour;
 36 C) the curvature of the pectoral muscle boundary can be convex, concave,
 37 a straight line or a mixture of these; D) the majority of the lower part of
 38 the pectoral muscle boundary is obscured due to overlapping fibro-glandular
 39 tissue. The pectoral muscle region tends to be a ‘triangular-shaped’ region
 40 located in the top left corner of a mammogram as depicted in Figure 1C.

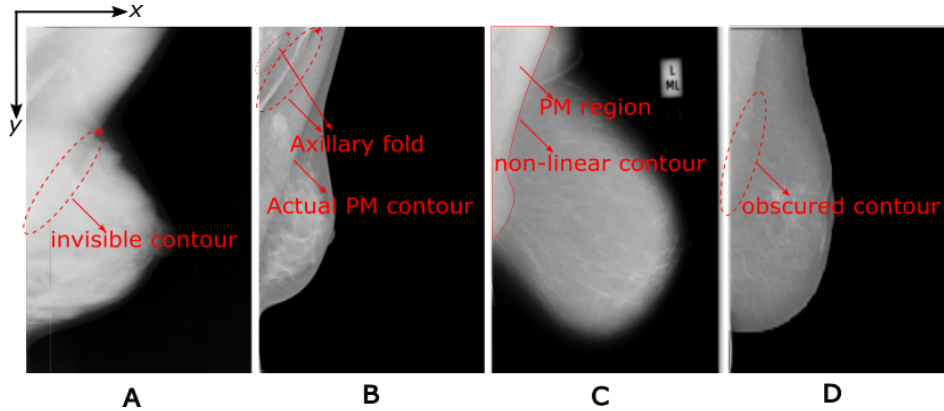


Figure 1: Different challenges in estimating the pectoral muscle boundary. Invisible pec-
 toral muscle boundary (A), multiple *axillary fold* (B), non-linear (or irregular) shape of
 the pectoral muscle boundary (C) and the lower part of the pectoral muscle boundary is
 obscured (D). PM indicates pectoral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

41 2. Literature Review

42 Although many methods have been developed for pectoral muscle segmen-
 43 tation, due to a lack of ground truth the majority of studies are evaluated

44 using the Mammographic Image Analysis Society (MIAS) database (Suck-
 45 ling et al., 1994). In early studies, straight-line based methods (Karssemeijer,
 46 1998; Aylward et al., 1998) using the Hough transform in conjunction with
 47 a gradient magnitude and a set of threshold values were used to estimate
 48 the pectoral muscle boundary. Unfortunately, these studies are unreliable in
 49 complex cases when the appearance of the pectoral muscle boundary is non-
 50 linear (or irregular), where the Hough transform fails to estimate a straight
 51 line. To compensate for the limitations of such methods, Chakraborty et al.
 52 (2012) developed a straight-line estimation technique based on texture and
 53 morphological features to find the initial boundary, followed by an itera-
 54 tive tuning procedure to produce a smooth curve. Although this approach
 55 improved the previous methods, it is sensitive to the pectoral muscle’s mor-
 56 phological properties, which can significantly affect the initial detection of
 57 the pectoral boundary.

58 Later, Kwok et al. (2004) and Ferrari et al. (2004) developed methods
 59 by combining straight-line and contour-based methods. Kwok et al. (2004)
 60 estimated the initial pectoral muscle boundary based on a straight-line ap-
 61 proximation technique, followed by a ‘cliff detection’ method to refine the
 62 initial boundary iteratively. Ferrari et al. (2004) proposed an approach based
 63 on a multiresolution technique using Gabor wavelet filters, which overcame
 64 the limitations of the straight-line based techniques used in (Kwok et al.,
 65 2004; Karssemeijer, 1998; Aylward et al., 1998; Chakraborty et al., 2012).
 66 There were 48 Gabor filters used to enhance the appearance of the edges
 67 within the region of interest containing the pectoral muscle. Subsequently,
 68 the magnitude value for each pixel was propagated using ‘edge-flow’ in the
 69 direction of the phase. Although both methods showed promising results,
 70 only a small number of images were used to evaluate the performance of the
 71 methods.

72 Adaptive thresholding-based methods were proposed by several authors
 73 (Czaplicka and Włodarczyk, 2012; Mustra and Grgic, 2013) to directly seg-
 74 ment the entire pectoral region. From our own experience, using an adaptive
 75 thresholding approach can only work if the majority of the pectoral region
 76 appears to have significant variation in intensity or texture appearance. In
 77 cases where the pectoral muscle boundary is overlapping with fibro-glandular
 78 tissues, the segmentation results are affected significantly. Another alterna-
 79 tive solution proposed in the literature is a region-growing based technique
 80 (Chen and Zwiggelaar, 2010). However, such an intensity-based technique
 81 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 geometry-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, Ram-pun 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

- 157 [et al., 2016](#)) were evaluated across different datasets.
- 158 3. None of the methods can automatically identify whether the pectoral
159 muscle is truly present in the image. A fully automated CAD system
160 should be able to recognise cases where the pectoral muscle region is
161 absent.
 - 162 4. Many studies ([Mustra and Grgic, 2013](#); [Chen and Zwiggelaar, 2010](#);
163 [Chakraborty et al., 2012](#); [Bora et al., 2016](#)) required user interaction,
164 such as seed initialisation and setting the degree of the polynomial
165 function.
 - 166 5. For deep learning-based methods ([Dubrovina et al., 2016](#); [Moeskops
167 et al., 2016](#)), networks were trained on patches and based on the in-
168 formation from the region’s surface (which increased false positives),
169 whereas our proposed network was trained based on the information
170 along the region’s boundary using the whole image.

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

187 Most pectoral muscle boundaries have unique appearances such as having
188 sharp intensity changes, and being morphologically smooth and continuous.
189 Modelling these characteristics manually (as proposed in ([Rampun et al.,
190 2017b](#); [Dubrovina et al., 2016](#); [Moeskops et al., 2016](#); [Taghanaki et al., 2017](#)))
191 was difficult and restricted the model’s capability in dealing with the vari-
192 ations of contour appearance; fortunately the HED network ([Xie and Tu,
193 2015](#)) can be used to learn these characteristics automatically, and with few

194 modifications it can be used to learn boundary cues. Furthermore, our moti-
 195 vation for training the proposed network based on contour appearance rather
 196 than the structure appearance of the pectoral muscle is two-fold: (a) overlap-
 197 ping structure information in both breast and pectoral muscle regions makes
 198 learning the pectoral muscle structure more difficult, yielding a large number
 199 of false positives, as visually shown in studies by [Dubrovina et al. \(2016\)](#),
 200 [Moeskops et al. \(2016\)](#), and our own experiment in Section 6.3; (b) usually
 201 there are only three types of possible contours in a mammogram: the *auxil-*
 202 *iary fold*, pectoral muscle boundary and breast boundary. By learning these
 203 cues only, the learning process became simpler because we have narrowed it
 204 down to specific problems. Therefore, this contributed to not only generat-
 205 ing a small number of false positives, but also simplified the post-processing
 206 step.

207 The contributions of our study are:

- 208 1. We have proposed a contour based CNN method that has learned the
 209 boundary representation rather than the appearance of the pectoral
 210 muscle region (as the current deep learning based methods for pectoral
 211 muscle segmentation in the literature have ([Dubrovina et al., 2016](#);
 212 [Moeskops et al., 2016](#))). Our approach not only reduced false positives
 213 but simplified the subsequent post processing steps.
- 214 2. We modify the original HED network by making it shorter (hence
 215 faster), having used an element-wise fusing operation instead of con-
 216 catenation (hence more accurate in locating the pectoral muscle bound-
 217 ary), and we introduced a weighted softmax loss function to deal with
 218 data imbalance between classes.
- 219 3. We conduct extensive experimental evaluation covering both full field
 220 digital mammograms (FFDM) and scanned film mammograms (SFM)
 221 using four different datasets (Mammographic Image Analysis Society
 222 (MIAS) ([Suckling et al., 1994](#)), Breast Cancer Digital Repository
 223 (BCDR) ([Lopez et al., 2012](#)), InBreast ([Moreira et al., 2011](#)), and
 224 Curated Breast Imaging Subset of Digital Database for Screening Mam-
 225 mography (CBIS-DDSM) ([Lee et al., 2017](#))), which to the best of our
 226 knowledge has been the largest validation study to date.
- 227 4. The proposed method has been fully automated and does not need any
 228 user intervention (such as seed initialisation, and selection of smooth-
 229 ing and curve parameters) and can recognise cases where the pectoral
 230 muscle was absent in the image.

231 3. Materials

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

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

244 Regarding ground truth generation, for the MIAS (Suckling et al., 1994)
 245 dataset, each contour for the pectoral muscle boundary was annotated by a
 246 clinician supervised closely by an expert radiologist. For the InBreast (Mor-
 247 eira et al., 2011) dataset annotations were provided by an expert radiologist,
 248 and for the BCDR (Lopez et al., 2012) and CBIS-DDSM (Lee et al., 2017)
 249 databases, pectoral muscle boundaries were provided by an experienced ob-
 250 server and verified by an expert radiologist.

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

257 4. Methodology

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

265 4.1. Pectoral Muscle Contour

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

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

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

$$c_1(x, y) = (0, 0 \leq y < N) \quad (2)$$

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

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

280 Figure 2 shows a step by step procedure for generating the pectoral muscle
 281 contours for training the CNN. Firstly, we applied the Canny edge detection
 282 technique to the whole pectoral muscle mask to get the pixels located along
 283 the contour. Secondly, in order to enrich contour information with neigh-
 284 bouring pixels, the edge is dilated using a line-shaped structuring element
 285 (ϵ) with the following properties: neighbourhood ($\eta = 5$) and orientation

286 ($\theta = 90^\circ$). The ‘Edge’ (E) sub-image in Figure 2 is the superimposed red
 287 square region in the pectoral muscle mask image. The ‘Dilated Edge’ (DE)
 288 sub-image in Figure 2 is the dilated edge derived from sub-image E, and the
 289 right-most image is the contour and its neighbouring pixels.

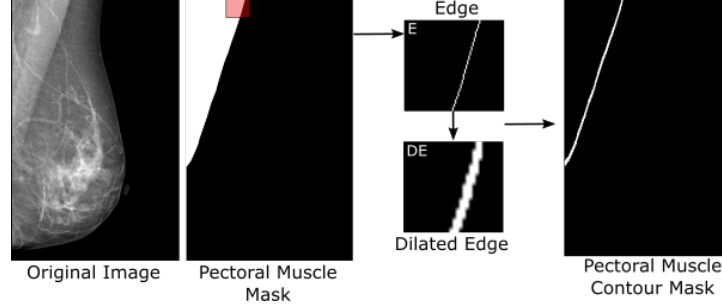


Figure 2: Contour generation to capture the pectoral muscle boundary and its surrounding neighbourhood pixels.

290 For training, we consider pixels with values ‘1’ in the image of the pectoral
 291 muscle contour mask (I_{pm}) as objects (e.g. class one) and pixel values equal to
 292 ‘0’ as non-objects (e.g. class two) which can be obtained using the following
 293 equation

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

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

$$\mathcal{T}^+ = \{I_{tr(+)}^1, I_{tr(+)}^2, I_{tr(+)}^3 \dots I_{tr(+)}^d\} \quad (5)$$

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

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

$$\mathcal{T}^- = \{I_{tr(-)}^1, I_{tr(-)}^2, I_{tr(-)}^3 \dots I_{tr(-)}^d\} \quad (7)$$

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

301 4.2. Network Architecture

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

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

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

- 332 1. We have modified the network to have 3 pooling layers and 4 side-
333 output maps. The final layers of the original HED network reduced the
334 resolution of the input image and provided a very coarse feature map.
335 The effect of this resultant coarse map on the final segmentation was
336 undesirable, as the very thick contour leads to a loss of accuracy when
337 detecting the pectoral boundary. With the removal of these layers, we

- 338 also obtained a faster network.
- 339 2. We have reduced the padding introduced in the first convolutional layer.
 340 In the original HED network, a large padding was needed as it is a
 341 deeper network, whereas our network was shorter.
 - 342 3. The cropping offset was calculated to have the resulting image centered
 343 before fusing and to avoid cropping relevant information.
 - 344 4. Instead of minimizing multiple loss functions, one per side-output map,
 345 and a global fused loss function obtained by concatenating the fea-
 346 ture maps at different scales, we compute a unique loss function from
 347 the element-wise fusing of side-output feature maps. By applying an
 348 element-wise fusing operation, the strongest activations are kept, and
 349 the global loss is computed taking into account the information from
 350 feature maps at different scales in a combined manner.
 - 351 5. We introduce a weighted softmax loss function, which accounts for
 352 the imbalance between contour and background pixels in the global
 353 loss function, whereas in the original HED network it was addressed
 354 independently at each side-output loss function.

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

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

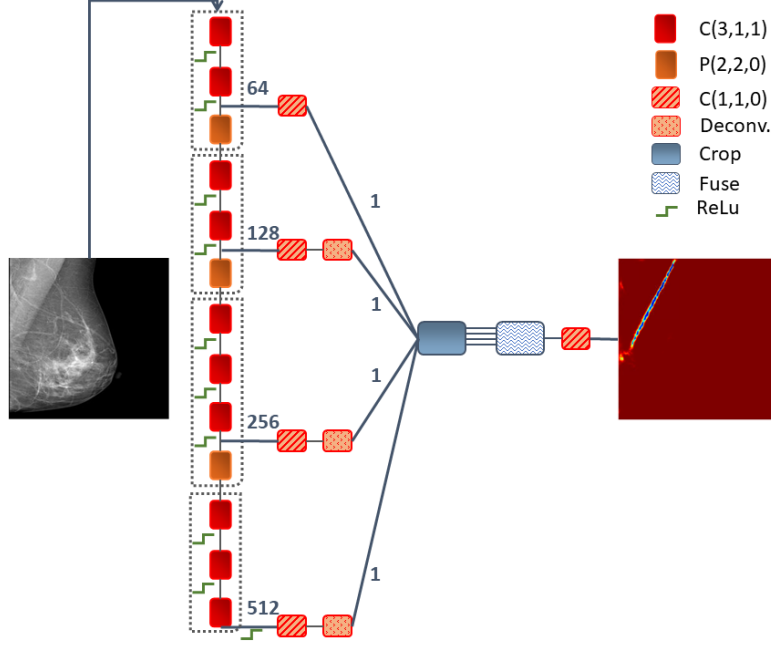


Figure 3: CNN for pectoral muscle contour segmentation, depicting also the input image and corresponding likelihood map. C: convolutional layer (kernel, stride, padding); P: max-pooling layer (kernel, stride, padding); Deconv: deconvolutional layer; Fuse: element-wise fusing; ReLu: Rectified Linear Unit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

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 over-fitting 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 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:

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

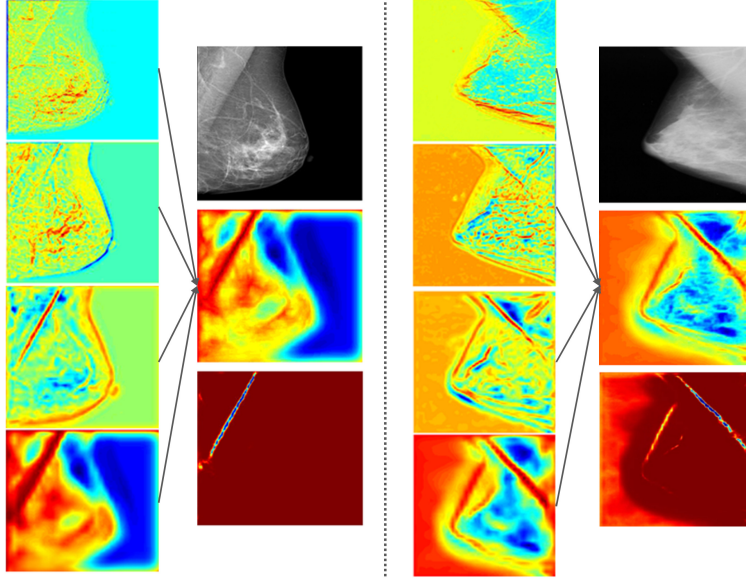


Figure 4: Side feature maps after deconvolution and cropping obtained for two example images from different datasets: BCDR (right) (Lopez et al., 2012) and MIAS (left) (Suckling et al., 1994). In both examples, the left column represents feature maps from finer to coarser, while the right column shows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

where f_k denotes the k -th 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

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

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; 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.

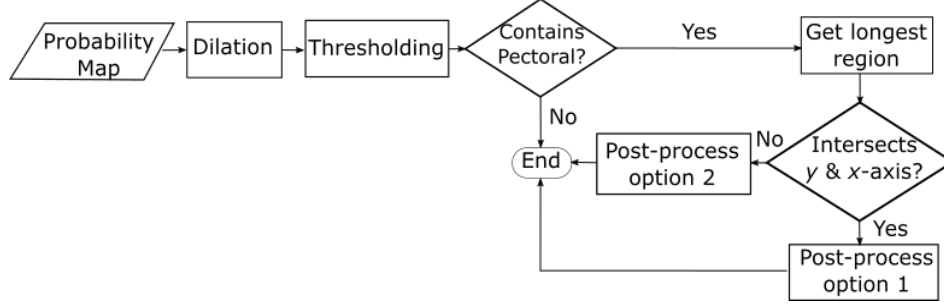


Figure 5: An overview of the post-processing approach to estimate the actual pectoral muscle boundary.

Figure 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 $\theta = 90^\circ$, resulting in I_{map}^ϵ . 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 $[0.1, \dots, 0.7]$ 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, Figure 6 shows a step by step representation for the flow chart in Figure 5.

As can be observed in Figure 6, applying $\epsilon_{\theta=90^\circ}^{\eta=5}$ (these values were determined empirically) to I_{map} resulted in a connected and solid contour in the I_{map}^ϵ . Image I_b was generated by thresholding I_{map}^ϵ . Finally, in $I_b^{L_r}$ we retained the longest region (L_r) with an orientation within $20^\circ \leq \theta \leq 90^\circ$, 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 $I_b^{L_r}$ located in the top row in Figure 6 shows it intersects both x - and y -axes, whereas the $I_b^{L_r}$ located in the bottom row in Figure 6 shows it intersects only the y -axis. To account for these two options, two post-processing

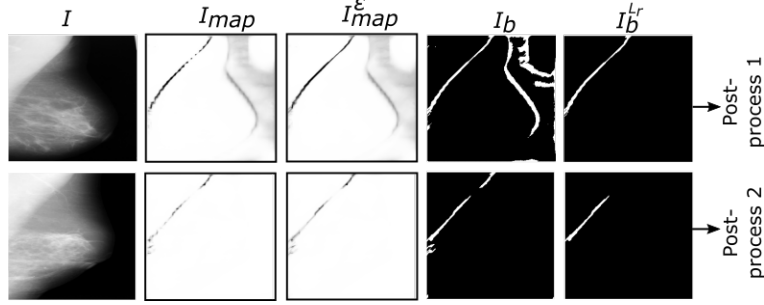


Figure 6: A graphical representation for the flow chart in Figure 5. Note that the I_b^{Lr} was an image that contained the longest region with $20^\circ \leq \theta \leq 90^\circ$.

approaches are proposed in the following subsections.

4.3.1. Post-processing Option One

Figure 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’.

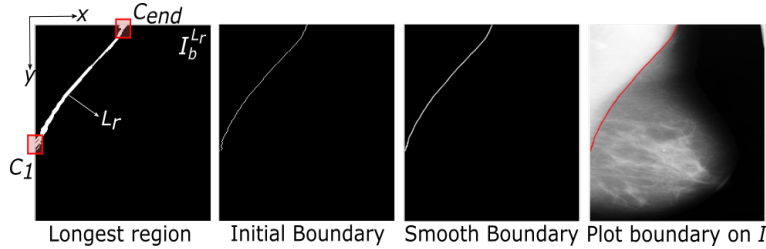


Figure 7: An overview for post-processing option one. The process starts from left to the right.

4.3.2. Post-processing Option Two

Figure 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

468 y_z to the left (y_u) and right (y_b) horizontally to identify associate contour
 469 candidates. Next, we removed false positives (yellow circle in image 8.2) by
 470 retaining the first connected pixels found in each column of the image and all
 471 remaining pixels are deleted. Subsequently, we determined C_b by taking the
 472 furthest pixel located within y_u and y_b followed by connecting a gap (or gaps)
 473 between contours using the straight line (red line in image 8.3) interpolation
 474 technique. We relocated each point based on the highest probability within
 475 a small 5×5 neighbourhood in the probability map. Finally, we applied the
 476 ‘moving average’ technique on C_b to get C_f (see image 9.6). Similar to the
 477 first post-processing step, to segment the pectoral muscle region we created
 478 a binary mask and filled in the region on the left side of C_f by replacing each
 479 pixel with ‘1’.

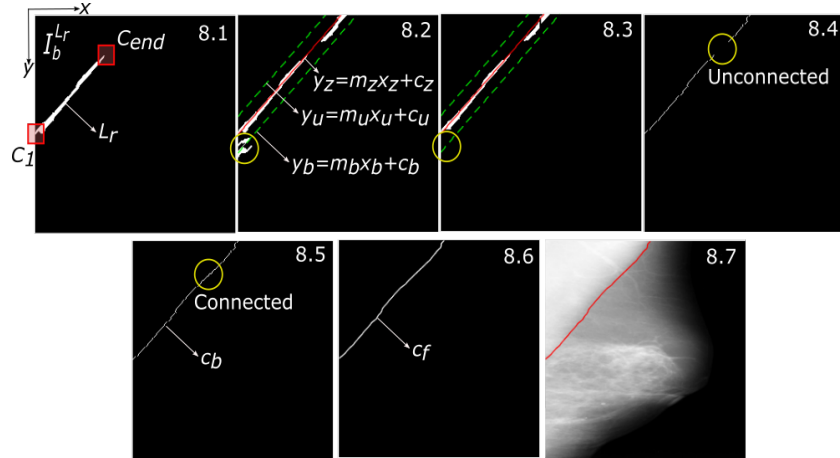


Figure 8: An overview for post-processing option two.

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 (\check{J}) coefficient, which measured 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 (\check{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 (\check{S}) and specificity (\bar{S}) to measure the proportions of true positives (TP) and true negatives (TN), respectively, and correctness (\check{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 $\check{J} = 96.9\%$ and $\check{D} = 98.8\%$ and a small $FPR = 0.1 \pm 0.8$.

For the MIAS database, we achieve $\check{J} = 94.6\%$ and $\check{D} = 97.5\%$, whereas for the InBreast database the proposed method produces values of $\check{J} = 92.6\%$ and $\check{D} = 95.6\%$. On a larger number of images (CBIS-DDSM) the Jaccard and Dice coefficients obtained are $\check{J} = 95.1\%$ and $\check{D} = 98.1\%$, respectively. Regarding \check{S} , the method achieves at least 95.2% with an average $\check{S} = 97.8\%$ for the four different databases. To summarise the results, on average our approach yields $\check{J} > 94\%$, $\check{D} > 97\%$, $\check{A} > 99\%$, $\check{S} > 97\%$, $\bar{S} > 99\%$ and $\check{C} > 97\%$ across various datasets, which is comparable with the existing methods. Furthermore, the method also produces small $FPR = 0.3 \pm 1.3$

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

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 seconds per image.

5.2. Qualitative Results

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

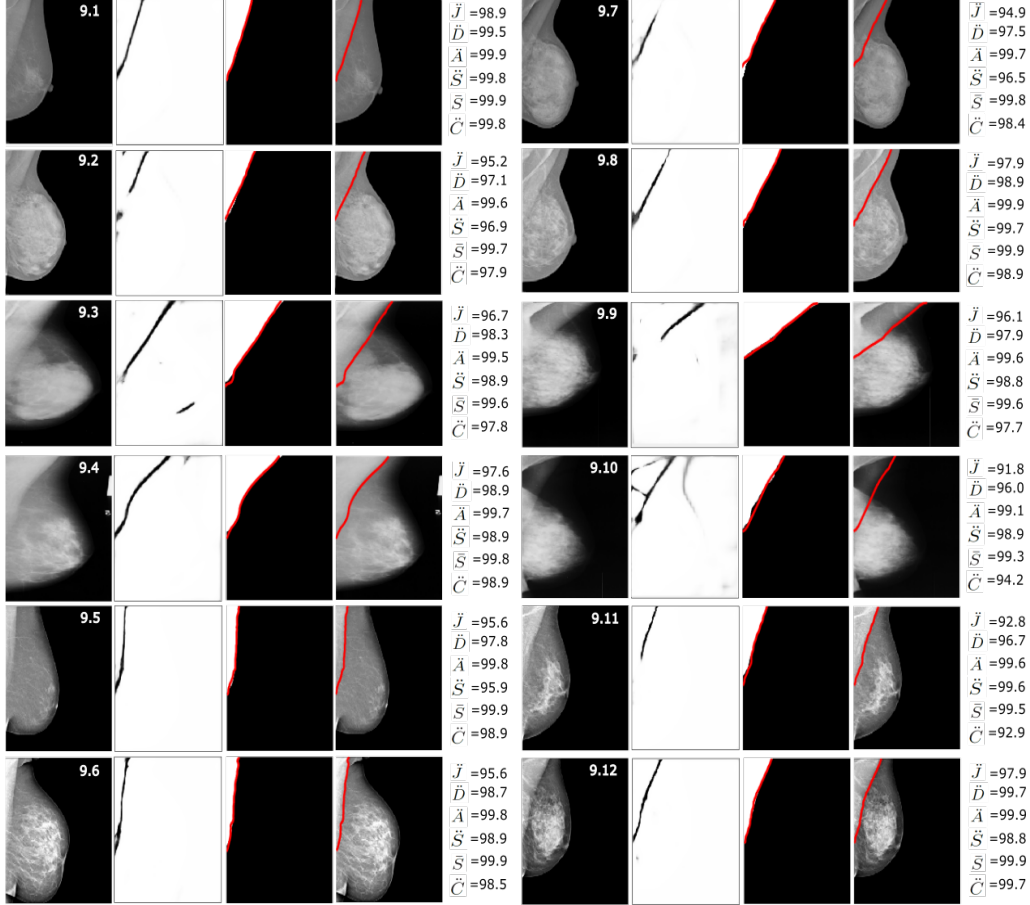


Figure 9: Examples of segmentation results (red line) with their corresponding ground truth. From left (first and sixth columns) to right this shows the original image, probability map, C_f superimposed on the ground truth image, C_f superimposed on the original image and evaluation results.

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 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

Figure 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

Figure 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_{map}^e 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 $\check{J} = 90.3\%$ and $\check{D} = 94.9\%$. For image 11.2 it can be observed that the I_{map}^e generated showed an accurate initial estimate for the pectoral muscle contour. The post-processing

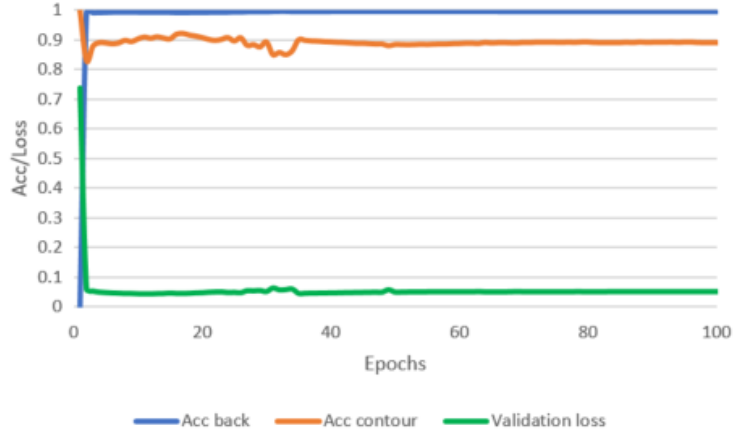


Figure 10: Validation accuracy and loss curves of the proposed network during training for an example network trained with the BCDR, InBreast and CBIS-DDSM datasets.

582 technique retained the longest contour and connected it with the contour located within y_b and y_z , which produces an accurate estimate with $\ddot{J} = 98.2\%$
583 and $\ddot{D} = 99.1\%$. In this case the proposed method was not affected by the
584 presence of multiple *axillary folds*. For image 11.3, where the shape of the
585 boundary is more complex, a high probability distributed along the contour
586 can be observed; by processing I_b with the simple post-processing step, evaluation
587 results achieve $\ddot{J} = 91.2\%$ and $\ddot{D} = 95.3\%$. When the pectoral muscle
588 contour was obscured as shown in image 11.4, the proposed method manages
589 to find the lower and upper parts of the contour. By connecting these contours
590 using the post-processing technique, the estimated C_f has evaluation
591 results of $\ddot{J} = 90.6\%$ and $\ddot{D} = 95.1\%$.
592

593 6.1. Comparative Study

594 A direct comparison is difficult due to the differences in evaluation techniques
595 and the number of images employed. However, for comparison, we have summarised
596 our results and present some of the existing methods in the literature in Tables 4
597 and 5. Note that we cover only those studies based on the datasets used in our study.
598 Although there are many methods developed in the literature, the majority of them
599 were evaluated qualitatively by expert radiologists (Kwok et al., 2004; Chen and
600 Zwiggelaar, 2010) or have been evaluated using their own private datasets. It can
601 be observed in Table 4 that our proposed method outperformed our previous method
602 (Rampun et al.,

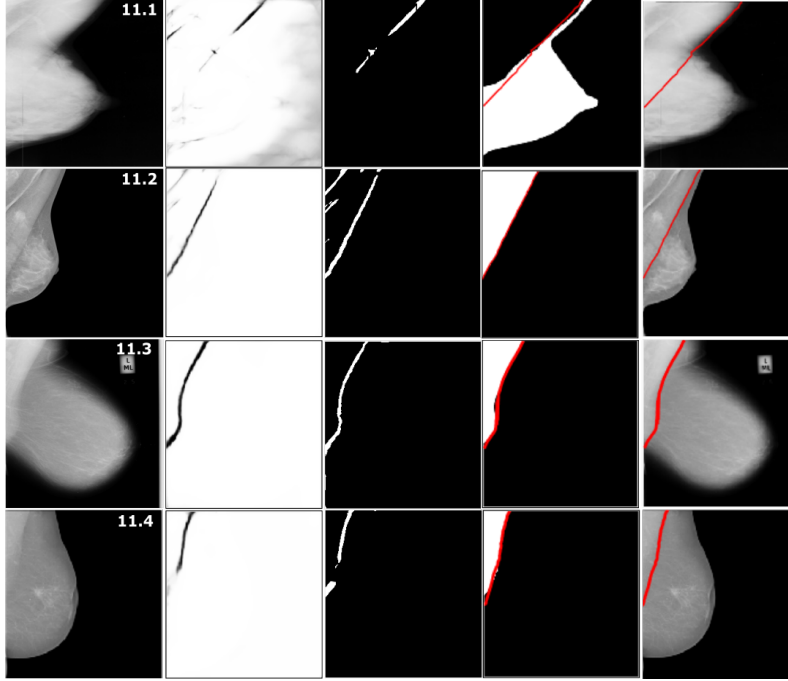


Figure 11: Segmentation results for cases shown in Figure 1. The second and the third column are the I_{map}^ϵ and I_b , respectively. From left to right this shows the original image, probability map, C_f superimposed on the ground truth image, and C_f superimposed on the original image.

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 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 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.

617 Taghanaki et al. (2017) achieved over 96% \bar{D} and \bar{J} across three datasets.
618 However, it should be noted that their results were based on the number of
619 pixels overlapping with the entire image. In our case, we calculated both
620 metrics based on the number of pixels overlapping with the pectoral muscle
621 region only. Moreover Taghanaki et al. (2017) did not use all images from
622 the MIAS and InBreast datasets.

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

623 In terms of the false negative and false positive rates obtained with
624 the MIAS dataset, our method produced $FNR=3.2\%$ and $FPR=0.6\%$, re-
625 spectively, which indicated that we quantitatively outperform recent studies
626 (Vikhe and Thool, 2017; Chen et al., 2015; Yoon et al., 2016; Liu et al.,
627 2014). Although the studies of Camilus et al. (2010) and Ferrari et al.
628 (2004) reported small false positives, their proposed methods produced large
629 false negatives of 5.58% and 5.77%, respectively. In a qualitative evaluation,
630 Kwok et al. (2004) used a five level assessment scale (exact, optimal, ade-
631 quate, sub-optimal and inadequate) and reported 83.9% of the segmentations
632 to be adequate or better. Chen and Zwiggelaar (2010), whose method was
633 tested based on 240 mammograms from the EPIC (European Prospective
634 Investigation on Cancer) dataset and used a four level assessment (accurate,

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

635 nearly accurate, acceptable and unacceptable), reported that 93.5% of their
636 pectoral segmentations are at least acceptable.

637 6.2. Visual Comparison

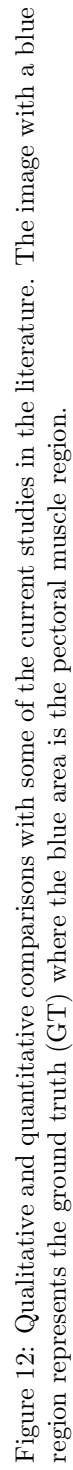
638 Figure 12 shows visual comparisons with some of the existing studies in
639 the literature taken from the MIAS and InBreast datasets. The segmentation
640 results of the other studies were taken from the authors’ papers. We have also
641 presented a quantitative comparison for a few cases where numerical results
642 were available from the authors’ papers (Kwok et al., 2004; Ferrari et al.,
643 2004; Rampun et al., 2017b). Note that for improved visual representation,
644 we have coloured the estimated pectoral muscle boundaries from the authors’
645 papers. For image *pdb151lx* it can be observed that the proposed method
646 quantitatively outperforms our previous method (Rampun et al., 2017b) by
647 at least 10% for both metrics. For this image the methods developed by
648 Kwok et al. (2004) and Chen et al. (2015) under segmented the lower part
649 of the pectoral muscle region. The method of Kwok et al. (2004) under
650 estimated the boundary and was reported as inadequate by their expert
651 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*, Ferrari et al. (2004) 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

690 explained in this paper yields more accurate segmentation results than the
691 methods developed by [Vikhe and Thool \(2017\)](#), [Chen et al. \(2015\)](#) and
692 [Rampun et al. \(2017b\)](#).



6.3. Learning Region's Structure

Figure 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. Figure 14 shows example patches extracted from different regions

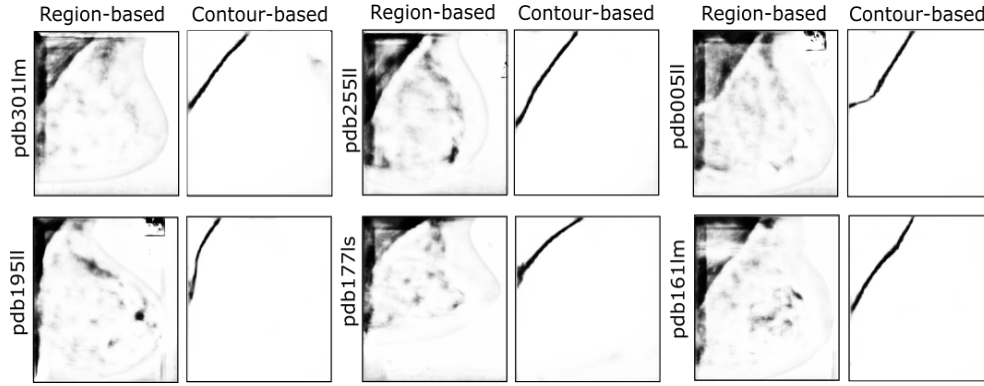


Figure 13: A visual comparison of the probability maps using region-based versus contour-based approaches taken from the MIAS database.

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.

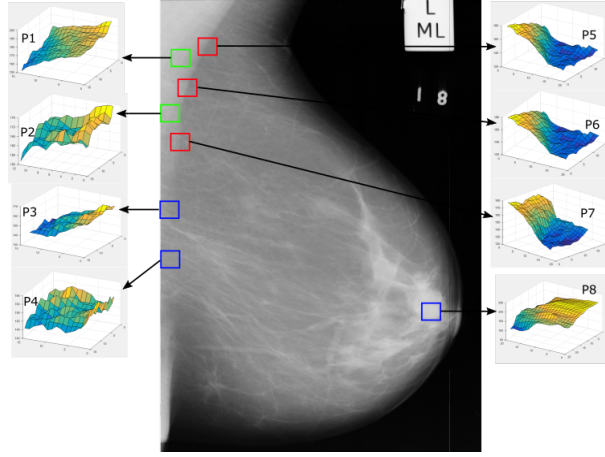


Figure 14: A 3D mesh visualisation for patches extracted from the breast region (blue boxes), pectoral muscle (green boxes) and boundary regions (red boxes).

6.4. Effects of Post-processing

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

6.5. Effects of Threshold Values

Figure 16 shows the performance evaluation of the proposed method using different threshold values when extracting initial candidates from the I_{map} .

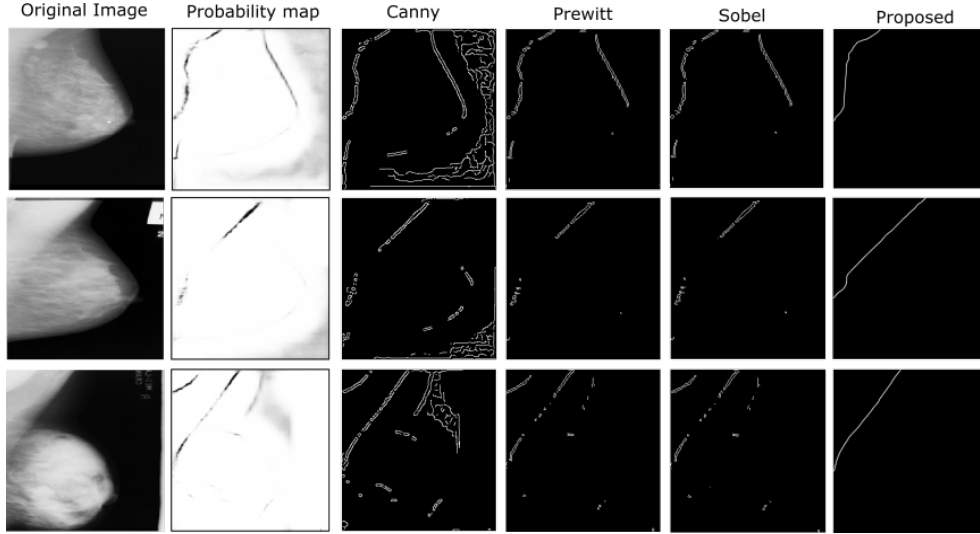


Figure 15: A visual comparison between contour detection using Canny, Prewitt, Sobel and the proposed post processing method.

730 The metrics \ddot{J} and \ddot{D} were chosen as evaluation metrics for all datasets. The
731 training and testing sets are as described in Table 2 where each database
732 was tested on a round robin basis. For this purpose, we tested 21 different
733 threshold values from 0.1 to 0.7 with an interval 0.03. It can be observed that
734 results for both metrics were consistent from 0.1 to 0.58. The evaluation re-
735 sults across different datasets decreased when using a threshold value larger
736 than 0.58. As can be observed, the performance of the proposed method
737 reduced after a threshold value of 0.58. Choosing a higher threshold value
738 (e.g. 0.8 or 0.9) further deteriorated the performance due to loss of bound-
739 ary/important cues in the binary image. Selecting a maximum threshold
740 value (e.g. 1) removed all boundaries hence producing an empty binary im-
741 age. On the other hand, choosing a smaller interval value (e.g. 0.01) did not
742 make a significant difference in terms of performance. This is because the
743 effect of a small interval value is only a small number of pixels resulting in
744 very similar binary images.

745 6.6. Visual Heat-maps Comparison

746 Figure 17 shows visual likelihood map comparisons between the original
747 HED and the proposed network (modified HED). It can be observed that our
748 network was more precise in locating the boundary of the pectoral muscle,

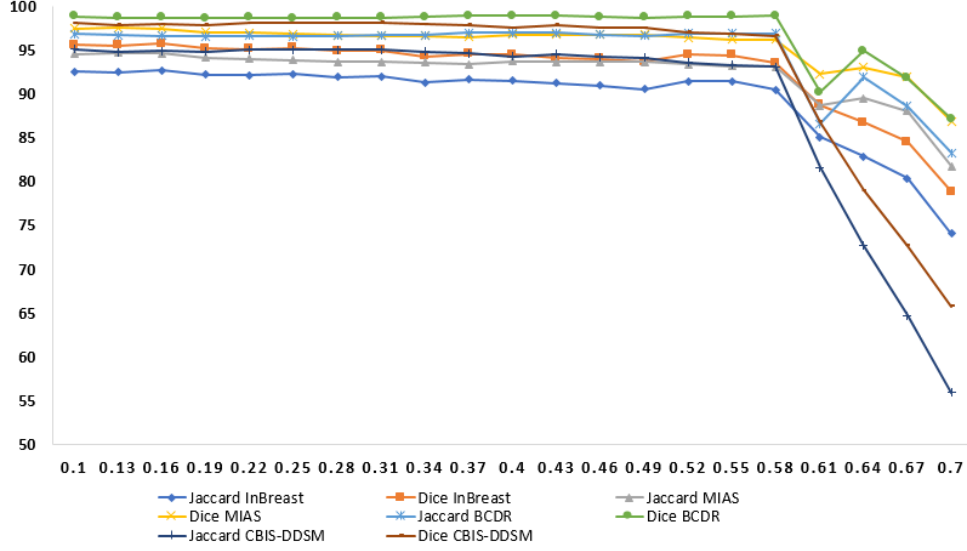


Figure 16: Performance evaluation using different threshold values for the \tilde{J} and \tilde{D} .

749 whereas the original HED can only approximately estimate the location. For
750 example, regions with high probability of being a contour (dark red) were
751 larger in the original HED heat-maps than in the modified HED heat-maps,
752 which made it more difficult to estimate the pectoral boundary in the post-
753 processing step. Moreover, this suggested that the number of false positives
754 (the number of pixels with dark red colour) in the heat-maps generated by the
755 original HED is much higher. In contrast, only pixels (and their neighbouring
756 pixels) located along the contour have high probability in the heat-maps
757 generated by our proposed network. This can be explained when the original
758 HED captured more finer and coarser details, yielding a coarser side-output
759 in each convolution layer. As a result, the original HED network generated
760 a blurry/coarser final output when fusing all the side-outputs from each
761 convolution layer.

762 6.7. HED versus modified HED

763 This section presents a quantitative comparison between the performance
764 of the original HED and our proposed network. Table 6 shows the exper-
765 imental results across different metrics used in this study. The resulting
766 probability maps produced by both networks fed into the post-processing
767 pipeline developed in our study. These quantitative results clearly show that

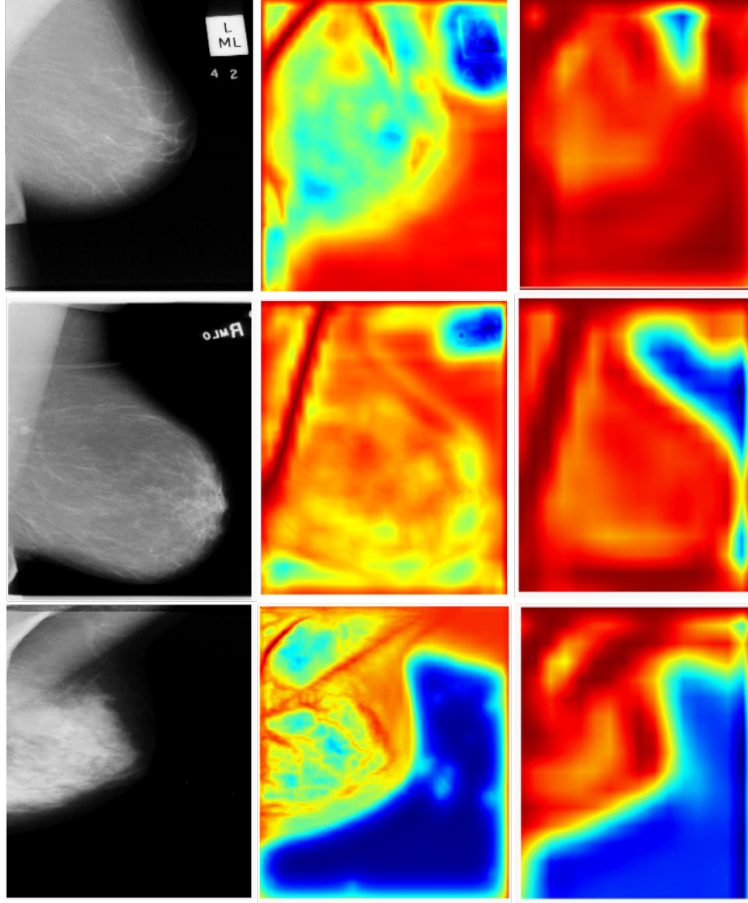


Figure 17: Visual heat-maps comparison between the modified HED (second column) and the original HED (third column). Dark red colour indicates higher probability of being an object (e.g. a contour).

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. Figure 18 shows some examples of probability maps produced by both networks. It can be observed that i) the 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), iii) the original HED was unable to find accurate location of the pectoral boundary

777 when it overlaps with breast tissue (e.g. sixth row), iv) the original HED un-
778 der estimated the locations of the pectoral muscle boundaries in most cases
779 (think boundary), and v) the proposed network produced more accurate lo-
780 cation, clearer probability map and more robust.

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

781 6.8. Choice of evaluation metrics

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

794 6.9. Cross validation

795 Quantitative results presented in this paper represent a single training
796 instance. We did not perform a cross-validation exercise during the train-
797 ing and validation phase mainly due to i) the number of training images is

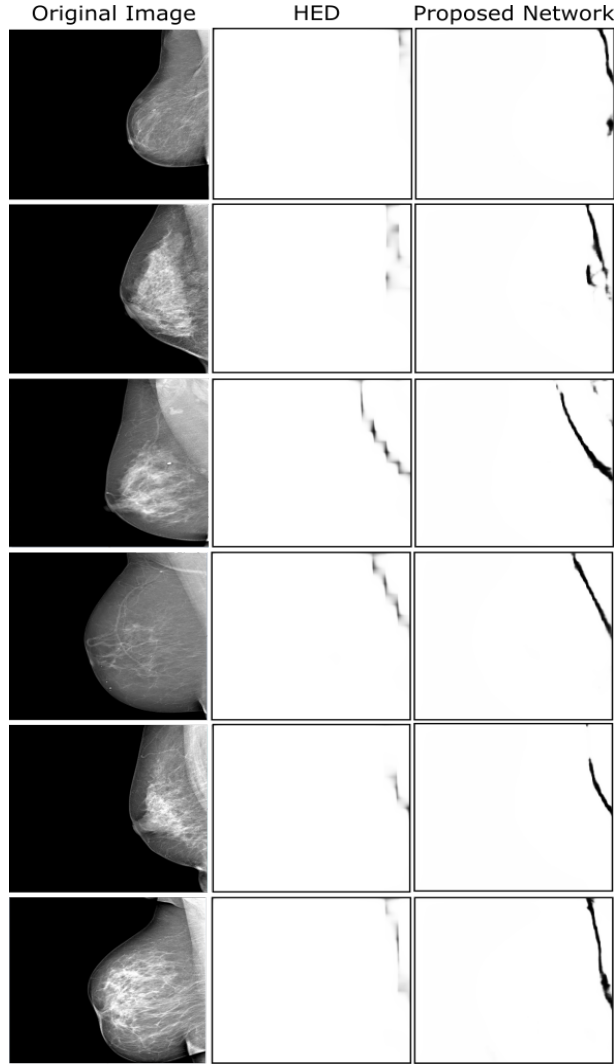


Figure 18: A visual comparison between probability maps produced by the original HED and our proposed network.

798 sufficient (in our case over 2200 to 3500), hence cross validation is unneces-
 799 sary, ii) cross-validation is extremely time consuming. In our case, a single
 800 training instance takes 7 hours on an Intel Xeon E5-1650 v3 processor, us-
 801 ing Nvidia Corporation’s Deep Learning GPU Training System (DIGITS)
 802 based on Caffe, with a Nvidia’s Quadro M6000 (12Gb) graphics card. Doing
 803 cross-validation, for example 3-fold cross validation of 10 runs in each fold,

would be $7 \times 30 = 210$ hours, 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 mammae 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 don't usually appear close to the pectoral muscle boundary ([Rampun et al., 2018c](#)).

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 [Musta and Grgic \(2013\)](#); [Kwok et al. \(2004\)](#); [Oliver et al. \(2014\)](#); [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.

Figure 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.

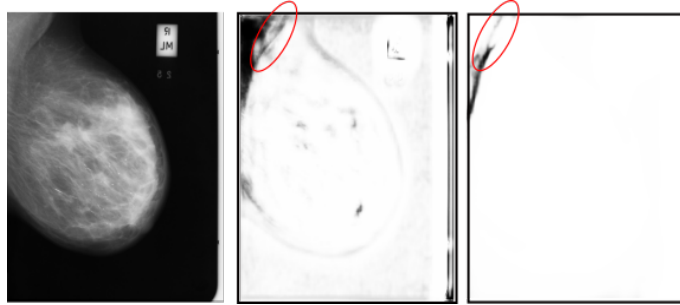


Figure 19: Illustration of combining probability maps generated by region-based (middle) approach and contour-based approach (right).

846

847 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_{map}^ϵ . Subsequently, we applied a thresholding operation on I_{map}^ϵ 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

863 approach in image segmentation. As a result, the proposed method is ro-
 864 bust and capable of reducing false positives/negatives resulting in a more
 865 accurate segmentation. In comparison to non-CNN methods, our proposed
 866 method is fully automated both in terms of its execution (some of the exist-
 867 ing methods require user interaction such as seed initialisation and choosing
 868 the degree for the polynomial curve) and modelling the appearance of the
 869 pectoral muscle. This yields a more robust model which is able to handle
 870 variety in appearance/shape of the pectoral boundary including when it is
 871 obscured or invisible. Most non-CNN methods require extensive knowledge
 872 of the appearance of the pectoral muscle boundary model in a mammogram
 873 to successfully develop a robust geometrical-based model. Unfortunately,
 874 such models usually fail to deal with obscured and invisible pectoral muscle
 875 due to significant difference between the actual model and the actual ap-
 876 pearance of the pectoral boundary. For example, some boundaries cannot
 877 be represented or modelled geometrically. Furthermore, in a case where the
 878 pectoral muscle is unavailable (hence no pectoral muscle) in a mammogram,
 879 our method is able to detect this automatically whereas all the non-CNN
 880 methods in the literature assume that each mammogram contains a pectoral
 881 muscle region. Finally, this study conducted the largest experimental valida-
 882 tion in the literature covering four different databases collected from different
 883 institutions.

884 In conclusion, we have proposed a contour-based approach by modifying
 885 the original HED network architecture to find the boundary of the pectoral
 886 muscle using a single-stream deep network divided into four blocks of convo-
 887 lution and pooling layers which are different from the patch-based approaches
 888 and region-based approaches (used by the studies of [Dubrovina et al. \(2016\)](#)
 889 and [Moeskops et al. \(2016\)](#)). Our network was designed and trained to specif-
 890 ically find ‘contour-like’ objects in mammograms. Experimental results based
 891 on four different datasets covering SFM and FFDM suggested that the pro-
 892 posed network can find ‘contour-like’ appearances between the breast and the
 893 pectoral muscle regions. In conjunction with the post-processing approaches
 894 used in this study, the probability maps generated by the proposed network
 895 can be enhanced to estimate the pectoral muscle boundary. Quantitative
 896 evaluation results showed that our method produced on average Jaccard and
 897 Dice values of $94.8 \pm 8.5\%$ and $97.5 \pm 6.3\%$, respectively, from four datasets,
 898 namely MIAS, InBreast, BCDR and CBIS-DDSM. The proposed method
 899 outperformed some of the previous ([Ferrari et al., 2004](#); [Kwok et al., 2004](#))
 900 and current ([Bora et al., 2016](#); [Rampun et al., 2017b](#)) methods quantita-

tively 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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