Improvements of an objective model of compressed breasts undergoing mammography: Generation and characterization of breast shapes

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Purpose: To develop a set of accurate 2D models of compressed breasts undergoing mammography or breast tomosynthesis, based on objective analysis, to accurately characterize mammograms with few linearly independent parameters, and to generate novel clinically realistic paired cranio-caudal (CC) and medio-lateral oblique (MLO) views of the breast.

Methods: We seek to improve on an existing model of compressed breasts by overcoming detector size bias, removing the nipple and non-mammary tissue, pairing the CC and MLO views from a single breast, and incorporating the pectoralis major muscle contour into the model. The outer breast shapes in 931 paired CC and MLO mammograms were automatically detected with an in-house developed segmentation algorithm. From these shapes three generic models (CC-only, MLO-only, and joint CC/MLO) with linearly independent components were constructed via principal component analysis (PCA). The ability of the models to represent mammograms not used for PCA was tested via leave-one-out cross-validation, by measuring the average distance error (ADE).

Results: The individual models based on six components were found to depict breast shapes with accuracy (mean ADE-CC = 0.81 mm, ADE-MLO = 1.64 mm, ADE-Pectoralis = 1.61 mm), outperforming the joint CC/MLO model ($P \leq 0.001$). The joint model based on 12 principal components contains 99.5% of the total variance of the data, and can be used to generate new clinically realistic paired CC and MLO breast shapes. This is achieved by generating random sets of 12 principal components, following the Gaussian distributions of the histograms of each component, which were obtained from the component values determined from the images in the mammography database used.

Conclusion: Our joint CC/MLO model can successfully generate paired CC and MLO view shapes of the same simulated breast, while the individual models can be used to represent with high accuracy clinical acquired mammograms with a small set of parameters. This is the first step toward objective 3D compressed breast models, useful for dosimetry and scatter correction research, among other applications. © 2017 American Association of Physicists in Medicine [<https://doi.org/10.1002/mp.12186>]

Key words: breast modeling, breast phantoms, image segmentation, mammography, tomosynthesis

1. INTRODUCTION

Mammography is considered the *gold standard* for detection of early breast cancer, the second leading cause of death in

women in developed countries after lung cancer.¹ Population-based screening programs with full field digital mammography (FFDM) have the potential to reduce mortality,² but still 15–30% of the cancers may be missed.^{3,4} In recent years, it

appears that the performance of the screening programs may be enhanced with the inclusion of digital breast tomosynthesis (DBT).^{5,6} However, the clinical performance of both modalities still has room for improvement.

The development of novel state-of-the-art image processing algorithms could help improve breast cancer detection and diagnosis with FFDM and DBT. Much of this research requires simulating realistic breast shapes undergoing mammography. Some examples of this research are scatter correction^{7–11} and lesion detection algorithms.^{12,13} However, other areas of research such as patient dosimetry,^{14–18} image registration,^{19,20} and 3D breast software phantoms^{21–28} could also benefit from objective shape models of compressed breasts.

Until now, most of the above mentioned studies use simplistic compressed breast models like a semi-elliptical approximation for the cranio-caudal (CC) mammography view or a subjective model for the medio-lateral oblique (MLO) view. This may limit the applicability of their results. Others developed more accurate compressed breast shapes from 3D uncompressed breast software phantoms, by using compression algorithms, but still result in a limited number of possible shapes.

Feng *et al.* developed for the first time an objective 2D model of the shapes of compressed breasts undergoing mammography.²⁹ However, there were some limitations in that work that could be overcome in order to have a more reliable model. In this work, we improve the accuracy, usability, and clinical relevance of their model. The need for improvement mainly lies in the detector size bias which could lead to a model more representative of smaller breasts than one of average size. Additionally, we now include three new features, not assessed in any of the previous models that increase the significance of the model. These features are the automatic modeling of the pectoralis muscle shape, an enhanced segmentation algorithm able to limit the region of interest to only the breast tissue within the mammogram, and a joint CC/MLO model including CC and MLO views from the same simulated breast.

As a result, we present a more accurate 2D model of compressed breasts undergoing mammography or breast tomosynthesis based on objective analysis, able to represent the shape of acquired clinical mammography views with a small set of parameters and also able to generate novel clinically realistic paired CC and MLO views from the same random breast.

2. METHODS

The methods follow the same general approach as in the work by Feng *et al.* (2013).²⁹ A mammography database undergoes automated edge detection, and afterwards principal component analysis (PCA)³⁰ is performed to represent the variance in the breast shapes to a small number of linearly independent variables. Even if we only use mammography images to build the model, our model is also valid for DBT since the central projection of DBT is geometrically equivalent to a mammographic acquisition. Three models are

created from this analysis: one for CC views, one for MLO views, and a joint CC/MLO model able to represent and generate both views of the same compressed breast undergoing mammography. A new mammography database with a larger detector size, enhanced edge detection algorithms, inclusion of the pectoralis muscle, and the joint model are used to improve the accuracy and relevance of the models with respect to the work by Feng *et al.* The full edge segmentation algorithm and all the PCA and statistical analysis are implemented in MATLAB® R2016a (MathWorks, Natick, MA, USA).

2.A. Mammography database

The mammography database used for the PCA consists of 982 paired CC and MLO view digital mammograms. This database consists of screening mammograms acquired at the Breast Imaging Center of Emory University, and was compiled retrospectively with IRB approval. All mammograms were visually inspected for correct positioning and adequate image quality (JRM). The mammograms were acquired using various equivalent Selenia Dimensions digital mammography systems (Hologic Inc, Bedford, MA, USA). These systems are equipped with 24×29 cm direct flat panel detectors with a pixel size of 70 μm . The average projected area (computed from the segmented contour of each mammogram), compressed breast thickness, and the employed compression force (retrieved from the DICOM header of the mammogram) were analyzed for both the CC and MLO views for comparison with other mammography databases found in the literature.

2.B. Automated edge detection

The automated edge detection algorithms are similar to those employed by Feng *et al.*, but with further optimizations. After automated detection of the breast contour, several processes are run to delineate only the actual breast tissue. The nipple is automatically detected and removed from the contour and the pectoralis muscle is delineated on the MLO view. In addition, since many mammograms include non-mammary tissue in the field of view, these tissues are removed before PCA analysis so an accurate breast shape model can be developed. Finally, the contours are sampled to a fixed number of points, used for the PCA. All 982 CC and MLO views are fully processed with the algorithm described below, which was validated by human observers.

2.B.1. Raw breast edge

Initially the mammogram is automatically thresholded to obtain a binary image, thus separating tissue from the background. Connected components are later extracted from this image and all the non-adjacent extraneous parts are excluded from the breast.³¹ A first raw breast edge for each CC and MLO view is then located using the Sobel gradient operator

and edge thinning.³¹ If the mammogram corresponds to the left breast, it is mirrored on the vertical axis to build a consistent database for all images, so the nipple always points in the same direction.

2.B.2. Nipple detection and removal

The nipple is located by detecting larger than average changes in the gradient of the breast contour curve. First, the normal vector of the raw edge is computed at every coordinate point. The data are limited to a range of interest comprising the coordinate points located between 1/4 and 3/4 of the total raw edge perimeter, starting from the top left corner of the image.

A running standard deviation is computed as follows. For every coordinate point, the normal vector values for W consecutive points are grouped together, where W is the total number of points in the raw edge divided by 50 (this value was selected by trial-and-error) (Fig. 1(a)). Then the standard deviation of the angles of the normal vectors within each group is computed and plotted (Fig. 1(b)). The background value (BG) of this profile is calculated as the mean of the values below half of the profile absolute maximum. Peaks at least three times greater than the BG level (again determined by trial-and-error) are detected. If found, it is assumed that the peaks correspond to the nipple location. Usually several consecutive peaks are found since the nipple often generates more than one change of direction on the breast contour (outwards and inwards). It is also assumed that the nipple is located within the coordinate points represented by the first and last peaks. Once identified, these profile points are removed and replaced with a 2nd order polynomial, computed from the surrounding points (Fig. 1(c)). The new points are generated with the same sample rate than the original points.

2.B.3. Lateral (CC) and inframammary fold (MLO) non-mammary tissue removal

To detect and remove the lateral non-mammary tissue on the CC view, and the inframammary fold tissue on the MLO view, the same strategy explained in section 2.B.2 is followed. However, for this case the search is limited to the coordinate points located after 3/4 of the total raw edge perimeter. If present, these features usually generate only one change of direction, represented as one peak in the profile. This change of direction occurs on the lower part of the breast contour and can reach more than 90° .

2.B.4. Medial non-mammary tissue removal in the CC view

The medial non-mammary tissue in the CC view does not always involve a pronounced change of direction from the breast contour of the mammogram, and hence the strategy of sections 2.B.2 and 2.B.3 cannot be used. To detect if this correction is necessary, the original image is thresholded again to the T percent of the original threshold level obtained in section 2.B.1, and then its raw sub-edge is computed. The analysis is limited to the coordinate points located within the first 1/4 of the total raw edge length (starting from the top left of the image).

Starting with $T = 10\%$, this value is progressively increased until the minimum distance ($D1$) between the raw original edge and raw sub-edge is below 1 cm (Fig. 2). Once this condition is met, the ratio between $D1$ (found at point P) and the distance between both profiles directly on the chest-wall side ($D2$) is computed (Fig. 2). If the ratio is less than 0.6, it is assumed that there is non-mammary tissue. If so, all the points from the chest-wall to P are removed and then replaced with a 2nd order polynomial computed from the

FIG. 1. Schematic of the method to detect and remove the nipple. See text for more details. [Color figure can be viewed at wileyonlinelibrary.com]

FIG. 2. Diagram of the method to detect and remove the medial non-mammary tissue. D1 is the closest distance between the original edge and the sub-edge (found at point P), while D2 is the distance between both edges directly on the chest-wall side. [Color figure can be viewed at wileyonlinelibrary.com]

points directly after P (Fig. 2). Both values 1 cm and 0.6 are determined by trial-and-error.

2.B.5. Pectoralis detection

The pectoralis muscle on the MLO view, is detected following a variant of the method described by Wei et al.³² A rectangular region of interest is generated, starting from the top left corner of the MLO raw edge [which is the (0, 0) coordinate]. The height is 90% of the maximum height coordinate

found on the MLO raw contour, and the width is 95% of the width displayed on the upper part of the MLO view, before the contour starts ascending in height. This ROI is further subdivided in 3 cm height sub-ROIs, with the same width. For every sub-ROI of the image, the histogram is computed (Fig. 3).

For the first sub-ROI, the most prominent local minimum of the histogram is detected following Wei et al. This is the minimum with the largest height differences between adjacent maxima (Fig. 3(a)). Every local minimum represents a set of points (Fig. 3(b)). The search is always limited to sets of points that generate a line that falls within -35° and -95° . Furthermore, in every set of points the outliers are removed, which are defined as those points with a standard deviation (SD) higher than twice the SD found when fitting all of them to a line.

For the next sub-ROIs, the local minimum of the histogram is selected if it generates a set of points that, in relation to the previous set: (a) has the highest correlation coefficient R-squared; (b) has the most similar slope; (c) are closest in distance. If no set of points is found in a sub-ROI, the search stops and the rest of the points are extrapolated (at the same sampling rate) by a 5th order polynomial from the last directly detected pectoralis point to the chest wall. Finally, all the collected points are fit to a 5th order polynomial (Fig. 3(c)).

Upon completions of these steps, the final breast contours of the CC and MLO views are resampled to 100 points in (x, y) coordinates. The pectoralis is also resampled to 35 points in (x, y) coordinates.

2.B.6. Validation

To validate the above described algorithms, we tested the accuracy of the process with human observers. First, upon

FIG. 3. Diagram of the method to detect and delineate the pectoralis muscle on the MLO view. Image (a) exhibits the histogram of the sub-ROI displayed on (b), which includes the points associated with the prominent local minima of the histogram. Image (c) shows all the points detected within the total pectoralis ROI, and their corresponding 5th order polynomial fit. [Color figure can be viewed at wileyonlinelibrary.com]

TABLE I. Average value $\pm$ standard deviation of the projected breast area, compressed breast thickness and compression force for both mammography views from our study population. Medians are shown in parentheses.

	Projected breast area (cm ²)	Compressed breast thickness (mm)	Compression force (N)
CC	163.1 $\pm$ 72.7 (151.4)	60.3 $\pm$ 13.3 (62)	102.9 $\pm$ 25.2 (101.0)
MLO	214.0 $\pm$ 74.7 (202.3)	60.7 $\pm$ 14.5 (62)	119.1 $\pm$ 32.3 (115.6)
P-values	< 0.001	0.55	< 0.001

completion of the development of the algorithm, the appropriateness of the segmentation of the edges of all 982 mammograms was evaluated by the first author (ARR). For independent validation, two samples of 50 paired two-view mammograms were assessed for accuracy of the segmentation algorithm, one by a radiology resident with a PhD in breast imaging (JvZ), and one by a PhD candidate with more than two years of experience in breast imaging (SV). For this assessment, the observers used a scale of 1 to 5, where 1 equals an inappropriate representation of the breast shape, 3 equals a sufficiently good representation, and 5 represents a perfectly segmented shape. Thus, 3 or higher was defined as a successful representation of the breast shape.

2.C. Principal component analysis: model generation

Following the same procedure as detailed in Feng et al., the subset of points representing the breast edges and the pectoralis muscle can be reduced to a smaller set of linearly independent variables via PCA, comprising most of the information present on the data points.³⁰ Three different models are created, each of them with its own set of linearly independent variables: a CC-only model, an MLO-only model, and a joint model considering the MLO and CC edges of the same breast. The pectoralis muscle contour is always considered as an appendix to the MLO edge.

For every model, a covariance matrix, $cov(X)$, defined as:

$$cov(X) = \frac{\sum_{i=1}^N (x_i - \bar{x})(x_i - \bar{x})^T}{N - 1} \quad (1)$$

where N is the total number of processed images, and x_i is the vector containing the (x,y) coordinates of the breast contour of the image i (for the joint model, x_i contains both the CC and the MLO edges). The n largest eigenvalues of the matrix render the n principal components of the model, which are represented by the corresponding eigenvectors (e_j). A matrix E with dimensions corresponding to the number of coordinates times n , is built assembling e_j . The matrix E can be used to build the modeled edge (t_m) of any segmented contour (t_i), used or not for the PCA analysis, using:

$$t_m = \bar{x} + \sum_{j=1}^n [(E^T E)^{-1} E^T (t_i - \bar{x})]_j e_j \quad (2)$$

where n is the number of principal components used to build E . The factors multiplying each e_j are hence the n first principal components that characterize t_i .

FIG. 4. Compressed breast thickness (in mm, extracted from the DICOM header) as function of the projected area of the breast in the mammogram (in cm², computed as the area enclosed by the automated segmented edge), for each of the 931 CC and MLO mammograms used to build our models. [Color figure can be viewed at wileyonlinelibrary.com]

TABLE II. Percentage of cases given each accuracy rating on the performance of the automated edge detection algorithm by the two expert observers. Each observer rated a different sample of 50 paired mammograms. The employed scale ranges from 5 (perfect) to 1 (inappropriate).

Rating	5	4	3	2	1
Observer 1	30%	54%	14%	2%	0%
Observer 2	22%	36%	38%	4%	0%

The purpose of the individual CC and MLO models is to characterize breast shapes with a small set of parameters (backward application), while the joint model is better to generate new, realistic, linked CC and MLO contours from a randomly generated breast (forward application).

Therefore, for the joint model, the histograms of the eigenvalues of the first 12 PCA parameters, found to be enough to represent the breast shape in detail, are computed and then fit with a Gaussian distribution (mean μ , standard deviation σ). For further characterization of this model, possible dependencies between the PCA parameters and the breast area and thickness are analyzed. Furthermore, the exact influence of each parameter j on the breast shape is studied after varying its value independently, from $(\mu_j - 2\sigma_j)$ to $(\mu_j + 2\sigma_j)$, while the other parameters are held constant at their mean values.

2.D. Testing of PCA-based edge representation of mammographic shape

The ability of the PCA models to characterize breast shapes with a small set of parameters is tested via leave-one-out cross-validation.³³ Each image j , of the total of k used for the main PCA model, was modeled with a PCA built from the other $k-1$ images. For each of these images, the modeled edge (t_m) is computed according to

FIG. 5. Examples of the edge segmentation performed by our algorithm for paired CC and MLO views, highlighting the areas that were removed. Example of paired views qualified as 5 by the independent resident radiologist (top), and a pair scored as 2 (bottom), due to the failure to completely remove the non-mammary tissue on the medial side of the CC view and to accurately follow the pectoralis muscle edge in the MLO view. [Color figure can be viewed at wileyonlinelibrary.com]

Eq. (2). The accuracy of t_m is calculated via the average distance error (ADE, in mm) between the modeled and the original edge t_i :

$$ADE = \frac{(T_m \cup T_i) - (T_m \cap T_i)}{0.5(L_i + L_t)} \quad (3)$$

where T_m and T_i are the areas of binary images created by shape filling the edge t_m and t_i , of length L_m and L_i respectively. The ADE is compared when using different number of principal components as well as between the joint and individual models at a fixed number of components, by

performing a paired t-test. The ADE is separately computed for the CC, MLO, and pectoralis muscle shape.

3. RESULTS

3.A. Mammography database

Table I shows the average values of the projected breast area, compressed breast thickness, and compression force for both CC and MLO views from the set of mammograms used to build our model. Only a weak relation between thickness

and projected breast area is found, after studying different possible relations among the three parameters (Fig. 4).

3.B. Automated edge detection

From the 982 paired mammograms, 51 (5.2%) were discarded by the human observer as our algorithm failed to successfully segment the breast contour. Therefore, our database was reduced to 931 paired mammograms. The ratings of both experienced observers on the accuracy of the edge segmentation are shown in Table II. Of the cases not scored as 5, observer number 1 reported problems in the pectoralis muscle in 89% percent of the cases and observer 2 in 59% percent of the cases. Similarly, observer 1 reported problems with the medial non-mammary tissue segmentation in 11% of the cases, and observer 2 in 29% of the cases. Almost all of the edges (98% for observer 1 and 96% for observer 2) were scored as at least successful representations of the breast shape (defined as a rating of 3 or higher).

Examples of the automated edge detection can be seen in Fig. 5. The delineated breast edges are overlaid as dots in yellow (see online version for color). The different anatomical parts considered as non-breast tissue that our algorithm aimed to detect and correct are indicated by arrows.

3.C. Principal component analysis

After performing PCA and obtaining the three different models, CC-only, MLO-only and joint CC and MLO, we observe in Fig. 6 that the individual models contain a larger proportion of the variance of the breast shapes for a given number of principal components used to build the model than the joint model. To reach 99% of cumulative variance, the CC-only model needs four components, the MLO-only model needs seven components, and the joint model requires at least 10 components. As expected, all the models converge toward 100% for higher number of parameters.

The first 12 principal components (labeled from alpha (α) to nu (ν)) of the joint CC and MLO model were successfully fit to Gaussian functions (Fig. 7). It was found that the first parameter alpha (α) was better fit to a two-term Gaussian (two-term $R^2 = 0.96$ versus one-term $R^2 = 0.82$). The same applies for the second parameter beta (β) (two-term $R^2 = 0.99$ versus one-term $R^2 = 0.95$). We note how the standard deviations of the Gaussian fits decrease with increasing order of the component.

3.D. PCA joint-model for novel breast shape generation (forward application)

We use the Gaussian fits (Fig. 7) of the parameters of the joint model for the generation of novel breast shapes. By taking the mean values of the distributions (for the first 12 parameters) we obtain an *average* compressed breast shape as shown in Fig. 8 (top), where a randomly generated shape is also plotted on the bottom for comparison. The projected area

Fig. 6. Cumulative percentage of the total variance represented by the models (CC-only, MLO-only and joint CC and MLO model), as a function of the number of principal components included.

of this model-generated average breast is 154.4 cm^2 in the CC view and 206.2 cm^2 in the MLO view (where 39.1 cm^2 corresponds to the area encompassed by the model-generated average pectoralis muscle). The average CC view breast can be approximated, by matching the area, to a semiellipse of radius 10.5 cm in the x direction and 10.2 cm in the y direction. Nevertheless, actually the average CC view is not symmetric on the horizontal axis since there is an area displacement toward the lateral side of the breast.

Figure 8 (top) also includes plots of the average breasts found by Feng et al. Two features can be seen in the comparison between those shapes and the ones generated here that show the impact of the changes incorporated in this new model. First, the current model results in larger average breasts, perhaps a demonstration that the previous database, being limited to breasts that fit in a $19 \times 23 \text{ cm}$ detector, introduced a size bias. Second, in addition to the smaller MLO average breast, the influence of the inclusion of the infra-mammary fold in the Feng et al. MLO view shape is apparent, resulting in a considerably different breast shape representation.

As supplementary material, a spreadsheet with the necessary data to apply this model and generate novel linked CC and MLO breast shapes is provided. In this spreadsheet, the user can select an estimate of the breast size to generate (*large, medium, small, random*), as well as turn on or off the generation of the pectoralis edge. An *a posteriori* condition was also implemented to prevent the pectoralis muscle shape to go beyond the MLO contour. Moreover, the user can generate a large batch of random paired breast profiles. This spreadsheet also includes diagrams showing the influence on the breast shape of each of the first 12 parameters. A strong relationship is found between the first parameter, alpha, and the compressed breast projected area (Fig. 9) and hence can be used to estimate breast size. No relationship among any of the other parameters with the projected breast area is found, as they simply regulate detailed

FIG. 7. Histograms and Gaussian fits of the eigenvalues of the first 12 (labeled from alpha to nu) principal components of the joint CC and MLO model. The first two components, alpha (α) and beta (β), were found to be better represented by a two-term Gaussian. All the R-squared parameters of the fits were above 0.95. [Color figure can be viewed at wileyonlinelibrary.com]

features of the breast shapes in both views and in the pectoralis muscle.

3.E. PCA for shape representation (backwards application)

For each of the analyzed shapes (CC, MLO, and pectoralis muscle), the individual models exhibit lower ADEs than the joint model at any particular number of components (Fig. 10), with $P \leq 0.001$.

All the models showed a consistent improvement to represent more accurately the different shapes with increasing number of principal components ($P \leq 0.08$), as seen in Fig. 10. In particular, when going from 2 to 6 components, the CC-only model average ADE decreases by 75% (from 3.21 to 0.81 mm), in the MLO-only model it decreases by 63% (from 4.40 to 1.64 mm), and with the joint model it decreases by 49% (from 4.90 to 2.47 mm, averaged for all shapes).

For the individual models, in order to reach an average ADE below 1 mm, the CC edge requires at least 5 components, the MLO shape requires 9 components, and the pectoralis shape needs at least 10 components. Some examples of the ADEs for CC and MLO images obtained with the

individual models using 2 and 6 principal components are displayed in Fig. 11.

4. DISCUSSION

We have developed three objective models of compressed breast shapes undergoing mammography, which improve the accuracy and clinical relevance of the work by Feng et al.²⁹ With our study, we provide the first step into more complex applications that require the use of objective and clinically relevant 2D and 3D models of compressed breasts undergoing mammography or tomosynthesis, either by modeling breast edges with a small set of parameters or by generating new random CC and MLO views from the same breast, based on objectively obtained models.

The mammography database we have employed to develop the models has similar size properties (Table I) than the ones used by other authors. The compressed breast thickness (60.3 mm in CC and 60.7 mm in MLO) is similar to the one reported by Young et al.³⁴ (56.3 mm in CC and 59.3 mm in MLO, using 87,122 images in the United Kingdom) and Branderhorst et al.³⁵ (60.7 mm using 1851 mammograms from the Netherlands, and 59.9 mm using 9188

FIG. 8. Paired CC and MLO shapes of the average breast (top), and from a randomly generated breast (bottom), using our 12-component joint model, and the corresponding list of the eigenvalues of these breast shapes. For comparison, the average shapes generated by Feng et al. based on a mammography database acquired with a smaller detector size are also included. The axes units are expressed in cm. [Color figure can be viewed at wileyonlinelibrary.com]

images from the US). Moreover, we have found an equivalent mean breast thickness between the two mammography views, as reported also by Timmers et al.³⁶ (59.1 mm in CC and 60.1 mm in MLO, using 179 mammograms in the Netherlands). This might be due to the use of a higher compression force in the MLO view with respect to the CC view. The average projected breast areas in each view, computed from the automatically detected edges by our algorithm, are smaller than the ones reported by Timmers et al., but still comparable.

The automated edge detection has proven to be successful, but the degree of complexity introduced in the algorithm leads to different levels of precision as confirmed by the validation study. This is the main limitation of this study, but it should not be significant since more than 95% of the detected edges are qualified as successful representations of the actual breast shapes. The problems in the segmentation algorithm have been found to be mainly localized in the pectoralis muscle and the medial non-mammary tissue segmentation. However, for the pectoralis, the observers reported randomly over- and under-estimations of the edge, thus its impact on the shape representation might be low.

FIG. 9. The alpha parameter (first component) of the joint model computed from every case used on the PCA as a function of the breast surface encapsulated by the segmented edges, for both the MLO and CC views. The data can be fit to a power function, showing how the MLO and CC increase in size in a similar fashion with increasing alpha. [Color figure can be viewed at wileyonlinelibrary.com]

The application of the PCA generated models can be in two different directions: backwards (by characterizing any breast edge contour of an obtained mammogram with a small set of parameters) and forwards (generating new random clinically relevant breast shapes). For the latter, a joint model (not present in the work by Feng et al.) allows us to generate objective paired CC and MLO views from a same randomly generated breast, increasing the potential applications of the model. The projected area of the average generated CC view (154.4 cm²) is between the mean and the median areas of the CC view mammograms in the database, pointing to the validity of the PCA. Furthermore, this value is in agreement with the one reported by Boone et al. for the average breast in the CC view (157.3 cm², from 82 patients in the USA).³⁷ Also, the average projected areas are significantly greater than the ones obtained by Feng et al. (Feng et al.: CC: 144 cm² and MLO: 191 cm² vs. this work: CC: 154 cm² and MLO: 206 cm²), overcoming the main bias of that study (based on mammograms acquired with a 19 × 23 cm flat panel detector).

We observe how the individual models contain a greater cumulative variance than the joint model for the same number of components (Fig. 7). Thus, they are more optimal for the backwards application, since we can achieve more accurate representations of breast shapes for a given number of components. Also, it has to be considered that CC and MLO views are independent. The ADEs of the individual models are similar to the ones reported by Feng et al., despite having a bigger variability within our database due to the larger detector size and higher number of mammograms employed. This might be caused by our enhanced edge detection algorithm, which removes some of the non-mammary features in the mammograms, such as the inframammary fold in the MLO view and small irregularities where the nipple is located.

FIG. 10. Whisker box plots comparing the ADE obtained with the individual models and the ADE from the joint model, for every analyzed shape (CC, MLO and pectoralis muscle). All the models showed a consistent improvement in representing the breast shape more accurately with an increasing number of components, showing both lower median values and lower values for the percentiles. The individual models perform better for all shapes in comparison to the joint model. [Color figure can be viewed at wileyonlinelibrary.com]

Note that the backwards application of our models is independent of the algorithm employed to segment the image, as long as it has similar aims as ours when it comes to detect only the actual breast tissue. In general, it is found that with the individual models, 4 components are enough to have an accurate modeling of a breast shape undergoing mammography.

The joint CC and MLO shapes model has been implemented on an Excel worksheet (see supplementary material) available for download as supplementary material, where the

user can automatically generate novel clinically relevant paired CC and MLO breast shapes, each from the same randomly generated breast. Different breast sizes (*large, medium, small, random*) can also be selected, which results in the spreadsheet using different values for the first component of the model, α . The pectoralis muscle can be turned on or off, since it has been found that sometimes the model can randomly generate pectoralis shapes that go beyond the MLO contour due to the independence of the parameters. The influence of the 12 first principal components on the breast shape

FIG. 11. Examples of modeled CC and MLO breast edges (not used in PCA analysis) and their average distance error, by using either 2 or 6 principal components with the individual models. [Color figure can be viewed at wileyonlinelibrary.com]

is also included allowing custom-generation of novel objective contours of mammography breast shapes.

This joint model could help in the development of 2D and 3D breast software phantoms and in the generation of large libraries of clinically relevant breast shapes. These libraries could be used in Monte Carlo simulations to compute scatter correction maps or accurate dosimetry values, both for mammography and digital breast tomosynthesis. With the individual models, new mammograms acquired in the clinic can be quickly characterized by a small set of parameters, and then matched to the corresponding closest scatter map within our library. This is a topic of current work.⁹

5. CONCLUSION

In this work, we develop a set of objective models of compressed breasts undergoing mammography. These models are a continuation of the work by Feng et al.,²⁹ and they overcome the main bias of that study since now we work with mammograms acquired with a standard flat panel detector size. Furthermore, we also improve the relevance and accuracy of the models as the breast shapes are automatically segmented to a region of interest containing only actual breast tissue, we model the pectoralis shape, and we obtain a joint model for CC and MLO paired views.

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CONFLICT OF INTEREST

Ioannis Sechopoulos has research and speaker agreements with Siemens, a research agreement with Toshiba and is a scientific advisor of Fischer Imaging.

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

Data S1. Spreadsheet that includes the objective model of compressed breast shapes