A SOFTWARE TOOL TO MEASURE THE GEOMETRIC DISTORTION IN X-RAY IMAGE SYSTEMS

Gabriel Prieto, Eduardo Guibelalde, Margarita Chevalier

Dept. Radiología. Fac. Medicina. Universidad Complutense de Madrid.
28040 Madrid (Spain)
gprietor@med.ucm.es , egc@med.ucm.es ,chevalier@med.ucm.es

ABSTRACT

A software tool is presented to measure the geometric distortion in images obtained with X-ray systems that provides a more objective method than the usual measurements over the image of a phantom with usual rulers. In a first step, this software has been applied to mammography images and makes use of the grid included into the CDMAM phantom (University Hospital Nijmegen).

For digital images, this software tool automatically locates the grid crossing points and obtains a set of corners (up to 237) that are used by the program to determine 6 different squares, at top, bottom, left, right and central positions. The sixth square is the largest that can be fitted in the grid (widest possible square). The distortion is calculated as ((length of left diagonal - length of right diagonal)/ length of left diagonal) (%) for the six positions. The algorithm error is of the order of 0.3%. The method might be applied to other radiological systems without any major changes to adjust the program code to other phantoms.

In this work a set of measurements for 54 CDMAM images, acquired in 11 different mammography systems from 6 manufacturers are presented. We can conclude that the distortion of all equipments is smaller than the recommendations for maximum distortions in primary displays (2%)

Keywords: Geometric distortion, mammography, CDMAM.

1. DESCRIPTION OF PURPOSE

To automate a method to measure the distortion in mammography systems, avoiding the errors, fluctuations and subjectivity that a manual measurement can introduce.

2. MATERIAL AND METHODS

We have developed our algorithms as a Java plugin inside ImageJ, the image manipulation program developed by Wayne Rasband [1]. Our software developments will be periodically updated in our website http://www.ucm.es/info/fismed/Digital_Imaging/Digital_imaging_archivos/slide0001.htm including object and source codes, manual instructions and several test images.

The CDMAM phantom consists of an aluminium base with gold discs of varying thicknesses and diameters, which is attached to a polymethyl-methacrylate cover. The discs are arranged in 16 rows and 16 columns. The lines that make the rows and columns determine a grid with up to 237 crossing points (Figure 1).
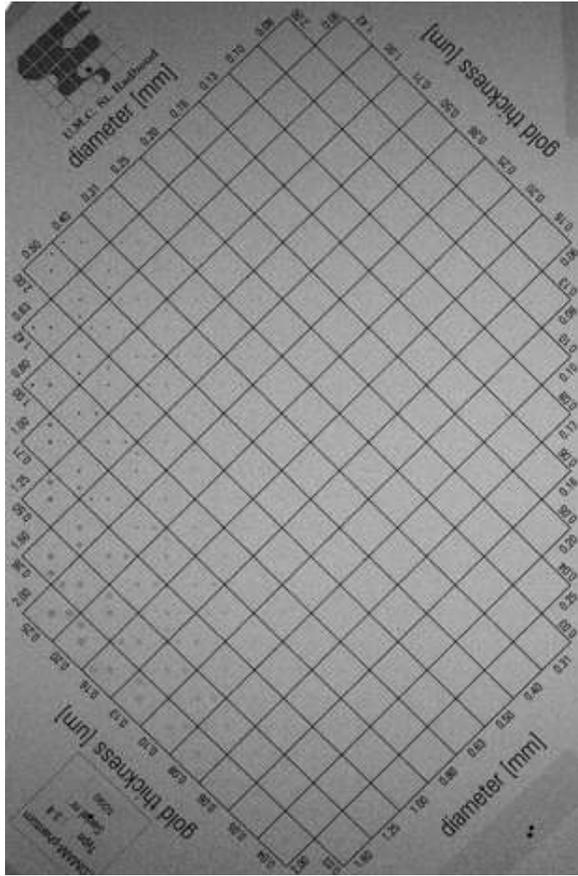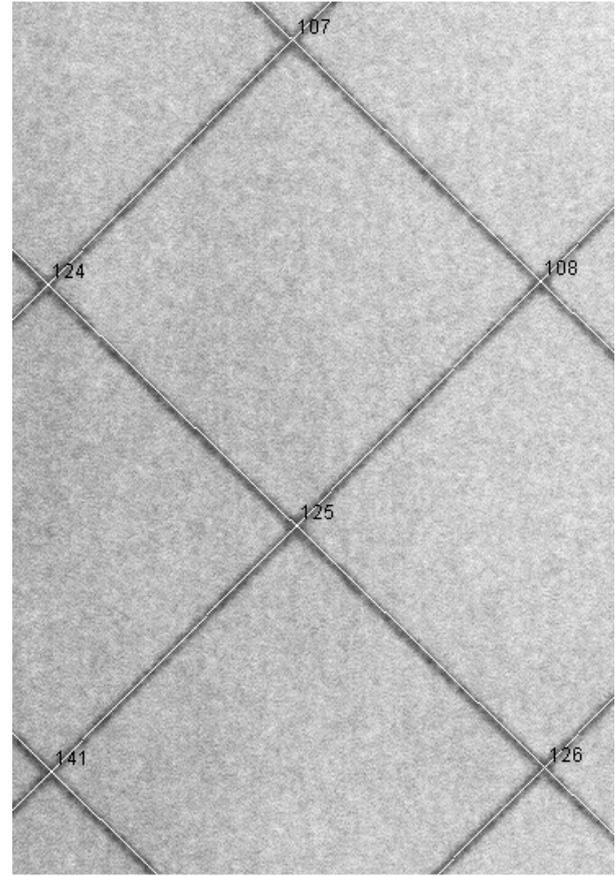
Figure 1. CDMAM image.

Figure 2. Grid superimposed

2.1. Detection of grid position.

Several methods have been applied to find the grid position for other purposes [2] [3]. The method used in this work was designed to be simple, time effective and shows a very small error, on the basis that we have complete information about the geometry of the CDMAM. This method has been described in some previous works [4] [5]. We have tested this algorithm with more than 100 images from instruments from different manufacturers and models. The error in the calculation of the crossing points of the grid is never larger than 2 – 3 pixels. Figure 2 shows the calculated grid and the crossing points superimposed to the CDMAM image.
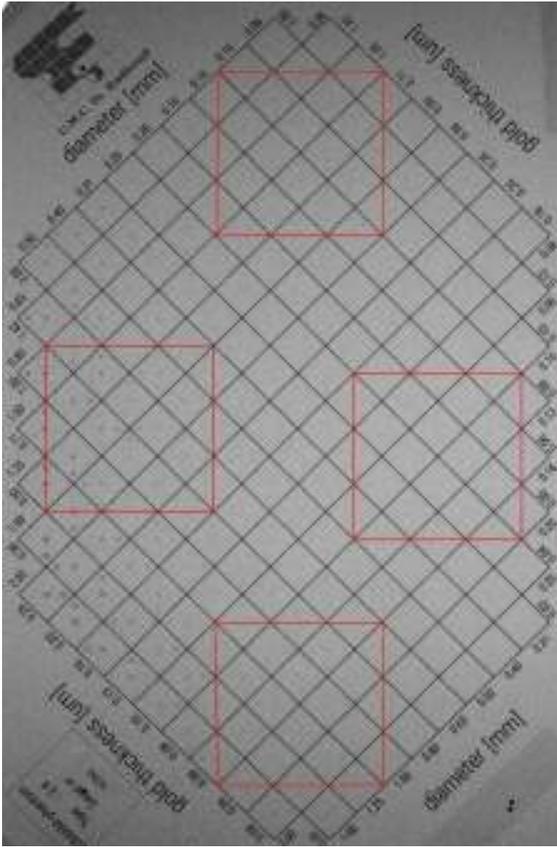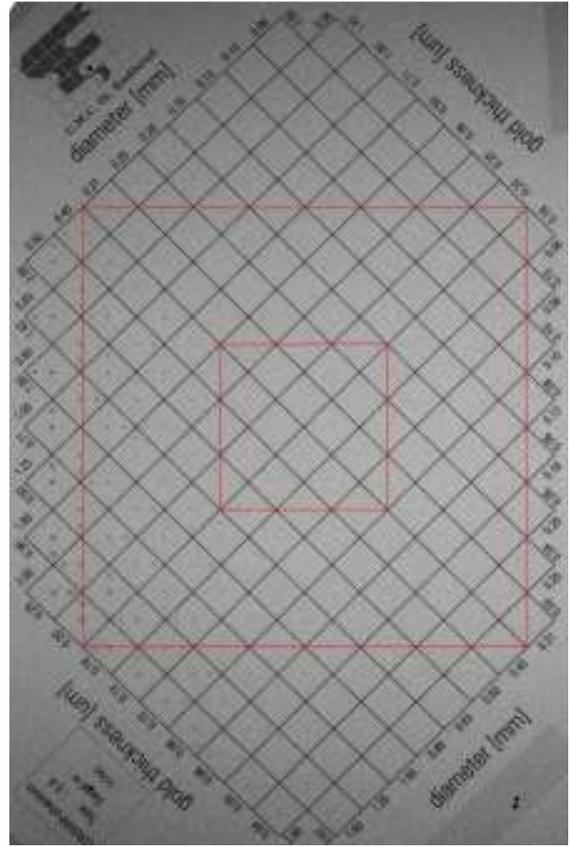
Figure 3. Top, bottom, right and left areas.

Figure 4. Wide and central areas.

2.2. Areas of distortion calculation.

Some authors have proposed methods to measure the distortion in medical displays [6]. These methods propose the measurement in square areas in the horizontal and vertical directions in each of the four quadrants of TG18-QC test pattern and within the whole pattern. Alike, in this method the distortion is calculated as ((length of left diagonal - length of right diagonal)/length of left diagonal) (%) for each square of figures 3 and 4. The algorithm error is of the order of 0.3% - 0.4% (2 – 3 pixels in the diagonal length), tested by visual inspection in the whole set of analyzed images.

3.3. Selection of areas and results.

The squares shown in figures 3 and 4 are the default squares to measure the distortion. Any case, the squares can be selected by the user in another areas of interest, using the interface of the program (Figure 5). The number of each corner is shown in Figure 7, assuming that the CDMAM is oriented as is shown in figures 3 and 4. The squares of figures 3 and 4 have been selected because they have a maximum size inside each region of interest, but another measures or situations could be of interest for other researchers. Figure 6 shows the program output.
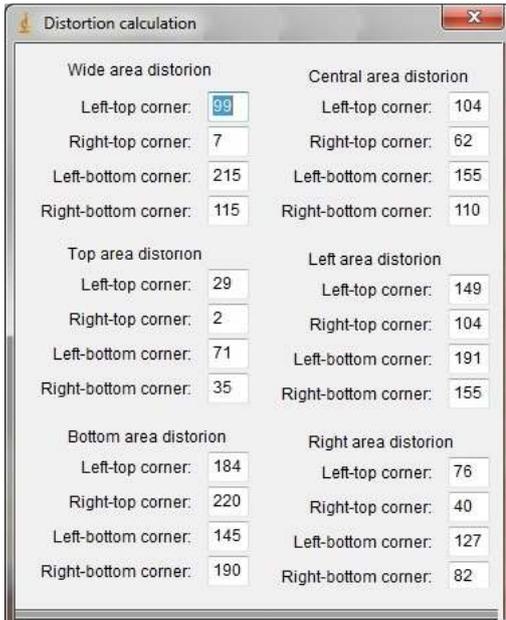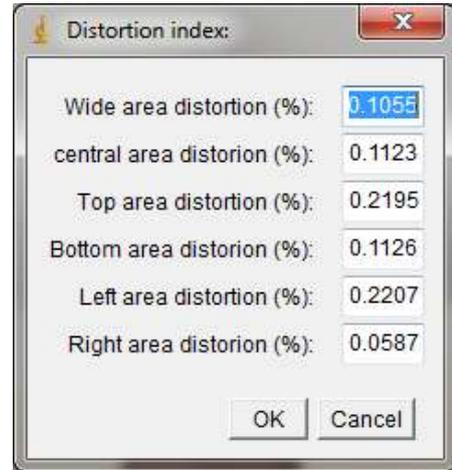
Figure 5. Corner selection for each square.
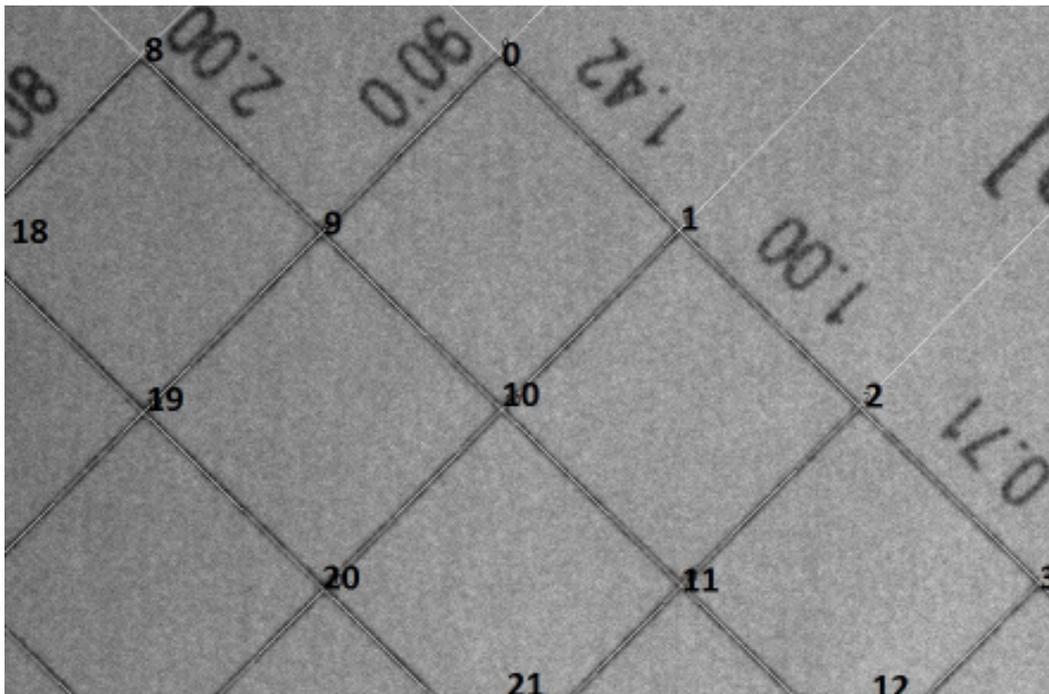

Figure 6. Program output.

Figure 7. Order of the corners inside the CDMAM

3.3. Similar areas using the TG-18 phantom.

The main reference that can be found in the literature for the image quality assessment related to geometry distortion is *E. Sahmei et al., "Assessment of display performance for medical imaging systems: Executive summary of AAPM TG18 report", 1205 Med. Phys. 32 .4. April 2005* [6]. The geometry distortion is proposed to be measured with a general-purpose phantom: TG-18. In our study we have measured this distortion in the CDMAM phantom, of exclusive use in mammography but, according to [6], we can define similar areas in the TG-18 to measure the equivalent distortion (see figures 8 and 9). Therefore, the measures of geometric distortion with these phantoms are equivalent.
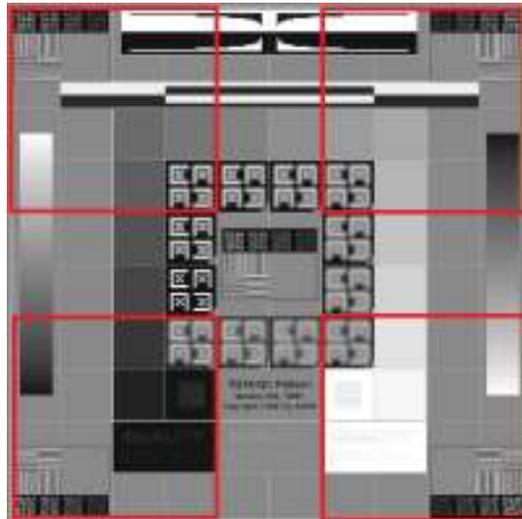

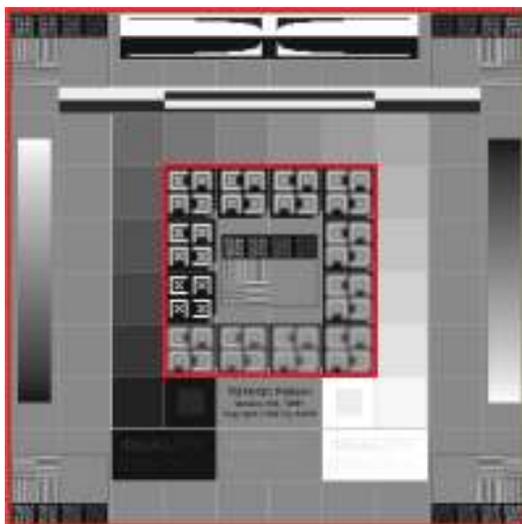Figure 8. Top, bottom, right and left areas.

Figure 4. Wide and central areas.

3. RESULTS

Equipment: General Electric Senograph 2000D.
Resolution: 100 μ/pixel.
Test set: 8 images.
Error (by visual inspection): 0.4%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%

Equipment: LORAD Hologic Selenia. S/N: H1KRHR832b7913.
Resolution: 50 μ/pixel.
Test set: 8 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%

Equipment: AGFA CR ADC_5148 S/N: 1259.
Resolution: 50 μ/pixel.
Test set: 6 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.1%	0.1%	0.1%	0.1%	0.2%	0.1%

Equipment: FUJI FILM AMULET S/N: 20003.
Resolution: 50 μ/pixel.
Test set: 6 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.1%	-0.1%	0.1%	0.1%	-0.4%	-0.1%

Equipment: FUJIFILM CR.
Resolution: 50 μ/pixel.
Test set: 6 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.0%	-0.1%	0.1%	-0.1%	0.2%	-0.1%

Equipment: SIEMENS Mammorat Novator DR S/N: 1072.
Resolution: 75 µ/pixel.
Test set: 6 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.1%	-0.1%	0.0%	-0.3%	-0.1%	0.0%

Equipment: SECTRA L30 S/N: 101430-10.
Resolution: 50 µ/pixel.
Test set: 8 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.3%	-0.3%	1.2%	-1.7%	-0.4%	-0.4%

Equipment: SECTRA L30 S/N: 101449-10.
Resolution: 50 µ/pixel.
Test set: 4 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.0%	-0.1%	1.6%	-1.5%	-0.2%	-0.1%

Equipment: SECTRA L30 S/N: 1014350-10.
Resolution: 50 µ/pixel.
Test set: 4 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.1%	-0.1%	1.5%	-1.7%	-0.2%	-0.2%

Equipment: SECTRA L30-MDM 1.5 S/N: 666.
Resolution: 50 µ/pixel.
Test set: 4 images.
Error (by visual inspection): 0.3%.

	Wide	Central	Top	Bottom	Left	Right
Average	0.7%	0.7%	1.9%	-0.8%	0.7%	0.6%

4. DISCUSSION

The distortion of all equipments is smaller than the recommendations for maximum distortions in primary displays (2%) [6]. In fact, the distortion is smaller than the error in all the experiments with the exception of Sectra models. For these systems the distortion in top and bottom squares is always around +/- 1.5%. We have verified this behaviour with different systems of the same model (L30). In this case, the distortion might be due to the scanning process in Sectra systems. The scanning geometry of these systems has a fixed distance between the detector and the X-ray source, and consequently the reference geometry of the acquired image is slightly curved, which is matched by a similar curvature of the patient support. The distortion figure of merit for this system is therefore negatively biased by the assumption of a flat reference system. For a correct measurement of the distortion for these systems, a slightly curved CDMAM should be available. However, the limits are acceptable (< 2%) even using a flat phantom.

5. CONCLUSION

The new software tool presented in this work can be used for automatic calculation of image geometric distortions (before the displaying step). The system is fast (from 15 s. to 60 s. for images with resolutions from 100 µ/pixel to 50 µ/pixel) and accurate. The distance from the automatically located crossing points to the actual positions has been tested by visual inspection for each image of the study. The difference is always smaller or equal to 3 pixels. This algorithm could also be applied to others radiological imaging techniques that use phantoms with square patterns or, at least, with objective points that could make a square.

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