Using Data Mining Techniques to Support Breast Cancer Diagnosis

Joana Diz[1], Goreti Marreiros[2], and Alberto Freitas[3]

[1] Institute of Engineering-Polytechnic of Porto, Porto, Portugal
[2] GECAD - Knowledge Engineering and Decision Support Group, Institute of Engineering-Polytechnic of Porto, Porto, Portugal
[3] Center for Health Technology and Services Research (CINTESIS) and Department of Health Information and Decision Sciences (CIDES), Faculty of Medicine, University of Porto, Portugal
joanamoreira.diz@gmail.com, mgt@isep.ipp.pt, alberto@med.up.pt

Abstract. More than ever, in breast cancer research, many computer aided diagnostic systems have been developed in order to reduce false-positives diagnosis. In this work, we present a data mining based approach which might support oncologists in the process of breast cancer classification and diagnose. A reliable database with 410 images was used containing microcalcifications, masses and also normal tissue findings. We applied two feature extraction techniques, specifically the gray level co-occurrence matrix and the gray level run length matrix, and for classification purposes several data mining classifiers were also used. The results revealed great percentages of positive predicted value (approximately 70%) and very good accuracy values in terms of distinction of mammographic findings (>65%) and classification of BI-RADS® scale (>75%). The best predictive method and the best performance on the distinction of microcalcifications found was the Random Forest classifier.

Keywords: Breast cancer diagnosis; Features extraction; Data mining techniques.

1 Introduction

Breast cancer is a public health problem that, despite not being the most lethal, has both high incidence and high mortality rate, especially among women.

According to data collected by the "Liga Portuguesa Contra o Cancro" [1] it is estimated that in Portugal, with a female population of about 5 million people, near 4500 new cases of breast cancer are detected annually and about 1500 women die from this disease each year, which is equivalent to 4 cases per day.

In a global way, and according to the International Agency for Research on Cancer (IARC), in 2012 there were estimated close to 1.7 million breast cancer diagnoses, which is approximately 11.9% of all worldwide cancers diagnosed in the same year, and about 522000 women have died from the disease in the same year worldwide [2].

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In the same study, 19.3 million new cancer cases are expected by 2025, and the largest increase will be in breast cancer [2].

As an attempt to counteract this trend, there is a need for implementation of early diagnosis and patient monitoring systems, as well as, better and more approachable health care. A quick advance of technology and the increasingly computerized resources will allow the realization of new platforms for medical care, which may include electronic recording and decision support systems.

The main objective of this work relied on the creation of an effective toolkit to support breast cancer diagnose by the application of data mining techniques. By this we intended to create a decision support approach that could be used either to assist professionals or to help students in the correct identification using learning platforms. It could improve the diagnose accuracy and treatment, became a tool to better understand the patterns of disease and be fundamental in training new specialists.

The application of classifying methods was later evaluated aiming to determine which features and classifiers have a better performance in identifying features on mammograms.

2 Breast Cancer

The breast cancer is a disease that reflects an uncontrolled growth of breast cells in the event of an error in the DNA sequence. About 95% of these cancers are carcinomas once they arise as breast epithelial elements [3]. In turn, usually about 80% of carcinomas are originated in the mammary ducts (DCIS) and 20% in the lobes (LCIS) [4, 5].

The favorable survival rate in breast cancer is due to two factors: the first one relies on the detection of the disease at an early stage through mammograms, and the second factor is due to advances in adjuvant systemic treatment such as chemotherapy and hormonal therapy for example.

2.1 Breast Cancer Types

Not all breast masses are synonymous of cancer. These are distinguished according to frequency of appearance, as is the case of cysts and fibroids, which appear and disappear in a given period, or as fibro adenomas and intraductal papilloma, which are abnormal growths that may indicate a risk factor. The masses clearly indicate that cancer is a carcinoma; a term used to describe a cancer that starts in the coating layer of organs (epithelial cells) such as the breast [6].

In breast tissue, a mass is an important change observed on a mammogram and can be cysts (non-cancerous fluid-filled sacs) and fibro adenomas (non-cancerous solid tumors) but a biopsy is always required to identify whether or not they are malignant. On the other hand, in case of the presence of a calcification, which are small deposits of calcium minerals, which can appear singly or in clusters [6].

2.2 Classification Criteria

In order to ensure the quality of collection and the data processing, the development of international guidelines has become essential to ensure the quality of data supplied by various sources [7].

The American College of Radiology (ACR) [8] is the copyright owner of a work entitled "Breast Imaging Reporting and Database System (BI-RADS®)" that contains a guide for the standardized mammographic opinion, including a lexicon of terminology, an organization of medical report as well as an evaluation framework and coding system. The BI-RADS® then suggests a standardized method for reporting breast imaging that does not presume to dictate individual decisions of case management.

Briefly described, the BI-RADS® guideline has six levels, level 0 being the inconclusive report or incomplete review; level 1 being the normal mammogram without lesions; levels 2 and 3 representing the benign findings and BI-RADS 3 the need of initial follow up; level 4 and 5 represent anomalies suspected and a risk of malignancy from 20 to 75%; and the final category, BI-RADS 6, shows a malignancy proven by biopsy that did not undergo surgery/treatment with 100% of risk of breast cancer [7, 8].

According to a study by Boyd [9] and later complete by several other studies [10, 11], breast density is the most important factor that influences the mammographic sensitivity. These studies were based on the concept of exposure of breast tissue as a relevant measure for breast cancer incidence. Various classification methods of breast density have emerged over the years [12] of which the most widely used worldwide is the ACR, developed in 2003, which identifies four types of mammographic density [8]. The model of classification and standardization presenting meets the following criteria:

(1) Predominantly lipomatous (< 25% glandular tissue);
(2) Density fibro granulate dispersed (25-50%);
(3) Heterogeneously dense breast (51-75%);
(4) Extremely dense breast (> 75% glandular tissue) [8].

3 Methodology

The main advantage of data mining techniques is the ability to provide a set of useful rules capable of discriminating between a series of supposed risks [13]. Classification is a fundamental task in data mining techniques and relies on a process of differentiating two or more classes by labelling each similar set of data in a single class. The application of classifying methods was evaluated with the objective to determine which features and classifiers have a better performance in identifying features on mammograms.

3.1 Data Description

The images used in this work were taken from the repository INbreast [14], developed by multiple institutions of the University of Porto and available to the public with

authors' consent. The INbreast includes a total of 410 images (115 patients), from which 90 patients are women whose both breasts were affected (four images per case) and 25 of the cases are mastectomy patients (two images per case). The sample also includes some types of findings (masses, calcifications, distortions and asymmetries) which were classified by specialists.

The available mammograms were firstly preprocessed in Matlab® and smoothed (with Gaussian low-pass and top-hat filtering) in order to prevent the loss of details that could be important for the following steps. The Gaussian filter was used to create a correlation kernel factor that was applied to the image [15, 16, 17]. Subsequent, the first method of extraction of characteristics was applied followed by the selection of the region of interest (ROI) and an image conversion into 4-bit, required to the second feature extraction methodology. In this way, a total of 410 images were processed and, in some cases, several injuries were observed on a single mammogram, giving a total of 439 characteristics, with respect to the multiple injuries found in a single image.

3.2 Features Extration

Features extraction is a key point that should be taken into account in the implementation of a decision support system. It recognizes breast tissue by selecting the most important features, and also due to its ability to describe and maximize differences in tissues and/or injuries [18]. Due to this, we selected texture as an important image characteristic that has been widely used in medical image analysis especially in its automatic classification [19, 20].

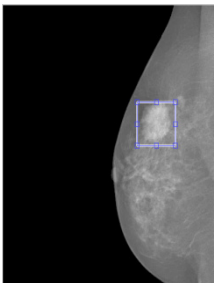

Fig. 1. Matlab selection of region of interest on a mammogram

In this work, two MATLAB® functions of feature-based matrices were used: GLCM (Gray-level co-occurrence matrix) and GLRLM (Gray-level run length matrix). The first is a statistical method of texture examination that considers the spatial relationship between the image pixels, and the second are based on computerizing the number of lines of grey levels at various angles [18, 19, 21].

The values of each feature extracted from the matrices above mentioned were removed twice at the same image, Table 1, the first for a ROI with a lesion finding, SRE_L for example, and the second for a clean/normal ROI, such as SRE_N. This technique allowed us to better understand the relationship between the normal tissue and a lesion for each mammogram.

Table 1. Features extracted

GLCM	GLRLM
Contrast ; Correlation; Energy ; Homogeneity.	Short run emphasis (SRE); Long run emphasis (LRE) ; Gray level non-uniformity (GLN); Run length non-uniformity (RLN); Run percentage (RP); Low Gray Level Run Emphasis (LGRE); High Gray Level Run Emphasis (HGRE).

The correlation between variables was later evaluated through SPSS®. Our case study revealed that the majority of variances are equal, showing a significant level (2-tailed) approximately to 0.001, which reveals that in addition to having significant correlation ($p < 0.05$) they also revealed significant interest ($p < 0.001$). This method allows us to remove of the GLN variable due to the fact that it is the only one that does not have a significant correlation with the lesion discrimination ($p > 0.05$).

3.3 Classification Methods

Several classification methods were used, such as: k-nearest Neighbor Support Vector Machine, Decision Tree (J48), Random Forest and Naive Bayes. The different classification methods were selected in terms of good accuracy on other databases and lack of results for comparison when using the INbreast database. The application of these different approaches was carried out in order to clarify which was the most efficient classifier for each case and compare with some related studies [17, 23], even if they were applied to other databases [22, 24, 25]. To apply these methods we use WEKA® software version 3.6.11 and ten-fold cross-validation.

To evaluate the influence of different classifications at the same dataset we created three different files. The first file has the BI-RADS classification with GLRLM outputs for each described case and was named BI-RADS file. The second includes both breast density classification made by radiologists and the GLCM matrix (without ROI selection) that we called BrD file. Finally, the last one was created to relate the finding type (mass, microcalcification or normal tissue) with GLRLM, for every image finding described (Characteristic file).

4 Results and Discussion

Therefore, and to analyze the results, they were compared in terms of some metrics. The area under the curve (AUC) represents a way to select optimal models, independently of the cost or the class distribution context. Using AUC values, researchers may trace ideal profiles and be aware of a greater efficiency of the method when AUC value is closer to one. Sensitivity and specificity are statistical measures

of the performance, the first referring to the test's ability to identify a condition correctly and the second metric, specificity, representing the proportion of negatives which are correctly identified as such. The positive predicted value (PPV) for each classifier was also included to better adapt the results with the clinical practice.

In order to find both the best predictor and the best method for breast cancer diagnosis, global accuracy was presented and analyzed in terms of the global percentage of success for each classifier.

First Scenario: In the first scenario we related the BI-RADS® classification with features extracted from GLRLM.

Table 2. Results for GLRLM with BI-RADS® subclass classification

Classifier	BI-RADS® subclass	PPV	AUC	Sensitivity	Specificity	Global Accuracy
Naïve Bayes	Benign	0.205	0.486	0.538	0.532	53.3%
	Malignant	0.837	0.486	0.532	0.538	
SVM - SMO	Benign	0.050	0.508	0.571	0.523	52.5%
	Malignant	0.965	0.508	0.523	0.571	
k-NN	Benign	0.657	0.789	0.724	0.707	71.4%
	Malignant	0.767	0.789	0.707	0.723	
J48	Benign	0.427	0.604	0.634	0.592	60.6%
	Malignant	0.771	0.604	0.592	0.633	
Random Forest	Benign	0.757	0.831	0.757	0.775	76.7%
	Malignant	0.775	0.831	0.775	0.757	

While conducting our study we concluded that the results of the chosen parameters were good for each classifier, however, the best predictor method was the Random Forest. With this classifier we were able to achieve values around 76.0% PPV, both for benign and malignant findings, which led us to conclude that this method has a good success rate as well as AUC (0.831), sensitivity and specificity (approximately 0,78 and 0,76 each). The results of this scenario also show that the Naïve Bayes and SVM-SMO revealed the worse percentages in terms of mean values for all measures.

From this analysis, we were able to conclude that using BI-RADS® classification for prediction has a large disadvantage because of its 5 classes. Due to this and to avoid inconsistencies derived from the different weight for each class we adopted the method of dividing BI-RADS® classes into benign and malignant, according to some studies conclusions [26, 27].

Second Scenario: The second tested scenario was based on the GLCM features' extraction related to BrD, according to ACR.

Table 3. Results of GLCM with BrD

Classifier	BrD by ACR	PPV	AUC	Sensitivity	Specificity	Global Accuracy
Naïve Bayes	1	0.592	0.725	0.534	0.791	34.5%
	2	0.206	0.480	0.276	0.615	
	3	0.165	0.596	0.250	0.753	
	4	0.538	0.750	0.182	0.959	
SVM - SMO	1	0.633	0.782	0.679	0.828	49.7%
	2	0.817	0.594	0.418	0.786	
	3	0.000	0.666	0.000	0.753	
	4	0.000	0.500	0.000	0.929	
k-NN	1	0.792	0.820	0.638	0.886	54.9%
	2	0.557	0.647	0.514	0.743	
	3	0.363	0.712	0.500	0.808	
	4	0.038	0.651	0.091	0.930	
J48	1	0.625	0.784	0.658	0.823	51.6%
	2	0.557	0.655	0.507	0.741	
	3	0.429	0.722	0.429	0.812	
	4	0.115	0.612	0.158	0.934	
Random Forest	1	0.725	0.829	0.690	0.864	58.7%
	2	0.603	0.715	0.556	0.770	
	3	0.516	0.785	0.553	0.844	
	4	0.115	0.704	0.200	0.935	

Comparing our results with the ones obtained in Fonseca work [22], which uses the same database, we realized that for k-NN and SVM methods the results are similar. According to fatty tissue the results for correctly classified instances (approximately 55%), corresponding to our 1 and 2 classes, are the ones with highest instances overall, being a contribution to the hit rate. In terms of Random Forest we obtained the best results, comparing to a previous work [22], since the accuracy for fatty and dense tissue was around 52.0% while we obtained a better result, with 58.7% accuracy.

Through this scenario we observed that in terms of density distinction, by using GLCM the results from classes' prediction presented a great range, maybe due to the different number of initial data in each class and also related to the features similarities extracted to neighboring classes as 1-2, 2-3 and so far. For Random Forest classifier, which was the better method, the PPV and sensitivity values were not invariants according to each class, ranging from 72.5% to BrD 1 and 11.5% to BrD 4. Once again the reason for these results could be related to the features' similarities or to the size of each class represented in the database. An effective approach to improve

these results could be to have a similar number of instances in each class or to group those four classes in half by way of creating a cutoff point at 50.0% of the glandular tissue.

Third Scenario: The last scenario analyzed was related to the type of finding observed for each case. In order to find the best predicting method, those findings were grouped into three subsets (3a, 3b and 3c). The first represents the previously given classification in the database (Mass, Micro and Normal); the second subset is only related to one type of reported lesion – microcalcification and the final subset concerns a general approach that reveals the presence of a lesion on the tissue, no matter its type.

Table 4. Results for 3a subgroup (mass, micro and normal tissue distinction)

Classifier	Subclass	PPV	AUC	Sensitivity	Specificity	Global Accuracy
Naïve Bayes	Mass	0.911	0.700	0.348	0.949	58.7%
	Micro	0.356	0.774	0.913	0.487	
	Normal	1.000	1.000	1.000	1.000	
SVM - SMO	Mass	0.000	0.605	0.000	0.770	76.9%
	Micro	1.000	0.705	0.726	1.000	
	Normal	1.000	1.000	1.000	1.000	
k-NN	Mass	0.228	0.636	0.315	0.787	70.8%
	Micro	0.813	0.737	0.736	0.653	
	Normal	1.000	1.000	1.000	1.000	
J48	Mass	0.000	0.600	0.000	0.770	76.9%
	Micro	1.000	0.703	0.726	1.000	
	Normal	1.000	1.000	1.000	1.000	
Random Forest	Mass	0.257	0.628	0.280	0.783	67.6%
	Micro	0.749	0.729	0.727	0.591	
	Normal	1.000	1.000	1.000	1.000	

Through analyzing the results obtained from subgroup 3a (Table 4), in terms of global percentage of correctly classified instances in distinguishing between mass, microcalcification and normal tissue, our tests revealed that for all classifiers, normal tissue show a percentage of 100.0% correctly classified instances. Despite this fact, classifiers such as Naïve Bayes or Random Forest revealed low values at the level of overall effectiveness and the best results were obtained using SVM-SMO and J48, both presenting 76.9% accuracy. Even though these last two methods have shown better global performance, by analyzing their results for each class individually, we found that none of them have correctly classified masses and achieved 100.0% of

PPV for microcalcifications. In turn, k-NN with an accuracy of 70.8% has classified every class, even though for masses it did not reveal promising results (PPV = 0.228 and sensitivity = 0.315).

Table 5. Results for 3b subgroup (microcalcification distinction)

Classifier	Subclass	PPV	AUC	Sensitivity	Specificity	Global Accuracy
Naïve Bayes	Micro	0.352	0.630	0.879	0.337	49.5%
	No micro	0.871	0.630	0.337	0.879	
SVM - SMO	Micro	1.000	0.500	0.000	---	72.5%
	No micro	0.000	0.500	0.726	0.725	
k-NN	Micro	0.798	0.573	0.727	0.280	63.8%
	No micro	0.208	0.573	0.280	0.727	
J48	Micro	1.000	0.492	0.726	---	72.5%
	No micro	0.000	0.492	0.000	0.671	
Random Forest	Micro	0.798	0.577	0.753	0.752	66.3%
	No micro	0.307	0.577	0.365	0.365	

By analyzing Table 5, we were able to recognize that there is no classifier that seems to be the best at all evaluated levels. Regardless of this and considering PPV, the best performance achieved for micros' identification was made by J48 and SVM-SMO, however, for other lesions, specifically for mass identification, the results obtained were the worst. Due to this, Naïve Bayes was considered the best test result evaluating the mean values and the best on distinguish masses, while Random Forest was regarded as the best in terms of global accuracy, showing the best results on microcalcifications' classification.

The final subset that was studied (3c) concerned a general approach that reveals the presence of a lesion on the tissue, no matter its type. By the results of this scenario we observed that all the individual methods accomplished the maximum value of prediction (100% of each field). Through this we can ensure that with our method all lesions were distinguished from normal tissue.

The conclusions made over this last scenario were interesting for the reason that masses are in lower number (267 micros and 101 masses), a fact emphasized in global accuracy percentages, which are 59.0% on subset 3a and 50.0% on subset 3b, approximately. Even though this global percentage was not optimal, it represents an interesting point for future investigation since it contradicts other studies which concluded that microcalcifications are a more predictable lesion than masses [28, 29].

5 Conclusions

With our results we can ensure the effectiveness of the developed method for cancer detection on a mammogram, through the use of injury classifiers (BI-RADS®) and breast density (BrD).

Some recent works have been using the INbreast database even when applied to other classification methods for malignancy [23, 30] or for fatty/dense tissue identification [17, 22]. The work developed by Carneiro et al. [17] has used a clustering k-means applied to some Haralick features and showed 85% of accuracy for identifying density classes. By comparing these results to the ones we obtained, we can conclude that clustered density classes would be a better method to identify them. Another classification method used by [23], linear discriminant analysis, has also presented great results with 89% of accuracy in classifying findings into benign and malignant. Once more, compared to our results the difference between the values could be explained by different pre-processing methods, despite the setting value of accuracy being close.

To better understand if the global accuracy values are reliable, we intend to apply the models proposed in this work to other databases in order to compare results. The techniques used on image pre-processing step can also be improved and ROI selection for GLRLM extraction features could be automatically selected in order to avoid misclassifications To implement these improvements a different software should be considered, since there is a need for faster and more efficient processing, a possible solution could be for instance use a language such as C++. Other findings should also be considered, such as bilateral asymmetry and architectural distortion.

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References

1. LPCC. Liga Portuguesa Contra o Cancro (February 13, 2014), http://www.ligacontracancro.pt/gca/index.php?id=14
2. Bray, F., Ren, J.S., Masuyer, E., Ferlay, J.: Global estimates of cancer prevalence for 27 sites in the adult population in 2008. International Journal of Cancer 132(5), 1133–1145 (2013)
3. Kumar, V., Abbas, A.K., Fausto, N., Aster, J.: Robbins and Cotran Pathologic Basis of Disease. Professional Edition: Expert Consult-Online. Elsevier Health Sciences (2009)
4. Khatib, O.M., Modjtabai, A.: Guidelines for the early detection and screening of breast cancer: EMRO Technical publications Series 30. World Health Organization (2006)
5. Health NIo. Breast Cancer. ADAM Medical Encyclopedia: PubMed Health (2012)
6. Society AC. American Cancer Society: Breast Cancer detailed guide2013, http://www.cancer.org/cancer/breastcancer/
7. Force UPST. Screening for breast cancer: US Preventive Services Task Force recommendation statement 151(10), 716 (2009)

8. Radiology ACo. ACR BI-RADS® Atlas: American College of Radiology(February 02, 2014), http://www.acr.org/Quality-Safety/Resources/BIRADS/About-BIRADS
9. Boyd, N.F., Martin, L.J., Bronskill, M., Yaffe, M.J., Duric, N., Minkin, S.: Breast tissue composition and susceptibility to breast cancer. Journal of the National Cancer Institute (2010)
10. Boyd, N.F., Martin, L.J., Yaffe, M.J., Minkin, S.: Mammographic density and breast cancer risk: current understanding and future prospects. Breast Cancer Research 13(6), 223 (2011)
11. Wang, A.T., Vachon, C.M., Brandt, K.R., Ghosh, K. (eds.): Breast Density and Breast Cancer Risk: A Practical Review. Mayo Clinic Proceedings. Elsevier (2014)
12. Gierach, G.L., Ichikawa, L., Kerlikowske, K., Brinton, L.A., Farhat, G.N., Vacek, P.M., et al.: Relationship between mammographic density and breast cancer death in the Breast Cancer Surveillance Consortium. Journal of the National Cancer Institute (2012)
13. Malucelli, A., Stein, J.A., Bastos, L., Carvalho, D., Cubas, M.R., Paraíso, E.C.: Classification of risk micro-areas using data mining. Revista de saude publica 44(2), 292–300 (2010)
14. Moreira, I.C., Amaral, I., Domingues, I., Cardoso, A., Cardoso, M.J., Cardoso, J.: INbreast: toward a full-field digital mammographic database. Academic Radiology 19(2), 236–248 (2012)
15. Teixeira, R.: Automatic Analysis of Mammography Images: Classification of Breast Density: MSc Dissertation; Universidade do Porto (2013)
16. Suri, J.S., Wilson, D.L., Laxminarayan, S.: Handbook of biomedical image analysis. Springer (2005)
17. Carneiro, P.: e A Patrocínio. Análise de atributos de intensidade e textura na classificação de densidade mamária. XXIV Congresso Brasileiro de Engenharia Biomédica (CBEB), Brazil (2014)
18. Meselhy, E.M., Faye, I., Belhaouari, S.B.: A statistical based feature extraction method for breast cancer diagnosis in digital mammogram using multiresolution representation. Computers in Biology and Medicine 42(1), 123–128 (2012)
19. Mohanty, A.K., Senapati, M.R., Beberta, S., Lenka, S.: Texture-based features for classification of mammograms using decision tree. Neural Computing and Applications 23(3-4), 1011–1017 (2013)
20. Chen, C.-H., Pau, L.-F., Wang, P.S.: Handbook of pattern recognition and computer vision. World Scientific (2010)
21. Nanni, L., Brahnam, S., Ghidoni, S., Menegatti, E., Barrier, T.: Different approaches for extracting information from the co-occurrence matrix. PloS One 8(12), e83554 (2013)
22. Da Fonseca, J.L., Cardoso, J.S., Domingues, I.: Pre-CADs in Breast Cancer. Idea 2(3) (2013)
23. Domingues, I., Sales, E., et al.: Inbreast-Database masses characterization. XXIII CBEB; Brazil (2012)
24. Bueno, G., et al.: Automatic breast parenchymal density classification integrated into a CADe system. International Journal of Computer Assisted Radiology and Surgery 6(3), 309–318 (2011)
25. Ramos-Pollán et al.: Discovering mammography-based machine learning classifiers for breast cancer diagnosis. Journal of Medical Systems 36(4), 2259–2269 (2012)
26. Lacquement, M.A., Mitchell, D., Hollingsworth, A.B.: Positive predictive value of the breast imaging reporting and data system. Journal of the American College of Surgeons 189(1), 34–40 (1999)

27. Obenauer, S., Hermann, K., Grabbe, E.: Applications and literature review of the BI-RADS classification. European Radiology 15(5), 1027–1036 (2005)
28. Amendolia, S.R., Bisogni, M.G., Bottigli, U., Ceccopieri, A., Delogu, P., Dipasquale, G., et al.: The CALMA project. Nuclear Instruments and Methods in Physics Research Section A: Accelerators, Spectrometers, Detectors and Associated Equipment 461(1), 428–429 (2001)
29. Bellotti, R., Bagnasco, S., Bottigli, U., Castellano, M., Cataldo, R., Catanzariti, E., et al.: The MAGIC-5 Project: medical applications on a GRID infrastructure connection. In: 2004 IEEE Nuclear Science Symposium Conference Record, IEEE (2004)
30. Matheus, B., Schiabel, H.: A CADx Scheme in Mammography: Considerations on a Novel Approach. ADVCOMP 2013. In: The Seventh International Conference on Advanced Engineering Computing and Applications in Sciences (2013)