SSJ01

Breast Imaging (Quantitative Imaging)

Sub-Events

SSJ01-01  3D Computer-Aided Detection (CAD) System for Breast Tomosynthesis in the Detection of Microcalcifications: Initial Experience

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PURPOSE

To evaluate the performance of a 3D computer-aided detection (CAD) system for breast tomosynthesis (DBT) in the detection of microcalcifications in comparison with 2D CAD for digital mammography.

METHOD AND MATERIALS

3D CAD (ImageChecker 1.0, Hologic) and 2D CAD systems (R2 ImageChecker CAD 9.3, Hologic) were retrospectively applied to combined DBT-digital mammograms of 68 women (mean age, 51 years; range, 30-77 years) with 68 microcalcifications (31 malignant [14 invasive, 17 DCIS], 37 benign; BI-RADS category 2 in 19, category 3 in 2, category 4 in 31, and category 5 in 16). Number of DBT reconstructed slices obtained per breast ranged from 36 to 76 (mean, 56.7). CAD marks were considered positive if the location of the corresponding lesions were correctly identified on at least one slice of DBT or one view of digital mammograms. Sensitivities for malignancy and for recalled lesions were defined as the number of lesions correctly marked divided by the total number of malignant lesions and by the number of the BI-RADS category 3, 4, or 5 lesions, respectively. To evaluate the false-positive mark rate, 20 mammograms with no clinical or radiologic abnormalities during 2-year follow-up in 20 women were used. Differences between 3D and 2D CAD systems were compared by using McNemar test and Wilcoxon signed rank test.

RESULTS

Sensitivities of 3D CAD were similar to those of 2D CAD for both malignancies (97% [30/31] vs. 100% [31/31], P = 1.0) and recalled lesions (97% [48/49] vs. 100% [49/49], P = 1.0). 2D CAD correctly marked one additional cancer at one view, which was missed by 3D CAD. For the 20 normal mammograms, mean false-positive marks per view with 3D CAD was similar to that of 2D CAD (0.13 vs. 0.14, P = 0.48).

CONCLUSION

3D CAD for DBT achieved 97% sensitivities for both malignant and recalled microcalcifications with 0.13 false-positive marks per view, which was comparable to those of 2D CAD.

CLINICAL RELEVANCE/APPLICATION

3D CAD is expected to reduce the interpretation time for radiologists in the detection of suspicious microcalcifications in reconstructed DBT slices with high sensitivity and an acceptable false positive rate.

SSJ01-02  Prediction of False-positive Recall from Screening Mammography Using Computer-extracted Breast Tissue Complexity Features: Data from the ACRIN 4006 trial

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PURPOSE
To investigate the feasibility to predict risk of false-positive recall from breast cancer screening with digital mammography based on computer-extracted parenchymal pattern features of breast tissue complexity.

METHOD AND MATERIALS

Digital mammography (DM) images from the ACRIN 4006 trial were retrospectively analyzed. The trial was a reader study to compare screening call-back rates from 2D DM versus a combination of 2D/digital breast tomosynthesis (DBT) in an enriched cohort of women. From a total of 550 women imaged, 76 were recalled on the basis of DM alone, from which 11 were true-positives. Images were acquired using a full-field digital mammography (FFDM) unit. All DM images sets consisted of bilateral CC and MLO views and were vendor post-processed ("For Presentation", Selenia Hologic Inc.). To characterize breast tissue complexity, breast percent density (PD) was estimated on a per-woman basis using previously validated automated software. In addition, thirteen texture features were extracted using a locally adaptive computerized parenchymal texture analysis algorithm. Logistic regression was performed to identify significant predictors of overall recall and false-positive recall respectively, adjusting for age and number of previous benign biopsies. The area under the curve (AUC) of the receiver operating characteristic (ROC) was used to evaluate model performance.

RESULTS

The logistic regression model has AUC=0.75 (95% CI 0.69-0.81) for predicting overall recall from DM and AUC=0.94 (95% CI 0.87 - 0.99) for predicting risk of false-positive recall; outperforming prediction based on age and number of previous benign biopsies alone that have AUC=0.64 (95% CI 0.57 - 0.70) and AUC=0.73 (95% CI 0.51 - 0.94) respectively. Significant predictors (p<0.05) are energy, inertia, inverse difference moment, sum average, sum variance, difference average, difference variance and difference entropy. Sensitivity for predicting false-positive recalls is 80% at a 100% cancer detection ROC operating point.

CONCLUSION

Prediction of false-positive recall from DM screening mammography could be improved with the inclusion of computer-extracted features of breast tissue complexity.

CLINICAL RELEVANCE/APPLICATION

Prediction models could identify women at high-risk for false-positive DM screening due to their breast tissue complexity, who may be offered supplemental modalities for breast cancer screening.

Fully Automated Volumetric Breast Density Estimation from Digital Breast Tomosynthesis Images: Multi-modality Comparison with Digital Mammography and Breast MRI

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PURPOSE

Accurate breast density estimation is important for breast cancer risk assessment and guiding personalized breast screening recommendations. We investigate the feasibility of fully-automated volumetric breast density estimation (VBD) from digital breast tomosynthesis (DBT), and compare to VBD estimates from digital mammography (DM) and breast MRI. Compared to 2D mammography, DBT visualizes the 3D distribution of fibroglandular tissue, having the potential to allow for more accurate VBD estimation.

METHOD AND MATERIALS

Bilateral DBT images, DM images (Selenia, Hologic Inc.) and sagittal MRI scans (GE LX echo speed, Siemens) were retrospectively collected from 63 women undergoing breast cancer screening within the course of one year (2010-11). A fully-automated algorithm was developed to segment the fibroglandular tissue and measure VBD from all DBT images. The proposed algorithm exploits the geometry of the acquisition of DBT sequences as well as the relationship between image intensity and tissue density and achieves 3D segmentation of the fibroglandular tissue by analyzing both the projection images and reconstructed DBT slices. For comparison, the DM images were processed with FDA-cleared software (Volpara 1.5, Matakina) and the MR images were processed with previously validated automated software to obtain corresponding VBD estimates. The Pearson's correlation and linear regression were used to compare the obtained multi-modality VBD estimates.

RESULTS

Substantial agreement is observed between bilateral VBD estimates from DBT images (r = 0.89, 95% CI: 0.83-0.93, p<0.001). Estimates of the total breast volume and percent volumetric breast density from DBT are highly correlated with DM with r = 0.99 (95% CI: 0.98-0.99) and r = 0.88 (95% CI: 0.81-0.93); as well as with the MR-based estimates with r = 0.95 (95% CI: 0.91-0.96) and r = 0.76 (95% CI: 0.63-0.85), respectively (p<0.001). Corresponding correlations between DM and MRI are r = 0.95 (95% CI: 0.92-0.97) and r = 0.73 (95% CI: 0.59-0.83).

CONCLUSION

Fully-automated 3D fibroglandular tissue segmentation and VBD estimation from DBT images is feasible and shows strong agreement with existing volumetric techniques based on DM and MRI images.

CLINICAL RELEVANCE/APPLICATION

Fully-automated quantitative VBD estimation from DBT could result into more accurate measures of the
Three-Compartment Breast Imaging and Quantitative Mammographic Image Analysis: Synergy for Improved Diagnosis


PURPOSE

To investigate whether knowledge of the biologic composition of breast lesions and the embedding parenchyma, derived through three-compartment breast (3CB) imaging, can improve upon existing mammographic quantitative image analysis (QIA) in estimating the probability of malignancy.

METHOD AND MATERIALS

3CB imaging is a novel imaging technique that derived biologic tissue composition measures from dual-energy mammography and a thickness phantom at about 110% of the dose of a regular mammogram. The study population consisted of 96 patients with 102 breast lesions imaged with dual-energy mammography prior to breast biopsy with final diagnosis resulting in 16 invasive ductal carcinomas, 10 ductal carcinoma in situ (DCIS), and 76 benign diagnoses. Analysis was three-fold: 1) The raw low-energy mammographic images were analyzed with an established in-house QIA method, 'QIA alone', 2) the 3-compartment breast (3CB) composition measure - derived from the dual-energy mammography - of water, lipid, and protein thickness were assessed, '3CB alone'), and 3) information from QIA and 3CB was combined, 'QIA+3CB'. Analysis was initiated from radiologist-indicated lesion centers and was otherwise fully automated. Steps of the QIA and 3CB methods were lesion segmentation, characterization, and subsequent classification for malignancy in leave-one-case-out cross-validation. Performance was assessed using Receiver Operating Characteristic (ROC) analysis with the area under the ROC curve (AUC) as figure of merit.

RESULTS

The AUC for distinguishing between benign and malignant lesions (invasive and DCIS) was 0.78 (standard error 0.06) for the 'QIA alone' method, 0.66 (0.06) for '3CB alone' method, and improved to 0.85 (0.05) for 'QIA+3CB' combined (p=0.05 with respect to 'QIA alone').

CONCLUSION

Combining knowledge of the composition of breast lesions and their periphery with an existing mammographic QIA method improved the distinction between benign and malignant lesions, which could help prevent unnecessary biopsies and improve diagnostic decision making.

CLINICAL RELEVANCE/APPLICATION

Three-Compartment Breast Imaging quantitatively assesses tissue composition of breast lesions and parenchyma and yields information largely independent from what can be gleaned from mammography alone, which could help increase biopsy yield while reducing unnecessary biopsies.

Classification of Breast Cancer Subtypes Using MRI Texture Features

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PURPOSE

Breast cancer subtypes have been classified based on tumor genotype variation and are indicators of disease free and overall survival. Using texture features extracted from magnetic resonance imaging (MRI) and a machine learning method, we investigated whether imaging characteristics could differentiate breast cancer subtypes.

METHOD AND MATERIALS

This retrospective study received institutional review board approval and need for informed consent waived. 178 women with invasive ductal carcinoma (IDC) and preoperative breast MRI were identified. Immunohistochemistry surrogates defined subtypes, and the distribution was: estrogen and progesterone receptor positive (ERPR+; n=95, 53.4%), HER2 receptor positive (HER2+; n=35, 19.6%) and triple negative (TN; n=48, 27.0%). Clinical and pathologic data were collected. Tumors were contoured on the fat-suppressed T1-weight pre- and three post-contrast images. Shape-, texture- and histogram-based features were extracted using in-house software (Computational Environment for Radiological Research). Support vector machine (SVM), a frequently used machine learning technique for classification problems, was used to identify significant image features and build a robust model to predict each IDC subtype.
RESULTS

SVM identified significant clinical, pathologic and imaging features. When the top 9 features were incorporated, the predictive model distinguished IDC subtypes with an overall accuracy of 83.4%. The model's accuracy for each subtype was 89.2% (ERPR+), 63.6% (HER2+) and 82.5% (TN). The nine features were: nuclear grade, tumor volume, presence of multi-centric disease, three texture features, and three histogram-based features. For these features, statistical analysis was performed using Kruskal-Wallis test. For all the 9 features, there was a statistically significant difference between ERPR+, HER2+ and TN subtypes with p < 0.0001.

CONCLUSION

We have developed a machine learning-based predictive model using texture features extracted from MRI that can distinguish IDC subtypes with significant predictive power.

CLINICAL RELEVANCE/APPLICATION

We were able to leverage computer-derived MRI phenotypic image-based biomarkers that reflect the genetic variability of different breast cancer subtypes, which are associated with different outcomes.

Relationship of Quantitative MRI-based Phenotypes and the Molecular Classifications of Breast Cancers in the TCGA/TCIA Dataset


PURPOSE

To investigate the performance of MRI-based phenotypes in predicting the molecular classification of breast cancers in The Cancer Genome Atlas dataset of NCI.

METHOD AND MATERIALS

Quantitative image analysis was performed on 98 de-identified, MRI studies depicting biopsy-proven breast cancers MRI studies from the NCI's multi-institutional The Cancer Imaging Archive and The Cancer Genome Atlas project. Immunohistochemistry molecular classification determined estrogen (ER+82/ER-16), progesterone (PR+75/PR-23) and HER2 (HER2+16/HER2-16) receptor status for each case. Computerized image-based phenotyping included: 1) 3D lesion segmentation based on a fuzzy c-means clustering algorithm; 2) computerized feature extraction; 3) leave-one-out linear stepwise feature selection; and 4) Linear Discriminant Analysis (LDA) as the prognostic predictive classifier. The performance of the classifier model for molecular subtyping was evaluated using jackknifing ROC analysis with area under the ROC curve (AUC) as the figure of merit.

RESULTS

Use of computer-extracted tumor phenotypes in for the task of distinguishing between molecular prognostic indicators, yielded AUC values of 0.79 (p-value < 0.0001), 0.68 (p-value = 0.0066), and 0.61 (p-value =0.126) in the tasks of distinguishing ER- vs ER+, PR- vs PR+, and HER2- vs HER2+, respectively. Features selected for the predictive tasks included volumetrics, texture (entropy), and kinetics for the predictive tasks.

CONCLUSION

The results from this study indicate that quantitative MRI analysis shows promise as a means for high-throughput image-based phenotyping in the discrimination of breast cancer subtypes, and potential. Merging imaging phenotypes with genomic data may lead to improved prognostic predictors.

CLINICAL RELEVANCE/APPLICATION

Computerized image-based phenotyping may yield quantitative predictive models of breast cancer for precision medicine.