RC215

Breast Series: Hot Topics (The In-Person Presentation is Supported by an Unrestricted Educational Grant from Hologic)

Monday, Nov. 26 8:30AM - 12:00PM Room: Arie Crown Theater

AI BR

AMA PRA Category 1 Credits ™: 3.50
ARRT Category A+ Credits: 4.00

FDA Discussions may include off-label uses.

Participants
Linda Moy, MD, New York, NY (*Moderator*) Nothing to Disclose
Fiona J. Gilbert, MD, Cambridge, United Kingdom (*Moderator*) Research Grant, Hologic, Inc; Research Grant, General Electric Company; Research Grant, GlaxoSmithKline plc; Research Consultant, Alphabet Inc

Sub-Events

RC215-01 Radiomics

Monday, Nov. 26 8:30AM - 8:50AM Room: Arie Crown Theater

Participants
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Active Handout:Karen Drukker

http://abstract.rsna.org/uploads/2018/18000478/RSNA2018_Drukker_Handout RC215-01.pdf

LEARNING OBJECTIVES

1) Identify the scientific premise, motivation, and increasing role of radiomics in medical imaging. 2) Compare 'conventional' radiomics methods and deep learning-based radiomics methods. 3) Assess some of the challenges for radiomics-based decision support systems in becoming powerful players in modern precision medicine.

RC215-02 Quantitative Diffusion-Weighted MRI of Estrogen Receptor-Positive, Lymph Node-Negative Invasive Breast Cancer: Association between Whole-Lesion Apparent Diffusion Coefficient Metrics and Recurrence Risk

Monday, Nov. 26 8:50AM - 9:00AM Room: Arie Crown Theater

Participants
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PURPOSE

To investigate possible associations between quantitative apparent diffusion coefficient (ADC) metrics derived from whole-lesion histogram analysis and breast cancer recurrence risk in patients with estrogen receptor (ER)-positive, lymph node-negative invasive breast cancer who underwent the Oncotype DX assay.

METHOD AND MATERIALS

Institutional review board approval was obtained for this retrospective study, which was conducted on 74 women (mean age, 49.3 years) with ER-positive, lymph node-negative invasive breast cancer who underwent the Oncotype DX assay and preoperative diffusion-weighted MRI from July 2015 to January 2018. Histogram analysis of pixel-based ADC data of whole tumors was performed by two radiologists using a software tool and various ADC histogram parameters (mean, minimum, maximum, and 5th, 25th, 50th, 75th, and 95th percentile ADCs) were extracted. The ADC difference value (defined as the difference between minimum and maximum ADC) was calculated to assess intratumoral heterogeneity. Associations between quantitative ADC metrics and Oncotype DX risk groups (low [recurrence score (RS) <18], intermediate (RS 18-30), and high [RS >30]) were evaluated by receiver operating characteristic (ROC) curve and logistic regression analyses.

RESULTS

Whole-lesion histogram analysis showed minimum ADCs, maximum ADCs, and ADC difference values were significantly different between low and non-low (ie, intermediate and high) risk groups (0.604, 1.478, and 0.874 × 10-3mm2/s versus 0.374, 1.687, and

1.321 × 10-3mm2/s, respectively; P<0.001, P=0.010, and P<0.001, respectively). The ADC difference value yielded the largest area under the ROC curve (0.771; 95% confidence interval [CI]: 0.650, 0.891; P<0.001) for differentiating the two groups. Multivariate regression analysis showed that the ADC difference value was the only significant factor associated with low Oncotype DX risk group (adjusted odds ratio = 0.998; 95% CI: 0.996, 0.999; P<0.001).

CONCLUSION

The ADC difference value derived from whole-lesion histogram analysis could be helpful for identifying ER-positive, lymph node-negative invasive breast cancer patients with low risk of recurrence.

CLINICAL RELEVANCE/APPLICATION

In estrogen receptor-positive, lymph node-negative breast cancer, the ADC difference value derived from whole-lesion histogram assessments might serve as quantitative biomarkers of recurrence risk.

RC215-03 Radiomic Phenotypes of Tumor Heterogeneity from Pre-Operative DCE-MRI Predict Breast Cancer Recurrence after 10-Year Follow-Up: Phenotype Discovery and Independent Validation

Monday, Nov. 26 9:00AM - 9:10AM Room: Arie Crown Theater

Participants
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PURPOSE

To validate intrinsic imaging phenotypes of tumor heterogeneity and evaluate their prognostic performance in predicting 10-year recurrence.

METHOD AND MATERIALS

Pre-treatment DCE-MRI scans of 94 women with primary invasive breast cancer and 10-year follow up data available were retrospectively analyzed from a clinical trial cohort at our institution (2002-2006). For each woman, a signal enhancement ratio map was generated for the most representative slice of the primary lesion from which morphologic features were calculated. Radiomic features (histogram, run-length, structural, and co-occurrence matrix features) were extracted and summarized over tumor quadrants. Intrinsic phenotypes of tumor heterogeneity were identified via unsupervised hierarchical clustering applied to the extracted feature vectors, with significant clusters found using Consensus Clustering and the SigClust method. Differences across phenotypes by hormone receptor status, tumor size, post-surgery therapy, TNM staging, and recurrence outcomes were assessed using Chi-square and Kruskal-Wallis tests. An independent dataset of 116 women diagnosed with primary invasive breast cancer (2002-2006), available via The Cancer Imaging Archive, was used to validate phenotype reproducibility. Survival probabilities across phenotypes were evaluated using Kaplan-Meier curves and phenotype cluster assignments were added to a baseline Cox proportional hazards model with established histopathologic prognostic factors to predict RFS.

RESULTS

Three significant phenotypes of low, medium, and high heterogeneity were identified in the discovery cohort and reproduced in the validation cohort (p<0.001). No recurrent cases were found in the low heterogeneity phenotype (p<0.001). Clinical stage, mitotic grade, lymph invasion, and nuclear grade were different across phenotypes (p<=0.02). Kaplan-Meier curves showed significant differences (p < 0.001) in RFS probabilities across phenotypes. The augmented model including phenotype assignment had a higher discriminatory capacity (c-statistic= 0.80) compared to a baseline model with only established prognostic factors (c-statistic= 0.65, p<0.01).

CONCLUSION

Intrinsic imaging phenotypes of tumor heterogeneity can predict 10-year recurrence as validated in an independent dataset.

CLINICAL RELEVANCE/APPLICATION

Radiomic phenotypes could provide a non-invasive characterization of tumor heterogeneity to augment personalized prognosis and treatment.

Honored Educators

Presenters or authors on this event have been recognized as RSNA Honored Educators for participating in multiple qualifying educational activities. Honored Educators are invested in furthering the profession of radiology by delivering high-quality educational content in their field of study. Learn how you can become an honored educator by visiting the website at: https://www.rsna.org/Honored-Educator-Award/ Mitchell D. Schnall, MD, PhD - 2013 Honored Educator

RC215-04 Robustness of Computer-aided Diagnosis of Breast Cancer Using Radiomics and Machine Learning Classification of 1,461 Lesions across Populations in China and the United States

Monday, Nov. 26 9:10AM - 9:20AM Room: Arie Crown Theater

Participants
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PURPOSE

To assess the performance of computer aided diagnosis (CADx) in breast lesions imaged with DCE-MR in two patient cohorts, one in China and one in the United States (US), using extracted radiomic features and machine learning classification.

METHOD AND MATERIALS

Dynamic contrast-enhanced magnetic resonance (DCE-MR) images of 1,461 breast lesions (from China, GE scanners: 300 benign lesions, 302 malignant cancers; from the US, Philips scanners: 268 benign lesions, 591 malignant cancers) were collected under HIPAA and IRB compliance. The lesions were segmented automatically using a fuzzy c-means method. Thirty-eight radiomic features describing size, shape, morphology, kinetics, and texture were extracted using previously reported methods. The performance of CADx for classification between benign lesions and malignant cancers was evaluated with two methodologies: (a) independent training and testing of the datasets, with each set serving as a training set while the other served as a testing set; and (b) ten-fold cross validation within each set. Classification was performed using support vector machines with optimization of the hyperparameters. The area under the ROC curve (AUC) served as figure of merit, with its value and standard error determined using the conventional binormal model. The AUCs resulting from (a) and (b) were compared within and between each methodology. Difference in AUC was significantly different when $p < 0.05$.

RESULTS

When radiomic features extracted from MRIs acquired in China were used to train the machine classifiers and independent testing was conducted on MRIs acquired in the US, AUC = 0.77 (0.02), while the reverse resulted in AUC = 0.79 (0.02). For cross-validation within each set, AUC = 0.82 (0.02) for the US database and AUC = 0.80 (0.02) for the China database. AUCs compared across methodologies failed to show significant difference.

CONCLUSION

Computer aided diagnosis of breast lesions demonstrated potential robustness across independent populations in both independent training/testing and in cross validation.

CLINICAL RELEVANCE/APPLICATION

Radiomic features extracted from DCE-MRI may be robust for classifying breast lesions as benign or malignant across two cohorts (one in China, one in US), enhancing translation to clinical use.

RC215-05 Radiogenomics

Monday, Nov. 26 9:20AM - 9:40AM Room: Arie Crown Theater

Participants
Lars J. Grimm, MD, Durham, NC (*Presenter*) Editorial Advisory Board, Medscape, LLC; Educational program support, Hologic, Inc

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LEARNING OBJECTIVES

1) Define radiogenomics and describe how it differs from radiomics. 2) Examine the limitations of current radiogenomics research. 3) Assess the utility of radiogenomics in clinical practice. 4) Develop a framework to evaluate future radiogenomics research.

RC215-06 Proteomic Expression Underlying Quantitative MRI Features in Breast Cancer: A Radioproteomics Study

Monday, Nov. 26 9:40AM - 9:50AM Room: Arie Crown Theater

Participants
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PURPOSE

The complementary analysis of breast cancer via radiology imaging and molecular pathology approaches has spurred radiogenomics and radioproteomics studies. We performed an investigation of the relationships between quantitative radiomic imaging phenotype data and underlying proteomic expression, with the goal of improving precise breast cancer diagnosis and cancer behavior characterization.

METHOD AND MATERIALS

We identified a retrospective cohort of 40 invasive breast cancer patients from a single medical center. Their integrated protein expression data were obtained from The Cancer Genome Atlas study. The proteomic data was acquired via Reverse Phase Protein Array (RPPA) to measure the expression of 217 breast cancer related proteins and phospho-proteins. Dynamic Contrast Enhanced Magnetic Resonance Imaging (DCE-MRI) data of the 40 patients were collected from clinical archive, all acquired with a 1.5T same-vendor scanner. A set of 30 radiomic imaging features were extracted from automatically-segmented tumor volume in all 40 DCE-MRIs to capture tumor morphological and contrast enhancement characteristics. Multivariate linear regression was used to map the associations between each imaging feature with each of the 217 protein expressions, controlling for patient age and cancer stage. A p value was obtained evaluating the significance of the association and was adjusted for multiple comparisons of the selected radiomic feature against every protein. Adjusted p values less than 0.05 were recorded.

RESULTS

The average patient age at scan was 38.7±12 years, 10 (25%) of which were pre- with the rest post-menopausal. We found a variety of expression of cancer related proteins were significantly associated (positively or negatively) with a subset of morphological and contrast enhancement kinetics related imaging features. For example, ERCC5 (a protein responsible for DNA repair following UV-induced damage) is negatively associated with the tumor brightness and contrast agent uptake rates. The full association map is shown in the attached figure.

CONCLUSION

Our study showed that the expression of several cancer related proteins were found to be linearly associated with quantitative DCE-MRI-derived phenotype features in invasive breast tumors.

CLINICAL RELEVANCE/APPLICATION

Radioproteomic studies of cancer can help to decipher how molecular mechanisms may regulate the development of specific tumor phenotypes.

RC215-07 Prediction of 21-gene Recurrence Score in Patients with Estrogen Receptor-positive Early-Stage Breast Cancer Using MRI-based Radiomics Nomogram

Monday, Nov. 26 9:50AM - 10:00AM Room: Arie Crown Theater

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PURPOSE

To develop a breast MRI-based radiomics nomogram including pathologic factors which can predict low-risk recurrence score (RS) on 21-gene RS assay in patients with estrogen receptor-positive early-stage breast cancer (EBC).

METHOD AND MATERIALS

From 2011 to 2017, a total of 547 tumors in 539 patients with EBC who underwent preoperative breast MRI were retrospectively included in this study. Among them, low-risk was 320 (58.5%), intermediate-risk was 180 (32.9%), and high-risk was 47 (8.6%). We extracted 744 quantitative MR radiomic features from computerized three-dimensional segmentations of each tumor generated computer-extracted image phenotypes (CEIP) within the intratumoral regions of early post-contrast T1-weighted images, percent enhancement (PE) map, signal enhancement ratio (SER) map, and T2-weighted images. We divided 547 cases into a training set (n=365) and a validation set (n=182). Elastic net was used for feature selection and radiomics score building. Multivariate logistic regression analysis was used to develop a prediction model, we incorporated the radiomics score and independent pathologic risk factors and build a radiomics nomogram. Internal validation for an independent validation set (n=182) was performed.

RESULTS

The radiomics score, which consisted of 24 selected CEIPs, was significantly associated with the prediction of recurrence (C-index, 0.769 for training set and 0.745 for validation set). Independent pathologic predictors contained in the nomogram were progesterone receptor status, nuclear grade, histologic grade, extensive intraductal component, lymphovascular invasion, P53, and Ki67 status, and their C-index was 0.858 for training set and 0.774 for validation set. Addition of radiomics score to the pathologic nomogram showed an incremental value of 0.054 and 0.092, respectively. Radiomics nomogram showed good prediction of low-risk RS, with a C-index of 0.912 for training set and 0.866 for validation set.

CONCLUSION

This study shows that a radiomics nomogram which incorporates the MRI-based radiomics score and pathologic features, can be used to help the preoperative individualized prediction of low-risk RS in patients with EBC.

CLINICAL RELEVANCE/APPLICATION

Prediction nomogram using breast MRI-based radiomics score and pathologic predictors can be used to facilitate the preoperative individualized prediction of low-risk RS on 21-gene RS assay in patients with EBC.

RC215-08 Can Histogram Analysis of Dynamic Contrast-Enhanced MRI and Apparent Diffusion Coefficient Map Predict Molecular Subtypes of Invasive Breast Cancers?

Monday, Nov. 26 10:00AM - 10:10AM Room: Arie Crown Theater

Participants
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PURPOSE

To evaluate if histogram analysis of dynamic contrast-enhanced (DCE) MRI and apparent diffusion coefficient (ADC) maps with diffusion-weighted imaging (DWI) can predict molecular subtypes of invasive breast cancers.

METHOD AND MATERIALS

In this HIPAA-compliant and IRB-approved study we retrospectively evaluated 91 consecutive patients from January 2011 to January 2013 with invasive ductal carcinoma of the breast who underwent multiparametric MRI with DCE and DWI at our institution. The exclusion criteria were 1) lesion smaller than 1 cm, 2) previous treatment for breast cancer, 3) pathology report unavailable, and 4) poor image quality. One experienced breast radiologist drew a region of interest on DCE MRI and ADC maps on the slice with the largest diameter of the solid portion of the lesion avoiding cystic areas and biopsy markers. The histogram analysis was performed and the mean, variance, kurtosis and skewness were calculated. Molecular breast cancer subtypes were derived by IHC surrogates. Tumors were classified as luminal A if either ER or PR was positive and HER2 was negative, Luminal B if either ER or PR was positive and HER2 positive, HER2-enriched if ER and PR were negative and HER2 positive and triple-negative if ER, PR and HER2 were negative. Nonparametric Mann-Whitney U test and Kruskal-Wallis were used to compare groups of molecular subtypes. P-values <0.05 were accepted to be statistically significant.

RESULTS

The histogram analysis of DCE images and ADC maps of 91 breast cancers demonstrated no significant difference among breast tumor molecular subtypes. Measurements of the mean, variance, kurtosis and skewness were used to compare luminal A/B with HER-2 enriched/triple-negative cancers, without significant results for both DCE (p-value = 0.405, 0.252, 0.667, 0.809) and ADC (0.204, 0.081, 0.941, 0.574), respectively. Histogram measurements were also used to compare luminal A with other subtypes and also demonstrated no significant difference for DCE (0.659, 0.162, 0.516, 0.833) and ADC (0.204, 0.222, 0.495, 0.896).

CONCLUSION

Histogram analysis of DCE MRI and ADC map cannot predict molecular subtypes of invasive breast cancers.

CLINICAL RELEVANCE/APPLICATION

Despite many valuable applications of histogram analysis in diagnostic imaging, it cannot predict molecular subtypes of invasive breast cancers.

RC215-09 CESM Enhancement Pattern and Intensity and Its Correlation to Breast Cancer Immunophenotype: Preliminary Results

Monday, Nov. 26 10:10AM - 10:20AM Room: Arie Crown Theater

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PURPOSE

The differences in the intensity and pattern of enhancement in CESM between breast carcinomas might result from the differences in the amount of contrast that leaked out from the blood vessels and timely arrested in the interstitium. The aim of this paper is to study the expression of podoplanin in cancer stroma and its relation to breast cancer immunophenotype.

METHOD AND MATERIALS

Patients with lesions enhancing on CESM were subjected to biopsy - material obtained during biopsies was histopathologically verified. In the present study we retrospectively investigated 97 invasive breast carcinomas diagnosed in 94 patients. This study was performed in compliance with the Declaration of Helsinki and it received the approval of Ethical Committee at the Regional Medical Chamber. For each tumor enhancing on CESM, the intensity and the pattern of enhancement were evaluated. The enhancement of contrast agent uptake was qualitatively assessed as weak/medium or strong ,while the pattern as heterogenous or homogenous. Lymphatic vessels were defined as strongly podoplanin-stained structures with lymphatic vessel characteristics , clearly distinguishable from other tissue structures and cells. We classified tumor stroma as: podoplanin-sparse and podoplanin-rich.

RESULTS

Strong enhancement on CESM was found more frequently in: large tumors (pT>1), node-positive carcinomas, in tumors with podoplanin-sparse stroma vs. tumors with podoplanin-rich stroma . We found no relationship between enhancement on CESM and: tumor grade, histological type of cancer, breast cancer immunophenotype and Ki-67LI. However, in luminal A tumors strong enhancement on CESM was insignificantly more frequent as compared to neoplasms with non-luminal A subtype .

CONCLUSION

In our study prognostic significance of selected CESM features was found for the first time: strong and heterogenous enhancement on CESM was related to poor patients' outcome. In this study, the aforementioned correlation was additionally confirmed by the relationship between strong enhancement on CESM and nodal involvement or large tumor size.

CLINICAL RELEVANCE/APPLICATION

Our results may suggest that intensity and pattern of enhancement on CESM might bring (together with the results of diagnostic imaging methods) not only the confirmation of presence or absence of tumor, but also prognostic information.

RC215-10 Development of MRI-based Radiomics Nomogram for the Prediction of Recurrence in Patients with Luminal-type Breast Cancer: A Nested Case-Control Study

Monday, Nov. 26 10:20AM - 10:30AM Room: Arie Crown Theater

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PURPOSE

To determine whether breast MRI-based radiomics nomogram including pathologic factors can predict recurrences or distant metastasis in patients with luminal-type breast cancer (LTBC).

METHOD AND MATERIALS

From 2006 to 2012, a total of 348 patients with LTBC who underwent preoperative breast MRI were retrospectively included in this study. Patients with recurrence were 174. Patients without recurrence were matched in terms of age, stage, and type of chemotherapy, and developed 174 nested case-control pairs. We extracted 804 quantitative MR radiomic features of computerized three-dimensional segmentations of each cancer generated computer-extracted image phenotypes (CEIP) within the intratumoral regions of early post-contrast T1-weighted images, percent enhancement (PE) map, signal enhancement ratio (SER) map, and T2-weighted images. We divided 174 case-control matches into a training set (n=232) and a validation set (n=116). Elastic net was used for feature selection and radiomics score building. Multivariate logistic regression analysis was used to develop the prediction model, we incorporated the radiomics score and independent pathologic risk factors and build a radiomics nomogram. Internal validation for an independent validation set (n=76) was performed.

RESULTS

The radiomics score, which consisted of 14 selected CEIPs, was significantly associated with the prediction of recurrence (C-index, 0.864 for training set and 0.815 for validation set). Independent pathologic predictors contained in the nomogram were progesterone receptor status, P53, lymphovascular invasion, Ki67 status, and lymph node ratio, and their C-index was 0.695 for training set and 0.701 for validation set. Addition of radiomics score to the pathologic nomogram showed an incremental value of 0.211 and 0.177, respectively. Radiomics nomogram showed good prediction of recurrence, with a C-index of 0.906 for training set and 0.878 for validation set.

CONCLUSION

This study shows that a radiomics nomogram which incorporates the MRI-based radiomics score and pathologic features, can be used to help the individualized prediction of local or distant recurrence in patients with LTBC.

CLINICAL RELEVANCE/APPLICATION

Nomogram using breast MRI-based radiomics score and pathologic predictors can be used to facilitate the individualized prediction of recurrence in patients with LTBC.

RC215-11 Horizons with Deep Learning

Monday, Nov. 26 10:40AM - 11:00AM Room: Arie Crown Theater

Participants
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LEARNING OBJECTIVES

1) To understand the importance implementing deep learning tools into a breast imager's workflow. 2) To understand applications of deep learning outside of detection and characterization of breast lesions.

RC215-12 Incorporating Patient Characteristics in Breast Cancer Screening with Deep Convolutional Neural (DCN) Network

Monday, Nov. 26 11:00AM - 11:10AM Room: Arie Crown Theater

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PURPOSE

To determine if the addition of patient characteristics obtained from the electronic health records may improve the ability of a DCN network to detect and classify lesions on screening mammography.

METHOD AND MATERIALS

This is a retrospective study of a DCN network trained on over 250,000 screening mammograms performed at our institution from 2010-2016. The patients were sorted according to the date of their latest exam and divided into training (first 80%), validation (next 10%), and test (last 10%) sets. In the test phase, only the most recent exam was used for each patient. Patient characteristics including age, family history of breast cancer, and history of prior examinations were extracted from the radiologist reports. The original high-resolution images and extracted side information were utilized as inputs by a multi-column DCN network to classify BI-RADS category. The model was evaluated using area under the receiver operating characteristic curve (AUC) analysis. Analysis was also performed after stratifying patients by age-group and breast density (dense vs non-dense).

RESULTS

The overall performance of the DCN network improved with the addition of patient characteristics in comparison to using images alone (AUC 0.750 vs 0.733). This improvement was especially notable for BI-RADS 0 cases, with an AUC of 0.664 vs 0.618. Performance also generally improved with increasing age, with an average AUC of 0.759 in patients over 70 years of age. Finally, performance of the model is superior in dense breasts vs non-dense breasts (AUC 0.740 vs AUC 0.707).

CONCLUSION

The performance of DCN networks in evaluating screening mammograms increases with the addition of patient characteristics information, especially in the abnormal BI-RADS 0 cases which are the most difficult to evaluate.

CLINICAL RELEVANCE/APPLICATION

End-to-end architectures of DCN networks, like ours, support the incorporation of patient characteristics to increase the accuracy of deep learning algorithms in breast cancer screening.

RC215-13 Detecting Breast Cancer in Mammography: A Deep Learning-Based Computer System versus 101 Radiologists

Monday, Nov. 26 11:10AM - 11:20AM Room: Arie Crown Theater

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PURPOSE

To compare the stand-alone performance of a computer-based detection system to that of radiologists in detecting breast cancer on digital mammography (DM).

METHOD AND MATERIALS

Nine multi-reader multi-case (MRMC) study datasets previously used for different performance evaluation purposes in seven countries were collected. Each dataset consisted of DM exams acquired with systems from four different vendors, multiple radiologists' assessments per exam (BI-RADS or probability-of-malignancy scores), and ground truth: yielding a total of 2,458 exams (608 malignant) and interpretations by 101 radiologists (28,373 independent exam interpretations). A deep learning-based computer system (Transpara, ScreenPoint Medical, Nijmegen, The Netherlands) was used to automatically analyze each exam, resulting in a score for suspiciousness of cancer (1-100). Independently for each dataset, the area under the receiver operating characteristic curve (AUC) and the sensitivity at the radiologists' specificity level (case recall) were compared between the computer and radiologists using MRMC analysis of variance.

RESULTS

The performance of the computer system was not significantly different to that of the average of radiologists in eight of nine datasets (AUC differences ranged between -2.6% and +2.5%, P>0.329) and was significantly better in the ninth (+4.6%, P=0.036). At the average specificity of the radiologists, the computer had an equal or higher sensitivity (+0-9%, P>0.083) in all datasets but one (-13%, P=0.066). Comparing individually, the computer had an AUC and sensitivity higher than 53% and 65% of all radiologists, respectively.

CONCLUSION

A computer system based on deep learning has an equivalent performance to radiologists for detecting breast cancer in mammography.

CLINICAL RELEVANCE/APPLICATION

Whether used for decision support (preventing overlook and interpretation errors that are relatively common in the reading of mammography) or as stand-alone readers, computer systems performing at radiologist-like level might herald a breakthrough in the breast cancer detection workflow with mammography. In some situations, where there is a lack of experienced breast radiologists, it might even allow the development or continuation of screening programs.

RC215-14 Improving Accuracy and Efficiency with Concurrent Use of Artificial Intelligence for Digital Breast Tomosynthesis Screening

Monday, Nov. 26 11:20AM - 11:30AM Room: Arie Crown Theater

Participants
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PURPOSE

Screening with Digital Breast Tomosynthesis (DBT) improves accuracy but prolongs reading time when compared to Full-Field Digital Mammography (FFDM) alone. A reader study evaluated concurrent use of Artificial Intelligence (AI) to shorten reading time, while maintaining or improving sensitivity and specificity.

METHOD AND MATERIALS

An AI system based on deep convolutional neural networks was developed to identify suspicious soft tissue and calcific lesions in DBT slices. Findings are outlined in slices, indicating AI's confidence of malignancy with 0-100 scores. A retrospective, fully-crossed, multi-reader, multi-case designed study compared performance of 24 radiologists reading 260 DBT cases both with and without AI. The case set included 65 cancer cases with 66 malignant lesions and 65 cases with biopsy-proven benign lesions. Readings with and without AI occurred in 2 visits separated by a memory washout period of at least 4 weeks. Performance was assessed by measuring Area Under the ROC Curve (AUC) for malignant lesions with AI versus without AI. Reading time, sensitivity, specificity and recall rate were also assessed.

RESULTS

Radiologist performance for detection of malignant lesions, measured by mean AUC, increased 0.057 with use of AI (95% CI: 0.028, 0.087; $p < 0.01$), from 0.795 without AI to 0.852 with AI. Reading time decreased 52.7% with use of AI (95% CI: 41.8%, 61.5%; $p < 0.01$), from 64.1 sec without AI to 30.4 sec with AI, using a normalizing transformation to appropriately assess reading times that

were not normally distributed. Sensitivity increased from 77.0% without AI to 85.0% with AI (8.0%; 95% CI: 2.6%, 13.4%; $p < 0.01$), specificity increased from 62.7% without AI to 69.6% with AI (6.9%; 95% CI: 3.0%, 10.8%; $p < 0.01$), and recall rate for non-cancers decreased from 38.0% without AI to 30.9% with AI (7.2%; 95% CI: 3.1%, 11.2%; $p < 0.01$).

CONCLUSION

Concurrent use of AI improves cancer detection with increases of 0.057 in AUC, 8.0% in sensitivity, and 6.9% in specificity; and decreases of 7.2% in recall rate and 52.7% in reading time.

CLINICAL RELEVANCE/APPLICATION

Radiologist's concurrent use of AI for DBT with certainty of finding scores increases detection of breast cancer with significant reduction in reading time while improving sensitivity and specificity.

RC215-15 Breast Cancer Temporal Risk Prediction by Deep Learning and Longitudinal Digital Mammogram Images

Monday, Nov. 26 11:30AM - 11:40AM Room: Arie Crown Theater

Participants
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PURPOSE

Mammographic breast density is a risk factor and recent studies showed deep learning may identify more predictive imaging risk features than breast density. We performed a study to investigate temporal breast cancer risk prediction by using deep learning models on longitudinal 'normal' screening mammograms acquired prior to diagnosis of breast cancer.

METHOD AND MATERIALS

We conducted a retrospective case-control study on a cohort of 226 patients (1:1 case-control ratio) who underwent standard mammographic screening at our institution during 2006-2013. The unilateral cancer cases (61.3±10.3YO) were all newly diagnosed at 2013 and confirmed by pathology. Asymptomatic cancer-free controls (60.1±10.0 YO) are matched to the cancer cases by age and year of the cancer-diagnosis imaging. All studied women did not have any prior biopsy or recall on mammography. For all cohort, a set of sequential prior 'normal' (negative or benign findings) screening mammogram exams acquired during 2006-2012 were collected (2-8 exams per patient), generating a total of 3263 'normal' images (913 for cancer cases, and 2350 for controls). Those prior images of the cancer-affected breast (for cancer cases) and side-matched breast (for controls) were used to predict the outcome (i.e., case/control status). We compared the prediction in terms of three time periods: (A) all priors from 2006 to 2012, (B) recent priors (1548 images) from 2010 to 2012, and (C) distant priors (1715 images) from 2006 to 2009. The outcome prediction was based on a pre-trained convolutional neural network model (ResNet-50) that was further fine-tuned on our mammograms. 10-fold cross-validation and AUC were used to measure model performance.

RESULTS

81% of cancers and 82% of controls were post- with the rest pre-menopausal, and neither menopausal status nor family history of breast cancer was associated with the outcome. AUC was 0.84 when using all priors, while it was 0.77 or 0.75 when using only the recent or only the distant priors, respectively.

CONCLUSION

Sequential recent or distant prior 'normal' screening mammograms can predict, and their combination is more predictive of, breast cancer development using deep learning models.

CLINICAL RELEVANCE/APPLICATION

Deep learning modeling on longitudinally acquired prior 'normal' screening mammogram images through up to 7 years earlier can enhance temporal prediction of breast cancer development.

RC215-16 Novel Radiomic Descriptor of Tumor Vascular Morphology Identifies Responders to Neo-Adjuvant Chemotherapy on Pre-Treatment Breast MRI

Monday, Nov. 26 11:40AM - 11:50AM Room: Arie Crown Theater

Awards
Trainee Research Prize - Medical Student

Participants
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Prateek Prasanna, Cleveland, OH (*Abstract Co-Author*) Nothing to Disclose
Maryam Etesami, MD, New Haven, CT (*Abstract Co-Author*) Nothing to Disclose
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PURPOSE

Despite significant interest in predicting treatment response prior to breast cancer neo-adjuvant chemotherapy (NAC) from DCE-MRI, prior work has focused on textural patterns of the tumor or parenchyma or deep learning-based approaches that lack direct biological interpretability. In this work, we introduce functional radiomic descriptors of vascular network disorder (VND) and evaluate whether differences in the complexity of tumor-associated vasculature on pre-treatment DCE-MRI can discriminate between patients who do and do not respond to NAC.

METHOD AND MATERIALS

1.5 or 3T DCE-MRI scans of 76 NAC recipients, 24 of whom had surgically confirmed pathological complete response (pCR), were retrospectively analyzed. Average pixel width and slice thickness were .77 mm and 1.22 mm, respectively. Patients were randomly divided into training (n=53, 14 pCR) and testing (n=23, 10 pCR) sets. A semi-interactive scheme was employed to segment the tumor and vascular network. Within a sliding window, vessel orientation was computed for a series of 2-dimensional representations of the vasculature relative to the tumor centroid. Statistics (mean, median, st. dev, skewness, and kurtosis) of the distribution of vessel orientations for each representation were computed, yielding 20 VND features total. Top VND features were selected in the training set using the Wilcoxon rank sum test via three-fold cross validation, then used to train a linear discriminant analysis classifier to predict response in the test set. Performance was compared against (1) intra- and peri-tumoral texture features and (2) a 3 layer LeNet convolutional neural network (CNN).

RESULTS

The top 4 VND features distinguished pCR with an AUC=0.75. pCR was characterized by reduced vascular disorder relative to non-pCR. VND performed comparably or better than other state of the art radiomic approaches, including intra- and peri-tumoral texture (AUC=.75) and deep learning (AUC=.67). Combining predictions from VND, texture features, and CNN yielded the best response prediction accuracy (AUC=0.80).

CONCLUSION

VND features, which capture chaotic vessel network architecture, appear to be associated with NAC response and added predictive value to established radiomic and deep learning approaches.

CLINICAL RELEVANCE/APPLICATION

Quantitative assessment of vessel network architecture as a functional radiomic biomarker could provide interpretable NAC response prediction in breast cancer.

RC215-17 Using Machine Learning to Assess Tumor Metastatic Lymph Nodes and Ki-67 Expression Aggressiveness from Breast MRI Using a Large Clinical Dataset of 300 Cancers from China

Monday, Nov. 26 11:50AM - 12:00PM Room: Arie Crown Theater

Participants
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PURPOSE

To evaluate quantitative MRI radiomics in the task of identifying metastatic versus nonmetastatic axillary lymph nodes and Ki-67 expression aggressiveness.

METHOD AND MATERIALS

Our research involved a HIPAA-compliant, DCE-MRI database of 300 breast cancer cases. The average age was 47.2 years with a standard deviation of 9.6 years and a range from 25 to 77 years with a median of 47 years. The clinical cohort included 48 low Ki-67 expression (Ki-67 proliferation index < 14%) and 252 cases with high Ki-67 expression (Ki-67 proliferation index >= 14%), indicating a range of tumor aggressiveness. The cohort also included 93 cases with axillary lymph node metastasis and 201 cases without metastasis. The images had been obtained with a gadodiamide-enhanced T1-weighted spoiled gradient-recalled acquisition in the steady state sequence. Primary lesions underwent computerized radiomic analysis in which tumor segmentation and extraction were automatically conducted on an existing CADx workstation. These computer-extracted features included MRI-based phenotypes from six categories: size, shape, morphology, enhancement texture, kinetics, and enhancement-variance kinetics. Radiomic features were input to a Bayesian artificial neural network classifier (BANN) and underwent leave-one-case-out cross validation. Area under the ROC curve (AUC) served as the figure of merit in the classification tasks.

RESULTS

In the task of identifying Ki-67 expression and lymph node status, the analyses of the various radiomic phenotypes yielded AUCs ranging from 0.50 (se = 0.05) to 0.69 (se = 0.04). The Ki-67 MRI-based tumor signature produced an AUC value of 0.71 (se = 0.04). In the task of assessing the status of axillary lymph nodes, the radiomics tumor signature yielded an AUC value of 0.67 (se = 0.03). Both signatures were found to be statistically different from random guessing.

CONCLUSION

Quantitative MRI radiomics conducted on depicted primary breast tumors can contribute to identifying aggressive tumors, including identifying Ki-67 expression and discriminating between metastatic and nonmetastatic lymph nodes, yielding automatic MRI-based prognostic markers for ultimate use in radiogenomics and patient care.

CLINICAL RELEVANCE/APPLICATION

The ability to assess automatically the potential aggressiveness of tumors may elucidate the characteristics of breast cancers for radiogenomics and for use in helping clinician estimate prognosis.