SSC08

## Informatics (Image Processing and Analysis)

Monday, Nov. 28 10:30AM - 12:00PM Room: S402AB

MR IN

*AMA PRA Category 1 Credits* ™: 1.50
ARRT Category A+ Credits: 1.50

Asim F. Choudhri, MD, Memphis, TN (*Moderator*) Nothing to Disclose
Srini Tridandapani, MD, PhD, Atlanta, GA (*Moderator*) Nothing to Disclose
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**Sub-Events**

### SSC08-01 Radiogenomic Analysis of The Cancer Genome Atlas (TCGA)/The Cancer Imaging Archive (TCIA) Head and Neck Squamous Cell Cancer (HNSCC) Cohort: Correlations between Genomic Features and Quantitative Imaging Features

Monday, Nov. 28 10:30AM - 10:40AM Room: S402AB

**Awards**
**Student Travel Stipend Award**

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#### PURPOSE

Radiogenomics is the study of the association between genomic features and imaging phenotypes, aiming to enhance the molecular drivers for image phenotypes of biological samples. With publicly available data from TCGA and TCIA on the same set of tumor samples, we assessed pathway-specific alterations as potential correlates of radiomics features in matched cases from TCGA/TCIA HNSCC database(s).

#### METHOD AND MATERIALS

Segmented gross tumor volumes from pretreatment CT scans in DICOM-RT format were processed in IBEX, yielding 360 radiomic features characterizing different tumor image phenotypes. TCGA genomic data of the same tumors including whole-genome gene expressions, copy number variations (CNV), DNA methylations, miRNA expressions, somatic mutations, and expressions of cancer-related proteins, were processed using TCGA-Assembler. We used regression analysis and gene set enrichment methods to identify individual genomic features and genetic pathways that are associated with tumor radiomic features, adjusting for known prognostic variables such as patient age, smoking status, tumor stage and subsite.

#### RESULTS

A total of 126 patient samples was analyzed. Most samples were AJCC stage IV (n=83) with tumors of the oral cavity (n=67), larynx (n=35), and oropharynx (n=20). Mean age was 59.8 (SD=11.35) and most were current (n=51) or former smokers (n=44). We identified 20, 154, 3, 438, 8641, and 814 statistically significant (Benjamini-Hochberg-adjusted p-value $\leq 0.05$) associations involving miRNA expressions, mutated genes, protein expressions, promoter region DNA methylations, transcriptional activities and CNVs of genetic pathways, respectively. Clinically relevant pathway associations have been identified, including the positive association between the expression level of ERK2 (a kinase important for cell proliferation and differentiation) and tumor size. All significant associations have been collected into a database for open-access querying/dissemination.

#### CONCLUSION

We identified a cohort of statistically significant associations between various genomic features and multiple kinds of radiomic phenotypes for HNSCC. These findings not only confirm known pathways, but may develop new knowledge about the genomic underpinnings of tumor imaging phenotypes.

#### CLINICAL RELEVANCE/APPLICATION

Quantitative analysis of standard-of-care images may inform upon tumor genomic status and identify pathway-depdendent features for risk/therapy stratification.

## SSC08-02 Quantitative MR Imaging Biomarkers to Assess Early Response of Breast Cancers to Neoadjuvant Chemotherapy (NACT)

Monday, Nov. 28 10:40AM - 10:50AM Room: S402AB

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Vivek Narayan, Boston, MA (*Abstract Co-Author*) Nothing to Disclose
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**CONCLUSION**

Initial results show correlation with multiple MR heterogeneity metrics to PR. The imaging biomarkers may be helpful to predict the NACT response in breast cancer patients after first cycle of NACT, early in the course of treatment, before usual size measurements would indicate response.

**Background**

To assess tumor response after the first cycle of neoadjuvant chemotherapy (NACT) using imaging biomarkers that quantify the tumor heterogeneity on MRI and further correlate these metrics to pathological response (PR).

**Evaluation**

45 biopsy proven breast cancers were evaluated using MRI on baseline and first post-NACT and compared with the PR (complete or significant PR [pCR] = tumor loss > 90% vs partial or no PR [non-pCR]). The average time between baseline and first post-NACT MRI was 30 days. The first post-NACT MRI was done 8-14 days after the first cycle of treatment. A breast-imaging radiologist segmented the cancer on pre-contrast and first post-contrast images of baseline and first post-NACT MRI in the 3D Slicer software. 57 metrics that quantify the shape, morphology, distribution statistics, geometry and texture were obtained for each cancer using the HeterogeneityCAD module in 3D Slicer. Statistical correlation of the PR was performed with the % change in metrics evaluated from baseline and first post-NACT cycle MRI using Mann-Whitney test.

**Discussion**

Percentage change in 26/57 metrics on pre-contrast and 28/57 metrics on post-contrast MRI showed significant difference between the pCR and non-pCR groups ($p<0.05$). Mean representative metrics for non-pCR on post-contrast MRI (as %): Energy: 22.9, Entropy: 33.2, Variance: 5.4, Uniformity: 26.6, Auto correlation: 42.0, Dissimilarity: 44.6. Mean of Metrics for PCR (as %): Energy: 44.1, Entropy: 55.2, Variance: 25.0, Uniformity: 45.7, Auto correlation: 68.9, Dissimilarity: 69.0. Standard morphological metrics such as volume, surface area, maximum 3D diameter and compactness do not show significant differences between the pCR and non-pCR groups.

## SSC08-03 Transport-Based Morphometry on Structural MRI Enables Reliable Differentiation of 16p11.2 Duplication and Deletion Carriers

Monday, Nov. 28 10:50AM - 11:00AM Room: S402AB

**Awards**
**Trainee Research Prize - Medical Student**

Shinjini Kundu, PhD, Pittsburgh, PA (*Presenter*) Nothing to Disclose
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Jeffrey Berman, PhD, Philadelphia, PA (*Abstract Co-Author*) Nothing to Disclose
Timothy Roberts, PhD, Philadelphia, PA (*Abstract Co-Author*) Nothing to Disclose
Randy L. Buckner, Charlestown, MA (*Abstract Co-Author*) Nothing to Disclose
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Pratik Mukherjee, MD, PhD, San Francisco, CA (*Abstract Co-Author*) Research Grant, General Electric Company Medical Adivisory Board, General Electric Company
Gustavo Rohde, PhD, Pittsburgh, PA (*Abstract Co-Author*) Nothing to Disclose

**PURPOSE**

Copy number variants (CNVs) in the 16p11.2 chromosomal locus (BP4-BP5) are associated with several neurodevelopmental disorders. This study aims to determine whether 16p11.2 deletion and duplication carriers can be differentiated based on structural MRI of the brain using Transport-Based Morphometry (TBM), and if so, whether regional white matter morphological changes that enable differentiation shed light on the underlying neurobiology of 16p11.2 CNVs.

**METHOD AND MATERIALS**

T1-weighted imaging was performed on 235 subjects (51 deletion carriers, 53 duplication carriers, 131 control subjects), including adults and children of both genders (4 – 63 years, mean age 22.4 ± 14.7; M:F ratio = 1.35). Deletion and duplication carriers had a range of neurodevelopmental diagnoses. Statistical Parametric Mapping (SPM12) was used to coregister and segment the white matter. Subsequently, TBM was applied to generate transport maps characterizing individual spatial tissue distribution compared to a common template image. Principal components analysis (PCA) was then applied for dimensionality reduction, and classification was performed using penalized linear discriminant analysis (PLDA) combined with a k-nearest neighbor (KNN) classifier (k = 15). Test accuracy was evaluated using leave-one-subject out cross-validation.

**RESULTS**

TBM enabled 100% test accuracy in predicting group membership (duplication, deletion, control) using white matter (100% sensitivity/specificity, Cohen's kappa = 1) and 95.7% using gray matter appearance alone (sensitivity = 96.1%, specificity = 98.9%, Cohen's kappa = 0.928). We identified a characteristic increase in white matter density (deletion carriers>controls>duplication carriers) in the following regions: occipital, splenium of corpus callosum, frontoparietal, inferior frontal, superior vermis of cerebellum, cerebellar hemispheric. Conversely, a decrease in the inferior temporal (duplication carrier>controls>deletion carriers) white matter was also observed.

**CONCLUSION**

TBM enables robust prediction of 16p11.2 CNVs using T1-weighted images alone. Furthermore, for the first time, characteristic white matter morphology differences that enable sensitive classification were visualized.

**CLINICAL RELEVANCE/APPLICATION**

TBM reveals structural changes in white matter caused by 16p11.2 CNVs, associated with many neurodevelopmental disorders, yielding new insight and potential biomarkers to monitor disease and treatment.

### SSC08-04 A Novel Bi-Input Convolutional Neural Network for Deconvolution-Free Estimation of Stroke MR Perfusion Parameters

Monday, Nov. 28 11:00AM - 11:10AM Room: S402AB

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Fabien Scalzo, PhD, Los Angeles, CA (*Abstract Co-Author*) Nothing to Disclose
Karthik V. Sarma, BSc, Los Angeles, CA (*Abstract Co-Author*) Nothing to Disclose
Suzie M. El-Saden, MD, Los Angeles, CA (*Abstract Co-Author*) Nothing to Disclose
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Corey W. Arnold, Los Angeles, CA (*Abstract Co-Author*) Nothing to Disclose

**PURPOSE**

Perfusion magnetic resonance (MR) images are often used in conjunction with diffusion weighted images during the assessment of acute ischemic stroke to distinguish between the likely salvageable tissue and infarcted core. Methods such as singular value decomposition have been developed to approximate perfusion parameters from these images. However, studies have shown that existing deconvolution algorithms can introduce distortions that influence the measurements. In this work, we present a novel bi-input convolutional neural network (bi-CNN) to approximate perfusion parameters without deconvolution. We applied the trained bi-CNN to approximate cerebral blood volume (CBV).

**METHOD AND MATERIALS**

MR perfusion data was collected retrospectively for a set of 11 patients who had acute ischemic stroke. The ground truth perfusion maps (i.e., CBV) and arterial input functions (AIFs) were generated from ASIST-Japan perfusion mismatch analyzer, with the resulting CBV values ranging between 0-201 ml/100g. A set of 87,600 training patches with associated AIFs and CBVs were randomly sampled from the source perfusion data. Each patch had a size of 3 x 3 x 70 (width x height x time), and the center of the patch was the voxel of interest for estimation.Our bi-CNN is a 5-layer model with two parts: 1) two separate 3D convolutional and nonlinear layers for the training patch and its AIF, and 2) three fully-connected layers that combine the output of the first part to produce an estimated CBV. The model was trained with batch gradient descent, with a momentum of 0.9.

**RESULTS**

A leave-one-brain-out validation was performed to estimate voxel-wise CBV values. The bi-CNN achieved an average mean squared error (MSE) of 3.799 ml/100g +/-3.715. CBV deficits (< 2.5 ml/100g) could be identified from the bi-CNN estimated maps.

**CONCLUSION**

Our patch-based bi-CNN model is capable of estimating CBV in stroke patients. The model can be potentially extended to other disease domains, such as perfusion analysis in cancer. Future work includes experimenting on a larger dataset and estimating other important perfusion parameters, such as time-to-maximum (Tmax).

**CLINICAL RELEVANCE/APPLICATION**

Convolutional neural networks can be trained to approximate stroke MR perfusion parameters (e.g., CBV) and are a potential alternative method for automated quantification of perfusion abnormalities.

### SSC08-05 Radiomic Response Assessment for Recurrent Glioblastoma Treated with Bevacizumab in the Brain Trial

Monday, Nov. 28 11:10AM - 11:20AM Room: S402AB

Patrick Grossmann, Boston, MA (*Presenter*) Nothing to Disclose
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Patrick Y. Wen, MD, Boston, MA (*Abstract Co-Author*) Research support, Agios Pharmaceuticals, Inc Research support, Angiochem Inc Research support, AstraZeneca PLC Research support, Exelixis, Inc Research support, F. Hoffmann-La Roche Ltd Research support, GlaxoSmithKline plc Research support, Karyopharm Therapeutics, Inc Research support, Novartis AG Research support, sanofi-aventis Group Research support, Regeneron Pharmaceuticals, Inc Research support, Vascular Biogenics Ltd Advisory Board, AbbVie Inc Advisory Board, Cavion Advisory Board, Celldex Therapeutics, Inc Advisory Board, Merck & Co, Inc Advisory Board, F. Hoffmann-La Roche Ltd Advisory Board, Midatech Pharma PLCAdvisory Board, Momenta Pharmaceuticals , IncAdvisory Board, Novartis AG Advisory Board, NovoCure Ltd Advisory Board, Sigma-Tau Pharmaceuticals, Inc Advisory Board, Vascular Biogenics Ltd Speaker, Merck & Co, Inc
Raymond Y. Huang, MD, PhD, Boston, MA (*Abstract Co-Author*) Nothing to Disclose
Hugo Aerts, PhD, Boston, MA (*Abstract Co-Author*) Stockholder, Genospace LLC

**PURPOSE**

To develop radiomic biomarkers for non-invasive response assessment of Bevacizumab (Avastin; Genentech) treatment in recurrent glioblastoma multiforme (GBM).

**METHOD AND MATERIALS**

We analyzed prospectively acquired data from the BRAIN trial. For 167 patients, we extracted 71 radiomic features each from normalized post-contrast T1-weighted and fluid attenuation inversion recovery (FLAIR) sequences at baseline (pre-treatment) and at first follow-up (six weeks post-treatment). For every imaging modality at baseline, we selected 10 comprehensive features using

an unsupervised feature selection approach that did not take clinical outcomes into account to limit overfitting. We investigated these features in terms of prognostic value for overall survival (OS), progression-free survival (PFS), as well as early (<3 month) and late (>9 month) progression.

**RESULTS**

T1 and FLAIR features showed only low pairwise correlation at baseline (mean positive and negative Pearson correlation of 0.3 and -0.13) indicating complementary effects of imaging modalities at the radiomic level. Features derived from T1 scans generally showed higher prognostic performances as compared to FLAIR (Fig. 1). A T1 derived textural-heterogeneity feature (gray-level non-uniformity) stratified patients into early and late progressors significantly at baseline (AUC 0.67, p=4.8x10-4); Kaplan-Meier analysis of this feature for OS showed moderate prognostic value at baseline (HR=1.8, p=7.2x10-4) and follow-up (HR=2, p=4x10-4). A multivariate Cox-regression model of supervised selected features stratified early and late progressors significantly at follow-up T1 scans in independent validation data (HR=2.8, p=5.8x10-4) after correcting for age, sex, and Karnofsky performance status.

**CONCLUSION**

For the first time, our study allows the definition of radiomic response phenotypes of Bevacizumab treatment in recurrent GBM by leveraging high-quality prospective trial data. Importantly, our data suggests the increased benefit of measuring radiomic patient profiles longitudinally after treatment has been initiated to monitor progression and resistance for immediate intervention and treatment adaptation.

**CLINICAL RELEVANCE/APPLICATION**

Through to the development of non-invasive imaging biomarkers predicting the effect of Bevacizumab treatment for patients with recurrent GBM, our study contributes to the promotion of precision medicine in oncology.

## SSC08-06 Radiogenomics Mapping of Non-small Cell Lung Cancer Shows Strong Correlations between Semantic Image Features and Metagenes

Monday, Nov. 28 11:20AM - 11:30AM Room: S402AB

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Sebastian Echegaray, MS, Stanford, CA (*Abstract Co-Author*) Nothing to Disclose
Ann N. Leung, MD, Stanford, CA (*Abstract Co-Author*) Nothing to Disclose
Olivier Gevaert, PhD, Stanford, CA (*Abstract Co-Author*) Nothing to Disclose

**PURPOSE**

To present a radiogenomic map linking RNA sequencing data with semantic image features for patients with non-small cell lung cancer (NSCLC).

**METHOD AND MATERIALS**

Under IRB approval, we studied 113 patients with NSCLC who had preoperative CT scans and tumor tissue collected between 04/07/2008 and 09/15/2014 at two medical centers. A thoracic radiologist annotated the CT of each tumor with 89 semantic image features using a template with a controlled vocabulary, reflecting radiologic features in tumor shape, margin, and texture as well as background lung characteristics. Next, total RNA was extracted from these tissue samples and converted into a library for paired-end RNA sequencing on Illumina Hiseq. The RNA sequencing data were clustered into 56 high quality metagenes and filtered for metagene homogeneity in five external, public gene expression cohorts totaling 1227 NSCLC patients. We updated a radiogenomics map between metagenes and semantic image features by using Pearson correlation metric with the False Discovery Rate (FDR). In addition, we established the prognostic relationship of metagenes using Cox proportional hazards modeling in five external cohorts.

**RESULTS**

We identified the top ten metagenes with the highest cluster homogeneity in consensus from five external cohorts. The defined metagenes are highly coexpressed genes to capture important biological processes including hypoxia, cell cycles, and immune response. Correlating metagenes and semantic features, we found 34 significant associations (P<0.05 and FDR<0.01). Ground glass opacity (P=0.005 and FDR<0.001) and nodule attenuation (P=0.008 and FDR=0.003) are strongly correlated with the metagene 19 that defines EGFR pathway. In addition, semantic features capturing presence of centrilobular emphysema (P=0.03) and emphysema severity (P=0.015) are both found to be significantly associated with survival outcomes of patients with NSCLC.

**CONCLUSION**

We built a radiogenomics map linking ten high-level metagenes capturing canonical pathways of NSCLC to observable imaging characteristics providing a strong association with survival.

**CLINICAL RELEVANCE/APPLICATION**

Semantic image features capturing tumor phenotypic characteristics can be used to non-invasively associate with molecular properties of NSCLC with prognostic implications.

## SSC08-07 Effect of Input Parameters on the Use of Convolutional Neural Networks in Distinguishing Between Malignant and Benign Breast Lesions Across Two Breast Imaging Modalities

Monday, Nov. 28 11:30AM - 11:40AM Room: S402AB

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**PURPOSE**

To investigate the effect of image formats on the use of deep convolutional neural networks (CNNs) in the task of distinguishing

between benign and malignant lesions on FFDM and breast ultrasound images

**METHOD AND MATERIALS**

Datasets included 1125 breast lesions [2393 regions of interest (ROIs)] on breast ultrasound and 219 breast lesions [607 ROIs] on full-field digital mammography (FFDM). Ultrasound ROIs were categorized as benign solid, benign cystic, or malignant; FFDM ROIs as either benign or malignant. Output from image ROIs subjected to pre-trained CNNs were classified in the diagnostic task using support vector machines (SVM). In order to fit the image size requirements of the pre-trained CNN, ultrasound ROIs were resized by various different scaling and padding methods, with classification performance being assessed for the different padding options. Performance levels of the deep learning were also compared to that obtained using 'traditional' CADx human-designed features. Five-fold cross validation (by lesion) was used to assess performance in the task of distinguishing between benign and malignant breast lesions, with area under the ROC curve (AUC) as the index of performance.

**RESULTS**

Mirror-padding resulted in the best performance (AUC=0.90 (Std Error=0.01)) compared to zero-padding (AUC=0.79 (SE=0.02)) and average-padding (AUC=0.81 (SE=0.01)). Also, extracted CNN features demonstrated rotational invariance despite the view-based asymmetry of ultrasound ROIs. The pre-trained CNN methods yielded similar diagnostic performance levels as compared to the conventional CADx methods (AUC = 0.90 vs 0.90 (SE = 0.01) for ultrasound; AUC = 0.81 vs 0.80 (SE = 0.01) for FFDM).

**CONCLUSION**

Deep learning demonstrated, across two breast imaging modalities, similar performance levels as compared to CADx in the diagnostic task. However, optimal choice of input ROIs in the CNN structure appears crucial in assuring high performance.

**CLINICAL RELEVANCE/APPLICATION**

Deep learning techniques show extreme promise in computer-aided diagnosis, however, performance levels are dependent on the type of pre-processing.

## SSC08-08 Development of a Novel Bayesian Network Interface for Radiology Diagnosis Support and Education

Monday, Nov. 28 11:40AM - 11:50AM Room: S402AB

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Tessa S. Cook, MD, PhD, Philadelphia, PA (*Abstract Co-Author*) Nothing to Disclose
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**CONCLUSION**

A prototype web-based interface (ARIES) was developed that streamlines interaction of radiologists with BNs. With further development and validation, we anticipate this could provide Radiology diagnosis and educational support.

**Background**

Bayesian networks (BNs) are forms of artificial intelligence that have shown promise for Radiology diagnosis support. Taking as input imaging and clinical key features (KFs) extracted by radiologists, BNs can output probability-ranked differential diagnoses (DDx) and suggest further imaging or testing to constrain the DDx. Moreover, because BNs illustrate probabilistic relationships between KFs and DDx, they offer a unique approach to Radiology education that emphasizes "bottom-up" diagnostic reasoning (i.e., DDx given KFs), as opposed to more traditional "top-down" approaches (i.e., KFs given DDx).

**Evaluation**

To translate BNs into clinical and educational practice, we developed ARIES (Adaptive Radiology Interpretation and Education System), an open-source, web-based interface that allows Radiologists to interact with expert-developed BNs representing various imaging domains (e.g., Neuroradiology). ARIES utilizes a commercially available BN backend (Netica, Vancouver, Canada) wrapped in a Java server, and was created using JavaScript, JQuery, and HighCharts. ARIES was developed in close collaboration with practicing radiologists, intended for use alongside a traditional PACS workstation.

**Discussion**

In Clinical Mode, ARIES displays buttons corresponding to relevant KFs. As KFs are selected, two sets of probability-ranked DDx are continuously updated ("radiographic DDx," based on imaging KFs alone, and "clinical DDx," using both disease prevalence and clinical KFs). Embedded sensitivity analysis highlights the next most discriminating KFs after each selection. In Education Mode, trainees are prompted to review clinically proven cases from an internal teaching file. After entering KFs and providing a DDx, automated feedback is provided comparing agreement between trainee- and expert-extracted KFs, and between trainee- and BN-generated DDx. ARIES also offers machine learning functionality, updating BN probability tables in real-time as cases are submitted to the interface.

## SSC08-09 Multiparametric Magnetic Resonance Imaging of the Prostate with Computer Aided Detection as the First Reader: Effect on Experienced Observer Performance

Monday, Nov. 28 11:50AM - 12:00PM Room: S402AB

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Simone Mazzetti, PhD, Candiolo, Italy (*Abstract Co-Author*) Nothing to Disclose
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Salvatore Pedalino, Candiolo, Italy (*Abstract Co-Author*) Nothing to Disclose
Filippo Russo, MD, Candiolo, Italy (*Abstract Co-Author*) Nothing to Disclose
Daniele Regge, MD, Torino, Italy (*Abstract Co-Author*) Speakers Bureau, General Electric Company

**PURPOSE**

To assess if the detection of prostate cancer (PCa) at multiparametric Magnetic Resonance Imaging (mp-MRI) is improved when Computer aided detection (CAD) is adopted as the first reader (FR-CAD) by the experienced radiologists. Secondary aims of this

study are to assess if CAD reduces reading time and interobserver variability.

## METHOD AND MATERIALS

3 experienced radiologists searched for PCa in 89 mp-MRI studies. First, radiologists reported the examinations by using the FR-CAD paradigm. In this case, they were asked to analyze the probability map of the CAD superimposed to the T2w, and to confirm those CAD marks that they consider to be PCa. After 6 weeks, cases were re-ordered randomly and readers reported them without the support of the CAD system (unassisted reading), by scrolling all MR sequences (i.e. T2w, DW and DCE). Lesion size, PIRADS (only in the unassisted reading), a five-point confidence score and interpretation time was recorded for both reading modalities. Per-patient and per-lesion sensitivity, and specificity were computed for both procedures and compared using the McNemar test. Inter-observer agreement between reviewers was evaluated using Fleiss Kappa statistics.

## RESULTS

The dataset comprised 35 patients having at least 1 clinically significant tumor (39 lesions) and 54 negative patients (at least 1 year follow up). Mean per-patient sensitivity of FR-CAD and unassisted reading did not differ significantly when considering lesion of all size and GS (81% vs 88%, p=0.105), while with the FR-CAD sensitivity increased significantly for patient having a GS>6 (81% vs 91%, p=0.046) and a maximum lesion diameter≥10 mm (80% vs 95%, p = 0.006). Specificity increased not significantly when using the FR-CAD (75.3% vs 78.4%, p = 0.25). The average reading time strongly decreased with the FR-CAD (220 s vs 60 s, p<0.0001). The inter-reader agreement also increased in the FR-CAD paradigm for both per-patient (0.55 vs 0.60) and per-lesion (0.46 vs 0.55) analysis.

## CONCLUSION

This preliminary study shows that FR-CAD can (I) improve sensitivity in detecting PCa with GS>6 and lesion diameter ≥ 10 mm, (II) increase inter-reader agreement and (III) reduce reading time.

## CLINICAL RELEVANCE/APPLICATION

FR-CAD for prostate cancer may be an attractive reading strategy into the routine clinical environment, especially if mp-MRI prostate imaging will be introduced to select patients candidate to biopsy.