TCIA Sessions at RSNA

The Cancer Imaging Archive has been presented numerous times by our staff at RSNA's Annual Meetings and many other researchers have submitted abstracts based on TCIA data. In order to enable the community to more easily see what is going on at past and upcoming RSNA meetings we have begun tracking them here. We now make a distinction between "TCIA-Sponsored" sessions and posters which are conducted by our internal team versus "Community" sessions which are being presented by our research community.

TCIA Sessions at RSNA 2019

Click here to browse the RSNA 2019 Program

TCIA-Initiated

- **All Day | AI050 | AI Community, Learning Center**
  - **Crowds Cure Cancer: Help Annotate Data from the Cancer Imaging Archive**
    - Attendees at this year's RSNA meeting are encouraged to participate in an exciting new activity that will provide valuable data to cancer researchers working in deep learning, radiomics and radiogenomics. This kiosk offers radiologist attendees an opportunity to participate in a 'crowd-sourcing' experiment to accelerate quantitative imaging research. Images are provided by The National Cancer Institute's Cancer Imaging Archive (http://www.cancerimagingarchive.net/), which is a massive public-access resource of cancer radiology images linked to genetic/proteomic, pathology images and clinical data. Many of these cases lack the tumor-location labels needed by computer scientists to jump-start their work on machine learning and quantitative imaging radiomics. Participants will be asked to spend a few minutes anonymously reviewing cases and visually marking their tumor locations. Upon completion, they will receive a ribbon to add to their RSNA badge acknowledging their participation. The data resulting from this process will be openly shared on TCIA with the radiology and computer science communities to accelerate cancer research.
- **Sunday 4:00-5:30 PM** | RCC13 | Room:
  - **Creating publicly-accessible radiology imaging resources for Machine Learning and AI**
    - Learn from leaders in the fields of radiology and AI about their experiences developing and leveraging publicly-accessible data resources for AI.
- **Monday 8:30-10:00 AM** | RCA21 | Room:
  - **An Introduction to Using the NIH/NCI's Cancer Imaging Archive (TCIA) (Hands-on)**
    - Access to large, high quality data is essential for researchers to understand disease and precision medicine pathways, especially in cancer. However HIPAA constraints make sharing medical images outside an individual institution a complex process. The NCI's Cancer Imaging Archive (TCIA) addresses this challenge by providing hosting and de-identification services which take the burden of data sharing off researchers. TCIA now contains over 100 unique data collections of more than 30 million images. Recognizing that images alone are not enough to conduct meaningful research, most collections are linked to rich supporting data including patient outcomes, treatment information, genomic / proteomic analyses, and expert image analyses (segmentations, annotations, and radiomic / radiogenomic features). This hands-on session will teach the skills needed to fully access our existing data as well as learn how to submit new data for potential inclusion in TCIA.
- **Monday 10:30-12:00 PM** | RCC22 | Room:
  - **Novel Discoveries Using the NCI's Cancer Imaging Archive (TCIA) Public Data Sets**
    - This didactic session will highlight popular data sets and major projects utilizing TCIA with presentations from leading researchers and data contributors. Attendees will also learn about a number of new, major NIH data collection initiatives that are ongoing or coming in the near future which they can leverage in their own research.
- **Wednesday 4:30-6:00 PM** | RCC45 | Room:
  - **Imaging in Proteogenomics Research**
    - Highlight research trends and major NIH new data programs in proteogenomics, and the potential contribution of imaging
- **Thursday 8:30-10:00 AM** | RC625 | Room:

- ## Radiomics: Informatics Tools and Databases
  - 1) Understand the role of challenges in facilitating reproducible radiomics research. 2) Learn about past challenges and lessons learned. 3) Learn about best practices based on experiences from multisite challenges. 4) Review the meaning and importance of interoperability for quantitative image analysis tools. 5) Review specific use cases motivating interoperable communication of the analysis results. 6) Learn about the tools that support interoperable communication of the analysis results using the DICOM standard. 7) Understand the importance of open science methods to facilitate reproducible radiomics research. 8) Become familiar with publicly available sites where you can download existing radiomic data sets, request to upload new radiomic/radiogenomic data sets, and manage your research projects, and learn about data citations and new data-centric journals which help enable researchers to receive academic credit for releasing well-annotated data sets to the public.

- **Thursday 4:30-6:00 PM** | RCC55 | Room:
  - ## Deep Learning-An Imaging Roadmap
    - Deep Learning,' an independent self-learning computational environment that uses multilayered computational neural nets, has generated considerable excitement (as well as concerns and misperceptions) in medical imaging. Deep learning computational techniques, such as convolutional neural networks (CNNs) generate multiple layer feature classifiers that extract disease relevant features from entire regions of medical images without the need for localization or pre-segmentation of lesions. Although CNNs require training on very large image datasets that encompass particular disease expressions, they can be diagnostically effective since no human input of segmentation features such as size, shape, margin sharpness, texture, and kinetics are required. But their immediate and future applicability as tools for unsupervised medical decision-making are, as yet, not well understood by most clinical radiologists. This overview session of Deep Learning will provide a clearer picture by presenters who are active in that field and who can clarify how the unique characteristics of Deep Learning could impact clinical radiology. It will address how radiologists can contribute to, and benefit from, this new technology. Topics of this multi-speaker session will cover: 1) the general principles of deep learning computational schemas and their mechanisms of handling image inputs and outputs. 2) new technology including hardware shifts in microprocessors from CPU's to GPU devices that offer significant computational advantages 3) how to ensure that Deep Learning results are consistently clinically relevant and meaningful including nodal element tuning and provability so as to assure medical care consistency and reproducibility. 4) how to develop and leverage datasets for deep learning on archives such as the NIH The Cancer Imaging Archive (TCIA) including requirements for input image dataset magnitude and completeness of disease spectrum representation. 5) how to embed essential non-imaging data needed as inputs, (e.g. EHR, outcome, cross-disciplinary metadata, and the data pre-processing required to make DICOM ready for Deep Learning. The presentations will be at a level understandable and relevant to the RSNA radiologist audience.

Community Sessions using TCIA Data

Do you have a TCIA-related presentation at RSNA that's not listed below? Contact the **helpdesk** to request it be added!

- **Sunday 10:55-11:05 AM** | SSA12-02 | Room:
  - **FalcoNet-GMC: A 3D Convolutional Neural Network Module for Instance Segmentation and Quantification of Distant Recurrence from Gynecological Cancers**
    - A multifunctional web-based auxiliary system for distant recurrence from gynecologic cancer will enhance the early detection for salvage treatment, with better segmentation by compartment weight maps.
- **Sunday 1:00-1:30 PM** | IN006-EB-SUB | Room:
  - **Reproducibility of Quantitative Features in Prostate mpMRI**
    - Multiparametric magnetic resonance imaging (mpMRI) has emerged as a non-invasive modality to diagnose and monitor prostate cancer. Quantitative metrics on the regions of abnormality in prostate mpMRI has shown to be predictive of clinically significant cancer defined by Gleason grade groups. In this study we evaluate the reproducibility of quantitative imaging features using repeated mpMRI on the same patients. We have shown that some quantitative imaging features are reproducible across sequential prostate mpMRI acquisition at a preset level of filters. A validated set of reproducible image features in mpMRI will allow us to develop a clinically reliable malignance risk stratification score. This will enable the possibility of using imaging as a surrogate to invasive biopsies
- **Monday 10:30-10:40 AM** | SSC03-01 | Room:
  - **Impact of Interobserver Variability in Manual Segmentation of Non-small Cell Lung Cancer (NSCLC) on Computed Tomography**
    - Discovery of predictive and prognostic radiomic features in cancer is currently of great interest to the radiologic community. Since there is no reliable automated means of segmenting lung cancer, tumor labeling is typically performed by imaging analysts, physician trainees and attending physicians. Here we examine the impact of level of specialty training on interobserver variability in manual segmentation of non-small cell lung cancer (NSCLC).
- **Monday 10:50-11:00 AM** | SSC03-03 | Room:
  - **Correlation-Incorporated Hierarchical Clustering of High-Dimensional Radiomic Features for Prognostic Phenotype Identification of EGFR-mutated Non-Small Cell Lung Cancer**
    - We propose a correlation-incorporated unsupervised hierarchical clustering algorithm and evaluate it in identifying computed tomography (CT) radiomic phenotypes of EGFR-mutated non-small cell lung cancer (NSCLC) in association with patient overall survival. CHCA effectively reduces the high dimensionality of radiomic features while allowing for robust identification of CT-based phenotypes of EGFR-mutated NSCLC that are associated with patient survival.
- **Tuesday 9:20-9:30 AM** |RC305-04 | Room:
  - **A Radiomics Nomogram Based on Multiregional Features Might Predict MGMT Promoter Methylation of Glioblastoma Patients**
    - To investigate multiregional features from multimodal MRI in reflecting O6-methylguanine methyltransferase (MGMT) promoter methylation status, and to establish visualized nomogram for MGMT methylation prediction of glioblastomas (GBM) patients. The radiomics nomogram based on multiregional features from multimodal MRI was proposed in our study, and could individually and visually predict MGMT status of GBM patients. In addition, the rEA and rNec areas of GBM play an important role in the prediction of MGMT methylation.
- **Wednesday 12:45-1:15 PM** | NR386-SD-WEB2 | Room: N/A

- **Radiogenomic Analysis of Glioblastoma on Pre-treatment Gd-T1w MRI Reveals Gender-specific Imaging Features and Signaling Pathways**
  - Recent epidemiological studies suggest that gender differences in Glioblastoma (GBM) influence the prognostic outcome of patients, and thus should be considered for targeted treatment. We hypothesize that (1) radiomic features from GBM sub-compartments (peri-tumoral edema, enhancing tumor, non-enhancing and necrotic core) on pre-treatment Gadolinium(Gd)-T1w MRI will have distinct imaging attributes that are prognostic of gender-specific survival, and (2) corresponding transcriptomic data can reveal signaling pathways that drive gender-specific tumor biology and treatment response.

- **Thursday 11:30-11:40 AM** | SSQ15-07 | Room: N/A
  - **Classification of IDH Mutation Status in Brain Tumors using Deep Learning**
    - Isocitrate dehydrogenase (IDH) mutation status is a widely recognized biomarker in diagnosing and treating primary brain tumors. Currently, it is determined using immunohistochemistry or gene sequencing on tissue specimens, acquired through biopsy or surgery. In this work, we developed a fully automated deep-learning network for non-invasive prediction of IDH mutation status using MRI.

- **Friday 8:30-10:00 AM** | RC825 | Room:
  - **Radiomics: From Image to Radiomics**
    - 1) Learn about the role of image annotations in radiology and their relevance to enabling interoperability and for communicating results and value for machine learning and decision support. 2) Become acquainted with important standards and tools that support the creation, management, and use of image annotations. 3) See case examples of image annotations in practice to enable developing applications that help the practice of radiology. 4) Understand the categories of, and the specific radiomic image features that can be computed from images. 5) Understand the effect and implications of image acquisition and reconstruction on radiomic image features. 6) Learn about workflows that drive the creation of predictive models from radiomic image features. 7) Understand the methods for and the potential value of correlating radiological images with genomic data for research and clinical care. 8) Learn how to access genomic and imaging data from databases such as The Cancer Genome Atlas (TCGA) and The Cancer Imaging Archive (TCIA) databases, respectively. 9) Learn about methods and tools for annotating regions within images and link them with semantic and computational features.10) Learn about methods and tools for analyzing molecular data, generating molecular features and associating them with imaging features. 11) Learn how deep learning can revolutionize interpretation of medical images.

TCIA Sessions at RSNA 2018

Click here to browse the RSNA 2018 Program

TCIA-Sponsored

- **All Day | AI030 | AI Community, Learning Center**
  - **Crowds Cure Cancer: Help Annotate Data from the Cancer Imaging Archive**
    - Attendees at this year's RSNA meeting are encouraged to participate in an exciting new activity that will provide valuable data to cancer researchers working in deep learning, radiomics and radiogenomics. This kiosk offers radiologist attendees an opportunity to participate in a 'crowd-sourcing' experiment to accelerate quantitative imaging research. Images are provided by The National Cancer Institute's Cancer Imaging Archive (http://www.cancerimagingarchive.net/), which is a massive public-access resource of cancer radiology images linked to genetic/proteomic, pathology images and clinical data. Many of these cases lack the tumor-location labels needed by computer scientists to jump-start their work on machine learning and quantitative imaging radiomics. Participants will be asked to spend a few minutes anonymously reviewing cases and visually marking their tumor locations. Upon completion, they will receive a ribbon to add to their RSNA badge acknowledging their participation. The data resulting from this process will be openly shared on TCIA with the radiology and computer science communities to accelerate cancer research.
- **Monday 12:30-2:00 PM** | RCB23 | Room: S401CD
  - **A Hands-on Introduction to Using the NIH/NCI's Cancer Imaging Archive (TCIA) (Hands-on)**
    - Access to large, high quality data is essential for researchers to understand disease and precision medicine pathways, especially in cancer. However HIPAA constraints make sharing medical images outside an individual institution a complex process. The NCI's Cancer Imaging Archive (TCIA) addresses this challenge by providing hosting and de-identification services which take the burden of data sharing off researchers. TCIA now contains over 80 unique data collections of more than 30 million images. Recognizing that images alone are not enough to conduct meaningful research, most collections are linked to rich supporting data including patient outcomes, treatment information, genomic / proteomic analyses, and expert image analyses (segmentations, annotations, and radiomic / radiogenomic features). This hands-on session will teach the skills needed to fully access TCIA's existing data as well as learn how to submit new data for potential inclusion in TCIA.
- **Tuesday 3:50-4:00 PM** | SSJ13-06 | Room: N230B
  - **Kaleidoscope: A Series Projection Visualization Tool for Review of DICOM Images for Protected Health Information**
    - Collections submitted to The Cancer Imaging Archive (TCIA) can approach one-million DICOM files. It is time consuming to review each image for burned-in-PHI, pixel data that contains names, dates, or other personal identifying information. Kaleidoscope was developed to increase throughput of visual review.
- **Wednesday 8:30-10:00 AM** | RC553 | Room: E451B
  - **Deep Learning: Applying Machine Learning to Multi-Disciplinary Precision Medicine Data Sets**
    - This didactic session will provide clinician researchers with examples of ongoing machine learning research in imaging combined with clinical and 'omics data sets, along with examples of where to find and how to link existing cancer image archive cases to other public-access stored databases that contain same-patient demographics, genetics, proteomic, and pathology images. Many of these disparate data types may be presently unfamiliar to imagers - such as mass spectroscopy data that arises from cellular proteomic analysis that propel the need for urgently forming new cross-disciplinary research teams. These datasets, often stored separately by different professional specialty teams, constitute critical complementary elements ultimately needed for reliable Machine Learning. This session pivots out from the clinical

images available in the NCI Cancer Imaging Archive (TCIA) collections that acts as the point of origin for linking same-patient demographics, pathology, proteomics, and genetic data so that machine learning efforts can be more scientifically robust.

- **Thursday 10:30-12:00 PM** | RCC52 | Room: S501ABC
  - **Novel Discoveries Using the NCI's Cancer Imaging Archive (TCIA) Public Data Sets**
    - This didactic session will highlight popular data sets and major projects utilizing TCIA with presentations from leading researchers and data contributors. Attendees will hear presentations about the following projects and data sets: • The Applied Proteogenomics OrganizationaL Learning and Outcomes (APOLLO) network • Cancer Proteomics Tumor Analysis Consortium (CPTAC) • Crowds Cure Cancer • Quantitative Imaging Network (QIN) Prostate MRI • Quantitative Image Informatics for Cancer Research (QIICR) • Digital Database for Screening Mammography • Head and Neck Squamous Cell Carcinoma (HNSCC) • 4D-Lung.
- **Presentations:**
  - Deep Learning in Cancer Imaging - Hugo Aerts
  - CBISDDSM: A curated mammography data set for use in computer-aided detection and diagnosis research - Daniel Rubin
  - Harmonizing TCIA image-related data using DICOM - Andrey Fedorov
  - Digital Pathology – Precision Medicine, Pathomics, and Decision Support - Joel Saltz

Community Sessions

Do you have a TCIA-related presentation at RSNA that's not listed below? Contact the **helpdesk** to request it be added!

- **All Day | QRR015 | QIRR, Learning Center**
  - **The Quantitative Image Feature Pipeline (QIFP): Automated Computation of Quantitative Image Features and Construction of Predictive Models**
    - Quantitative image features computed from medical images (i.e., radiomics [1]) can be useful components of biomarkers of diseases including cancer that can be used for treatment selection, assessing response to treatment, and for predicting clinical outcome. As the field evolves, it is still important to discover the best quantitative imaging features for use in associative and predictive models for each cancer type and imaging modality to predict response to existing and new therapeutics, to identify cancer subtypes, and to correlate with cancer genomics. Challenges to progress include the dearth of shared software algorithms, architectures, and tools required to compute, compare, evaluate, and disseminate these quantitative imaging features to researchers and, eventually, to use them for clinical trials and patient management. Our project tackles these challenges with the Stanford Quantitative Imaging Feature Pipeline (QIFP)*, an open source and server-based software system, that gives researchers capabilities for characterizing images of tumors and surrounding tissues. These features can be passed to resident machine learning algorithms to build predictive models, which in turn can be used in multi-center clinical trials with eventual translation to clinical care. The QIFP also allows researchers to add their own algorithms, written in any language for any platform and deployed in Docker containers, for computing novel quantitative image features and for building predictive models for their own studies, and for the benefit of the community. In this way, the QIFP facilitates assessment of the incremental value of new vs. existing feature sets and machine learning algorithms for the development and qualification of imaging biomarkers. *funded by NIH U01 CA187947
- **All Day | QRR014 | QIRR, Learning Center**
  - **ePAD 2018: Expanded Platform to Support Using New Quantitative Imaging Biomarkers in the Clinical Research Workflow**
    - Quantitative imaging ('radiomics') is an emerging field that holds promise for making radiology image interpretation more objective and reproducible, with the potential of better characterizing and diagnosing lesions. As the number of quantitative imaging algorithms explodes, however, there is a pressing need for integrating these algorithms into image interpretation workflows in reading rooms of the future. The electronic Physician Annotation Device (ePAD; http://epad.stanford.edu) [1] is an open source tool that enables radiomics algorithms to be deployed in research workflows such as clinical trials. ePAD captures image annotations from radiologists as they view images and executes radiomics feature algorithms, storing all the results in the Annotation and Image Markup (AIM) [2] format, enabling interoperability of annotations. ePAD has a modular design, and is extensible for adding new tools and quantitative imaging applications that the community is developing. In the past year we have made substantial new developments and enhancements in the ePAD platform that are helping to bring new quantitative imaging methods to the reading room of the future: (1) integration of ePAD into the Quantitative Imaging Feature Pipeline (QIFP) [3], an open source and server-based software system for creating and executing image feature pipelines, (2) recent harmonization of AIM with DICOM, with support for the new DICOM-SR/AIM object, permitting interoperability with vendor platforms and support for new radiomics advancements, (3) expansion of ePAD plugins to incorporate new radiomics image feature algorithms, and (4) new applications that leverage radiomics features for decision support. The

ePAD interface has been enhanced with a new Javascript user interface to fit seamlessly into the radiologist research workflow and produces structured reports of lesion features to improve clinical decision making. ePAD is being used internationally with over 300 users who created 21,000+ image annotations, as well in national research projects of The Cancer Genome Atlas.

- **All Day | QRR020 | QIRR, Learning Center**
  - **Cancer Imaging Phenomics Toolkit (CaPTk): A Software Platform Leveraging Quantitative Radio(geno)mic Analytics for Computational Oncology**
    - Computational research has provided the scientific community with sophisticated algorithms towards gaining a comprehensive understanding of fundamental oncologic mechanisms, while providing substantive insight into the biological basis of disease susceptibility and treatment response, as well as potentially leading to the identification of new therapeutic targets. Rapid deployment and translation of such algorithms via an integrative and easy-to-use platform is required to maximize their benefit in clinical practice. CaPTk1 is a platform that makes this translation possible, thereby enabling clinical researchers to conduct quantitative analyses without requiring a substantial computational background. It can thus be seamlessly integrated into the typical quantification and analysis workflow of a radiologist, emphasizing its clinical potential. CaPTk is a growing software platform focusing on image analysis and machine learning tools for brain, breast and lung cancer, based on a two-tier functionality: Extraction of diverse and complementary features (e.g. textural, morphologic, kinetic) from multimodal imaging. Integration of the extracted features, via multivariate machine learning, into non-invasive diagnostic, prognostic and predictive models.
- **Monday 9:20-9:30 AM** | RC205-04 | Room: S406B
  - **Probabilistic Atlases of Pre-Treatment MRI Reveal Hemispheric and Lobe-Specific Spatial Distributions across Molecular Sub-Types of Diffuse Gliomas**
    - Recent WHO classification of diffuse gliomas defined 3 subtypes based on their molecular status: Isocitrate dehydrogenase wild type (IDH-WT), IDH mutant with 1p/19q intact (IDHmut-noncodel), and IDH mutant with 1p/19q co-deletion (IDHmut-codel). Each category represents different prognosis and chemo-sensitivity thus impacting treatment decisions. Previous studies have linked tumor location with patient outcome. In this feasibility study, we developed population atlases of pre-treatment MRI lesions to evaluate whether IDH-WT, IDHmut-codel, IDHmut-noncodel tumors will have spatial proclivity to hemispheric or lobe-specific locations based on their frequency of occurrence.
- **Monday 1:50- 2:00 PM** | MSRO23-03 | Room: E450A
  - **Using Artificial Intelligence to Predict Oropharyngeal Cancer Recurrence After Radiation Therapy**
    - HPV derived oropharyngeal cancers are less aggressive and more radiosensitive compared to non-HPV derived oropharyngeal cancers. In the HPV era, treatment de-escalation is one of the main areas of focus for clinical trials. However, recurrences still occur in HPV derived disease and can follow unique patterns, so it is important to identify patients at high risk of recurrence and ensure that they do not receive de-intensified treatment. Artificial intelligence can be used to analyze radiomic signatures and potentially predict recurrence. This would allow for personalized treatment planning based on radiographic risk profiles. Our purpose was to demonstrate that deep learning models have the potential to assess radiographic risk factors for oropharyngeal cancer recurrence.
- **Tuesday 3:20-3:30 PM** | SSJ22-03 | Room: N227B
  - **Implementation of a CT Reference Library Containing Manufacturer-Neural Projection Data, Images, and Clinical Metadata**
    - A manufacturer-neutral CT projection data (PD) format (DICOM-CT-PD) has been previously developed and used to allow access to CT PD and the scanner information required for image reconstruction. Access to such data was not previously possible, limiting the ability of

reconstruction scientists to work with patient data. In this work, we aim to construct a reference DICOM-CT-PD library containing patient PD with corresponding images and clinically relevant metadata, and to publish this library for public access.

- **Wednesday 11:20-11:30 AM** | SSK09-06 | Room: N226
    - **Radiologically Defined Tumor Necrosis in Clear Cell Renal Cell Carcinoma as a Surrogate of Pathologically-Defined Tumor Necrosis, Staging, and as a Size-Independent Prognostic Biomarker**
        - Pathologically defined tumor necrosis (PDTN) in clear cell renal cell carcinoma (ccRCC) has been considered as a prognostic factor. We aimed to measure radiologically-defined tumor necrosis (RDTN) of ccRCC and explore its association with PDTN, stage/grade, and with survival outcomes in a multi-institutional cohort.
- **Wednesday 11:30-11:40 AM** | SSK09-07 | Room: N226
    - **Developing a Sex-Specific Stratification System for Renal Cell Carcinoma Patients Using CT-Based Abdominal Fat and Muscle Quantification and Tumor Molecular Phenotyping**
        - Imaging biomarkers of metabolism such as tumor glucose uptake, patient muscle mass, and patient visceral fat have the ability to predict outcomes in cancer patients. Recent evidence has demonstrated sex differences in these metabolic measurements both on the imaging and the molecular levels. We wanted to determine if muscle mass and visceral fat measured by CT and molecular profiling of tumor glycolytic metabolism could be combined to develop a multiparametric sex-specific stratification system for RCC patients.
- **Wednesday 3:00-3:10 PM** | SSM12-01 | Room: E535B
    - **Quantitative DCE-MRI Features Can Complement Molecular Markers for Predicting Tumor Infiltrating Lymphocytes in Breast Cancer: Model Discovery and Independent Validation**
        - We retrospectively analyzed two breast cancer cohorts, with 126 patients from the cancer genome atlas (TCGA) as discovery cohort and 106 patients from ACRIN 6657/I-SPY 1 TRIAL as validation cohort. 17 computational features were extracted from DCE MRI to characterize functional tumor volume, tumor morphology and texture as well as parenchymal enhancement patterns. The percentage of stromal TILs was evaluated on hematoxylin and eosin stained histologic whole-tumor sections by two experienced pathologists. From tumor molecular data, we computed two markers as surrogates for TILs, including the non-synonymous somatic mutational burden and cytolytic activity score. First, we evaluated the associations between individual DCE-MRI features and TILs read by pathologists. Multiple hypotheses testing was corrected by the Benjamini-Hochberg method using false discovery rate (FDR). Next, we built a composite prediction model for TILs by combining DCE-MRI features with molecular surrogates. Finally, we independently validated the prognostic significance of the built TILs model in the I-SPY cohort.
- **Thursday 4:30-6:00 PM** | RC718C | Room: N229
    - **Making Sense of Big Imaging Data: What Comes Next?**
        - The practice of medicine is undergoing seismic shifts from being primarily experience-based to data-driven. Further, the emergence of data-driven quantitative diagnostic, prognostic, and predictive methods will see an exponential increase in coming years due to the emergence of tools that can mine large amounts of data across sites. Such systems are already in place for many data types, and tools for analyses of radiological data are just emerging, and are likely to change the practice of radiology forever from a semantic lexicon based discipline to one that is increasingly analytical, driven by machine learning algorithms. The power of these analytics is primarily limited by access to sufficiently large data sets of highly curated patients, with images, co-variates, treatments and outcomes. In the field of cancer, the Cancer Image Archive (TCIA) houses over 30 million radiographic images that can be mined for associations with multiple core data elements (CDE) and this has been used extensively to generate predictive

and prognostic models. Although 30 million sounds like a lot, it is a mall fraction of the >100 million radiological exams that are acquired annually in the U.S. Going forward, tools are being developed that will allow sharing of processed image data along with CDEs without the need to share images themselves, lowing the barriers to building large cohorts. These will likely take decades to deploy, however. In the meantime tools are being deployed to prospectively capture data within single institutions to automatically build and populate focused cohorts.

- **Friday 10:30-10:40 AM** | SST07-01 | Room: E353A
    - **Radiogenomic Analysis Identifies Multiple Therapeutically Relevant Subtypes for Head and Neck Squamous Cell Carcinoma**
        - This study included 113 HNSCC patients from The Cancer Genome Atlas Head-Neck Squamous Cell Carcinoma (TCGA-HNSC) project. Molecular phenotypes investigated were RNA-defined HPV infection, 5 epigenomic subtypes discovered by MethylMix, 4 mRNA subtypes by TCGA group, and 5 common somatic gene mutations. In total, 2,131 quantitative image features were extracted from pre-treatment CT scans. Discriminative features were selected using the Minimum Redundancy Maximum Relevance (mRMR) algorithm. Afterwards, we applied logistic regression model with the least absolute shrinkage and selection operator (LASSO) to build binary classifiers for predicting each molecular subtype. All classifiers were trained using nested stratified 10-fold cross-validation repeated 10 times and the performance metric was the average area under the Receiver Operator Characteristic (ROC) curve (AUC) of the outer loop of the nested cross-validation. Additionally, an HPV prediction model was developed using the entire TCGA-HNSC cohort, and was validated by an independent validation cohort (N = 53).

TCIA Sessions at RSNA 2017

TCIA-Sponsored

- **All Day | ML005 | Machine Learning Community, Learning Center**
  - **Crowds Cure Cancer: Help Annotate Data from The Cancer Imaging Archive**
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- **Wednesday 8:30-10:00 AM** | RCC41 | Room: S501ABC
  - **Research Opportunities Using the NIH The Cancer Imaging Archive (TCIA) That Links Cancer Imaging to Clinical Data, Genomics, Proteomics, Quantitative Imaging and Deep Learning**
    - Diagnostic images, analyzed by expert radiologists with computational analytic tools assistance can offer reliable, reproducible data that connect tumor tissue genetics, proteomics and pathology images. This didactic session will highlight major projects utilizing TCIA with presentations from leading researchers using projects such as the Moonshot/APOLLO, proteomics (CPTAC Phase III), The Cancer Genome Atlas (TCGA), Immunotherapy, Challenges, Precision Medicine, NCI Quantitative Imaging Network.
- **Wednesday 4:30-6:00 PM** | RCC45 | Room: S501ABC
  - **Deep Learning—An Imaging Roadmap**
    - Deep Learning,' an independent self-learning computational environment that uses multilayered computational neural nets, has generated considerable excitement (as well as concerns and misperceptions) in medical imaging. Deep learning computational techniques, such as convolutional neural networks (CNNs) generate multiple layer feature classifiers that extract disease relevant features from entire regions of medical images without the need for localization or pre-segmentation of lesions. Although CNNs require training on very large image datasets that encompass particular disease expressions, they can be diagnostically effective since no human input of segmentation features such as size, shape, margin sharpness, texture, and kinetics are required. But their immediate and future applicability as tools for unsupervised medical decision-making are, as yet, not well understood by most clinical radiologists. This overview session of Deep Learning will provide a clearer picture by presenters who are active in that field and who can clarify how the unique characteristics of Deep Learning could impact clinical radiology. It will address how radiologists can contribute to, and benefit from, this new technology. Topics of this multi-speaker session will cover: 1) the general principles of deep learning computational schemas and their mechanisms of handling image inputs and outputs. 2) new technology including hardware shifts in microprocessors from CPU's to GPU devices that offer significant computational advantages 3) how to ensure that Deep Learning results are consistently clinically relevant and meaningful including nodal element tuning and provability so as to assure medical care consistency and reproducibility. 4) how to develop and leverage datasets for deep learning on archives such as the NIH The Cancer Imaging Archive (TCIA) including requirements for input image dataset magnitude and completeness of disease spectrum representation. 5) how to embed essential

non-imaging data needed as inputs, (e.g. EHR, outcome, cross-disciplinary metadata, and the data pre-processing required to make DICOM ready for Deep Learning. The presentations will be at a level understandable and relevant to the RSNA radiologist audience.

- **Thursday 2:30-4:00 PM** | RCB54 | Room: S401CD
  - **Using Publicly Accessible 'Big Data' from the NIH/NCI's Cancer Imaging Archive (TCIA) to Research Quantitative Radiomics, Proteomics, Genetics and Pathology (Hands-on)**
    - Access to large, high quality data is essential for researchers to understand disease and precision medicine pathways, especially in cancer. However HIPAA constraints make sharing diagnostic clinical images outside an individual institution a complex process. The NCI's Cancer Imaging Archive (TCIA) addresses this challenge by providing hosting and de-identification services which take the burden of data sharing off researchers. TCIA now contains over 70 unique data collections of more than 28 million images. Recognizing that images alone are not enough to conduct meaningful research, most collections are linked to rich supporting data including patient outcomes, treatment information, genomic / proteomic analyses, and expert image analyses (segmentations, annotations, and radiomic / radiogenomic features). This hands-on session will teach the skills needed to fully access TCIA's existing data as well as learn how to submit new data for potential inclusion in TCIA.

Community sessions

Do you have a TCIA-related presentation at RSNA that's not listed below? Contact the **helpdesk** to request it be added!

- **Monday 9:10-9:20 AM** | RC205-03 | Room: S406B
  - Radiogenomics Analysis in Hemodynamic Abnormality of Patients with Newly Diagnosed Glioblastomas: Combination with TCIA Database
- **Monday 3:00-3:10 PM** | SSE02-01 | Room: E450A
  - Phenotypic Biomarkers of Intra-Tumor Heterogeneity in Breast DCE-MRI Can Augment Tumor Volume Measures in Predicting Survival after Neoadjuvant Chemotherapy for Locally Advanced Breast Cancer: Results from the ACRIN 6657/I-SPY-1 Trial
- **Tuesday 8:30-10:00 AM** | RC325 | Room: S404AB
  - Radiomics Mini-Course: From Image to Omics
    - Image Annotation and Semantic Labeling
    - Image Feature Computation and Considerations
    - Correlating Image Features with Multi-Omics Data
- **Tuesday 4:30-6:00 PM** | RC425 | Room: S103CD
  - Radiomics Mini-Course: Informatics Tools and Databases
    - The Role of Challenges and Their Requirements
    - Quantitative Image Analysis Tools: Communicating Quantitative Image Analysis Results
    - Public Databases for Radiomics Research: Current Status and Future Directions
- **Wednesday 3:10-3:20 PM** | SSM12-02 | Room: S404CD
  - Personalized Survival Prediction Using Random Forest Survival Model on MR Radiomic Features in Gliomas
- **Wednesday 3:40-3:50 PM** | SSM12-05 | Room: S404CD
  - A Clinically-Actionable Fully Convolutional Network for Brain Tumor Segmentation
- **Lakeside Learning Center Exhibits**
  - DICOM4QI Demonstration and Connectathon: Structured Communication of Quantitative Image Analysis Results Using the DICOM Standard (Meet-the-Experts Schedule: Mon/Tues/Weds 12:15pm - 1:15pm)
  - The Quantitative Image Feature Pipeline (QIFP): Automated Radiomic Feature Extraction to Derive Associations with and Prediction of Clinical Variables from Image Features (Meet-the-Experts Schedule: Mon/Tues/Weds 12:15pm - 1:15pm)
  - Cancer Imaging Phenomics Toolkit (CaPTk): A Radio(geno)mics Software Platform Leveraging Quantitative Imaging Analytics for Computational Oncology (Meet-the-Experts Schedule: Tues/Weds /Thurs 12:15pm - 1:15pm)
  - Standardizing Radiomic Feature Descriptions for Quantitative Imaging: A Preliminary Report of the Cooperative Efforts of the NCI's QIN PET-CT Subgroup (Meet-the-Experts Schedule: Mon/Tues /Weds 12:15pm - 1:15pm)

RSNA 2016 Sessions Using TCIA

TCIA-Sponsored Sessions

Imaging Integration with Cancer Genomics/Proteomics: Methodologies Leveraging the Cancer Imaging Archive

Thursday 8:30-10:00 AM | RCC51 | Room: S501ABC

The Cancer Imaging Archive: Using 'Big Data' for the study of Cancer Radiomics, Proteomics, Genetics and Pathology (Hands-on)

Thursday 4:30-6:00 PM | RCA55 | Room: S401AB

User Community Sessions

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 10:30-10:40 AM | SSC08-01 | Room: S402AB

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

Monday 11:20-11:30 AM | SSC08-06 | Room: S402AB

Targeting Glucose Metabolism in Brain Tumor Initiating Cells: An Novel Therapeutic Approach for Radiosensitization

Monday 11:50-12:00 PM | MSRO25-09 | Room: S103CD

Practical Radiogenomics: Lessons Learned from the Cancer Genome Atlas

Tuesday 9:40-10:10 AM | RC305-06 | Room: S102AB

Comparison of Novel Multi-level Otsu and Conventional PET Segmentation Methods for Measuring FDG Metabolic Tumor Volume in Patients with Soft Tissue Sarcoma

Tuesday 11:20-11:30 AM | RC311-12 | Room: S505AB

The Quantitative Image Feature Pipeline (QIFP) for Discovery, Validation, and Translation of Cancer Imaging Biomarkers

Thursday 12:15-12:45 PM | IN251-SD-THA2 | IN Community, Learning Center Station #2

Reproducibility of CT Texture Parameters by Leveraging Publically Available Patient Imaging Datasets

Thursday 12:15-12:45 PM | IN255-SD-THA6 | IN Community, Learning Center

Station #6

Interoperable Communication of Quantitative Image Analysis Results Using the DICOM Standard

All Day | QRR003 | QIRR, Learning Center

Early Implementation of Radiomics into Clinical Use: How Radiomic Data Can Change Clinical Care of Patients

All Day | IN109-ED-X