TCIA Sessions at RSNA 2018

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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).