Session: Lightning talks – day 1

RadxTools for assessing tumor treatment response on imaging

Hyemin Um and Thomas DeSilvio, Andrew Janowczyk, Manmeet Ahluwalia, Sharon Stein, Anant Madabhushi, Pallavi Tiwari, and Satish E. Viswanath

Case Western Reserve University, Cleveland, OH

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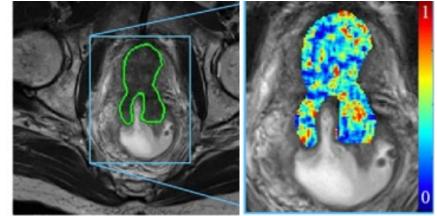




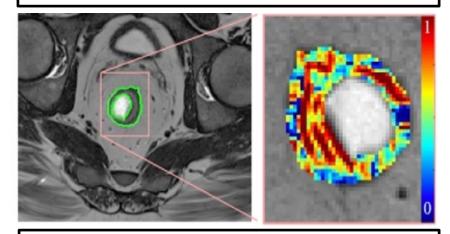


The Challenge: Identifying Treatment Response

- 1.6 million patients in U.S. undergo chemotherapy or radiation as first-line cancer treatment
- Expert identification of responder vs. non-responder on post-treatment imaging is challenging
- Unmet need for image analytics tools to quantify treatment response in oncology via routine imaging



Responder



Non-responder

Adapted from Antunes et al. JMRI 2020









RadxTools

- Suite of 3 open-source tools to characterize tumor treatment response on standard-of-care MR/CT imaging
- 1. RadTx capture subtle lesion perturbations in response to therapy
 - CoLlAGe
 - Topology
- 2. RadPathFuse MRI-histopathology co-registration
- **3.** RadQC quality control of radiomic features
- Integrated into informatics platforms for widespread use by the radiomics/imaging community and oncology working groups

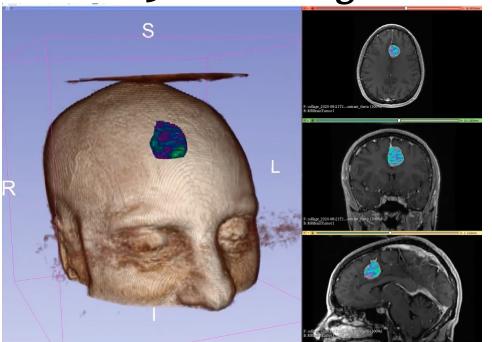




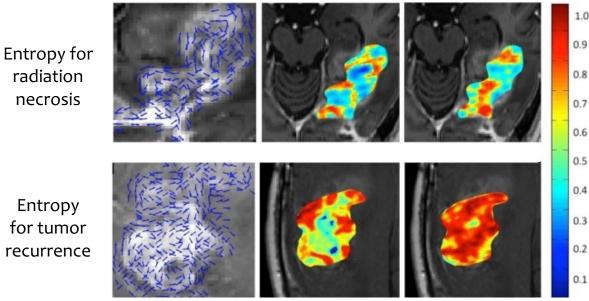


RadTx: CoLlAGe Module

3D Slicer Plugin



Use Case: Brain Tumors



CoLlAGe features shown to distinguish radiation effects from recurrent tumor on post-treatment T1w MRI with an accuracy of 88.5% [1].

Purpose: Measure anisotropic differences in disease pathologies via local entropy of voxel-level gradient orientations

Available Platforms: Python PIP, 3D Slicer, CapTK

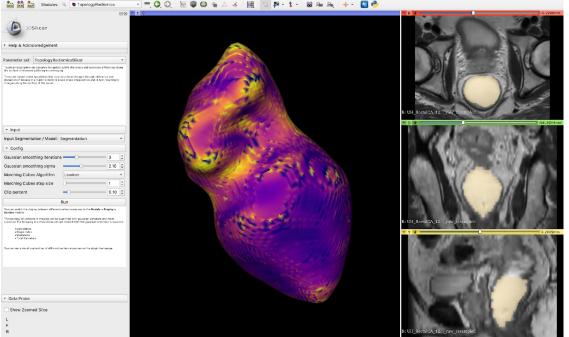




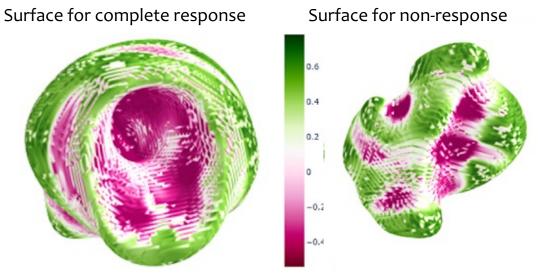


RadTx: Topology Module

3D Slicer Plugin



Use Case: Rectal Cancer



Tumor topology features predict pathologic complete response to neoadjuvant CRT on pre-treatment T2w MRI with an AUC of 0.95 [2].

Purpose: Quantify morphometric sharpness and surface curvature differences between responders vs. non-responders to treatment **Available Platforms:** Python PIP, 3D Slicer, Jupyter Notebook



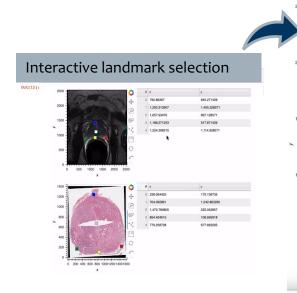


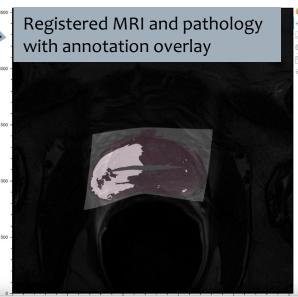


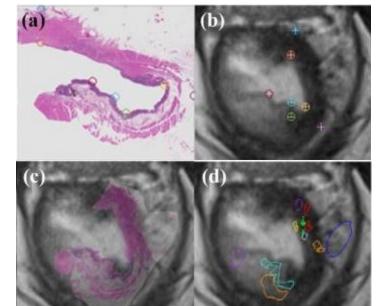


RadPathFuse

Jupyter Notebook







Use Case: Rectal Cancer

Co-registered pathology and MRI sections (c-d) reveal excellent structural alignment, with a registration error of 2-3 pixels [3]. Landmarks used for registration displayed in different colors on the pathology slide (a) and MR slice (b).

Purpose: Interactive workflow to generate deeply annotated pathologyvalidated radiographic datasets via rigorous co-registration of MRI/CT and histopathology specimens

Available Platforms: Jupyter Notebook





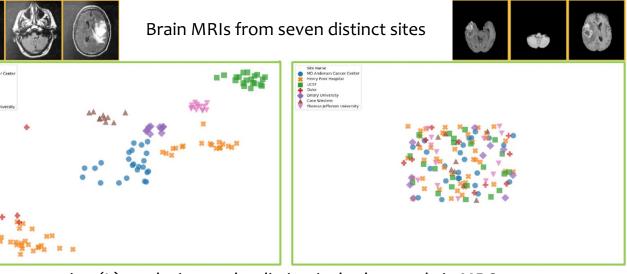


RadQC: MRQy

Python PIP

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Use Case: TCGA-GBM



Before processing (L), each site can be distinctively clustered via MRQy measures, revealing potential batch effects. After processing (R), the data fall within a single merged cluster [4].

Purpose: Enables quality control of MRI data to quantify and evaluate impact of imaging and institutional variations (e.g., scanners, protocols) **Available Platforms:** Python PIP









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