TCGA Breast Phenotype Research Group Data sets

Data Citation

Morris, Elizabeth, Burnside, Elizabeth, Whitman, Gary, Zuley, Margarita, Bonaccio, Ermelinda, Ganott, Marie, … Giger, Maryellen L. (2014). Using Computer-extracted Image Phenotypes from Tumors on Breast MRI to Predict Stage. The Cancer Imaging Archive. http://doi.org/10.7937/K9/TCIA.2014.8SIPIY6G

Description

At the time of our study, 108 cases with breast MRI data were available in the TCGA-BRCA collection. In order to minimize variations in image quality across the multi-institutional cases we included only breast MRI studies acquired on GE 1.5 Tesla magnet strength scanners (GE Medical Systems, Milwaukee,Wisconsin, USA) scanners, yielding a total of 93 cases. We then excluded cases that had missing images in the dynamic sequence (1 patient), or at the time did not have gene expression analysis available in the TCGA Data Portal (8 patients). After these criteria, a dataset of 84 breast cancer patients resulted, with MRIs from four institutions: Memorial Sloan Kettering Cancer Center, the Mayo Clinic, the University of Pittsburgh Medical Center, and the Roswell Park Cancer Institute. The resulting cases contributed by each institution were 9 (date range 1999-2002), 5 (1999-2003), 46 (1999-2004), and 24 (1999-2002), respectively. The dataset of biopsy proven invasive breast cancers included 74 (88%) ductal, 8 (10%) lobular, and 2 (2%) mixed. Of these, 73 (87%) were ER+, 67 (80%) were PR+, and 19 (23%) were HER2+. Various types of analyses were conducted using the combined imaging, genomic, and clinical data. Those analyses are described within several manuscripts created by the group (cited below).

Publication Citation

- Guo W, Li H, Zhu Y, Lan L, Yang S, Drukker K, Morris E, Burnside E, Whitman G, Giger ML*, Ji Y*: Prediction of clinical phenotypes in invasive breast carcinomas from the integration of radiomics and genomics data. J Medical Imaging 2(4), 041007 (Oct-Dec 2015). doi: 10.1117/1.JMI.2.4.041007
- Burnside E, Drukker K, Li H, Bonaccio E, Zuley M, Ganott M, Net JM, Sutton E, Brandt K, Whitman G, Conzen S, Lan L, Ji Y, Zhu Y, Jaffe C, Huang E, Freymann J, Kirby J, Morris EA*, Giger ML*: Using computer-extracted image phenotypes from tumors on breast MRI to predict breast cancer pathologic stage. Cancer doi: 10.1002/cncr.29791, 2015.
- Zhu Y, Li H, Guo W, Drukker K, Lan L, Giger ML*, Ji Y*: Deciphering genomic underpinnings of quantitative MRI-based radiomic phenotypes of invasive breast carcinoma. Nature – Scientific Reports 5:17787. doi: 10.1038/srep17787, 2015.
- Li H, Zhu Y, Burnside ES, …. Perou CM, Ji Y*, Giger ML*: MRI radiomics signatures for predicting the risk of breast cancer recurrence as given by research versions of gene assays of MammaPrint, Oncotype DX, and PAM50. Radiology. doi: 10.1148/radiol.2016152110, 2016.
- Li H, Zhu Y, Burnside ES, …. Perou CM, Ji Y, Giger ML: Quantitative MRI radiomics in the prediction of molecular classifications of breast cancer subtypes in the TCGA/TCIA Dataset. npj Breast Cancer (2016) 2, 16012; doi:10.1038/npjbcancer.2016.12; published online 11 May 2016.

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- Image Data: DICOM – Save/open this file to initiate our Java Web Start download manager to begin your download
- Radiologist Annotations/Markup: tcga breast radiologist reads.xls
- 3D Lesion Segmentations & Quantitative Radiomic Features
  - 3D Segmentations
    - Readme instructions
    - Note: With regards to the naming structure, *S2-1.les: S2 means DCE-MRI sequence 2, lesion #1. Sometimes, there are multiple DCE-MRI sequences on TCIA data, and so the team used the sequence that corresponded to the one on which the radiologists annotated the truth.
  - Quantitative Radiomics
    - Note: please reference these data extracted using version **V2010** of the UChicago MRI Quantitative Radiomics workstation
- Multi-gene assays including MammaPrint, Oncotype DX, and PAM50: Perou TCGA BRCA MRIs+PAM50+GHI21+NKI70 MAILED.xlsx
- TCGA Clinical Data (from TCGA Data Portal, archived in case of subsequent updates made by TCGA): brca-clinicalforwiki.xls