

# Prostate Fused-MRI-Pathology

## Summary

This collection comprises a total of 28 3 Tesla T1-weighted, T2-weighted, Diffusion weighted and Dynamic Contrast Enhanced prostate MRI along with accompanying digitized histopathology (H&Estained) images of corresponding radical prostatectomy specimens. The MRI scans also have a mapping of extent of prostate cancer on them [1]. Each surgically excised prostate specimen was originally sectioned and quartered resulting in 4 slides for each section. Each of these individual slides was digitized at 20x magnification using an Aperio slide scanner resulting in a set of 4 .svs images. Each of the 4 .svs images were then digitally stitched together to constitute a pseudo-whole mount section (.tiff) using the program in [2]. Annotations of cancer presence on the pseudo-whole mount sections were made by an expert pathologist. Slice correspondences were established between the individual T2w MRI and stitched pseudo-whole mount sections by the program in [3] and checked for accuracy by an expert pathologist and radiologist. Deformable co-registration [4] was employed to spatially co-registered the corresponding radiologic and histopathologic tissue sections to map disease extent onto the corresponding MRI scans.

Data collection and analysis was provided by Anant Madabhushi, PhD, Case Western Reserve University and Michael D. Feldman, MD, PhD, Hospital at the University of Pennsylvania. This work was supported by NIH R01CA136535.


## References

1. Singanamalli, A. , Rusu, M. , Sparks, R. E., Shih, N. N., Ziober, A. , Wang, L. , Tomaszewski, J. , Rosen, M. , Feldman, M. and Madabhushi, A. (2016), **Identifying in vivo DCE MRI markers associated with microvessel architecture and gleason grades of prostate cancer.** *J. Magn. Reson. Imaging*, 43: 149-158. doi: [10.1002/jmri.24975](https://doi.org/10.1002/jmri.24975) (PMID:26110513).
2. Toth, R, Feldman, M, Yu, D, Tomaszewski, J, Madabhushi, A. “**Histostitcher™: An Informatics Software Platform for Reconstructing Whole-Mount Prostate Histology using the Extensible Imaging Platform (XIP™) Framework,**” *Journal of Pathology Informatics*, vol. 5, pg. 8, 2014 (PMID: 24843820, PMCID: PMC4023035).
3. Xiao, G, Bloch, N, Chappelw, J, Genega, E, Rofsky, N, Lenkinsky, R, Tomaszewski, J, Feldman, M, Rosen, M, Madabhushi, A. “**Determining Histology-MRI Slice Correspondences for Defining MRI-based Disease Signatures of Prostate Cancer,**” Special Issue of Computerized Medical Imaging and Graphics on Whole Slide Microscopic Image Processing, vol. 35[7-8], pp. 568-78, 2011 (PMID: 21255974).
4. Chappelw, J, Bloch, N., Rofsky, N, Genega, E, Lenkinski, R, DeWolf, W, Madabhushi, A. “**Elastic Registration of Multimodal Prostate MRI and Histology via Multi-Attribute Combined Mutual Information,**” *Medical Physics*, vol. 38[4], pp. 2005-2018, 2011 (PMID: 21626933).

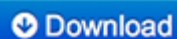
## Data Access

### Data Access

Click the **Download** button to save a ".tcia" manifest file to your computer, which you must open with the [NBIA Data Retriever](#) . Click the **Search** button to open our Data Portal, where you can browse the data collection and/or download a subset of its contents.

Data Type	Download all or Query/Filter
Images (DICOM, 4.4 GB)	 
Annotated Whole Slide Pathology Images (76.8 GB)	 

Fused Rad-Path Matlab Files



Please note that Box has a 15GB download limit, so you will need to download images in batches.

Click the Versions tab for more info about data releases.

### Detailed Description

## Detailed Description

Collection Statistics	Radiology Image Statistics	Pathology Image Statistics
Modalities	MRI	Pathology, Matlab
Number of Participants	28	16
Number of Studies	29	N/A
Number of Series	325	N/A
Number of Images	32,508	114
Image Size (GB)	4.4	76.8

## Supporting Documentation

The data set is fully described in the following publications:

1. Singanamalli, A. , Rusu, M. , Sparks, R. E., Shih, N. N., Ziober, A. , Wang, L. , Tomaszewski, J. , Rosen, M. , Feldman, M. and Madabhushi, A. (2016), **Identifying in vivo DCE MRI markers associated with microvessel architecture and gleason grades of prostate cancer.** J. Magn. Reson. Imaging, 43: 149-158. doi: [10.1002/jmri.24975](https://doi.org/10.1002/jmri.24975) (PMID:26110513).
2. Toth, R, Feldman, M, Yu, D, Tomaszewski, J, Madabhushi, A, “**Histostitcher™: An Informatics Software Platform for Reconstructing Whole-Mount Prostate Histology using the Extensible Imaging Platform (XIP™) Framework,**” *Journal of Pathology Informatics*, vol. 5, pg. 8, 2014 (PMID: 24843820, PMCID: PMC4023035).
3. Xiao, G, Bloch, N, Chappelow, J, Genega, E, Rofsky, N, Lenkinsky, R, Tomaszewski, J, Feldman, M, Rosen, M, Madabhushi, A, “**Determining Histology-MRI Slice Correspondences for Defining MRI-based Disease Signatures of Prostate Cancer,**” Special Issue of Computerized Medical Imaging and Graphics on Whole Slide Microscopic Image Processing, vol. 35[7-8], pp. 568-78, 2011 (PMID: 21255974).
4. Chappelow, J, Bloch, N., Rofsky, N, Genega, E, Lenkinski, R, DeWolf, W, Madabhushi, A, “**Elastic Registration of Multimodal Prostate MRI and Histology via Multi-Attribute Combined Mutual Information,**” *Medical Physics*, vol. 38[4], pp. 2005-2018, 2011 (PMID: 21626933).

## Pathology and Matlab Data

Reconstructed, annotated whole slide pathology as well as fused Rad-Path matlab objects are also available at <https://pathology.cancerimagingarchive.net/pathdata/>.

### Citations & Data Usage Policy

## Citations & Data Usage Policy

Users of this data must abide by the [Creative Commons Attribution 3.0 Unported License](https://creativecommons.org/licenses/by/3.0/) under which it has been published. Attribution should include references to the following citations:

### Data Citation

Madabhushi, A., & Feldman, M. (2016). **Fused Radiology-Pathology Prostate Dataset** . The Cancer Imaging Archive. doi: [10.7937/K9/TCIA.2016.TLPMRIAM](https://doi.org/10.7937/K9/TCIA.2016.TLPMRIAM)

### Publication Citation

1. Singanamalli, A. , Rusu, M. , Sparks, R. E., Shih, N. N., Ziober, A. , Wang, L. , Tomaszewski, J. , Rosen, M. , Feldman, M. and Madabhushi, A. (2016), **Identifying in vivo DCE MRI markers associated with microvessel architecture and gleason grades of prostate cancer**. J. Magn. Reson. Imaging, 43: 149-158. doi: [10.1002/jmri.24975](https://doi.org/10.1002/jmri.24975) (PMID:26110513).
2. Toth, R, Feldman, M, Yu, D, Tomaszewski, J, Madabhushi, A, “**Histostitcher™: An Informatics Software Platform for Reconstructing Whole-Mount Prostate Histology using the Extensible Imaging Platform (XIP™) Framework**,” *Journal of Pathology Informatics*, vol. 5, pg. 8, 2014 (PMID: 24843820, PMCID: PMC4023035).
3. Xiao, G, Bloch, N, Chappelow, J, Genega, E, Rofsky, N, Lenkinsky, R, Tomaszewski, J, Feldman, M, Rosen, M, Madabhushi, A, “**Determining Histology-MRI Slice Correspondences for Defining MRI-based Disease Signatures of Prostate Cancer**,” Special Issue of Computerized Medical Imaging and Graphics on Whole Slide Microscopic Image Processing, vol. 35[7-8], pp. 568-78, 2011 (PMID: 21255974). <https://doi.org/10.1016/j.compmedimag.2010.12.003>
4. Chappelow, J, Bloch, N., Rofsky, N, Genega, E, Lenkinski, R, DeWolf, W, Madabhushi, A, “**Elastic Registration of Multimodal Prostate MRI and Histology via Multi-Attribute Combined Mutual Information**,” *Medical Physics*, vol. 38[4], pp. 2005-2018, 2011 (PMID: 21626933).

### TCIA Citation





Clark K, Vendt B, Smith K, Freymann J, Kirby J, Koppel P, Moore S, Phillips S, Maffitt D, Pringle M, Tarbox L, Prior F. **The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository**, *Journal of Digital Imaging*, Volume 26, Number 6, December, 2013, pp 1045-1057. ([paper](#))

## Other Publications Using This Data

TCIA maintains [a list of publications](#) that leverage our data. At this time we are not aware of any publications based on this data. If you have a publication you'd like to add, please [contact the TCIA Helpdesk](#).

### Versions

#### Version 1 (Current) Updated 11-30-2016

Data Type	Download all or Query/Filter
Images (DICOM, 4.4 GB)	  (Requires the <a href="#">NBIA Data Retriever</a> .)
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