Ivy Glioblastoma Atlas Project (IvyGAP)

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Summary

This data collection consists of MRI/CT scan data for brain tumor patients that form the cohort for the resource Ivy Glioblastoma Atlas Project (Ivy GAP). There are 390 studies for 39 patients that include pre-surgery, post-surgery and follow up scans. The Ivy GAP is a collaborative partnership between the Ben and Catherine Ivy Foundation, which generously provided the financial support, the Allen Institute for Brain Science, and the Ben and Catherine Ivy Center for Advanced Brain Tumor Treatment. The goal of the project is to provide online resources to scientists and physicians dedicated to the development of innovative treatments and diagnostics that will enhance the quality of life and survival of patients with brain cancer.

These resources represent an unprecedented platform for exploring the anatomic and genetic basis of glioblastoma at the cellular and molecular levels. In addition to the DICOM images in TCIA there are two interactive databases linked together by de-identified tumor specimen numbers to facilitate comparisons across data modalities:

1. Ivy Glioblastoma Atlas Project - An open/public database providing in situ hybridization (ISH) and RNA sequencing (RNA-Seq) data, which map gene expression across the anatomic structures and putative cancer stem cell clusters in glioblastoma. The associated histological dataset is annotated and is suitable for neuropathological examination.
2. Ivy GAP Clinical and Genomic Database - A database offering detailed clinical, genomic, and expression array data sets that are designed to elucidate the pathways involved in glioblastoma development and progression. This database requires registration for access.

The Ivy GAP is described in the resource paper (70 authors not all listed here) : Puchalski, R. B., Shah, N., …, Foltz, G. D. (2018). **An anatomic transcriptional atlas of human glioblastoma.** In Science (Vol. 360, Issue 6389, pp. 660–663). https://doi.org/10.1126/science.aaf2666

For scientific or other inquiries about this dataset, please contact the TCIA Helpdesk.

Data Access

Data Access

Some data in this collection contains images that could potentially be used to reconstruct a human face. To safeguard the privacy of participants, users must sign and submit a TCIA Restricted License Agreement to help@cancerimagingarchive.net before accessing the data.

Data Type	Download all or Query/Filter	License
Images (DICOM, 130.4GB)	*Download Search* (Download requires the NBIA Data Retriever)	TCIA Restricted

Click the Versions tab for more info about data releases.

Additional Resources for this Dataset

IvyGap provides access to additional resources for this data.

- Summary ISH, RNA, gene expression and clinical data
- Detailed clinical, genomic, and expression array data

- Pathology images

Third Party Analyses of this Dataset

TCIA encourages the community to publish your analyses of our datasets. Below is a list of such third party analyses published using this Collection:

- SDTM datasets of clinical data and measurements for selected cancer collections to TCIA (DI-Cubed-Reports)
- Multi-Institutional Paired Expert Segmentations and Radiomic Features of the Ivy GAP Dataset

Detailed Description

Detailed Description

Collection Statistics	
Modalities	MR
Number of Participants	39
Number of Studies	390
Number of Series	5223
Number of Images	846743
Image Size (GB)	130.4

Supporting Documentation

In addition to the DICOM images in TCIA there are two additional databases linked together by de-identified tumor specimen numbers to facilitate comparisons across data modalities:

1. The Ivy Glioblastoma Atlas Project web site includes the following data:
    a. ISH: Image data at cellular resolution of *in situ* hybridization (ISH) tissue sections and adjacent hematoxylin and eosin (H&E)-stained sections annotated for anatomic structures
        i. **Anatomic Structures ISH Survey**: Primary screen of 8 tumors with probes for 343 genes enriched in glioblastoma.
        ii. **Anatomic Structures ISH for Enriched Genes**: Subsequent screen of 29 tumors with probes for 37 genes enriched in glioblastoma structures identified in Anatomic Structures RNA-Seq Study (see below).
        iii. **Cancer Stem Cells ISH Survey**: Primary screen of 16 tumors with probes for 55 genes enriched in putative cancer stem cells, resulting in a 20 probe reference set, which was then used in an extensive screen of 42 tumors.
        iv. **Cancer Stem Cells ISH for Enriched Genes**: Subsequent screen of 37 tumors with probes for 76 genes enriched in clusters of putative cancer stem cells identified in the Cancer Stem Cells RNA-Seq Study (see below).
    b. RNA-Seq: RNA sequencing data for anatomic structures identified in the Anatomic Structures ISH Survey and putative cancer stem cell clusters isolated by laser microdissection
        i. **Anatomic Structures RNA-Seq**: Screen of 5 structures (Leading Edge, Infiltrating Tumor, Cellular Tumor, Microvascular Proliferation, and Pseudopalisading Cells Around Necrosis) identified by H&E staining. A total of 122 RNA samples were generated from 10 tumors.

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ii. **Cancer Stem Cells RNA-Seq**: Screen of 35 clusters of putative cancer stem cells identified by ISH with a 17 reference probe subset (validated in the Cancer Stem Cells ISH Survey). A total of 148 RNA samples were generated from 34 tumors.

c. Specimen Metadata: De-identified clinical data for each patient and tumor.

2. The Ivy GAP Clinical and Genomic Database contains detailed clinical information including pathology images, genomic data, and prospectively collected outcomes data. This site requires separate registration.
3. Additionally, the pathology images from this study are also available externally from here on Amazon Web Services (AWS).

Citations & Data Usage Policy

Citations & Data Usage Policy

Users must abide by the TCIA Data Usage Policy and Restrictions. Attribution should include references to the following citations:

Data Citation

Shah, N., Feng, X., Lankerovich, M., Puchalski, R. B., & Keogh, B. (2016). **Data from Ivy Glioblastoma Atlas Project (IvyGAP) [Data set].** The Cancer Imaging Archive. https://doi.org/10.7937/K9/TCIA.2016.XLwaN6nL

Publication Citation

Puchalski RB, Shah N, Miller J, Dalley R, Nomura SR, Yoon J-G, Smith KA, Lankerovich M, Bertagnolli D, Bickley K, Boe AF, Brouner K, Butler S, Caldejon S, Chapin M, Datta S, Dee N, Desta T, Dolbeare T, Dotson N, Ebbert A, Feng D, Feng X, Fisher M, Gee G, Goldy J, Gourley L, Gregor BW, Gu G, Hejazinia N, Hohmann J, Hothi P, Howard R, Joines K, Kriedberg A, Kuan L, Lau C, Lee F, Lee H, Lemon T, Long F, Mastan N, Mott E, Murthy C, Ngo K, Olson E, Reding M, Riley Z, Rosen D, Sandman D, Shapovalova N, Slaughterbeck CR, Sodt A, Stockdale G, Szafer A, Wakeman W, Wohnoutka PE, White SJ, Marsh D, Rostomily RC, Ng L, Dang C, Jones A, Keogh B, Gittleman HR, Barnholtz-Sloan JS, Cimino PJ, Uppin MS, Keene CD, Farrokhi FR, Lathia JD, Berens ME, Iavarone A, Bernard A, Lein E, Phillips JW, Rostad SW, Cobbs C, Hawrylycz MJ, Foltz GD. (2018). **An anatomic transcriptional atlas of human glioblastoma.** Science, 360(6389), 660–663. https://doi.org/10.1126/science.aaf2666

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. (2013). **The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository.** Journal of Digital Imaging, 26(6), 1045–1057. https://doi.org/10.1007/s10278-013-9622-7

Other Publications Using This Data

TCIA maintains a list of publications that leverage our data. If you have a publication you'd like to add, please contact TCIA's Helpdesk.

1. Beig, N., Bera, K., Prasanna, P., Antunes, J., Correa, R., Singh, S., . . . Tiwari, P. (2020). Radiogenomic-Based Survival Risk Stratification of Tumor Habitat on Gd-T1w MRI Is Associated with Biological Processes in Glioblastoma. Clin Cancer Res. doi:10.1158/1078-0432.CCR-19-2556

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2. Gevaert, O., Nabian, M., Bakr, S., Everaert, C., Shinde, J., Manukyan, A., . . . Pochet, N. (2020). Imaging-AMARETTO: An Imaging Genomics Software Tool to Interrogate Multiomics Networks for Relevance to Radiography and Histopathology Imaging Biomarkers of Clinical Outcomes. JCO Clin Cancer Inform, 4, 421-435. doi:10.1200/CCI.19.00125
3. Le, N. Q. K., Hung, T. N. K., Do, D. T., Lam, L. H. T., Dang, L. H., & Huynh, T.-T. (2021). Radiomics-based machine learning model for efficiently classifying transcriptome subtypes in glioblastoma patients from MRI. Comput Biol Med, 132, 104320. doi:10.1016/j.compbiomed.2021.104320
4. Mi, E., Mauricaite, R., Pakzad-Shahabi, L., Chen, J., Ho, A., & Williams, M. (2022). Deep learning-based quantification of temporalis muscle has prognostic value in patients with glioblastoma. Br J Cancer, 126(2), 196-203. doi:10.1038/s41416-021-01590-9
5. Miller, T. E., Liau, B. B., Wallace, L. C., Morton, A. R., Xie, Q., Dixit, D., . . . Rich, J. N. (2017). Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. Nature, 547(7663), 355. doi:10.1038/nature23000
6. Puchalski, R. B., Shah, N., Miller, J., Dalley, R., Nomura, S. R., Yoon, J.-G., . . . Foltz, G. D. (2018). An anatomic transcriptional atlas of human glioblastoma. Science, 360(6389), 660-663. doi:10.1126/science.aaf2666
7. Soike, M. H., McTyre, E. R., Shah, N., Puchalski, R. B., Holmes, J. A., Paulsson, A. K., . . . Strowd, R. E. (2018). Glioblastoma radiomics: can genomic and molecular characteristics correlate with imaging response patterns? Neuroradiology, 1-9. doi:10.1007/s00234-018-2060-y
8. van der Voort, S. R., Incekara, F., Wijnenga, M. M. J., Kapsas, G., Gahrmann, R., Schouten, J. W., . . . Klein, S. (2022). Combined molecular subtyping, grading, and segmentation of glioma using multi-task deep learning. Neuro Oncol. doi:10.1093/neuonc/noac166
9. Verma, R., Hill, V. B., Statsevych, V., Bera, K., Correa, R., Leo, P., . . . Tiwari, P. (2022). Stable and Discriminatory Radiomic Features from the Tumor and Its Habitat Associated with Progression-Free Survival in Glioblastoma: A Multi-Institutional Study. American Journal of Neuroradiology, 43(8), 1115-1123. doi:10.3174/ajnr.A7591
10. Vo, V. T. A., Kim, S., Hua, T. N. M., Oh, J., & Jeong, Y. (2022). Iron commensalism of mesenchymal glioblastoma promotes ferroptosis susceptibility upon dopamine treatment. Communications Biology, 5(1). doi:10.1038/s42003-022-03538-y
11. Zander, E., Ardeleanu, A., Singleton, R., Bede, B., Wu, Y., & Zheng, S. (2022). A functional artificial neural network for noninvasive pretreatment evaluation of glioblastoma patients. Neurooncol Adv, 4(1), vdab167. doi:10.1093/noajnl/vdab167
12. Zheng, S., & Tao, W. (2021). Identification of Novel Transcriptome Signature as a Potential Prognostic Biomarker for Anti-Angiogenic Therapy in Glioblastoma Multiforme. Cancers (Basel), 13(5). doi:10.3390/cancers13051013

Altmetrics

Versions

Version 1 (Current): Updated 2016/12/30

Data Type	Download all or Query/Filter
Images (DICOM, 130.4GB)	*Download* *Search* (Download requires the NBIA Data Retriever)
Summary ISH, RNA, gene expression and clinical data (external)	*Search*

Detailed clinical, genomic, and expression array data (external)	*Search*
Pathology images (external)	*Search*

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