Glioblastoma multiforme: exploratory radiogenomic analysis by using quantitative image features (TCGA-GBM-QI-Radiogenomics)

Description

PURPOSE:

To derive quantitative image features from magnetic resonance (MR) images that characterize the radiographic phenotype of glioblastoma multiforme (GBM) lesions and to create radiogenomic maps associating these features with various molecular data.

MATERIALS AND METHODS:

Clinical, molecular, and MR imaging data for GBMs in 55 patients were obtained from the The Cancer Genome Atlas Glioblastoma Multiforme Collection (TCGA-GBM) collection after local ethics committee and institutional review board approval. Regions of interest (ROIs) corresponding to enhancing necrotic portions of tumor and peritumoral edema were drawn and saved in AIM format. Quantitative image features were derived from these ROIs. Robust quantitative image features were defined on the basis of an intraclass correlation coefficient of 0.6 for a digital algorithmic modification and a test-retest anal ysis. The robust features were visualized by using hierarchic clustering and were correlated with survival by using Cox proportional hazards modeling. Next, these robust image features were correlated with manual radiologist annotations from the Visually Accessible Rembrandt Images (VASARI) feature set and GBM molecular subgroups by using nonparametric statistical tests. A bioinformatic algorithm was used to create gene expression modules, defined as a set of coexpressed genes together with a multivariate model of cancer driver genes predictive of the module's expression pattern. Modules were correlated with robust image features by using the Spearman correlation test to create radiogenomic maps and to link robust image features with molecular pathways.

RESULTS:

Eighteen image features passed the robustness analysis and were further analyzed for the three types of ROIs, for a total of 54 image features. Three enhancement features were significantly correlated with survival, 77 significant correlations were found between robust quantitative features and the VASARI feature set, and seven image features were correlated with molecular subgroups ($P < .05$ for all). A radiogenomics map was created to link image f eatures with gene expression modules and allowed linkage of 56% (30 of 54) of the image features with biologic processes.

CONCLUSION:

Radiogenomic approaches in GBM have the potential to predict clinical and molecular characteristics of tumors noninvasively.

Data Access

Data Access

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Segmentations (ZIP, 597kB)	*Download*	CC BY 3.0
Segmentation Summary (XLS, 123kB)	*Download*	CC BY 3.0

Collections Used in this Third Party Analysis

Below is a list of the Collections used in these analyses:

Source Data Type	Download all or Query/Filter	License
Corresponding Original Images from TCGA-GBM (DICOM, 1.73 GB)	*Download* (Requires NBIA Data Retriever)	TCIA Restricted

- TCGA-GBM

Detailed Description

Detailed Description

Image Segmentation summary spreadsheet: tcga-gbm segmentation summary.xls

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

Gevaert O, Mitchell LA, Achrol AS, Xu J, Echegaray S, Steinberg GK, Cheshier SH, Napel S, Zaharchuk G, Plevritis SK. (2014). **Glioblastoma multiforme: exploratory radiogenomic analysis by using quantitative image features**. The Cancer Imaging Archive. https://doi.org/10.7937/K9/TCIA.2014.RJEFTJBU

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

In addition to the dataset citation above, please be sure to cite the following if you utilize these data in your research:

Publication Citation

Gevaert, O., Mitchell, L. A., Achrol, A. S., Xu, J., Echegaray, S., Steinberg, G. K., Cheshier, S. H., Napel, S., Zaharchuk, G., & Plevritis, S. K. (2014). **Glioblastoma Multiforme: Exploratory Radiogenomic Analysis by Using Quantitative Image Features**. Radiology, 273(1), 168–174. https://doi.org/10.1148/radiol.14131731

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Versions

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4 The Cancer Genome Atlas Glioblastoma Multiforme Collection (TCGA-GBM) patients were removed from the collection, which had been previously analyzed by this group. Since the images are no longer available this Analysis Result dataset was updated accordingly.

Version 1: 2014/11/05

Data Type	Download all or Query/Filter
Image Data (DICOM)	No longer available. See v2 note.
Segmentations (ZIP)	Download
Segmentation Summary (XLS)	Download