MR Imaging Predictors of Molecular Profile and Survival: Multi-institutional Study of the TCGA Glioblastoma Data Set (TCGA-GBM-Radiogenomics)

Description

PURPOSE:

To conduct a comprehensive analysis of radiologist-made assessments of glioblastoma (GBM) tumor size and composition by using a community-developed controlled terminology of magnetic resonance (MR) imaging visual features as they relate to genetic alterations, gene expression class, and patient survival.

MATERIALS AND METHODS:

Because all study patients had been previously deidentified by the Cancer Genome Atlas (TCGA), a publicly available data set that contains no linkage to patient identifiers and that is HIPAA compliant, no institutional review board approval was required. Presurgical MR images of 75 patients with GBM with genetic data in the TCGA portal were rated by three neuroradiologists for size, location, and tumor morphology by using a standardized feature set. Interrater agreements were analyzed by using the Krippendorff statistic and intraclass correlation coefficient. Associations between survival, tumor size, and morphology were determined by using multivariate Cox regression models; associations between imaging features and genomics were studied by using the Fisher exact test.

RESULTS:

Interrater analysis showed significant agreement in terms of contrast material enhancement, nonenhancement, necrosis, edema, and size variables. Contrast-enhanced tumor volume and longest axis length of tumor were strongly associated with poor survival (respectively, hazard ratio: 8.84, P = .0253, and hazard ratio: 1.02, P = .00973), even after adjusting for Karnofsky performance score (P = .0208). Proneural class GBM had significantly lower levels of contrast enhancement (P = .02) than other subtypes, while mesenchymal GBM showed lower levels of nonenhanced tumor (P < .01).

CONCLUSION:

This analysis demonstrates a method for consistent image feature annotation capable of reproducibly characterizing brain tumors; this study shows that radiologists' estimations of macroscopic imaging features can be combined with genetic alterations and gene expression subtypes to provide deeper insight to the underlying biologic properties of GBM subsets.

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Data Access

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- TCGA-GBM

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Gutman DA, Cooper LA, Hwang SN, Holder CA, Gao J, Aurora TD, Dunn WD Jr, Scarpace L, Mikkelsen T, Jain R, Wintermark M, Jilwan M, Raghavan P, Huang E, Clifford RJ, Mongkolwat P, Kleper V, Freymann J, Kirby J, Zinn PO, Moreno CS, Jaffe C, Colen R, Rubin DL, Saltz J, Flanders A, Brat DJ. (2014). **MR Imaging Predictors of Molecular Profile and Survival: Multi-institutional Study of the TCGA Glioblastoma Data Set**. The Cancer Imaging Archive. https://doi.org/10.7937/K9/TCIA.2014.4HTXYRCN

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, Volume 26, Number 6, pp 1045-1057. DOI: https://doi.org/10.1007/s10278-013-9622-7

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Publication Citation

Gutman DA, Cooper LA, Hwang SN, Holder CA, Gao J, Aurora TD, Dunn WD Jr, Scarpace L, Mikkelsen T, Jain R, Wintermark M, Jilwan M, Raghavan P, Huang E, Clifford RJ, Mongkolwat P, Kleper V, Freymann J, Kirby J, Zinn PO, Moreno CS, Jaffe C, Colen R, Rubin DL, Saltz J, Flanders A, Brat DJ. (2013) **MR imaging predictors of molecular profile and survival: multi-institutional study of the TCGA glioblastoma data set**. Radiology. 2013 May;267(2):560-9. DOI:10.1148/radiol.13120118

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