Prediction of Outcome Using Clinical, Imaging, and Genetic Information
Summary

To date, no study has attempted to integrate imaging biomarkers and tumor gene expression into a statistical model that could constitute a more robust predictor of patient outcome than either biomarkers or gene expression alone. This study explored whether such a model could allow reliable prediction of patient survival and time to tumor recurrence based on a combination of magnetic resonance imaging (MRI) features and tumor gene expression.

The study aimed to incorporate glioblastoma imaging features and genomic biomarkers into statistical models in order to reliably predict patient outcomes. MRI images of 70 glioblastoma multiforme (GBM) patients were reviewed by six neuroradiologists using the VASARI scoring system; 620 angiogenesis genes were tested. Patient outcome was measured as duration of survival and time to recurrence. Eight MRI features were associated with survival (unadjusted p-value <0.05). Ependymal extension (feature F19) was correlated with the shortest survival (p=0.0012). Expression of ANG and TGFB2 genes correlated with shorter survival. CCL5 and TNF genes correlated with longer survival. A statistical model incorporating F19 with expression of the above genes correctly predicted survival for 82% of patients. Left hemispheric tumor location (feature F2) correlated with the longest time to recurrence (p=0.0084). An optimal linear regression model was constructed to include F2 and expression of the STAT1, ARHGAP24, and SSTR2 genes. This study demonstrated that a subset of VASARI imaging features does correlate with survival and time to recurrence. Linear regression models incorporating one or multiple imaging features and tumor gene expression can reliably predict patient outcome.

Preliminary analysis has been derived from Round 1 of the VASARI Research Project and presented at the following conferences:

- RSNA 2011 Annual Meeting: Prediction of Glioblastoma Multiforme (GBM) Time to Recurrence Using MRI Image Features and Gene Expression

The study is still ongoing and is now being reviewed with the inclusion of Round 2 data as well.
Supporting Documentation and Metadata

Shared Lists
The following shared lists have been created to easily obtain the subset of The Cancer Genome Atlas (TCGA)-GBM images relevant to this study.

- **TCGA-GBM Outcome Prediction**: Consists of only the 70 subjects from Round 1 of the VASARI Research Project which were utilized in preliminary analysis.

*Note: See Section 3.7 of TCIA User Guide for help with Shared Lists.*

Clinical and genetic data
Corresponding gene, survival, and recurrence data was obtained from TCGA Data Portal. The following text file contains the full list of sample IDs from the data portal which were used in the preliminary analysis:

- tca-gbm_outcome_sample_ids.txt