

**IDENTIFYING A 229-GENE SIGNATURE TO DISCRIMINATE ANAPLASTIC
ASTROCYTOMA FROM GLIOBLASTOMA USING META-ANALYSIS OF MULTIPLE
MICROARRAY DATASETS**

N. Tursynbek , G. Ghahramany , S. Nabavi , and A. Zollanvari
*'Electrical and Computer Engineering Department at Nazarbayev University
(Astana, Kazakhstan)*

School of Natural Sciences, Blinn College (TX 77840 USA)

*³Institute for Systems Genomics, University of Connecticut (CT 06030 USA)
nurislam.tursynbek@nu.edu.kz*

Keywords: Glioblastoma Multiforme; Anaplastic Astrocytoma; Predictive Meta-analysis; Microarrays

Introduction: Gliomas are the most common type of primary malignant brain tumors and are graded into I to IV according to their increasing malignancy. Classification of Grade III (anaplastic astrocytoma) and IV (glioblastoma multiforme) is important not only because of the difference in the survival time of patients but also because of the significant guidance provided for therapeutic decisions.

Results: In this study, we conducted a predictive meta-analysis of multiple Affymetrix U133 microarrays to identify a set of signature genes that can distinguish glioblastoma multiforme from anaplastic astrocytoma. Our classifier, which was based on the nearest shrunken centroids, contained 229 genes and achieved an accuracy, sensitivity, specificity, and J index of 75%, 78.5%, 74.1%, and 52.6%, respectively, using a dataset cross-validation procedure. Based on the identified gene signature, we found 13 pathways, most of which have been already linked in a number of sporadic studies to high-grade gliomas.

Conclusion: The results of this study can be potentially used: (1) to shed light on the molecular mechanisms underlying the formation of malignant gliomas; and (2) to match malignant glioma individuals with treatment strategies based on their gene expression profiles.