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Mathematical modeling of patient-matched genomic profiles predicts brain cancer survival and drug targets

Researchers at the Scientific Computing and Imaging (SCI) Institute at the University of Utah have used novel mathematical modeling of patient-matched genomic profiles to uncover a previously unknown global pattern of DNA aberrations that is correlated with, and possibly causally related to, brain cancer survival.

This new link between a glioblastoma multiforme (GBM) brain tumor's genome and a patient's prognosis offers insights into the cancer's formation and growth, and suggests promising targets for drug therapy. GBM – the most common brain cancer in adults – causes over 10,000 deaths each year in the US alone, often within one year of diagnosis. Despite extensive studies with the latest tools and the collection of copious amounts of data, the best prognostic indicator of GBM prior to the discovery of this genome-wide pattern was the patient's age at diagnosis.

In an article published in the journal *PLoS One* on January 23, 2012, Orly Alter, USTAR associate professor of bioengineering and human genetics at SCI, and her students, Cheng H. Lee, Benjamin O. Alpert and Preethi Sankaranarayanan, compared GBM and normal genomic profiles from the same set of patients. These datasets, from The Cancer Genome Atlas, a national effort to accelerate cure for cancer, were published in 2008.

By using a comparative mathematical decomposition – a framework for modeling the two patient-matched composite datasets – Alter and her students separated the tumor-exclusive pattern from genomic variations that occur in the normal human genome as well as from variations that are due to inconsistent experimental protocols. They showed that the prognostic value of the global pattern is similar to, yet independent of, that of age. Therefore, combined with age, the pattern makes a better predictor than age alone.

This mathematical modeling makes it possible to similarly use recent high-throughput biotechnologies in the personalized prognosis and treatment of GBM and other cancers.

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To read the January 23, 2012 article in *PLoS One* go to:
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