OMICS International
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4th International Conference and Exhibition on
Biometrics & Biostatistics

November 16-18, 2015   San Antonio, USA

Glioma classification and translational application in clinics

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Gliomas are the most common type of primary brain tumors in adults and a significant cause of cancer-related mortality. Defining glioma sub-types based on objective genetic and molecular signatures may allow for a more rational, patient specific approach to therapy in the future. Applying two unsupervised machine-learning methods to 159 glioma patient gene expression profiles ranging from low to high grade gliomas, we have established a glioma classification model containing six distinct sub-types. These sub-types are validated using three additional data-sets and annotated for underlying molecular functions. To translate this glioma classification model into clinical application, we developed a web-based tool, GliomaPredict, for assigning new patients into our molecular sub-types. The classification model also facilitates us to study glioma progression mechanism in cohered and to design targeted clinical trials.

Biography

Aiguo Li is a Senior Bioinformatician in Neuro-Oncology Branch, National Cancer Institute, National Institutes of Health. Her research interests include glioma tumor biomarker identification and prognostic studies, and tumor molecular and functional classification. The goals of her research are to understand the underlying molecular mechanisms of glioma tumorigenesis and its progression; and developing novel therapeutic approaches for curing glioma patients. In the past, she has established a glioma molecular classification model containing six sub-types and further translated this model into a clinically useful tool – GliomaPredict, which allows clinicians and researchers to assign new patients to the existing sub-types. The focus of her research is, currently, on understanding the glioma tumor's heterogeneity and infiltration mechanism by integrative analysis of multi-dimensional high throughput data of glioma patients and glioma stem cell lines.

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J Appl Computat Math 2015
ISSN: 2168-9679, JACM an open access journal

Biostatistics 2015
November 16-18, 2015

Volume 4 Issue 5

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