

OVERVIEW

Professor Xiaolong Fan at Beijing Normal University and his colleagues both in Beijing and Sweden, try to find ways to classify brain tumors according to the known pathogenesis processes. This could help with diagnoses and maybe could avoid unnecessary treatment.

The results have been published in Proceedings of the National Academy of Sciences of the United States of America (www.pnas.org/cgi/doi/10.1073/pnas.1313814111).

"In this process of this study, we have found that Qlucore has been very helpful in supporting a biologist without sufficient mathematic background to apply bioinformatics approaches in their studies. This has been essential for the implementation of the project."

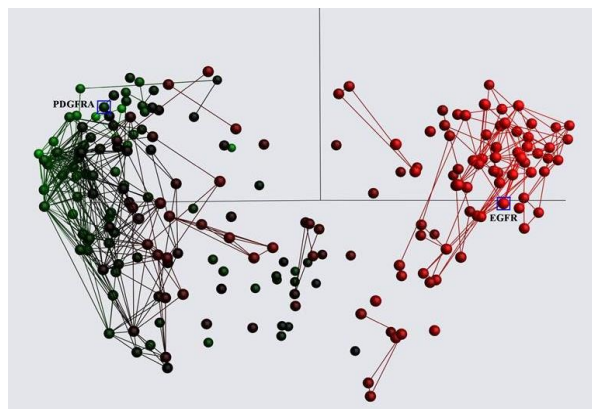
Statistical analysis could improve understanding and treatment of different brain tumors

TECHNICAL SITUATION

There are many different types of brain tumor with different survival rates and different methods for treatment. However, today many brain tumors are difficult to clearly diagnose, leading to poor prognoses for patients. Diagnosis today is mainly done by morphological appearance. However, this does not closely correlate with the pathogenesis mechanisms and diagnosis based on morphology may have hampered the discovery of a cure for brain tumors and other types of cancers.

SOLUTION

To come up with the classification, the researchers studied two gene co-expression modules around key signaling pathways that are conserved between neural development and the formation of gliomas. In the search for patterns, they use publicly available datasets from three continents, including gene expression data, genomic data and clinical data. To analyze these datasets and look for links, Qlucore Omics Explorer was used.



Differential expression of the two gene modules, EGFR and PDGFRA, could help with understanding glioma pathogenesis and identifying new glioma therapeutic targets. Image courtesy of Xiaolong Fan.

Glioma classification case study

Based on the expression patterns of these two modules, adult low-grade and high-grade gliomas could be classified into three major subtypes that are distinct in prognosis, genetic abnormalities and correlation to the cell lineages and differentiation stages of glial genesis but independent of glioma morphology.

The three subtypes are EM, PM and EMLowPMlow gliomas.

EM gliomas were associated with higher age at diagnosis, poorer prognosis, and stronger expression of neural stem cell and astrogenesis genes. Both PM and EMLowPMlow gliomas were associated with younger age at diagnosis and better prognosis. In addition, PM gliomas were enriched in the expression of oligodendrogenesis genes, whereas EMLowPMlow gliomas were enriched in the signatures of mature neurons and oligodendrocytes.

BENEFITS

With the support of the program a new classification was proposed and published. Qlucore Omics Explorers enables biologists to analyze data of themselves. It has been easy to bring data together from different sources and start to analyze.

For More information
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