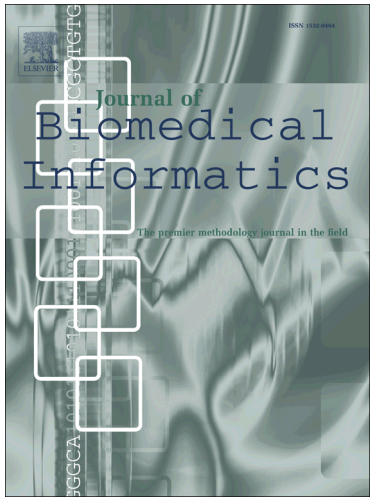

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Drug repurposing for glioblastoma based on molecular subtypes

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Abstract

A recent multi-platform analysis by The Cancer Genome Atlas identified four distinct molecular subtypes for glioblastoma (GBM) and demonstrated that the subtypes correlate with clinical phenotypes and treatment responses. In this study, we developed a computational drug repurposing approach to predict GBM drugs based on the molecular subtypes. Our approach leverages the genomic signature for each GBM subtype, and integrates the human cancer genomics with mouse phenotype data to identify the opportunity of reusing the FDA-approved agents to treat specific GBM subtypes. Specifically, we first constructed the phenotype profile for each GBM subtype using their genomic signatures. For each approved drug, we also constructed a phenotype profile using the drug target genes. Then we developed an algorithm to match and prioritize drugs based on their phenotypic similarities to the GBM subtypes. Our approach is highly generalizable for other disorders if provided with a list of disorder-specific genes. We first evaluated the approach in predicting drugs for the whole GBM. For a combined set of

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