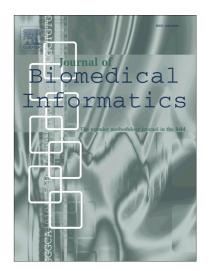
Accepted Manuscript

Drug repurposing for glioblastoma based on molecular subtypes

Yang Chen, Rong Xu

PII:S1532-0464(16)30132-0DOI:http://dx.doi.org/10.1016/j.jbi.2016.09.019Reference:YJBIN 2653To appear in:Journal of Biomedical InformaticsReceived Date:5 January 2016Revised Date:23 August 2016Accepted Date:27 September 2016



Please cite this article as: Chen, Y., Xu, R., Drug repurposing for glioblastoma based on molecular subtypes, *Journal of Biomedical Informatics* (2016), doi: http://dx.doi.org/10.1016/j.jbi.2016.09.019

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

Drug repurposing for glioblastoma based on molecular subtypes

Yang Chen^a, Rong Xu^{a,*}

^aDepartment of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland OH, 44106

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

Preprint submitted to Elsevier

^{*}Corresponding author

Email address: rxx@case.edu (Rong Xu)

Download English Version:

https://daneshyari.com/en/article/4966943

Download Persian Version:

https://daneshyari.com/article/4966943

Daneshyari.com