

Accepted Manuscript

Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power

Alex Graudenzi, Davide Maspero, Marzia Di Filippo, Marco Gnugnolo, Claudio Isella, Giancarlo Mauri, Enzo Medico, Marco Antoniotti, Chiara Damani

PII: S1532-0464(18)30184-9
DOI: <https://doi.org/10.1016/j.jbi.2018.09.010>
Reference: YJBIN 3055

To appear in: *Journal of Biomedical Informatics*

Received Date: 9 July 2018
Accepted Date: 14 September 2018

Please cite this article as: Graudenzi, A., Maspero, D., Filippo, M.D., Gnugnolo, M., Isella, C., Mauri, G., Medico, E., Antoniotti, M., Damani, C., Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power, *Journal of Biomedical Informatics* (2018), doi: <https://doi.org/10.1016/j.jbi.2018.09.010>

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.



Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power

Alex Graudenzi^{a,b}, Davide Maspero^{c,b}, Marzia Di Filippo^{c,d}, Marco Gnugnolo^{c,d}, Claudio Isella^{e,f}, Giancarlo Mauri^{a,d}, Enzo Medico^{e,f}, Marco Antoniotti^{a,g}, Chiara Damani^{a,d,h}

^a*Department of Informatics, Systems and Communication, University of Milan-Bicocca, Milan, Italy*

^b*Equal contributors*

^c*Department of Biotechnology and Biosciences, University Milano-Bicocca, Milan, Italy*

^d*SYSBIO Centre of Systems Biology, University Milano-Bicocca, Milan, Italy*

^e*University of Torino, Department of Oncology, Candiolo, Torino, Italy*

^f*Candiolo Cancer Institute, FPO, IRCCS, Candiolo, Torino, Italy*

^g*Milan Center for Neuroscience, University of Milan-Bicocca, Monza, Italy*

^h*Corresponding author: email: chiara.damiani@unimib.it; address: Viale Sarca 336 I-20126 - Milan (MI), Italy; phone: +39-02-64487918*

Abstract

Effective stratification of cancer patients on the basis of their molecular make-up is a key open challenge. Given the altered and heterogenous nature of cancer metabolism, we here propose to use the overall expression of central carbon metabolism as biomarker to characterize groups of patients with important characteristics, such as response to *ad-hoc* therapeutic strategies and survival expectancy.

To this end, we here introduce the data integration framework named *Metabolic Reaction Enrichment Analysis (MaREA)*, which strives to characterize the metabolic deregulations that distinguish cancer phenotypes, by projecting RNA-seq data onto metabolic networks, without requiring metabolic measurements. **MaREA** computes a score for each network reaction, based on the expression of the set of genes encoding for the associated enzyme(s). The scores are first used as features for cluster analysis and then to rank and visualize in an organized fashion the metabolic deregulations that distinguish cancer sub-types.

We applied our method to recent lung and breast cancer RNA-seq datasets

Download English Version:

<https://daneshyari.com/en/article/11020966>

Download Persian Version:

<https://daneshyari.com/article/11020966>

[Daneshyari.com](https://daneshyari.com)