Accepted Manuscript

Grouped gene selection and multi-classification of acute leukemia via new regularized multinomial regression



Juntao Li, Yanyan Wang, Tao Jiang, Huimin Xiao, Xuekun Song

PII:	S0378-1119(18)30489-X
DOI:	doi:10.1016/j.gene.2018.05.012
Reference:	GENE 42823
To appear in:	Gene
Received date:	24 December 2017
Revised date:	26 April 2018
Accepted date:	2 May 2018

Please cite this article as: Juntao Li, Yanyan Wang, Tao Jiang, Huimin Xiao, Xuekun Song , Grouped gene selection and multi-classification of acute leukemia via new regularized multinomial regression. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Gene(2017), doi:10.1016/j.gene.2018.05.012

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

Grouped Gene Selection and Multi-classification of Acute Leukemia via New Regularized Multinomial Regression

Juntao Li^a, Yanyan Wang^{a*}, Tao Jiang^b, Huimin Xiao^b and Xuekun Song^c

^a School of Mathematics and Information Science, Henan Normal University, Xinxiang

453007, China.

E-mail: juntaolimail@126.com, yanyanwangmail@126.com

^b School of Computer and Information Engineering, Henan University of Economics

and Law, Zhengzhou 450002, China.

E-mail: Jiangtaoxxx@126.com, huiminxiao@126.com

^c School of Information Technology, Henan University of Chinese Medicine,

Zhengzhou 450046, China.

E-mail: bioinformatics_son@126.com

Abstract

Diagnosing acute leukemia is the necessary prerequisite to treating it. Multiclassification on the gene expression data of acute leukemia is help for diagnosing it which contains B-cell acute lymphoblastic leukemia (BALL), T-cell acute lymphoblastic leukemia (TALL) and acute myeloid leukemia (AML). However, selecting cancer-causing genes is a challenging problem in performing multiclassification. In this paper, weighted gene co-expression networks are employed to

^{*} Corresponding author. E-mail address: yanyanwangmail@126.com.

Download English Version:

https://daneshyari.com/en/article/8644816

Download Persian Version:

https://daneshyari.com/article/8644816

Daneshyari.com