

Author's Accepted Manuscript

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PII: S0010-4825(16)30195-0
DOI: <http://dx.doi.org/10.1016/j.compbio.2016.08.004>
Reference: CBM2471

To appear in: *Computers in Biology and Medicine*

Received date: 21 March 2016
Revised date: 3 August 2016
Accepted date: 3 August 2016

Cite this article as: Weng Howe Chan, Mohd Saberi Mohamad, Safaai Deris, Nazar Zaki, Shahreen Kasim, Sigeru Omatu, Juan Manuel Corchado and Hany Al Ashwal, Identification of Informative Genes and Pathways using an Improved Penalized Support Vector Machine with a Weighting Scheme, *Computers in Biology and Medicine*, <http://dx.doi.org/10.1016/j.compbio.2016.08.004>

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Identification of Informative Genes and Pathways using an Improved Penalized Support Vector Machine with a Weighting Scheme

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Abstract: Incorporation of pathway knowledge into microarray analysis has brought better biological interpretation of the analysis outcome. However, most pathway data are manually curated without specific biological context. Non-informative genes could be included when the pathway data is used for analysis of context specific data

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