

## Accepted Manuscript

Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles

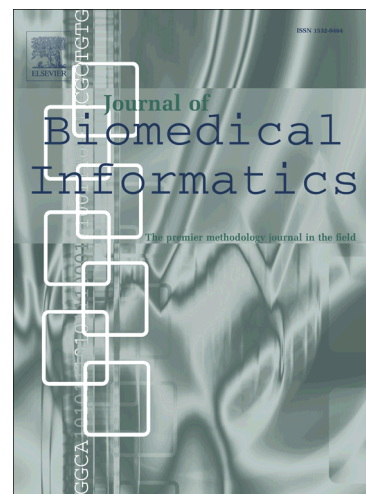
Nelson Kibinge, Naoaki Ono, Masafumi Horie, Tetsuo Sato, Tadao Sugiura, Md. Altaf-Ul-Amin, Akira Saito, Shigehiko Kanaya

PII: S1532-0464(16)30024-7

DOI: <http://dx.doi.org/10.1016/j.jbi.2016.04.002>

Reference: YJBIN 2559

To appear in: *Journal of Biomedical Informatics*



Please cite this article as: Kibinge, N., Ono, N., Horie, M., Sato, T., Sugiura, T., Altaf-Ul-Amin, Md., Saito, A., Kanaya, S., Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles, *Journal of Biomedical Informatics* (2016), doi: <http://dx.doi.org/10.1016/j.jbi.2016.04.002>

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.

# Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles

Nelson Kibinge<sup>a</sup>, Naoaki Ono<sup>a</sup>, Masafumi Horie<sup>b</sup>, Tetsuo Sato<sup>a</sup>, Tadao Sugiura<sup>a</sup>, Md. Altaf-Ul-Amin<sup>a</sup>, Akira Saito<sup>b</sup>, Shigehiko Kanaya<sup>a,\*</sup>

<sup>a</sup>*Graduate School of Information Science, Nara Institute of Science and Technology, Takayama 8916-5, Ikoma, Nara 630-0192, Japan*

<sup>b</sup>*Department of Respiratory Medicine, Graduate School of Medicine, University of Tokyo, 7-3-1, Hongo, Bunkyo-ku, Tokyo 113-0033, Japan*

---

## Abstract

Conventionally, workflows examining transcription regulation networks from gene expression data involve distinct analytical steps. There is a need for pipelines that unify data mining and inference deduction into a singular framework to enhance interpretation and hypotheses generation. We propose a workflow that merges network construction with gene expression data mining focusing on regulation processes in the context of transcription factor driven gene regulation. The pipeline implements pathway-based modularization of expression profiles into functional units to improve biological interpretation. The integrated workflow was implemented as a web application software (TransReguloNet) with functions that enable pathway visualization and comparison of transcription factor activity between sample conditions defined in the experimental design. The pipeline merges differential expression, network construction, pathway-based abstraction, clustering and visualization. The framework was applied in analysis of actual expression datasets related to lung, breast and prostate cancer.

*Keywords:* Biological interpretation; Pathway-based modularization; Gene regulation; Transcription factors

---

\*Corresponding author

*Email address:* s-kanaya@gtc.naist.jp (Shigehiko Kanaya)

Download English Version:

<https://daneshyari.com/en/article/6927790>

Download Persian Version:

<https://daneshyari.com/article/6927790>

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