

Accepted Manuscript

Evaluation of artificial time series microarray data for dynamic gene regulatory network inference

P. Xenitidis , I. Seimenis , S. Kakolyris , A. Adamopoulos

PII: S0022-5193(17)30218-7
DOI: [10.1016/j.jtbi.2017.05.010](https://doi.org/10.1016/j.jtbi.2017.05.010)
Reference: YJTBI 9067



To appear in: *Journal of Theoretical Biology*

Received date: 25 July 2016
Revised date: 13 March 2017
Accepted date: 5 May 2017

Please cite this article as: P. Xenitidis , I. Seimenis , S. Kakolyris , A. Adamopoulos , Evaluation of artificial time series microarray data for dynamic gene regulatory network inference, *Journal of Theoretical Biology* (2017), doi: [10.1016/j.jtbi.2017.05.010](https://doi.org/10.1016/j.jtbi.2017.05.010)

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.

Highlights

- The influence of a number of factors on the inference of a gene regulatory network using microarray data was examined.
- The amount of information in microarray data was evaluated using a system theory approach.
- The relationship between the inference performance in the time domain and the true system parameter identification was investigated. .
- Crucial factors were examined using a real GRN and acquired results confirmed simulation findings with artificial data.
- Different initial conditions were used as an alternative triggering approach.

ACCEPTED MANUSCRIPT

Download English Version:

<https://daneshyari.com/en/article/5759940>

Download Persian Version:

<https://daneshyari.com/article/5759940>

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