



## NARROMI: a noise and redundancy reduction technique improves accuracy of gene regulatory network inference.

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Titre NARROMI: a noise and redundancy reduction technique improves accuracy of gene regulatory network inference.

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**MOTIVATION:** Reconstruction of gene regulatory networks (GRNs) is of utmost interest to biologists and is vital for understanding the complex regulatory mechanisms within the cell. Despite various methods developed for reconstruction of GRNs from gene expression profiles, they are notorious for high false positive rate owing to the noise inherited in the data, especially for the dataset with a large number of genes but a small number of samples.

**RESULTS:** In this work, we present a novel method, namely NARROMI, to improve the accuracy of GRN inference by combining ordinary differential equation-based recursive optimization (RO) and information theory-based mutual information (MI). In the proposed algorithm, the noisy regulations with low pairwise correlations are first removed by using MI, and the redundant regulations from indirect regulators are further excluded by RO to improve the accuracy of inferred GRNs. In particular, the RO step can help to determine regulatory directions without prior knowledge of regulators. The results on benchmark datasets from Dialogue for Reverse Engineering Assessments and Methods challenge and experimentally determined GRN of Escherichia coli show that NARROMI significantly outperforms other popular methods in terms of false positive rates and accuracy.

**AVAILABILITY:** All the source data and code are available at: <http://csb.shu.edu.cn/narromi.htm> [13].

URL de la notice <http://okina.univ-angers.fr/publications/ua7618> [14]

DOI 10.1093/bioinformatics/bts619 [15]

Lien vers le document <http://www.ncbi.nlm.nih.gov/pubmed/23080116> [16]  
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### Liens

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