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

**MATLAB source code, dataset and tutorial**

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**Introduction:**

**NARROMI** is a MATLAB program for inferring gene regulatory networks from gene expression data. It is a novel method combining ordinary differential equation based recursive optimization (RO) and information-theory based mutual information (MI). In this algorithm, both noisy regulations with low pair-wise correlations and redundant regulations from indirect regulators are removed by measuring MI and implementing RO, respectively. Moreover, the dimension shrinking technique improves the efficiency of optimization and further the accuracy of network inference. In particular, our approach is the first one to handle the redundancy problem in GRNs for model based network inference methods.

**Download:**

Source Code: NARROMI;

Datasets: Ecoli\_Data;

Tutorial: Tutorial for NARROMI.

**Contact:**

The MATLAB codes and dataset are free to use. If you encounter any problem, please do not hesitate to contact us at [zhang-xiujun@163.com](mailto:zhang-xiujun@163.com) or [zhaoxingming@gmail.com](mailto:zhaoxingming@gmail.com) or [hao@info.univ-angers.fr](mailto:hao@info.univ-angers.fr) or [lnchen@sibs.ac.cn](mailto:lnchen@sibs.ac.cn). Thanks!