**Inferring GRNs from Gene Expression Data by PC-Algorithm Based on Conditional Mutual Information**

**MATLAB source code, datasets and validation files**

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**Introduction:**

**PCA-CMI** is a MATLAB program for inferring gene regulatory networks from gene expression data.

It is a novel method based on path consistency algorithm and conditional mutual information, which consider the non-linear dependence and topological structure of GRNs. In this algorithm, the (conditional) dependence between a pair of genes is represented by the CMI between them. With the general hypothesis of Gaussian distribution underlying gene expression data, CMI between a pair of genes is computed by a concise formula involving the covariance matrices of the related gene expression profiles.

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