Causal discovery from omics information using Bayesian network

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Abstract

Since rapid development and cost down of a next generation sequencer, an importance of omics (genome, transcriptome, epigenome and etc.) data analysis for personalized medicine about diagnosis, treatment and prevention is remarkably increasing.

Moreover, it is expected that more good evidence is obtained by integration of those omics information, epidemiology data and phenotyping data of experimental animals with meta information of an environment about gene-phenotype and gene-environment interactions.

Under such a background, we develop omics data analysis system for causal discovery about diseases and phenotypes using clustering, meta-analysis, Bayesian network and directed acyclic graph. Further, we investigate epigenome data analysis about DNA methylation and histone modification applying existing system.

In the present study, we use public omics and epidemiology data for a cancer as a trial because we have investigated about transcriptional controls in a cancer cell and retrotransposons related to transcription control, and epigenetic alterations are related to causes for cancer and a control of retrotransposon.

We expect that the system to be useful for discoveries of biomarkers for diagnosis and drug targets, and a research of disease mechanisms.

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