

遺伝子発現データからの新しい因果推論手法の検証

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概要: 生命情報解析において因果推論は非常に重要である。代表的な因果推論手法として有向グラフによるベイジアンネットワークが挙げられるが、本手法はノード数が60くらいで計算限界なのが難点である。そのため、ARACNe[1]と呼ばれる相互情報量と無向グラフによるマルコフネットワークを用いた解析が実施されてきた[2]。近年、新たなアルゴリズムで推定した相互情報量とChow-LiuアルゴリズムによるForest Structure Learning (FSL)という構造学習手法が提案された[3]。今回発表者はNCBI GEOに収載された数種の公共データに本手法を適用した。本発表ではその結果と今後の研究の進め方について議論したい。

キーワード: 因果推論, ベイジアンネットワーク, マルコフネットワーク, 相互情報量, ARACNe, Chow-Liu アルゴリズム, Forest Structure Learning

A novel causal inference method from gene expression

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Abstract: A causal inference is a very important for life science study. A typical causal inference method is a Bayesian network using a directed graph, however, this method has the disadvantage that it has upto 60 nodes and its computational limit. For this reason, analysis using a Markov network based on mutual information and undirected graph called ARACNe[1] has been performed[2]. In recent years, a structure learning method called Forest Structure Learning (FSL) using the mutual information estimated by a new algorithm and the Chow-Liu algorithm has been proposed[3]. We applied the method to several public datasets stored on NCBI GEO. In this presentation, we would like to discuss the results and future research.

Keywords: Causal inference, Bayesian network, Markov network, Mutual information, ARACNe, Chow-Liu algorithm, Forest Structure Learning

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