

研究论文

结合基因表达数据和ChIP-chip数据的酵母转录调控模块的识别

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摘要:

活细胞依赖其众多的转录调控模块来实现复杂的生物功能, 识别转录调控模块对深入理解细胞的功能及其转录机制有着重要的意义。本文结合酵母基因表达数据和ChIP-chip数据, 提出了一种转录调控模块识别算法。该算法通过采用不同的 P 值阈值分别得到了核心集和粗糙集, 然后对核心集和粗糙集进行判别, 最后对基因进行扩展之后得到基因转录调控模块。将该算法运用到两个酵母基因表达数据中, 得到了一些具有显著生物学意义的基因转录调控模块。与其它算法相比, 该算法不仅可以识别含有较多基因的转录调控模块, 而且可以识别一些其它算法不能识别的基因转录调控模块。识别得到的基因转录调控模块有着不同的生物学功能, 并且有助于进一步理解酵母的转录调控机制。

关键词: 基因表达数据 ChIP-chip数据 转录调控模块 调控因子 酵母

Yeast Transcriptional Regulatory Module Identification by Integrating Gene Expression Data and ChIP-chip Data

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Abstract:

A living cell can carry out complex biological functions depending on its transcriptional regulatory modules. Therefore, identifying transcriptional regulatory modules is very important for understanding cell function and its transcription mechanism. Integrating gene expression profiles and ChIP-chip data, a transcriptional regulatory module identifying algorithm is developed. The algorithm introduces local correlation into ChIP-chip data and obtains the core and loose sets of transcriptional regulatory modules by using two different P value thresholds. Then the core and loose sets are distinguished and the genes in them are expanded. Finally the transcriptional regulatory modules are obtained. Some transcriptional regulatory modules with significant biological meanings are obtained from two different yeast gene expression profiles by using this algorithm. The comparison with other algorithms shows that this algorithm can identify not only modules with more genes, but also modules that other algorithms can not identify. These identified transcriptional modules are helpful for further understanding yeast transcription mechanism.

Keywords: Gene expression data ChIP-chip data Transcriptional regulatory module Regulatory factor Yeast

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