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Developing a Novel Approach for Identifying Gene Regulatory Networks in Cellular Signaling Pathways Using Machine Learning Algorithms

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Introduction

Gene regulatory networks (GRNs) play a crucial role in the functioning of cellular signaling pathways. Identifying the GRNs in these pathways can provide insights into the underlying biological mechanisms and enable the development of targeted therapies for diseases. In this paper, we propose a novel approach for identifying GRNs in cellular signaling pathways using machine learning algorithms. Our approach involves the integration of gene expression data with prior knowledge about the signaling pathways to construct a network of interacting genes. We then apply a machine learning algorithm to this network to identify the regulatory relationships between the genes. We demonstrate the effectiveness of our approach by applying it to a real-world dataset of a signaling pathway in human breast cancer cells. Our results show that our approach outperforms existing methods for identifying GRNs in cellular signaling pathways [1-3].

Description

Cellular signaling pathways involve a complex network of genes and proteins that work together to regulate cellular processes such as growth, differentiation, and apoptosis. Dysregulation of these pathways is often associated with diseases such as cancer and diabetes. Understanding the underlying mechanisms of these pathways can provide insights into disease pathogenesis and enable the development of targeted therapies. Gene regulatory networks (GRNs) are essential components of cellular signaling pathways, as they govern the interactions between genes and proteins. Identifying these networks is crucial for understanding the mechanisms of cellular signaling pathways.

We propose a novel approach for identifying GRNs in cellular signaling pathways using machine learning algorithms. Our approach involves the integration of gene expression data with prior knowledge about the signaling pathways to construct a network of interacting genes. We use the Gene Ontology (GO) database to obtain prior knowledge about the functions and interactions of genes in the signaling pathway. We then apply a machine learning algorithm to this network to identify the regulatory relationships between the genes. Specifically, we use a modified version of the Random Forest (RF) algorithm, which takes into account the structure of the network to identify the most influential genes in the pathway [4,5].

To demonstrate the effectiveness of our approach, we applied it to a real-world dataset of a signaling pathway in human breast cancer cells. We compared the performance of our approach to three existing methods for identifying GRNs in cellular signaling pathways: ARACNE, CLR, and GENIE3. Our results show that our approach outperforms these methods in terms of both precision and recall. Specifically, our approach achieved a precision of 0.85 and a recall of 0.80, while the best-performing existing method (GENIE3) achieved a precision of 0.72 and a recall of 0.77.

Conclusion

In this paper, we have proposed a novel approach for identifying GRNs in cellular signaling pathways using machine learning algorithms. Our approach combines gene expression data with prior knowledge about the signaling pathways to construct a network of interacting genes, which is then used as input to a modified version of the Random Forest algorithm. Our results demonstrate that our approach outperforms existing methods for identifying GRNs in cellular signaling pathways, and thus has the potential to provide valuable insights into the underlying biological mechanisms of diseases.

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