

# A method of extracting disease-related microRNAs through the propagation algorithm using the environmental factor based global miRNA network

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**Abstract.** MicroRNAs (miRNA) are known to be involved in the development of various diseases. Hence various scientists in the field have been utilized computational analyses to determine the relationship between miRNA and diseases. However, the knowledge of miRNA and disease is still very limited. Therefore, we combined Environmental Factor (EF) data to a miRNA global network. Increasing research has shown that relationship between miRNAs and EFs play a significant role in classifying types of diseases. Environmental Factors consist of radiation, drugs, viruses, alcohol, cigarettes, and stress. Our global network considered all the interactions between every pair of miRNAs, which has led to precise analyses in comparison to local networks. As a result, our approaches' performance demonstrated its effectiveness in identifying disease-related miRNA and this is the area under the ROC curve (AUC) of 74.46%. Furthermore, comparative experiment has shown that our approach performs comparable to other existing methods with an accuracy of 94%, 90% and 96% for breast cancer, colonic cancer, and lung cancer respectively. In conclusion, these results support that our research has broadened new biological insights on identifying disease-related miRNAs.

Keywords: miRNA, disease, environmental factor, network, propagation algorithm

## 1. Introduction

MicroRNAs (miRNAs) are small non-coding RNAs that are composed of 19-22 nucleotides. They play an important role in the regulation of cell proliferation, growth, and apoptosis based on the base-pairing to the 3' untranslated-regions (UTRs) of their target mRNAs at post-transcriptional level. Growing evidence indicates that miRNAs have been associated with the pathogenesis of the disease. Therefore, discerning the relationship between miRNAs and diseases has become an important goal in the biological context. However, identifying disease-related miRNAs with existing experimental setup might be laborious and time-consuming. In addition, many researchers also face a difficult problem of limited knowledge on miRNA. Therefore a number of computational approaches have been developed

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