# Article information:

用于疾病相关circRNA预测的深度学习模型：综述 - PubMed
<https://pubmed.ncbi.nlm.nih.gov/36130259/>

# Article summary:

1. This article reviews the use of deep learning models for predicting disease-associated circRNAs.

2. It outlines three methods based on feature generation, type discrimination, and hybrid approaches.

3. It evaluates seven benchmark models for balanced and unbalanced classification tasks, and discusses the advantages and limitations of each method.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

The article is generally reliable and trustworthy in its content. The authors provide a comprehensive overview of the current state of research into deep learning models for predicting disease-associated circRNAs, as well as an evaluation of seven benchmark models for balanced and unbalanced classification tasks. The authors also discuss the advantages and limitations of each method, providing insights into potential biases and their sources.

The article does not appear to be one-sided or promotional in any way; it presents both sides equally by discussing both the advantages and limitations of each method. Furthermore, it does not appear to contain any unsupported claims or missing points of consideration; all claims are supported by evidence from other studies or experiments conducted by the authors themselves. Additionally, all possible risks are noted throughout the article, ensuring that readers are aware of any potential issues with using deep learning models for predicting disease-associated circRNAs.

In conclusion, this article is reliable and trustworthy in its content; it provides a comprehensive overview of current research into deep learning models for predicting disease-associated circRNAs while noting all possible risks associated with using such methods.

# Topics for further research:

* Deep learning models for disease prediction
* Circular RNAs and disease association
* Evaluation of benchmark models for classification tasks
* Advantages and limitations of deep learning models
* Potential biases in deep learning models
* Risks associated with using deep learning models for disease prediction

# Report location:

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