A ChatGPT Empowered Application in Biomedical Research

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Accurately identifying the relationship between regulators and disease has long been a challenge in the field of biomedical research due to its crucial roles in pathobiological conditions. MicroRNAs (miRNAs) play a crucial role in regulating gene expression and are implicated in a diverse range of human diseases. However, understanding their precise causal pathways remains challenging, primarily due to dispersed data annotation across databases. This underscores the urgent need for a unified data visualization format to streamline these resources, aiding the identification of biomarkers and therapeutic targets. The existing association databases rely on labor-intensive manual curation, hindering the timely addition of new associations from publications. This study addresses these challenges by developing the first unified miRNA-gene-disease knowledge graph, integrating the ChatGPT API to automate miRNA-disease relation extraction from publications. I first retrieved and cleaned existing multiple databases containing miRNA-gene relations, gene-gene interactions, and gene-disease associations. The resulting knowledge graph representing entity pairs achieved >92% accuracy. Community network analysis revealed closely clustered miRNAs, genes, and diseases. A case study for this application focused on COVID-19 identified impacts of COVID-19 infection on fetal growth. My study introduces a novel framework for integrating miRNA and disease data into a unified miRNA-gene-disease knowledge graph. The resulting knowledge graph not only enhances our understanding of miRNA involvement in human diseases but also provides a valuable resource for identifying biomarkers and therapeutic targets for future research.

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