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Korea designs advanced AI model for accelerating therapeutic gene target discovery

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New AI model leverages hypergraphs to quickly and accurately identify therapeutic gene targets for diseases



Identifying therapeutic gene targets is essential for advancing personalised medicine and addressing the genetic basis of diseases. However, traditional experimental methods for discovering these targets are costly and time-consuming. While deep learning has shown promise in identifying biomarker genes, it has struggled to identify therapeutic genes.

To address this challenge, researchers from Pusan National University, South Korea have developed an innovative method, the Hypergraph Interactive Transformer (HIT), which accurately and quickly identifies therapeutic gene targets using hypergraphs and attention-based learning.

The HIT model utilises hypergraphs, which, unlike traditional graphs, can connect multiple nodes with a single hyperedge. This allows HIT to effectively model complex biological relationships by constructing gene and disease hypergraphs from multiple biological datasets, capturing connections between genes, diseases, and various ontologies like gene, disease, and human phenotype ontologies.

"HIT can accelerate the discovery of novel therapeutic gene targets and contribute to the understanding of disease mechanisms. This could advance personalized medicine by enabling treatments tailored to a patient's genetic profile and improving early disease detection in clinical settings", said the researchers.