DeepOmicsNet: 名疾患遺伝子予測のためのマルチオミクス深層学習モデル
DeepOmicsNet: A Multi-Omics Deep Learning Model for Disease Gene Prediction

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Advances in sequencing have generated massive multi-omics data, yet integrating these diverse layers to uncover disease-associated genes remains challenging. We propose DeepOmicsNet, a deep learning framework combining gene expression, methylation, and protein interaction data to predict genes linked to disease. The model utilizes convolutional and attention-based layers to capture complex biological patterns and weigh the contribution of each omics source. We evaluated DeepOmicsNet using TCGA datasets across multiple cancer type. It achieved high performance (AUC > 0.90), outperforming baseline models like MOFA and logistic regression. Importantly, the model identified novel gene candidates, some supported by literature and pathway databases. To enhance interpretability, we applied SHAP analysis, revealing omics-specific contributions varying across disease contexts. This insight aids biological understanding and hypothesis generation. A web tool is also provided for custom data input and visualization. DeepOmicsNet offers a powerful, interpretable approach to multi-omics integration and has potential in biomarker discovery and precision medicine.