# NeuroXNet: A Novel Hierarchical Based, Blood Biomarker Driven, Deep Learning Model With miRNA Drug Discovery Pipeline for Neurological Disease Diagnosis and Treatment Using in silico Modeling, MRI Imaging and Genomic Data

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Neurodegenerative diseases and cancerous brain tumors cause millions of patients worldwide to be fatally ill each year. Current diagnosis and treatment of these neurological conditions take many days, are sometimes inaccurate, costly, and may use invasive approaches that could endanger the patient's life. Thus, this study's purpose is the creation of a novel hierarchical deep learning model, NeuroXNet, which utilizes MRI images and genomic data to diagnose both neurodegenerative diseases like Alzheimer's disease, Parkinson's disease, and MCI as well as cancerous brain tumors, including glioma, meningioma, and pituitary tumors. Moreover, the model helps identify blood-based biomarkers using differentially expressed gene analysis to aid in diagnosing the six neurological conditions. Gene expression data is identified, protein network analysis, fold enrichment analysis, and gene ontology analysis is done for each class. Examples of hub genes found for meningioma tumors include CDK1, CCNA2, AURKA, BUB1. These proteins have degrees greater than 76 and fold enrichment values over 100. The model then uses these proteins to create a miRNA drug discovery pipeline to discover new therapeutics. Furthermore, the model uses patient genomic data to rank treatment options based on survival rate. The NeuroXNet model achieves a training accuracy of 99.70%, a validation accuracy of 100%, and a test accuracy of 94.71% in the multi-class diagnosis of the disease classes. Being the first such model in published literature, NeuroXNet reduces the chances of misdiagnosis, finds new methods for diagnosis and treatment, assesses treatment options, and does so in a time/cost-efficient manner compared to current procedures with multiple results that have never been reported or published before.

**Awards Won:**