

REVOLUTIONIZING BIOMEDICAL RESEARCH: INTEGRATING CUTTING-EDGE AI/ML TO UNLEASH INNOVATION IN DRUG DISCOVERY AND THERAPEUTICS DEVELOPMENT

Machine Learning Identifies Genes Linked To Neurological Disorders Induced By Equine Encephalitis Viruses (EEV, Traumatic Brain Injuries (TBI), And Organophosphorus Nerve Agents (OPNA)

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Venezuelan, eastern, and western equine encephalitis viruses (collectively referred to as equine encephalitis viruses (EEV)) cause serious neurological disease and are a significant threat to the civilian population and the warfighter. Likewise, organophosphorus nerve agents (OPNA) are highly toxic chemicals that pose serious health threats to both military and civilian personnel around the world. However, limited research exists on EEV and OPNA pathogenesis, but comparative analysis with traumatic brain injuries (TBI) reveals commonalities, including the occurrence of seizures. Examining molecular characteristics like gene expression profiles may offer insights into medical countermeasures (MCMs) for TBI, EEV infection and OPNA neuropathologies and sequelae. In this study, we collected transcriptomic datasets for neurological disorders caused by TBI, EEV infection, and OPNA exposure. A framework was implemented to normalize and integrate gene expression datasets derived from various platforms. Effective machine learning approaches were developed to identify critical genes that are associated, either shared or specific, with TBI, EEV, and OPNA. With the aid of deep neural networks, we were able to extract important association signals for an accurate prediction of different neurological disorders by using integrated gene expression datasets of VEEV, OPNA, and TBI samples. The identified neuropathologic features underwent analysis for gene product attributes and functions by gene ontology and pathway analyses, aiding in gaining mechanistic insights into the fundamental biology of these neurological disorders.

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