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Machine Learning Approach for Understanding the Effect of CD33 and TREM2 in Alzheimer's Disease

Jisu Jeong[1], Wookyung Yu[1,*]

[1] *Department of Brain Sciences, Daegu Gyeongbuk Institute of Science and Technology*
**Corresponding author: wkyu@dgist.ac.kr*

Neuroinflammation is a pathological hallmark of Alzheimer's disease (AD), and microglia, the brain's resident phagocyte, are pivotal for the immune response observed in AD. Recent Genome Wide Association Studies (GWAS) have identified about 20 gene variants associated with an increased risk of late-onset AD (LOAD), the most prevalent AD form. These methods strongly implicate some genes, especially related to the immune response and the triggering receptor expressed in myeloid cells 2 protein (TREM2). We focused on two microglial receptors CD33 and TREM2. Recently, data science with artificial intelligence technology has been extensively applied to genomics. We expect to employ machine learning techniques for understanding of the public sequencing data. Utilizing K-Nearest Neighbors (K-NN) and Support Vector Machine(SVM) models, we anticipate that by integrating biological knowledge and machine learning-based computer science techniques for genomic data analysis, we can uncover new phenomena that could not be identified solely through conventional data analysis methods.