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Predicting Risk of Opioid Addiction: Evaluation of Genetic Factors Using Machine Learning Algorithms

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We previously published the development of a multi-variant genetic probability risk model in a small case cohort study that included 37 patients with a known addiction to prescription opioids or heroin, as well as 30 age- and gender-matched controls. The performance characteristics of this algorithm were then determined by blinded deployment in 138 additional subjects. Overall test performance was promising with an AUC>0.80. To further test the generalizability of the model we requested access to data, and dna from >2000 subjects included GWAS studies from the NIDA Center for Genetic Studies. We will present the results of the blinded deployment of the genetic as well as genetic and phenotype (age, sex, substance abuse history) models in this sample set. The results of a second optimized AI model of the combined samples (458 OUD cases and 506 controls) as well as a model including and excluding individuals of African descent will also be presented. Correlation with nicotine, cannabis use disorders, as well as alcohol dependence/abuse was variable and will be reviewed in the context of OUD. Our results using materials and data originally collected for GWAS studies is promising and confirms the performance characteristics of our primary model. Additional predictive modeling for other substance use disorders using previously characterized data and samples will be limited by the primary study design and data collection but should be aggressively pursued.