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Predicting Development of Opioid Use Disorder Among Chronic Pain Patients Using Genomics, Social, and Clinical Factors within the All of Us Research Dataset

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The opioid epidemic remains a major public health crisis. Patients experiencing chronic pain are more likely to become dependent with up to 50% of patients on chronic opioid therapy meeting criteria to be diagnosed with opioid use disorder (OUD). It is essential to risk stratify which chronic pain patients are highest at risk for OUD. As risk for opioid addiction is likely multifactorial, such predictive models should include a diverse set of variables; therefore, the objective of this study was to leverage machine learning to predict OUD among chronic pain patients using genomic, social, and clinical factors within the AllofUs Research dataset. Initially, we used machine learning to predict OUD among chronic pain patients using >50 risk factors that included social determinants of health, educational background, income, co-substance use, comorbidities, psychiatric illnesses, and demographic data. Performance of the neural network, random forest, and logistic regression models demonstrated an area under the receiver operating characteristics curve of 0.82, 0.79, and 0.81, respectively, but had poor specificity (<0.1 for each model). Next, we utilized the HAIL platform to perform genome wide association analyses to identify genomic markers correlated with OUD. We will further improve our predictive models by both optimizing machine learning parameters and by incorporating genomic risk factors into the approach. As risk for OUD is likely multifactorial, predictive models using a wide array of patient-specific features, including genomics, may provide clinicians with a decision support tool to help determine OUD risk among chronic pain patients.

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