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Pain to Opioid use disorder Pattern Through Sequence (POPS): Genetic, Behavioral, and Environmental Roots

Background: While changes in policy have attempted to stem opioid use disorder (OUD) caused by prescription opioids, imprecise policy actions often create compromise at the cost of chronic pain patient treatment. We leveraged the AI infrastructure of the All of Us program to capture the predictive relationship between pain, opioid analgesic prescribing, and later diagnosis of OUD. We call our predictive score the “Pain to Opioid use disorder Pattern through Sequence” or POPS.
Method: We developed a longitudinal long and short-term memory system (LSTM) model using a sample of 24,200 (N case=12,100) patients matched on electronic health record data, ethnicity, age, and sex. We then created a longitudinal probability of OUD for the entirety of the All of Us EHR Sample (N=358,677). We related the POPS to common correlates of OUD. Finally, we used the genetic sequence data to conduct a genome-wide association study (GWAS).
Results: The model showed stronger prediction than most clinical predictors of OUD (AUC =.829, OR = 5.75 for each quantile increase in the probability of OUD, P < 2e1-6) and greatly out-predicted a chronic pain (OR = 2.280) and long-term prescription of opioid analgesics (OR = 1.822) phenotype. POPS significantly and weakly related to common correlates of OUD, such as psychiatric diagnosis and social determinants of health. Across ancestries, genome-wide data found 7 associated loci.
Conclusion: The POPS more effectively captures OUD risk than chronic opioid prescription. Future work will expand the genome-wide analyses to include drug repurposing to target this vulnerability.

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