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POLYGENIC SCORING AND THE CRIMINAL LEGAL SYSTEM

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ABSTRACT

Behavioral genetics has long sought to associate genetic variations with observed behavioral, social, or psychological traits. One area of behavioral genetics of particular interest to the criminal legal community has been research on genetics, antisocial or violent behavior, and criminal wrongdoing. In earlier eras of genomic research, these efforts often proposed candidate genes that, alone or in combination with identified environmental factors, would heighten risks for violent behavior and criminal activity. But these efforts largely lacked scientific validity, reliability, and explainability. Polygenic risk scores ("PRS"), which calculate whole genomic risk for complex conditions, may reinvigorate interest in genomic explanations for criminal behavior. This Article considers the ethical, legal, and social implications that such work occasions in the criminal legal system.

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I. INTRODUCTION

Imagine that a judge imposing a prison sentence for a criminal defendant who has pleaded guilty makes her sentencing decision based, at least in part, on a "recidivism risk score," an algorithmically derived measure of an individual's relative risk of reoffending.[1] Unlike prior generations of recidivism risk assessments, this tool includes not only background biographical characteristics about the defendant, but also a genetic component — a polygenic "risk score." This score purports to measure the relative likelihood that individuals with genetic profiles similar to the defendant's will exhibit antisocial, aggressive, or violent behavior.[2]

Or imagine that a school system, seeking medical history as part of the new student enrollment process, develops or accesses a similar polygenic "risk score" for each student. The school might provide additional social or academic support for students deemed at "high risk" for antisocial behavior. Or perhaps the school might segregate such students from one another,[3] surveil them more intensely, or share that data

1. *See, e.g.*, State v. Loomis, 881 N.W.2d 749 (Wis. 2016) (rejecting a constitutional challenge to a trial judge's use of an algorithmically derived "recidivism risk score" in determining the length or fact of imprisonment in sentencing in a criminal case).

2. *See* Colleen M. Berryessa, Nicole A. Martinez-Martin & Megan A. Allyse, *Ethical, Legal and Social Issues Surrounding Research on Genetic Contributions to Anti-Social Behavior*, 18 AGGRESSION & VIOLENT BEHAV. 605, 608 (2013).

3. *See* Sarah Zhang, *DNA Got a Kid Kicked Out of School — And It'll Happen Again*, WIRED (Feb. 1, 2016, 7:00 AM), https://www.wired.com/2016/02/schools-kicked-boy-based-dna/ [https://perma.cc/PC3L-TWZL] (reporting the story of a California middle school student removed from school because he had genetic markers for cystic fibrosis, but no manifested disease, where other students with cystic fibrosis were present).

with law enforcement for purposes of developing a "heat list" of probable future offenders.[4]

Or perhaps a state enacts a "red flag" law that includes, among its "risk factors," "genetic or biological determinants."[5] "Red flag" laws empower certain individuals "to petition a court to allow law enforcement to temporarily remove firearms, and temporarily prohibit the purchase or possession of firearms from an individual that is determined by the court to be a danger to themselves or others . . . ."[6] "Risk factors" are individual characteristics that may support an order for firearm removal. The law further calls for the names of individuals subject to "red flag" orders to be entered into the "National Instant Criminal Background Check System until such time it has been determined by the court that they no longer pose a threat to themselves or to others . . . ."[7]

Although these scenarios have not yet come to pass, they are only slight variations on reality. Recidivism risk scores are widely used in courts to inform bail and sentencing decisions, though these have not (yet) included genetic data.[8] Schools and local police departments have attempted to identify and surveil "at risk" students based on confidential information, including educational and child welfare records.[9] Meanwhile, the National League of Cities, an advocacy organization representing municipal leaders, has promoted the "red flag" law

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4. *See* Neil Bedi & Kathleen McGrory, *Pasco's Sheriff Uses Grades and Abuse Histories to Label Schoolchildren Potential Criminals. The Kids and Their Parents Don't Know.*, TAMPA BAY TIMES (Nov. 19, 2020), https://projects.tampabay.com/projects/2020/investigations/police-pasco-sheriff-targeted/school-data/ [https://perma.cc/9VCQ-KTL5] (describing Florida police program that kept track of, surveilled, and harassed middle and high schoolers in the county whom police deemed likely to "fall into a life of crime" based on criteria that included whether students had bad grades or had experienced household abuse and trauma).

5. *See* NAT'L LEAGUE OF CITIES, 2021 PROPOSED NATIONAL MUNICIPAL POLICY AMENDMENTS & RESOLUTIONS 152–53 (2021) (setting out NCL Resolution #51, "In support of federal legislation to incentivize states to enact extreme risk protection order laws and to enact a federal extreme risk protection order law to reduce firearm related suicides, murder-suicides and family fires").

6. *Id.* at 153.

7. *Id.*

8. *See* Julia Angwin, Jeff Larson, Surya Mattu & Lauren Kirchner, *Machine Bias*, PROPUBLICA (May 23, 2016), https://www.propublica.org/article/machine-bias-risk-assessments-in-criminal-sentencing [https://perma.cc/37U6-TSC4] ("[R]isk assessments . . . are increasingly common in courtrooms across the nation. . . . In Arizona, Colorado, Delaware, Kentucky, Louisiana, Oklahoma, Virginia, Washington and Wisconsin, the results of such assessments are given to judges during criminal sentencing.").

9. *See* Bedi & McGrory, *supra* note 4. Meanwhile, some researchers have advocated for "personalized education," along the lines of "personalized medicine," based on widespread polygenic scoring for "educational attainment" or other traits. *See* Erik Parens, *The Genes We're Dealt*, AEON (Nov. 10, 2020), https://aeon.co/essays/social-genomics-can-combat-inequality-or-be-used-to-justify-it [https://perma.cc/WYB4-VU52] (describing with skepticism progressive proponents of behavioral genetics as supporting a future of "'precision education', where educational interventions are tailored to children's genomes" (citing KATHRYN ASBURY & ROBERT PLOMIN, G IS FOR GENES: THE IMPACT OF GENETICS ON EDUCATION AND ACHIEVEMENT (2013))).

described above,[10] and twenty-one states have so far enacted some form of "red flag" legislation.[11]

Nor would such interventions be the first time genetic risk data intersects with the criminal legal system. Behavioral genetics has long sought to associate genetic variations with observed behavioral, social, or psychological traits. One area of behavioral genetics of particular interest to the criminal legal community has been research on genetics, antisocial or violent behavior, and criminal wrongdoing. In an earlier era of genomic research, these efforts often proposed "candidate genes" that, alone or in combination with identified environmental factors, would heighten risks for particular behavioral outcomes, like violence or criminal activity.[12] Among the most prominent examples of this approach involved variants of the monoamine oxidase A ("MAOA") gene. Studies purported to show that, among children who had been maltreated, those with a genetic variant giving rise to low levels of MAOA activity were more likely to exhibit violent behavior than those with high MAOA activity.[13] Unfortunately, these efforts proved to be "a spectacular failure because of methodological limitations and an oversimplified biology."[14]

Now, polygenic risk scores ("PRS") have reinvigorated interest in genomic explanations for complex behaviors, including violence and crime.[15] PRS calculate whole genome risk for complex conditions, utilizing genome-wide association studies to generate a "single quantitative measure of genetic predisposition" for a trait or outcome of interest.[16] Importantly, researchers caution that PRS "do not predict

10. *See* NAT'L LEAGUE OF CITIES, *supra* note 5, at 152–53.

11. *See Extreme Risk Laws*, EVERYTOWN FOR GUN SAFETY, https://www.everytown.org/solutions/extreme-risk-laws/ [https://perma.cc/LWR9-JXEK]. To date, no enacted "red flag" law explicitly includes genetic data as a relevant risk factor.

12. *See* Laramie E. Duncan, Michael Ostacher & Jacob Ballon, *How Genome-Wide Association Studies (GWAS) Made Traditional Candidate Gene Studies Obsolete*, 44 NEUROPSYCHOPHARMACOLOGY 1518, 1518 n.2 (2019) ("[T]he term 'candidate gene study' refers to traditional candidate gene studies, meaning studies that test for an association between one or a small number of polymorphisms and a phenotype of interest (e.g. depression), without examining genome-wide data." (emphasis omitted)).

13. *See* Avshalom Caspi, Joseph McClay, Terrie E. Moffitt, Jonathan Mill, Judy Martin, Ian W. Craig et al., *Role of Genotype in the Cycle of Violence in Maltreated Children*, 297 SCIENCE 851, 853 (2002).

14. Callie H. Burt, *Challenging the Utility of Polygenic Scores for Social Science: Environmental Confounding, Downward Causation, and Unknown Biology*, 46 BEHAV. & BRAIN SCIS., May 13. 2022, at 1.

15. *See* Duncan et al., *supra* note 12, at 1522; J.C. Barnes, Hexuan Lu, Ryan T. Motz, Peter T. Tanksley, Rachel Kail, Amber L. Beckley et al., *The Propensity for Aggressive Behavior and Lifetime Incarceration Risk: A test for Gene-Environment Interaction (G × E) Using Whole-Genome Data*, 49 AGGRESSION & VIOLENT BEHAV., Nov.–Dec. 2019, at 8.

16. Burt, *supra* note 14, at 6 (quoting Melinda C. Mills, Nicola Barban & Felix C. Tropf, *The Sociogenomics of Polygenic Scores of Reproductive Behavior and Their Relationship to Other Fertility Traits*, 4 RSF: RUSSELL SAGE FOUND. J. SOC. SCIS. 122 (2018)).

complex social outcomes with any degree of efficacy or accuracy and, therefore, should not be used for individual prediction."[17]

Yet, such precautionary instructions may well be insufficient and impair the integration of PRS within the criminal legal system. After all, police investigating crime[18] and judges imposing sentences of imprisonment[19] routinely rely on questionable algorithmic tools to do their work.

This Article thus considers the ethical, legal, and social implications that PRS might occasion in the criminal legal system. Part II draws on the experience of the criminal legal system with prior behavioral predictive tools, including MAOA and recidivism risk assessment. Part III then turns to PRS, querying whether the improvements of PRS over older tools make their use less problematic. At least for now, this Article concludes that PRS remain underdeveloped and should not be utilized. More broadly, the Article argues that PRS in the criminal legal system risk unwarranted genetic essentialism and are likely to be as infected with racial bias as the criminal legal system they seek to inform. A brief conclusion follows.

II. PRIOR PREDICTIVE PRACTICES

The history of behavioral genetics is fraught, as are practices of predictive policing and risk assessment in the criminal legal system. This Part tackles that history in two pieces. Section II.A describes the rise and fall of the candidate gene approach to behavioral genetics, including its intersection with the criminal legal system. Section II.B turns to contemporary predictive practices, including risk assessment tools widely used in courts in making bail and sentencing decisions. Together, these separate histories give rise to a range of concerns that polygenic risk prediction will need to answer if it is to be used to promote justice.

A. A Gene for Crime?

Following the Human Genome Project, which sought to produce the first full sequence of a human genome, behavioral genetics looked to establish causal genes for a wide array of behavioral traits. As a recent consensus report on behavioral genomics observed, "the 1990s

17. Burt, *supra* note 14, at 7.

18. *See* Maneka Sinha, *The Automated Fourth Amendment*, 73 EMORY L.J. 589, 605–17 (2024) (describing the range of algorithmic tools police use to "generate suspicion of a crime, of a person responsible for a crime, or of both" and explaining how and why "there are many documented instances of policing technology getting it wrong").

19. *See* State v. Loomis, 881 N.W.2d 749, 754 (Wis. 2016) (affirming sentence of imprisonment where trial judge relied, at least in part, on recidivism risk score).

were marked by a series of genetic studies hailed in the press for finding the 'gay gene,' the 'intelligence gene,' and the 'warrior gene.'"[20] Many of these studies were "candidate gene" or "candidate gene-environment" studies, which proposed specific genetic variations that, alone or in combination with identified environmental factors, would heighten risks for the particular behavioral outcome of interest.[21] Often, the "candidate gene" was selected because researchers hypothesized that the gene's known neurochemical activity might be relevant to the trait being studied.[22] These studies, in other words, hypothesized a causal mechanism, and set out to determine if a relationship between gene and observed outcome could be established.

In 2002, researchers announced a link between the MAOA gene, childhood maltreatment, and subsequent violent behavior.[23] The MAOA gene is involved in the breakdown of neurotransmitters, including norepinephrine, serotonin, and dopamine, and researchers hypothesized that variants of this gene might yield variation in impulsive and violent behavior.[24] What they found reinforced that belief: "of the 442 males in their study, those with a genetic variant called MAOA-L (the low activity form of the MAOA gene) were more likely to exhibit violent behavior if they had been maltreated as children compared to those with the genetic variant MAOA-H (the high activity form of the MAOA gene)."[25]

Yet, by the early 2000s, researchers were beginning to doubt the power of "candidate gene" studies, particularly in the context of behavioral genomics.[26] Most of the findings from these studies, including for MAOA, could not be consistently replicated.[27] The flaws in "candidate gene" studies, it emerged, were foundational. First, complex traits are biologically complex. "Although thousands of diseases and disorders are produced by this monogenic (one gene: one behavior) model, complex behavioral phenotypes such as antisocial, maladaptive, and violent

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20. Michelle N. Meyer, Paul S. Appelbaum, Daniel J. Benjamin, Shawneequa L. Callier, Nathaniel Comfort, Dalton Conley et al., *Wrestling with Social and Behavioral Genomics: Risks, Potential Benefits, and Ethical Responsibility*, 53 HASTINGS CTR. REP. S2, S12 (2023) (citations omitted).

21. *See* Duncan et. al., *supra* note 12, at 1518 n.2.

22. *See* Meyer et al., *supra* note 20, at S12.

23. *See* Caspi et al., *supra* note 13, at 851.

24. *See id.*

25. Nita A. Farahany, Roderick T. Kennedy & Brandon L. Garrett, *Genetic Evidence, MAOA, and* State v. Yepez, 50 N.M. L. REV. 469, 473 (2020) (emphasis omitted).

26. *See* Meyer et al., *supra* note 20, at S12 ("By the start of the 2000s, however, it became clear that (with some exceptions, including rare forms of common diseases like breast cancer and Parkinson's) many of those original positive findings about strong associations between single candidate genes and common phenotypes were illusions.").

27. Farahany et al., *supra* note 25, at 477 ("When researchers in 2011 conducted a thorough review of the first ten years of candidate-gene studies using candidate genes in psychiatry, they found that while 96% of initial novel findings were significant, they were only replicated 27% of the time.").

behavior, are *not* produced by such a simple genetic model."[28] Rather than one or a few genetic variations informing a complex behavioral trait, such traits are polygenic in nature.[29] This means that the effect of any single gene or gene variant on the trait of interest is likely to be quite small.[30] "Candidate gene" studies missed this forest for the trees for a second reason: small sample sizes. In a study of only several hundred individuals, small genetic variations could take on outsized significance.[31] In hindsight, the "candidate gene" era of behavioral genomics has been described as documenting "illusions,"[32] "studying pure noise,"[33] and "a spectacular failure."[34]

Notwithstanding the scientific community's rejection of "candidate gene" research, the criminal legal system was asked to embrace it, in at least some circumstances. Most often, criminal defendants have relied on MAOA research at sentencing to argue that their possession of an MAOA-L gene variant and a childhood afflicted with trauma should be mitigating circumstances weighing in favor of a shorter or less harsh criminal sentence.[35] On at least two occasions, defendants sought the admission of this research during the guilt phase of their trial, arguing that the presence of an MAOA-L variant and childhood trauma rendered them incapable of the requisite intent for the crime with which they were charged.[36] In many — but not all — of these cases, courts did admit or consider MAOA research. Notably, in the most recent decision on the matter, the New Mexico Supreme Court concluded that the district court had not abused its discretion in excluding evidence regarding MAOA for determining the defendant's guilt or innocence.[37]

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28. *Id.* at 478.

29. *Id.*

30. *Id.* at 479.

31. *See* Meyer et al., *supra* note 20, at S12 ("What was initially cast as a series of triumphant discoveries came to be seen as systemic publication bias that favored positive results generated by underpowered studies (that is, from samples with too few individuals).").

32. Meyer et al., *supra* note 20, at S12.

33. Burt, *supra* note 14, at 2 (quoting psychiatric geneticist Matthew Keller).

34. *Id.* at 1.

35. *See* Sally McSwiggan, Bernice Elger & Paul S. Appelbaum, *The Forensic Use of Behavioral Genetics in Criminal Proceedings: Case of the MAOA-L Genotype*, 50 INT'L J. L. & PSYCHIATRY 17, 19 tbl.1 (2017).

36. *Id.* (describing proceedings in *Yepez* and *Waldroup* cases); *see* State v. Yepez, 483 P.3d 576, 578 (N.M. 2021); State v. Waldroup, No. E2010-01906-CCA-R3-CD, 2011 WL 5051677, at *1 (Tenn. Crim. App. 2011); *see also* Farahany et al., *supra* note 25, at 472 ("At trial, Mr. Yepez sought to present evidence of his inability to form the specific intent necessary for a jury to find him guilty of first-degree murder.").

37. *Yepez*, 483 P.3d at 589 ("We hold that evidence of mere genetic susceptibility to a given mental condition is not relevant on the issue of deliberate intent, at least in the absence of evidence that such susceptibility is so well understood and has such strong predictive value as to be clinically validated as an indicator of the mental condition."); *see also* Shawneequa Callier & Anya E.R. Prince, *The Legal Uncertainties of Sociogenomic Polygenic Scores*, 38 HARV. J.L. & TECH. 553, 573 (2024) (discussing *Yepez*).

When this research has been introduced in criminal proceedings, however, it has not always been received in the way it was intended. Indeed, Nita Farahany has described MAOA and related neurobiological research as having "double-edged potential" because it can "denigrate defendants' characters and . . . demonstrate defendants' likely future dangerousness."[38] Despite a lack of scientific validity, supposed genetic explanations for violent behavior have continued to be of interest to defense counsel, prosecutors, and others working in the criminal legal system.

In sum, the history of behavioral genetics in general, and of MAOA in particular, is a cautionary tale about overinterpreting genetic correlation as genetic causation and extrapolating from research to criminal law.

B. Recidivism Risk Assessment

While MAOA research originated in the behavioral genomics/scientific community, many other tools used in the criminal legal system are created, designed, and intended solely for criminal legal use. This is the case for recidivism risk assessment software.

Modern recidivism risk assessment tools are machine learning models that generate relative "risk scores" of an individual criminal defendant's likelihood of recidivism. Among the best known and most widely used tools of this type is the Correctional Offender Management Profiling for Alternative Sanctions ("COMPAS"), a privately developed proprietary tool from Northpointe, Inc. (now doing business as Equivant).[39] COMPAS calculates its recidivism scores based on an interview with a defendant and information in the defendant's criminal file.[40] COMPAS is designed to measure both "dynamic factors," including personal beliefs and trust, and "static factors," like a defendant's family criminal history and age at first arrest.[41]

Based on the data collected, COMPAS produces risk scores, which are reported on an easy-to-read 10-point bar chart.[42] These scores —

38. Nita A. Farahany, *Neuroscience and Behavioral Genetics in US Criminal Law: An Empirical Analysis*, 2 J.L. & BIOSCIENCES 485, 489 (2015); *see also* McSwiggan et al., *supra* note 35, at 21 ("Evidence of a genetic risk for aggression admitted in mitigation nonetheless may have been considered as an aggravating circumstance insofar as it heightened the risk of future dangerous behavior.").

39. *See* Natalie Ram, *Innovating Criminal Justice*, 112 NW. U. L. REV. 659, 683–84 (2018); *see also* Angwin et al., *supra* note 8 (describing COMPAS and its popularity).

40. *See* State v. Loomis, 881 N.W.2d 749, 754, 761 (Wis. 2016) (describing then-Northpointe's explanation about the information inputs used to generate COMPAS scores); *see also* Ram, *supra* note 39, at 684 (describing COMPAS).

41. *See* Katherine Freeman, Note, *Algorithmic Injustice: How the Wisconsin Supreme Court Failed to Protect Due Process Rights in* State v. Loomis, 18 N.C. J.L. & TECH. 75, 79 (2016).

42. *See Loomis*, 881 N.W.2d at 754; Freeman, *supra* note 41, at 81.

which include scales for "pretrial misconduct," "general recidivism," and "violent recidivism," among others[43] — are intended to represent a relative risk. Defendants with higher scores are deemed at higher risk of reoffending than other individuals in the same "norm group."[44]

These scores are alluring in their supposed simplicity and veneer of objectivity, so it is little surprise that COMPAS has come to be widely used — including beyond its intended purposes. Consider the *Loomis* case. In that case, Eric Loomis pled guilty to fleeing the police and driving a stolen car.[45] The trial court's pre-sentence report included a COMPAS recidivism risk score, and Loomis was deemed at high risk of committing another crime.[46] The pre-sentence report also cautioned that "risk scores are not intended to determine the severity of the sentence or whether an offender is incarcerated."[47] This instruction reflected Northpointe's own description of COMPAS as "inform[ing] decisions regarding the placement, supervision and case management of offenders."[48] Nonetheless, the trial court cited Loomis's COMPAS score when sentencing Loomis to six years imprisonment.[49] The Wisconsin Supreme Court affirmed that sentence, turning aside Loomis's argument that a sentence based on a COMPAS score violates due process.[50]

There are also reasons to doubt the validity and reliability of COMPAS and other tools like it. Researchers have documented that "COMPAS predictions are no better, in terms of accuracy, false positives and false negatives, than untrained human laypersons . . . ."[51]

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43. NORTHPOINTE INC. D/B/A EQUIVANT, PRACTITIONER'S GUIDE TO COMPAS CORE § 4.1, at 30 (2019) [hereinafter COMPAS PRACTITIONER'S GUIDE], https://www.equivant.com/wp-content/uploads/Practitioners-Guide-to-COMPAS-Core-040419.pdf [https://perma.cc/MK6H-ASAN].

44. *See* Freeman, *supra* note 41, at 81–82; *see also Loomis*, 881 N.W.2d at 754. Northpointe has identified eight norm subgroups: "(1) male prison/parole, (2) male jail, (3) male probation, (4) male composite, (5) female prison/parole, (6) female jail, (7) female probation and (8) female composite." COMPAS PRACTITIONER'S GUIDE, *supra* note 43, § 2.9, at 11.

45. *Loomis*, 881 N.W.2d at 754.

46. *Id.* at 754–55; Ethan Chiel, *Secret Algorithms that Predict Future Criminals Get a Thumbs Up from Wisconsin Supreme Court*, SPLINTER (July 27, 2016, 8:00 PM), https://www.splinter.com/secret-algorithms-that-predict-future-criminals-get-a-t-1793860613 [https://perma.cc/E2D7-BTN4].

47. *Loomis*, 881 N.W.2d at 755 (emphasis omitted).

48. COMPAS PRACTITIONER'S GUIDE, *supra* note 43, at 1.

49. Chiel, *supra* note 46.

50. *Loomis*, 881 N.W.2d at 753, 772 ("We determine that because the circuit court explained that its consideration of the COMPAS risk scores was supported by other independent factors, its use was not determinative in deciding whether Loomis could be supervised safely and effectively in the community. Therefore, the circuit court did not erroneously exercise its discretion.").

51. Christoph Engel, Lorenz Linhardt & Marcel Schubert, *Code Is Law: How COMPAS Affects the Way the Judiciary Handles the Risk of Recidivism*, A.I. & L., Feb. 9, 2024, at 3; *see also* Angwin et al., *supra* note 8 ("The score proved remarkably unreliable in forecasting violent crime: Only 20 percent of the people predicted to commit violent crimes actually went

Moreover, there are fundamental concerns about racial bias that may run through the training data from which these algorithmic systems "learn" due to racial bias in the criminal legal system writ large (a garbage in/garbage out concern).[52] Indeed, researchers have found that recidivism risk assessment tools, including COMPAS, may be racially biased.[53] In one prominent study, ProPublica analyzed COMPAS scores for more than 7,000 people arrested in 2013 and 2014 and compared these scores to the actual incidence of recidivism for those individuals.[54] ProPublica concluded that COMPAS scores were unreliable predictors of violent crime in general: "Only 20 percent of the people predicted to commit violent crimes actually went on to do so."[55] Worse yet, "[t]he formula was particularly likely to falsely flag black defendants as future criminals, wrongly labeling them this way at almost twice the rate as white defendants," while "[w]hite defendants were mislabeled as low risk more often than black defendants."[56] Subsequent studies have documented similar overprediction of future risk for other groups, including Hispanic individuals[57] and women.[58]

In addition, there may be unease about technical decisions in software tools like COMPAS such as which criteria to include and how to

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on to do so. When a full range of crimes were taken into account — including misdemeanors such as driving with an expired license — the algorithm was somewhat more accurate than a coin flip. Of those deemed likely to re-offend, 61 percent were arrested for any subsequent crimes within two years.").

52. *See, e.g.*, Sandra G. Mayson, *Bias In, Bias Out*, 128 YALE L.J. 2218, 2251 (2019) ("[P]rediction functions like a mirror. . . . If there is racial disparity in the data, there will be racial disparity in prediction too.").

53. *See* Cecelia Klingele, *The Promises and Perils of Evidence-Based Corrections*, 91 NOTRE DAME L. REV. 537, 577 (2015) ("A significant body of literature has found that risk assessment tools disproportionately classify minorities and the poor as higher risk, often due to factors outside their control, such as familial background and education, potentially subjecting them to harsher treatment throughout the penal system."); *Loomis*, 881 N.W.2d at 763 ("[T]here is concern that risk assessment tools may disproportionately classify minority offenders as higher risk, often due to factors that may be outside their control, such as familial background and education."); Angwin et al., *supra* note 8 (observing that ProPublica's study "turned up significant racial disparities").

54. Angwin et al., *supra* note 8.

55. *Id.*

56. *Id.*

57. *See* Melissa Hamilton, *The Biased Algorithm: Evidence of Disparate Impact on Hispanics*, 56 AM. CRIM. L. REV. 1553, 1577 (2019) ("Using multiple definitions of algorithmic unfairness, results consistently showed that COMPAS, a popular risk tool, is not well calibrated for Hispanics. . . . The tool fails to accurately predict actual outcomes in a linear manner and overpredicts risk for Hispanics. Overall, there is cumulative evidence of disparate impact.").

58. *See* Melissa Hamilton, *The Sexist Algorithm*, 37 BEHAV. SCIS. & L. 145, 154 (2019) ("When agencies, such as the one studied here, decline to incorporate gendered scoring, it is unsurprising that risk outcomes will present disparate impact on women. The unfortunate consequence is that the risk tool overclassifies women and thus more of them are likely to be unfairly treated in criminal justice decisions and be subject to unnecessary levels of supervision."). *See generally* Engel et al., *supra* note 51, at 3 (observing that "COMPAS has met with considerable criticism" and collecting sources).

weight them (a black box concern). Black box concerns are particularly salient in the context of recidivism risk scores like those generated by COMPAS, given the proprietary claims made over this software. While Northpointe has made available the 137-question survey that provides the informational input for COMPAS, it has refused to disclose how that information is used or weighted to arrive at a particular recidivism risk score.[59] Instead, Northpointe has asserted that its algorithmic system is a trade secret.[60] These proprietary claims have rendered genuine independent validation and verification of COMPAS and similar systems difficult, if not impossible, to accomplish.[61]

Taken together, challenges to the growing use of recidivism risk assessment tools span the gamut. Recidivism risk assessment tools raise concerns about accuracy and bias; they also demand scrutiny about the role of secrecy in criminal legal tools, about the ability to adequately validate and verify these tools notwithstanding assertions of secrecy, and about how these tools have been stretched beyond even their validated use cases. Many of these same challenges may well emerge with respect to the use of PRS models in the criminal legal system as well.

III. THE FUTURE OF GENOMIC RISK PREDICTION

Polygenic risk scores have been greeted as a new "golden age" for behavioral genomics, following the downfall of the "candidate gene" approach.[62] In basic terms, PRS owe their existence to genome-wide association studies ("GWAS"). GWAS seek to identify genetic variations across the human genome that correlate with an observed outcome or trait.[63] For most traits, each such variation has only a small impact.[64] PRS represent the cumulative relationship between the many identified genetic variants and the trait of interest. In other words, PRS are a "massively polygenic, additive model" that yield "genetic summary scores" by aggregating genetic variations "weighted by their effect sizes."[65] Perhaps surprisingly, many PRS include all identified genetic variations in their calculations, without regard to the statistical significance

59. *See* State v. Loomis, 881 N.W.2d 749, 761 (Wis. 2016); Freeman, *supra* note 41, at 80 (describing the survey).

60. *Loomis*, 881 N.W.2d at 761 ("Northpointe, Inc., the developer of COMPAS, considers COMPAS a proprietary instrument and a trade secret.").

61. *See* Ram, *supra* note 39, at 686–90.

62. Burt, *supra* note 14, at 1.

63. Meyer et al., *supra* note 20, at S12–S13.

64. *Id.*

65. Burt, *supra* note 14, at 6.

of a particular genetic variation to the target trait (an "all SNPs" model).[66]

In significant ways, PRS answer the flaws of the "candidate gene" approach that they succeeded. Where "candidate gene" studies were underpowered, PRS studies often examine the genomes of hundreds of thousands of individuals.[67] Where "candidate gene" studies modeled a too-simple biological causal story, PRS studies adhere to a new "Fourth Law of Behavioral Genetics: A typical human behavioral trait is associated with very many genetic variants, each of which accounts for a very small percentage of the behavioral variability."[68] And where "candidate gene" studies "proceeded from a hypothesis about an association between a single gene and a phenotype or outcome," PRS studies are virtuously "hypothesis free."[69] That is, PRS studies do not attempt to uncover how or why certain genetic variations produce or effect a behavioral outcome, nor do they seek out genetic variations based on a theory of causal relationship.

Given these methodological improvements, renewed interest in the utility of behavioral genomics is understandable, including from actors in the criminal legal system. Police investigating crime or identifying "high risk" individuals, judges making bail or sentencing determinations, or courts deciding whether to issue a "red flag" order or involuntary civil commitment may hope to put PRS to use. As with many other forensic methods, criminal legal actors may believe that PRS can offer an objective, scientific, and bias-free tool to supplement or replace faulty human judgment.[70]

But this Part identifies at least four reasons to doubt that PRS can, at least at present, ameliorate rather than exacerbate harms within the criminal legal system.

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66. *Id.* at 7. "SNP" stands for "single nucleotide polymorphism," which refers to a variation between individuals in a single base pair of DNA — a single "rung" on the double-helix ladder of DNA's structure. *See* Natalie Ram, *DNA by the Entirety*, 115 COLUM. L. REV. 873, 879 (2015). More specifically, SNPs typically include those variations "where two (or more) alternative nucleotides are common (>1%) in the population." Burt, *supra* note 14, at 4 tbl.1 (defining "SNP"). Researchers constructing PRS models must decide which SNPs identified through GWAS comparisons to include in their models. An "all SNPs" model is what it sounds like: a model that includes all available SNPs, rather than a subset of SNPs that meet some measure of statistical significance. Burt, *supra* note 14, at 7 ("[M]ost PGSs are constructed from all available SNPs regardless of their statistical significance in the GWAS.").

67. *See* Meyer et al., *supra* note 20, at S12 ("GWASs with several thousand participants were augmented with tens of thousands and then hundreds of thousands, and those larger samples provided finer resolution to identify smaller effects, which turned out to be numerous.").

68. *Id.* at S12–S13 (internal quotation marks omitted).

69. *Id.* at S12 ("Indeed, being 'hypothesis free' was one of the virtues hailed by scientists who used the methodology.").

70. *See* Ram, *supra* note 39, at 681–82, 685 (describing such assumptions, and their flaws, in the context of other forensic methods).

A. PRS Do Not Tell a Causal Story

Owing to their "hypothesis free" method, the genome-wide approach of PRS studies "by itself permits researchers to identify only correlations between [genetic variations] and phenotypes."[71] An identified genetic variation may have no causal relationship to the trait being studied at all.[72] Even if a particular genetic variation is causally related to a trait, geneticists are unlikely to understand that relationship, particularly where psychiatric or behavioral traits are at issue.[73] Moreover, many researchers working on PRS "explicitly deemphasiz[e] inquiry into causal variant(s) or biological pathways."[74]

The absence of a focus on causal pathways in PRS development and use raises concerns should PRS be incorporated in the criminal legal system. PRS proponents argue that PRS could "provide an inexpensive way to more expansively identify those at high genetic risk of problems . . . and intervene in advance with, for example, extra support or placement into a different learning environment."[75] But PRS are at least equally likely to provide yet another tool for identifying and punishing individuals after a crime has occurred, rather than for identifying at risk individuals and providing ex ante support that might prevent wrongdoing.[76] Indeed, there is good reason to believe that PRS are

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71. Meyer et al., *supra* note 20, at S13.

72. *See id.*

73. *See id.* ("There has been some limited success in learning about causal pathways from GWASs of disease phenotypes. Even fewer insights about causal mechanisms have emerged from GWASs of psychiatric phenotypes and fewer still from GWASs of nonpsychiatric behavioral phenotypes.").

74. Burt, *supra* note 14, at 5. Burt also suggests that the genetic variations on which PRS rely — single nucleotide polymorphisms ("SNPs") — are not well suited to "tag" various other forms of genetic variation, including some that may be disproportionately responsible for causal effects. *Id.* at 5 ("Crucially, rare and more likely deleterious variants are not well tagged by SNPs, given that SNPs tag haplotypes defined by shared common variants, and most haplotypes will not contain the rare variants (or they wouldn't be rare). Additionally, other variant forms — indels, copy number variants (CNVs), and [structural variants] — are not measured in GWASs, and many are not well-tagged by common SNPs."). This may suggest more fundamental methodological limitations in the PRS approach to behavioral genetics.

75. Burt, *supra* note 14, at 8.

76. Often, policing wins out over competing approaches to responding to crime. *Compare* Sam Levin, *These US Cities Defunded Police: 'We're Transferring Money to the Community*,*'* GUARDIAN (Mar. 11, 2021, 11:03 AM EST), https://www.theguardian.com/us-news/2021/mar/07/us-cities-defund-police-transferring-money-community [https://perma.cc/6LFZ-8H83] (documenting how the "defund the police" movement sought, in many cities, to urge officials to "prioritize the programs that have been defunded over the years that would address root causes of crime and poverty, like education, healthcare and homeless services") *with* Char Adams, *Cities Vowed in 2020 to Cut Police Funding — but Budgets Expanded in 2021*, NBC NEWS (Dec. 28, 2021, 6:33 PM EST), https://www.nbcnews.com/news/nbcblk/cities-vowed-2020-cut-police-funding-budgets-expanded-2021-rcna9864 [https://perma.cc/G396-DJJX] (documenting how many cities subsequently restored police budgets). The allocation and use of city funds are not the same as the

more likely to inform ex post punishments than ex ante interventions. That is so because PRS do not enrich our understanding of which genetic variants are *causally related* to behavioral outcomes or why those variants have that effect.[77] Without a causal story, it is difficult, if not impossible, to sort out what interventions might be genetically relevant in preventing an undesirable outcome from manifesting. Indeed, some prominent researchers "are skeptical that GWAS (even with much improved data and methods) will ever yield much knowledge about genetic causal mechanisms for behavioral or social phenotypes."[78] Insofar as PRS researchers actively discourage inquiry into biological pathways, this is likely to further reinforce PRS as a predictive tool, but not a preventive one.

Moreover, the lack of a causal story in behavioral PRS is likely to manifest another harm commonly leveled at criminal legal tools: reinforcing racial bias in the criminal legal system.[79] Given the lack of a causal relationship between the genetic variations that make up a PRS model and the prevalence of racial bias throughout the criminal legal system, it will be difficult to discern whether a PRS model reflects racial or other bias in an individual's environment or rather measures something separate from it. To see how environmental bias might creep into a purely genetic score, consider a thought experiment on the relationship between genes, environment, and discrimination:

> [I]magine a system where red-haired children are barred from school. In such a system, genetic variants linked to red hair would be identified by GWASs as genetic causes of educational attainment. However, neither an individuals' red hair, nor the genetic variants contributing to red hair, are appropriately conceived as causes of differences in educational attainment in this hypothetical case . . . . The "difference that makes a difference" is not red hair but the social-institutional policies excluding people with red hair . . . .[80]

Because communities of color experience over-policing, over-surveillance, and disproportionate arrest, charging, and conviction in the

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use of scientific data, of course, but similar competing interests of ex ante versus ex post interventions exist in both scenarios, particularly in the real world of scarce public resources. At least one story of the "defund the police" movement of the early 2020s is that when cities had to prioritize, they mostly chose ex post policing and punishment.

77. Meyer et al., *supra* note 20, at S13.

78. *Id.*

79. *See supra* notes 53–57 (describing this concern with respect to recidivism risk assessments).

80. Burt, *supra* note 14, at 10–11.

criminal legal system, genetic variations associated with skin pigmentation may well crop up in PRS models for traits associated with criminal wrongdoing. To be clear, this is *not* because there is a genetic causal relationship between skin color and criminal wrongdoing. Rather, a PRS model that is intended to measure genetic difference may instead reflect structural bias found in the criminal legal system. As with recidivism risk assessment tools, PRS use in the criminal legal system is likely to suffer from a garbage in/garbage out problem.[81]

B. PRS Do Not Tell an Individualized Story

Using PRS in the criminal legal system is also problematic because PRS do not tell an individualized story. As described at the outset, researchers caution that PRS "do not predict complex social outcomes with any degree of efficacy or accuracy and, therefore, should not be used for individual prediction."[82] More pointedly, it is "misguided" to associate a PRS with "individual propensity."[83] This may be particularly so for behavioral and "all SNPs" PRS models.[84] Current research suggests that "all SNPs" PRS models "are more environmentally confounded than those that use (more stringent) [thresholds for statistical significance]."[85] Existing models "may explain more variance," but perhaps only "because they capture environmental influences as well as genetic ones."[86]

Yet, use of PRS in the criminal legal system would likely be in the form of individualized predictions of future behavior. A judge imposing a sentence or length of imprisonment in reliance on PRS would be taking that score into account as an individualized prediction of future risk. So too would police identifying "high risk" individuals and courts making individualized determinations of future risk under "red flag" or civil commitment statutes.

Such uses of PRS in the criminal legal system would be dismaying, but not surprising — we have seen much the same pattern with recidivism risk assessments. As described above, although recidivism "risk scores are not intended to determine the severity of the sentence or whether an offender is incarcerated,"[87] courts have used these tools for

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81. *See* Mayson, *supra* note 52, at 2224.

82. Burt, *supra* note 14, at 7; *see also* Daphne O. Martschenko & Lucas J. Matthews, *Genomics, Behavior, and Social Outcomes*, HASTINGS CTR.: BIOETHICS BRIEFINGS (Dec. 1, 2020), https://www.thehastingscenter.org/briefingbook/genomics-behavior-and-social-outcomes/ [https://perma.cc/9CFS-GTBZ] ("[M]any scientists emphasize that PGS cannot accurately predict the outcomes of *individuals* . . . ."); Meyer et al., *supra* note 20, at S25 (observing that most PRS are only "very weak predictors of individual outcomes").

83. Burt, *supra* note 14, at 13.

84. *See supra* note 66 and accompanying text.

85. Burt, *supra* note 14, at 7.

86. *Id.*

87. State v. Loomis, 881 N.W.2d 749, 755 (Wis. 2016) (emphasis omitted).

just that purpose.[88] Similarly, the misuse of PRS to target individuals for investigation or to support individualized determinations regarding bail, sentencing, or other judicial decisions would take a scientific research tool and put it to scientifically unsound use.

At least in part, such misuse reflects the differing standards for validity and reliability applicable to traditional scientific research, the admission of expert evidence at trial, and the use of technology in policing investigations, bail determinations, and sentencing decisions.[89] Scientific evidence introduced in a criminal trial must meet certain requirements, such as those set out in Federal Rule of Evidence 702, the *Daubert* standard, and the older *Frye* standard still in use in some state courts.[90] These rules aim to ensure that only rigorous and validated scientific evidence is admitted. In practice, however, these rules are susceptible to manipulation by savvy prosecutors, incurious judges, and profit-minded private developers.[91] Police investigative methods, bail determinations, and sentencing decisions are subject to even laxer standards, as evidentiary standards need not be met in those contexts.[92] Under these standards, it is often difficult for a court to properly identify, much less preclude, unscientific uses of scientific research tools.

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88. *Id.* at 753–54; Chiel, *supra* note 46; *see supra* Section II.B.

89. As described in Section III.B, concerns about the use of PRS models beyond their established validity and reliability are also present when PRS are misused to make predictions about individual propensity, and the same issues regarding evidentiary standards apply in that context.

90. *See* Maneka Sinha, *Radically Reimagining Forensic Evidence*, 73 ALA. L. REV. 879, 908–10 (2022) (describing these standards); Frye v. United States, 293 F. 1013, 1014 (D.C. Cir. 1923) (announcing that expert opinion evidence is admissible only if the scientific method on which the opinion is based has gained "general acceptance in the particular field in which it belongs"); Daubert v. Merrell Dow Pharms., 509 U.S. 579, 592–94 (1993) (supplanting the *Frye* test in federal courts by requiring judges themselves to assess "whether the reasoning or methodology underlying the [expert] testimony is scientifically valid" and suggesting several factors for judges to consider in assessing methodological reliability including (1) testing, (2) peer review and publication, (3) standards and controls, (4) error rate, and (5) general acceptance in the relevant scientific community); FED. R. EVID. 702 advisory committee's note to 2000 amendment (codifying the *Daubert* standard and outlining the "non-exclusive checklist for trial courts to use in assessing the reliability of scientific expert testimony").

91. *See* Sinha, *supra* note 90, at 910–13, 927–37 (describing how "segments of the forensic community have worked to facilitate the admission of unsound forensic evidence in criminal cases," including by "leverag[ing] an understanding of the *Daubert* factors to manufacture a perception that their method is reliable — thereby winning it widespread admissibility — despite significant data to the contrary").

92. *See* Sinha, *supra* note 18, at 618–27 (describing standards for investigative reliability, which is generally "assessed under a flexible, totality of circumstances test"); Maneka Sinha, *Junk Science at Sentencing*, 89 GEO. WASH. L. REV. 52, 87 (2021) ("By and large, trial-stage evidentiary rules do not apply at sentencing.").

C. PRS Are Population Specific

PRS are not portable from one population to another.[93] That is, PRS "created by studying one 'genetic ancestral population' cannot be generalized or applied to another genetic ancestral population to make predictions about that population."[94] The concept of "genetic ancestral population" is itself fraught, particularly if described at the continental level.[95] But the portability (or lack thereof) of PRS from one "genetic ancestral population" to another means that at a basic level, a PRS developed from the genomic data of individuals of European descent tells us relatively little about the polygenic risks for other populations.[96] Indeed, PRS developed from the genetic data of "European ancestries participants are *most* predictive of European DNA samples, and *least* predictive of African-ancestries DNA samples."[97]

This reality is particularly salient when considering the use of PRS models in the criminal legal system.[98] "[T]he largest biobanks today include overrepresentation of people of 'European genetic ancestry . . . .'"[99] Meanwhile, the criminal legal system is disproportionately composed of people of color.[100] For many people of color, it would be scientifically invalid to use a PRS modeled on populations of European descent.[101] Yet, that is what the use of PRS in the criminal legal system would likely produce. The serious mismatch between the populations present in large biobanks and those overrepresented in the criminal legal system thus undermines the utility of PRS use in the latter.

Once again, one might wonder how a scientifically invalid use could come to pass, but the unfortunate reality is that this happens

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93. Meyer et al., *supra* note 20, at S16.

94. *Id.* at S15.

95. *Id.* at S16.

96. *Id.* at S15; Burt, *supra* note 14, at 5 ("This ancestral variation in LD and haplotypes is one biological reason why GWAS findings do not 'port well' or generalize across ancestral groups.").

97. Martschenko & Matthews, *supra* note 82.

98. *See* Callier & Prince, *supra* note 37, at 560–62 (discussing the problems of portability and emphasizing that these concerns are especially salient when polygenic scores are incorporated into settings beyond the medical realm).

99. Meyer et al., *supra* note 20, at S16.

100. *See, e.g.*, Margaret Bull Kovera, *Racial Disparities in the Criminal Justice System: Prevalence, Causes, and a Search for Solutions*, 75 J. SOC. ISSUES 1139, 1140–51 (2019) (reviewing literature documenting racial disparities in the criminal legal system across policing, prison populations, and participation in juries).

101. Of course, communities or "people of color" and individuals of "European genetic ancestry" are not exclusive of one another. It is inappropriate to conflate genetic ancestry with "social groupings such as race and ethnicity." Meyer et al., *supra* note 20, at S15. As I have explained elsewhere, "America's history of slavery, and the sexual violence that often accompanied it," renders many self-identified Black Americans individuals of European descent. Natalie Ram, *Investigative Genetic Genealogy and the Problem of Familial Forensic Identification*, *in* CONSUMER GENETIC TECHNOLOGIES: ETHICAL AND LEGAL CONSIDERATIONS (I. Glenn Cohen, Nita Farahany, Henry T. Greely & Carmel Shachar, eds., 2021).

routinely. The field of forensic evidence is littered with not-sciences.[102] Moreover, even genetic sciences, which have the best track record among forensic methods, have been pushed beyond the scope of their validated use cases.[103] The use of PRS models beyond their intended use or validated scope, accordingly, would not raise wholly new concerns about the use of scientific tools in unscientific ways in the criminal legal system. But insofar as greater care should be taken (and it should!) to prevent such misuse, the incorporation of PRS models should be closely scrutinized.

D. PRS Are a Black Box

Finally, use of PRS models in the criminal legal system is likely to be problematic because these models are, or soon will be, technological black boxes. The black box nature of PRS models is not only a reflection of the "correlation, not causation" effect that they purport to measure; it is also a function of the fact that "the technological and statistical tools for creating [PRS] are complex . . . ."[104] As one research team has explained, existing PRS models "are unlikely to adapt well to high-dimensional genomic data owing to their low model complexity (i.e., insufficient number of model parameters)."[105] Researchers increasingly look to machine learning models to generate more complex PRS.[106] But highly complex, machine learning models are frequently black box tools, which carry concerns of their own. As Cynthia Rudin explains, "A black box model could be either (1) a function that is too

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102. *See generally* COMM. ON IDENTIFYING THE NEEDS OF THE FORENSIC SCIS. CMTY., NAT'L RSCH. COUNCIL, STRENGTHENING FORENSIC SCIENCE IN THE UNITED STATES: A PATH FORWARD 107–08 (2009) ("Much forensic evidence — including, for example, bite marks and firearm and toolmark identifications — is introduced in criminal trials without any meaningful scientific validation, determination of error rates, or reliability testing to explain the limits of the discipline."); PRESIDENT'S COUNCIL OF ADVISORS ON SCI. & TECH., FORENSIC SCIENCE IN CRIMINAL COURTS: ENSURING SCIENTIFIC VALIDITY OF FEATURE-COMPARISON METHODS 67–123 (2016) (assessing an array of forensic disciplines for scientific validity and reliability and concluding that many — including bitemark analysis, firearms analysis, footwear analysis, and hair analysis — lack foundational validity, while other forms of forensic evidence — including complex DNA mixture analysis and latent fingerprint analysis — are subject to greater error rates or limitations than typically acknowledged).

103. *See, e.g.*, Susan Walsh, *Forensic DNA Phenotyping*, LAW ENFORCEMENT USE OF PROBABILISTIC GENOTYPING, FORENSIC DNA PHENOTYPING, AND FORENSIC INVESTIGATIVE GENETIC GENEALOGY TECHNOLOGIES: A WORKSHOP (Mar. 14, 2024), https://www.nationalacademies.org/event/41774_03-2024_law-enforcement-use-of-probabilistic-genotyping-forensic-dna-phenotyping-and-forensic-investigative-genetic-genealogy-technologies-a-workshop-public-session [https://perma.cc/37FS-89AP] (discussing DNA phenotyping tools for law enforcement investigation and explaining that these tools should "NEVER" be used to "provide a single image based solely on DNA").

104. Meyer et al., *supra* note 20, at S13.

105. Xiaopu Zhou, Yu Chen, Fanny C. F. Ip, Yuanbing Jiang, Han Cao, Ge Lv et al., *Deep Learning-Based Polygenic Risk Analysis for Alzheimer's Disease Prediction*, 3 COMMC'NS MED., Apr. 6, 2023, at 2.

106. *Id.*

complicated for any human to comprehend, or (2) a function that is proprietary."[107] COMPAS is an example of the latter. PRS may well be both, given their technological complexity and the likelihood that PRS models will be developed using data sets or algorithms over which proprietary rights may be asserted. Although "[t]he consequences of these two types of black box are different," Rudin suggests they are also "related."[108]

As I have explained elsewhere, black box tools raise serious concerns for criminal justice.[109] Black box tools may be more difficult to subject to independent validation and verification, which may lead to lower quality algorithmic systems.[110] Moreover, the black box nature of an algorithmic tool may compromise a criminal defendant's ability to mount a successful constitutional or other challenge to the use of that tool.[111] As Maneka Sinha has put it, bluntly, where black box tools are at issue, "because how such technology works is not readily knowable, an accused person who was subjected to a police intrusion based on the output of [a black box] technology cannot check its work either."[112] While there may be methods that can help to render machine learning models "explainable," such methods may themselves be "problematic."[113]

IV. CONCLUSION

Are PRS fit for use in the criminal legal system? Not yet, and perhaps not ever. To be sure, PRS models are a significant methodological improvement over the earlier era of "candidate genes." Still, both foundational and methodological questions remain about whether PRS models for complex behavioral traits relevant to the criminal legal system can be developed in a way that is scientifically valid and reliable — and a reflection of causally-relevant behavioral genetic risk rather than environmental injustice. At present, PRS for complex behavioral traits

107. Cynthia Rudin, *Stop Explaining Black Box Machine Learning Models for High Stakes Decisions and Use Interpretable Models Instead*, 1 NATURE MACH. INTEL. 206, 206 (2019).

108. *Id.* at Supp. 1, app'x A.

109. *See* Ram, *supra* note 39, at 686–99 (describing "the harms of criminal justice secrecy"); *see also supra* Section II.B (noting that black box algorithms like COMPAS pose challenges for criminal justice).

110. *See* Ram, *supra* note 39, at 688.

111. *See id.* at 692–99 (arguing that black box tools can impair a defendant's rights to "vindicate their due process and confrontation rights at trial and their due process interests at sentencing" and observing that the black box nature of these tools may "also hamstring defendants and courts alike in their efforts to ensure that the government does not engage in unreasonable searches").

112. Sinha, *supra* note 18, at 601.

113. Rudin, *supra* note 107, at 206 (explaining that "explainable ML" models are "often not reliable, and can be misleading" and arguing that, at least for high stakes decisions including those in the criminal legal system, "inherently interpretable" are preferrable).

run many of the same risks for misuse that already occur in recidivism risk assessment, including bias, use beyond validated and intended applications, and reliance on "black box" technology. Existing experience with recidivism risk assessment tools should warn us off exacerbating these harms through the inclusion of additional algorithmic tools.