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Commentary

Essentialism and Exclusion: Racism in Cancer Risk Prediction Models

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COMMENTARY

Abstract

Cancer risk prediction models have the potential to revolutionize the science and practice of cancer prevention and control by identifying the likelihood that a patient will develop cancer at some point in the future, likely experience more benefit than harm from a given intervention, and survive their cancer for a certain number of years. The ability of risk prediction models to produce estimates that are valid and reliable for people from diverse socio-demographic backgrounds—and consequently their utility for broadening the reach of precision medicine to marginalized populations—depends on ensuring that the risk factors included in the model are represented as thoroughly and as accurately as possible. However, cancer risk prediction models created in the United States have a critical limitation, the origins of which stem from the country's earliest days: they either erroneously treat the social construct of race as an immutable biological factor (ie, they "essentialize" race), or they exclude from the model those socio-contextual factors that are associated with both race and health outcomes. Models that essentialize race and/or exclude socio-contextual factors sometimes incorporate "race corrections" that adjust a patient's risk estimate up or down based on their race. This commentary discusses the origins of race corrections, potential flaws with such corrections, and strategies for developing cohorts for developing risk prediction models that do not essentialize race or exclude key socio-contextual factors. Such models will help move the science of cancer prevention and control towards its goal of eliminating cancer disparities and achieving health equity.

Cancer risk prediction models are anticipated to play a key role in precision medicine for cancer prevention, detection, and treatment. However, almost all risk prediction models created in the United States have a critical limitation: they either ignore race or implicitly treat race as a biological factor when, in reality, it is a social construct created in the sixteenth century to justify enslaving Africans (1-3) and the genocide of indigenous peoples (4,5). It now reflects nationality, ethnicity, and/or physical characteristics (6). This means that any apparent effects of race on health outcomes are not shaped by biology but instead by long-standing systemic oppression and social inequities that reflect unequal access to power, prestige, resources, and opportunity (7). Ignoring these powerful social forces harms patients (8).

In this commentary, we describe how 2 ways of treating race in risk prediction models—including a "race correction" that adjusts risk estimates for Black patients and excluding the socio-contextual factors that shape health outcomes—harm Black people in the United States. We focus on Black people in the United States because most other marginalized populations are represented infrequently in risk prediction research.

Racial Essentialism

A recent report describes how some models and algorithms that predict a variety of health outcomes, including breast cancer risk, rectal cancer survival, in-hospital mortality from heart failure, pulmonary function, and kidney function, include a race correction that adjusts the predictive number up or down if the patient is identified as Black (either by a health-care provider or by the patient themselves) (6). However, adjustments are not typically based on empirical evidence of a biological or genetic pathway that places Black patients at higher or lower risk. Instead, some adjustments first originated from medical knowledge that was created during a time when science was used to promote racist beliefs about the biological characteristics of Black people (1). For example, in the mid-nineteenth century, Samuel Cartwright used spirometry to assert that enslaved Black people in America had approximately 20% lower pulmonary function than White people, and further, that this difference was attributable to innate biological differences rather than environmental and social conditions (3,9). He prescribed hard labor—such as that imposed by slavery—as a way of

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"vitalizing the blood" (2). Many modern spirometers automatically adjust the results shown to clinicians in a way that Black patients' "normal" lung function is 12%-15% lower than that for White patients (10). However, the standards do not account for the possibility that perhaps lower lung function among Black people is not normal but rather the consequence of being disproportionately exposed to factors known to affect lung health, such as toxic environmental exposures (11).

Race-based adjustments are not uncommon in cancer risk prediction models (12-14). Many adjustments are based on epidemiological observations of higher incidence of cancer among Black individuals (15). Although these adjustments allow models to produce estimates that reflect the incidence of disease in the US population, they are problematic because they implicitly essentialize and/or mischaracterize race in several ways. For example, they assume that race is a categorical factor with clear boundaries between "Black" and "White." However, we are aware of no risk prediction models that allow users to indicate biracial or multiracial ancestry, though biracial and multiracial people have existed in the United States for centuries. In addition, the race adjustment confers the same risk estimate for Black individuals regardless of their geographic origin (ie, people in the United States whose ancestors were enslaved; people who recently immigrated to the United States from Kenya; people who recently immigrated to the United States from Brazil). However, there is ample evidence that cancer screening and incidence varies widely among countries, immigrant status, and years spent in the United States (16-20). Such ecological data provide evidence against biological explanations of cancer incidence in favor of evidence for environmental explanations. Race-specific models, such as that described by Gail et al. (21), are intended to obviate the need for a race correction while accommodating the possibility that models developed for White people may not be valid for racially or ethnically marginalized populations. However, they may also inadvertently essentialize race as a biological construct if they do not include socio-contextual factors known to affect risk. For example, having lower socioeconomic position (SEP), experiencing racial discrimination, and being born in a state that had Jim Crow laws is associated with increased risk of developing breast cancer (22-24).

"Correcting" for race in cancer risk prediction models, and health prediction models in general, can result in Black patients being deemed ineligible for services that they would receive had the race "correction" not been applied to their risk estimate. For example, the "correction" to the estimated glomular filtration rate results in Black patients appearing to have better kidney function than would be indicated without the correction (6). This could result in delayed referrals to transplant or other specialist care. In the context of cancer risk prediction models, "correcting" for Black race can harm diagnostic accuracy (25) and result in lower risk estimates for breast cancer (6). In the age of risk-stratified screening (26), this could result in Black patients being ineligible for high-risk screening options based solely on their race—not on their cancer risk. Race corrections are also a concern in cancer mortality and survival prediction models. For instance, 1 rectal cancer prediction model predicts shorter cancer-specific survival for Black patients, which could limit their access to more aggressive therapeutics (6).

To fully address the race correction problem, additional research is needed to identify what other exposures explain disease incidence or mortality more accurately. Including a race adjustment to address problems with model fit or inequitable health-care access for Black individuals instead of seeking to understand why the model or policy does not provide equitable benefits stunts progress in reducing health disparities.

Exclusion

Another way in which using "race corrections" harms people is by mischaracterizing the cause of health disparities as an immutable person-level characteristic—"biological" race—instead of acknowledging that interconnected macro-level systems, institutions, processes, and social forces produce and reinforce racial disparities in health (ie, structural racism) (27). Researchers have known for many years that as a result of structural racism, Black people in the United States are disproportionately affected by socio-contextual factors that harm health, including having a lower social class and experiencing housing instability, racism, discrimination, and segregated neighborhoods. Residential segregation can be harmful because it often leads to economic disinvestment, increased exposure to environmental toxins, and less access to health-promoting resources (healthy food options, green space) than White neighborhoods at similar levels of income (28-31). These and other social determinants of health are associated with cancer risk; however, they are not included in cancer risk prediction models.

Excluding socio-contextual factors known to shape health outcomes not only poses a threat to the validity and reliability of risk prediction models, but it also has the potential to do social harm to Black people by seeming to attribute their poor health—which originates in socio-contextual injustices—to their biology or behavior. To address this concern, some researchers have recommended creating scores that summarize social risk factors and incorporating those into risk prediction models (32), but research to implement such recommendations is needed. This concern becomes particularly salient when considering the practical logistics of including socio-contextual factors in risk prediction models (eg, which of several dozens of socio-contextual factors to include, how to measure them, at what point in the lifespan they affect health).

Another key issue surrounding creating risk prediction models that apply to people from many racial and ethnic groups is that there are no datasets that have the data researchers need, in the large numbers of participants that would be needed, to be able to create and validate risk prediction models. For example, the Nurses' Health Study, which was used to create the Rosner-Colditz breast cancer risk prediction model (33), contains 1 216 701 women followed from 1976. The cohort is approximately 97% White, reflecting women entering nursing before that time. Multiple recent cohorts have expanded the racial and ethnic composition, but models still largely apply to White women. The Black Women's Health Study has developed a breast cancer risk prediction model for African American women, but the cohort (N = 55 879) is relatively new and does not apply to men (34). The Jackson Heart Study (N = 5301) is a community-based cohort from Jackson, Mississippi, that has validated cardiovascular risk models for Black people (35). Both these cohorts might serve as models for the development of future, nationally representative cohorts.

Call to Action

Research in other domains demonstrates that, if there is sufficient creativity, motivation, and institutional commitment and resources, many seemingly impossible tasks can be achieved.

For example, in 1990, a sum of 3 billion US dollars and 15 years of support were allocated to the Human Genome Project (36). It is reasonable to assume that, if governments and funding agencies made equally strong commitments to providing equivalent funding and resources to understanding and addressing social determinants of health, much progress could be made in alleviating health inequities. We challenge funding agencies to make this commitment.

We need more data to begin to address the current limitations of the use of race and social determinants in risk prediction models. As a result, we call on funders to support the development of cohorts that will enable us to understand how to incorporate socio-contextual factors in cancer risk prediction models. Some cohorts are already collecting variables such as area-level zip codes and individual-level psychosocial variables, such as experiences of discrimination and stress. However, to collect the highest-quality data and integrate it into health systems, transdisciplinary teams of researchers with specific expertise from a variety of areas, including social epidemiology and bioinformatics, are needed. Such efforts will be expensive but critically necessary to eliminate health inequities and ensure the health of the entire US population. Funding agencies should consider increasing the allowable funding per grant to achieve this; the maximum funding for several key US National Institutes of Health mechanisms have remained the same since at least the year 2003 (37): $100 000 in direct costs over 2 years for R03s, $275 000 over 2 years for R21s, and $2 500 000 over 5 years for R01s. Adjusted for inflation to the year 2021, these amount to approximately $69 000 in direct costs for R03s, $191 000 for R21s, and $1 700 000 for R01s (38). Clearly, additional funds must be allocated to retain the purchasing power of research dollars.

In our own work with the Your Disease Risk suite of risk assessment tools (39), we have been working to identify ways to better address socio-contextual factors. The process is long and unfinished, but in the last several years we have supplemented correction factors that allow estimates to be consistent with population-wide data with exposures that are disproportionately experienced by marginalized groups. For example, for our bladder cancer risk prediction model, we include occupational exposures and drinking well water; for lung cancer prediction, we include occupational exposures and air pollution. Other researchers might conduct similar investigations that ask whether adding socio-contextual variables to existing risk prediction models increases the validity of those models.

New or expanded cohorts that assess the social determinants of health should consider the following.

Socio-economic position (SEP) and risk. Following the example of the Black Women's Health Study and the Jackson Heart Study, cohorts should be geo-coded so they can be linked to area-level measures of SEP. They should also include individual-level SEP measures that extend beyond education, income, and occupation for Black people (31,40). Ample research has indicated that higher levels of education and income do not have the same health protective effect for Black people compared with White people (41), yet few current datasets include sufficient sample sizes of Black people, particularly at higher levels of SEP, and alternative measures of SEP to explore. Including childhood socio-economic status or measures of wealth at multiple levels would help researchers understand SEP and social mobility over the life course and identify more precise SEP measures that are associated with cancer risk.

Intersectional analyses. Cohorts should be diverse along a variety of factors (eg, racially, ethnically, socioeconomically, geographically, gender diversity) to allow for quantitative analyses that examine how the intersection of multiple social identities and processes affect cancer risk and other health outcomes (42,43). The health disparities literature is often siloed in terms of racial and ethnic disparities, socioeconomic disparities, and rural or urban disparities; this effectively ignores people living at the intersection of multiple socially disadvantaged identities. Moreover, siloed work often ignores some research that suggests that middle- to high-income Black people have wider obesity-related disparities than White people, a major cancer risk factor (44).

Until such cohorts are developed, we suggest that risk prediction model developers take the following actions.

Critically interrogate what is meant by the inclusion of race. If it is meant to represent a potential biological mechanism or serve as a proxy for a socio-environmental indicator, include a direct measure of the biological or socio-environmental factor instead. Where data are not available, describe the hypothesized relationship and purported mechanisms (7,45).

Consider adding contextual variables related to inequality. Most cohorts include zip codes of where people live, allowing the modelers to calculate residential segregation, a contextual variable that has been shown to be associated with multiple cancers, including breast cancer (46). Furthermore, innovative measures of structural racism have shown that high Black–White structural racism in a variety of domains, including job and employment status, political participation, educational attainment, and judicial treatment, are associated with higher odds of myocardial infarction for Black people but not White people (47). These measures could be useful contextual variables to consider in risk prediction with some additional research.

Link data sets to historical and contemporary environmental toxins. An example is brown fields that have been shown in some cases to lead to cancer "hot spots," which are also more likely to be located in neighborhoods with a higher proportion of people of color.

Additional Challenges and Considerations

We acknowledge that integrating social determinants of health into clinical care presents substantial challenges (48). To appropriately integrate social determinants of health and other nonclinical factors into clinical cancer risk prediction models, we need research, infrastructure, and funding to facilitate standardizing measurement of individual- and area-level variables across hospitals and integrating this data into electronic health records (49,50). Another important consideration is to balance the need to develop risk prediction models that are valid and also practically useful within the context of the health-care system. For example, a model that includes 100 variables might be more valid than a model with 20, but if the more comprehensive model is never used because it is too burdensome, it will not advance the health of individuals or populations (51).

We also clarify that, although the issues in this commentary were discussed in terms of Black individuals in the United States, they are also relevant to other marginalized racial and ethnic groups. For example, Latinos, American Indians, Alaska Natives, Native Hawaiians, and Pacific Islanders also experience the health effects of intergenerational trauma, racism, colonialism, and forced removal from their homelands. Future research should examine how to engage in risk prediction modeling research with these groups, despite the relatively small populations available, to ensure that advances in precision medicine

do not bypass these already marginalized and medically underserved groups. Ultimately, a substantial investment needs to be made for larger cohorts that include sufficient numbers of multiple racial and ethnic groups in order to gain a thorough understanding of cancer etiology, biology, and treatment and thereby reduce cancer disparities (52).

Many risk prediction models treat race in essentialist terms and exclude powerful socio-contextual forces that are related to race and health outcomes. Such mischaracterizations, even when inadvertent, have the potential to distract researchers and funders from prioritizing initiatives to understand and alleviate the socio-contextual root causes of health disparities. More importantly, however, such mischaracterizations increase the possibility that health-care providers, scientists, policy makers, and the public conclude that the increased risk of cancer and other health problems in Black people in the United States is due to something immutable and inherent in their biology rather than modifiable consequences of centuries of White supremacy ideology that purposefully seeks to create and maintain a racist caste system (53).

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Data Availability

No new data were generated or analyzed in support of this research.

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