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Principles and methods for transferring polygenic risk scores across global populations

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Competing interests

The authors declare no competing interests.

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Abstract

Polygenic risk scores (PRSs) summarize the genetic predisposition of a complex human trait or disease and may become a valuable tool for advancing precision medicine. However, PRSs that are developed in populations of predominantly European genetic ancestries can increase health disparities due to poor predictive performance in individuals of diverse and complex genetic ancestries. We describe genetic and modifiable risk factors that limit the transferability of PRSs across populations and review the strengths and weaknesses of existing PRS construction methods for diverse ancestries. Developing PRSs that benefit global populations in research and clinical settings provides an opportunity for innovation and is essential for health equity.

Introduction

Genome-wide association studies (GWAS) have discovered thousands of variants associated with complex human traits, illustrating the high polygenicity of many common diseases and emphasizing the potential of leveraging these findings for genetic prediction of health outcomes. Although each individual associated variant accounts for a small proportion of phenotypic variance, aggregating information across multiple variants into a single score creates a compendium of an individual's genetic predisposition for a given complex trait or disease. Calculated as a sum of alleles weighted by their estimated effect sizes, these cumulative genetic profiles are commonly referred to as polygenic risk scores (PRSs) when derived for a binary disease outcome or polygenic scores when calculated for a general trait.

PRSs have the potential to advance precision medicine by improving disease stratification and prioritization of high-risk individuals for appropriate interventions, enabling more accurate diagnoses and predicting therapeutic outcomes¹. Nearly two decades of GWAS have provided a rich foundation of discoveries to facilitate PRS construction². However, more than 85% of GWAS have been undertaken in individuals of European ancestries, and PRSs derived from these studies can be substantially less predictive for other genetic ancestries, potentially exacerbating health disparities^{3,4}. The growing recognition of this issue has spurred methodological innovations to integrate data from diverse populations, enabling more powerful analyses of existing studies, as well as the establishment of new biobanks, consortia and data collection initiatives of diverse populations⁵.

Here, we consider the principles and methods of applying PRSs across global populations, complementing existing reviews on PRS methodology and clinical utility^{1,6-10}. Specifically, we consider how genetic and non-genetic factors impact PRS performance, how new methods might improve their transferability across populations and implications for PRS clinical utility. We describe the technical challenges associated with the development of PRS predictive modelling within the context of social and environmental influences, and discuss the evaluation of model performance and clinical utility in populations of diverse ancestral backgrounds. These aspects are especially important given that many individuals have complex genetic ancestries shaped by recent admixture (Fig. 1). In addition to these challenges, we highlight emerging resources and opportunities for the development of new methods to enable more widespread and equitable translation of PRSs.

Genetic factors influencing PRS performance

PRSs have lower accuracy in cross-population prediction when the target sample is genetically distant from the discovery GWAS sample, regardless of the PRS construction method^{3,11-16} (Fig. 2a,b). This is akin to agricultural genetics, in which the accuracy of genomic prediction decreases as the genetic distance between the training and target populations increases¹⁷⁻²⁰. Several genetic factors can influence the genetic architecture of a complex trait and may limit the transferability of PRSs across populations, including differences in heritability, causal allele frequencies, allelic effect sizes and linkage disequilibrium (LD) patterns.

Heritability, the percentage of variation in a trait attributed to genetics, can differ across populations. Array heritability²¹, the proportion of phenotypic variation that can be captured by the additive effects of SNPs assayed and imputed from a GWAS array, limits the prediction accuracy of a PRS based on common genetic variation in a given population²²⁻²⁶. As heritability measures the relative contribution of genetic factors to total inter-individual trait variation in a specific population or context, differences in sociocultural factors, environmental exposures and measurement errors between populations that affect total phenotypic variance can alter heritability estimates and influence the accuracy of PRSs (discussed further below). It has been shown that even within a relatively homogeneous population, heritability – and thus the predictive accuracy of PRSs – can differ by major demographic variables such as age, sex and socioeconomic status^{27,28}.

The transferability of PRSs across populations might also be impacted by differences in the frequency of causal variants and their allelic effect sizes (Fig. 2c). These factors can vary due to demographic histories (such as mutations in historical migrant groups followed by genetic drift or population bottlenecks) or gene by environment interactions. Although existing studies have shown extensive genetic overlap across ancestries for a range of complex traits and diseases both at the variant level and the genome-wide level (via cross-population genetic correlation analyses), especially between European and East Asian populations²⁹⁻³², widespread allelic effect heterogeneity has also been observed^{33,34}. Even assuming identical allelic effects, population differences in allele frequencies can impact the amount of phenotypic variance explained by these variants, and thus PRS performance. As the vast majority of GWAS have been conducted in individuals of European ancestries, most existing PRSs have been constructed from variants that are common in European populations, which may have substantially lower frequencies in other populations. Moreover, causal variants in non-European ancestry populations may not be detectable in European ancestry GWAS due to low allele frequencies in European ancestries, and thus limited statistical power, further reducing the generalizability of PRSs.

The marked differences in LD patterns across populations can also impact PRS transferability. For example, the size of LD blocks is, on average, much smaller in African populations than in European or East Asian populations^{35,36}. As a result, many more variants are needed to capture the same level of genetic variation in African populations than in other populations. Many of the variants used in PRS construction are not causal but are merely in LD with causal variants, and many early genotyping arrays were designed based on European-enriched variants. Thus, differences in LD across populations can affect the transferability of PRSs derived from European GWAS (Fig. 2d). Taken together, the number of causal alleles and their allelic effect size distributions^{25,26} coupled with their frequencies and local LD patterns can have a complex impact on the performance of PRSs across populations. Furthermore, although most PRSs only capture additive genetic effects tagged by assayed or imputed variants, non-linear genetic effects including allelic heterogeneity, haplotype effects and gene by gene interactions can influence the genetic basis of a complex trait or disease³⁷ and further complicate the transferability of PRSs.

It is important to recognize that the analysis and comparison of genetic architecture of a trait or disease between populations depend on how the continuum of genetic ancestry is operationalized into discrete categories and population labels (Box 1). However, genetic diversity exists even within populations with a relatively high degree of genetic similarity or within geographically constrained regions³⁸. Genetic admixture presents further challenges to the characterization of genetic architecture and the development of PRS construction methods because the genomes of individuals are mosaics of their ancestors, and when individuals have different local genetic ancestries across the genome, the genetic effects can broadly vary from individual to individual.

Recent theoretical and empirical studies have attempted to separate the contributions of the different genetic factors discussed above to the transferability of PRSs across diverse populations. These studies support the view that allelic effects of causal variants are similar across ancestries, and the attenuation of PRS accuracies can be primarily attributed to

differences in allele frequencies and LD structure, although none of the factors can fully explain the power loss^{23,32,39,40}. In addition, improving PRS accuracy in African-ancestry populations can be especially challenging due to the existence of a much larger number of genetic variants in these groups⁴¹. Although these findings are promising to facilitate the dissection of cross-population genetic architecture and inform the development of PRS construction methods, our current understanding of the genetic basis of complex traits and common diseases is still hindered by small sample sizes for under-represented populations. A full accounting of the genetic architecture across the phenotypic spectrum and diverse ancestries, and its impact on the transferability of PRSs, requires continued expansion of non-European genomic resources and a comprehensive catalogue of global genetic and phenotypic variation.

Social and environmental factors influencing PRS performance

Many complex diseases arise from both genetic and environmental risk factors, which may together impact PRS performance across populations. Environmental factors include individual-level exposures (such as cigarette smoking, diet or physical activity), and macro-environmental factors (such as health policies or neighbourhood characteristics including degree of urbanization, green space, available facilities, environmental noise and air pollution, and so on). Risk factors and health outcomes may be shaped by the broader conditions in which populations live, work and age, referred to as social determinants of health (SDOH) (Fig. 3a). SDOH relate to an individual's place in society, including access to healthcare resources, and capture experiences of social exclusion, such as racism and discrimination. For disease-specific PRS development and evaluation, there is a need to create a conceptual framework that specifies relationships between PRSs, genetic ancestry and specific social and environmental risk factors.

SDOH encompass a wide array of factors, each of which may act differently in relation to PRSs, as an effect modifier, a confounder or a partial mediator of the observed PRS effects (Fig. 3b,c). To understand and account for the influence of SDOH, these factors must first be accurately measured and operationalized. For instance, if the contribution of important environmental risk factors is lower in the training versus testing populations, the proportion of variance in the trait explained by the PRS may appear lower in the target population. Using structured approaches such as directed acyclic graphs^{42,43} to clarify assumptions and inform appropriate analytic strategies, for example covariate adjustment for population structure⁴⁴, may help interpret differences in PRS accuracy. As an example, directed acyclic graphs can identify scenarios in which PRS effects may be partially mediated by genetically inferred ancestry, leading to a different interpretation of adjusted estimates of PRS performance compared with a case in which ancestry acts as a confounder^{45,46}. Furthermore, as PRS performance is context-dependent, identifying and characterizing gene–environment interactions may inform PRS implementation efforts by identifying groups of individuals who may experience a greater or smaller degree of risk stratification benefits from PRS. For example, previous studies have reported a synergistic interaction effect between PRSs and childhood trauma on depression, suggesting that individuals with both high PRSs and exposure to childhood trauma are particularly at risk for developing depression and could form a target group for interventions⁴⁷. However, efforts to replicate

this effect have led to mixed results⁴⁸, and evidence supporting robust PRSs by environment interactions in general has been limited to date⁷.

It is important to assess the potential impact of PRS implementation on health disparities and recognize that genetic factors do not capture the full understanding of an individual's health. The contribution of heritable factors can vary depending on how a disparity is quantified. In the United States, individuals identified as African American or Black, Hispanic or Latino and Native American are disproportionately affected by numerous conditions, such as hypertension⁴⁹, chronic kidney disease^{50,51} and certain cancers⁵²⁻⁵⁵, compared with those identified as white. Trends in the incidence of such conditions that are not easily attributed to diagnostic biases or differences in risk factor profiles may offer clues to a potential role of genetic factors. Disparities in mortality are largely driven by inequities in healthcare access, although for certain cancers, germ-line genetic factors have been shown to underlie differences in the prevalence of actionable tumour mutations between populations^{55,56}. In this context, race poses a unique confounding challenge because it is correlated with measures of SDOH and genetic ancestry, hence setting the stage for confounding of PRS associations when considering trait predictions.

If disease susceptibility varies across ancestral groups, the degree of admixture and the extent to which SDOH and other modifiable factors correlate with genetic ancestry will affect PRS performance. If differences in disease risk between two ancestral populations arise partly due to differences in the frequencies of risk alleles, we would expect to observe an enrichment of one ancestry in cases compared with controls at specific loci in the genome (Fig. 3d). Admixture mapping can be used to identify genetic loci that contribute to differences in disease risk, while controlling for global ancestral differences as well as confounding due to non-genetic factors that differ between populations, thus providing insights into the genetic causes of health disparities in recently admixed populations. To date, admixture mapping has refined important risk loci for prostate cancer⁵⁷, breast cancer⁵⁸, asthma⁵⁹, multiple sclerosis⁶⁰ and coronary heart disease⁶¹, which may complement PRS development efforts by uncovering ancestry-specific causal variants.

Methods to improve PRS transferability across populations

Recent shifts in GWAS towards increasing the diversity of populations included^{33,34,62,63}, in parallel with rapid advances in methods that leverage these more diverse studies as well as existing Eurocentric GWAS, aim to improve the transferability of PRSs across populations. These methods can be broadly grouped into approaches that combine or jointly model population-specific summary statistics (Table 1).

One approach combines GWAS from multiple ancestry groups using fixed-effect meta-analysis and constructs PRSs using the meta-GWAS and a single-population PRS method. This approach is widely used in many large-scale multi-ancestry GWAS and can improve the transferability of PRSs relative to population-specific PRSs^{34,62,63}. However, it can require potentially difficult parsing of mixed LD patterns in the meta-GWAS and makes strong assumptions of homogeneous allelic effects across ancestries, which may limit the accuracy of the resulting PRSs. Restricting the meta-analysis to variants that are

common across all populations will further limit PRS transferability. More flexible meta-analysis methods, such as ShaPRS⁶⁴ that incorporates heterogeneity of SNP effects across GWAS coupled with an appropriate LD reference panel for the derived summary statistics, might improve downstream PRS performance. Alternatively, another approach linearly combines PRSs constructed from each population-specific discovery GWAS using clumping and *P*-value thresholding (C + T)^{65,66}; this method improved risk prediction in recently admixed individuals⁶⁷. Subsequent work in combining PRSs across populations has replaced C + T with more sophisticated polygenic prediction methods to further improve prediction^{68,69}. However, this method cannot fully exploit cross-population models of genetic architecture that incorporate heritability, genetic correlation and polygenicity to inform PRS construction.

Another approach uses one large-scale GWAS – often conducted in European populations and termed the ‘auxiliary GWAS’ – to improve prediction in a target non-European population where there are smaller GWAS. This method leverages the observation that many causal signals are shared among populations²⁹ and cross-ancestry genetic correlations for human complex traits and diseases are often moderate to high^{30,31,70}. For example, XP-BLUP⁷¹ builds PRSs using a two-component linear mixed-effects model, with one component including variants that show associations in the auxiliary GWAS and the other component including all available variants in the target data set to capture the polygenic background. XPASS(+)⁷² uses a bivariate linear mixed-effects model with a multivariate normal prior to jointly model SNP effect sizes from the auxiliary and non-European GWAS. BridgePRS⁷³ fits a Bayesian ridge regression to the auxiliary GWAS and uses the posterior SNP effect size estimates as the prior when fitting a second Bayesian ridge regression to the GWAS in the target non-European population. TL-Multi⁷⁴ transfers the SNP weights estimated by Lassosum⁷⁵ in the auxiliary GWAS to the target population, with an assumption that effect sizes across populations are largely similar. SDPRX⁷⁶ models the auxiliary and non-European GWAS using a hierarchical non-parametric Bayesian model with a prior that characterizes the joint effect size distribution of each variant in the two populations to be null, population-specific or shared with correlation.

Recent work has also allowed for the modelling of GWAS summary statistics from more than two populations. For example, CT-SLEB⁴¹ expanded the C + T algorithm to the multi-ancestry setting for SNP selection, and uses an empirical Bayes algorithm for computationally efficient SNP effect size estimation. TL-PRS⁷⁷ fine-tunes effect sizes estimated from large-scale training GWAS to the target population using transfer learning and a gradient descent algorithm. PROSPER⁷⁸ uses a combination of LASSO (L1) and Ridge (L2) penalties to regularize SNP effect sizes, encouraging a sparse genetic architecture within populations and similar genetic effects across populations. ME-Bayes SL⁷⁹ performs Bayesian hierarchical modelling of SNP effect size distributions under a multivariate spike-and-slab prior and integrates information across different tuning parameter settings and ancestry groups using ensemble learning. Lastly, PRS-CSx⁶⁸ extended the single-population polygenic prediction method, PRS-CS⁸⁰, to jointly model GWAS summary statistics from an arbitrary number of populations, using Bayesian regression and a continuous shrinkage prior on SNP effect sizes that is coupled across populations.

Although these methods have different variant selection procedures or make different assumptions about the prior distribution of SNP effect sizes, they all aim to account for different degrees of polygenicity of the underlying SNP effect size distribution, integrate GWAS summary statistics from two or more populations in a principled statistical framework that accounts for allele frequency and LD differences, and leverage cross-ancestry genetic correlation to borrow information from well-powered European GWAS to improve PRS performance in non-European populations.

Other work has incorporated information beyond GWAS for the trait of interest into PRS construction algorithms. For example, XPXP⁸¹ extends XPASS to enable joint modelling of multiple genetically correlated traits in both auxiliary and target populations. X-Wing⁸² expands the modelling framework of PRS-CSx to allow for annotation-dependent priors and uses trans-ancestry local genetic correlation to up-weight variants whose effect sizes are more concordant across populations. PolyPred-S+/PolyPred-P+⁶⁹ uses functionally informed statistical fine-mapping to identify and prioritize functional variants, whose effects are often more portable than tagging variants due to assumed shared mechanisms of biology⁸³ and minimal impact of differential LD patterns across populations. The fine-mapping informed PRSs can then be combined with population-specific genome-wide PRSs to capture signals at polygenic loci that are difficult to fine-map.

Considerations of PRS methods for diverse populations

Although methodological developments can help improve PRS transferability, several limitations merit consideration. First, many of the methods require a validation data set with individual-level phenotypes and genotypes to tune an algorithm's hyper-parameters. Although this can maximize the accuracy of PRSs for specific populations, it also increases the risk of overfitting. In addition, there may not exist a sufficiently large independent validation data set in the target non-European population, especially when the hyper-parameter space is large. Fully Bayesian models⁸⁴, pseudo-validation methods^{74,75} and repeated learning techniques^{82,85} that can automatically learn model parameters from summary-level data may facilitate cross-population PRS development.

Second, many methods require categorizing individuals into a genetic ancestry group before a PRS can be optimized and applied (Box 1). However, this poses challenges when implementing the PRS in clinical settings, where admixed individuals can be difficult to assign to a discrete population cluster, and genetically inferred ancestry can differ from self-reported race or ethnicity.

A third consideration is that existing methods need to balance trade-offs between prediction accuracy and computational complexity. For example, the infinitesimal model, which assumes that prior SNP effect sizes are independent and normally distributed, has a closed-form posterior distribution and is highly scalable^{41,72,73,81}. However, this approach shrinks the effects of all variants towards zero at the same constant rate, and is thus less adaptive to varying genetic architectures. More sophisticated Bayesian methods assume that the prior distribution is a mixture of two or more normals^{76,86,87}, which allows for flexible modelling of the genetic architecture but makes model fitting challenging and

potentially unstable. Continuous shrinkage priors^{68,80} can balance modelling flexibility and computational efficiency, but full posterior inference remains infeasible to scale to all common variants across the genome. As a result, most Bayesian methods use HapMap3 variants to construct PRSs. Although they might have provided a good balance between computational cost and genetic variation captured within European populations, HapMap3 variants do not tag genetic variation in non-European populations equally well and can miss population-specific signals. This coupled with unequal imputation accuracy across populations can limit the transferability of PRSs.

Fourth, although it has been shown that the polygenic background can modify the penetrance of monogenic variants^{88,89}, studies and methods that explore the integration of genome-wide rare and common variants for prediction are limited⁹⁰⁻⁹³. The prediction accuracy of rare and low-frequency variants across populations has not been systematically assessed, although a recent study suggests that rare coding variants will likely contribute only modestly to population risk stratification⁹⁴. Whether rare variants provide value for the prediction of complex traits depends on the number of rare causal variants and their effect sizes, which will likely be trait-specific. Although the contribution of rare high-penetrance variants to overall trait variation may be small relative to common-variant PRSs, they can be valuable to identify high-risk individuals.

Finally, the methods described above primarily use GWAS summary statistics from relatively homogeneous populations as input and only model allele frequency and LD differences at the continental level. Much work remains to develop best practices to integrate GWAS from admixed or under-represented populations (such as the PAGE study³³) with large genomic diversity and heterogeneous LD patterns. As noted above, mismatch between the LD structure of the GWAS discovery sample and the reference panel is likely an important contributing factor to the loss in PRS prediction accuracy. Moreover, when the target sample is admixed, most methods weight population-specific PRSs globally without modelling local ancestry and individual-level proportions of admixture. Initial attempts to infer local ancestry tracts, estimate local ancestry-specific effect sizes⁹⁵ and build local ancestry-aware PRSs^{40,96} have shown increased power for loci discovery and improved prediction accuracy in admixed populations. A recently developed method, GAUDI⁹⁷, explicitly models local ancestry using a fused LASSO framework that encourages similar effects across ancestries but allows for population-specific effects. These methods, however, have only been evaluated in two-way recently admixed populations, and the predictive performance of PRSs has not been fully benchmarked against other cross-ancestry polygenic prediction methods.

Benchmarking PRS methods may require a reference-standardized set-up⁹⁸, whereby a common set of variants and individuals are used to build reference panels and assess the accuracy of PRSs. However, the optimal prediction method might depend on a range of factors including the genetic architecture, the diversity and sample size of the discovery GWAS, and the ancestry composition of the target sample⁹⁹. For example, clumping and fine-mapping based methods may work well for traits that have a handful of large-effect causal variants but not as well when predicting highly polygenic traits. In contrast, genome-wide PRS approaches may capture signals that do not reach statistical significance,

but they may also include a large number of non-informative variants when the genetic architecture is sparse and the power of GWAS is limited. Future methodological efforts that focus on integrating multiple data modalities (such as variants across the allele frequency spectrum, functional annotations and cross-ancestry fine-mapping results^{100,101}) from diverse resources and better local and global ancestry modelling in a computationally efficient and robust framework, coupled with increasing size of non-European genomic resources, hold promise to improve the accuracy and generalizability of PRSs.

Evaluation of PRS clinical utility

Demonstrating the clinical utility of PRSs across diverse populations requires careful consideration of suitable performance metrics, which depend on the intended use of the PRS in a specific clinical context. The area under the receiver operating characteristic curve (AUC) for binary health outcomes and the C-index, an analogous measure of concordance for time to event outcomes¹⁰², are widely used to report discriminatory abilities of PRSs. The AUC can take values between 0.5 and 1.0, ranging from completely random, clinically useless predictions to perfect classification. In practice, the AUC of a PRS has an upper bound based on disease heritability and is thus always less than 1. For many common complex diseases, such as breast cancer¹⁰³⁻¹⁰⁶, coronary heart disease^{107,108} and type 2 diabetes mellitus^{84,107}, the best-performing PRS has achieved AUC values in the range of 0.6–0.7 across different populations, demonstrating moderate discriminatory abilities. However, the AUC and related measures do not account for disease rates in the underlying population, and therefore cannot be translated directly into the predictive value of PRSs at the individual level and provide little insight regarding clinical utility¹⁰⁹.

Many studies use rank-based risk classifications to identify high-risk individuals and report, for example, an odds ratio that compares individuals in the top decile of the PRS distribution with those around the median. These measures, however, depend on the reference population for the PRS distribution. Metrics of PRS utility are also affected by operationalization of the PRS. For instance, when a PRS cut-off is used for classifying individuals as high risk, it is important to select an optimal threshold that maximizes discrimination. This requires calibration of the PRS distributions across populations, which can have different mean values and spread (Fig. 4). Existing studies express polygenic risk on the same scale across ancestrally diverse individuals by removing gross cross-population differences in the mean and variance of the PRS distribution that can be captured by genetic principal components^{84,110-112}; however, these methods could remove real risk differences explainable by genetic and non-genetic risk factors that are correlated with population structure, reducing the predictive power of PRSs.

In general, relative risk estimates (such as those based on the odds ratio) do not provide information that can be readily translated to risk thresholds for clinical action, such as diagnostic and treatment decisions. Instead, these typically require estimates on the absolute risk scale. Positive and negative predictive values, which represent the proportions of individuals who test positive (or negative) who will (or will not) have the disease, respectively, give absolute risk estimates and are more clinically relevant metrics. For diseases that have clinical guidelines based on absolute risk thresholds (for example, breast

cancer and coronary heart disease), absolute risk models with and without the PRS can be compared to quantify the expected increase in individuals who now meet this threshold. Additionally, we can examine the increase in disease cases detected among the high-risk individuals identified using the PRS^{108,113}. Measures of net reclassification indices¹¹⁴ – which summarize the net number of cases and controls who move into higher and lower risk categories, respectively, according to a new model compared with an existing model – can be used to evaluate the added value of PRSs in relation to existing clinical risk factors¹¹⁵. However, net reclassification indices, similar to the AUC, do not take into account disease rates in the underlying population and do not directly quantify clinical utility. In addition, caution is needed for inappropriate use of such measures in the absence of predefined risk categories¹¹⁶. When specific risk thresholds are not available, one can also carry out decision curve analysis¹¹⁷ to evaluate the net benefit associated with decision-making at different absolute risk thresholds under alternative models¹¹⁸. An important consideration, when evaluating the added value of PRSs in diverse populations, is whether existing risk-threshold guidelines themselves are universally suitable across groups that may have different loss–benefit balances for underlying decisions.

For diseases that do not have established absolute risk models, absolute risk can be estimated by combining overall or relative risk estimates with disease incidence rates observed internally in cohort studies or approximated by external information on population incidence rates^{119,120}. Studies evaluating absolute risk have shown that PRSs for some common diseases, even with their modest discriminatory performance, can now identify a substantial fraction of the population who would be considered as high risk to warrant drug therapy, or invasive and potentially costly interventions not appropriate for the general population¹⁰⁸. However, as rates of many diseases as well as SDOH are typically estimated with stratification by self-identified race or ethnicity, and are known to vary widely by racial groups, it is particularly important to incorporate absolute risk considerations when the utility of PRSs is being evaluated across diverse populations. Future research is merited to explore the ability of genetic ancestry to explain known variations in disease incidence rates across population groups¹²¹. Furthermore, as the severity, prognosis and financial burdens of diseases can vary widely by socioeconomic status, it will be important to demonstrate the utility of PRSs considering the risk of different types of adverse outcomes.

Another dimension of PRS performance that is not commonly assessed is the uncertainty in relative and absolute risks derived from the PRS and the stability of PRS-based risk classifications across different PRS modelling approaches and choice of LD reference panels. Recent work has demonstrated substantial variability in individual-specific PRS estimates for 13 complex traits¹²². As an example, for high-density lipoprotein (HDL) PRSs, the 95% credible interval for an individual at the 90th PRS percentile spans widely between the 41st and 99th percentiles. There are multiple sources of uncertainty in PRSs, including error in estimates of SNP weights, and this is likely to be higher for non-European ancestry populations because of the smaller sample sizes used to create PRSs. Quantifying the impact of this uncertainty on clinical decisions will be important for PRS implementation across diverse populations.

The appropriate choice of clinical utility metrics must also be considered in the development stage of PRSs in diverse ancestry settings. Current multi-ancestry methods allow the development of improved population-specific PRSs by borrowing data across diverse multi-ancestry populations. Although these approaches have the advantage of being able to generate the best possible PRS for a given ancestry group using all existing data, in a country such as the United States where there are many diverse groups, and many admixed sub-groups, delivery of optimized PRSs for each distinct group is not practical. Additionally, optimizing PRSs for each ancestry group separately might still exacerbate inequity in their performance across groups because of differences in sample sizes and genetic architecture of traits across groups. Therefore, an alternative goal may be to develop more universal PRSs that can be applied across populations by using suitable loss functions that take into account fairness constraints so that prediction performance is not driven by a majority group. Although there is an emerging body of literature in machine learning theory to incorporate different types of fairness constraints¹²³⁻¹²⁶, considerations of such a framework are currently lacking in PRS development. An additional challenge relates to defining what fairness means in the context of PRSs and prioritizing trade-offs, as simultaneously satisfying all constraints may not be feasible¹²⁷.

Remaining challenges and future directions

As we strive towards creating and improving PRSs across diverse populations, several challenges lie ahead. First, in the shift away from the use of race and ethnicity in biomedical research and clinical practice, genetic ancestry is often put forth as a suitable replacement¹²⁸. Although this has numerous advantages, the use of discrete population categories, including groups derived from genetic ancestry or genetic similarity, is also problematic¹²⁹. Global ancestry cut-offs used to create more homogeneous groups are often arbitrary, study-specific and primarily driven by considerations of statistical power. Sensitivity analyses at different ancestry thresholds are typically not performed or reported. The most fundamental consideration for PRS accuracy is the genetic distance between the PRS training population, such as the source GWAS sample, and the target population where the PRS is intended to be applied¹⁵. Gauging expected PRS performance using genetic distance does not require forming discrete population clusters, and the development of robust PRSs in the future will benefit from this approach.

Although race, a socially defined construct, is not an acceptable proxy for genetic ancestry or patterns of admixture, it remains extensively used in administrative databases, disease surveillance systems and healthcare records in the United States, and thus has been used in the design and analysis of GWAS. Participants are sampled or enrolled based on race and/or ethnicity rather than genetic ancestry, which can induce systematic differences in ascertainment, phenotyping and measurement of potential confounders or effect modifiers, especially for SDOH. In some GWAS, samples have been genotyped using different arrays depending on participants' race (self-reported or assigned by healthcare providers), which has implications for imputation quality and downstream analyses¹³⁰. Ignoring race/ethnicity, especially when it is a study design feature, can bias estimates of PRS accuracy when considering continuous measures of genetic diversity. Differences in study design are a major source of heterogeneity in GWAS meta-analyses, and this heterogeneity

can disproportionately affect studies conducted in admixed and non-European ancestry populations. Together with the smaller GWAS sample sizes in these populations, this may further reduce the signal-to-noise ratio in data used to construct PRSs and limit PRS transferability and generalizability.

Another challenge in transitioning to continuous genetic ancestry relates to operationalizing analyses that require additional inputs, such as incidence or mortality rates. This issue applies not only to integration of PRSs with population-level health indicators but also to more basic analyses, such as converting heritability estimates from the observed to the liability scale using lifetime risks¹³¹. Although tracking disease morbidity and mortality by race or ethnicity is suboptimal, these metrics are not collected alongside genetic ancestry, and outside the United States, surveillance systems such as disease registries are often agnostic to any metrics of race, ethnicity or ancestry. In developing countries and low-resource settings, surveillance systems may be extremely limited, leading to sparse or non-existent data on disease burden and non-genetic risk factors. Further, as observed variations in disease incidence, outcomes and mortality rates by race, ethnicity and other categorical descriptors (such as immigration status) could be due to life experiences and environmental exposures unrelated to genetics, removing such proxy information prematurely can hinder contextualizing clinical utility of PRSs in the absolute risk scale.

This leads to a broader but related challenge for PRS translation. Once a PRS demonstrating acceptable within-population and cross-population predictive performance has been developed, an appropriate statistical framework for integrating the PRS with other clinical predictors and established risk assessment tools must be established. For conditions with existing risk calculators, the simplest approach is to multiply risk estimates generated by the PRS and the clinical model. However, this assumes that PRSs are independent of other predictors, which may not be valid for all health outcomes, especially if the PRS captures indirect genetic effects partly mediated by clinical or modifiable risk factors. Furthermore, most existing models were not developed and validated in ancestrally diverse populations. For instance, pooled cohort equations, QRISK and Framingham scores for atherosclerotic cardiovascular disease have shown worse performance in African Americans, African Caribbeans and South Asians based on studies in the United States and the United Kingdom^{132,133}. Lung cancer screening criteria from the US Preventive Services Task Force have been shown to significantly underestimate screening eligibility in African Americans compared with white Americans¹³⁴. This disparity was attenuated, but not eliminated, with the PLCOm2012 model¹³⁵. Therefore, even if PRS-based risk estimates are well calibrated, the accuracy of the overall risk prediction model may suffer due to poor performance of the non-genetic components.

Simultaneously combining data on all relevant risk factors, including family history^{136,137} and relevant pre-existing conditions, into a framework that returns a single estimate of absolute risk would accelerate the uptake of PRSs into clinical practice. Currently, few such models exist, and they have been validated only in individuals of European ancestries¹³⁸. For instance, the BOADICEA model for breast and ovarian cancer has successfully integrated modifiable risk factors with rare, high-penetrance mutations and PRSs^{139,140}. A PRS for coronary heart disease was shown to be largely uncorrelated with pooled cohort equations

and QRISK, suggesting that incorporating PRSs may further improve these models if they are transferable across ancestries¹⁴¹. Given the population differences in performance that exist for both genetic and non-genetic predictors, developing reliable risk prediction tools will likely require fitting and validating new ancestry-aware models that incorporate joint effects of PRSs and other risk factors. To achieve this, large cohorts would be needed to measure the calibration of the joint model. The All of US Research Program¹⁴² is one such promising cohort. In addition, multiple medical centres have created their own biobanks. Forming a network of these types of cohorts would provide additional avenues to evaluate whether the developed models offer accurate predictions in terms of calibration.

Generating new data in under-represented populations will undoubtedly have the largest impact on precision medicine efforts by providing the information necessary to develop effective, evidence-based tools, including PRSs. For instance, African populations have the greatest genetic diversity, the largest number of population-specific alleles and the smallest LD blocks, providing a wealth of information to enable globally relevant genetic discoveries^{143,144}. However, until systems are in place to support large-scale collection of genetic, clinical and epidemiologic data in Africa and globally¹⁴⁴, and until such data collection efforts mature, utilizing existing resources remains important. Furthermore, the success of new data collection efforts will require a commitment to transparency and community engagement in order to build trust with populations who have been historically under-represented and exploited in biomedical research. To improve participation and ensure ethical translation of genetic discoveries, concerns regarding potential for misinterpretation, stigma and discrimination, conflicts of interest, data sovereignty and premature commercialization of PRSs must be understood and addressed^{145,146}.

Data aggregation and pooling efforts are crucial for advancing genetic research in under-represented populations, and must be supported by the development of best practices for phenotyping and data harmonization. Use of external controls may be an effective way of leveraging limited resources, particularly for studies of rare conditions using whole-genome sequencing; however, matching closely on genetic ancestry is critical for avoiding bias and this may be more challenging for admixed populations¹⁴⁷. Imputation with more diverse reference panels, such as TOPMed¹⁴⁸, will improve the utility of existing genetic data, but this will not fully compensate for the bias in genotyping arrays that were optimized for European LD structure towards alleles that segregate at intermediate frequencies in non-African populations¹⁴⁹⁻¹⁵². Until whole-genome sequencing data are more widely available, choice of genotyping arrays and imputation panels will continue to limit PRS transferability and accuracy, especially for highly polymorphic and complex regions, such as HLA^{152,153}.

Understanding the primary drivers of health disparities is critical for contextualizing PRS performance and informing appropriate public health interventions. In addition to comprehensively measuring different dimensions of SDOH, methods are needed to account for complex confounding structures and population stratification that may arise. Detailed information on social constructs, environmental exposures and behavioural factors is often absent from genomic studies, and these variables are less amenable to pooling across studies due to differences in data collection and exposure assessment. Careful consideration of

non-genetic risk factors is important both for PRS evaluation and for covariate adjustment in GWAS used to generate summary statistics for PRS development⁴⁴. Some variables or underlying constructs may only be applicable to specific countries or communities. For instance, although race or ethnicity is an imperfect surrogate for the effects of discrimination and access to health care, for studies conducted in the United States it might be the only available measure of these constructs¹⁵⁴. Methods are thus needed for reconciling risk information captured by genetic ancestry and other population descriptors, and PRS evaluations will continue to need to account for disparities that cannot be explained by genetic ancestry alone. Although GWAS have historically prioritized achieving large sample sizes by including the minimal set of covariates available across the largest number of individuals or studies, smaller studies with deep phenotyping and more comprehensive risk factor assessment will be equally important for PRS development.

Conclusions

Although progress has been made towards the improvement of PRS prediction accuracy in non-European populations, substantial efforts are needed to improve PRS transferability, integrate PRSs into routine health care and equitably deliver PRS to global populations. In addition to further narrowing the gap in the prediction and stratification capabilities of PRSs between European and non-European populations, novel statistical and computational methods are needed to construct, validate and optimize PRSs that can be applied to any individual along the continuum of genetic ancestry. Admixture-aware and clinically informative metrics are also needed to assess the accuracy, calibration, uncertainty and stability of PRS prediction in ancestrally diverse samples. These methodological development efforts must be coupled with data generation initiatives to diversify samples in genomic research as well as to collect and harmonize measures for SDOH across studies. Release of ancestry-specific GWAS summary statistics¹⁵⁵ in addition to multi-ancestry meta-analysis results is critical to the characterization of the comparative genetic architectures between populations and will facilitate the development of more flexible and accurate PRS construction methods (as shown in Table 1). A comprehensive catalogue of genetic, phenotypic, environmental and behavioural variation in diverse populations will not only inform and facilitate the development of more accurate and generalizable PRSs but also help disentangle the genetic and non-genetic contributions to disease burden and health disparities between populations, and characterize the relationships between PRSs and social and environmental factors.

Finally, future work is critically needed to contextualize PRS performance in real-world healthcare settings, and to develop integrative clinical models that combine PRSs with established risk factors into reliable and unbiased absolute risk assessment tools for patients of diverse ancestral and sociocultural backgrounds. Importantly, all PRS development, evaluation and implementation efforts should adhere to the latest reporting standards¹⁵⁶ and promote data sharing and transparency to facilitate reproducibility, replication and benchmarking¹⁵⁷.

Encouragingly, the field is rapidly advancing on all fronts, including method development, data generation and clinical implementation. For example, the National Institutes of Health

(NIH)-funded Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium (<https://primedconsortium.org>) is developing methods and pooling genomic and phenotypic information to improve the use of PRSs for disease prediction in diverse populations. The growth of global biobanks and national health registries⁵ has substantially expanded sample diversity, accelerated genomic discovery and already informed PRS construction, evaluation and interpretation¹⁵⁸. The emerging data sets from medical systems linked to electronic health records and a range of physical measurements and questionnaires on lifestyle, family history, socioeconomic factors and environment, such as the All of Us Research Program¹⁴² (<https://allofus.nih.gov>), the BioMe Biobank, the Mayo Clinic Biobank, the Vanderbilt's BioVU resource, the Mass General Brigham Biobank and the UCLA Precision Health Biobank, will substantially expand data from groups that are historically under-represented in biomedical research and provide unprecedented opportunities to contextualize PRSs of specific diseases in real-world clinical settings. The NIH-initiated Electronic Medical Records and Genomics (eMERGE) IV study (<https://emerge-network.org>) has pioneered the return and communication of PRS results along with monogenic risks, family history and clinical risk assessments via a genome-informed risk assessment report to participants and their healthcare providers across ten conditions^{159,160}, and will assess the uptake of care recommendations after the return of results. By combining new PRS construction methods, evaluation metrics, data resources and clinical implementation efforts that focus on diverse populations, the PRS may be well suited to realize its potential to advance precision medicine that benefits global populations.

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Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium

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Glossary

Absolute risk

The probability that a person or group of individuals who are free of a certain disease at a given point in time will develop that disease over a certain time period. Absolute risks are typically expressed as proportions from 0 to 100%.

Admixture

The process by which two or more previously separated populations come into contact, often through migration, generating a descendant population with a mixed mosaic of genetic material.

Admixture mapping

An approach that consists of inferring local genetic ancestry and testing for association between local ancestry segments derived from different ancestral populations and the phenotype.

Area under the receiver operating characteristic curve

(AUC). The ability of a model to discriminate between diseased and disease-free individuals is calculated as the AUC, which compares the true positive rate (sensitivity) with the false positive rate (1 – specificity). An AUC of 0.50 indicates that the classification accuracy of a model is equal to chance; an AUC of 1.0 indicates perfect discrimination.

Clumping

A procedure that iteratively selects the variant with the lowest *P*-value within a specified window from genome-wide association study (GWAS) results and removes nearby variants that are correlated with the selected variants above a specific linkage disequilibrium (LD) threshold.

Genetic architecture

The genetic basis of a trait described by the number, frequency and magnitude of effect size of genetic variants contributing to its heritability.

Genetic correlation

The correlation between the genetic influences on two traits, or the proportion of variance that two traits share due to genetics.

Haplotype

A cluster of polymorphisms or alleles that typically reside near each other on a chromosome and tend to be inherited together.

Linkage disequilibrium

(LD). Non-random association of alleles at different genetic loci, often measured as the square of the correlation coefficient between two alleles. LD is, on average, lower in African populations compared with European and Asian populations.

Meta-analysis

Statistical analysis that combines results from multiple studies.

Net reclassification indices

Metrics that measure the extent to which a new model improves classification as compared with an old model, calculated as the difference between the proportion of individuals who are correctly reclassified and the proportion of individuals who are incorrectly reclassified.

P-value thresholding

A procedure that selects the genetic variants whose *P*-value is below a threshold in a genome-wide association study (GWAS).

Polygenic risk scores

(PRSs; also known as genetic risk scores). Single values that quantify an individual's genetic predisposition to a discrete health outcome, calculated as a sum of alleles weighted by effect sizes corresponding to a relative magnitude of association.

Polygenic scores

Single values that quantify an individual's genetic predisposition calculated as a sum of trait-associated alleles weighted by their additive, per-allele effect sizes, typically derived from genome-wide association studies (GWAS).

Population structure

The presence of multiple genetically distinct subpopulations that differ in their allele frequencies and mean phenotypic values. Not accounting for this structure can lead to spurious associations in genome-wide association studies (GWAS) and polygenic risk score (PRS) analyses.

Relative risk

The probability that a certain health outcome will occur in a person or group of individuals relative to the probability that this event will occur in a reference population. Relative risks are typically expressed as ratios, with 1.0 indicating no difference between the comparison groups.

Risk stratification

The process of classifying and ordering individuals according to their specific risk estimates.

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Box 1**Population descriptors and concepts**

Historically, most genetic association studies have involved assigning participants to discrete clusters to facilitate statistical analyses. Variability in criteria for defining such clusters and inconsistent use of labels for the resulting populations not only creates challenges for analysis and interpretation but might also contribute to harmful misuse of findings from genome-wide association studies (GWAS) and polygenic risk scores (PRSs). Here, we provide a brief overview of common population descriptors and discuss distinct, but related, concepts of ancestry¹⁶¹ that are relevant for genetic association studies.

Race, ethnicity and ancestry

Both race and ethnicity have a history of being used as a misleading shorthand for groups of individuals with shared genetic ancestry. Race is a socially constructed system for classifying humans based on erroneous beliefs about innate biological differences, often proxied by physical features (such as skin colour) and sociocultural characteristics. Ethnicity is a sociopolitical identity that is assumed by or assigned to a group of individuals, typically in a contiguous geographic area, based on shared heritage and cultural similarities, such as language, religion or beliefs. Individuals of the same ethnicity often share genetic or genealogical heritage, but as this system varies globally, in certain regions ethnicity may be primarily a sociocultural identity. Ancestry is a complex and context-dependent term that encompasses both the biological and social components of an individual's or population's descent. In the western world, it has an aspect of both sociocultural and continental origin, whereas in the eastern and southern hemispheres there is an aspect of either shared genealogical or genetic heritage, or both, on a smaller regional scale. Race and/or ethnicity should not be conflated with ancestry or used as synonyms for population genetic differences.

Different types of ancestry

Unlike race or ethnicity, which are subjective constructs, genetic ancestry is a fixed characteristic of the genome. Genealogical ancestry describes an individual's lineage based on family trees of known ancestors that have been traced back over multiple generations. Genealogical ancestry is inferred using oral and written historical records, and, more recently, genetic information. Genetic ancestry refers to segments of an individual's genome that have been inherited through a subset of realized paths from their ancestors, and unlike genealogical ancestry does not require reconstructing a family pedigree. The complete record of coalescent and recombination events (that is, the convergence of two lineages into a single population and the process of shuffling of alleles on the chromosome to produce novel combinations of alleles, respectively) in the history of an individual's genetic lineage is called an ancestral recombination graph, which is the fundamental representation of genetic ancestry. Genetic similarity is a quantitative measure of genetic sharing between individuals or populations. Most studies that develop and evaluate PRSs approximate genetic ancestry from measures of genetic similarity, typically with respect to reference ancestral populations. We note that these

types of ancestry are rarely distinguished in the literature and the research community frequently uses genetic ancestry as a catch-all term for all dimensions of ancestry. Throughout our review of PRS methods we refer to genetically inferred ancestry, unless otherwise specified. When describing findings from the literature, we use the same terminology, including population labels, as the original publication(s).

Measuring genetic ancestry

Coalescent models provide a statistical framework for reconstructing evolutionary history to determine how alleles sampled from a group of individuals link to a common ancestor. Quantitative models for ancestry inference incorporate patterns of linkage disequilibrium (LD) and allele frequencies, which are also fundamental features for describing the genetic architecture of complex traits. Global (genome-wide) genetic ancestry is the proportion of contributions of different assumed proxy ancestral populations to an individual or a group of individuals' overall genetic make-up. Global ancestry can be inferred using both model-based¹⁶² and data-driven methods^{163,164}. Local ancestry is the genetic ancestry of an individual at a particular location in a chromosomal segment. Local ancestry can be inferred by computational approaches, often using discriminative modelling¹⁶⁵ or generative hidden Markov models¹⁶⁶ with modifications to improve on efficiency, accuracy and the number of ancestral populations considered¹⁶⁷⁻¹⁶⁹.

Admixture

Populations from which an individual or group of individuals have inherited their genome are referred to as ancestral populations. Admixture is the process that brings together individuals from two or more ancestral populations that were previously isolated for a period of evolutionary time, allowing distinct haplotypes to be combined in a gene pool. Although admixture is a pervasive phenomenon, the term 'admixed' typically refers to individuals with recent admixture (<100 generations). For much of human history, admixture has occurred through mass migration, colonization or forced displacement. However, in today's increasingly globalized and interconnected society, novel patterns of recent admixture are emerging and shaping the ancestry of modern human populations (Fig. 1). Genetic ancestry in admixed populations varies between individuals and along haplotypes. The proportion of populations contributing to an individual's genome can be represented on global and local levels that both attempt to determine the ancestral origin of polymorphisms or chromosomal segments in the admixed individual.

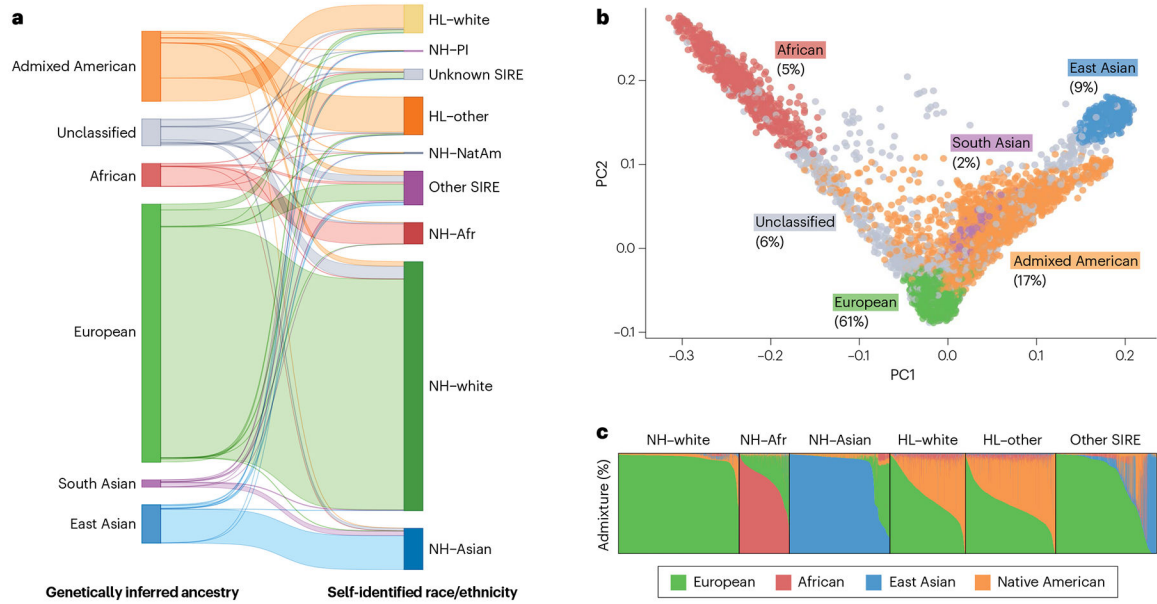


Fig. 1 | Complex genetic ancestries and admixture using data from UCLA-ATLAS.

a, Comparison between genetically inferred ancestry and self-identified race and ethnicity (SIRE): Hispanic/Latino (HL), non-Hispanic/Latino (NH), Pacific Islander (PI), Native American (NatAm) and African/African American (Afr). Genetically inferred ancestry labels are assigned based on proximity to 1000 Genomes reference populations in principal component (PC) space using the *k*-nearest neighbour algorithm. SIRE is a composite label based on separate entries in the ‘Race’ and ‘Ethnicity’ fields extracted from medical records. **b**, First two PCs of the genetic data. Each dot represents an individual, with colours corresponding to their assigned genetically inferred ancestry cluster. A non-trivial percentage of individuals could not be categorized into a ‘homogeneous’ or ‘continental’ population. **c**, Unsupervised clustering of the genetic data. Each column represents the proportion of the global genetic ancestry of an individual with respect to 1000 Genomes reference populations.

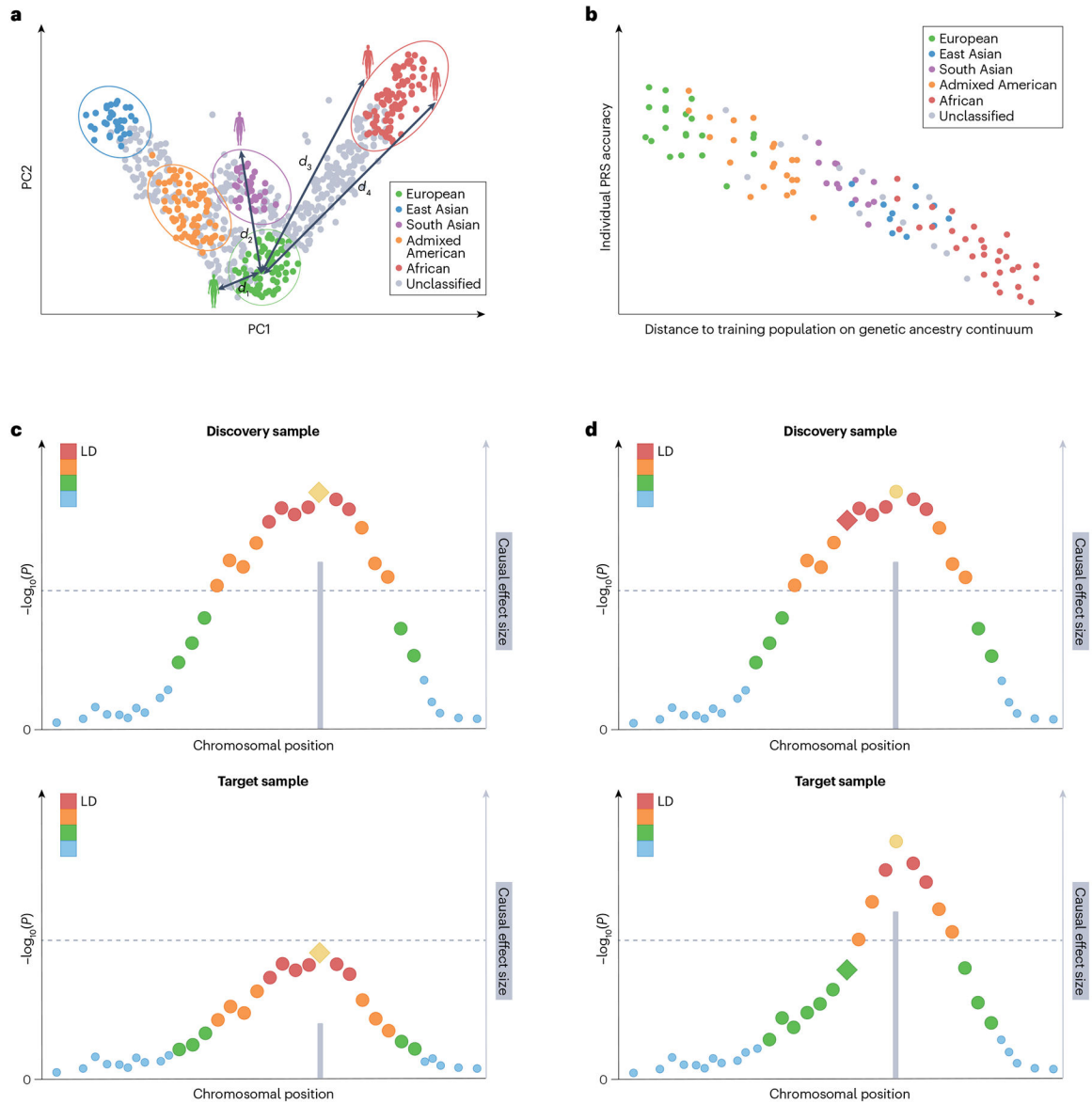


Fig. 2 |. Genetic factors that can influence PRS performance.

a, First two principal components (PCs) of the genetic data. Each dot represents an individual. Individuals are assigned discrete population labels by applying arbitrary cut-offs to the genetic ancestry continuum. Different colours represent different population labels. Grey dots represent individuals who are unclassified. A genetic distance (d) can be calculated between each individual and the centre of the discovery genome-wide association study (GWAS) samples in the PC space. **b**, Prediction accuracy of the polygenic risk score (PRS) shows individual to individual variation and decreases along the genetic ancestry continuum when the genetic distance between the training and target samples increases. **c**, Differences in causal allelic effect size between the discovery (upper graph) and target (lower graph) samples can influence the accuracy of PRS across populations. **d**, Differences in linkage disequilibrium (LD) patterns between the discovery (upper graph) and target (lower graph) samples can influence the accuracy of PRS across populations. In panels **c**

and **d**, each dot represents the marginal association strength of a genetic variant. The lead (most associated) variant in yellow represents the causal variant and the grey bar represents its effect size. Other variants are coloured by descending degrees of LD with the causal variant (ordered red, orange, green and blue dots). Diamond represents the variant (which may be a tagging variant) used in PRS construction. Dashed line represents genome-wide significance.

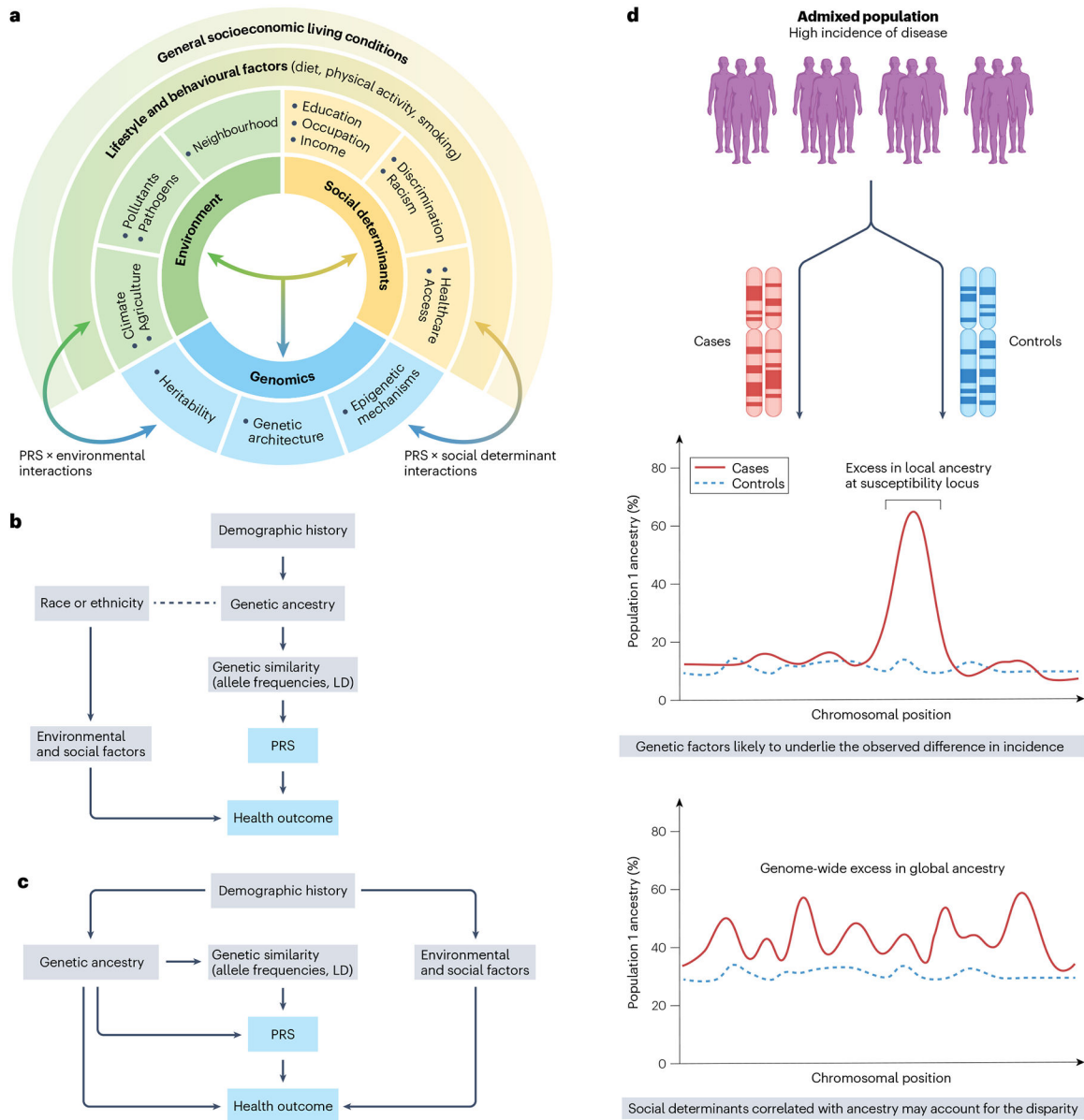


Fig. 3 | Interplay between social, environmental and genetic determinants of health.

a. Complex interrelationship among different risk factors for ill health and poor disease outcomes. These include living and working conditions (such as environmental exposures and social determinants of health (SDOH)) and genomic factors. **b.** Race and/or ethnicity can confound polygenic risk score (PRS) associations with health outcomes if a correlation exists with genetic ancestry (dotted line). In this case, correction for population structure using methods such as principal component analysis (PCA) that captures similarity in allele frequencies and linkage disequilibrium (LD) structure that arises due to shared demographic histories between populations can mitigate the confounding effect. **c.** Residual confounding may bias PRS associations when genetic ancestry is correlated with environmental and/or social factors due to shared demographic histories. For instance, when asthma is the health outcome and exposure to air pollution is the non-genetic risk factor, standard methods such

as PCA may under-correct for population structure. **d**, Admixture mapping detects disease-associated loci and patterns of excess local ancestry that help disentangle the contribution of genetic factors to observed disparities in risk.

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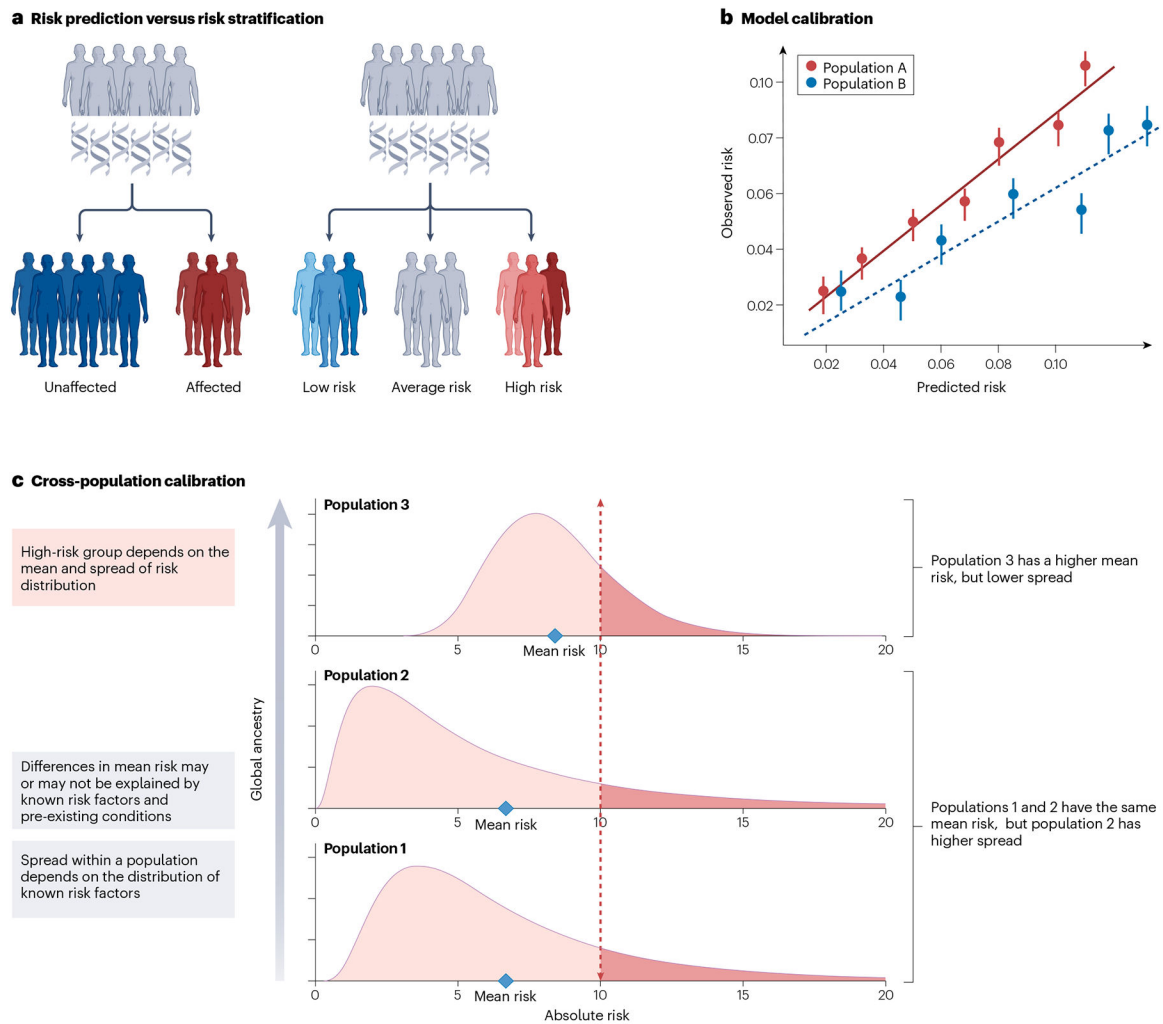


Fig. 4 | Considerations for the assessment of PRS clinical utility.

a, Visual representation of the difference between risk prediction and risk stratification. **b**, An example of model calibration, that is, the agreement between observed and estimated disease risk. Accurate estimation of absolute risks requires well-calibrated models. For instance, risks are systematically overestimated for Population B compared with Population A. **c**, Cross-population calibration of the polygenic risk score (PRS) distributions, which can have different mean and spread. Differences in calibration between populations arise due to a combination of the genetic and clinical risk factors. Cross-population calibration is important when selecting a single cut-off to identify individuals as high risk across samples with diverse ancestral and sociocultural backgrounds.

Table 1 | Polygenic prediction methods integrating GWAS summary statistics from diverse populations

Category	Method	Input	Variants for prediction	Need validation data set	Tuning parameters	Algorithm	Ref.
Combining approaches	Meta-analysis	Population-specific GWAS and LD	Up to all 1000 Genomes common variants	Optional	Depends on the single-population PRS method	Fixed-effect meta-analysis and a single-population PRS method	62
	ShaPRS	Population-specific GWAS and LD	Up to all 1000 Genomes common variants	Optional	Depends on the single-population PRS method	Meta-analysis accounting for heterogeneity between GWAS and a single-population PRS method	64
	MultiPRS	Population-specific GWAS and LD	Up to all 1000 Genomes common variants, depending on the C + T parameters	Yes	C + T parameters and linear combination weights for population-specific PRS	C + T	67
Joint modelling of two populations	XP-BLUP	GWAS in the auxiliary population; individual-level data for the target population	Genotyped SNPs in the target data set	Yes	F -value threshold for the auxiliary GWAS (optional)	Local FDR for variant selection; restricted maximum likelihood (ReML) for model fitting; best linear unbiased prediction	71
	XPASS(+)	GWAS and LD from the auxiliary and target populations	All available variants	No	None	Best linear unbiased prediction and conjugate gradient for solving linear systems	72
	BridgePRS	GWAS and LD from the auxiliary and target populations; individual-level data for the auxiliary population	All available variants	Yes	Ridge shrinkage parameters and linear combination weights for PRS generated under different prior parameters and loci selection criteria	Best linear unbiased prediction	73
Joint modelling of two or more populations	TL-Multi	GWAS and LD from the auxiliary and target populations	HapMap3	Optional	Regularization parameters in LASSO	Coordinate descent for model fitting	74
	SDPRX	GWAS and LD from the auxiliary and target populations	HapMap3	Yes	Linear combination weights for population-specific PRS	Markov chain Monte Carlo	76
Joint modelling of two or more populations	CT-SLEB	Population-specific GWAS and LD	Up to all 1000 Genomes common variants, depending on the C + T parameters	Yes	C + T parameters and parameters in the super learning model (such as LASSO, ridge regression and neural networks)	Two-dimensional C + T; empirical Bayes (for SNP effect estimation); super learning (for combining PRSs generated under different C + T parameters)	41
	TL-PRS/MTL-PRS	Population-specific GWAS and LD	HapMap3	Yes	Learning rate and number of iterations in the gradient descent algorithm	Gradient descent for model fitting	77

Category	Method	Input	Variants for prediction	Need validation data set	Tuning parameters	Algorithm	Ref.
	PROSPER	Population-specific GWAS and LD	HapMap3 + MEGA chip array	Yes	Regularization parameters in LASSO, ridge regression and LD matrix estimation; tuning parameters in the ensemble regression	Coordinate descent and super learning (for combining PRSs generated under different tuning parameters)	78
	ME-Bayes SL	Population-specific GWAS and LD	HapMap3 + MEGA chip array	Yes	Parameters in the super learning model (such as linear regression, ridge regression and elastic net)	LDpred2 (for estimating causal SNP proportions and heritability); ME-Bayes (for SNP effect estimation); super learning (for combining PRSs generated under different ME-Bayes parameters)	79
	PRS-CS(- auto)	Population-specific GWAS and LD	HapMap3	Optional	The global shrinkage parameter and linear combination weights for population-specific PRS; none for the auto algorithm	Markov chain Monte Carlo	68
Incorporating information beyond GWAS	XPXP	Population-specific GWAS (for both the target trait and its genetically correlated traits) and LD	All available variants	No	None	Best linear unbiased prediction and conjugate gradient for solving linear systems	81
	X-Wing	Population-specific GWAS and LD	HapMap3	No	None	Scan statistics (for local genetic correlation estimation); Markov chain Monte Carlo (for PRS model fitting); summary statistics based repeated learning (for combining population-specific PRSs)	82
	PolyPred-S+/ PolyPred-P+	Population-specific GWAS and LD; functional annotations	All available variants for PolyFun-pred; HapMap3 for SBayesR and PRS-CS	Yes	Linear combination weights for population-specific PRS	PolyFun + SuSIE (for fine-mapping informed PRS) and Markov chain Monte Carlo (for SBayesR and PRS-CS)	69

C + T, clumping and P -value thresholding; FDR, false discovery rate; GWAS, genome-wide association studies; LD, linkage disequilibrium; PRS, polygenic risk score.