Twelve Tests of the Additive Genetic Model of Social Mobility

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Abstract: An additive genetic model of social mobility predicts that intergenerational transmission of social status operates entirely through genetic inheritance, with no role for environment. In the model, any differences in transmission rates across places and time must reflect differences in assortative mating or measurement error. The model generates sharp, testable predictions for status correlations across immediate family members and extended kin, and I test twelve of them using linked U.S. census data on over 50 million white Americans from 1850 to 1940. The model fails on multiple dimensions. Using the model's method to identify latent transmission rates, estimates vary widely and implausibly across states and birth cohorts, yet independent measures of assortative mating show little corresponding variation, violating a key restriction of the model. Sibling correlations substantially exceed father-son correlations, the opposite of what the model predicts. Fathers who raise the child (adoptive or stepfathers) predict adult outcomes as strongly as the father who provides the genes. These findings reject the claim that inherited genetic endowments alone explain social mobility. Persistent economic and social environments play a quantitatively important role.

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1. Introduction

Children from richer families tend to become richer adults, while children from poorer families tend to remain poor. A large body of research points to environmental mechanisms behind this persistence. Wealthier parents sort into better neighborhoods, which have lasting causal effects on children's outcomes (Chetty and Hendren, 2018). Poorer families face credit constraints that limit investments in early childhood skills, and so access to health care, food assistance, and cash transfers can improve children's long-run outcomes (Aizer et al., 2016; Bailey et al., 2024; Barr et al., 2022; Goodman-Bacon, 2021). Advantaged parents are also better connected to other high-income families, giving their children access to networks and opportunities, a form of social capital linked to upward mobility (Chetty et al., 2022, 2026). Taken together, this evidence points to a common conclusion: differences in family and social environments are key determinants of intergenerational mobility.

An additive genetic model offers a stark alternative. In this view, each child is born with a genetic potential for economic success equal to the average of the parents' potentials plus biological luck, often called the "genetic lottery."[1] This potential is fixed at conception and inherited from parents, so childhood environments do not alter long-run outcomes. Neighborhoods do not make children more successful; they sort families with similar genetic potential into the same places. A stronger safety net does not improve long-run prospects; it may raise observed income temporarily but childhood interventions fade out and do not change what is passed on to children. The only force that can permanently change persistence is assortative mating: where spouses have similar genetic potential, persistence is high; where marriage is more random, it falls.

Under the genetic model, standard measures of mobility are misleading. Because underlying genetic potential is fundamentally unobservable, researchers must rely on proxies such as income, education, and occupation, but these are noisy measures, and the resulting measurement error attenuates the observed link between parents and children. A parent-child income rank correlation of about 0.35 therefore does not imply that advantages fade within three or four generations. Once corrected for measurement error, the implied transmission rate may rise to 0.7 or 0.8, meaning that status advantages could persist for ten to fifteen generations.[2]

[1] While not advocating an additive genetic model, see Harden (2021).

[2] A transmission rate of 0.35 implies that about 4% of an initial status gap remains after three transmission steps (0.35^3), whereas a rate of 0.7 implies about 34% remains (0.7^3). Measurement error in latent endowments does not imply that the underlying trait is purely genetic; it may reflect a combination of cultural, social, and other persistent influences (Collado et al., 2023).

The same logic reinterprets cross-country differences in mobility as differences in measurement, not in opportunity. Sweden appears more mobile than the United States not because its policies help poor children climb, but because a compressed wage structure and low-cost access to higher education weaken the link between genetic potential and income or educational attainment. Policy can change the noise in the measurement, but not the underlying rate of transmission; that is, unless it changes assortative mating on genetic potential.

Gregory Clark, the leading proponent of this view, presents extensive evidence consistent with a genetic interpretation of mobility (Clark, 2014, 2023). He argues that social mobility is largely "indistinguishable from genetic inheritance," drawing on data from many countries, especially England. Several patterns align with the model's predictions. Mobility across multiple generations is lower than standard two-generation estimates, suggesting observed outcomes indeed imperfectly capture latent status. Similar patterns of low multigenerational mobility have been documented by others, lending support to the measurement error argument even if the authors do not attribute this persistence to genetic transmission.[3] Yet some of the English evidence points more specifically toward genetics.[4] Using four centuries of English data, Clark finds sibling correlations similar to parent–child correlations, which is difficult to reconcile with strong shared environmental effects. Status correlations across extended kin decay in a pattern consistent with genetic distance. Mothers predict children's outcomes as strongly as fathers, and birth order and parental death have limited long-run effects (Clark and Cummins, 2024a,b). Taken together, these findings support a view in which inherited endowments play a dominant role in status persistence.

This paper tests whether the additive genetic model withstands systematic empirical scrutiny, taking the model as given and evaluating its predictions. In the model, all observed status correlations are governed by two parameters: assortative mating on genetic potential, m, and the reliability with which observed outcomes measure latent endowment, θ.[5] Once these parameters are known, the model predicts precise correlations across a wide range of relatives, including parents and children, grandparents, uncles, cousins, and in-laws.

[3] For example, see Adermon et al. (2021); **?**); Belloc et al. (2024); Solon (2018); Stuhler (2024); Modalsli and Vosters (2024); Ward et al. (2025).

[4] Clark and Kristensen (2026) argue that an additive genetic model fits the pattern of extended-kin correlations in Danish and Swedish register data as well, though Collado et al. (2023) argue the opposite for Sweden. The disagreement is partly over model specification; see (Clark and Kristensen, 2026).

[5] In Clark (2023), θ corresponds to the heritability coefficient h^2, the share of variation in observed outcomes attributable to genetic endowment. More generally, one can decompose measurement error into two distinct sources: imperfect observability of the latent "social ability" on which individuals match and which they transmit to offspring, and imperfect heritability of latent social ability (see Clark and Kristensen (2026)).

The structure of the model makes it possible to recover assortative mating and measurement error in more than one way. Relationships that differ only one step in genetic distance, such as fathers and sons versus grandfathers and grandsons, help to uncover the underlying rate of transmission. Relationships that add a marriage step but no additional genetic distance, such as between sons and their father-*in-laws*, help uncover assortative mating because they reflect sorting in marriage rather than biological inheritance. If the model provides a consistent account of mobility, these different kinship correlations should all point to the same values of assortative mating on genetic potential m and measurement error θ. Moreover, these values should agree across states and birth cohorts: places and periods with high transmission should also have higher assortative mating, while those with low transmission should have lower assortative mating. In other words, a model with just two parameters but many distinct kinship correlations is over-identified and can be tested by whether these independent pieces of evidence agree.

Besides these positive predictions, the genetic model also yields clear null predictions. If adult outcomes are entirely determined by inherited endowment, then environmental shocks within families, such as parental death or adoption, should not have persistent effects on adult status.

I test these predictions using linked U.S. census records from 1850 to 1940, covering more than 50 million white Americans up to three generations apart.[6] The census data are well suited to this task. The samples are large enough to estimate kinship correlations precisely. The long time span makes it possible to link extended kin (siblings, cousins, in-laws, uncles, and grandparents) within the same population. And the sheer scale of the data reveals natural experiments, such as twins, parental death, adoption, and remarriage, that are rare in surveys. I organize twelve tests into three groups (Table 1): internal consistency across states and cohorts, gender symmetry in genetic transmission, and the irrelevance of family environment for adult outcomes.

The model fails on several tests, though not equally strongly. I begin by testing its internal consistency, and it clearly does. I estimate the transmission rate separately by U.S. state and birth cohort using the ratio of the grandfather-grandson correlation (two genetic steps) to the grandfather-father correlation (one genetic step).[7] These estimates vary widely across places and over time. The model allows such variation, but because the environment plays no role, it attributes all differences

[6]The American racial experience poses a challenge to the additive genetic framework: Black-white economic gaps narrowed at uneven rates after 1865 despite near-complete barriers to intermarriage for a century (Collins and Wanamaker, 2022; Ferrara, 2022; Althoff and Reichardt, 2024). I therefore restrict attention to white Americans, which stacks the deck in favor of the genetic model.

[7]In the model, each correlation reflects both genetic distance and measurement error. Taking the ratio cancels measurement error, isolating the effect of genetic distance.

Table 1: Testable Predictions of the Additive Genetic Model

Test	**If Model holds**	**Verdict**
Prediction 1: Internal Consistency		
1. Across states	Variation in transmission driven by variation in assortative mating	Rejected, large
2. Across cohorts	Variation in transmission driven by variation in assortative mating	Rejected, large
3. Consistency of b and m	Independent estimates of b and m are consistent	Rejected, large
4. Sibling vs. parent-child	Sibling correlation $\leq$ parent-child correlation	Rejected, large
Prediction 2: Gender Symmetry		
5. Gender symmetry (grandparents)	Maternal and paternal lineages have equal effects	Rejected, small
6. Gender symmetry (parents)	Father's and mother's education have equal effects	Rejected, large
7. Gender-symmetric siblings	Brother-brother, sister-sister, and mixed correlations equal	Rejected, large
Prediction 3: Family Environment		
8. Living vs. dead irrelevant	Dead parents predict outcomes as well as living parents	Rejected, small
9. Twins and age gap	Twin corr. exceeds sibling corr. by genetic prediction; age gap irrelevant	Mixed, small
10. Birth order irrelevant	No within-family differences in outcomes by birth order	Rejected, small
11. Family size irrelevant	Family size has no effect on child outcomes	Mixed, small
12. Bio parents more predictive	Adopted/stepchildren have zero or reduced corr. with rearing father; bio father predicts more than rearing father	Rejected, large

across states to assortative mating. The implied levels of sorting, however, are not plausible: they range from negative to nearly one and shift sharply even across adjacent birth cohorts.

For example, transmission is lower in Pennsylvania than in Alabama, consistent with higher social mobility and greater equality of opportunity in the industrialized North rather than the agrarian South. Under the model, this difference must be driven entirely by sorting, implying strongly negative assortative mating in Pennsylvania ($m \approx -0.25$) and perfect assortment in Alabama ($m \approx 1$).

A second approach to estimating assortment uses a different set of relatives. A son's correlation with his father-in-law combines one marriage link and one genetic link, while his correlation with his own father reflects a genetic link alone. The ratio therefore isolates sorting through marriage. Unlike the wide variation in the first measure, this ratio is remarkably stable: in almost every state, a father-in-law's occupational rank predicts a son-in-law's nearly as well as a father's.

To see how these two ways of estimating assortment are internally inconsistent, consider Pennsylvania and Alabama again. The first measure places these states at opposite extremes, with negative sorting in Pennsylvania and near-perfect sorting in Alabama. If that were true, a father-in-law should predict the son-in-law's outcome nearly as well as a father in Alabama, but be negatively correlated in Pennsylvania. Instead, the father-in-law correlation is positive and nearly the same as the father correlation in both states. In the data, the father and father-in-law correlations move together far more tightly than the genetic model predicts, as if a common environmental factor drives both. More broadly, the first measure implies large variation in sorting across states and cohorts, while the second shows almost none.

The in-law correlations are not the only inconsistency. The data include many types of blood relatives (siblings, uncles, cousins), and the model implies that correlations should decline in a specific way as genetic distance increases. In the data, they do not. The rate at which correlations decline across relative types differs widely across states for many different measures of social status, including educational attainment, occupational status, and wage income. In short, the model's over-identification restrictions fail.

Setting internal inconsistencies aside, the model's core implication that family environment should not matter is also rejected. Sibling correlations exceed parent–child correlations, consistent with shared environment increasing similarity among siblings. Sibling correlations decline with age gaps, indicating that siblings closer in age have more similar outcomes due to having shared environments. A mother's education is a stronger predictor of children's outcomes than a father's

education, and mothers matter especially more for daughters. The death of a mother between censuses predicts lower children's educational attainment. Birth order also affects economic outcomes, even though siblings should have similar genetic endowments under the model.

A final test exploits the difference between biological and rearing fathers: one transmits genes, the other does not. As Clark puts it, "if genetics matters most, then the outcomes for adopted children will be largely uncorrelated with those of their adoptive parents but highly correlated with those of their biological parents" (Clark, 2014, p. 29). I track children who move across households between censuses, appearing first with a biological father and later with an adoptive or stepfather, and include both fathers' occupations in the same regression predicting the child's adult outcome. The genetic model predicts that the biological father's coefficient should at least exceed the rearing father's.[8] This prediction fails: for occupation score and education, the adoptive father's coefficient exceeds the biological father's, and for wage income the two are statistically indistinguishable. The father who raises the child predicts adult outcomes at least as well as, and often better than, the father who provides the genes.

Not all empirical tests of the model fail equally, and distinguishing between marginal and decisive failures is informative. Shocks within families produce detectable but modest effects: birth order, parental death, and family size all matter, yet the magnitudes are small and sometimes statistically indistinguishable from zero. Taken in isolation, these results might suggest that the family environment plays only a limited role. But small estimated effects do not necessarily imply that families or childhood environment are unimportant. Instead, they may reflect the limited role of financial resources, or the ability of families to insure against disruptions through remarriage, informal transfers from extended kin, or community networks (Ager et al., 2021; Bleakley and Ferrie, 2016).

The model's largest failures point toward persistent shared environments. Sibling correlations exceed parent-child correlations in nearly every state, and a man's father-in-law predicts his occupational attainment almost as strongly as his own father.[9] Since the father-in-law never raised the son-in-law or shared his household, this correlation is difficult to attribute to parenting or direct investment; it more plausibly operates through shared local environments such as labor markets, schools, networks, and community institutions (Chetty and Hendren, 2018; Chetty et al.,

[8]The stepfather's only genetic link to the child runs through the mother via assortative mating, so his predicted coefficient equals a fraction r of the biological father's, where r is the spousal correlation in observed outcomes. Because we do not know how adoptees are matched to adoptive parents, the adoptive father's coefficient need not be zero, but it should be smaller than the biological father's.

[9]This result is also consistent with historical research during this period, including (Buckles et al., 2023; Olivetti and Paserman, 2015; Eriksson et al., 2026).

2026). Rearing parents do predict outcomes as strongly as biological parents, which confirms that household environments matter. But the father-in-law results suggest that important environmental channels extend beyond the household to shared features of the local community.

The contribution of this paper is not any single test but the combination: bringing multiple predictions of one model to the same population and showing that the model fails on multiple margins. My results across different relatives are most closely related to Collado et al. (2023), who test the additive genetic model using extended kin correlations in Swedish administrative data. The results are complementary: they reject the model in a modern Scandinavian welfare state, while I reject it in American history, where institutional context and data sources are entirely different. Several of the individual tests I apply have precedents in the literature, sometimes using the same historical U.S. census data.[10] Gould et al. (2020) use variation from parental death, divorce, and family size to show that the parent-child correlation in education is causally related to the amount of time each parent spends with the child, a finding consistent with some results here. My results on adoptees also contribute to a large literature showing that non-biological parents predict children's wealth, income, and education, including studies of adoptees and children conceived through in vitro fertilization (Björklund et al., 2006; Black et al., 2020; Fagereng et al., 2021; Lundborg et al., 2025; Sacerdote, 2007).

2. The Additive Genetic Model and Testable Predictions

2.1 The Model

The additive genetic model starts from a simple decomposition. Any economic outcome y_g reflects a latent endowment x_g that transmits across generations and a residual ε_g that does not:

$$y_g = x_g + \varepsilon_g \tag{1}$$

Economists since Becker and Tomes (1979) have modeled intergenerational transmission through latent endowments, but they typically interpret x_g broadly: it could be genetic ability, cultural norms, work habits, social connections, or anything else that persists across generations. The additive genetic model makes the stronger claim that x_g is literally the genetic endowment, and excludes any role for shared family environment or family investment. In particular, outcomes are assumed to be additively separable in genes and shocks, ruling out gene–environment interactions. The model also

[10] On birth order, see Cools et al. (2024). On parental or grandparental death, see Dupraz and Ferrara (2025); Goldstein (2025); Jensen and Zhang (ming); Ward et al. (2025). On the outcomes of adopted children, see Moriguchi and Parman (2015).

assumes stationarity: the variances of x and ε are constant across generations, so θ and all kinship correlations are stable over time.

Because the model is genetic, the child's endowment is the average of the parents' endowments, plus a random shock due to the "genetic lottery" or recombination:

$$x_g = \frac{1}{2}\left(x^f_{g-1} + x^m_{g-1}\right) + e_g \tag{2}$$

Equation 2 cannot be estimated directly because latent genetic endowment x is unobservable; only the outcome y is observed.

Let m denote the correlation between spouses' latent endowments. In a regression of the child's endowment on the father's endowment alone, the coefficient is

$$b = \frac{1+m}{2} \tag{3}$$

If the father's endowment predicts the mother's endowment (because $m > 0$), then it also predicts the portion of the child's endowment inherited from the mother. This raises the one-parent coefficient above 0.5. The parameter b governs nearly all latent kinship correlations in the model: each additional step of genetic distance reduces the latent correlation by a factor of b. Since b depends only on m, assortative mating is the single free parameter that controls intergenerational persistence. But m is not observed directly, because no dataset records genetic endowments. Researchers can only estimate correlations using observable outcomes like income, education, or occupation.

To link m to observables, standard genetic models assume that spouses sort on what they can observe (phenotype), not on latent endowment (genotype) (Clark, 2023; Collado et al., 2023). Let r be the spousal correlation in observables and let $\theta = \text{Var}(x)/\text{Var}(y)$ be the share of outcome variance attributable to genetic endowment. In the genetics literature, this quantity corresponds to narrow-sense heritability, but I use the reliability-ratio notation common in economics. Because sorting occurs on both the endowment and luck rather than just the endowment, the spousal correlation r on observables exceeds the correlation in endowments m:

$$m = \theta r \tag{4}$$

Since $\theta < 1$, spouses who appear similar in outcomes (r) are less similar in their underlying endowments ($m < r$).[11]

Matching on observables also inflates the observed parent-child correlation. A lucky father ($\varepsilon^f > 0$) appears more successful than his endowment, and because partners sort on observables, he marries a woman with a higher genetic endowment than his genes alone would predict. Their child inherits the average of both parents' endowments, so the father's luck raises the child's expected endowment indirectly, through the mother. The observed parent-child regression coefficient is:

$$\beta = \theta\left(\frac{1+r}{2}\right) \tag{5}$$

Note that because this is the relationship between observed outcomes, it is attenuated by the θ reliability ratio.

From these building blocks, Clark (2023) shows the predicted correlations for every kinship pair (parents, grandparents, siblings, uncles, cousins, in-laws, etc.), summarized in Table 2.[12] The intuition is straightforward. Relatives are correlated because they share genetic material, and each additional step of genetic distance reduces the correlation by a constant factor, $b = \frac{1+m}{2}$. Siblings share both parents and therefore correlate at θb. An uncle and nephew are separated by two genetic steps and correlate at θb^2. First cousins are separated by three steps and correlate at θb^3.

Correlations are stronger when relatives are connected through a direct line of descent, such as parent-child or grandparent-grandchild relationships. In these cases, the connection includes not only genetic transmission but also an additional channel created by assortative mating on observable outcomes. Siblings do not have this additional correlation because this is not a direct lineage link.

[11] Clark and Kristensen (2026) parameterize the model with separate heritability (h^2) and measurement attenuation (θ) parameters, so that $m = h^2 r$ and observed correlations are attenuated by θh^2 rather than by θ alone. This effectively decomposes my single reliability ratio into two components: how much of the latent trait is genetic (h^2) and how well the observed outcome captures the latent trait (θ). The distinction does not affect any of the testable predictions in this paper. All identifying ratios cancel the attenuation factor whether it is θ or θh^2, and the qualitative predictions (e.g., that sibling correlations should not exceed parent-child correlations) hold under either parameterization.

[12] Clark references (Gimelfarb, 1981) for deriving these relationships.

Table 2: Predicted Correlations Under the Additive Genetic Model

Kinship pair	Notation	**Predicted Correlation**
Parent–child	$\rho_{f,s}$	$\theta\left(\frac{1+r}{2}\right)$
Sibling	ρ_{sib}	$\theta\left(\frac{1+m}{2}\right)$
Grandparent–grandchild	$\rho_{gf,gs}$	$\theta\left(\frac{1+m}{2}\right)\left(\frac{1+r}{2}\right)$
Uncle–nephew	ρ_{un}	$\theta\left(\frac{1+m}{2}\right)^2$
First cousin	ρ_c	$\theta\left(\frac{1+m}{2}\right)^3$
Father-in-law–son	$\rho_{fil,s}$	$r\theta\left(\frac{1+r}{2}\right)$

$\theta = \mathrm{Var}(x)/\mathrm{Var}(y)$ is the reliability ratio. $m = \theta r$ is the spousal correlation in latent endowments; r is the spousal correlation in observed outcomes. Sibling, uncle–nephew, and first cousins depend on m through $b = (1+m)/2$ but not on r directly, because the connecting path is not a direct lineage. Direct-lineage pairs (parent–child, grandparent–grandchild) and spousal links (groom–father-in-law) include $(1+r)/2$ factors because the observed outcome of one member reveals the spouse's latent endowment through assortative mating.

Table 3: Identifying Ratios Under the Additive Genetic Model

Ratio	Formula	Identifies
Grandfather / father	$\frac{\rho_{gf,gs}}{\rho_{gf,f}}$	$b = \frac{1+m}{2}$
Uncle–nephew / sibling	$\frac{\rho_{un}}{\rho_{sib}}$	$b = \frac{1+m}{2}$
Cousin / uncle–nephew	$\frac{\rho_c}{\rho_{un}}$	$b = \frac{1+m}{2}$
$\sqrt{\text{Cousin / sibling}}$	$\sqrt{\frac{\rho_c}{\rho_{sib}}}$	$b = \frac{1+m}{2}$
Father-in-law–son / father–son	$\frac{\rho_{fil,s}}{\rho_{f,s}}$	$r = \frac{m}{\theta}$

Notation follows Table 2.

2.2 *Testable Predictions of the Additive Genetic Model*

The model generates many testable predictions, which I group into three sets (Table 1).

First, the model requires strong internal consistency. No single kinship correlation identifies the latent parameters θ, m, or r, but ratios of correlations at adjacent kinship distances cancel the shared parameters and isolate the transmission rate $b = (1+m)/2$ (Table 3). The reliability ratio θ cancels because it attenuates every correlation equally (I discuss a relaxation of this assumption in Appendix C). A separate ratio, the father-in-law–son correlation divided by the father–son correlation, recovers assortative mating on observables r. If the model is correct, every ratio in Table 3 should return the same value of b, and the two measures of assortative mating should agree. These identifying ratios should all agree regardless of which kinship pair is used.

An advantage of the U.S. data is that I can obtain more power for this test by calculating these ratios by state and birth cohort, allowing me to assess whether these approaches produce similar parameter values within each context. I therefore estimate m and r by state (Test 1) and by birth cohort (Test 2) to test whether they are strongly correlated. I also use a different set of relatives (uncles, cousins, and siblings) by state (Test 3) to estimate b. Measurement error may vary by state and generation, which I discuss in this section. As a final consistency check, the model predicts that parent–child correlations *exceed* sibling correlations, since the former involve matching on observables (r) while the latter do not ($m < r$). If siblings are systematically more correlated than the model predicts, shared household environment is the most natural explanation (Test 4).

The second set of predictions follows from the symmetry of genetic transmission across gender. Because a child's endowment is the unweighted average of both parents' endowments (Equation 2), maternal and paternal lineages should have equal predictive power (Test 5), and mothers' and fathers' education should have equal effects on the child's education (Test 6). For the same reason, sibling correlations should not depend on the gender composition of the pair (Test 7). Observed correlations may still differ by gender if measurement error θ is gender-specific, a possibility I address in this section.

Third, the child's endowment (x_g) is determined at conception, so features of the rearing environment should have no effect on transmission. If a father dies when his child is young, environmental theories predict worse outcomes for the child and weaker father–child correlations. The genetic model predicts neither, since transmission occurs at conception (Test 8). Twins should be more correlated than non-twin siblings by a fixed genetic factor, and the age gap between non-twin siblings should not affect their correlation (Test 9). Birth order (Test 10) and family size (Test

11) should also be irrelevant. Non-biological children, whether adopted or living with a stepparent, should have smaller correlations with their household head's outcomes than their biological parent, since fewer or no genes are shared. A within-child design that observes the same child first with a biological father and then with a stepfather or adoptive parent sharpens this test by holding the child's genotype constant (Test 12).

3. Data

The underlying data are the IPUMS full-count digitized U.S. censuses from 1850 to 1940 (Ruggles et al., 2024).[13] Each census records household composition, allowing me to infer likely parent-child relationships during childhood and then link individuals across censuses to observe adult outcomes.[14] Cross-census links use the Census Tree crosswalk files of Buckles et al. (2023), which provide links across all census pairs from 1850 to 1940 using genealogical records and probabilistic matching on name, age, and birthplace. Linkage is imperfect: not all individuals are successfully linked, and representativeness biases are more severe across racial groups (Ward, 2023). I focus throughout on the white population, where linkage rates are highest. Across all twelve tests, the analysis samples cover approximately 58 million unique white Americans observed in censuses from 1850 to 1940.[15]

Linked samples are non-random, with linkage rates varying by age, education, urban status, and region, so raw correlations may be biased relative to the population of interest. I address this using inverse probability weights (IPW) following Bailey et al. (2020). For each linked dataset, I estimate a probit model predicting selection into the linked sample as a function of demographics, education, occupation, and state of residence, and construct weights as the inverse of the predicted probability of linkage. All estimates in this paper apply these weights; Appendix B.11 provides details. Each test requires a different dataset, constructed from different combinations of censuses and family relationships (siblings, twins, step-parents, adopted children, uncles). Appendix B provides construction details for each.

[13] The 1950 census has been released but has not been fully cleaned; the current digitization has known errors in income and education variables that make it unreliable for the analyses in this paper. The 1890 census manuscripts were destroyed by fire and are not available.

[14] The 1850–1870 censuses do not record relationship to household head, so parent–child links in those years are inferred from co-residence patterns. This limitation affects only the multigenerational sample used in Tests 1–4; the remaining datasets rely on later censuses where relationships are recorded directly.

[15] This count is obtained by collecting all unique person identifiers from each test's regression sample and deduplicating across census years using the Census Tree crosswalk, which tracks the same individual across multiple censuses. The largest contributing samples are the intergenerational father-son pairs (30 million pairs), sibling pairs with education (22 million pairs), and multigenerational grandfather-father-grandson triplets (7.6 million triplets).

I use three outcome measures. The first is an occupation-based score from Ward (2023), which also adjusts for regional differences in occupational standing to account for large economic gaps across space.[16] Occupations are difficult to rank precisely, so I also use two directly observed measures from the 1940 census: years of schooling, available for all individuals, and wage income, available for wage workers. Wherever possible, I report results for all three outcomes. Education is the only outcome observed for women, since most did not report an occupation in this era.

The model's predictions are stated in terms of correlations, which are scale-invariant. All results are presented as standardized correlations or, where regression coefficients are reported, as coefficients on variables standardized to mean zero and unit variance.

4. Results

4.1 Prediction 1: Internal Consistency

The first set of tests asks whether estimates of assortative mating are consistent across different types of kin. I do this by calculating the identifying ratios shown in Table 3 separately by state and birth cohort and comparing the resulting estimates. These ratios are estimated using an instrumental variables approach. For example, the latent transmission rate b and assortative mating m can be recovered by instrumenting the father's outcome with the grandfather's outcome. In this setup, the first stage is the grandfather-father (i.e., father-son) correlation, and the reduced form is the grandfather–grandson correlation. These tests require multigenerational data that observe grandfathers, fathers, biological uncles, and siblings. Appendix B.1 describes the construction of the multigenerational linked data.

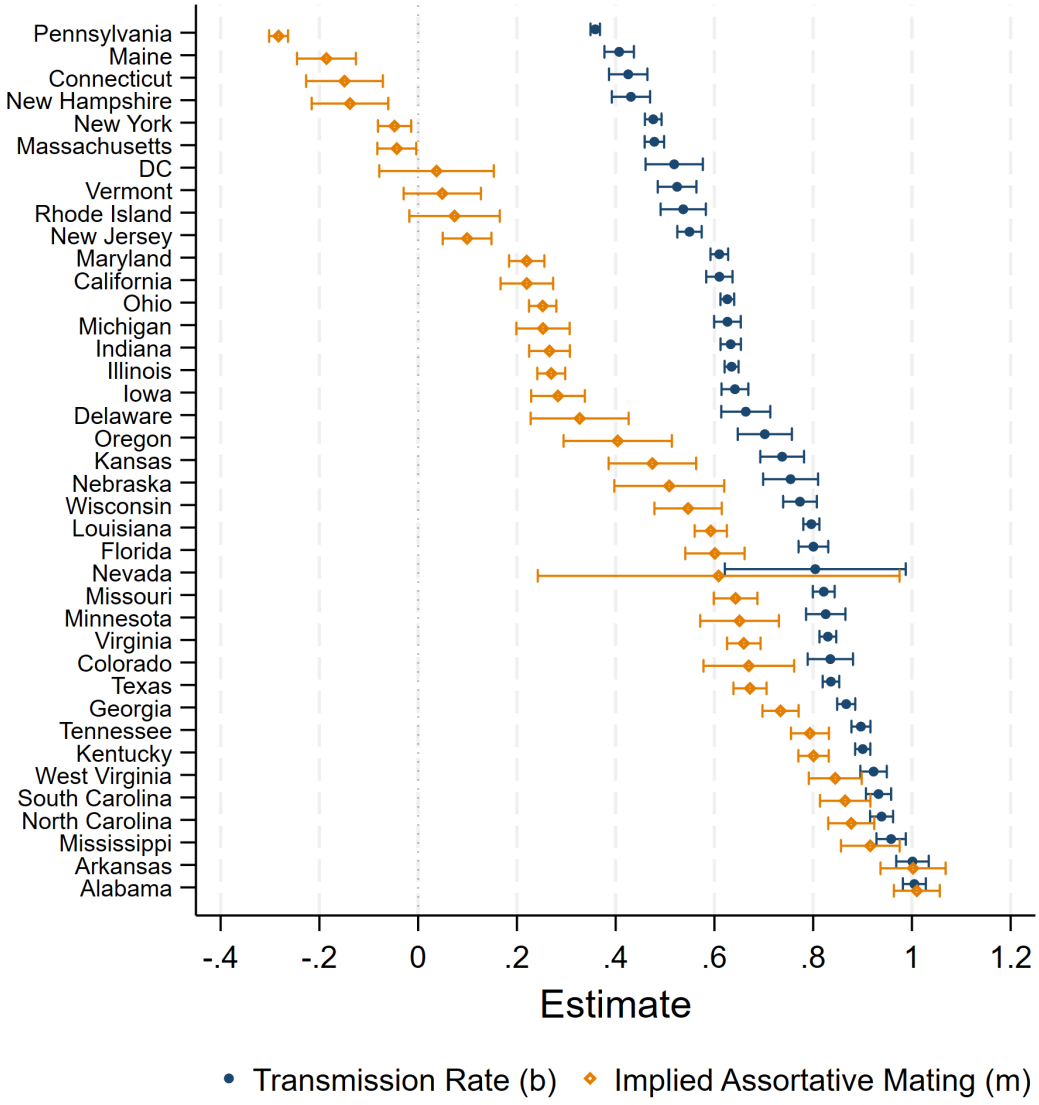
4.1.1 Test 1: Assortative Mating Explains State Variation

In this first test, I estimate assortative mating in two independent ways and compare the results. First, I estimate the transmission rate b_{state} using the ratio of the grandfather–grandson correlation to the grandfather–father correlation. This identifies the implied assortative mating on genetic potential parameter m_{state}. Second, I estimate assortative mating on observables using the ratio of the father-in-law–son correlation to the father–son correlation, which identifies r_{state}. The additive

[16] A common alternative is the IPUMS occupational income score, which assigns each occupation its median income from the 1950 census. This measure is problematic when applied to earlier periods because the relative standing of occupations changes over time: farmers, for example, were a large and middle-income group in the nineteenth century but a shrinking one by 1940. The score I use instead adjusts occupation titles using contemporaneously available information in each census, specifically literacy (available 1850 to 1930) and years of education (available in 1940), to rank occupations by their human capital levels within cells defined by occupation, race, and region. I also assess robustness to the LIDO score from Saavedra and Twinam (2020).

genetic model predicts that variation in the transmission rate across states, b_{state}, is entirely driven by variation in assortative mating.[17]

Figure 1: Estimates of the transmission rate and implied assortative mating vary widely across states.



Notes: Each state's transmission rate $\hat{b}_{state}$ (navy circles) and implied assortative mating $\hat{m}_{state} = 2\hat{b}_{state} - 1$ (orange diamonds) are estimated from the grandfather-grandson / grandfather-father ratio, implemented as an IV regression. States sorted by $\hat{b}_{state}$. Sample is limited to white males and uses standardized occupation scores by state (Ward, 2023).

[17] States are defined by the father's state of residence, which is also where the grandson was raised.

Figure 1 presents $\hat{b}_{state}$ and the implied $\hat{m}_{state} = 2\hat{b}_{state} - 1$ for each state, sorted by $\hat{b}_{state}$. The results show wide geographic variation. The sample is restricted to white men, and occupation scores are standardized within each state, so the variation reflects neither racial composition nor differences in state-level occupational distributions. The latent transmission rate $\hat{b}_{state}$ ranges from 0.36 to 1.01, with Southern states at the high end and Northeastern states well below.

The model allows b_{state} to vary across populations if assortative mating varies, but the range of implied $\hat{m}_{state}$ values is implausibly wide. Several Southern states have estimates at or above 1.0, which is the theoretical maximum ($b = 1$ requires perfect assortative mating, $m = 1$). Several Northeastern states have implied $\hat{m}_{state}$ values that are negative: Pennsylvania, Maine, New Hampshire, and Connecticut all have point estimates below zero, with confidence intervals that exclude positive values. While negative assortative mating is theoretically possible (Becker, 1973), it is without much empirical precedent: spousal correlations in education, often the only outcome systematically observed for women across countries and time periods, are nearly universally positive. Further, the model requires entirely different marriage patterns across states, from strongly negative in New England to strongly positive in parts of the South.

An important point to recall here is that this variation across space does not reflect differences in measurement error. One might think that if occupation titles are more informative in some states than others, the reliability ratio θ_{state} would vary, adding additional variation to the estimates across states. But the ratio strategy cancels measurement error by design, so the variation in Figure 1 cannot be due to differences in how well occupation scores capture latent status.

Setting the implausible parameter values aside, I next ask whether different ways of estimating assortative mating agree with each other. Now I estimate assortative mating on observables, r_{state} using the same multigenerational data: the ratio of the father's correlation with his father-in-law (the maternal grandfather) to his correlation with his own father (the paternal grandfather). The two measures, m_{state} and r_{state} will not be numerically identical due to measurement error $m_{state} = \theta_{state} \cdot r_{state}$. But if the model is correct, they should be strongly related across states: places with higher implied $\hat{m}_{state}$ should also have sons more tightly linked to the father in law.

Figure 2 plots the two measures of assortative mating against each other across states: the y-axis shows the estimate of $\hat{r}_{state}$, and the x-axis shows the estimate of $\hat{m}_{state}$. The relationship is weak (slope $= 0.10$, $R^2 = 0.23$). The two estimates do not line up, rejecting a key restriction of the additive genetic model.

The only explanation for this discrepancy is that measurement error, θ_{state}, varies substantially across states. If the reliability ratio differs, the father-in-law ratio identifies $r_{state} = m_{state}/\theta_{state}$ rather than m_{state}, and the two measures need not agree exactly. I can simply use the ratio of the assortative mating measures to calculate θ_{state}, and check if the values are reasonable. Panel B of Figure 2 plots the distribution of these implied values. Six states require $\hat{\theta}_{state} < 0$, and the cross-state variation is far wider than any plausible differences in how well occupation scores capture latent status.

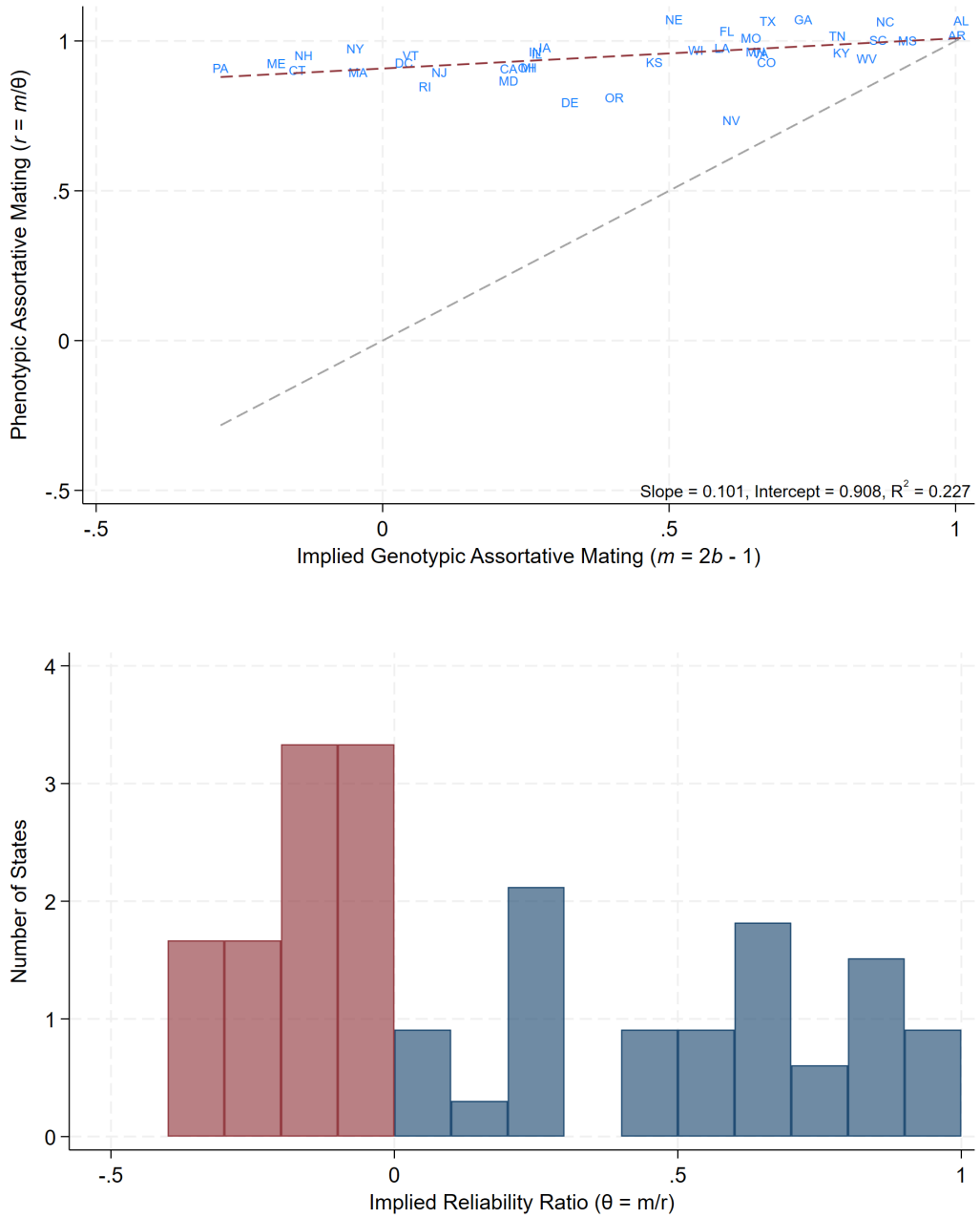
Four robustness checks confirm this rejection of the model's overidentifying restrictions. Appendix Figure A1 repeats the analysis using the uncle-sibling ratio in place of the grandfather-father IV, with similar results. Appendix Figure A2 replaces occupation scores with years of education, a variable observed directly in the 1940 census and free of the assumptions involved in assigning occupations a score. The results hold: the education assortative mating ratio is flat across states while the uncle-sibling education IV varies widely. Appendix Figure A6 replaces the occupation score in the grandfather-father-grandson correlations from Ward (2023) with the LIDO index of Saavedra and Twinam (2020), a predicted-income measure preferred by some in the literature. The disconnect between m_{state} and r_{state} is, if anything, stronger. Finally, the assortative mating ratio relies on the father-in-law link, which passes through a woman's cross-census linkage. In the Census Tree crosswalk files (Buckles et al., 2023), women are linked primarily through genealogical records that track surname changes at marriage, while men can also be linked through a machine learning algorithm trained on name, age, and birthplace. If the mixed linking method introduces asymmetric measurement error, the father-in-law ratio could be distorted. Appendix Figure A5 repeats the analysis restricting all cross-census links to genealogical records only, placing men and women on equal footing. The results are unchanged.

4.1.2 Test 2: Assortative Mating Explains Cohort Variation

In this test, instead of estimating b, m, and r by state, I do so at the national level by five-year birth cohort of the grandchild. One could argue that the state-level analysis may be biased by migration or intermarriage across states, violating an implicit closed population assumption.[18] Doing so at the national level avoids this issue. Figure 3 plots $\hat{b}_c$ and the implied $\hat{m}_c = 2\hat{b}_c - 1$ over time, with shaded bands showing 95% confidence intervals.

[18] Appendix Figure A3 restricts the sample to a closed population, keeping only linkages where all seven family members (grandchild, father, mother, and four grandparents) were born in the same state. The basic inconsistency between kinship correlations remain.

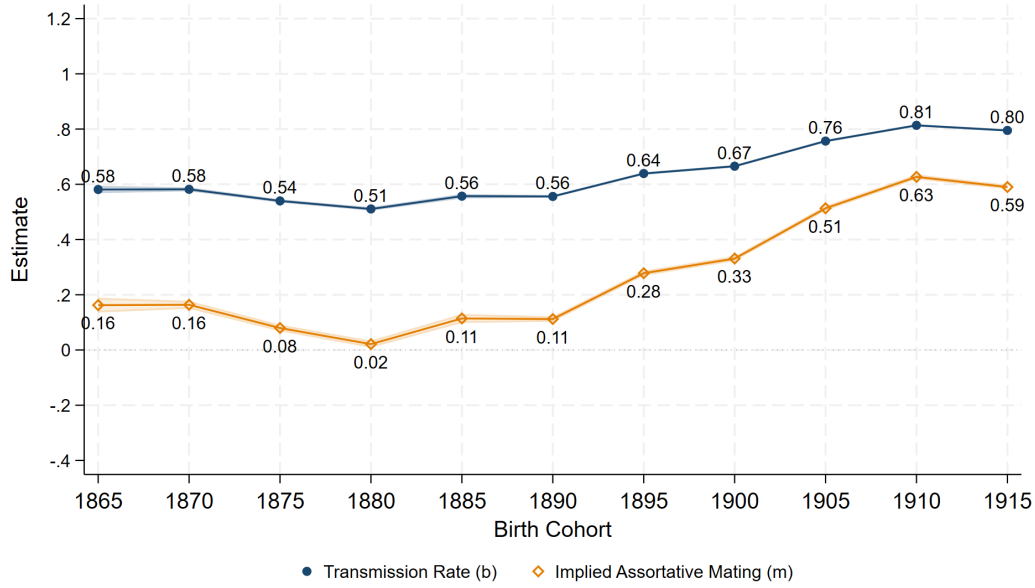
Figure 2: Two independent estimates of assortative mating are unrelated across states.



Notes: Panel (a): the x-axis plots the implied genotypic assortative mating $\hat{m}_{state} = 2\hat{b}_{state} - 1$ from the grandfather-father IV; the y-axis plots phenotypic assortative mating $\hat{r}_{state}$ (father/maternal-grandfather correlation divided by father/paternal-grandfather correlation). Under the genetic model with $\theta_{state} = 1$, the two should be equal (gray dashed 45-degree line); with $\theta_{state} < 1$, r_{state} should be proportionally larger. The OLS slope is far below the predicted relationship. Panel (b): the distribution of the implied $\hat{\theta}_{state} = \hat{m}_{state}/\hat{r}_{state}$ that each state would require for the two estimates to be consistent. The dashed line marks Clark's preferred $\theta = 0.8$; dotted lines mark $\theta = 0$ and $\theta = 1$. Navy bars fall in the valid $[0,1]$ range; maroon bars fall outside.

Once again, the transmission estimates vary substantially across birth cohorts: $\hat{b}_c$ ranges from 0.51 for the 1880 cohort to 0.81 for the 1910 cohort. Variation in $\hat{b}_c$ across cohorts is not itself surprising (Olivetti and Paserman, 2015; Jácome et al., 2025; Althoff et al., 2025; Abramitzky et al., 2025; Ward, 2023), but the additive genetic model attributes all of this variation to changes in assortative mating. If the model is true, this implies large changes in the marriage market across short periods of time. For cohorts born in the 1870s and 1880s, $\hat{m}_c$ falls to 0.02–0.16, meaning assortative mating was close to random. Between the 1880 and 1910 birth cohorts, $\hat{m}_c$ rises from 0.02 to 0.63, a swing that would require a wholesale transformation of marriage patterns within a single generation.

Figure 3: Estimates of $\hat{b}_c$ and implied $\hat{m}_c$ vary substantially across birth cohorts.



Notes: Each five-year birth cohort produces an IV estimate of the transmission rate $\hat{b}_c$ (navy, solid circles) and the implied assortative mating $\hat{m}_c = 2\hat{b}_c - 1$ (orange, hollow diamonds). Shaded bands show 95% confidence intervals. White males, cohorts 1865–1915.

As in the state-level analysis, I test whether independent estimates of assortative mating agree across cohorts. If changes in transmission were truly driven by changes in sorting in the marriage market, cohorts with higher transmission should also have stronger father-in-law–son correlations, and cohorts with lower transmission should have weaker ones.

However, as in the state-level analysis, the two measures show no consistent relationship. Figure 4 plots the two independent estimates by cohort: the father-in-law ratio $\hat{r}_c$ on the y-axis and the implied assortative mating parameter $\hat{m}_c = 2\hat{b}_c - 1$, derived from the grandfather–father IV estimate, on the x-axis. Under the model, $m_c = \theta_c r_c$, implying that the relationship should have slope $1/\theta_c$.

Instead, the correlation is weak and not statistically significant (slope $= 0.05$, $R^2 = 0.22$). The father-in-law ratio varies little across cohorts, while $\hat{m}_c$ varies widely, mirroring the pattern observed across states.[19]

4.1.3 Test 3: Consistency of b and m

The preceding tests relied on direct-lineage correlations (grandfather-father-grandson chains) to estimate the underlying b_{state}. But the additive genetic model provides multiple ways to estimate it (Table 3): the uncle/sibling ratio, the cousin/uncle ratio, and the square root of cousin/sibling, each of which cancels measurement error. For these kinship types, all can be observed in the 1940 census, where education and wage income are recorded alongside occupation scores. If the model is correct, all strategies must agree.

Figure 5 displays three alternative estimates of $\hat{b}$ by state. The uncle-sibling ratio varies considerably across states, ranging from roughly 0.5 to 0.8, while the cousin-uncle ratio clusters tightly near or above one. The square root of cousin/sibling estimate falls systematically between the other two. Under the genetic model, all three ratios recover b and should agree. The same failure appears when using wage income (Appendix Figure A8). Appendix Figure A7 adds the grandfather-father IV, which is available only for occupation scores. All four strategies disagree.

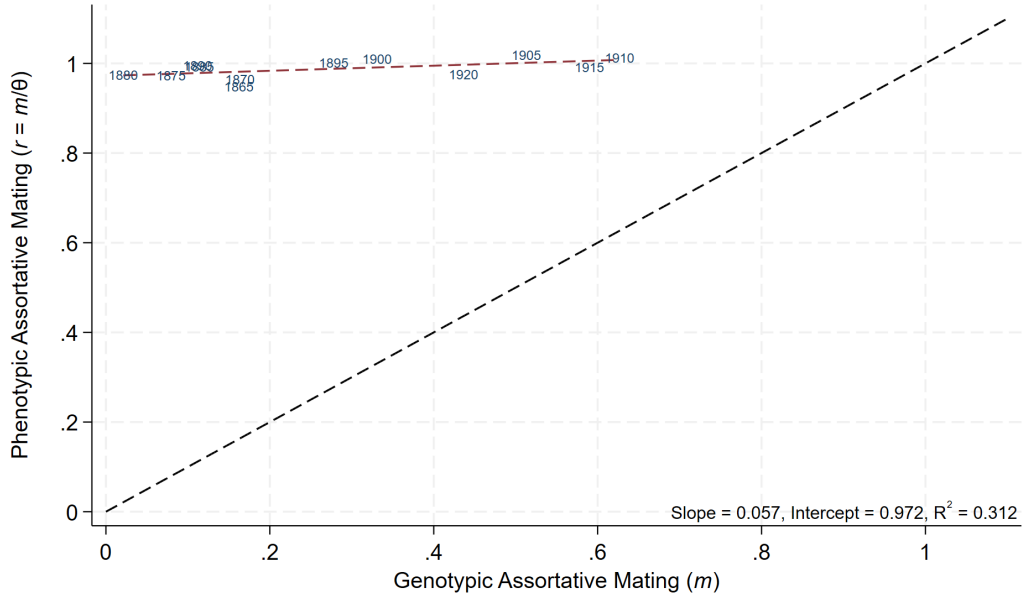
One notable feature of the disagreement is what the cousin–sibling ratio implies on its own. Using the national moments (Table A1), this ratio implies a transmission rate of $b \approx 0.9$, corresponding to an assortative mating parameter of $m \approx 0.8$. This would require very high levels of genetic assortment, well above the spousal correlation in latent genetic factors for educational attainment of 0.37 estimated from Norwegian genomic data after correcting for measurement error in polygenic scores (Torvik et al., 2022; Sunde et al., 2025), and would further imply that assortment on observables, r, is even higher.

Additional moments also help rule out generation-specific measurement error as the source of the overidentification failure (e.g., $\theta_{G1} \neq \theta_{G2} \neq \theta_{G3}$). One test is the ratio of cousin to sibling correlations, since both relationships involve individuals born in roughly the same generation. If measurement error differed across generations, it would not affect this ratio. But as just noted, this ratio implies implausibly high values of b and m, which is itself evidence against the model. A second test exploits the fact that generation-specific measurement error should imply equality

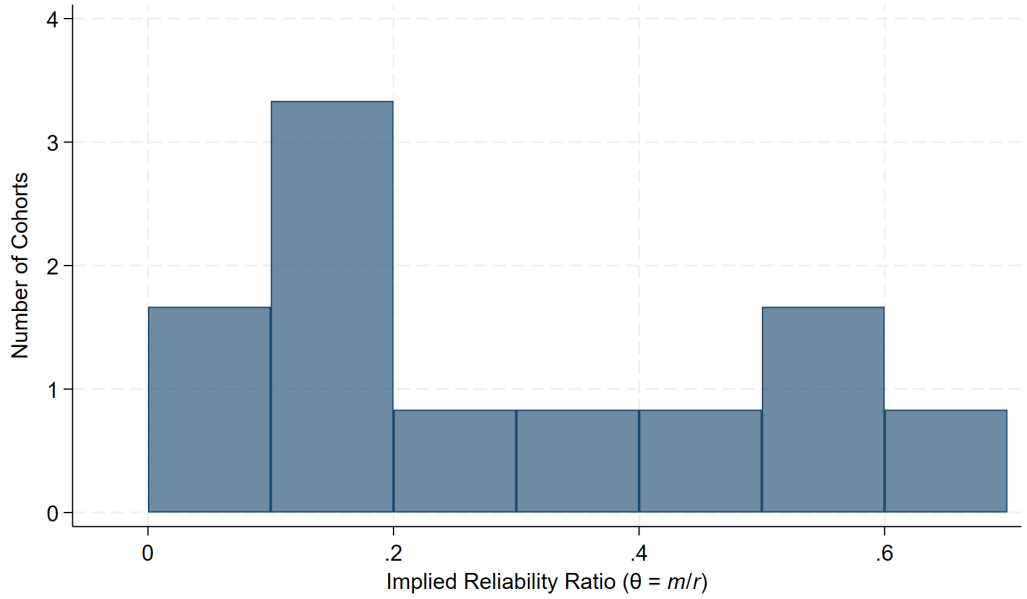
[19] These estimates do not require all individuals to have an observable maternal grandfather. The result is also not driven by compositional differences. When the sample is restricted to cases where the paternal grandfather, maternal grandfather, father, and child all have valid occupation scores, the same pattern appears (Appendix Figure A4).

Figure 4: Latent and observed assortative mating are weakly related across cohorts.

(a) Implied $\hat{m}_c$ from grandfather-father IV vs. observed spousal correlation r_c from father-in-law ratio



(b) Implied reliability ratio $\hat{\theta}_c = \hat{m}_c / r_c$ by cohort



Notes: Panel (a) plots implied assortative mating $\hat{m}_c = 2\hat{b}_c - 1$ (from the grandfather-grandson IV) against the observed spousal correlation r_c (from father-in-law correlations) by five-year birth cohort, 1865–1920. The model predicts $r_c = m_c / \theta_c$, so points should fall above the 45-degree line along a ray with slope $1/\theta_c$. Panel (b) shows the implied reliability ratio $\hat{\theta}_c = \hat{m}_c / r_c$ that each cohort would require for the two estimates to be consistent. The implied $\hat{\theta}_c$ ranges from 0.02 to 0.62, far wider than any plausible cross-cohort differences in measurement quality. Dashed lines mark $\theta_c = 0$ and $\theta_c = 1$.

between the grandfather–grandson/grandfather–father ratio and the cousin/uncle–nephew ratio.[20] I estimate this for occupation scores and find in Figure A7 that these correlations also do not line up. Therefore, it does not appear that generation-specific measurement error explains the inconsistencies with the additive genetic model.

Nor can linkage error explain the pattern. Cousins are the most distant kin type and therefore the most likely to be linked falsely. False positive cousin matches (non-cousins misidentified as cousins) would attenuate the cousin correlation toward zero, pushing the cousin/uncle ratio *down* (Bailey et al., 2020). Since the ratio systematically exceeds one, linkage error works against the finding: even replacing 10% of cousin links with random pairs is sufficient to bring the ratio below one (Appendix Figure A10).

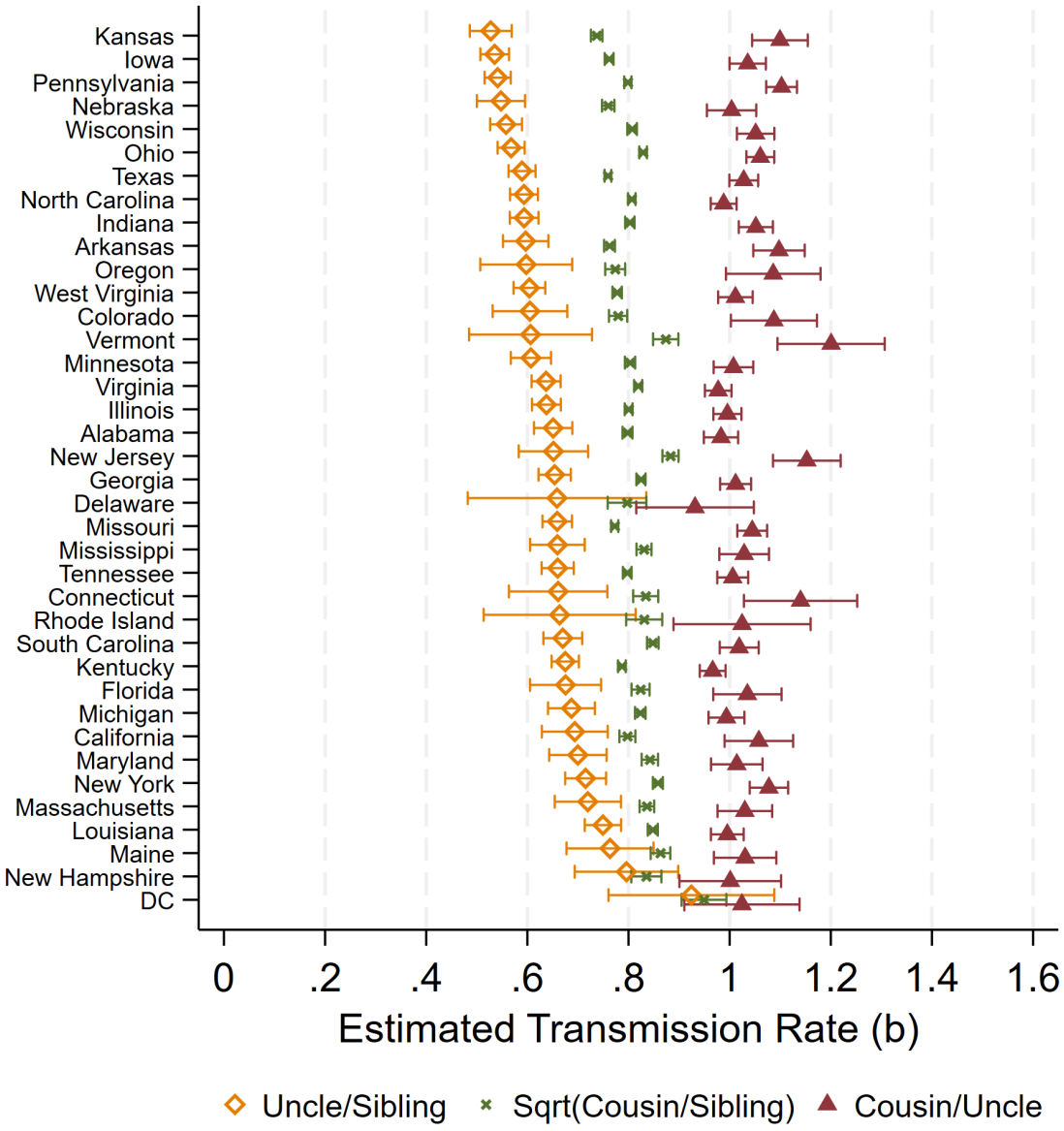
4.1.4 Test 4: Sibling vs. Parent-Child Correlations

I have so far used a rich variety of relationship types to show that the additive genetic model is internally inconsistent. But the comparison between sibling and parent-child correlations is particularly revealing because the two models predict opposite directions. Under the environmental view, siblings should be more correlated: they share the same household, neighborhood, and schools, while parents and children grow up in different eras. The genetic model predicts the reverse. Observing a father's outcome reveals something about the mother he married, and therefore about what the child inherits. Formally, the parent-child correlation is $\theta(1+r)/2$ and the sibling correlation is $\theta(1+m)/2$, and since $r > m$, the genetic model predicts the parent-child correlation exceeds the sibling correlation. The direction of the difference thus tells us which model is right.

I compute the father-son correlation using the intergenerational data (Appendix B.2) and the brother-brother correlation using the sibling data (Appendix B.3), measuring outcomes in adulthood (1940). At the national level, the brother correlation exceeds the father-son correlation for both occupation (0.43 vs. 0.39) and education (0.46 vs. 0.40, Table A1). This is not driven by a few outlier states. Figure 6 plots the sibling correlation against the parent-child correlation for each state,

[20] The grandfather–grandson correlation is attenuated by $\sqrt{\theta_{G3}\theta_{G1}}$, while the grandfather–father correlation is attenuated by $\sqrt{\theta_{G2}\theta_{G1}}$, so their ratio is attenuated by $\sqrt{\frac{\theta_{G3}}{\theta_{G2}}}$. The same attenuation bias applies to the cousin/uncle–nephew ratio. Cousin correlations are attenuated by θ_{G3}, while the uncle–nephew correlation is attenuated by $\sqrt{\theta_{G2}\theta_{G3}}$. Taking the ratio also yields $\sqrt{\frac{\theta_{G3}}{\theta_{G2}}}$. See Appendix C.

Figure 5: Independent estimates of the transmission rate disagree across states.



Notes: Each state's transmission rate $\hat{b}$ is estimated using three independent lateral-kin ratios applied to years of schooling in 1940: uncle/sibling (orange diamonds), the square root of cousin/sibling (green X's), and cousin/uncle (maroon triangles). Under the genetic model, all three recover b and should agree. The grandfather-father ratio is unavailable for education because grandparents' schooling is not observed. States sorted by the uncle-sibling estimate. Appendix Figure A7 repeats the analysis for occupation scores, with similar results.

for both occupation scores (Panel a) and education (Panel b): every state lies above the 45-degree line, and every difference is statistically significant.[21]

I am far from the first to document that the sibling correlation exceeds the parent-child correlation (e.g., see discussion in Björklund and Jäntti (2020)). Clark and Kristensen (2026) acknowledge that sibling correlations exceed the genetic prediction in Danish and Swedish data but argue that this family effect "is not transmitted to the children of these siblings, cousins" (p. 14). If that were true, however, the sibling correlation would be inflated by the transient family effect while the cousin correlation would not. The square root of the cousin-to-sibling ratio in Test 3 should therefore be a *lower* bound on the genetic prediction of b. Yet even this lower bound implies an assortative mating parameter of $m \approx 0.8$, and an even higher level of assortment on observables, r.

The sibling correlation exceeds the father–son correlation, even though the standard genetic model predicts the opposite. How large is this discrepancy relative to the model's prediction? Using the correlation formulas from Table 2, the father–son correlation is related to the sibling correlation as

$$\rho_{\text{father-son}} = \rho_{\text{sibling}} \times \frac{1+r}{1+m}. \tag{6}$$

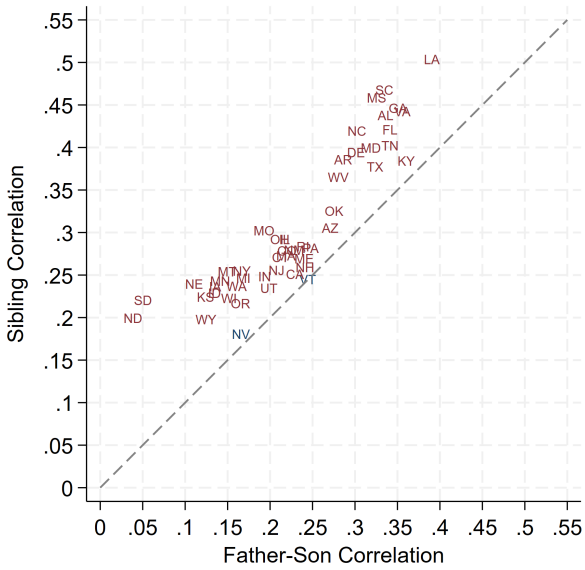
Using the estimated parameters from Tests 1–3 ($\hat{r} \approx 0.96$ and $\hat{m} \approx 0.42$ on average), the ratio $(1+r)/(1+m) \approx 1.4$. The model therefore predicts that father–son correlations should be about 40% higher than sibling correlations, whereas in the data they are roughly 15% lower.

The gap between what the model predicts and what the data show can be quantified state by state. Since I observe the sibling correlation and can estimate $\hat{r}_{state}$ and $\hat{m}_{state}$ for each state, the model delivers a direct prediction for the father–son correlation required for internal consistency. Figure 7 plots these predicted values against the actual correlations in the data. Two failures stand out. First, the observed father–son correlation falls below the sibling correlation in virtually every state, which already points toward shared family environment as an important driver of transmission. Second, the gap between predicted and observed father–son correlations is large: the genetic model requires father–son correlations far above anything seen in the data.

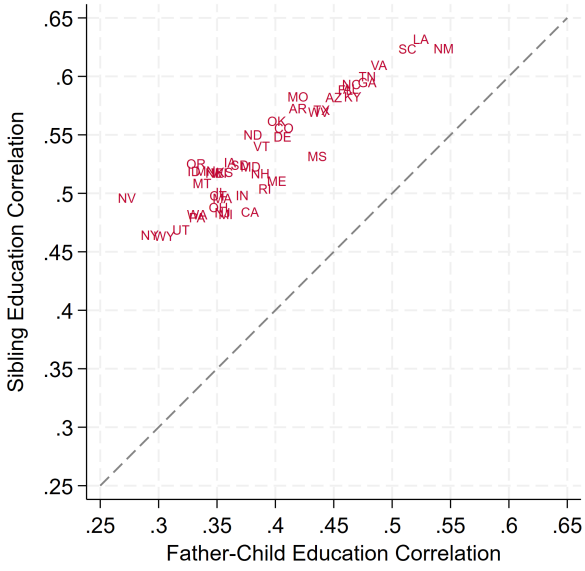
[21] The same pattern appears at the next rung of the kinship ladder. Grandparents and uncles are both at genetic distance 2 from the child, so the model predicts grandparents should slightly exceed uncles (because the direct-lineage path is inflated by phenotype matching). Instead, the uncle-nephew correlation exceeds the grandfather-grandson correlation in nearly every state (Appendix Figure A12), consistent with same-generation environmental channels such as mentoring or labor market connections. Appendix Table A2 extends this comparison to education, further disaggregating by biological and married-in kin.

Figure 6: Sibling correlations exceed parent-child correlations in every state.

(a) Occupation scores

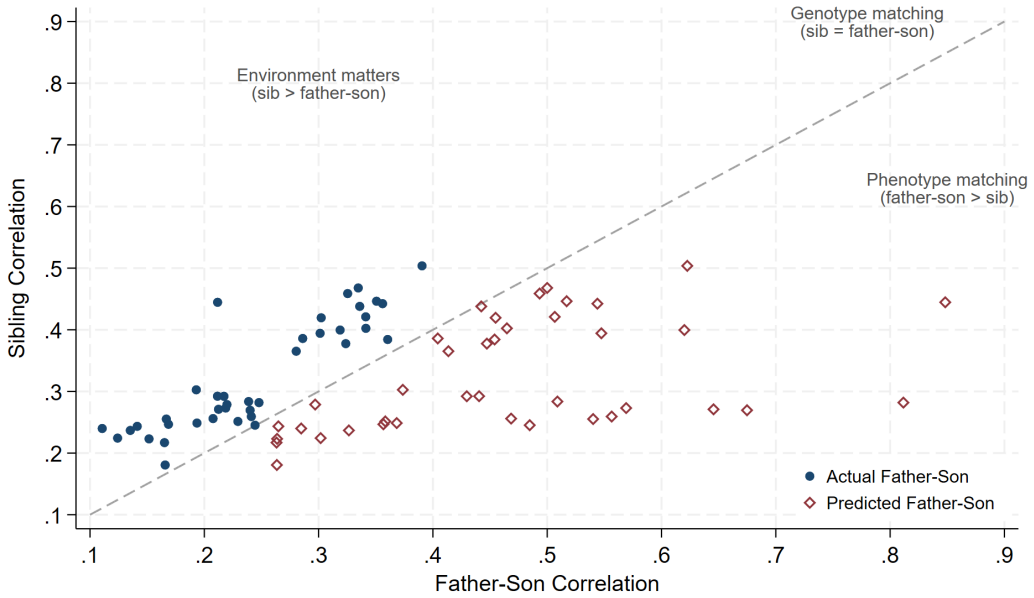


(b) Education



Notes: Each point represents a state. The 45-degree line marks the genetic model's prediction of equality. States above the line have sibling correlations exceeding parent-child correlations, consistent with shared environment effects. Panel (a): brother-brother vs. father-son correlations in occupation scores (white males, 1940). Panel (b): sibling vs. father-child correlations in years of schooling (1940).

Figure 7: Model-predicted father-son correlations far exceed actual values.



Notes: Sibling correlations (y-axis) plotted against actual (navy) and model-predicted (orange) father-son correlations (x-axis), by state. Predicted values use Equation 6: $\rho_{\text{fs}} = \rho_{\text{sib}} \times (1+r)/(1+m)$, where we plug state-level estimates of the sibling correlation, r_{state} and m_{state}.

4.2 Prediction 2: Gender Symmetry

The additive genetic model predicts that transmission is symmetric across gender. Each parent contributes half of the child's genetic endowment regardless of sex, so maternal and paternal lineages should have equal effects, and sibling correlations should not depend on the gender composition of the pair. I test these predictions using occupation scores and education.

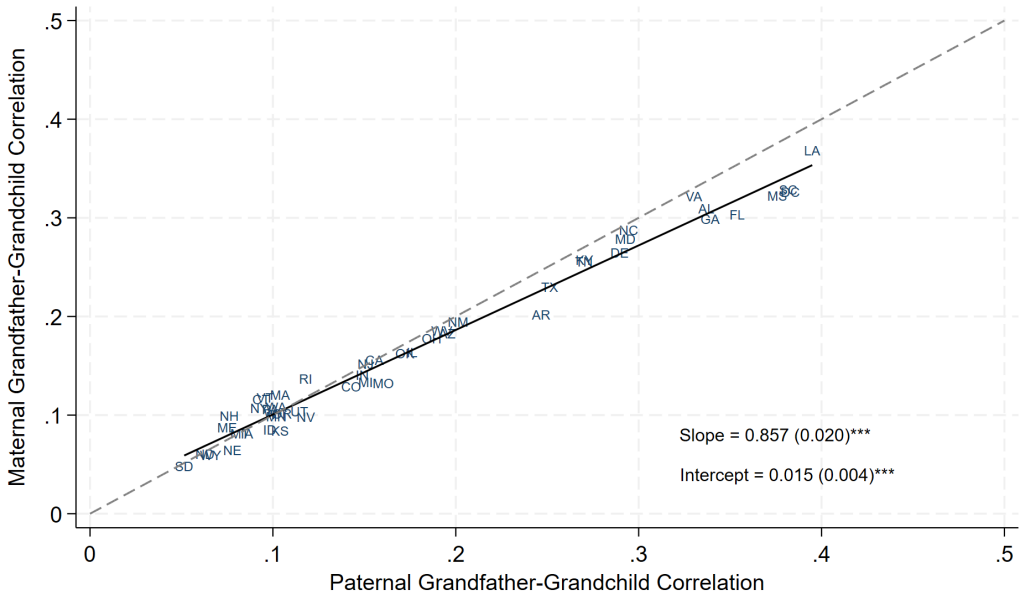
4.2.1 Tests 5–6: Gender Symmetry

Under the additive genetic model, both grandfathers are at genetic distance 2 from the grandchild, and both mothers and father contribute equally, so the paternal and maternal grandfather correlations should be the same (Test 5). Any asymmetry would suggest that the type of lineage matters, for instance if patrilineal cultural transmission is stronger due to occupational networks or inheritance norms.

Figure 8 plots the maternal grandfather correlation against the paternal grandfather correlation for each state. Under the additive genetic model, all states should fall on the 45-degree line. The fitted slope is 0.86, which is statistically different from 1: paternal grandfather correlations are slightly stronger in states with greater intergenerational transmission. This rejects the strict prediction of

the additive genetic model. However, the deviations from the 45-degree line are small. Most states cluster near the line, and the overall pattern is not a dramatic departure from the claim that mothers and fathers matter similarly for occupational transmission. Of course, symmetry between maternal and paternal lineages would not itself imply a genetic mechanism, since environmental channels could also operate symmetrically through both parents.

Figure 8: Paternal and maternal grandfather correlations are roughly equal across states.



Notes: Each point represents a state. The 45-degree line marks perfect gender symmetry. The solid line is the OLS fit. White males, occupation scores.

A more direct test (Test 6) of gender symmetry asks whether the mother's and father's education have equal effects on the child's education (Appendix B.6). I identify children ages 5–14 in the 1920 census who have both parents present, link all three family members to the 1940 census, and observe each person's years of schooling. This yields 3.8 million child-parent triads where education is measured for all three in the same census.

Table A3 reports the horse race results. Pooling all children, the mother's coefficient (0.27) exceeds the father's (0.24), statistically rejecting the genetic model's prediction that parental effects should be equal. The difference is modest overall, but clearer patterns emerge when the sample is split by child gender. For sons, the father's coefficient slightly exceeds the mother's (0.25 vs. 0.24), a difference statistically significant at the 5 percent level. For daughters, however, the mother's coefficient (0.30) is much larger than the father's (0.22). This pattern suggests that mothers'

education had a particularly strong influence on daughters, consistent with same-sex role modeling or gender-specific norms surrounding schooling in this period.

The stronger association between mothers' education and daughters' education appears in every state (Panel A of Figure 9). Southern states show the largest maternal premium, possibly reflecting stricter gender norms that made daughters' schooling more dependent on their mothers' education. For sons, the pattern is weaker and less uniform: some states fall below the 45-degree line (father stronger), while many others lie near or above it, indicating that the small father-son advantage in the pooled estimates is not consistent across states. More broadly, these findings align with evidence during this period that mothers play an important role in forming children's human capital Althoff et al. (2025); Espín-Sánchez et al. (2023).

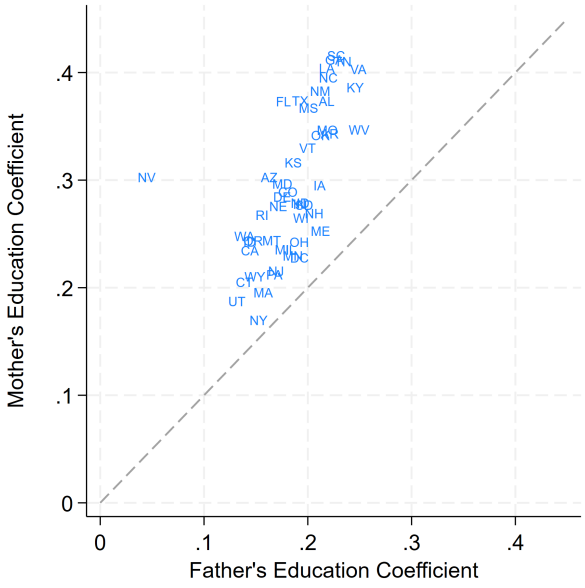
4.2.2 Test 7: Gender-Symmetric Sibling Correlations

TThere are no gender-specific terms in the standard additive genetic model. Sons and daughters each inherit half of their parents' latent endowment on average, so the model predicts that sibling correlations should not depend on the gender composition of the pair. In other words, brother–brother, brother–sister, and sister–sister pairs should all have the same expected correlation (Test 7). If instead gender-specific environmental channels matter, one might expect higher correlations for same-sex siblings, particularly for sisters given the stronger mother–daughter associations observed above. Gender-specific measurement error may be an issue with this comparison, however, where education reflects genetic potential differently by sex, a point which we will address below.

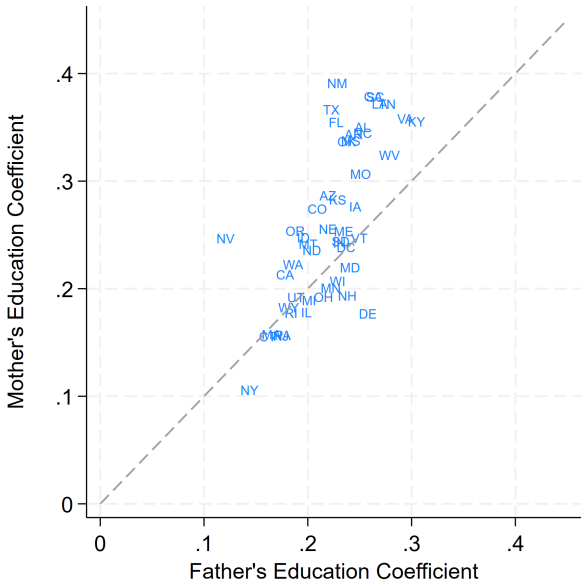
I test whether gender composition matters using the sibling data (Appendix B.3) and education (years of schooling) measured in the 1940 census for adults age 25 and older. Brother-brother pairs have an education correlation of 0.46, brother-sister pairs show a nearly identical correlation of 0.47, but sister-sister pairs are substantially more correlated at 0.55. The sister-sister premium is large and precisely estimated, well outside the confidence intervals of the other two pair types. Figure 10 shows that this result is not driven by a few unusual states: sister-sister correlations exceed brother-brother correlations in every state, with an intercept of 0.117 well above the 45-degree line.

This pattern, where sister-sister correlations exceed brother-brother and brother-sister correlations by a wide margin, is inconsistent with the pure genetic model's prediction of equality. The sister-sister premium is remarkably stable across states in absolute terms, suggesting a common mechanism rather than local variation in norms or institutions. One explanation is that women's educational attainment in this era was more heavily shaped by family-level decisions. Parents chose whether and how far to educate their daughters, and sisters in the same household faced the same parental

Figure 9: Mother's education predicts daughters' education better than father's in nearly every state; the father-son pattern is weaker.



(a) Daughters

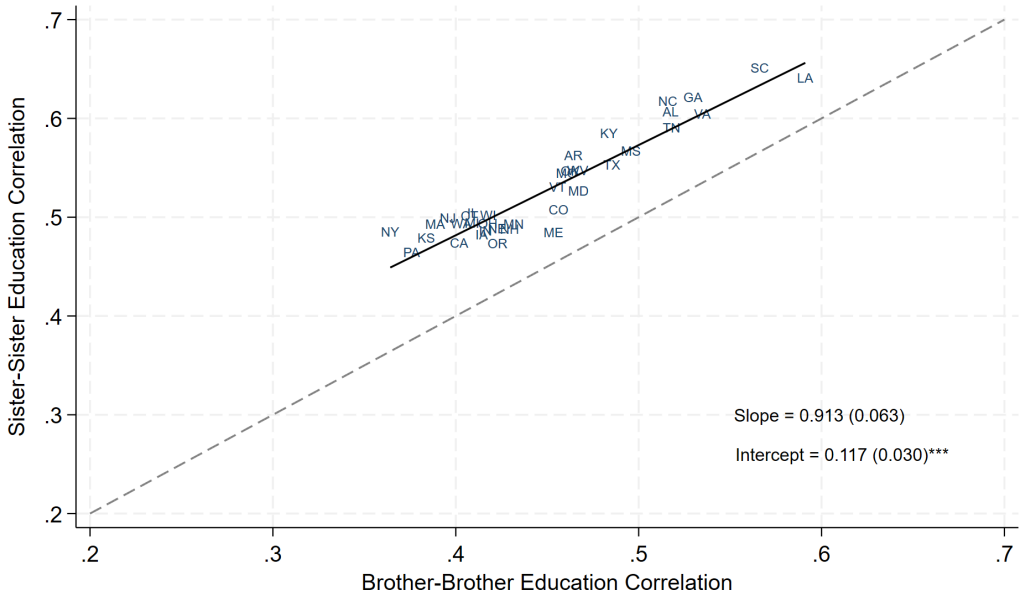


(b) Sons

Notes: Each point represents a state. The y-axis plots the coefficient on mother's education; the x-axis plots the coefficient on father's education from the same horse race regression. The 45-degree line marks equal coefficients. Panel (a): for daughters, nearly every state lies above the line, indicating that mother's education is the stronger predictor. Panel (b): for sons, the pattern is more mixed, with states scattered on both sides of the line. Children ages 5–14 in 1920 linked with both parents to 1940; education measured as years of schooling.

calculus. Brothers' schooling may have been more responsive to individual-level factors like ability or outside labor market opportunities, producing more variation within families even when the family-level mean was similar.

Figure 10: Sister-sister education correlations exceed brother-brother correlations in every state.



Notes: Sister-sister education correlations (y-axis) plotted against brother-brother education correlations (x-axis), by state. The dashed line is the 45-degree line. Under the genetic model, all states should fall on this line. The solid line is the fitted regression. Education measured as years of schooling in the 1940 census, adults age 25 and older.

An alternative explanation is gender-specific measurement error. Under the genetic model, siblings share the same fraction of genetic endowment regardless of sex, so the true sibling correlation is a single number. But if education captures that latent endowment with different reliability for men and women, the *observed* correlations will differ by pair type. Note that this explanation is itself somewhat surprising in context: the higher sister-sister correlation implies that education is a *better* proxy for women's latent ability than for men's, the opposite of the argument above that brothers' schooling was more responsive to individual ability.

Regardless, the measurement error story makes a testable prediction. If gender-specific attenuation is the only reason same-sex correlations differ, the brother-sister correlation should fall between the two, at the geometric mean: $\sqrt{0.46 \times 0.55} = 0.50$. The actual brother-sister correlation is 0.47, below this prediction and closer to the brother-brother value. Gender-specific measurement error therefore does not explain the pattern, suggesting that the sister-sister premium reflects a genuine

environmental channel. In the next set of predictions, we test whether some observable changes in family environment impacts child outcomes.

4.3 Prediction 3: Family Environment

The additive genetic model implies that family environment (the resources, investments, and circumstances of a child's upbringing) should be irrelevant to for the child's outcomes and intergenerational transmission. Several of the following tests show small effect sizes from shocks within the family. These results should be read in light of the prior evidence: a genetics-only model of transmission fails to be internally consistent. Therefore, they help to reveal which mechanisms were important for child outcomes.

4.3.1 Test 8: Living vs. Dead Parents

If genetic transmission is the sole mechanism, a parent who dies should predict the child's outcome just as well as a surviving parent, since genes were passed at conception. Under environmental models, however, parental death removes a key source of investment, role modeling, and economic resources, and should weaken the parent-child correlation.

The identification strategy exploits widowhood (Appendix B.5): children living with a widowed mother or widowed father in the 1910 census have lost a parent.[22] Linking these children back to the 1900 census recovers the parents' characteristics, and linking forward to 1940 reveals the child's adult outcome. A control group of children from the same 1910 census whose parents are both alive provides the comparison, with all parental outcomes measured in 1900. In the education sample, 167,557 children (4.7 percent) lost their father compared to 3.4 million whose fathers survived; 106,013 (3.1 percent) lost their mother compared to 3.3 million whose mothers survived. The occupation sample (sons only) contains 93,876 paternal-death cases and 1.8 million controls.

I estimate the regression separately for paternal and maternal death:

$$y_{i,\text{child}} = \alpha + \beta_1 y_{\text{parent}} + \beta_2 \text{ParentDied}_i + \beta_3 (\text{ParentDied}_i \times y_{\text{parent}}) + \varepsilon_i \tag{7}$$

where β_3 tests whether the parent-child transmission slope differs when the parent is deceased. Under environmental models, $\beta_2 < 0$ (a direct negative effect of parental death) and β_3 may also differ from zero if parental death disrupts the transmission mechanism. The strict prediction of the genetic model is $\beta_2 = \beta_3 = 0$. I do not have data on the cause of death and so the identification strategy is the cleanest. One might expect this test to be biased toward finding a negative effect,

[22] Widowhood is identified by marital status code 5 (`marst`=5) in the census.

since a common health shock, for example, could cause the parent's death and long-term harm to the child. Under the genetic model, however, any impact of such shocks is temporary and should fade by adulthood. I estimate effects on both sons' occupations and children's education (observed in 1940).

Table 4 reports the results. The genetic model is rejected on both the intercept and the slope. On the intercept (β_2): children who lost their father have 0.08 standard deviations less education than children whose fathers survived, and children who lost their mother have 0.14 standard deviations less. Parental death lowers children's outcomes even after controlling for the parent's own status. On the slope (β_3): the interaction terms are negative and significant in every specification, meaning that intergenerational transmission itself is weaker when a parent has died. A high-status parent passes on less of that advantage if they die before the child reaches adulthood. The patterns are similar for sons and daughters, though father's death is associated with a larger level gap for sons, and mother's death with a larger gap for daughters.[23]

These are not causal estimates; early parental death is correlated with poverty, poor health, and other disadvantages that independently affect children's outcomes. The results nonetheless reject the genetic model's strict prediction that $\beta_2 = \beta_3 = 0$. Yet the magnitudes are small, and could be interpreted as evidence that nature dominates nurture. Recall, however, that sibling correlations exceeded parent-child correlations, suggesting that the broader family environment matters for children's outcomes beyond the direct contribution of any single parent. Further, remarriage, extended kin, and community institutions may have partially insured children against the loss of a parent, dampening the observed effect.[24]

4.3.2 Test 9: Twins and Age Gap

Age gaps between siblings provide a useful test of the additive genetic model because it predicts a very specific pattern for the correlation across spacing. For siblings with zero age gap (twins), the correlation should exceed the regular sibling correlation because some twins are identical and share all of their genes, whereas ordinary siblings differ due to the randomness of recombination. If there is no clear twin premium, this suggests that genetic inheritance plays a limited role. Beyond twins, however, the genetic model predicts a flat profile. Siblings born one year apart and those born ten

[23] Appendix Table A4 reports the same specification using sons' occupation scores: the results are qualitatively similar, with smaller but statistically significant associations.

[24] Other work using quasi-experimental variation has found larger effects. Goldstein (2025) exploits mining accidents and finds a substantial impact on sons' outcomes; Dupraz and Ferrara (2025) use Civil War deaths and reach a similar conclusion.

Table 4: Education Transmission: Effects of Parental Death

	(1) All Children	(2) Sons	(3) Daughters
Panel A: Father Death			
Father's Occupation	0.307	0.315	0.293
	(0.000)	(0.001)	(0.001)
Father Died (before 1910)	-0.081	-0.107	-0.043
	(0.002)	(0.003)	(0.003)
Father Died × Father's Occupation	-0.020	-0.020	-0.025
	(0.002)	(0.002)	(0.003)
Observations	5,026,337	2,786,193	2,240,144
R-squared	0.093	0.097	0.087
Panel B: Mother Death			
Father's Occupation	0.307	0.316	0.294
	(0.000)	(0.001)	(0.001)
Mother Died (before 1910)	-0.137	-0.124	-0.154
	(0.002)	(0.003)	(0.003)
Mother Died × Father's Occupation	-0.027	-0.026	-0.028
	(0.002)	(0.003)	(0.004)
Observations	4,892,502	2,708,247	2,184,255
R-squared	0.093	0.097	0.088

Notes: All variables standardized to mean zero and unit variance. Father death identified from children living with a widowed mother in 1910; mother death from children living with a widowed father. Robust standard errors in parentheses.

years apart inherit from the same two parents, so the expected genetic similarity is unchanged. Once the twin premium is removed, the correlation should be roughly constant across all other age gaps.

Environmental models imply a different pattern. Siblings born close together experience more similar childhood environments. They are more likely to attend the same schools at the same time, face the same local economic conditions, and share parental time and household resources at similar stages of development. As the age gap increases, these shared experiences diverge, so the sibling correlation should decline with birth spacing rather than remain flat. If only environment matters and genes do not, one would predict a linear profile between sibling correlations and age gaps.

I identify twins from the 1900 census as siblings born in the same month and year (Appendix B.4), the only census that records month of birth. I then link them forward to 1940 and compare their occupation and education correlation to that of non-twin siblings at various age gaps. One limitation is that the data do not distinguish monozygotic from dizygotic twins.

The results suggest that both genetics and shared environment contribute to intergenerational transmission. The figure reveals a clear monotonic decline in sibling correlations as age gaps widen, from 0.37 at 1–2 years apart to 0.34 at 10–14 years (Figure 11). Under the genetic model, this line should be flat: all siblings inherit from the same two parents regardless of when they are born. The observed decline indicates that siblings born close together share more of the same childhood environment and are therefore more similar. At the same time, twins have a correlation of 0.43, a premium of 0.06 over siblings 1–2 years apart that is statistically significant and consistent with a role for genetics, since identical twins share the same DNA. Panel B shows that a similar pattern holds for education: the twin premium is even larger (0.56 vs. 0.49) and the decline across age gaps is steeper.

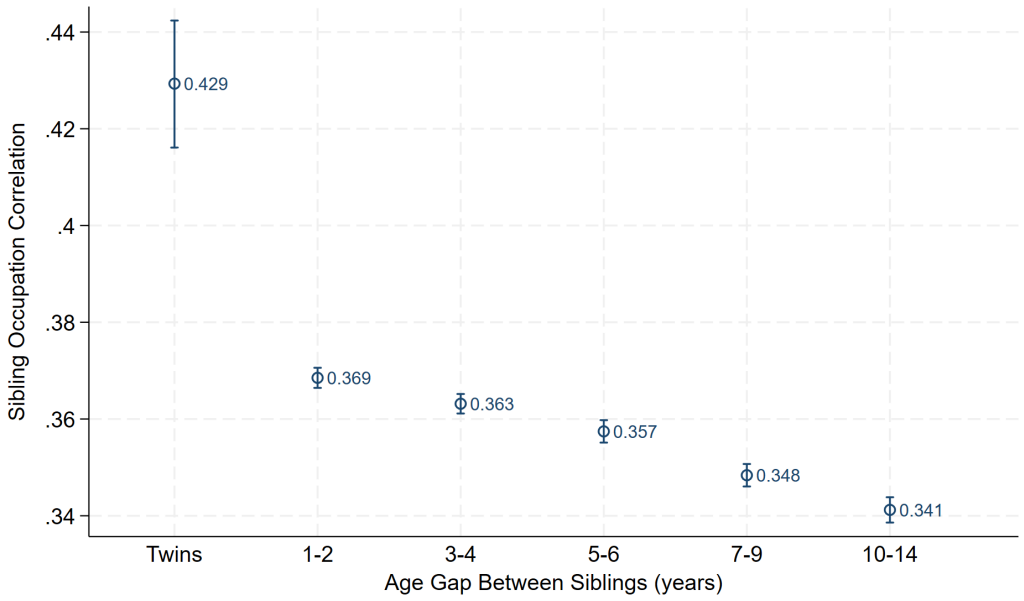
4.3.3 Test 10: Birth Order

Does birth order affect adult outcomes? Each child's endowment is determined at conception regardless of birth order, so the genetic model predicts no birth order effects. But first-borns may benefit from undivided parental attention, primogeniture norms, different parental expectations, or simply more resources before younger siblings arrive.

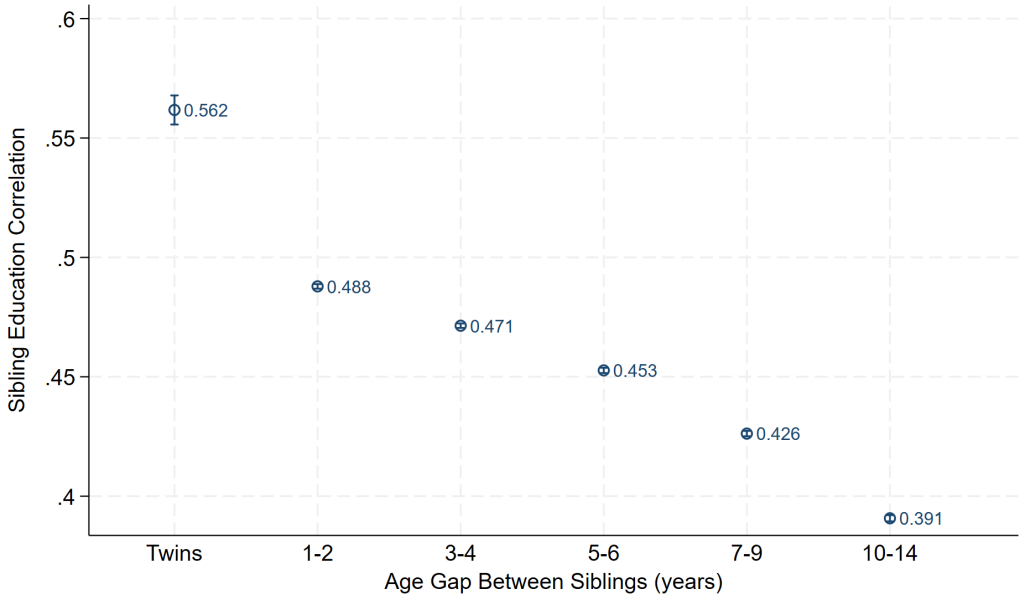
Using the intergenerational data (Appendix B.2), I identify birth order within families using children's ages in the childhood census and estimate birth order effects with and without family fixed effects. The family fixed effects compare siblings within the same family, holding constant all family-level characteristics.

Figure 11: Sibling correlations decline with age gap, and twins show a substantial premium.

(a) Occupation scores



(b) Years of education



Notes: Sibling correlations by age gap. Under the genetic model, the correlation should be flat across age gaps because all siblings inherit from the same two parents. Panel A: white male sibling pairs, occupation scores measured in 1940. Panel B: all white sibling pairs (brother-brother, sister-sister, and brother-sister), years of education measured in 1940 for adults age 25 and older.

Table 5 reports the results, controlling for family and birth year fixed effects.[25] First-born children have systematically higher occupation scores and education than later-born siblings. The effects are small: within the same family, fifth-born children score about 0.04 standard deviations lower than first-borns on occupation and education. Wage effects are small but significant for second- through fourth-borns. These magnitudes are consistent with Cools et al. (2024), who use a similar family fixed effects strategy on linked U.S. census data and find a firstborn occupational premium of 2.5–3.8 percent of a standard deviation. The effects are small, but the genetic model predicts exactly zero, and occupation and education effects are statistically significant at every birth order position.

Table 5: Birth Order Effects on Child Outcomes (Family Fixed Effects)

	Occupation	Education	Wage Income
First-born	Ref.	Ref.	Ref.
Second-born	-0.024	-0.047	-0.017
	(0.001)	(0.001)	(0.001)
Third-born	-0.030	-0.048	-0.020
	(0.002)	(0.002)	(0.002)
Fourth-born	-0.035	-0.048	-0.014
	(0.003)	(0.003)	(0.003)
Fifth-born+	-0.036	-0.038	-0.004
	(0.006)	(0.006)	(0.007)
N	6,985,692	4,975,175	4,289,915

Standard errors clustered at the family level in parentheses. All regressions include family and birth year fixed effects. Since all children are observed in 1940, birth year fixed effects are algebraically equivalent to mother's age at birth fixed effects within the family fixed effects model. All outcomes standardized to mean zero and unit variance nationally. Occupation: adjusted occupation score. Education: years of schooling (age $\geq$ 25). Wage: wage income (wage workers, classwkr=2). White males.

If birth order effects operate through environmental channels, they should vary with family resources. Table 6 interacts birth order dummies with father's standardized occupation score (mean zero, standard deviation one). For occupation and education, the interaction is positive: the first-born advantage is smaller in high-status families. The education interaction rises from 0.046 for second-borns to 0.073 for fifth-borns and above, consistent with high-status families sustaining investment across multiple children. The occupation interactions are more modest but stable across birth order positions. For wages, however, the interactions are close to zero or slightly negative, which complicates a simple resource dilution interpretation. One possibility is that father's occupational status influences investments in human capital (schooling, skill formation) more directly than it

[25] Since all children are observed in the 1940 census, a child's birth year is a one-to-one function of their age (birth year $=$ 1940 $-$ age). Within the family fixed effects model, the mother's birth year is absorbed as a family-level constant, so the birth year fixed effects are algebraically equivalent to mother's age at birth fixed effects.

influences wage outcomes, which depend on local labor market conditions. Regardless, under the genetic model, birth order effects should be zero at every level of father's status, so there is no scope for a systematic interaction in either direction. Appendix Table A5 extends the analysis to daughters and finds that birth order effects on education are weaker for women than for men.

Table 6: Birth Order Effects Interacted with Father's Occupational Status

	Occupation		Education		Wage Income	
	Main	× Father	Main	× Father	Main	× Father
First-born	Ref.	—	Ref.	—	Ref.	—
Second-born	-0.020	0.048	-0.043	0.046	-0.018	-0.001
	(0.001)	(0.001)	(0.001)	(0.001)	(0.001)	(0.001)
Third-born	-0.025	0.043	-0.041	0.054	-0.022	-0.017
	(0.002)	(0.001)	(0.002)	(0.002)	(0.002)	(0.002)
Fourth-born	-0.030	0.040	-0.037	0.062	-0.020	-0.022
	(0.003)	(0.003)	(0.003)	(0.003)	(0.004)	(0.003)
Fifth-born+	-0.029	0.052	-0.025	0.073	-0.017	-0.037
	(0.006)	(0.006)	(0.007)	(0.007)	(0.008)	(0.008)
N	6,638,426		4,709,538		4,058,694	

Standard errors clustered at the family level in parentheses. All regressions include family and birth year fixed effects. columns report the birth order coefficient at the mean of father's status. columns report the interaction between birth order dummies and father's standardized occupation score (mean 0, SD 1). A positive interaction means the birth order penalty is smaller (or reversed) for children of higher-status fathers. White males.

4.3.4 Test 11: Family Size

A related question is whether family size affects the strength of intergenerational transmission. Each child's genetic endowment is independent of how many siblings they have, so the genetic model predicts no family size effects. But larger families spread parental resources thinner, which could weaken the father-child correlation or lower the level of child outcomes.

I test this prediction using both OLS and an instrumental variables strategy following Black et al. (2005), which exploits twin births as an exogenous shock to family size. Family size is measured as the number of children observed in the father's household in the 1900 census. This is a snapshot rather than completed fertility: some families were still growing, and older children may have already left. A twin birth at parity n increases the number of children in the household by one without reflecting deliberate parental choice. To avoid endogenous responses to the twin birth, I restrict the outcome sample to children born prior to the twin event. This design is not without limitations. If parents reallocate resources toward older children following a twin birth, as documented by Rosenzweig and Zhang (2009), such responses would attenuate the negative

effect of larger family size. From the perspective of the environmental model, the IV estimates may therefore be conservative. For this reason, I also report OLS estimates.

Twins are identified in the 1900 Census as children within the same household who share both age and birth month (Appendix B.2). I present results for twin births at parity 2 (affecting first-born children), parity 3 (affecting first- and second-born children), and parity 4 (affecting the first through third-born children).

Figure 12 reports both the OLS and IV estimates. The effects are uniformly small: all point estimates are less than 0.06 standard deviations per additional sibling, and several confidence intervals span zero. The largest effect is for wage income when instrumenting with a twin at the fourth birth order (-0.06 standard deviations). Appendix Table A6 interacts father's occupation with family size, and these interactions are also small, with many insignificant. The results suggest that an exogenous increase in family size does not substantially affect adult outcomes, consistent with the genetic model. That said, the effect is per sibling: across realistic family size differences in this period, the cumulative effect could be meaningful (e.g., three additional siblings would imply roughly -0.18 standard deviations).

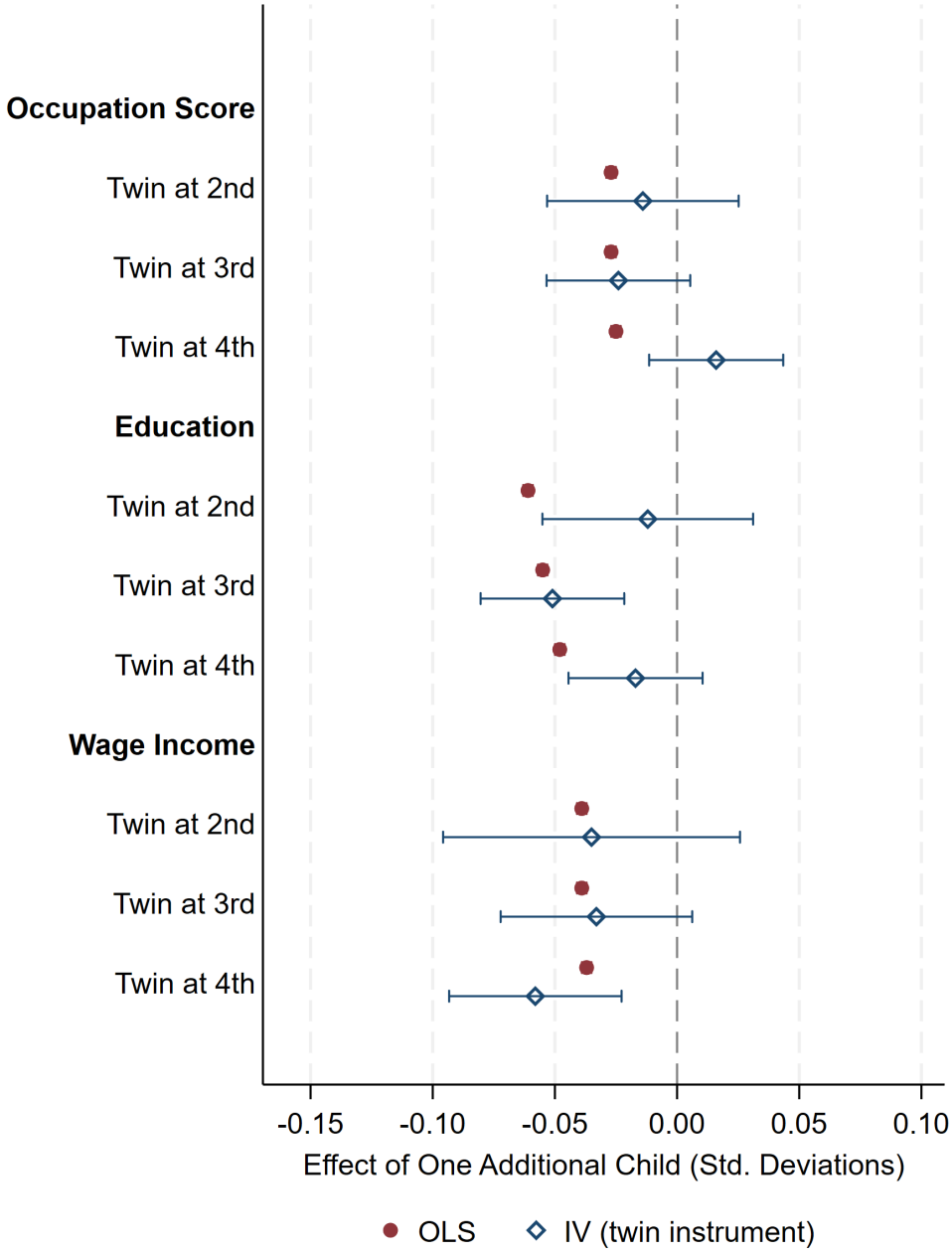
4.3.5 Test 12: Biological Parents More Predictive

The additive genetic model predicts that adopted children should have zero correlation between their adult outcomes and their adoptive father's occupation, since no genes are shared and (absent selective placement) the adoptive family has no genetic link to the biological parents. For stepchildren, the prediction is less stark: the stepfather shares no genes with the child, but his genetic relationship to the child is analogous to a father-in-law's (one genetic step via the mother and one marriage step). Assortative mating means the stepfather's occupation proxies for the mother's genetic endowment, creating an indirect channel. The model therefore predicts a reduced stepfather-child correlation, not zero.

I identify adopted children and stepchildren in the 1900, 1910, and 1920 censuses using detailed relationship codes[26] (Appendix B.7), link them forward to 1940 to observe their adult occupation scores, and compute the father-child occupation correlation separately by relationship type.

[26]Adopted children are identified by RELATE codes 302 and 304; stepchildren by code 303. The census did not specifically ask about adoption but it is inferred from the "relationship to head of family" question (Moriguchi and Parman, 2015). All instances of "adopted son" or "adopted daughter" were self-reported by the household. Measurement error therefore runs in both directions: many formally adopted children were likely recorded simply as "son" or "daughter" and are missed, while some children listed as "adopted" may have been informally taken in by extended family and would not meet modern definitions of adoption.

Figure 12: Family size effects on child outcomes: OLS vs. IV (twin instrument).



Notes: Each row reports the effect of one additional child on the child's standardized adult outcome. OLS (maroon circles) and IV (navy diamonds) with 95% confidence intervals. The IV instruments number of children with a twin birth at the indicated position; the outcome sample includes only children born before the twin. The dashed line marks zero, the genetic model's prediction. Appendix Table A7 reports point estimates, standard errors, sample sizes, and first-stage F-statistics.

Both adopted and stepchildren show substantial correlations with their rearing father's occupation, rejecting the genetic model's prediction (Table 7). Biological children have a correlation of 0.37, stepchildren 0.33, and adopted children 0.28.[27] The adopted children's correlation of 0.28 is well above the zero predicted by the model, providing evidence for environmental transmission since no genetic channel connects them to their adoptive father (though selective placement could contribute, a point I return to later). Two recent studies of the Orphan Train Movement reach similar conclusions, where the foster parent's income score predicts the child's income score Abrahams and Keniston (2025); Bullard and Van Leeuwen (2025). Both non-biological groups fall below the biological baseline, consistent with some genetic contribution but also longer environmental exposure, but the stepchildren's correlation of 0.33 is close to the biological level. The pattern holds for education and wage income as well.

An alternative approach is to estimate the correlation of adult outcomes between siblings raised by the same father, comparing biological-biological pairs to biological-adopted and biological-step pairs. If adult outcomes are determined entirely by inherited endowment, biological and adopted siblings should have no correlation since they share no genes. But the results show positive correlations for biological-adopted sibling pairs for occupation, educational attainment, and wages (Appendix Table A8).

Table 7: Father-Child Correlations by Relationship Type and Outcome

	Biological	Adopted	Stepchild
Occupation	0.373	0.283	0.330
	(0.000)	(0.007)	(0.002)
Education	0.325	0.281	0.281
	(0.000)	(0.008)	(0.002)
Wage Income	0.205	0.146	0.185
	(0.000)	(0.009)	(0.003)
N	15,892,316	17,920	155,917

Note: Correlations between father's occupation score and child's outcome. Father's occupation from childhood census (1900–1920); child's outcomes from 1940. Standard errors in parentheses. Education: years of schooling, standardized within 5-year age bands (age $\geq$ 25). Wage income standardized within 5-year age bands; wage workers only. White males. Predicted zero for adopted and stepchildren.

This cross-child comparison has two limitations. First, children coded as "adopted" in early censuses may include extended kin raised by relatives, such as nephews raised by uncles or grandchildren raised by grandparents. If so, the "non-biological" group has some genetic relatedness

[27] Sample sizes are 15.9 million biological, 155,917 stepchildren, and 17,920 adopted children.

to the household head, and part of the observed correlation reflects shared genes rather than environment. Second, the comparison is across different children: biological, step, and adopted children may differ in unobserved ways that affect both selection into the household and adult outcomes.

A within-child design mitigates both concerns by predicting each adopted child's outcomes from both their biological and adoptive father's outcomes. Because the same child is observed with both fathers, unobserved child characteristics that affect selection into adoption and later-life outcomes are less likely to confound the comparison. And because the biological father is observed directly, any genetic similarity between the child and the adoptive household is less likely to be mistaken for environmental influence. I stack two cohorts: children recorded as adopted in the 1910 census who appear as biological in 1900, and children recorded as adopted in the 1920 census who appear as biological in 1910 (Appendix B.9). In both cohorts I restrict to children ages 0–5 in the earlier census to ensure they will still be in the household ten years later. Where the adoptive father can be linked back to the earlier census, I verify that he is a different person from the biological father and drop confirmed same-person cases; adoptive fathers who cannot be linked back are retained under the assumption that they are different people. To address the concern that some "adopted" children may have been placed with extended kin rather than unrelated families, I drop cases where the biological father and the adoptive father share the same surname. About 16 percent of the sample has matching surnames, consistent with placement within extended families. Dropping these cases yields 1,679 children for whom I observe both a biological father and an adoptive father, along with the child's 1940 outcomes.

Panel A of Table 8 presents the adoptee results, with all variables standardized. The adoptive father's coefficient (0.28) exceeds the biological father's (0.22) for occupation, though the difference is not statistically significant. For education, the adoptive father's coefficient (0.23) is nearly double the biological father's (0.13), a difference significant at the 5 percent level. For wages, the biological father's coefficient is larger but the difference is not significant. The father who raised the child predicts adult outcomes at least as well as the father who provided the genes, a direct rejection of the model's central prediction.

I replicate this design using stepchildren. I stack two cohorts: children living as biological offspring in the 1900 census who appear as stepchildren in 1910, and children biological in 1910 who appear as stepchildren in 1920 (Appendix B.8).[28] I verify that the child's mother is the same person in both census years, confirming that the biological father died or left and the mother

[28] Biological children are identified by RELATE code 301; stepchildren by code 303.

remarried.[29] This design yields 15,478 children for whom I observe both a verified biological father and a verified stepfather.

The stepfather design is a weaker test than the adoptee design because assortative remarriage creates an indirect channel through the mother's genes: the stepfather's occupation is correlated with the mother's latent endowment, which the child inherits. But the biological father carries both a direct genetic contribution and this indirect channel, so in a horse race regression his coefficient should still exceed the stepfather's.

Panel B of Table 8 presents the stepfather results. For occupation scores, the stepfather's coefficient (0.25) exceeds the biological father's (0.21), a difference significant at the 5 percent level ($p = 0.012$). This is the opposite of what the genetic model predicts: the father who raises the child matters more than the father who provided the genes. For education, the biological father's coefficient (0.22) exceeds the stepfather's (0.19), but the difference is not statistically significant ($p = 0.079$). For wage income, the two coefficients are identical (0.15). Across all three outcomes, the two fathers' coefficients are statistically indistinguishable or favor the stepfather, reinforcing the adoptee results.

[29] I also link the stepfather back to the earlier census and confirm that he is a different person from the biological father. About 25% of linkable stepfathers turn out to be the same man as the biological father, most likely cases where the man was truly a stepfather in both years but was recorded as "father" in one census and "stepfather" in the next. Dropping these cases has little effect on the results.

Table 8: Biological vs. Non-Biological Father: Horse Race

	Occ. Score	Education	Wage Income
	(1)	(2)	(3)
Panel A: Biological vs. Adoptive Father			
Bio Father's Occ.	0.218	0.134	0.155
	(0.027)	(0.027)	(0.032)
Adoptive Father's Occ.	0.278	0.234	0.085
	(0.027)	(0.029)	(0.032)
R^2	0.169	0.099	0.042
p(Bio = Adopt)	0.186	0.030	0.163
N	1,679	1,649	1,242
Panel B: Biological vs. Step Father			
Bio Father's Occ.	0.214	0.220	0.146
	(0.009)	(0.010)	(0.011)
Step Father's Occ.	0.253	0.192	0.146
	(0.009)	(0.009)	(0.011)
R^2	0.157	0.125	0.060
p(Bio = Step)	0.012	0.079	1.000
N	15,478	15,195	11,445

Note: All outcomes standardized (mean 0, SD 1). Panel A: sample stacks two cohorts of adopted children: adopted in 1910 linked back to 1900, and adopted in 1920 linked back to 1910, where they appear as biological (related=301) with a different father. Confirmed same-person fathers are dropped; unlinked adoptive fathers retained. Restricted to children ages 0–5 in the biological census year. Cases where the biological and adoptive father share the same surname are dropped to exclude possible extended kin placements. Panel B: sample stacks two cohorts of stepchildren: biological in 1900 then stepchild in 1910, and biological in 1910 then stepchild in 1920. Different-father status verified by linking the step father back to the biological census year. Sample restricted to children whose mother is the same person in both censuses. Education standardized within 5-year age bands; age $\geq$ 25 in 1940. Wage income standardized within 5-year age bands; wage workers only. White males only. Robust standard errors in parentheses.

5. Discussion

The twelve tests in this paper reject the additive genetic model on multiple margins, including internal consistency, gender symmetry, and environmental irrelevance.[30]

What do these failures collectively imply? The most informative pattern is the contrast between small and large environmental effects. Specific environmental shocks (parental death, birth order, family size) have detectable but economically small effects. In fact, these results are consistent with some evidence from English genealogical data (Clark, 2023; Clark and Cummins, 2024a,b). A proponent of the genetic model could view these results in isolation as consistent with a world where nature dominates nurture. But the broader tests tell a different story. Sibling correlations exceed parent-child correlations in nearly every state and for both occupation and education, indicating that forces shared between siblings matter beyond what genetics alone can explain. Stepfathers and adoptive fathers predict children's adult outcomes as well as biological fathers in a within-child design. These results point to an important role for the family environment broadly defined. Gender-specific mechanisms also appear to be important: mothers have larger correlations with daughters than with sons, and sisters are more strongly correlated than brothers, suggesting that same-sex parent-child interactions influence transmission in ways the additive genetic model does not accommodate. The importance of mothers relative to fathers has also been documented by others using indirect methods to uncover mothers' status (Althoff et al., 2025; Espín-Sánchez et al., 2023).

The strong father-in-law correlations help separate household from broader environmental mechanisms. A man's father-in-law predicts his occupational attainment almost as well as his own father, for every state and birth cohort. Some of this correlation reflects assortative mating: the daughter married someone from a similar background. But assortative mating alone should produce a father-in-law correlation below the father-son correlation. The near equality of the two correlations is too large for sorting alone to explain. The father-in-law did not raise the son-in-law and never shared his household, so the correlation cannot operate through parenting or other within-family inputs. A more plausible explanation is that both families are affected by the same local environment: the same labor markets, schools, networks, and community norms (Chetty and Hendren, 2018; Chetty et al., 2026; Card et al., 2022). The persistence of occupational status, in this view, operates less through what fathers do and more through the communities in which families live.

[30] Clark has also advanced a stronger claim: that transmission rates are constant across societies and historical periods (Clark, 2014). The results in Tests 1–3 reject this as well, since estimated transmission rates vary substantially across U.S. states and birth cohorts.

All twelve tests in this paper use only white Americans, a sample restriction that favors the genetic model by ignoring the large environmental variation across race throughout American history. Yet even within this restricted sample, the model fails repeatedly. The experience of Black Americans poses a separate and distinct challenge, one that operates at the group level. Under the additive genetic model, convergence in economic status between groups can occur only through intermarriage, because without intermarriage the model implies that the underlying status distributions of the two groups cannot converge. Black–white marriage was legally prohibited across much of the United States until 1967, and rates remained small for decades after. Despite this near-complete absence of cross-racial marriage, Black–white economic gaps narrowed substantially over the twentieth century, and mobility patterns appear to change across cohorts (Durlauf et al., 2024; Jácome et al., 2025). The timing of convergence tracked institutional and environmental changes, not intermarriage: the Great Migration, investments in Black schooling and improvements in school quality, World War II labor shortages, and the dismantling of Jim Crow (Margo, 2016; Collins and Wanamaker, 2022; Aaronson and Mazumder, 2011; Ferrara, 2022; Carruthers and Wanamaker, 2017; Jones and Schmick, 2025). A consistent theme in this literature is that place-based factors, such as local labor markets and legal institutions, affected outcomes for Black individuals (Althoff and Reichardt, 2024; Card et al., 2022; Collins and Wanamaker, 2014). These forces operated at the group level, shifting economic outcomes for Black Americans without the intermarriage that the additive genetic model requires for convergence. A model in which intermarriage is the sole mechanism for group convergence cannot account for these patterns.

6. Conclusion

The additive genetic model's appeal lies in its simplicity: a few parameters generate precise predictions for every kinship correlation, from siblings to distant in-laws. This paper first tests whether those predictions hold in linked U.S. census data. They do not: independent identification strategies yield systematically inconsistent parameter estimates, and the model cannot match the observed correlations across relative types. But even if the correlations fit well, they do not imply solely a genetic mechanism. If transmission is truly genetic, then environmental variation within families should not matter: a father's death should not affect his child's adult outcomes, birth order and family size should be irrelevant, and stepfathers and adoptive fathers should predict children's outcomes far less well than biological fathers. These predictions also fail. Variation in transmission across states and cohorts is unrelated to assortative mating, and stepfathers, fathers-in-law, and adoptive fathers predict children's outcomes about as well as biological fathers.

None of this implies that genetics is irrelevant.[31] The claim rejected here is narrower: not that genes matter, but that genes are all that matters. The results instead reject a restrictive model in which intergenerational persistence arises solely through the transmission of genetic endowments, while remaining consistent with frameworks in which genetic predispositions operate alongside, or interact with, social and institutional environments.

[31] For example, see the growing literature on how polygenic scores predict education, income, and wealth (Barth et al., 2020; Carvalho, 2025; Harden, 2021).

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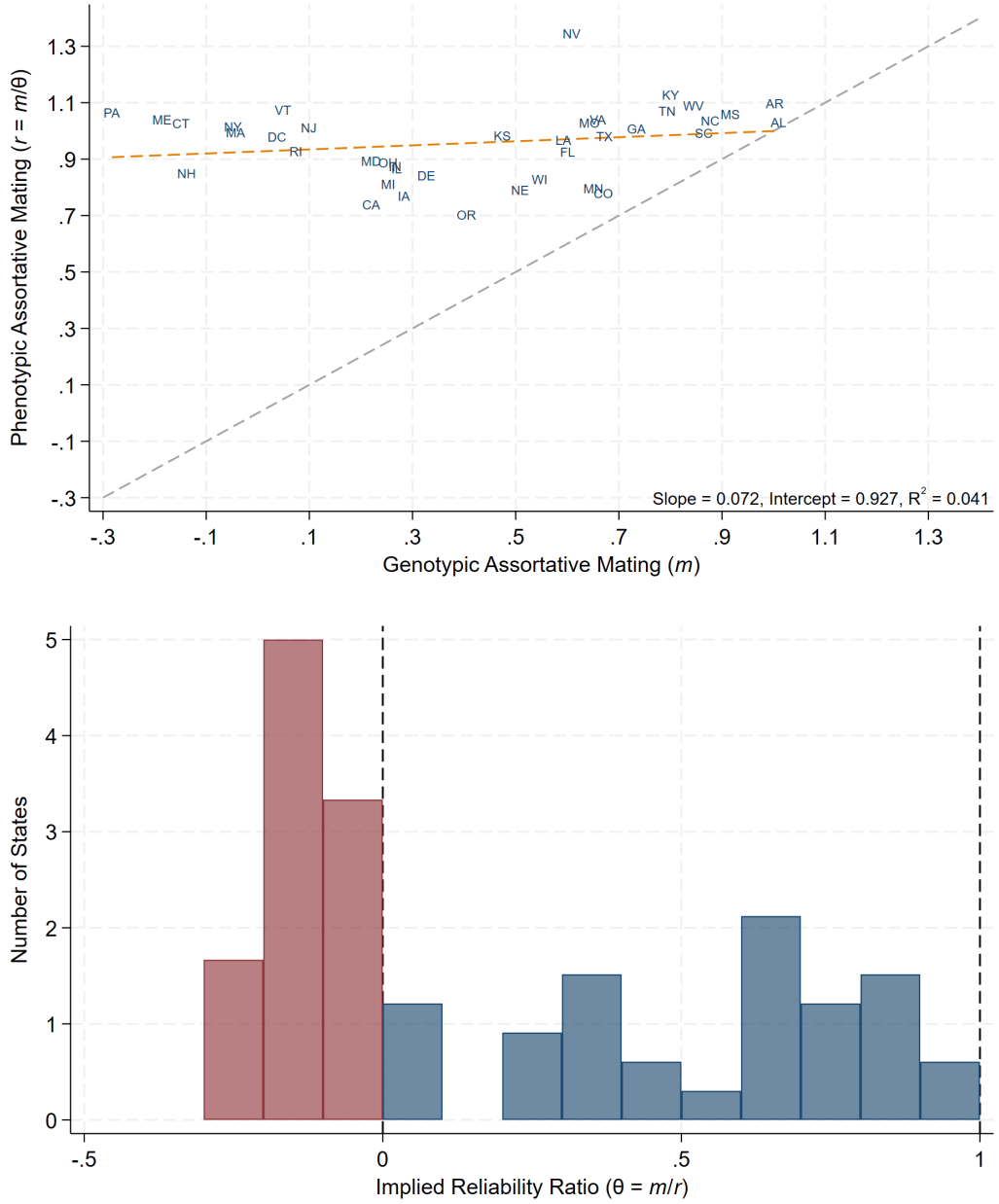
Online Appendix for

Twelve Tests of the Additive Genetic Model of Social Mobility

March 24, 2026

A. Additional Tables and Figures

Figure A1: Latent and observed assortative mating are unrelated across states.



Notes: See Section 4.1.1. Panel A plots latent assortative mating $\hat{m} = 2\hat{b} - 1$ (from the uncle-sibling ratio) against the observed spousal correlation $\hat{r}$ (from father-in-law correlations). The model predicts $r = m/\theta$. Panel B shows the distribution of the implied $\hat{\theta} = \hat{m}/\hat{r}$ that each state would require for the two estimates to be consistent. Navy bars fall in the valid $[0,1]$ range; maroon bars fall outside.

Table A1: National-Level Kinship Correlations and Identifying Ratios

Panel A: Kinship Correlations

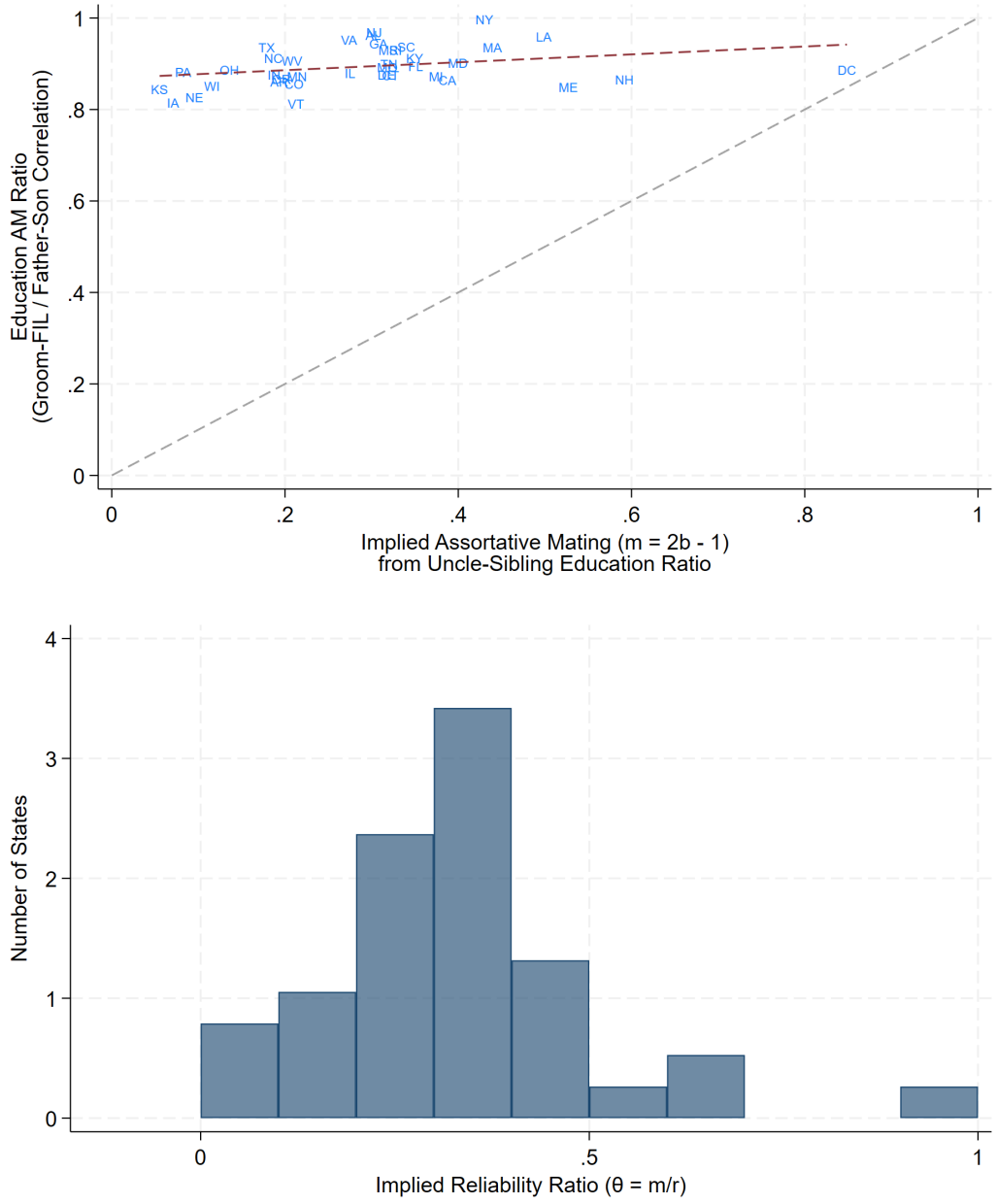
	Occupation		Education	
	Correlation	N	Correlation	N
Father-son ($\rho_{f,s}$)	0.394[a]	9,169,520	0.395[c]	2,297,410
Father-daughter ($\rho_{f,d}$)	–	–	0.426[c]	1,536,382
Mother-son ($\rho_{m,s}$)	–	–	0.390[c]	2,297,410
Mother-daughter ($\rho_{m,d}$)	–	–	0.453[c]	1,536,382
Brother (ρ_{bb})	0.430[a]	5,550,647	0.463[d]	6,939,375
Sister (ρ_{ss})	–	–	0.551[d]	4,531,298
Brother-sister (ρ_{bs})	–	–	0.467[d]	10,901,237
Grandfather-grandson ($\rho_{gf,gs}$)	0.278[a]	9,268,739	–	–
Grandfather-father ($\rho_{gf,f}$)	0.445[a]	8,051,666	–	–
Uncle-nephew (ρ_{un})	0.361[a]	5,171,434	0.370[e]	1,648,713
Cousin (ρ_{cous})	0.337[a]	7,502,131	0.390[e]	7,269,151
Male-Male	–	–	0.380[e]	2,274,241
Male-Female	–	–	0.382[e]	1,781,626
Female-Male	–	–	0.385[e]	1,785,528
Female-Female	–	–	0.424[e]	1,427,756
Groom-FIL ($\rho_{groom,FIL}$)	0.416[b]	2,003,501	–	–
Father-FIL ($\rho_{f,FIL}$)	0.441[b]	2,003,501	–	–

Panel B: Identifying Ratios

	Identifies	Occupation	Education
Grandfather / father ($\rho_{gf,gs}/\rho_{gf,f}$)	b	0.624	–
Uncle / sibling (ρ_{un}/ρ_{sib})	b	0.840	0.799
Cousin / uncle (ρ_c/ρ_{un})	b	0.932	1.054
$\sqrt{\text{Cousin / sibling}}$ ($\sqrt{\rho_c/\rho_{sib}}$)	b	0.885	0.918
Groom-FIL / father-son ($\rho_{groom,FIL}/\rho_{f,s}$)	m or r	1.056	–

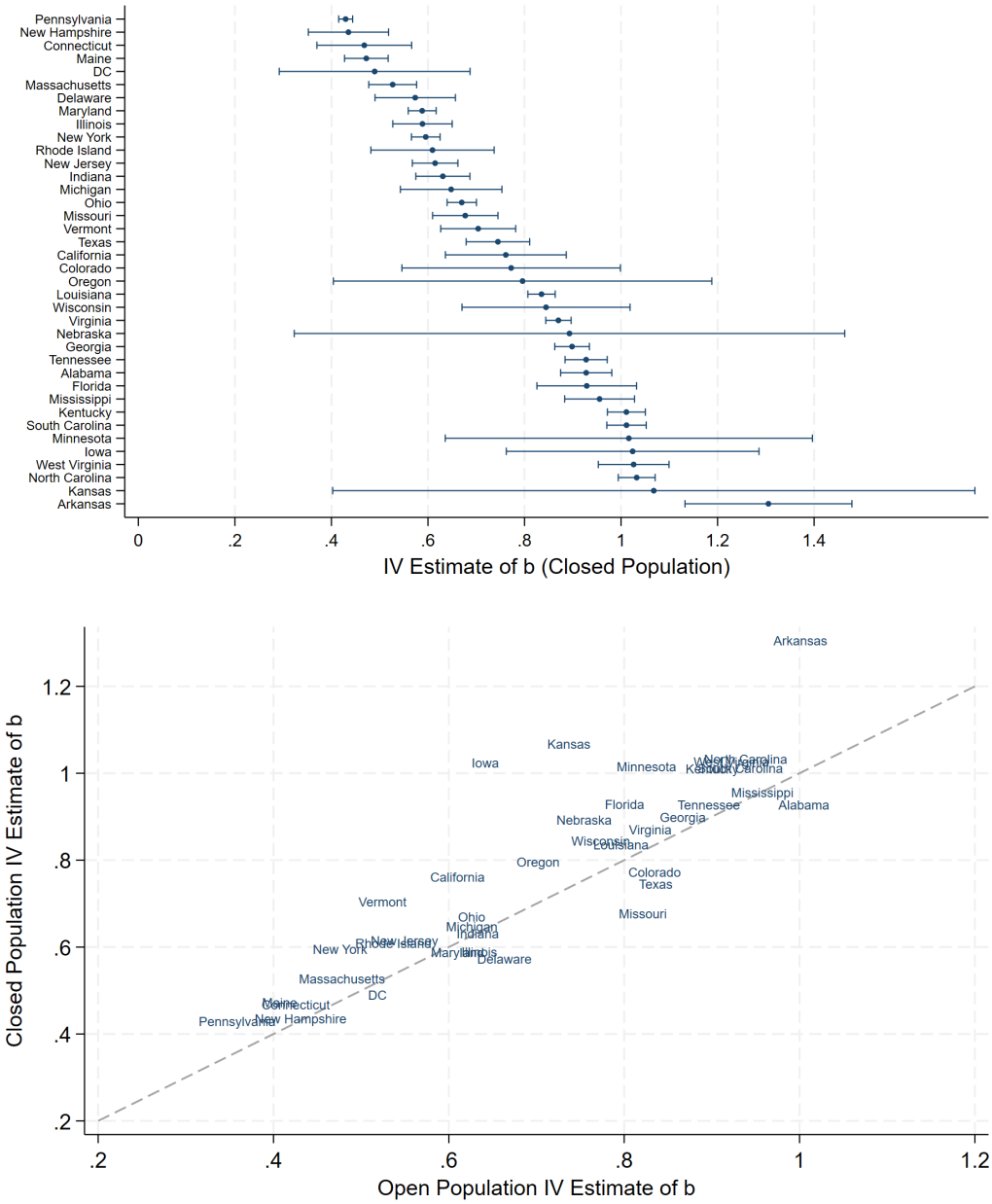
Notes: Panel A reports IPW-weighted Pearson correlations. Occupation correlations use the adjusted SONG score from Ward (2023) and are restricted to white men. Sibling, uncle-nephew, and cousin pairs each keep one match per focal person (alphabetically first by identifier) to avoid inflating sample sizes. Education correlations use years of schooling from the 1940 census. Grandfather-generation education is not observed; those cells are left blank. Panel B evaluates the identifying ratios from Table 3 at the national correlations. Under the additive genetic model, all four ratios identifying $b = (1+m)/2$ should yield the same value, and m (the spousal correlation in latent endowments) must lie between 0 and 1. Under genotype matching the groom-FIL ratio identifies m; under phenotype matching it identifies $r = m/\theta$. Data sources: [a]Multigenerational data (Appendix B.1). [b]Assortative mating data: married couples in 1940 linked back to their fathers in 1910 via the childhood census crosswalk. [c]Parent education data (Appendix B.6). [d]Sibling data (Appendix B.3). [e]Uncle and cousin data (Appendix B.10).

Figure A2: The assortative mating disconnect persists when using education instead of occupation scores.



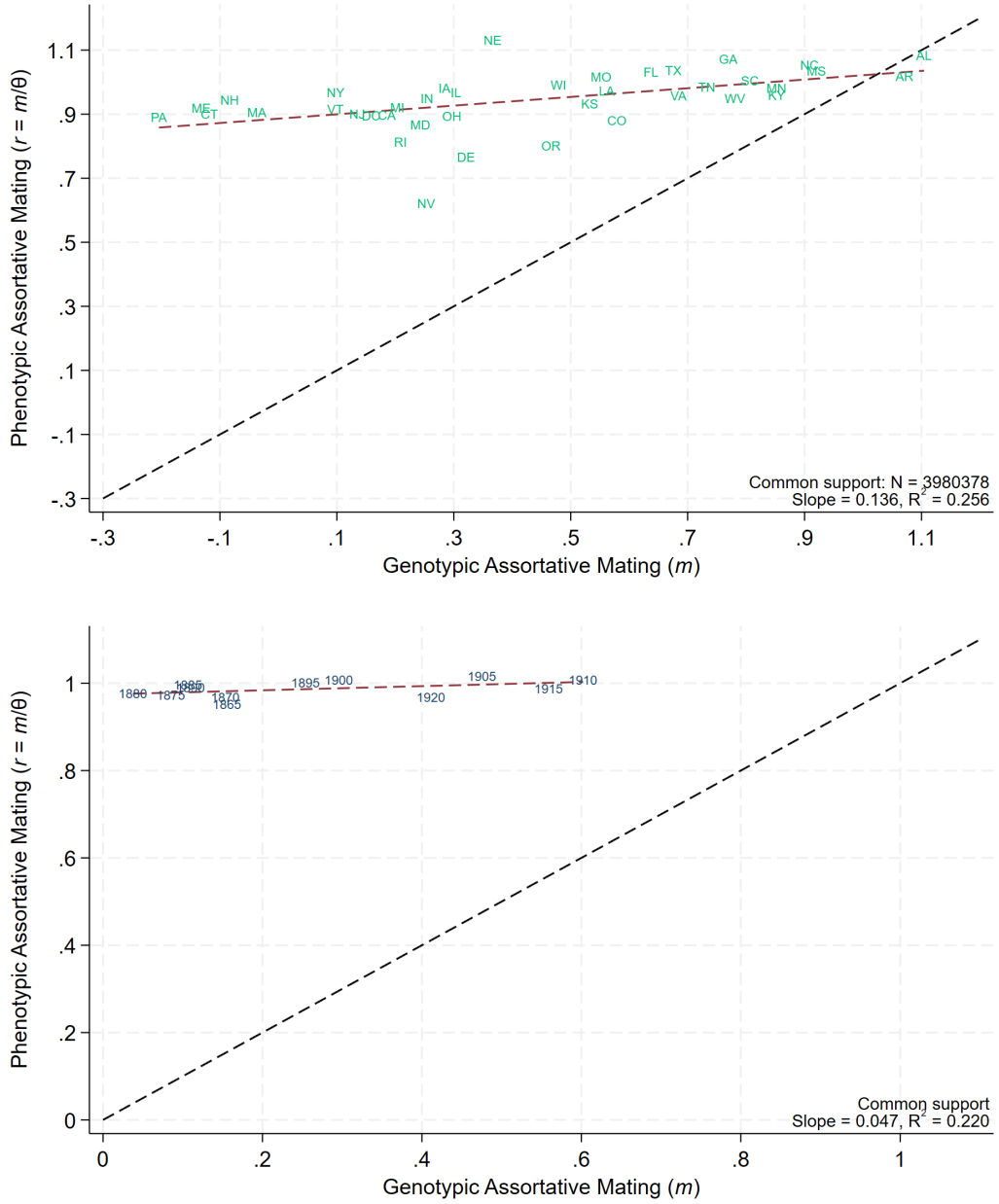
Notes: See Section 4.1.1. Education is measured as years of schooling from the 1940 census, residualized by age. The AM ratio is the groom/father-in-law education correlation divided by the father/son education correlation, computed by state. The x-axis plots implied assortative mating $\hat{m} = 2\hat{b} - 1$ from the uncle-sibling education IV (Figure 5). The gray dashed line shows the 45-degree line ($\theta = 1$); the maroon dashed line is the OLS fit (slope $= 0.086$, $R^2 = 0.095$). Panel B shows the distribution of implied $\hat{\theta} = \hat{m}/\hat{r}$ by state. $N = 732{,}017$ trios across 38 states.

Figure A3: Geographic variation in $\hat{b}$ persists under a closed-population restriction.



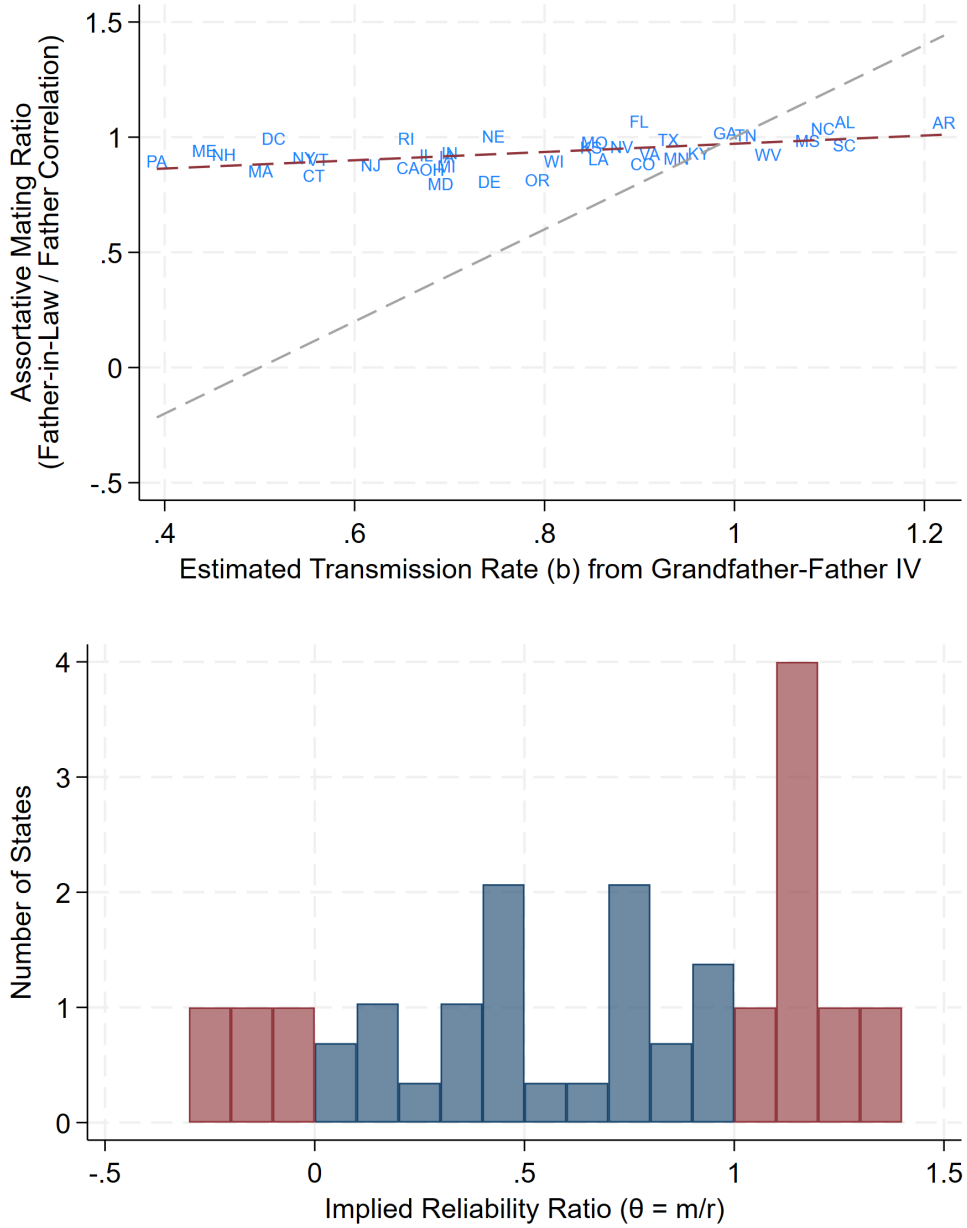
Notes: See Section 4.1.2. Panel A restricts the sample to families where all seven members (grandchild, father, mother, and four grandparents) were born in the same state ($N = 2{,}430{,}424$). Panel B plots the closed-population estimate (y-axis) against the open-population estimate (x-axis) for each state. Points near the 45-degree line indicate that cross-state migration does not drive the geographic variation. The closed-population restriction produces slightly higher estimates of $\hat{b}$ on average.

Figure A4: The disconnect between two measures of assortative mating persists under a common-support restriction.



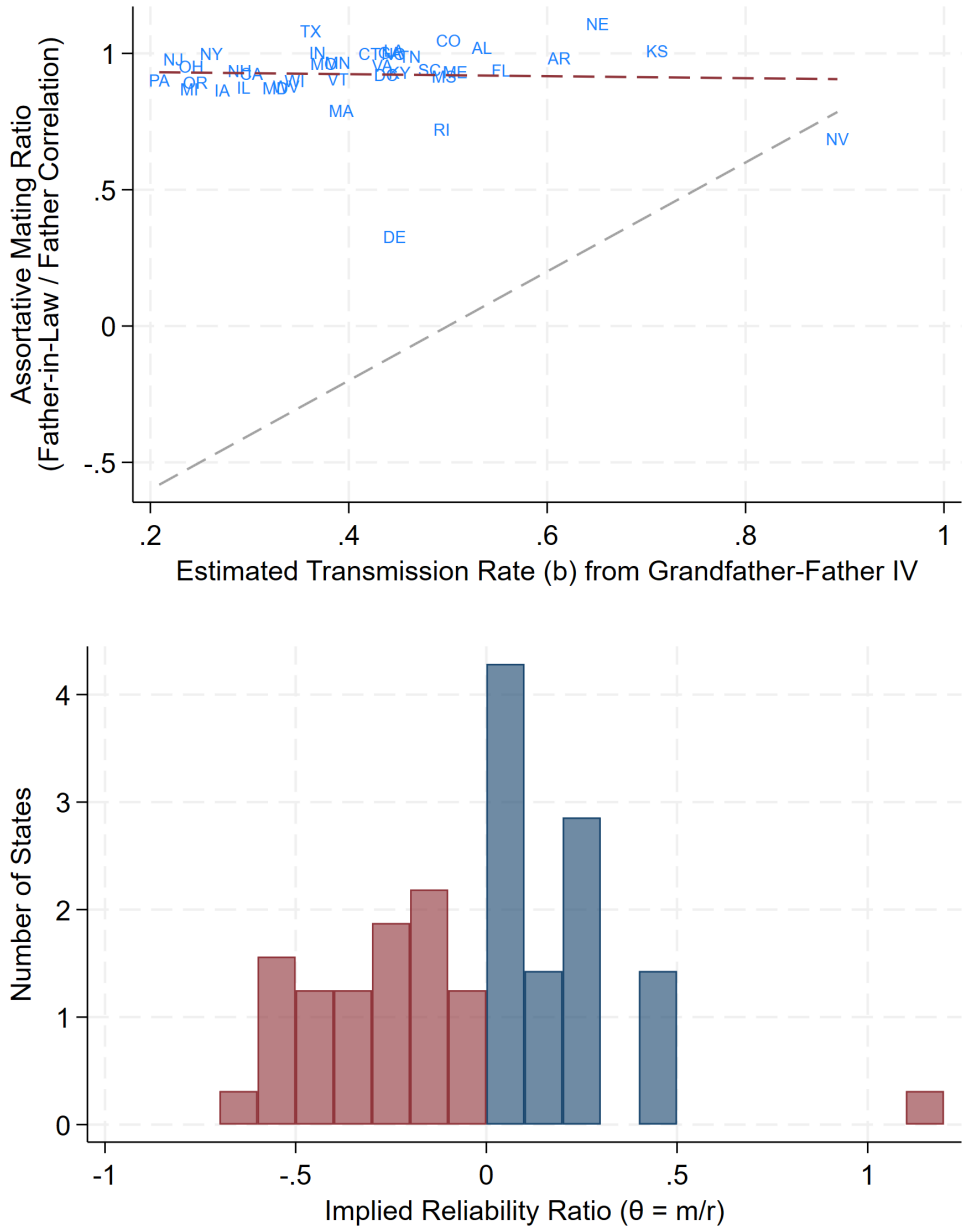
Notes: See Sections 4.1.1–4.1.2. The sample is restricted to families where paternal grandfather, maternal grandfather, father, and child all have valid occupation scores. The grandfather-father IV (implied $\hat{m} = 2\hat{b} - 1$) and the father-in-law ratio ($\hat{r} = \rho_{\text{groom,FIL}} / \rho_{\text{father,son}}$) are computed on this common-support sample. Panel A plots the two estimates by state; Panel B plots them by birth cohort. The disconnect between $\hat{m}$ and $\hat{r}$ persists: the implied $\hat{m}$ from direct-lineage transmission is systematically lower than the spousal correlation $\hat{r}$ estimated from in-law ratios.

Figure A5: The assortative mating disconnect persists when restricting to genealogical links only.



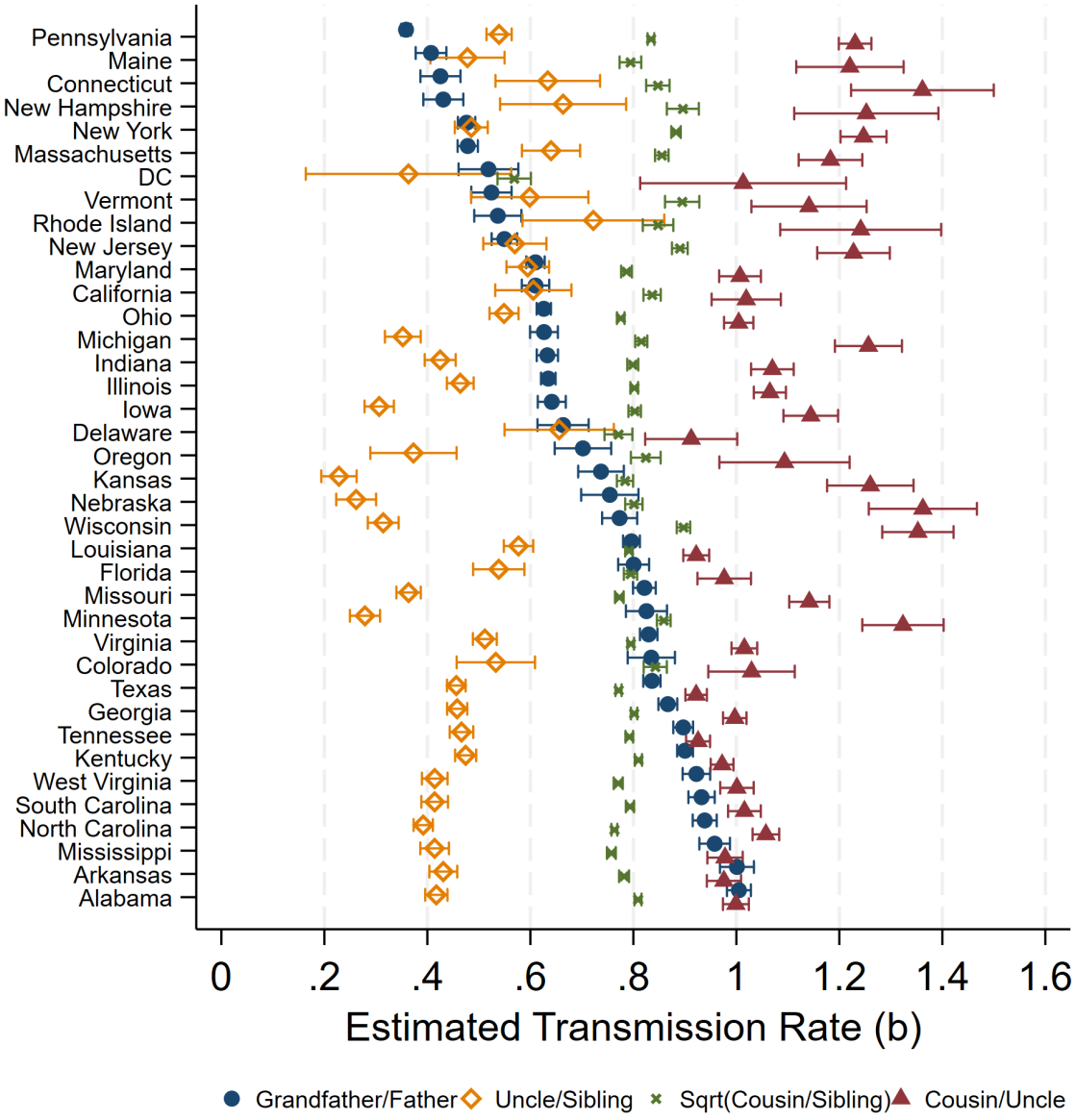
Notes: See Section 4.1.1. This figure replicates Figure 2 restricting all cross-census person links to genealogical records from the Census Tree (Buckles et al., 2023), excluding the machine-learning-based links that apply primarily to men. Panel (a) plots the assortative mating ratio against $\hat{b}_{state}$ from the grandfather-father IV; Panel (b) shows the distribution of implied $\hat{\theta}_{state}$. The disconnect between the two measures of assortative mating is unchanged.

Figure A6: The assortative mating disconnect persists with an alternative occupation measure (LIDO).



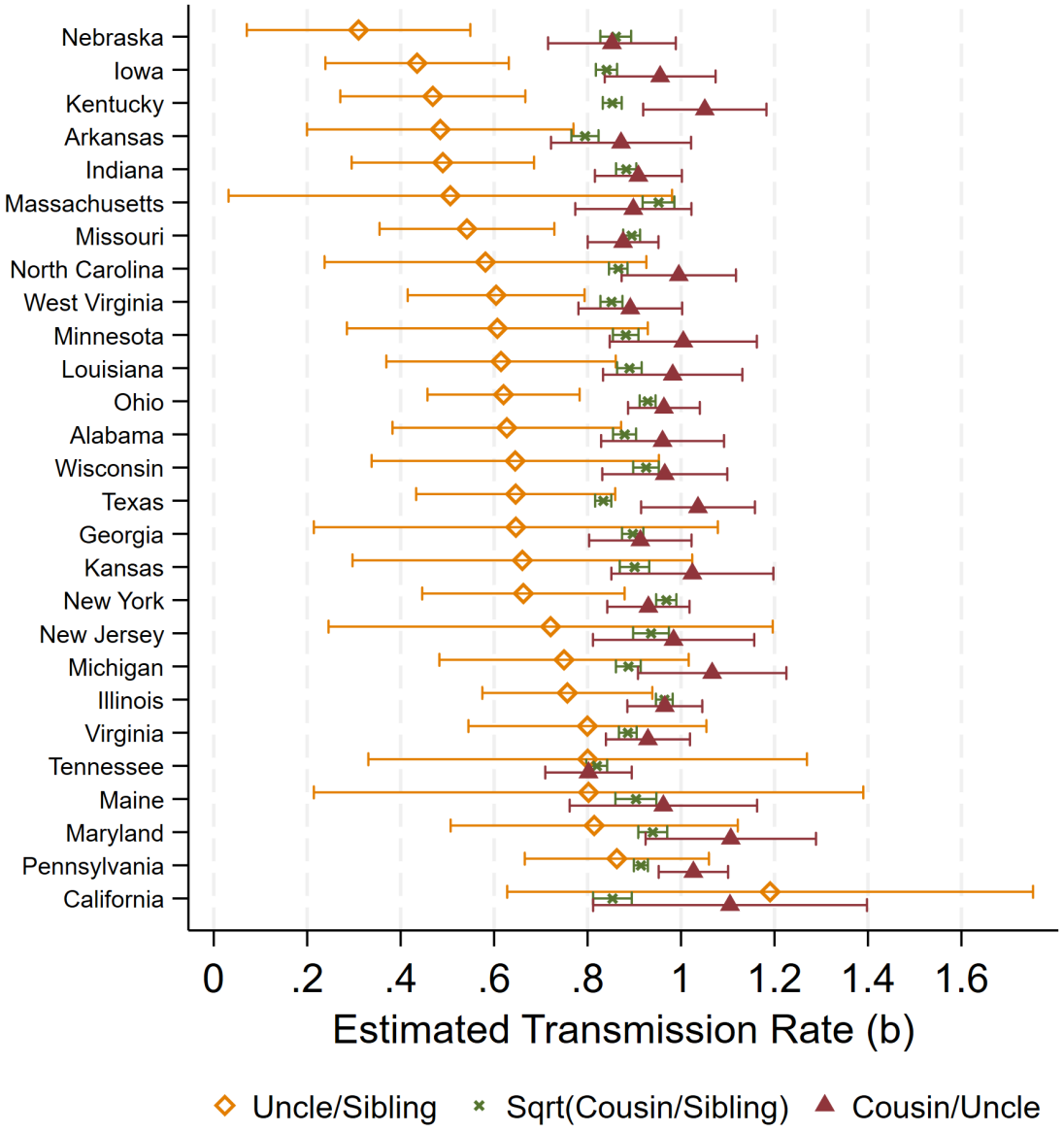
Notes: See Section 4.1.1. This figure replicates Figure 2 replacing the occupation percentile score with the standardized LIDO index of Saavedra and Twinam (2020), a predicted-income measure constructed from occupation, industry, and demographics via lasso regression. Panel (a) plots the assortative mating ratio against $\hat{b}_{state}$ from the grandfather-father IV; Panel (b) shows the distribution of implied $\hat{\theta}_{state}$. The two measures of assortative mating are completely unrelated across states ($R^2 = 0.00$).

Figure A7: Independent estimates of the transmission rate disagree across states: occupation scores.



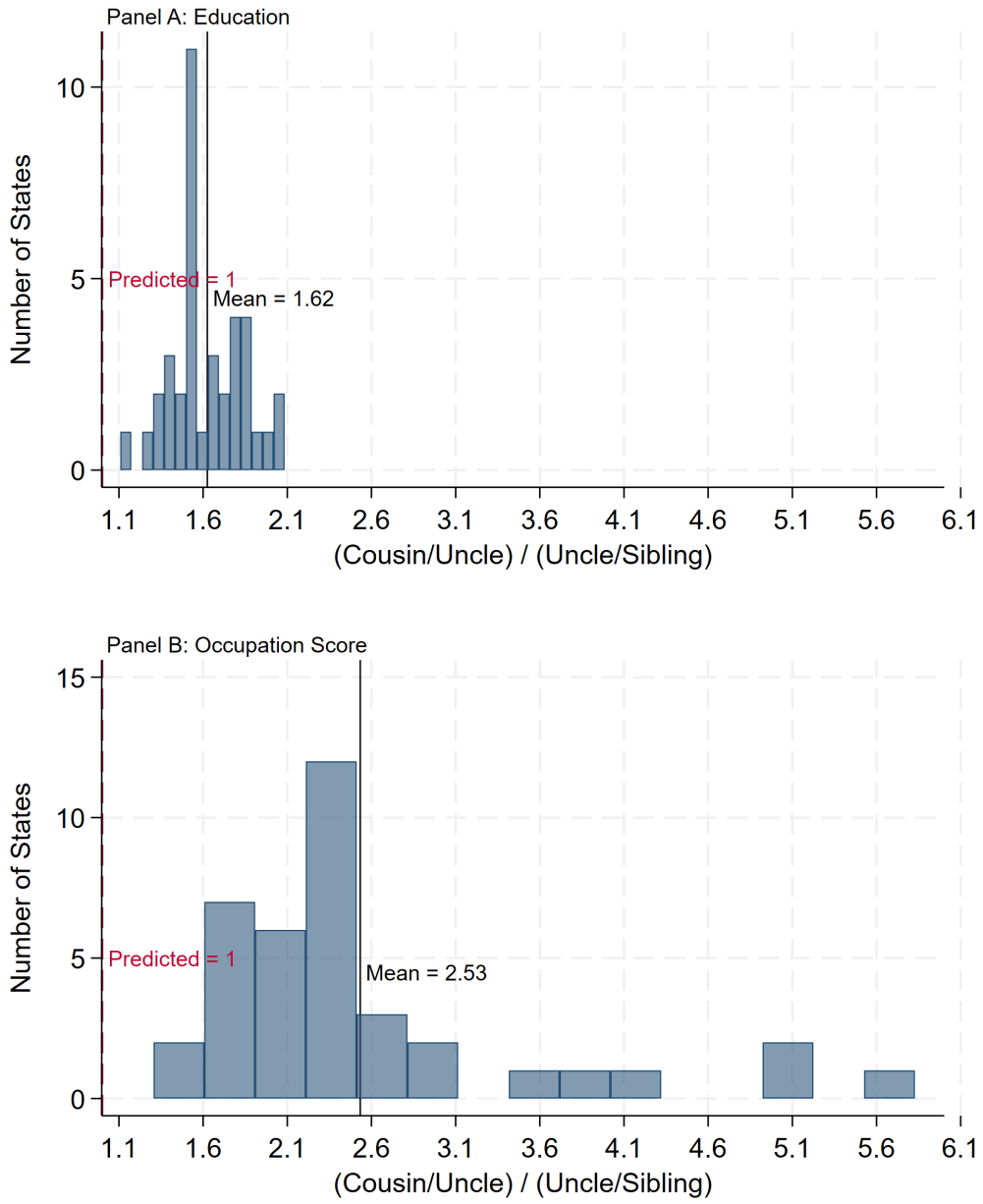
Each state's transmission rate $\hat{b}$ is estimated using four identification strategies applied to occupation scores: grandfather/father (navy circles), uncle/sibling (orange diamonds), the square root of cousin/sibling (green X's), and cousin/uncle (maroon triangles). Under the genetic model, all four recover b and should agree. States sorted by the grandfather-father estimate.

Figure A8: Overidentification failure using wage income.



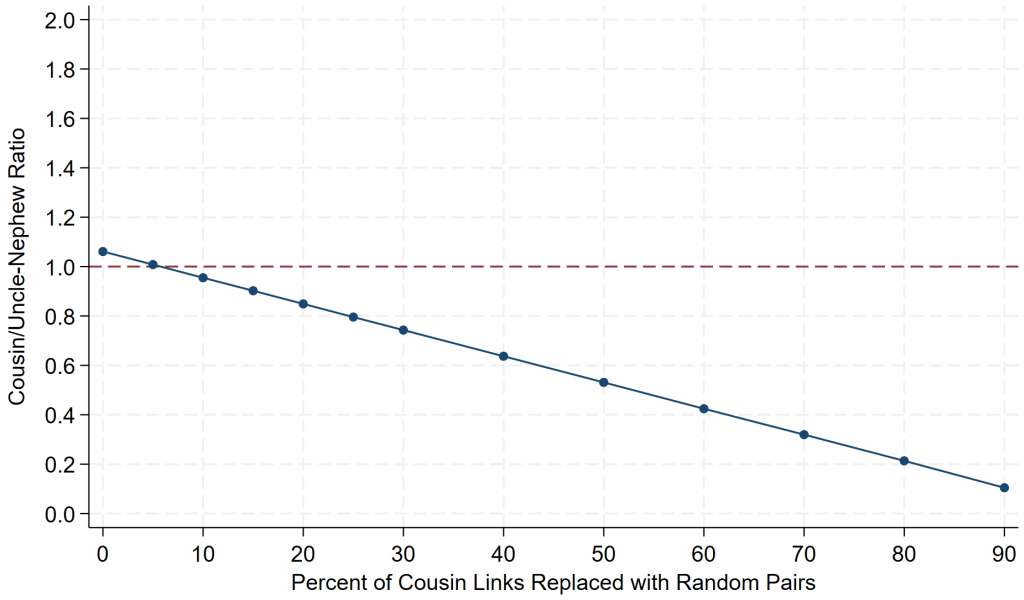
Each state's transmission rate b is estimated using three identification strategies applied to standardized wage income: the uncle/sibling ratio (orange diamonds), the square root of cousin/sibling (green X's), and the cousin/uncle ratio (maroon triangles). The sample is restricted to white men in 1940 who report positive wage income as employees. Wages are standardized within five-year age bands. Estimates are noisier than those using occupation scores or education because the sample is restricted to wage workers. States sorted by the uncle-sibling estimate.

Figure A9: Two independent estimates of $\hat{b}$ disagree: the cousin/uncle ratio systematically exceeds the uncle/sibling ratio.



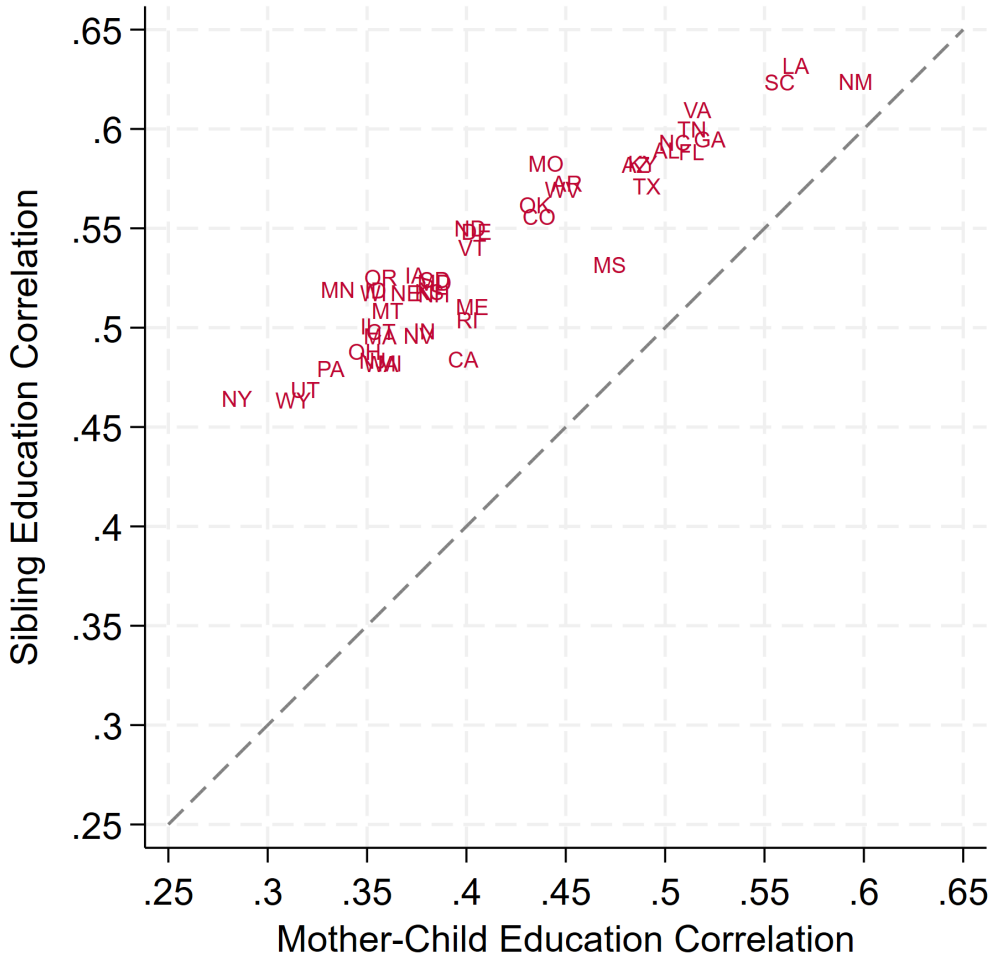
Notes: See Section 4.1.3. Each bar represents a state. The ratio plotted is $\hat{b}_{\text{cousin/uncle}} / \hat{b}_{\text{uncle/sibling}}$, which should equal 1 under the genetic model. Panel A uses education (38 states, mean = 1.62). Panel B uses occupation scores (mean = 2.53). Both means are significantly different from one at the 1 percent level. The dashed line marks the genetic model prediction of 1.

Figure A10: False positive cousin links cannot explain the overidentification failure.



Notes: See Section 4.1.3. The baseline cousin/uncle-nephew education correlation ratio is 1.06, exceeding the model's prediction of 1.0. To assess sensitivity to linkage error, I randomly replace $X\%$ of cousin pairs with random individuals drawn from the same marginal distribution of 1940 education and recompute the ratio. False positive cousin links attenuate the cousin correlation toward zero, pushing the ratio down. Even 5% contamination brings the ratio near 1.0, and 10% pushes it below. Since the observed ratio exceeds one, linkage error works against the finding.

Figure A11: Sibling education correlations exceed mother-child correlations in every state.



Notes: See Section 4.1.4. Each point represents a state. The 45-degree line marks the genetic model's prediction of equality. Every state lies above the line, and every difference is statistically significant. The father-child version of this figure appears in the main text (Figure 6, Panel b). Education measured as years of schooling in 1940.

Table A2: Extended Kin Education Correlations

Relationship	Correlation	95% CI	N
Panel A: By kin type (all focal children)			
Bio uncle	0.390	[0.389, 0.391]	3,382,571
Bio aunt	0.327	[0.326, 0.329]	1,470,640
Married-in uncle	0.281	[0.279, 0.283]	962,109
Married-in aunt	0.402	[0.401, 0.403]	2,844,767
Panel B: By kin type and focal child sex			
Bio uncle – Nephew	0.391	[0.390, 0.392]	1,918,955
Bio uncle – Niece	0.391	[0.389, 0.392]	1,463,616
Bio aunt – Nephew	0.319	[0.317, 0.321]	831,883
Bio aunt – Niece	0.341	[0.339, 0.343]	638,757
Married-in uncle – Nephew	0.277	[0.275, 0.280]	546,970
Married-in uncle – Niece	0.287	[0.284, 0.290]	415,139
Married-in aunt – Nephew	0.394	[0.393, 0.395]	1,616,883
Married-in aunt – Niece	0.415	[0.414, 0.417]	1,227,884

Note: Education measured as years of schooling from the 1940 census. White adults age 25+. Paternal lineage: bio uncle = father's brother; bio aunt = father's sister. Married-in kin identified via the 1940 spousal crosswalk from bio kin (married-in aunt = wife of bio uncle; married-in uncle = husband of bio aunt). Under the genetic model, all biological kin at distance two should have equal correlations ($\rho = \theta b^2 \approx 0.17$), and married-in kin should have weaker correlations ($\rho = r \cdot \theta b^2 = m b^2$).

Table A3: Mother's vs. Father's Education: Predicting Child's Education

	(1) Father Only	(2) Mother Only	(3) Horse Race		
			All	Sons	Daughters
Father's Education	0.410		0.238	0.252	0.222
			(0.001)		
Mother's Education		0.420	0.265	0.235	0.296
			(0.001)		
R^2			0.209	0.186	0.236
p(Father = Mother)			0.000	0.024	0.000
N	3,833,792	3,833,792	3,833,792	2,297,410	1,536,382

Note: Children ages 5–14 in 1920, linked with both parents to 1940. Columns (1) and (2) report bivariate correlations. Columns (3)–(5) report standardized coefficients from a joint regression. Education measured as years of schooling from the 1940 census. White families only. Robust standard errors in parentheses. Predicted: father and mother coefficients should be equal.

Table A4: Intergenerational Occupation Transmission: Parent Death (Sons)

	(1) Father Death	(2) Mother Death
Father's Occupation	0.429***	0.430***
	(0.001)	(0.001)
Father Died (before 1910)	-0.010***	
	(0.003)	
Father Died × Father's Occupation	-0.008***	
	(0.003)	
Mother Died (before 1910)		-0.068***
		(0.004)
Mother Died × Father's Occupation		0.010***
		(0.004)
Observations	1,933,957	1,885,082
R-squared	0.197	0.197

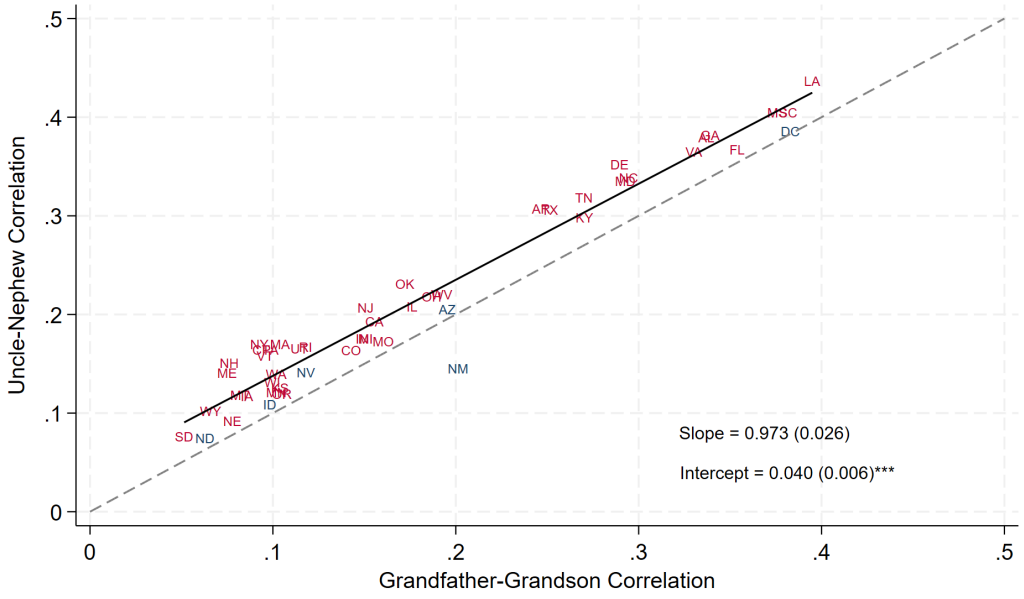
Standard errors in parentheses

All variables standardized to mean zero and unit variance.

Robust standard errors in parentheses.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Figure A12: Uncle-nephew correlations exceed grandparent-grandchild correlations in most states.



Notes: See Section 4.1.4. Each point represents a state. The 45-degree line marks equality. States above the line have uncle correlations exceeding grandparent correlations, consistent with cultural rather than genetic transmission. White males, occupation scores.

Table A5: Birth Order Effects on Education by Gender (Family Fixed Effects)

	Sons (Main Effect)	× Female (Interaction)	Daughters (Implied)
Female		0.078	
		(0.001)	
First-born	Ref.	Ref.	Ref.
Second-born	-0.040	0.017	-0.023
	(0.001)	(0.001)	(0.001)
Third-born	-0.047	0.025	-0.021
	(0.002)	(0.002)	(0.002)
Fourth-born	-0.039	0.030	-0.009
	(0.002)	(0.002)	(0.002)
Fifth-born+	-0.026	0.036	0.009
	(0.003)	(0.003)	(0.003)
N		10,320,643	

Standard errors clustered at the family level in parentheses. Single regression with family and birth year fixed effects. column reports birth order coefficients for males (reference gender). column reports the interaction between birth order dummies and a female indicator. column reports the implied effect for females (main + interaction), with standard errors from `lincom`. Education is years of schooling, standardized to mean zero and unit variance pooled across genders (age $\geq$ 25). White children.

Table A6: Family Size and Intergenerational Transmission: Twins Instrumental Variable

	Occ. Score (Std.)		Education (Std.)		Wage Income (Std.)	
	OLS	IV	OLS	IV	OLS	IV
	(1)	(2)	(3)	(4)	(5)	(6)
Twin at 2nd Birth (sample: first-born children)						
Number of Children	-0.026***	-0.013	-0.064***	-0.012	-0.040***	-0.036
	(0.001)	(0.020)	(0.001)	(0.022)	(0.001)	(0.031)
Father × Num. Children	0.009***	0.026	-0.029***	0.008	-0.017***	0.045
	(0.001)	(0.021)	(0.001)	(0.022)	(0.001)	(0.031)
First-Stage *F*		1057.5		1029.4		578.5
N	1,342,489	1,342,489	1,448,635	1,448,635	759,898	759,898
Twin at 3rd Birth (sample: 1st and 2nd children)						
Number of Children	-0.025***	-0.024	-0.058***	-0.053***	-0.040***	-0.033*
	(0.001)	(0.015)	(0.001)	(0.015)	(0.001)	(0.020)
Father × Num. Children	0.009***	-0.003	-0.026***	-0.033**	-0.016***	-0.025
	(0.001)	(0.016)	(0.001)	(0.015)	(0.001)	(0.020)
First-Stage *F*		2209.6		2152.9		1260.7
N	1,876,191	1,876,191	2,007,813	2,007,813	1,044,322	1,044,322
Twin at 4th Birth (sample: 1st, 2nd, and 3rd children)						
Number of Children	-0.023***	0.021	-0.052***	-0.017	-0.039***	-0.058***
	(0.001)	(0.014)	(0.001)	(0.014)	(0.001)	(0.019)
Father × Num. Children	0.009***	0.029*	-0.023***	-0.001	-0.015***	0.003
	(0.001)	(0.015)	(0.001)	(0.015)	(0.001)	(0.018)
First-Stage *F*		2630.0		2559.2		1538.1
N	1,854,009	1,854,009	1,973,340	1,973,340	1,015,045	1,015,045

Standard errors clustered at the household level in parentheses. * p<0.10, ** p<0.05, *** p<0.01. Sample: white males observed as children (relate = 3) in the 1900 full-count census and linked to 1940 for outcomes. All outcomes standardized to mean zero, unit variance. Father's occupation score (standardized), age in 1940, and age squared included as controls in all specifications. Following Black et al. (2005), the outcome sample includes only children born strictly before the potential twin birth position. Birth order dummies included for twin at 3rd and 4th birth specifications. Wage income restricted to male wage workers (classwkr = 2) with positive earnings. Both Number of Children and the Father × Number of Children interaction are instrumented using the twin indicator and its interaction with father's occupation score. First-stage *F* is the squared *t*-statistic on the twin instrument in the first-stage regression for Number of Children.

Table A7: Family Size Effects on Child Outcomes: Twins Instrumental Variable

	Occ. Score (Std.)		Education (Std.)		Wage Income (Std.)	
	OLS	IV	OLS	IV	OLS	IV
	(1)	(2)	(3)	(4)	(5)	(6)
Twin at 2nd Birth (sample: first-born children)						
Number of Children	-0.027***	-0.014	-0.061***	-0.012	-0.039***	-0.035
	(0.001)	(0.020)	(0.001)	(0.022)	(0.001)	(0.031)
First-Stage F		1056.8		1029.3		594.9
N	1,342,489	1,342,489	1,448,635	1,448,635	759,898	759,898
Twin at 3rd Birth (sample: 1st and 2nd children)						
Number of Children	-0.027***	-0.024	-0.055***	-0.051***	-0.039***	-0.033*
	(0.001)	(0.015)	(0.001)	(0.015)	(0.001)	(0.020)
First-Stage F		2179.7		2126.2		1260.3
N	1,876,191	1,876,191	2,007,813	2,007,813	1,044,322	1,044,322
Twin at 4th Birth (sample: 1st, 2nd, and 3rd children)						
Number of Children	-0.025***	0.016	-0.048***	-0.017	-0.037***	-0.058***
	(0.001)	(0.014)	(0.001)	(0.014)	(0.001)	(0.018)
First-Stage F		2549.9		2479.2		1486.4
N	1,854,009	1,854,009	1,973,340	1,973,340	1,015,045	1,015,045

Standard errors clustered at the household level in parentheses. * p<0.10, ** p<0.05, *** p<0.01. Sample: white males observed as children (relate = 3) in the 1900 full-count census and linked to 1940 for outcomes. All outcomes standardized to mean zero, unit variance. Father's occupation score, age in 1940, and age squared included as controls in all specifications. Following Black et al. (2005), the outcome sample includes only children born strictly before the potential twin birth position. Birth order dummies included for twin at 3rd and 4th birth specifications. Wage income restricted to male wage workers (classwkr = 2) with positive earnings. First-stage F is the squared t-statistic on the twin instrument in the first-stage regression for Number of Children.

Table A8: Within-Family Sibling Correlations by Relationship Type

Sibling Pair Type	Occupation	Education	Wage Income
Bio-Bio	0.421	0.514	0.315
	[0.420, 0.421]	[0.513, 0.514]	[0.314, 0.316]
	N= 7922499	N= 6318367	N= 2957194
Bio-Adopted	0.212	0.339	0.191
	[0.175, 0.248]	[0.302, 0.374]	[0.131, 0.250]
	N= 2,675	N= 2,297	N= 1,011
Bio-Step	0.331	0.365	0.217
	[0.324, 0.338]	[0.357, 0.373]	[0.205, 0.229]
	N= 59,627	N= 49,396	N= 23,300

Note: Correlations between adult outcomes of siblings raised by the same father. Bio-Bio = both biological children. Bio-Adopted = one biological, one adopted (RELATE 302/304). Bio-Step = one biological, one stepchild (RELATE 303). All variables standardized to mean zero and unit variance within 5-year age bands. Education: years of schooling (age $\geq$ 25). Wage: wage income (wage workers only). 95% confidence intervals shown in brackets. White males only. Under pure genetic transmission, Bio-Adopted correlation should equal zero.

B. Data Construction

All datasets are constructed from the fully digitized U.S. censuses of 1850 through 1940, available through IPUMS (Ruggles et al., 2024). Individuals are linked across censuses using the Census Tree crosswalk files of Buckles et al. (2023). These crosswalk files provide pairwise links between adjacent census pairs (e.g., 1900 to 1910, 1910 to 1920). I merge all pairwise links into a single master linkage file that tracks each individual across every census in which they appear, creating a life-course record from childhood through adulthood. When links conflict (for example, if person A in 1900 is linked to person B in 1910, and person B in 1910 is linked to person C in 1920, but person A in 1900 is linked to a different person D in 1920), I discard all links for that individual to avoid introducing false matches. The primary outcome is the adjusted Song score from Ward (2023), which ranks occupations by their human capital levels using literacy (1850–1930) and years of education (1940) within cells defined by occupation, race, and region, as described in Section 3. Education (years of schooling) is available for all individuals in the 1940 census.

B.1 Multigenerational Data (Three Generations)

The multigenerational dataset links grandfathers, fathers, and grandsons across three censuses. The construction proceeds in three steps. First, I identify sons (generation 3, hereafter G3) living with their fathers (G2) in a childhood census (1880, 1900, 1910, or 1920) using the IPUMS household structure variables (`poploc`). Second, I link each G2 father back to an earlier census (ranging from 1850 to 1910) where he appeared as a child, and I identify his father (G1, the grandfather) in that earlier household. Third, I link the G3 grandson forward to the 1940 census to observe his adult occupation. All cross-census linkages use the person-level crosswalk files of Buckles et al. (2023), which provide probabilistic links based on name, age, and birthplace.

I merge adjusted Song scores for all three generations. This score ranks each individual's occupation by human capital levels, by birth cohort, race, and region, rescaled to a 0–100 percentile. The sample is restricted to white males with non-missing occupation scores for all three generations. For the state-level analysis, I further restrict to states that had achieved statehood by 1880, dropping Arizona, Idaho, Montana, New Mexico, North Dakota, Oklahoma, South Dakota, Utah, Washington, and Wyoming. States with fewer than 100 triads are excluded. The final analysis sample contains approximately 8.8 million grandfather-father-grandson triads spanning 37 states.

The identification strategy uses the ratio of the grandparent-grandchild to the father-grandfather correlation, which cancels measurement error and recovers the latent transmission rate b (Section

2). I implement this ratio as an IV regression, instrumenting the father's occupation score with the grandfather's, which provides standard errors for the estimated transmission rate.

B.2 Intergenerational Data (Two Generations)

The intergenerational dataset links fathers to sons across two censuses. For each childhood census (1900, 1910, and 1920), I identify father-child pairs using the IPUMS parent pointer variables (`poploc`) and the relationship crosswalk files. The father's occupation score is measured in the childhood census, and the son is linked forward to the 1940 census using the crosswalk files of Buckles et al. (2023) to observe his adult occupation. The unit of observation is a father-son pair.

Several tests augment this baseline dataset with additional variables. For the birth order analysis, I calculate each child's birth order within the set of children sharing the same father in the childhood census, ranking children by age. For the family size analysis, I merge the number of own children present in the household (`nchild`) from the childhood census to capture the father's total fertility at the time of observation. In both cases, the sample is restricted to white males with valid father and son occupation scores.

B.3 Sibling Data

The sibling dataset identifies pairs of siblings observed in the same household during childhood and linked forward to 1940. The construction uses sibling crosswalk files that identify all pairwise sibling combinations within each household across four childhood censuses (1900, 1910, 1920, and 1930). Each crosswalk file records the identifiers of two siblings, their father, and their mother. I process each childhood census separately. For each sibling pair, I link both individuals forward to 1940 using the crosswalk files of Buckles et al. (2023), retaining only pairs where both siblings are successfully linked. I also link the father and mother forward to 1940 when possible, which allows the same file to support both sibling and parent-child analyses.

After appending sibling pairs identified from all four childhood censuses, I drop duplicate pairs (individuals linked from multiple earlier censuses). Note that all pairwise combinations appear in both directions (sibling *i*-*j* and *j*-*i*); I retain both for flexibility in computing correlations but account for this when constructing unique pairs.

For occupation-based analyses (brother-brother correlations), I merge 1940 adjusted occupation scores for both siblings and restrict to white male pairs. For education-based analyses (brother-sister and sister-sister correlations), I use years of schooling recorded in the 1940 census. The age gap between siblings is computed from their reported ages in the childhood census. This dataset supports

the sibling-versus-parent-child correlation comparison (Test 4), the sibling age gap analysis, and the gender-symmetric education correlations.

B.4 Twin Data

Twins are identified from the 1900 census, which uniquely reports month of birth (`birthmo`) in addition to birth year. I start with the 1900 sibling crosswalk file, which contains all pairwise sibling combinations within households. For each pair, I merge birth month, birth year, age, sex, and race from the 1900 full-count census. I classify a pair as twins if both siblings share the same birth month and birth year (excluding cases where either value is missing or zero). I cannot distinguish identical from fraternal twins.

The sample is restricted to white male pairs to match the occupation-based analysis. I remove duplicate pairs by creating a canonical pair identifier (alphabetically ordered) and keeping one observation per pair. Both twins are linked forward to 1940 using the crosswalk files of Buckles et al. (2023), and 1940 adjusted occupation scores are merged for each. The final sample contains approximately 3.1 million brother pairs from the 1900 census, of which roughly 14,800 are twin pairs and the remainder are non-twin siblings. Non-twin siblings are grouped by age gap (1–2 years, 3–4 years, 5–6 years, 7–9 years, 10–14 years), and pairs with an age gap of 15 or more years are dropped.

B.5 Parental Death Data

This dataset exploits widowhood to identify children who lost a parent between 1900 and 1910. The construction requires linking individuals across three censuses (1900, 1910, and 1940) and proceeds in several steps.

Step 1: Identify children and parental marital status in 1910. I load the full-count 1910 census and keep all children ages 0–15 who have at least one parent present in the household (identified via `momloc` and `poploc`). For each child, I merge the mother's and father's characteristics, including marital status. I flag paternal death as cases where the mother is present and widowed (`marst` = 5) and no father is present. Maternal death is flagged symmetrically: the father is present and widowed with no mother present. The 1910 census contains approximately 30.0 million children with at least one parent identified.

Step 2: Link children to the 1900 and 1940 censuses. Each child identified in 1910 is linked backward to the 1900 census and forward to the 1940 census using the crosswalk files of Buckles et al.

(2023). I retain only children who are successfully linked to both censuses, yielding approximately 4.3 million children.

Step 3: Recover the father's occupation from 1900. For children linked to 1900, I identify the father in the 1900 household using the father crosswalk file (constructed from `poploc`). The father's adjusted occupation score is merged from the 1900 occupation score file. Children without a father present in 1900 or without a valid father occupation score are dropped. The sample after this step contains approximately 3.8 million children.

Step 4: Merge child outcomes from 1940. I merge each child's 1940 occupation score and years of education. Education is recoded from IPUMS detailed education codes to approximate years of schooling. Occupation scores are available for sons who report an occupation; education is available for both sons and daughters. The final sample contains approximately 2.0 million sons with occupation scores and 3.7 million children (sons and daughters) with education data.

For the analysis, the treatment group consists of children whose father (or mother) died between 1900 and 1910, identified by the surviving parent's widowed status in 1910. The control group consists of children whose father (or mother) remained alive and present.

B.6 Parent Education Data

This dataset tests whether mother's and father's education have symmetric effects on children's education, as the additive genetic model predicts (since the child's endowment is the average of both parents', Equation 2). I use the 1920 census as the starting point because it is the latest childhood census that allows children to reach adulthood by 1940, and education is only recorded in the 1940 census.

Step 1: Build child-mother-father triads in 1920. I load the father crosswalk for 1920, which links children to their fathers using household structure. Separately, I load the mother crosswalk for 1920. I merge these two files, retaining only children who have both a father and a mother identified in 1920. I then merge child characteristics (race, sex, state) from the 1920 full-count census. The sample is restricted to white children ages 5–14, yielding approximately 17.0 million child-mother-father triads (8.6 million sons and 8.4 million daughters).

Step 2: Link all three family members to 1940. I link the child, father, and mother each to the 1940 census using separate applications of the crosswalk files. For each individual, I merge years of schooling from 1940, recoded from IPUMS detailed education codes (`educd`) to approximate years of schooling. Individuals with missing education are dropped. The final sample retains only

triads where all three family members have valid education data in 1940, yielding approximately 3.8 million triads (2.3 million sons and 1.5 million daughters).

Mean education in the sample is approximately 10.4 years for children, 7.3 years for fathers, and 7.4 years for mothers, reflecting the generational increase in schooling over this period.

B.7 Adopted Children and Stepchildren Data

This dataset classifies father-child pairs by the child's biological relationship to the household head, using the detailed relationship codes (`RELATE`) recorded in the 1900 and 1910 censuses. Under the additive genetic model, adopted children share zero genes with their adoptive parent, so the father-child occupation correlation should be zero. Stepchildren also share zero genes with the stepfather, but assortative remarriage creates an indirect genetic channel through the mother, so the predicted correlation is reduced but not zero (see Section 4.3.5).

For each census year (1900, 1910, and 1920), I proceed as follows. I load the father crosswalk file, which identifies each child's father (household head). I merge the child's relationship code, race, and sex from the full-count census file. Children are classified into three categories: biological (RELATE code 301), adopted (codes 302 and 304), and stepchild (code 303). The sample is restricted to white males ages 0–15. I merge the father's adjusted occupation score from the corresponding census year's occupation score file, and link the child forward to 1940 to obtain the child's adult occupation score.

After appending pairs from all three census years, I drop duplicate children (those linked from multiple earlier censuses), retaining the first observation. The final sample contains approximately 16.1 million father-son pairs: 15.9 million biological, 17,920 adopted, and 155,917 stepchildren. The small number of adopted children reflects the rarity of formal adoption in this period and the fact that many informal adoptions were not recorded as such in census relationship codes.

I also construct education and wage outcomes from the 1940 census. Education is measured as years of schooling (for individuals age 25 and older), converted to percentile ranks within five-year age bands. Wage income is taken from the 1940 census (`incwage`), restricted to wage workers, and similarly percentile-ranked within age bands.

B.8 Biological vs. Step Father Data

This dataset identifies children who transition from a biological father's household to a stepfather's household between consecutive census years, providing a within-child comparison of biological

versus environmental transmission. Under the genetic model, the biological father's occupation should predict the child's outcome more strongly than the stepfather's. The stepfather still has some predictive power through assortative remarriage: his phenotype correlates with the mother's endowment, and the child inherits from the mother. In a bivariate regression, the model predicts the stepfather's coefficient should be a fraction r of the biological father's (Section 4.3.5).

The analysis stacks two cohorts. Cohort 1 uses children biological in 1900 who become stepchildren in 1910; Cohort 2 uses children biological in 1910 who become stepchildren in 1920. The procedure is identical for each cohort.

Step 1: Identify biological children. I load the father crosswalk for the earlier census and merge RELATE codes from the full-count census. I keep only white male children ages 0–15 who are classified as biological children (RELATE code 301).

Step 2: Link children to the later census and identify stepchildren. I link each child forward using the crosswalk files. Separately, I load the later census's father crosswalk and merge RELATE codes, keeping only children classified as stepchildren (RELATE code 303). I merge these two files, retaining only children who appear as biological in the earlier census and as stepchildren in the later census with a different household head. I verify that the biological father and stepfather are different people by linking the stepfather back to the earlier census through the crosswalk files and confirming his identity differs from the biological father's. About 25% of linkable stepfathers turn out to be the same person as the biological father; these are dropped. To confirm the interpretation that the biological father died (or left) and the mother remarried, I also verify that the child's mother is the same person in both census years.

Step 3: Stack cohorts and merge occupation scores. I link each child forward to 1940, merge adult occupation scores, and append the two cohorts. Duplicate children appearing in both cohorts are dropped. The final stacked sample contains 15,478 observations. Mean occupation scores are 51.6 for biological fathers, 52.0 for stepfathers, and 56.0 for children.

B.9 Biological vs. Adoptive Father Data

This dataset identifies children who appear as adopted in one census but were observed as biological children with a different father in the preceding census, providing a within-child comparison of biological versus adoptive fathers. Because adopted children share zero genes with their adoptive father, the genetic model predicts that the biological father's occupation should predict the child's outcome more strongly than the adoptive father's.

The analysis stacks two cohorts. Cohort 1 uses children adopted in 1910 who were biological in 1900; Cohort 2 uses children adopted in 1920 who were biological in 1910. The procedure is identical for each cohort.

Step 1: Identify adopted children. I load the father crosswalk for the later census and merge RELATE codes from the full-count census. I keep white children ages 0–18 classified as adopted (RELATE codes 302 and 304).

Step 2: Link children back and identify biological fathers. I link each adopted child back to the earlier census using the crosswalk files. In the earlier census, I identify children classified as biological (RELATE code 301) and merge their father's identity. I retain only children who appear as biological in the earlier census and as adopted in the later census. To remove cases where the "adoptive" father is actually the same person as the biological father, I link the adoptive father back to the earlier census through the crosswalk files and drop confirmed same-person cases. Adoptive fathers who cannot be linked back are retained under the assumption that they are different people. I restrict the sample to children ages 0–5 in the earlier census to ensure they spent most of their formative years with the adoptive family.

Step 3: Stack cohorts and merge outcomes. I link each child forward to 1940, merge occupation scores, education, and wage income, and append the two cohorts. Duplicate children appearing in both cohorts are dropped. The final stacked sample contains 1,998 observations. Mean occupation scores are 46.8 for biological fathers, 52.6 for adoptive fathers, and 54.3 for children. Education regressions use 1,961 observations (restricting to age 25 and older with non-missing education) and wage regressions use 1,476 observations (restricting to wage workers with positive earnings).

B.10 Uncle Data

Uncles are defined as brothers of the father (paternal uncles). Under the additive genetic model, the uncle-nephew correlation should be lower than the sibling correlation by a factor of $(1 + m)/2$, because uncles are one genetic step further removed on the lateral-kin ladder (Table 2).

I construct uncle-nephew pairs using the multigenerational data (Appendix B.1). Uncles are identified as G2 fathers who share the same paternal grandfather as the focal child's father but are not the focal child's own father. This yields uncle-nephew pairs where the uncle is a paternal uncle.

The nephew's occupation score is measured in 1940. The uncle's occupation score is measured in a prior census in which the uncle was observed as a household head, using the same adjusted scores as the father generation. I merge adjusted occupation scores for both individuals and drop

duplicate uncle-nephew pairs. The final sample contains approximately 3.5 million uncle-nephew pairs. For state-level analyses, I apply the same state restrictions as the multigenerational analysis (dropping states without statehood by 1880) and additionally exclude Nevada due to insufficient sample size. I compute uncle-nephew and father-son correlations separately within each remaining state and compare the ratio of the two correlations to the predicted decay factor.

B.11 Inverse Probability Weights

Cross-census linkage is non-random. Individuals who are successfully linked from childhood censuses to 1940 differ systematically from the general population: they are more likely to be rural, male, US-born, and to have common names and stable residential patterns (Bailey et al., 2020). If these characteristics also predict the outcomes of interest (occupation scores, education), then correlations estimated on the linked sample may not represent population parameters. I construct inverse probability weights (IPW) for each linked dataset following Bailey et al. (2020).

The procedure is the same for each dataset. I extract unique focal individuals from the linked sample and merge their demographic characteristics from the 1940 full-count census. I pool these linked individuals with the target population: all white, US-born adults ages 18–60 in the 1940 census (with age ranges adjusted for datasets that require completed education or specific life-cycle stages). I then estimate a probit model predicting inclusion in the linked sample:

$$\Pr(\text{linked}_i = 1 \mid X_i) = \Phi\Big(\beta_0 + \beta_1 \cdot \text{educ}_i + \beta_2 \cdot \text{urban}_i + \textstyle\sum_k \gamma_k \cdot \text{relate}_{ik} + \delta_0 \cdot \text{female}_i + \text{female}_i \times \big(\delta_1 \cdot \text{educ}_i + \delta_2 \cdot \text{urban}_i + \textstyle\sum_k \lambda_k \cdot \text{relate}_{ik}\big) + \text{age FE}_i + \text{occ FE}_i + \text{state FE}_i\Big)$$

where educ is years of schooling, urban is an urban/rural indicator, relate_{ik} is a set of household relationship indicators, age FE is a set of decadal age group indicators, occ FE is a set of broad occupation category indicators (white collar, farmer, craftsman, operative, unskilled, no occupation), and state FE is a full set of state fixed effects. Education, urban status, and household relationship enter both as main effects and interacted with a female indicator, allowing the selection process to differ by sex.

I construct weights as $w_i = (1 - \hat{p}_i)/\hat{p}_i$, normalized so that the weighted linked sample sums to the same total as the unlinked population. I winsorize the weights at the 1st and 99th percentiles to limit the influence of extreme values. This yields six separate weight files, one for each linked dataset: the multigenerational sample (three generations), the intergenerational sample (two generations), the sibling sample, the uncle-nephew sample, the cousin sample, and the parent education sample.

All correlations, regressions, and IV estimates reported in this paper apply these weights.

C. Generation-Specific Measurement Error

A concern with the multigenerational identification strategy is that measurement error may differ across generations. Grandfathers (G1) are observed in early censuses (1850–1910), fathers and uncles (G2) in later censuses (1900–1930), and grandchildren, siblings, nephews, and cousins (G3) in the 1940 census. If occupation titles become more precisely measured over time, or if the mapping from occupations to economic status changes, the reliability ratio $\theta_g = \text{Var}(x)/\text{Var}(y_g)$ may vary across generations.

Allow the reliability ratio to differ: θ_{G1} for G1, θ_{G2} for G2, and θ_{G3} for G3. Under the additive genetic model, the latent endowment variance $\text{Var}(x)$ is constant across generations (a consequence of stationarity), but the environmental variance $\text{Var}(\varepsilon_g)$ may differ, so $\text{Var}(y_g) = \text{Var}(x) + \text{Var}(\varepsilon_g)$ and θ_g can vary. Each observed correlation between a kinship pair involves two specific generations, and the attenuation depends on the reliability ratios of those two generations. Direct-lineage pairs also involve the phenotype-matching parameter $r_g = m/\theta_g$, which varies across generations when θ does:

$$
\begin{aligned}
\text{Corr}(y_{\text{father}}, y_{\text{son}}) &= \frac{1 + r_{G2}}{2} \sqrt{\theta_{G2}\,\theta_{G3}} \\
\text{Corr}(y_{\text{grandfather}}, y_{\text{grandson}}) &= \frac{1 + r_{G1}}{2} \cdot b \sqrt{\theta_{G1}\,\theta_{G3}} \\
\text{Corr}(y_{\text{grandfather}}, y_{\text{father}}) &= \frac{1 + r_{G1}}{2} \sqrt{\theta_{G1}\,\theta_{G2}} \\
\text{Corr}(y_{\text{uncle}}, y_{\text{nephew}}) &= b^2 \sqrt{\theta_{G2}\,\theta_{G3}} \\
\text{Corr}(y_{\text{sib}_1}, y_{\text{sib}_2}) &= b\,\theta_{G3} \\
\text{Corr}(y_{\text{cousin}_1}, y_{\text{cousin}_2}) &= b^3\,\theta_{G3}
\end{aligned}
$$

When $\theta_{G1} = \theta_{G2} = \theta_{G3} = \theta$, these reduce to the standard expressions in Table 2. When θ varies by generation, the three identification ratios no longer all recover b. Table A9 shows how each ratio is affected.

The grandfather-father and uncle-sibling ratios have opposite bias directions: one depends on $\sqrt{\theta_{G3}/\theta_{G2}}$ and the other on $\sqrt{\theta_{G2}/\theta_{G3}}$. The key implication is that the grandfather-father and cousin/uncle-nephew ratios share the same bias factor $\sqrt{\theta_{G3}/\theta_{G2}}$, so they should produce the same estimate of b regardless of how measurement error varies across generations. If they disagree, generation-specific measurement error cannot explain the discrepancy.

Table A9: Identification Ratios Under Generation-Specific Measurement Error

Ratio	Constant θ	Generation-specific θ
Grandfather / father	b	$b\sqrt{\theta_{G3}/\theta_{G2}}$
Uncle-nephew / sibling	b	$b\sqrt{\theta_{G2}/\theta_{G3}}$
Cousin / uncle-nephew	b	$b\sqrt{\theta_{G3}/\theta_{G2}}$

Generation-specific reliability ratios: θ_{G1} (G1: grandparents), θ_{G2} (G2: fathers, uncles), θ_{G3} (G3: grandchildren, siblings, nephews, cousins). The G1 reliability θ_{G1} does not appear in any ratio because it enters both the numerator and denominator of the grandfather-father ratio and cancels.

Figure 5 reports the grandfather-father, uncle-sibling, and cousin/uncle-nephew ratios by state. The cousin/uncle-nephew estimates are systematically larger than the grandfather-father estimates in nearly every state, the opposite of agreement. Generation-specific measurement error cannot explain this pattern: it predicts the two should be equal. I cannot fully verify this restriction by birth cohort, because uncles and cousins are not observed by cohort in the same way as the multigenerational grandfather-father-grandson chain. The state-level comparison, however, directly addresses the concern.