Room at the top: biological lock-in of social advantage

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1 Introduction

Charles Murray (1995) warned of "a merging of the cognitive elite with the affluent". On the opposite side of the political spectrum, Karl Marx (1844) wrote "I am ugly, but I can buy the most beautiful woman…. the effect of ugliness, its repelling power, is destroyed by money." These quotations suggest that social advantages, such as wealth, caste or status, may be transformed into biological advantages in the next generation, via assortative mating between socially and genetically advantaged people. We call this process biological lock-in.

Figures 1 and 2 illustrate the idea using data for spouse pairs from UK Biobank. Figures 1 plots one partner's mean polygenic score for educational attainment (PSEA) against a measure of the other partner's actual educational attainment: possession of a university degree. University graduates had spouses with higher PSEA.[1] Figure 2 plots one partner's PSEA against another measure of social status: income.

These figures do not prove that biological lock-in is taking place: since an individual's own PSEA correlates with both their educational attainment, and their income, both figures could be a result of partner selection on a purely genetic basis. In this paper, we test the theory more rigorously, using environmental shocks to social status that are unlikely to be correlated with own genetics. First, we develop a simple theory of biological lock-in, to illustrate how its effects vary with social structure.

2 Theory

The population is size 1. There is a single binary genetic trait and a single social trait. Individuals i thus have $G_i \in \{0, 1\}$ and $S_i \in \{0, 1\}$; write $\tau_i = (G_i, S_i)$ to fully describe i's type. We will call individuals with $\tau_i = (1, 1)$, $(1, 0)$, $(0, 1)$ and $(0, 0)$, b-types, g-types, s-types and n-types respectively. The proportion of the population with $G_i = 1$ is denoted by γ, and the population proportion with $S_i = 1$ is denoted by σ. In generation 1, G_i and S_i are assumed independent, so e.g. the proportion of b-types is $\gamma\sigma$.

Higher values of G_i and S_i are assumed to be attractive in the marriage market. Indeed, individuals are divided into two classes, H and L, for the purpose of marital matching. Within H and L, all individuals form spouse pairs at random. Class H is of size θ: we assume $\gamma\sigma < \theta \le \min\{\gamma, \sigma\}$. We also assume γ and σ are not too different:

$$\text{Either } \sigma < \gamma < (1 + \sigma)/2 \text{ or } \gamma < \sigma < (1 + \gamma)/2. \tag{1}$$

Married pairs have two children and each randomly inherits one parent's genetic trait and one parent's social trait. As a result, σ and γ stay constant over generations.

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[1] To minimize concerns about genetic stratification, i.e. correlations between genetics and non-genetic forms of inherited advantage, PSEA is residualized by the first 100 principal components of UK Biobank array data.
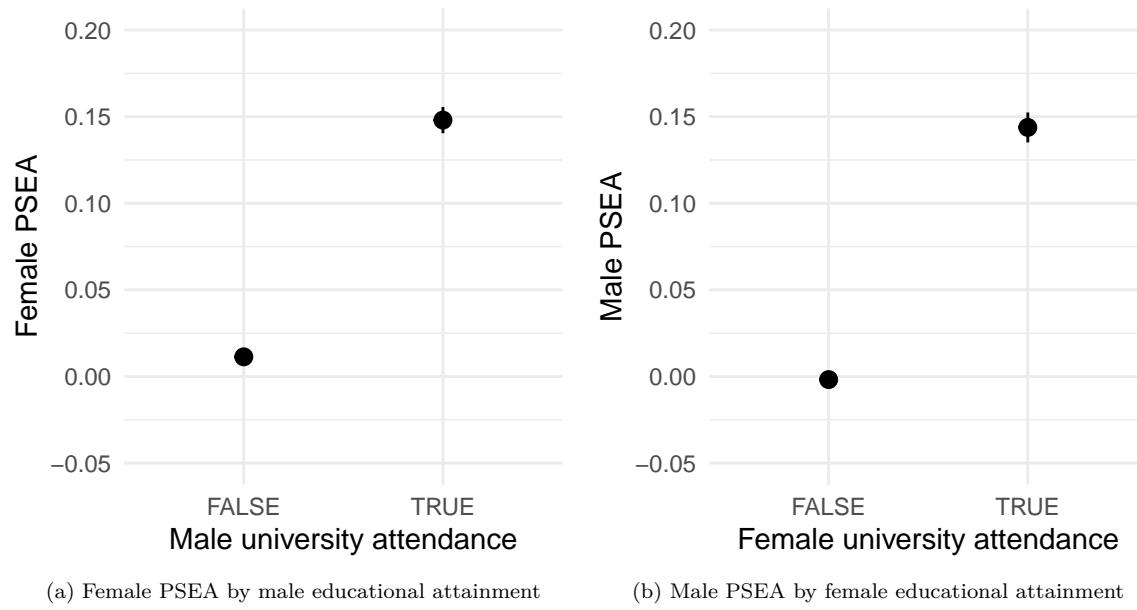
(a) Female PSEA by male educational attainment (b) Male PSEA by female educational attainment

Figure 1: Social and genetic advantage among spouse pairs in UK Biobank

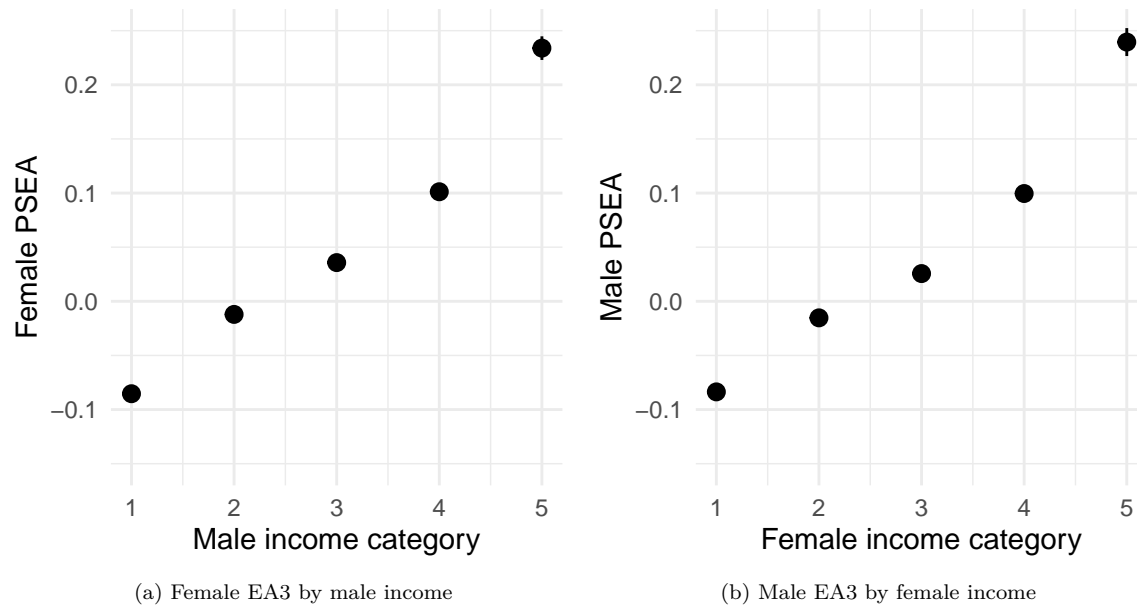(a) Female EA3 by male income (b) Male EA3 by female income

Figure 2: Social and genetic advantage among spouse pairs in UK Biobank

B-types with $\tau_i = (1,1)$ are always in H. N-types with $\tau_i = (0,0)$ are always in L. Where the other groups fit depends on the nature of the society. Of the $\theta - \gamma\sigma$ non-b-types in H, a proportion k are s-types and the remaining $1 - k$ are g-types.

The value of k gives the level of social stratification in the society's marriage market. When k is close to 1, individuals' place in the marriage market is largely determined by social status, and genetics alone rarely gives access to the high matching group. When k is close to 0, "good genes" play a larger role in the marriage market, and social status alone rarely gives access to the high group.

To build intuition, we start with two extreme examples. Suppose first that $k = 1$ and that $\theta = \sigma$. This is a caste society where marital matching is entirely driven by social status. All individuals in H (L) have $S_i = 1$ ($S_i = 0$), and so do their children. On the other hand, the proportion of individuals with $G_i = 1$ stays at γ within both groups. Thus, over generations, the distributions of G_i and S_i remain independent in the population.

Suppose next that $k = 0$ and $\theta = \gamma$. This society is socially egalitarian: only genetics matter for marital matching. All individuals in H (L) have $G_i = 1$ ($G_i = 0$), and so do their children. The proportion of individuals with $S_i = 1$ stays at σ within both groups; hence, again, G_i and S_i remain independent over generations.

In between these cases, G_i and S_i will become positively correlated. We examine the correlation in the second generation.

Proposition 1. *The second-generation correlation between G_i and S_i is concave in k. If θ is close enough to $\min\{\sigma, \gamma\}$, then the correlation has a maximum at $k \in (0, 1)$.*

The logic behind Proposition 1 is simple. As we have seen, when spouse matching is entirely on the basis of social status, or entirely on the basis of genetics, no correlation arises between the two. However, when spouses are selected on the basis of both genetics and social status, then some s-types, who only have high social status, marry some g-types, who only have valuable genetic capital. As a result, some of their children inherit both (or neither), and this increases the correlation between genetics and social status.

Figure 3 plots the second generation correlation coefficient of S_i and G_i against k, for $\gamma = \sigma = \theta = 0.5$.

Some points are in order. First, the "marriage market" here is a reduced form mechanism, encompassing that makes a difference to partner choice. For example, if earned income affects attractiveness in the marriage market, then society's level of meritocracy in the labour market will correlate with the value of k: a more meritocratic labour market will allow people with low social status but high human capital (partly genetically determined) to earn more, and therefore to enter the high group.

Second, the contents of G – what counts as "good genes" in the marriage market – are themselves likely to vary across societies. For instance, standards of physical attractiveness vary historically. Similarly, it is plausible that what counted as a "good match", in terms of personality, physical and intellectual characteristics, differed between medieval European nobility and contemporary society.

The model predicts variation in the strength of biological lock-in. In particular, in "caste societies" where there is complete endogamy within social status groups, there is no scope for biological lock-in, because marriage partners do not trade off genetics for social status. The model also assumes that social status is inherited randomly from one parent, in the same way a genetic allele is inherited. This assumption can be weakened. For example, if social status is inherited deterministically from the father, then the results remain unchanged (for each pair of parents, just assume that one randomly chosen parent is the father).

Another possibility is that cultural rules may assign status more or less strictly. Suppose that if both parents have $S_i = 1$, then the children always inherit $S_i = 1$. However, if only one parent has $S_i = 1$, then children inherit $S_i = 1$ with probability α. A higher value of α corresponds to a more "expansive" inheritance rule for social status. For example, while British noble titles descend only to the first born son, on Europe the status of nobility were granted to all children, creating a separate quasi-caste. (TODO: check details!) The original
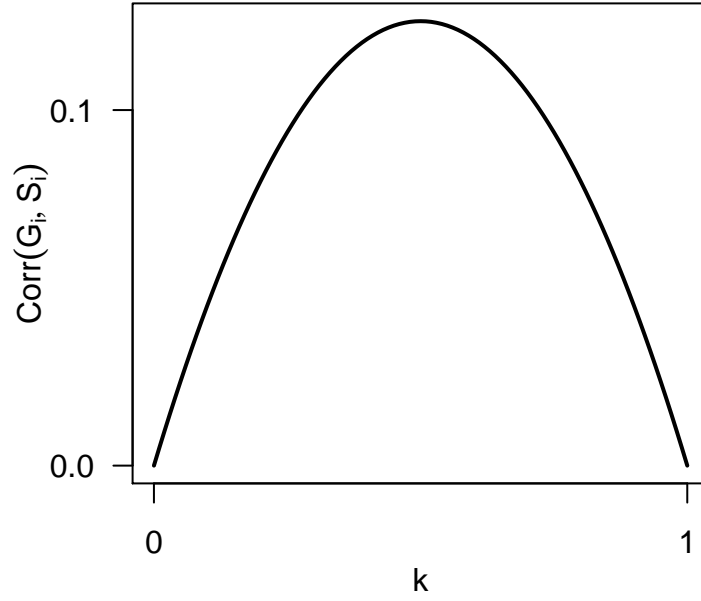
Figure 3: Social stratification and biological lock-in: theory

model corresponds to $\alpha = \frac{1}{2}$.[2] Our second result shows that a more expansive inheritance rule strengthens the correlation between genetics and status.

Proposition 2. *The second-generation correlation between G_i and S_i increases in α.*

This is because when the inheritance rule is generous, children of b-types and other types are relatively more likely to end up as b-types, inheriting both genetics and social status.

TODO: Points about the theory - Contents of G itself will vary across societies DONE - Marriage market is "reduced form" for everything that affects partner matching. DONE - No correlation if $k = 0$ and $\theta = \sigma$, i.e. if there is complete endogamy within social statuses. DONE - Model assumes that social status descends randomly. (We can investigate varying this.) - Differences with meritocracy. Meritocracy models of this phenomenon have that G causes S. Here G may not play any causal role in determining status. - A more complex model with continuous S and G would still have the same results (maybe discuss in appendix)?

3   Data

As mentioned above, simple correlations between one partner's social status and the other partner's genetics do not prove that biological lock-in is taking place, because one's social status correlates with one's own genetics. To demonstrate biological lock-in, we therefore need a source of social advantage which is exogenous to genetics. One possibility is birth order. It is well known that earlier-born children receive more parental care and have better life outcomes. (XXX is it? Go check.) On the other hand, early- and late-born full siblings have the same ex ante expected genetic endowment. [3] We can therefore use birth order as an exogenous shock to social status.

We use data from UK Biobank, a study of about 500,000 individuals.

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[2]If $\alpha \neq \frac{1}{2}$, the size of the high-status group increases or decreases over time. Population shares could be stabilized by adding noise to the inheritance process, however.

[3]This might not be the case, if parents' choice of whether to have more children is endogenous to the genetic endowment of their earlier children. We will check for this below.

TODO: describe N for birth order, describe PSEA calculation. TODO: look at mechanisms by which birth order might affect university TODO: get IQ data, control for it TODO: subset to spouses with children TODO: overall index of social status?

4 Results

Ideally we would instrument social status with birth order. However, our measures of social status are noisy and incomplete. For example, we know whether subjects went to university, but not which university they went to, and we only have rough categorical data on household income. Birth order likely affects both these and other measures of social advantage. So, an instrumental variables approach would probably fall foul of the exclusion restriction.

Instead, we conduct a mediation analysis, following the strategy of Heckman and Pinto (2013). We first regress our measures of own social status (i.e. income and education) on birth order. Then, we regress spouse's PSEA on birth order, with and without controlling for social status. Under the assumption that birth order is exogenous to own genetics, these regressions identify the effect of birth order, plus other environmental variables that correlate with it, on own social status and spouse's genetics. Also, if the estimated effect of birth order on spouse's PSEA changes when social status is included, that is evidence that social status mediates the effect of birth order.
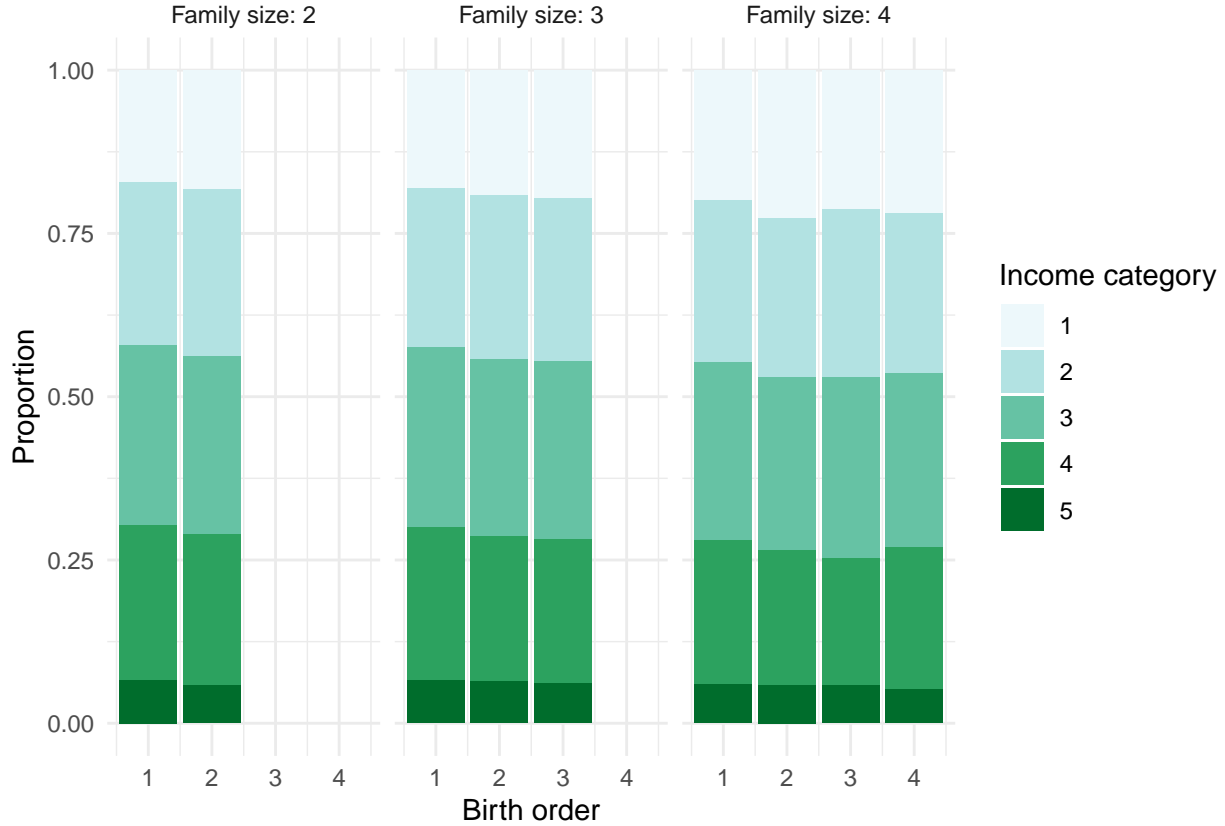
TODO: clarify the empirical model, you may need help….

TODO: reduced form TODO: estimate individual income from job SIC codes? ASHE gives data

5

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## `summarise()` regrouping output by 'Birth order' (override with `.groups` argument)
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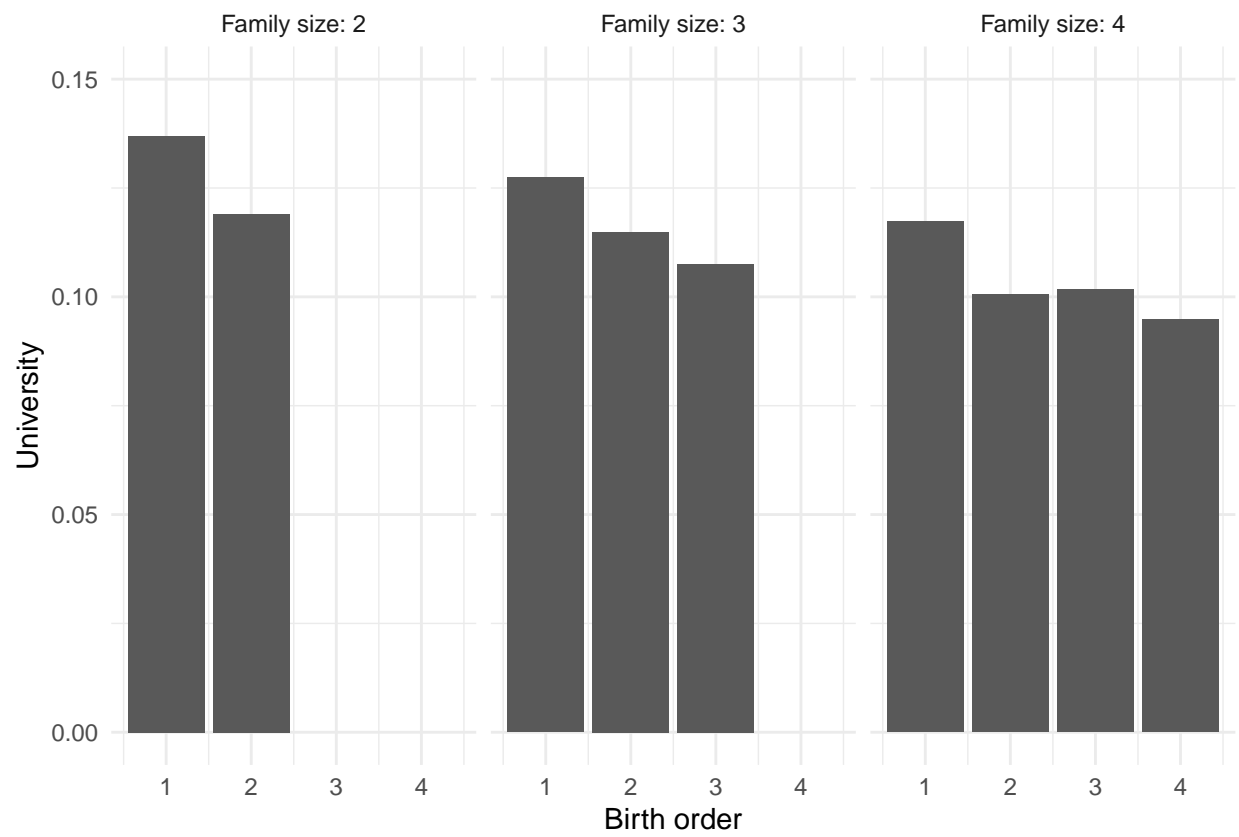
5.1 Regressions

We run regressions instrumenting one spouse's educational attainment with their birth order. We control for overall family (i.e. sibling group) size. Without this, then birth order would correlate with family size, which itself may correlate with genetics, since parents of different family sizes might have different genetic endowments. Indeed, respondents with more siblings overall have substantially lower PSEA. We also control for subject's own PSEA. Lastly, we allow the effect of birth order to vary depending on total family size.

Table 1 shows instrumental variables regressions using 2 stage least squares. We use only subjects with between 2 and 8 siblings. Column 1 pools men and women. Columns 2 and 3 run separate regressions by sex. The effect is positive for both male and female subjects, but twice as strong, and significant, for males.

Although all children of the same parents have identical expected values of polygenic scores, it is conceivable that parents might select family size on the basis of genetics. For example, if the first child had a phenotype reflecting a high (or low) polygenic score, then that might affect the parents' decision to have a second child. To check this we regress birth order directly on PSEA. As before, we control for family size and allow the effect of birth order to vary depending on family size. Birth order variables are not jointly significant (anova p 0.178) and their effect sizes are of the order of 0.01 of a standard deviation of PSEA.

Table 1: Effects of educational attainment on spouse's EA3

	All spouses' EA3	Female spouses' EA3	Male spouses' EA3
University	0.440 **	0.351	0.610 *
	(0.161)	(0.187)	(0.295)
EA3	0.033 ***	0.035 ***	0.029 **
	(0.005)	(0.007)	(0.009)
Family size dummies	Y	Y	Y
R2	-0.007	-0.002	-0.019
N	340061	170663	169398
Sargan test (p)	0.467	0.407	0.844

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$. Educational attainment instrumented by birth order.

6 Appendix

6.1 Proof of Proposition 1

Write b_t, g_t, s_t, n_t for the population proportion of each type in generation $t = 1, 2, \dots$. Sometimes we drop the subscript. Since G_i and S_i are independent in generation 1,

$$b_1 = \gamma\sigma;$$
$$g_1 = \gamma(1-\sigma);$$
$$s_1 = (1-\gamma)\sigma;$$
$$n_1 = (1-\gamma)(1-\sigma).$$

Within either group $J \in \{H, L\}$, write the proportion of types in generation t as b_J, g_J, s_J, n_J for the respective types.

Dividing children up by their parents' types, we can calculate the proportion with each of the four types:

	b_J	g_J	s_J	n_J
b_J	$1; 0; 0; 0$	$\frac{1}{2}; \frac{1}{2}; 0; 0$	$\frac{1}{2}; 0; \frac{1}{2}; 0$	$\frac{1}{4}; \frac{1}{4}; \frac{1}{4}; \frac{1}{4}$
g_J	$\frac{1}{2}; \frac{1}{2}; 0; 0$	$0; 1; 0; 0$	$\frac{1}{4}; \frac{1}{4}; \frac{1}{4}; \frac{1}{4}$	$0; \frac{1}{2}; 0; \frac{1}{2}$
s_J	$\frac{1}{2}; 0; \frac{1}{2}; 0$	$\frac{1}{4}; \frac{1}{4}; \frac{1}{4}; \frac{1}{4}$	$0; 0; 1; 0$	$0; 0; \frac{1}{2}; \frac{1}{2}$
n_J	$\frac{1}{4}; \frac{1}{4}; \frac{1}{4}; \frac{1}{4}$	$0; \frac{1}{2}; 0; \frac{1}{2}$	$0; 0; \frac{1}{2}; \frac{1}{2}$	$0; 0; 0; 1$

Table 2: Proportions of children born from different types of parents (b-type; g-type; s-type; n-type)

Summing these in each group, and using that $n_H = 0$ and $b_L = 0$, gives the proportion of children of each

type in each group:

$$b_{J,t+1} = b_J + \rho_J$$
$$g_{J,t+1} = g_J - \rho_J$$
$$s_{J,t+1} = s_J - \rho_J$$
$$n_{J,t+1} = n_J + \rho_J$$

where

$$\rho_J \equiv \frac{1}{2} g_J s_J.$$

In words, when a group contains both g-types and s-types, some of them marry each other and produce some b- and n-type offspring: this increases the correlation between G_i and S_i.

Summing over the groups, we can write the new generation's proportion of types in the whole population as

$$b_{t+1} = b_t + \rho$$
$$g_{t+1} = g_t - \rho$$
$$s_{t+1} = s_t - \rho$$
$$n_{t+1} = n_t + \rho$$

where

$$\rho \equiv \theta \rho_H + (1 - \theta) \rho_L.$$

We can now calculate the covariance between G and S in the second generation. The covariance is just $E(G_i S_i) - E(G_i)E(S_i)$; in general, at generation t, this is $b_t - \gamma\sigma$. For $t = 2$ this is just equal to ρ.

In the first generation, we can calculate:

$$b_{H,1} = \gamma\sigma/\theta;$$
$$g_{H,1} = (1 - k)\phi/\theta$$
$$s_{H,1} = k\phi/\theta;$$
$$n_{H,1} = 0;$$

where

$$\phi \equiv \theta - \gamma\sigma.$$

Similarly:

$$b_{L,1} = 0;$$
$$g_{L,1} = \frac{\gamma(1 - \sigma) - \phi(1 - k)}{1 - \theta}$$
$$s_{L,1} = \frac{(1 - \gamma)\sigma - \phi k}{1 - \theta}$$
$$n_{L,1} = \frac{(1 - \gamma)(1 - \sigma)}{1 - \theta};$$

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and from these

$$\rho_H = \frac{1}{2}\frac{\phi^2 k(1-k)}{\theta^2};$$

$$\rho_L = \frac{1}{2}\frac{[\gamma(1-\sigma)-\phi(1-k)][(1-\gamma)\sigma-\phi k]}{(1-\theta)^2}.$$

Hence:

$$\rho = \frac{1}{2}\frac{\phi^2 k(1-k)}{\theta} +$$
$$\frac{1}{2}\frac{[\gamma(1-\sigma)-\phi(1-k)][(1-\gamma)\sigma-\phi k]}{(1-\theta)}.$$

Note that when $k = 1$ and $\theta = \sigma$, ρ evaluates to 0. Similarly, when $k = 0$ and $\theta = \gamma$, ρ evaluates to 0. This confirms the claims in the main text about the two extreme example societies.

ρ is a quadratic in k. Differentiating ρ by k gives

$$\frac{d\rho}{dk} = \frac{1}{2\theta}\phi^2(1-2k) + \frac{1}{2(1-\theta)}[\phi^2(1-2k)+\phi(\sigma-\gamma)]$$
$$= \frac{1}{2\theta(1-\theta)}\phi^2(1-2k) + \frac{1}{2(1-\theta)}\phi(\sigma-\gamma)$$
$$= \frac{1}{2(1-\theta)}\left[\frac{\phi^2}{\theta}(1-2k)+\phi(\sigma-\gamma)\right]. \tag{2}$$

This is decreasing in k, proving that ρ is concave.

We find the maximum for ρ by solving the first order condition. In (2), setting the term in square brackets to 0 gives:

$$k = \frac{1}{2} + \frac{1}{2}\frac{\theta}{\theta-\gamma\sigma}(\sigma-\gamma). \tag{3}$$

We need to show this is strictly between 0 and 1 as θ approaches σ or γ.

First assume $\sigma < \gamma$. As $\theta \to \sigma$, the expression (3) approaches $k = \frac{1}{2} + \frac{1}{2}\frac{(\sigma-\gamma)}{(1-\gamma)}$. The requirement for this to be interior is that $|\sigma-\gamma| < |1-\gamma|$. For $\sigma < \gamma$ this is equivalent to $\gamma < (1+\sigma)/2$, which holds by condition (1).

Next assume $\gamma < \sigma$. As $\theta \to \gamma$, (3) approaches $k = \frac{1}{2} + \frac{1}{2}\frac{(\sigma-\gamma)}{(1-\sigma)}$. This is interior when $|\sigma-\gamma| < |1-\sigma|$, equivalently when $\sigma < (1+\gamma)/2$, which again holds by (1).

6.2 Proof of Proposition 2

We can rewrite table 2 as:

	b_J	g_J	s_J	n_J
b_J	$1;0;0;0$	$\alpha;1-\alpha;0;0$	$\frac{1}{2};0;\frac{1}{2};0$	$\frac{\alpha}{2};\frac{1-\alpha}{2};\frac{\alpha}{2};\frac{1-\alpha}{2}$
g_J	$\alpha;1-\alpha;0;0$	$0;1;0;0$	$\frac{\alpha}{2};\frac{1-\alpha}{2};\frac{\alpha}{2};\frac{1-\alpha}{2}$	$0;\frac{1}{2};0;\frac{1}{2}$
s_J	$\frac{1}{2};0;\frac{1}{2};0$	$\frac{\alpha}{2};\frac{1-\alpha}{2};\frac{\alpha}{2};\frac{1-\alpha}{2}$	$0;0;1;0$	$0;0;\frac{1}{2};\frac{1}{2}$
n_J	$\frac{\alpha}{2};\frac{1-\alpha}{2};\frac{\alpha}{2};\frac{1-\alpha}{2}$	$0;\frac{1}{2};0;\frac{1}{2}$	$0;0;\frac{1}{2};\frac{1}{2}$	$0;0;0;1$

Table 3: Proportions of children born, α-rule for social inheritance

Again, summing over types within groups and then over groups, we get

$$b_{t+1} = b_t - \theta(1-2\alpha)b_t g_t + \alpha g_t s_t$$
$$g_{t+1} = g_t + \theta(1-2\alpha)b_t g_t - \alpha g_t s_t$$
$$s_{t+1} = s_t - (1-\alpha)g_t s_t$$
$$n_{t+1} = n_t + (1-\alpha)g_t s_t$$

as the intergenerational difference equation in type shares. As before, plug in first generation type-shares to get:

$$b_2 = b_1 - \theta(1-2\alpha)b_{H,1}g_{H,1} + \alpha\rho_\alpha$$
$$g_2 = g_1 + \theta(1-2\alpha)b_{H,1}g_{H,1} - \alpha\rho_\alpha$$
$$s_2 = s_1 - (1-\alpha)\rho_\alpha$$
$$n_2 = n_1 + (1-\alpha)\rho_\alpha$$

where

$$\rho_\alpha = \theta(g_H s_H) + (1-\theta)(g_L s_L).$$

Calculating the second-generation covariance as $b_2 - \gamma\sigma = b_2 - b_1$ gives:

$$\alpha[\theta(g_H s_H) + (1-\theta)(g_L s_L)] - \theta(1-2\alpha)b_{H,1}g_{H,1}$$

and plugging in values for the first generation as before gives

$$\alpha\frac{k(1-k)\phi^2}{\theta} + \alpha\frac{[\gamma(1-\sigma) - \phi(1-k)][(1-\gamma)\sigma - \phi k]}{1-\theta}$$
$$-(1-2\alpha)\frac{\gamma\sigma(1-k)\phi}{\theta}.$$

This expression equals the old value of ρ when $\alpha = \frac{1}{2}$. It is also increasing in α, since all the fractions in it are positive.