

ONLINE APPENDIX, NOT FOR PUBLICATION

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APPENDIX A AN EXTENSION OF THE ONE-SEX MULTIGENERATIONAL MODEL WITH MARRIAGE

In this section, I extend Matras' two-generation social reproduction model in equation (7) to multiple generations. Specifically, I add parameters that characterize the likelihood of marriage in each generation and grandparents' socioeconomic characteristics. The model is specified as

$$s_{j|ikl,c} = f_{ikl,c} \cdot m_{ikl,c} \cdot r_{ikl,c} \cdot p_{Y_n=j|Y_{n-1}=i, Y_{n-2}=k, Y_{n-3}=l, \bar{Y}=c} \quad (\text{a.1})$$

where $s_{j|ikl,c}$ denotes the number of men in the offspring generation who are in class j ($j = 1, \dots, J$) with fathers in class i ($i = 1, \dots, I$), grandfathers in class k ($k = 1, \dots, K$), and great-grandfathers in class l ($l = 1, \dots, L$); $m_{ikl,c}$ denotes the probability of getting married (or the average number of marriages) for men in the parent generation, $f_{ikl,c}$; and $r_{ikl,c}$ denotes the expected number of sons born to men, in each marriage, in the parent generation. The extra subscript c ($c = 1, \dots, C$) refers to this person's ancestral traits that do not change over generations (e.g., an indicator of remote family history of slavery or royalty). More generally, if the model parameters depend on the socioeconomic status of all prior generations, $\bar{\mathbf{Y}}_{n-1} = \{Y_1, Y_2, \dots, Y_{n-1}\}$, the model can be expressed as

$$s_{Y_n} = \sum_{Y_1} \cdots \sum_{Y_{n-1}} f_{\bar{\mathbf{Y}}_{n-1}} \cdot m_{\bar{\mathbf{Y}}_{n-1}} \cdot r_{\bar{\mathbf{Y}}_{n-1}} \cdot p_{Y_n|\bar{\mathbf{Y}}_{n-1}} \quad (\text{a.2})$$

To predict the number of descendants in the n^{th} generation, we rely on the recursive relationship shown in equation (8). The resulting model is written as,

$$\begin{aligned} s_{Y_n}^{(n)} &= \sum_{Y_1} \cdots \sum_{Y_{n-1}} f_{Y_1} \cdot m_{Y_1} \cdot r_{Y_1} \cdot p_{Y_2|Y_1} \cdot m_{\bar{\mathbf{Y}}_2} \cdot r_{\bar{\mathbf{Y}}_2} \cdot p_{Y_3|\bar{\mathbf{Y}}_2} \cdots m_{\bar{\mathbf{Y}}_{n-1}} \cdot r_{\bar{\mathbf{Y}}_{n-1}} \cdot p_{Y_n|\bar{\mathbf{Y}}_{n-1}} \\ &= \sum_{Y_1} \cdots \sum_{Y_{n-1}} f_{Y_1} \cdot \prod_{i=1}^{n-1} m_{\bar{\mathbf{Y}}_i} \cdot r_{\bar{\mathbf{Y}}_i} \cdot p_{Y_{i+1}|\bar{\mathbf{Y}}_i} \end{aligned} \quad (\text{a.3})$$

The marriage (m), fertility (r), and social mobility (p) terms can be modeled by generalized linear models as functions of independent variables. For example, marriage outcomes are often assumed to be dichotomous if the probability of getting married is considered, or non-negative counts if the number of marriages is considered. The latter applies to populations that have high rates of multi-partner fertility or polygamy. The marriage term thus can be characterized by a logit or negative binomial function. Reproduction outcomes are often assumed to follow a Poisson distribution with

a possible overdispersion parameter and modeled by the negative binomial function. The mobility term can be modeled by multinomial logistic models when multiple categories of social statuses are used as the dependent variable. This model is restricted to influences of the father, grandfather, and great-grandfather, but similar recursive models can incorporate influences from more generations or paternal and maternal sides of the family.

When the marriage component is added, the Kitagawa method can still be used to partition the social reproduction effect in equation (20) into demography and mobility effects. Below, I illustrate the method assuming that m , r , and p depend only on the socioeconomic characteristics of the parent generation, but the method can also be used when characteristics of more generations are considered. I first partition the SRE into the demographic part that combines marriage and reproduction effects and the mobility part.

$$SRE_{k|j} = (m_k r_k - m_j r_j) \cdot \frac{(p_{Y_2=k|Y_1=k} + p_{Y_2=k|Y_1=j})}{2} + \frac{(m_k r_k + m_j r_j)}{2} \cdot (p_{Y_2=k|Y_1=k} - p_{Y_2=k|Y_1=j}). \quad (\text{a.4})$$

For the term $(m_k r_k - m_j r_j)$, I repeat the Kitagawa decomposition method and separate the marriage and reproduction effects:

$$SRE_{k|j} = \left((m_k - m_j) \cdot \frac{(r_k + r_j)}{2} + (r_k - r_j) \cdot \frac{(m_k + m_j)}{2} \right) \cdot \frac{(p_{Y_2=k|Y_1=k} + p_{Y_2=k|Y_1=j})}{2} + \frac{(m_k r_k + m_j r_j)}{2} \cdot (p_{Y_2=k|Y_1=k} - p_{Y_2=k|Y_1=j}). \quad (\text{a.5})$$

Let $\bar{m} = \frac{m_k + m_j}{2}$, $\bar{r} = \frac{r_k + r_j}{2}$, $\bar{m}\bar{r} = \frac{m_k r_k + m_j r_j}{2}$, and $\bar{p} = \frac{p_{Y_2=k|Y_1=k} + p_{Y_2=k|Y_1=j}}{2}$, and the above equation can be further simplified as

$$SRE_{k|j} = \underbrace{(m_k - m_j) \cdot \bar{r} \cdot \bar{p}}_{\text{marriage effect}} + \underbrace{(r_k - r_j) \cdot \bar{m} \cdot \bar{p}}_{\text{reproduction effect}} + \underbrace{\bar{m}\bar{r} \cdot (p_{Y_2=k|Y_1=k} - p_{Y_2=k|Y_1=j})}_{\text{mobility effect}}. \quad (\text{a.6})$$

The marriage effect shows differences in SRE attributed to differences in marriage rates of high-status and low-status fathers, fixing the reproductive rates of fathers and mobility probabilities of their offspring at the mean levels, \bar{r} and \bar{p} . The reproduction effect shows differences in SRE attributed to differences in reproductive rates of high-status and low-status fathers, fixing the marriage rates of fathers and mobility probabilities of their offspring at the mean levels, \bar{m} and \bar{p} . The mobility effect refers to differences in SRE due to differences in mobility probabilities of offspring from high-status and low-status fathers, fixing fathers' demographic rates at the mean

level, \overline{mr} . We can also use Das Gupta's 1993 decomposition method discussed in Section 4.3 to decompose SRE as follows. The Das Gupta's method is particularly useful when the demographic rates contains multiple factors.

$$\text{marriage effect} = \left[\frac{r_k \cdot p_{Y_2=k|Y_1=k} + r_j \cdot p_{Y_2=k|Y_1=j}}{3} + \frac{r_k \cdot p_{Y_2=k|Y_1=j} + r_j \cdot p_{Y_2=k|Y_1=k}}{6} \right] \cdot (m_k - m_j) \quad (\text{a.7})$$

$$\text{reproduction effect} = \left[\frac{m_k \cdot p_{Y_2=k|Y_1=k} + m_j \cdot p_{Y_2=k|Y_1=j}}{3} + \frac{m_k \cdot p_{Y_2=k|Y_1=j} + m_j \cdot p_{Y_2=k|Y_1=k}}{6} \right] \cdot (r_k - r_j) \quad (\text{a.8})$$

$$\text{mobility effect} = \left[\frac{m_k \cdot r_k + m_j \cdot r_j}{3} + \frac{m_k \cdot r_j + m_j \cdot r_k}{6} \right] \cdot (p_{Y_2=k|Y_1=k} - p_{Y_2=k|Y_1=j}) \quad (\text{a.9})$$

APPENDIX B AGE-CLASSIFIED MODELS

Regular mobility models often ignore the age structure of the parent or the offspring generation. Such a simplification does not affect our understanding of the long-term behaviors of a Markov chain, namely, the chances that individuals will achieve a certain social class conditional on their parent’s or ancestor’s social status. Yet, the distribution of fathers or sons, even after accounting for the reproduction factor, reflects only the overall size of each generation, not the population structure at a given point in time. From a demographic perspective, all accurate representations of population growth—or “transformations of occupation structure” (Duncan 1966a)—depend on age-specific fertility and mortality rates. In his classic work on population projection, P. H. Leslie (1945: 183) showed that “the age distribution of the survivors and descendants of the original population at successive intervals of time” can be derived from simple matrix multiplication, assuming the regime of mortality and fertility is time-constant or year-to-year change in mortality and fertility is known. Keyfitz (1964) introduced this method to the study of human populations. Specifically, let $r_{i,t}$ refer to age-specific fertility rates, often based on five-year age groups, for social class i and age group t ; $r_{i,t}$ is a positive number for men within the reproductive age range and zero otherwise. In addition, let $\frac{{}_5L_{i,t+5}}{{}_5L_{i,t}}$ refer to the life table function of surviving from age t to $t + 5$ for social class i . The social reproduction models shown in equation (7) thus can be represented as

$$s_{j,1} = \sum_{i=1}^I \sum_{t=1}^T f_{i,t} \cdot r_{i,t} \cdot p_{Y_2=j|Y_1=i} \quad (j = 1, 2, \dots, J) \quad (\text{a.10})$$

$$s_{j,t+5} = s_{j,t} \cdot \frac{{}_5L_{j,t+5}}{{}_5L_{j,t}} \quad (\text{a.11})$$

$$f_{i,t+5} = f_{i,t} \cdot \frac{{}_5L_{i,t+5}}{{}_5L_{i,t}} \quad (\text{a.12})$$

Note that this model assumes social attainment is completed at birth, and no intragenerational mobility is allowed for either the father or son generation. Predictions based on these assumptions may detract from the exact number of incumbents in each social class, but this will not affect conclusions regarding the overall social trend from an intergenerational perspective. The matrix forms of similar models based on the Leslie matrix are described in Matras (1967) and Mare (1997).

APPENDIX C A GENERALIZATION OF THE SRE DECOMPOSITION METHOD

In this section, I generalize the decomposition method for parent and grandparent SRE described in Section 4.3 to multiple generations. First, following the decomposition method for grandparents illustrated in equations (23)–(26), we can derive the decomposition for four generations. To simplify the notations below, I use r_1, r_2, r_3 to indicate the reproduction of the great-grandparent, grandparent, and parent generation, respectively, and $p_1, p_2,$ and p_3 to indicate the mobility probability of grandparents, parents, and offspring generation conditional on all prior generations, respectively.²⁷

The total effect of great-grandparents is thus expressed as

$$\text{TSRE}_{k|j}^{GGP} = \sum_{Y_2} \sum_{Y_3} r_1 \cdot p_1 \cdot r_2 \cdot p_2 \cdot r_3 \cdot p_3 - \sum_{Y_2} \sum_{Y_3} r'_1 \cdot p'_1 \cdot r'_2 \cdot p'_2 \cdot r'_3 \cdot p'_3$$

which can then be partitioned using Das Gupta's method for rates of six factors. For example, the demography effect from the first generation r_1 versus r'_1 is:

$$\begin{aligned} \text{demography effect (1)} &= \sum_{Y_2} \sum_{Y_3} \left[\frac{p_1 r_2 p_2 r_3 p_3 + p'_1 r'_2 p'_2 r'_3 p'_3}{6} \right. \\ &+ \frac{p_1 r_2 p_2 r_3 p'_3 + p_1 r_2 p_2 r'_3 p_3 + p_1 r_2 p'_2 r_3 p_3 + p_1 r'_2 p_2 r_3 p_3 + p'_1 r_2 p_2 r_3 p_3}{30} \\ &+ \frac{p_1 r_2 p_2 r'_3 p'_3 + p_1 r_2 p'_2 r_3 p'_3 + p_1 r_2 p'_2 r'_3 p_3 + p_1 r'_2 p_2 r_3 p'_3 + p_1 r'_2 p_2 r'_3 p_3}{60} \\ &\left. + \frac{p_1 r'_2 p'_2 r_3 p_3 + p'_1 r_2 p_2 r_3 p'_3 + p'_1 r_2 p_2 r'_3 p_3 + p'_1 r_2 p'_2 r_3 p_3 + p'_1 r'_2 p_2 r_3 p_3}{60} \right] \\ &\cdot (r_1 - r'_1) \end{aligned} \tag{a.13}$$

Demography effects (2)–(3) and mobility effects (1)–(3) can be derived easily by interchanging the terms in equation (a.13). The total effect of great-grandparents is equal to the sum of all separate effects.

Overall, the total effect of an N^{th} ancestor defined in equation (19) can be decomposed into $2N$ terms, including demographic effects and mobility effects from each of the N prior generations. Below, I apply the decomposition method of rates as the product of P factors proposed by Das Gupta (1993). To simplify the notations for demographic and mobility parameters in each generation, I

²⁷For example, $r_1 = r_k, r'_1 = r_j, r_2 = r_{kk}, r'_2 = r_{jj}, r_3 = r_{kkk}, r'_3 = r_{kjj}, p_1 = p_{Y_2=k|Y_1=k}, p'_1 = p_{Y_2=j|Y_1=j}, p_2 = p_{Y_3=k|Y_2=k, Y_1=k}, p'_2 = p_{Y_3=k|Y_2=j, Y_1=j}, p_3 = p_{Y_4=k|Y_3=k, Y_2=k, Y_1=k},$ and $p'_3 = p_{Y_4=k|Y_3=k, Y_2=j, Y_1=j}.$

denote the demographic parameter in the n^{th} generation ($n = 1 \cdots N$) as follows,

$$r_n = r_{Y_n|\bar{Y}_{n-1,k}} \text{ and } r'_n = r_{Y_n|\bar{Y}_{n-1,j}}.$$

I use r and r' to differentiate between two ancestors in the founding generation with social status k and j , respectively. Similarly, the mobility parameters in the n^{th} generation are

$$p_n = p_{Y_{n+1}|\bar{Y}_{n,k}} \text{ and } p'_n = p_{Y_{n+1}|\bar{Y}_{n,j}}.$$

Suppose the elements r and p are members of the set $\mathbb{A} = \{r_1, \dots, r_N, p_1, \dots, p_N\}$ and r' and p' are members of set \mathbb{A}' . The set \mathbb{A} , excluding one element A_n (e.g., r_n), is defined as $\mathbb{A} \setminus A_n$ (or $\mathbb{A} \setminus r_n$). The $\text{TSRE}_{k|j}^{(n)} = \sum_{Y_2} \cdots \sum_{Y_{N-1}} r_1 \cdots r_{N-1} \cdot p_1 \cdots p_{N-1} - r'_1 \cdots r'_{N-1} \cdot p'_1 \cdots p'_{N-1}$ can be decomposed into the sum of the demography effect (n) and mobility effect (n) from the n^{th} generation. For example, Das Gupta (1993: 15–16) described the decomposition of $(r_1 \cdots r_{N-1} \cdot p_1 \cdots p_{N-1}) - (r'_1 \cdots r'_{N-1} \cdot p'_1 \cdots p'_{N-1})$ as

$$\begin{aligned} \text{demography effect } (n) = & \sum_{t=1}^N \frac{\text{sum of all } (2N-1) \text{ terms with } (2N-t) \text{ from the set } \mathbb{A} \setminus r_n \text{ and } (t-1) \\ & \text{from the set } \mathbb{A}' \setminus r'_n \text{ or } (2N-t) \text{ terms from } \mathbb{A}' \setminus r'_n \text{ and } (t-1) \text{ from } \mathbb{A} \setminus r_n}{2N \cdot \binom{2N-1}{t-1}} \\ & \cdot (r_n - r'_n) \end{aligned} \tag{a.14}$$

More formally, I introduce the following notations to define the demography effect in equation (a.14). Let \mathbb{B}_{2N-t} denote subsets of $\mathbb{A} \setminus A_n$ with a cardinality of $2N-t$ (i.e., $|\mathbb{B}| = 2N-t$). Given that there are $\binom{2N-1}{2N-t}$ of such subsets, each subset i is denoted by

$$\mathbb{B}_{2N-t,i} = \{B_{2N-t,i} : B_{2N-t,i} \in \mathbb{A} \setminus A_n\}.$$

The complement of the set $\mathbb{B}_{2N-t,i}$ can be written as $\bar{\mathbb{B}}_{2N-t,i}$, which satisfies that $\bar{\mathbb{B}}_{2N-t,i} = \mathbb{B}_{t-1,i}$ with the cardinality of $t-1$. Taking our illustration of the total effect of grandparents with $N=2$ as an example, the set $\mathbb{B}_{21} = \{r_2, p_2\}$ is one subset with cardinality 2 of the set $\mathbb{A} \setminus r_1 = \{r_2, p_1, p_2\}$. Other subsets include $\mathbb{B}_{22} = \{r_2, p_1\}$ and $\mathbb{B}_{23} = \{p_1, p_2\}$, where the total number of subsets with cardinality 2 is $\binom{3}{2} = 3$. The complement set of \mathbb{B}_{21} in the counterpart set of \mathbb{A}' is $\bar{\mathbb{B}}'_{21} = \mathbb{B}'_{11} = \{p'_1\}$.

$$\text{demography effect } (n) = \frac{\sum_{t=1}^N \sum_{i=1}^{\binom{2N-1}{2N-t}} \left(\prod_{B \in \mathbb{B}_{2N-t}} B_{2N-t,i} \cdot \prod_{B' \in \mathbb{B}'_{t-1}} B'_{t-1,i} + \prod_{B' \in \mathbb{B}'_{2N-t}} B'_{2N-t,i} \cdot \prod_{B \in \mathbb{B}_{t-1}} B_{t-1,i} \right)}{2N \cdot \binom{2N-1}{t-1}} \cdot (r_n - r'_n) \quad (\text{a.15})$$

Likewise, if the set \mathbb{B} is a subset of $\mathbb{A} \setminus p_n$, the mobility effect can be written as

$$\text{mobility effect } (n) = \frac{\sum_{t=1}^N \sum_{i=1}^{\binom{2N-1}{2N-t}} \left(\prod_{B \in \mathbb{B}_{2N-t}} B_{2N-t,i} \cdot \prod_{B' \in \mathbb{B}'_{t-1}} B'_{t-1,i} + \prod_{B' \in \mathbb{B}'_{2N-t}} B'_{2N-t,i} \cdot \prod_{B \in \mathbb{B}_{t-1}} B_{t-1,i} \right)}{2N \cdot \binom{2N-1}{t-1}} \cdot (p_n - p'_n) \quad (\text{a.16})$$

APPENDIX D EQUILIBRIUM EFFECTS

In this section, I show the equilibrium of Markov chain models with demography. Recall that in regular Markovian mobility models with a time-invariant transition matrix, the effect of a family's initial social status will disappear in the long run. After enough generations, the probability distribution of descendants from high-status and low-status families will converge to the same equilibrium. However, as illustrated in the paper, this property does not hold when considering families' reproductive behaviors. According to the definition in equation (27), the long-term mobility effect in equation (27) is defined as

$$\text{LSRE} = \lim_{t \rightarrow \infty} \begin{pmatrix} \mathbf{S}_{k|k}^{(t)} \\ \mathbf{S}_{k|j}^{(t)} \end{pmatrix}.$$

Now we assume $\mathbf{S}^{(t)} = \mathbf{F}^{(0)} \cdot \mathbf{C}^t$, where $\mathbf{C} = \mathbf{R} \cdot \mathbf{P}$, a combination of the reproduction and mobility components. According to the Perron-Frobenius theorem, \mathbf{C} would be a square matrix with positive entries and a unique dominant eigenvalue.²⁸ The long-term behavior of $\mathbf{S}^{(t)}$ would depend on the largest eigenvalue of \mathbf{C} .

To see this, we assume \mathbf{C} has n linearly independent left eigenvectors $\mathbf{v}_1, \mathbf{v}_2 \dots \mathbf{v}_n$ with corresponding eigenvalues of $\lambda_1, \lambda_2, \dots \lambda_n$. Assume the eigenvalues are ordered so that $|\lambda_1| > \dots \geq |\lambda_{n-1}| \geq |\lambda_n|$. For the social class distribution in the first generation $\mathbf{S}^{(1)}$, we can write this vector as the linear combination of the eigenvectors of \mathbf{C} :

$$\mathbf{S}^{(1)} = a_1 \mathbf{v}_1 + a_2 \mathbf{v}_2 + \dots + a_n \mathbf{v}_n \tag{a.17}$$

where $a_1 \dots a_n$ are scalars and $a_1 \neq 0$. Then, multiplying both sides by \mathbf{C} produces

$$\mathbf{S}^{(1)} \cdot \mathbf{C} = (a_1 \mathbf{v}_1 + a_2 \mathbf{v}_2 + \dots + a_n \mathbf{v}_n) \cdot \mathbf{C} \tag{a.18}$$

Using the spectral decomposition theorem,

$$\mathbf{S}^{(1)} \cdot \mathbf{C} = a_1(\lambda_1 \mathbf{v}_1) + a_2(\lambda_2 \mathbf{v}_2) + \dots + a_n(\lambda_n \mathbf{v}_n). \tag{a.19}$$

²⁸This assumption implies that the number of social classes is the same for fathers and sons, and the marriage, fertility, and mobility matrices have no structural 0s. That is, men in different social classes may get married and have sons, and all sons may stay in the same social class as their fathers or move to other classes.

Repeating the multiplication on both sides produces

$$\mathbf{S}^{(1)} \cdot \mathbf{C}^{t-1} = a_1(\lambda_1^{t-1}\mathbf{v}_1) + a_2(\lambda_2^{t-1}\mathbf{v}_2) + \dots + a_n(\lambda_n^{t-1}\mathbf{v}_t) = \mathbf{S}^{(t)}. \quad (\text{a.20})$$

As λ_1 is assumed to be larger in absolute value than the other eigenvalues, it follows that each of the fractions $\frac{\lambda_2}{\lambda_1}, \frac{\lambda_3}{\lambda_1} \dots \frac{\lambda_n}{\lambda_1}$ is less than 1 in absolute value. Each of the factors $\left(\frac{\lambda_2}{\lambda_1}\right)^{t-1}, \left(\frac{\lambda_3}{\lambda_1}\right)^{t-1} \dots \left(\frac{\lambda_n}{\lambda_1}\right)^{t-1}$ must converge to 0 as $t - 1$ approaches infinity. Therefore, we have the following relationship

$$\mathbf{S}^{(t)} \simeq a_1 (\lambda_1^{t-1}\mathbf{v}_1). \quad (\text{a.21})$$

For the initial vector $\mathbf{F}^{(0)} = [f_1, f_2, \dots, f_n]$, let $\mathbf{F}_k^{(0)} = [0, \dots, f_k = 1, \dots, 0]$ and $\mathbf{F}_j^{(0)} = [0, \dots, f_j = 1, \dots, 0]$, so that the entire initial cohort is located in a single class. Assume $a_1 = a_{1k}$, when $\mathbf{S}^{(1)} = \mathbf{F}_k^{(0)}\mathbf{C}$, and $a_1 = a_{1j}$, when $\mathbf{S}^{(1)} = \mathbf{F}_j^{(0)}\mathbf{C}$. After t generations, the long-term social reproduction effect would converge to

$$\text{LSRE} = \lim_{t \rightarrow \infty} \left(\frac{a_{1k}\lambda_1^{t-1}\mathbf{v}_1}{a_{1j}\lambda_1^{t-1}\mathbf{v}_1} \right) = \frac{a_{1k}}{a_{1j}}. \quad (\text{a.22})$$

APPENDIX E ADDITIONAL RANDOM MATING FUNCTIONS

In the main analysis, I define the random mating rule as follows:

$$\mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) = \frac{\mathbf{N}_i^m \mathbf{N}_j^f}{(\mathbf{N}^m + \mathbf{N}^f)/2} \quad (\text{a.23})$$

where $\mathbf{N}^m = \sum_i \mathbf{N}_i^m$ and $\mathbf{N}^f = \sum_j \mathbf{N}_j^f$. Compared to the assortative mating rule, random mating assumes the number of marriages between men in class i and women in class j is only constrained by the abundance of mates.

The random mating rule can be defined differently depending on our assumption about the constraint imposed by the size of male and female populations. For example, random mating rules can be defined as

$$\begin{aligned} \mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) &= \frac{\mathbf{N}_i^m + \mathbf{N}_j^f}{2} && (\text{arithmetic mean}) \\ \mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) &= \sqrt{\mathbf{N}_i^m \mathbf{N}_j^f} && (\text{geometric mean}) \\ \mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) &= a\mathbf{N}_i^m + (1-a)\mathbf{N}_j^f, \quad 0 \leq a \leq 1, && (\text{weighted mean}) \\ \mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) &= \mathbf{N}_i^m && (\text{male dominance}) \\ \mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) &= \mathbf{N}_j^f && (\text{female dominance}) \\ \mu_{ij}(\mathbf{N}^m, \mathbf{N}^f) &= \min(\mathbf{N}_i^m, \mathbf{N}_j^f) && (\text{minimum abundance}) \end{aligned}$$

These functions are all considered as random mating because the number of marriages does not depend on parameters related to individual preferences between different class groups.

**APPENDIX F ADDITIONAL TABLES USED IN THE ILLUSTRATIVE EX-
AMPLES**

Appendix Table S1. Two-Generation Reproduction and Social Mobility Models, Historical Data

Father's Occupation	Gross Reproduction Rate		Mobility Model: Son's Occupation							
	(Poisson Regression)		(Multinomial Logistic Regression, Base = 1. Upper nonmanual)							
			2. Lower nonmanual	3. Upper manual	4. Lower manual	5. Farming				
2. Lower nonmanual	-0.100***	(0.02)	0.607***	(0.05)	0.371***	(0.079)	0.108*	(0.061)	-0.161*	(0.093)
3. Upper manual	0.004	(0.015)	0.732***	(0.048)	2.234***	(0.057)	1.686***	(0.048)	1.145***	(0.065)
4. Lower manual	-0.004	(0.014)	0.675***	(0.047)	1.595***	(0.06)	2.418***	(0.045)	1.432***	(0.061)
5. Farming	0.161***	(0.012)	-0.908***	(0.043)	0.280***	(0.056)	0.667***	(0.039)	3.803***	(0.047)
Intercept	0.956***	(0.011)	0.037	(0.027)	-1.355***	(0.043)	-0.394***	(0.031)	-1.388***	(0.043)
<i>n</i>	27,734		78,133							
Log likelihood	-57,136									
AIC	114,283		163,900							

Source: IPUMS Linked Representative Samples, 1850–1930 (final data release June 2010).

Notes: Standard errors are in parentheses. The Gross Reproduction Rates and mobility probabilities estimated from these models are presented in Table 1.

* $p < .05$; ** $p < .01$; *** $p < .001$ (two-tailed test).

Appendix Table S2. Three-Generation Reproduction and Social Mobility Models, Historical Data

	Gross Reproduction Rate		Mobility Model: Son's Occupation							
	(Poisson Regression)		(Multinomial Logistic Regression, Base = 1. Upper nonmanual)							
			2. Lower nonmanual	3. Upper manual	4. Lower manual	5. Farming				
Father's Occupation										
1. Upper nonmanual (reference)										
2. Lower nonmanual	-0.058**	(0.028)	0.196**	(0.076)	0.182*	(0.11)	0.203**	(0.088)	-0.079	(0.128)
3. Upper manual	0.013	(0.017)	0.323***	(0.054)	0.878***	(0.066)	0.721***	(0.055)	0.775***	(0.068)
4. Lower manual	0.029*	(0.016)	0.411***	(0.053)	0.620***	(0.068)	1.057***	(0.053)	0.785***	(0.065)
5. Farming	0.111***	(0.015)	0.136***	(0.045)	0.183***	(0.061)	0.640***	(0.047)	1.294***	(0.054)
Grandfather's Occupation										
1. Upper nonmanual (reference)										
2. Lower nonmanual	-0.085***	(0.02)	0.574***	(0.052)	0.342***	(0.08)	0.077	(0.062)	-0.131	(0.094)
3. Upper manual	0.004	(0.016)	0.612***	(0.051)	1.907***	(0.061)	1.443***	(0.051)	0.959***	(0.068)
4. Lower manual	-0.016	(0.015)	0.545***	(0.05)	1.388***	(0.063)	2.092***	(0.048)	1.192***	(0.064)
5. Farming	0.098***	(0.013)	-0.934***	(0.048)	0.290***	(0.061)	0.469***	(0.043)	3.306***	(0.05)
Intercept	0.916***	(0.014)	-0.099***	(0.036)	-1.625***	(0.055)	-0.848***	(0.042)	-2.080***	(0.058)
<i>n</i>	27,734		78,133							
Log likelihood	-57,104									
AIC	114,226.5		162,099.0							

Source: IPUMS Linked Representative Samples, 1850–1930 (final data release June 2010).

Notes: Standard errors are in parentheses. The Gross Reproduction Rates and mobility probabilities estimated from these models are presented in Table 2.

* $p < .05$; ** $p < .01$; *** $p < .001$ (two-tailed test).

Appendix Table S3. Two-Generation Reproduction and Social Mobility Models, Contemporary Data

Father's Occupation	Gross Reproduction Rate		Mobility Model: Son's Occupation							
	(Poisson Regression)		2. Lower nonmanual		3. Upper manual		4. Lower manual		5. Farming	
1. Upper nonmanual (reference)										
2. Lower nonmanual	-0.016	(0.059)	0.711***	(0.154)	0.619***	(0.157)	0.773***	(0.171)	-0.419	(0.645)
3. Upper manual	-0.032	(0.043)	0.789***	(0.122)	1.373***	(0.116)	1.230***	(0.132)	0.353	(0.387)
4. Lower manual	-0.021	(0.047)	1.083***	(0.141)	1.496***	(0.136)	1.808***	(0.145)	1.396***	(0.36)
5. Farming	0.11	(0.072)	0.312	(0.268)	1.575***	(0.215)	1.360***	(0.24)	3.514***	(0.352)
Intercept	0.375***	(0.034)	-0.535***	(0.088)	-0.535***	(0.088)	-0.945***	(0.101)	-3.219***	(0.273)
<i>n</i>	2,689		4,142							
Log likelihood	-3,457									
AIC	6,924.4		11,609.8							

Source: Panel Study of Income Dynamics, 1968–2015.

Notes: Standard errors are in parentheses. The Gross Reproduction Rates and mobility probabilities estimated from these models are presented in Table 1.

* $p < .05$; ** $p < .01$; *** $p < .001$ (two-tailed test).

Appendix Table S4. Three-Generation Reproduction and Social Mobility Models, Contemporary Data

	Gross Reproduction Rate		Mobility Model: Son's Occupation							
	(Poisson Regression)		2. Lower nonmanual		3. Upper manual		4. Lower manual		5. Farming	
Father's Occupation										
1. Upper nonmanual (reference)										
2. Lower nonmanual	-0.059	(0.072)	0.17	(0.184)	-0.105	(0.198)	0.306	(0.214)	0.241	(0.664)
3. Upper manual	0.029	(0.058)	0.442***	(0.156)	0.686***	(0.157)	0.620***	(0.181)	0.890*	(0.507)
4. Lower manual	0.01	(0.057)	0.435***	(0.154)	0.679***	(0.154)	0.966***	(0.174)	0.703	(0.493)
5. Farming	0.129**	(0.058)	0.052	(0.171)	1.049***	(0.159)	1.033***	(0.181)	1.217***	(0.472)
Grandfather's Occupation										
1. Upper nonmanual (reference)										
2. Lower nonmanual	-0.018	(0.059)	0.659***	(0.156)	0.547***	(0.159)	0.681***	(0.174)	-0.498	(0.647)
3. Upper manual	-0.051	(0.044)	0.715***	(0.126)	1.166***	(0.12)	1.031***	(0.136)	0.142	(0.394)
4. Lower manual	-0.045	(0.049)	1.019***	(0.145)	1.272***	(0.14)	1.569***	(0.15)	1.177***	(0.369)
5. Farming	0.035	(0.076)	0.387	(0.278)	1.136***	(0.226)	0.985***	(0.251)	3.065***	(0.387)
Intercept	0.354***	(0.051)	-0.757***	(0.131)	-1.000***	(0.136)	-1.509***	(0.16)	-3.818***	(0.458)
<i>n</i>	2,690									
Log likelihood	-3,452.0									
AIC	6,921.9									

Source: Panel Study of Income Dynamics, 1968–2015.

Notes: Standard errors are in parentheses. The Gross Reproduction Rates and mobility probabilities estimated from these models are presented in Table 2.

* $p < .05$; ** $p < .01$; *** $p < .001$ (two-tailed test).

APPENDIX G R CODES USED IN THE ANALYSIS OF THE PSID DATA

```

1 #####
2 ### Implementation of Various Joint Demography-Social Mobility ###
3 ### Models: ###
4 ### (1) 2g and 3g mobility table construction ###
5 ### (2) Ratio and difference measures of mobility effects ###
6 ### (3) Ratio and difference measures of social reproduction ###
7 ### effects ###
8 ### (4) Effect decomposition ###
9 ### (5) Long-term social reproduction effects ###
10 ### (6) Two-sex social reproduction models ###
11 ### Supplementary to: ###
12 ### "Multigenerational Social Mobility: A Demographic Approach" ###
13 ### Author: Xi Song ###
14 #####
15 library(readstata13)
16 library(tidyr)
17 library(dplyr)
18 library(expm)
19 library(nnet)
20 library(reshape)
21 require(boot)
22 library(parallel)
23
24 psid.male <- read.dta13("psid_mobility.dta", nonint.factors=T) %>%
25   select(c(f_id, sex, occ, occ_f, occ_m, occ_ff, occ_fm, occ_mf, occ_mm, occ_gf, sex)) %>%
26     drop_na(occ, occ_f, occ_gf) %>% filter(sex==1)
27 ##### Table 1 #####
28 # Two-Generation Mobility Transition Matrix and Gross
29 # Reproduction Rates
30 #####
31 # Describe 2-generation mobility table (transition matrix)
32
33 summary(m1 <- multinom(occ ~ relevel(as.factor(occ_f), ref = "1"), data = psid.male))
34
35 data.2g <- cbind(psid.male, fitted=fitted(m1))
36 mobility2g <- data.2g %>%
37   group_by(occ_f) %>%
38   summarise(son1=mean(fitted.1), son2=mean(fitted.2), son3=mean(fitted.3), son4=mean(fitted
39     .4), son5=mean(fitted.5))
40 with(psid.male, addmargins(table(occ_f, occ)))
41 # Describe fertility by occupation
42
43 sons.count <- psid.male %>% filter(f_id != 0) %>% arrange(-f_id) %>% group_by(f_id, occ_f)
44   %>% summarise(sons.count=n())
45
46 summary(m2 <- glm(sons.count ~ relevel(as.factor(occ_f), ref = "1"), family="poisson", data=
47   sons.count))
48 GRR1 <- exp(c(0, rep(coefficients(m2)[1],4))+coefficients(m2))
49
50 ##### Table 2 #####
51 # Three-Generation Mobility Transition Matrix and Gross
52 # Reproduction Rates
53 #####
54 # Describe 3-generation mobility table
55 summary(m3 <- multinom(occ ~ relevel(as.factor(occ_gf), ref = "1")+relevel(as.factor(occ_f),
56   ref = "1"), data = psid.male))
57 data.3g <- cbind(psid.male, fitted=fitted(m3))
58 mobility3g <- data.3g %>%
59   group_by(occ_gf, occ_f) %>%

```

```

59   summarise(son1=mean(fitted.1), son2=mean(fitted.2), son3=mean(fitted.3), son4=mean(fitted
      .4), son5=mean(fitted.5))
60 with(psid.male, addmargins(table(occ_f, occ, occ_gf)))
61
62 # Describe fertility by occupation
63 sons.count2 <- psid.male %>% filter(f_id != 0) %>% arrange(-f_id) %>% group_by(f_id, occ_gf,
      occ_f) %>% summarise(sons.count2=n())
64
65 summary(m4 <- glm(sons.count2 ~ relevel(as.factor(occ_gf), ref = "1")+relevel(as.factor(occ_
      f), ref = "1"), family="poisson", data=sons.count2))
66 intercept <- coefficients(m4)[1]
67 gf_coef <- c(0, coefficients(m4)[2:5])
68 f_coef <- c(0, coefficients(m4)[6:9])
69
70 GRR2 <- exp(intercept) * (exp(gf_coef) %x% exp(f_coef))
71
72
73 ##### Table 3 #####
74 # Ratio Measures of Mobility Effects and Social Reproduction
75 # Effects by Comparing Upper Nonmanual and Lower Nonmanual
76 # Families in Producing Offspring in Upper Nonmanual
77 # Occupations
78 #####
79
80 # net and total mobility effect of p
81 mobility2g <- as.matrix(mobility2g[1:5, 2:6])
82 mobility2g[1,1]/mobility2g[2,1]
83
84 # net mobility effect of gp
85 mobility3g <- as.matrix(mobility3g[1:25, 3:7])
86 mobility3g[1,1]/mobility3g[7,1] #assume p and gp in the same class
87
88 # total mobility effect of gp
89 G0.1 <- c(1,0,0,0,0)
90 G0.2 <- c(0,1,0,0,0)
91 (G0.1 %*% mobility2g %*% mobility3g[1:5,]) [1,1]/(G0.2%*%mobility2g%*%mobility3g[6:10,]) [1,1]
92
93 # SRE of parents
94 SRE.f <- (GRR1[1]*mobility2g[1,1])/(GRR1[2]*mobility2g[2,1])
95
96 # NSRE of grandparents
97 NSRE.gf <- (GRR2[1]*mobility3g[1,1])/(GRR2[7]*mobility3g[7,1])
98
99 # TSRE of grandparents
100
101 G1.1 <- G0.1 %*% diag(GRR1) %*% mobility2g
102 G2.1 <- G1.1 %*% diag(GRR2[1:5]) %*% mobility3g[1:5,]
103
104 G1.2 <- G0.2 %*% diag(GRR1) %*% mobility2g
105 G2.2 <- G1.2 %*% diag(GRR2[6:10]) %*% mobility3g[6:10,]
106
107 TSRE.gf <- G2.1[1]/G2.2[1]
108
109 # bootstrap standard errors
110
111 bs <- function(formula1, formula2, formula3, formula4, data, indices) {
112   d1 = data[indices,]
113
114   m1 = multinom(formula1, data=d1, maxit=1000, trace=FALSE)
115   data.2g <- cbind(d1, fitted=fitted(m1))
116   mobility2g <- data.2g %>% group_by(occ_f) %>%
117     summarise(son1=mean(fitted.1), son2=mean(fitted.2), son3=mean(fitted.3), son4=mean(
      fitted.4), son5=mean(fitted.5))
118
119   sons.count <- d1 %>% filter(f_id != 0) %>% arrange(-f_id) %>%
120     group_by(f_id, occ_f) %>% summarise(sons.count=n())

```

```

121 m2 = glm(formula2, family="poisson", data=sons.count, maxit=1000, trace=FALSE)
122 GRR1 <- exp(c(0, rep(coefficients(m2)[1],4))+coefficients(m2))
123
124 m3 = multinom(formula3, data=d1, maxit=1000, trace=FALSE)
125 data.3g <- cbind(d1, fitted=fitted(m3))
126 mobility3g <- data.3g %>% group_by(occ_gf, occ_f) %>%
127   summarise(son1=mean(fitted.1), son2=mean(fitted.2), son3=mean(fitted.3), son4=mean(
128     fitted.4), son5=mean(fitted.5))
129
130 sons.count2 <- d1 %>% filter(f_id != 0) %>% arrange(-f_id) %>% group_by(f_id, occ_gf, occ_
131   f) %>% summarise(sons.count2=n())
132
133 m4 = glm(formula4, family="poisson", data=sons.count2, maxit=1000, trace=FALSE)
134 GRR2 <- exp(coefficients(m4)[1]) * (exp(c(0, coefficients(m4)[2:5])) %x% exp(c(0,
135   coefficients(m4)[6:9])))
136
137 mobility2g = as.matrix(mobility2g[1:5, 2:6])
138 mobility.f = mobility2g[1,1]/mobility2g[2,1]
139
140 mobility3g = as.matrix(mobility3g[1:25, 3:7])
141 n.mobility.gf = mobility3g[1,1]/mobility3g[7,1]
142
143 G0.1 <- c(1,0,0,0,0); G0.2 <- c(0,1,0,0,0)
144 t.mobility.gf = (G0.1 %>% mobility2g %>% mobility3g[1:5,])[1,1]/(G0.2 %>% mobility2g %>%
145   mobility3g[6:10,])[1,1]
146
147 SRE.f = (GRR1[1]*mobility2g[1,1])/(GRR1[2]*mobility2g[2,1])
148 NSRE.gf = (GRR2[1]*mobility3g[1,1])/(GRR2[7]*mobility3g[7,1])
149
150 G1.1 <- G0.1 %>% diag(GRR1) %>% mobility2g
151 G2.1 <- G1.1 %>% diag(GRR2[1:5]) %>% mobility3g[1:5,]
152 G1.2 <- G0.2 %>% diag(GRR1) %>% mobility2g
153 G2.2 <- G1.2 %>% diag(GRR2[6:10]) %>% mobility3g[6:10,]
154 TSRE.gf = G2.1[1]/G2.2[1]
155
156 estimates = rbind(mobility.f, SRE.f, n.mobility.gf, t.mobility.gf, NSRE.gf, TSRE.gf)
157
158 return(t(estimates))
159 }
160
161 # enable parallel
162
163 cl <- makeCluster(2)
164 clusterExport(cl, "multinom")
165
166 # 1000 replications
167 set.seed(1984)
168
169 #system.time(boot(data=psid.male, statistic=bs, R=1000, parallel = "multicore", ncpus=2,
170   formula=occ ~ relevel(as.factor(occ_f), ref = "1")))
171
172 results <- boot(
173   data=psid.male, statistic=bs, R=1000, parallel = "multicore", ncpus=2, cl=cl, formula1=occ
174     ~ relevel(as.factor(occ_f), ref = "1"), formula2=sons.count ~ relevel(as.factor(occ_f
175     ), ref = "1"), formula3=occ ~ relevel(as.factor(occ_gf), ref = "1")+relevel(as.factor(
176     occ_f), ref = "1"),
177   formula4=sons.count2 ~ relevel(as.factor(occ_gf), ref = "1")+relevel(as.factor(occ_f), ref
178     = "1")
179 )
180
181 ##### Table 4 #####
182 # Effect Decomposition Based on Difference Measures of
183 # Social Reproduction Effects by Comparing Upper Nonmanual
184 # and Lower Nonmanual Families in Producing Offspring in
185 # Upper Nonmanual Occupations
186 #####

```

```

178
179 # Kitagawa SRE decomposition of SRE.f
180 kita.demo.eff.f <- (GRR1[1]-GRR1[2])*(mobility2g[1,1]+mobility2g[2,1])/2
181 kita.mobi.eff.f <- (GRR1[1]+GRR1[2])/2*(mobility2g[1,1]-mobility2g[2,1])
182
183 # Kitagawa SRE decomposition of TSRE.gf
184 kita.demo.eff.gf <- sum((GRR1[1]*GRR2[1:5]-GRR1[2]*GRR2[5+1:5])*(mobility2g[1,1:5]*
185   mobility3g[1:5,1]+mobility2g[2,1:5]*mobility3g[5+1:5,1])/2)
186 kita.mobi.eff.gf <- sum((GRR1[1]*GRR2[1:5]+GRR1[2]*GRR2[5+1:5])/2*(mobility2g[1,1:5]*
187   mobility3g[1:5,1]-mobility2g[2,1:5]*mobility3g[5+1:5,1]))
188
189 # Das Gupta SRE decomposition of TSRE.gf
190 r1 <-GRR1[1]; r1prime <- GRR1[2]
191 r2 <- GRR2[1:5]; r2prime <- GRR2[5+1:5]
192 p1 <- mobility2g[1,1:5]; p1prime <- mobility2g[2,1:5]
193 p2 <- mobility3g[1:5,1]; p2prime <- mobility3g[5+1:5,1]
194
195 das.demo.eff.1.gf <-
196   sum(((p1*r2*p2+p1prime*r2prime*p2prime)/4
197     +(p1*r2*p2prime+p1*r2prime*p2+p1prime*r2*p2+p1prime*r2prime*p2+p1prime*r2*p2prime+p1*
198       r2prime*p2prime)/12)*(r1-r1prime))
199 das.demo.eff.2.gf <-
200   sum(((p1*r1*p2+p1prime*r1prime*p2prime)/4
201     +(p1*r1*p2prime+p1*r1prime*p2+p1prime*r1*p2+p1prime*r1prime*p2+p1prime*r1*p2prime+p1*
202       r1prime*p2prime)/12)*(r2-r2prime))
203 das.mobi.eff.1.gf <-
204   sum(((r1*r2*p2+r1prime*r2prime*p2prime)/4
205     +(r1*r2*p2prime+r1*r2prime*p2+r1prime*r2*p2+r1prime*r2prime*p2+r1prime*r2*p2prime+r1*
206       r2prime*p2prime)/12)*(p1-p1prime))
207 das.mobi.eff.2.gf <-
208   sum(((r1*r2*p1+r1prime*r2prime*p1prime)/4
209     +(r1*r2*p1prime+r1*r2prime*p1+r1prime*r2*p1+r1prime*r2prime*p1+r1prime*r2*p1prime+r1*
210       r2prime*p1prime)/12)*(p2-p2prime))
211
212 ##### Table 5 #####
213 # Long-Term Social Reproduction Effects
214 #####
215 # Long-term SRE (we assume mobility is Markovian)
216
217 C <- diag(GRR1) %>% mobility2g
218
219 G1.1 <- GO.1 %>% C
220 G2.1 <- G1.1 %>% C
221 G5.1 <- GO.1 %>% (C %^(5))
222 G10.1 <- GO.1 %>% (C %^(10))
223
224 G1.2 <- GO.2 %>% C
225 G2.2 <- G1.2 %>% C
226 G5.2 <- GO.2 %>% (C %^(5))
227 G10.2 <- GO.2 %>% (C %^(10))
228
229 eL <- eigen(t(C)) #left eigenvector
230 L <- eL$values
231 V <- eL$vectors
232 G1.1 %>% V %>% solve(t(V)%%V)
233 G1.2 %>% V %>% solve(t(V)%%V)
234
235 ##### Table 6 #####
236 # Two-Sex Assortative Mating and Force of Attraction
237 # (age 25-60)
238 #####

```

```

237 psid <- read.dta13("psid_mobility.dta", nonint.factors=T) %>% select(c(f_id, m_id, occ, occ_
    f, occ_m, sex)) %>% drop_na(occ, occ_f, occ_m)
238
239 child.count <- psid %>% filter(f_id != 0 | m_id != 0) %>% arrange(-f_id, -m_id) %>% group_by
    (f_id, m_id, occ_f, occ_m) %>% summarise(child.count=n())
240 summary(m5 <- glm(child.count ~ relevel(as.factor(occ_f), ref = "1")+relevel(as.factor(occ_m
    ), ref = "1"), family="poisson", data=child.count))
241 intercept <- coefficients(m5)[1]
242 f_coef <- c(0, coefficients(m5)[2:5])
243 m_coef <- c(0, coefficients(m5)[6:9])
244
245 GRR.son <- GRR.daughter <- exp(intercept) * (exp(f_coef) %x% exp(m_coef))
246
247 mobility.samesex.son <- with(filter(psid, sex==1), prop.table(table(occ_f, occ), 1))
248 mobility.samesex.daughter <- with(filter(psid, sex==2), prop.table(table(occ_m, occ), 1))
249
250 mobility.samesex.son <- matrix(rep(mobility.samesex.son,each=5), ncol=5)
251 mobility.samesex.daughter <- matrix(rep(t(mobility.samesex.daughter),5) , ncol=5, byrow=TRUE
    )
252
253 mobility.2sex.son <- with(filter(psid, sex==1), ftable(prop.table(table(occ_f, occ_m, occ),
    c(1,2))))
254 mobility.2sex.daughter <- with(filter(psid, sex==2), ftable(prop.table(table(occ_f, occ_m,
    occ), c(1,2))))
255
256 mobility.perfect <- diag(rep(1, 5))
257 mobility.perfect.son <- matrix(rep(mobility.perfect,each=5), ncol=5)
258 mobility.perfect.daughter <- matrix(rep(t(mobility.perfect),5) , ncol=5, byrow=TRUE)
259
260 N.male.0 <- apply(with(psid, table(occ_f, occ_m)), 1, sum)
261 N.female.0 <- apply(with(psid, table(occ_f, occ_m)), 2, sum)
262
263 mu.0 <- with(psid, table(occ_f, occ_m))
264 alpha <- matrix(rep(0, 25), 5, 5)
265 for (i in 1:5) for (j in 1:5) alpha[i,j] <- mu.0[i,j]*(N.male.0[i]+N.female.0[j])/(N.male.0[
    i]*N.female.0[j])
266
267 random.0 <- matrix(rep(0,25), 5, 5)
268 for (i in 1:5) for (j in 1:5) random.0[i,j] <- N.male.0[i]*N.female.0[j]/sum(N.male.0)
269
270 endogamous.0 <- diag(pmin(N.male.0, N.female.0))
271
272
273 ##### Table 7 #####
274 # Ratio Measures of Social Reproduction Effects Under
275 # Different Mating and Mobility Rules
276 #####
277
278 mobility.list.son <- list(mobility.samesex.son, mobility.2sex.son, mobility.perfect.son)
279 mobility.list.daughter <- list(mobility.samesex.daughter, mobility.2sex.daughter, mobility.
    perfect.daughter)
280
281 mating.list <- list(random.0, endogamous.0, mu.0)
282
283 TSRE.ratio <- rep(0,9)
284 TSRE.diff <- rep(0,9)
285
286 count = 1
287 for (x in 1:3) {
288   for (y in 1:3) {
289
290     new.mobility.son <- matrix(0, 25, 125)
291     new.mobility.daughter <- matrix(0, 25, 125)
292
293     for (i in 1:25) {
294       new.mobility.son[i, ((i-1)*5+1):(i*5)] <- mobility.list.son[[y]][i,]

```

```

295     new.mobility.daughter[i, ((i-1)*5+1):(i*5)] <- mobility.list.daughter[[y]][i,]
296   }
297
298   G1.son <- t((as.vector(t(mating.list[[x]]))* GRR.son)) %% new.mobility.son
299   G1.daughter <- t((as.vector(t(mating.list[[x]]))* GRR.daughter)) %% new.mobility.
300     daughter
301
302   TSRE.ratio[count] <- (sum(G1.son[,1]+G1.daughter[,1])/(N.male.0[1]+N.female.0[1])/2)
303     /(sum(G1.son[,((7-1)*5+1)]+G1.daughter[,((7-1)*5+1)])/(N.male.0[2]+N.female
304     .0[2])/2)
305   TSRE.diff[count] <- (sum(G1.son[,1]+G1.daughter[,1])/(N.male.0[1]+N.female.0[1])/2)
306     -(sum(G1.son[,((7-1)*5+1)]+G1.daughter[,((7-1)*5+1)])/(N.male.0[2]+N.female
307     .0[2])/2)
308
309   count <- count + 1
310 }

```