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## A “Lineage” Matrix Population Model of The Rendille of Northern Kenya

by

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Revised August 2006

### ABSTRACT

The Rendille tribe of Northern Kenya is an “age-group society” in which cohorts of similarly aged males known as “age sets” are organized along periodic lines of descent. This paper develops a matrix population model that reveals the genealogical dynamics inherent in the Rendille social organization. The rules governing marriage as they relate to lineage considerations substantially reduce the size and the growth rate of the population; they also induce periodicity in the demographics, and dramatically favour one of the age-set lines. More generally, the analysis suggests that matrix population modeling is a powerful tool for analyzing the social dynamics of age-group societies.

## 1. Introduction

Ethnographers have classified societies that are formally organized according to age and/or lineage as “age-group” societies. Such societies are found around the world and have been classified in set-theoretic terms by Stewart (1977). “Age-set” societies are those that recruit similar aged males into cohorts – age sets – whose members transit the lifecycle together. “Paternal-linking” societies are societies that link a father’s age-set with the sons in lineages. This paper examines a particular age-group society, the Rendille of northern Kenya, incorporating both forms of age-group organization, age sets and paternal linking. The operation of the Rendille age-group rules is well described by a genealogical (lineage-based) matrix population model. The solution to the model reveals the population dynamics inherent in the age-group marriage rules and dramatic differences in the evolution of the various lineages.

A historical description of the Rendille age-group system is presented in Table 1 (reproduced from Engineer, Roth and Welling, 2006). The system’s history is remarkably regular: every 14 years a new age set of males roughly between the ages of 14-30 is initiated. Three age sets make up what the Rendille call a *fahan*. A *fahan* is a “genealogical generation”, which we denote by the index  $n$ . The age sets are also organized along three lines of descent: each *fahan*  $n$  contains age sets  $X_n$ ,  $Y_n$  and  $Z_n$ , one from each of the three lineages denoted  $X$ ,  $Y$  and  $Z$ . Sons belong to the *fahan* subsequent to that of their fathers. For example, an “early-born” son of an age-set  $X_n$  father is initiated into age set  $X_{n+1}$ . Thus, 42 years separates the initiation of fathers and their early-born sons. “Late-born” sons are initiated into the age set that follows that of their early-born brothers, e.g., a late-born son of an age-set  $X_n$  father is initiated into age set  $Y_{n+1}$ .

In Stewart’s (1977) categorization of age-group societies, Rendille society is described as a “negative paternal-linking society” which maintains fathers and early-born sons in the same lineage. In the case of the Rendille, the paternal-linking rules require a minimum three age-set interval between the initiation of father and sons. Early-born sons are initiated into the next age-set that belongs to the same age-set line as their fathers. The lines of descent between fathers and early-born sons correspond to a 3-age-set lineage cycle and late-born sons fall out of step with their father’s lineage cycle. The reader is referred to Engineer, Roth and Welling (2005) for a more complete description of the Rendille age-group system, its history, and for evidence that the Rendille in fact closely adhere to the age-group rules.

To study the population dynamics of the Rendille age-group system, we develop a matrix population model that groups daughters in relation to their father’s age-set and lineage. The marriage customs and age-group rules are then used to identify marriages between daughter

cohorts and men of various lineages. The model is maternal in that reproductive rates only depend on when women marry not whom. The maternal reproductive assumption permits a matrix analysis with fixed coefficients.<sup>1</sup> With a maternal model, the process of mothers begetting daughters determines all of the population dynamics. In particular, the model is described by a system of difference equations that relate how daughters beget daughters by lineage, *fahan*, and birth order.

Using stable population theory, we prove that the population dynamics of the *fahan*-based model yield convergence to a constant growth path. The rules governing marriage according to lineage: substantially reduce the level and the growth rate of the population, induce periodicity in the demographics, and dramatically favours one of the age-set lines. We show these results apply generally over the range of parameters that are demographically realistic. Perturbation analysis allows us to measure the contribution of each vital coefficient to population growth. Growth elasticities with respect to the vital coefficients are calculated and compared to simulation results.

This paper builds on previous work. The history and structure of the Rendille age-group rules is discussed in detail by Engineer, Roth and Welling (2006). They outline a macro-dynamic model that is consistent with Rendille age-group organization according to Beaman's (1981) ethnographic study. Simulations are then used to analyse the population dynamics and age structure induced by the social institutions represented in the model; the simulation analysis is akin to "experimental history" wherein the study of historical counterfactuals sheds light on the process of institutional change (cf. Hammel 1979). In a separate paper, Engineer, Kang, Roth and Welling (2006) construct a formal "overlapping generations model" of the Rendille age-group rules and show that the population dynamics can be studied from either the age-cohort or the genealogical perspective.<sup>2</sup> Their calibrated macro-simulation model is based on Roth's (1993, 1999) data. The model is used to explore the political economy dynamic generated by conflicting interests of the various lineages.

The present paper links matrix population models not only to the analysis of age-group systems but also to overlapping generations modeling more generally. Here, the formal genealogical overlapping generations model of Engineer, Kang, Roth and Welling (2005) is described in more

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<sup>1</sup> Engineer, Roth and Welling (2006) make a strong case for the maternal reproductive assumption. Amongst the Rendille, women are not allowed to bear children until they marry. Married women space bearing children roughly every three years; the Rendille live a nomadic existence in dessert environment making it difficult to carrying more than one infant at a time. All women marry; there is no shortage of husbands as polygyny is allowed. Women may continue to bear children and raise them as their husband's even after their husband has died.

<sup>2</sup> The overlapping generations model is a widely used theoretical model used in economics. It has for the most part not been used as an applied demographic model and genealogy is ignored. See Engineer and Welling (2004) for a further description and reference to the literature.

detail and solved analytically using Perron-Frobenius matrix methods. The mathematical analysis provides a rigorous consistency check on the macro-simulation analysis in the other papers. More importantly, the analytical solution provides general results that show that the simulation-based conclusions of Engineer et al (2005) extend over historically relevant regions of the parameter space.<sup>3</sup>

The paper proceeds as follows. Section 2 lays out the elements of the dynamic model. The steady state is characterized analytically in Section 3. Section 5 examines perturbations to the model. Section 5 concludes.

## 2. The dynamical system

In this section we state the assumptions upon which the genealogical matrix population model is based, illustrate the model dynamics with the aid of a flow diagram, and then proceed to derive the system of equations governing the dynamics.

### *Assumptions of the model*

Our model postulates the existence of generation groups distinguished by lineage and *fahan*, the basic units of genealogical and generational distance used by the Rendille. Recall from Table 1 that a *fahan* is to a three age-set epoch equal to  $3 \times 14 = 42$  years with each epoch cycling through the lineages X, Y, and Z. This cyclical feature of the Rendille age-group system makes it possible to construct a genealogical model that is congruent with the age-set formulation. Because marriage and child-rearing activities are conceived as relations among the ordered generation groups, additional assumptions that address the coordination of these processes in real time are unnecessary. This is in contrast to the overlapping generations model of Engineer, Kang, Roth and Welling (2005) based on temporally situated age sets (cf. the “simplifying assumption” of Engineer et al 2005).

Assumption G1 (Lineages). Individuals are assigned to one of three lineages denoted by X, Y, and Z. Lineage assignment is patrilineal: an individual belongs to lineage k only if his/her father belongs to lineage k. (The converse also holds if a “climbing” rule is assumed.) Without loss of generality, the *Teeria* are associated with lineage X and non-*Teeria* are associated with lineages Y and Z.

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<sup>3</sup> Axtell (2000) discusses the potential complementarities between mathematical and simulation analysis in the social sciences, even when the mathematical model is explicitly soluble.

A generation group, male or female, is identified by its lineage and *fahan*. For the female generation groups, we also need to distinguish between the early-born and late-born in each female generation group in order to pin down the population dynamics. This is because differential timing of birth leads to differences in the age at which daughters marry, even if they belong to the same lineage.

Assumption G2. (Generation groups). Males are grouped by *fahan* and lineage while females are grouped by *fahan*, lineage, and birth order (early- vs. late-born). Generation [*Fahan*]  $n$  consists of male generation groups ( $X_n, Y_n, Z_n$ ) and female generation groups ( $X_n, X'_n, Y_n, Y'_n, Z_n, Z'_n$ ). Late-born female groups are denoted by the symbol ( $'$ ).

Note that daughters are identified by their father's lineage, i.e., if the father is born into lineage  $X$ , the daughter is also associated with lineage  $X$ . Thus,  $X'_{n+1}$  represents late-born daughters from lineage  $X$ , born to fathers of *fahan*  $n$ .

Because age-at-marriage for women is heterogeneous with respect to lineage and birth order, we assign each female generation group a parameter governing the proportion of women marrying young.

Assumption G3 (Marriage timing by lineage). Of each female generation group  $k=X, X', Y, Y', Z, Z'$ , a fixed proportion  $p_k$  are women-marrying-young and  $(1 - p_k)$  are women-marrying-old. The  $p_k$ 's satisfy the following:

- *Sepaade* restricts the majority of early-born daughters of Teeria men to be women-marrying-old:  $p_X \leq 0.4$ .
- The vast majority of early-born daughters in the non-Teeria lines are women-marrying-young:  $p_Y = p_Z = p \geq 0.8$ .
- Virtually all late-born daughters are women-marrying-young:  $p_{X'} = p_{Y'} = p_{Z'} = p'$ , and  $p \leq p'$ .

Assumption G4 (Marriage and lines of descent). All women marry. All men marry (if possible). Men and women of particular generation groups marry and rear children according to the following table:

Men of generation group ...	... Are eligible to marry women-marrying-old (women-marrying-young) from groups:	... Rear daughters belonging to groups:
$X_n$	$Z'_{n-1}, X_n ( X'_n, Y_n )$	$X_{n+1}, X'_{n+1}$
$Y_n$	$X'_n, Y_n ( Y'_n, Z_n )$	$Y_{n+1}, Y'_{n+1}$

$Z_n$	$Y'_n, Z_n (Z'_n, X_{n+1})$	$Z_{n+1}, Z'_{n+1}$
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Assumption G5 (Net Reproductive Rates). Women-marrying-young each rear  $n_1^y$  early-born daughters and  $n_2^y$  late-born daughters, where  $n_1^y \geq n_2^y > 0$ . Women-marrying-old each rear  $n^o$  early-born daughters. These net reproductive rates are fixed and satisfy the restrictions  $n^y \equiv n_1^y + n_2^y \geq n^o$  and  $n^o \geq n_2^y > 0$ .

In summary, Assumption G1 and G2 define the model primitives to be lineages and generation groups. Assumption G3 assigns group-specific marriage parameters – proportions of women marrying young – that vary by lineage but not by *fahan*. Assumption G4 states that participation in marriage is universal and restricts the possible marital relations between generation groups, conditional on the woman's age at marriage. Assumption G5 imposes uniform reproductive rates on women-marrying-young and women-marrying-old and restricts the reproductive capacity of the latter relative to the former. Assumptions G4 and G5 form the core of the maternal reproductive assumption.

#### *Life-cycle flows*

To develop intuition for the population dynamics, we constructed a life-cycle flow diagram that represents the maternal model as a Markov chain with growth. In Figure 1, the Markov states correspond to sizes of the six female generation groups extant at any time: X, X', Y, Y', Z, and Z'. Transitions between states are understood to be reproductive flows with mothers of one lineage rearing daughters of another lineage by virtue of marrying fathers who belong to that lineage. In the flow diagram, the nodes represent the states and the edges represent the state transitions. The arrows are labeled with the conditional rearing rates and the reproductive flows are read from mother's group to daughter's group. For instance, there are four flows into the X state from the Z', X, X', and Y states. That is, daughters of group X are reared by mothers of groups Z', X, X', and Y. This is a direct translation of the maternal equation for group X. The other states are treated similarly.

(Figure 1 here )

#### *The maternal equations*

Assumptions G1-G5 yield the following system of maternal equations:

$$\begin{aligned}
X_{n+1} &= no \cdot (1-p_Z)Z'_{n-1} + no \cdot (1-p_X)X_n + ny1 \cdot p_X X'_n + ny1 \cdot p_Y Y_n \\
X'_{n+1} &= ny2 \cdot p_X X'_n + ny2 \cdot p_Y Y_n \\
Y_{n+1} &= no \cdot (1-p_X)X'_n + no \cdot (1-p_Y)Y_n + ny1 \cdot p_Y Y'_n + ny1 \cdot p_Z Z_n \\
Y'_{n+1} &= ny2 \cdot p_Y Y'_n + ny2 \cdot p_Z Z_n \\
Z_{n+1} &= no \cdot (1-p_Y)Y'_n + no \cdot (1-p_Z)Z_n + ny1 \cdot p_Z Z'_n + ny1 \cdot p_X X_{n+1} \\
Z'_{n+1} &= ny2 \cdot p_Z Z'_n + ny2 \cdot p_X X_{n+1}
\end{aligned}$$

The system is linear, second-order, and homogeneous. Observe that, conditional on birth order, the differences only show up in the proportion that marry young in each generation group ( $p_k$ ). In the next section, we characterize the explicit solution to the maternal system.

To understand how these equations are derived, consider the intergenerational mapping from mother to daughter group given in Table A. The mapping is based on the age-at-marriage rules specific to each lineage (Assumption G4). Specifically, the table identifies the daughter groups that marry men of *fahan*  $n$  and become mothers of daughter groups of *fahan*  $n+1$ . Notice that the daughter groups marrying men of *fahan*  $n$  are spread over *fahans*  $n-1$ ,  $n$ , and  $n+1$ . This spread arises due to the variation within a group in terms of the timing of marriage (young or old) and of child bearing (early- or late-born).

Table A. Mother generation groups identified with daughter generation groups  $N+1$

DAUGHTER GROUPS $N+1$	IDENTIFIED MOTHER GROUPS (DAUGHTER GROUPS MARRYING MEN OF FAHAN $N$ )							
	$Z'_{n-1}$	$X_n$	$X'_n$	$Y_n$	$Y'_n$	$Z_n$	$Z'_n$	$X_{n+1}$
$X_{n+1}$	WMO	WMO	WMY	WMY				
$X'_{n+1}$			WMY	WMY				
$Y_{n+1}$			WMO	WMO	WMY	WMY		
$Y'_{n+1}$					WMY	WMY		
$Z_{n+1}$					WMO	WMO	WMY	WMY
$Z'_{n+1}$							WMY	WMY

WMY – women (mothers) marrying young, WMO – women (mothers) marrying old

Each lineage marries its men once per *fahan*. Men of lineage Y from *fahan*  $n$  sire daughters  $Y_{n+1}$  and  $Y'_{n+1}$ . Consider early-born daughters  $Y_{n+1}$  in the far left column. Reading across the row, we see that four groups of *fahan*  $n$  daughters marry into lineage Y and become mothers bearing children  $Y_{n+1}$ . These mothers comprise  $X'_n$  and  $Y_n$  daughters marrying old, and  $Y'_n$  and  $Z_n$  daughters marrying young. Now consider late-born daughters  $Y'_{n+1}$ . These daughters come from only those groups able to marry young:  $Y'_n$  and  $Z_n$ . Men of lineage Y never marry  $Z'$  or  $X$  daughters because these daughters are born in the same period as when the men are supposed marry, thus they are too young to marry.

Under Assumptions G4 and G5, the size of each daughter group is simply the number of mothers rearing daughters into that group multiplied by the associated net reproductive rate. Then it is straightforward to derive the maternal equations for lineage Y:

$$\begin{aligned} Y_{n+1} &= n_0 \cdot (1-p_X) X'_n + n_0 \cdot (1-p_Y) Y_n + n_{y1} \cdot p_Y Y'_n + n_{y1} \cdot p_Z Z_n \\ Y'_{n+1} &= n_{y2} \cdot p_Y Y'_n + n_{y2} \cdot p_Z Z_n \end{aligned}$$

The maternal equations for lineages X and Z are derived similarly. This establishes the system of maternal equations asserted above.

### 3. The steady state

In the model, mothers beget daughters within and across cohorts at different rates associated with different vital coefficients, which suggests that population growth and the age distribution will change over time. When the reproductive flows are balanced so that all maternal cohorts grow at the same constant rate, we say that the dynamical system has reached a *steady state*.

PROPOSITION. The system of maternal equations has a unique and stable steady state characterized by the largest root of the characteristic equation,  $f(r) = 0$ .

*Proof.* The details are left to the Appendix. Briefly, the proof proceeds as follows. First, we transform the maternal equations into a first-order system  $\mathbf{x}_{n+1} = A\mathbf{x}_n$  where  $\mathbf{x}$  is a vector of state variables, one for each maternal group, and  $A$  is a square transition matrix. With a parameter restriction, the transition matrix  $A$  has special properties that allow us to apply the Perron-Frobenius theorem for nonnegative matrices. We then argue that the system has a unique and stable steady state as a direct implication of the theorem. The reader is referred to Tuljapurkar & Caswell Ch. 2 for a more comprehensive treatment of these and other matrix methods.

Below, we characterize steady state growth and prove the growth propositions in the text, assuming that there exists a unique and stable steady state.

#### *Characterizing the steady state*

In the steady state, all extant groups grow at the same rate. Let  $r^*$  be the gross rate of steady-state growth. If  $r^*$  is known, the steady-state population dynamics are simply:

$$X_{n+1} = r^* X_n \quad Y_{n+1} = r^* Y_n \quad Z_{n+1} = r^* Z_n$$



$$X'_{n+1} = r^* X'_n \quad Y'_{n+1} = r^* Y'_n \quad Z'_{n+1} = r^* Z'_n$$

Substituting into the maternal equations,

$$r^* X_n = no \cdot (1-p_Z)(r^*)^{-1} Z'_n + no \cdot (1-p_X) X_n + ny1 \cdot p_X X'_n + ny1 \cdot p_Y Y_n$$

$$r^* X'_n = ny2 \cdot p_X X'_n + ny2 \cdot p_Y Y_n$$

$$r^* Y_n = no \cdot (1-p_X) X'_n + no \cdot (1-p_Y) Y_n + ny1 \cdot p_Y Y'_n + ny1 \cdot p_Z Z_n$$

$$r^* Y'_n = ny2 \cdot p_Y Y'_n + ny2 \cdot p_Z Z_n$$

$$r^* Z_n = no \cdot (1-p_Y) Y'_n + no \cdot (1-p_Z) Z_n + ny1 \cdot p_Z Z'_n + ny1 \cdot p_X r^* X_n$$

$$r^* Z'_n = ny2 \cdot p_Z Z'_n + ny2 \cdot p_X r^* X_n$$

we obtain a system of six linear homogeneous equations. In matrix form:

$$\mathbf{x}_{n+1} = r^* \mathbf{x}_n = \Lambda(r^*) \cdot \mathbf{x}_n$$

$$[\Lambda(r^*) - r^* \cdot \mathbf{I}] \mathbf{x}_n = 0$$

where:  $\mathbf{x}_n \equiv (X_n, X'_n, Y_n, Y'_n, Z_n, Z'_n)$

and:

$$\Lambda(r^*) \equiv \begin{pmatrix} no(1-p_X) & ny1 \cdot p_X & ny1 \cdot p_Y & & & no(1-p_Z)(r^*)^{-1} \\ & ny2 \cdot p_X & ny2 \cdot p_Y & & & \\ & no(1-p_X) & no(1-p_Y) & ny1 \cdot p_Y & ny1 \cdot p_Z & \\ & & & ny2 \cdot p_Y & ny2 \cdot p_Z & \\ ny1 \cdot p_X r^* & & & no(1-p_Y) & no(1-p_Z) & ny1 \cdot p_Z \\ ny2 \cdot p_X r^* & & & & & ny2 \cdot p_Z \end{pmatrix}$$

and  $\mathbf{I}$  is the identity matrix. Characterizing the steady state is then equivalent to solving an ordinary eigenvalue problem. The solution is obtained by finding the roots of the characteristic polynomial  $f(r) = \det [\Lambda(r) - r \cdot \mathbf{I}]$  taking  $r^*$  to be the largest root.

After simplifying, the characteristic polynomial reduces to:

$$f(r) = (r^2 - b_X r + c_X)(r^2 - b_Y r + c_Y)(r^2 - b_Z r + c_Z) - r^4 (ny1)^3 \cdot p_X p_Y p_Z$$

$$\begin{aligned} \text{where } b_x &= n_o(1-p_x) + n_y2 \cdot p_z & c_x &= n_o \cdot n_y2(p_z - p_x) \\ b_y &= n_o(1-p_y) + n_y2 \cdot p_x & c_y &= n_o \cdot n_y2(p_x - p_y) \\ b_z &= n_o(1-p_z) + n_y2 \cdot p_y & c_z &= n_o \cdot n_y2(p_y - p_z) \end{aligned}$$

Interestingly, there is a correspondence between the three factors that comprise the first term in  $f(r)$  and three lineage “subsystems” constituting a partition of the life-cycle flow diagram. For example, the second term,  $r^2 - b_y r + c_y$ , can be derived as the characteristic polynomial  $f_y(r)$  that solves the maternal equations:

$$\begin{aligned} r^* X'_n &= n_y2 \cdot p_x X'_n + n_y2 \cdot p_y Y_n \\ r^* Y_n &= n_o \cdot (1-p_x) X'_n + n_o \cdot (1-p_y) Y_n \end{aligned}$$

These are the same equations for  $X'_n$  and  $Y_n$  above minus the interaction terms  $v \cdot p_y Y'_n$  and  $v \cdot p_z Z_n$ . In the flow diagram, one can visualize an isolated subsystem comprised of  $X'$  and  $Y$  with no flows coming in or out of the subsystem. Similarly, the other terms of  $f(r)$  can be derived as characteristic polynomials:  $f_x(r) = r^2 - b_x r + c_x$  from the closed maternal system of  $Z'_n$  and  $X_n$ , and  $f_z(r) = r^2 - b_z r + c_z$  from  $Y'_n$  and  $Z_n$ . The characteristic polynomial can thus be written as:

$$f(r) = f_x(r) \cdot f_y(r) \cdot f_z(r) - r^4 (n_y1)^3 \cdot p_x p_y p_z$$

Viewing the characteristic polynomial from the subsystems perspective allows us to intuit the propositions and their implications. This is particularly true of the case of complete *Sepaade* where  $p_x = 0$  thus annihilating the fourth interaction term.

To simplify the analysis and concentrate on the impact of *Sepaade* we assume that the two non-Teeria lineages are symmetric with respect to the proportion of early born women who marry young, and that all three lineages are symmetric with respect to the proportion of late born women who marry young. That is,  $p_y = p_z = p$ , and  $p'_y = p'_z = p'$ . Substituting:

$$f(r) = (r^2 - br + c)^2 (r^2 - b_x r + c_x) - r^4 (n_y1)^3 \cdot p^2 p_x$$

$$\begin{aligned} \text{where: } b &= n_o(1-p) + n_y2 \cdot p' & c &= n_o \cdot n_y2(p' - p) \\ b_x &= n_o(1-p_x) + n_y2 \cdot p' & c_x &= n_o \cdot n_y2(p' - p_x) \end{aligned}$$

Note that  $f(r)$  is of degree six. The largest root  $r^*$  can be computed numerically but we can also write down qualitative conditions for steady state growth in terms of the parameters. These will be inequalities based on the boundary condition  $f(r^*) = f(1) = 0$ .

### *Growth in the steady state*

The growth propositions place restrictions on the vital parameters  $n_0$ ,  $n_{y1}$ ,  $n_{y2}$  – these are interpreted as net reproductive rates from mother to daughter, consistent with our maternal model assumption. Though women that marry young have more children than those that marry old,  $n_{y1} > n_0$ , we assume that women that marry young bear no more children in their middle age (third period of life) than do women who marry old,  $n_{y2} \leq n_0$ . This assumption is consistent the evidence that women-marrying-old try to have as many children as possible, whereas women-marrying-young are likely to have already of borne at least one son and may not be interested in more children in her middle age. (Recall sons look after moms.)

ASSUMPTION.  $n_{y2} \leq n_0$ , and  $n_{y2} \cdot p' \leq 1$

The assumption allows us to prove a useful lemma, which establishes the necessary and sufficient condition for growth.

LEMMA.  $f(1) (<, =, >) 0$  iff  $r^* (>, =, <) 1$ .

*Proof.* See the Appendix.

The lemma, in turn, yields the main growth proposition directly.

PROPOSITION. A necessary and sufficient condition for steady state growth  $r^* \geq (\leq) 1$  is given by:

$$(n_{y1})^3 p^2 p_x \geq (\leq) [(1-n_0)(1-n_{y2} \cdot p') + (1-n_{y2})n_0 \cdot p]^2 \cdot [(1-n_0)(1-n_{y2} \cdot p') + (1-n_{y2})n_0 \cdot p_x]$$

*Proof:* Rewriting the characteristic polynomial, we have:

$$\begin{aligned} f(r) &= (r^2 - br + c)^2 (r^2 - b_x r + c_x) - r^4 (n_{y1})^3 \cdot p^2 p_x \\ &= [(r - n_0)(r - n_{y2} \cdot p') + (r - n_{y2})n_0 \cdot p]^2 \cdot [(r - n_0)(r - n_{y2} \cdot p') + (r - n_{y2})n_0 \cdot p_x] - r^4 (n_{y1})^3 \cdot p^2 p_x \end{aligned}$$

Then:

$$f(1) = [(1 - n_0)(1 - n_{y2} \cdot p') + (1 - n_{y2})n_0 \cdot p]^2 \cdot [(1 - n_0)(1 - n_{y2} \cdot p') + (1 - n_{y2})n_0 \cdot p_x] - (n_{y1})^3 \cdot p^2 p_x$$

By the Lemma,  $f(1) (<, =, >) 0$  iff  $r^* (>, =, <) 1$  which yields the desired condition and proves the Proposition.

We can now apply the proposition to study some special parametric cases:

1. Full symmetry:  $p_X = p = p'$

$$r^* \geq (\leq) 1 \Leftrightarrow (ny_1 + ny_2)p + no(1-p) \geq (\leq) 1$$

2. Partial symmetry:  $p_X = p \neq p'$

$$r^* \geq (\leq) 1 \Leftrightarrow (ny_1 + ny_2)p + no(1-p) + (1-no)ny_2(p'-p) \geq (\leq) 1$$

3. Complete *Sepaade*:  $p_X = 0$

$$r^* \geq (\leq) 1 \Leftrightarrow [(1-no)(1-ny_2 \cdot p') + (1-ny_2)no \cdot p]^2 (1-no)(1-ny_2 \cdot p') \leq (\geq) 0$$

4. Incomplete *Sepaade*:  $p_X > 0$

$$r^* \geq (\leq) 1 \Leftrightarrow [(1-no)(1-ny_2 \cdot p') + (1-ny_2)no \cdot p]^2 [(1-no)(1-ny_2 \cdot p') + (1-ny_2)no \cdot p_x] \leq (\geq) (ny_1)^3 p^2 p_x$$

The growth rate  $r^*$  describes the growth rate of the total population in the steady state. All lineages will  $r^*$  in the steady state when there are active flows connecting all groups (see the flow diagram). This condition is always satisfied except for the case of Complete *Sepaade*.

The case of Complete *Sepaade* is conceptually distinct because it shuts off key flows that may result in lineages growing at separate rates and possibly dying out. This possibility can be seen directly from the flow diagram. Setting  $p_X = 0$  shuts off all flows from lineage X into lineage Z. In particular, there become no external flows into lineage Z'. The best lineage Z' can do is sustain itself in the special case of  $ny_2 \cdot p_Z = 1$  and  $p_Z = 1$ . Otherwise, it slowly dies out. If it dies out then there are no flows into the subsystem formed by Z and Y'. Recall that the growth rate of this subsystem can be described by  $f_Z(r) = r^2 - br + c$ . But there are a large range of parameter values for which this population declines and dies out. Then there are no flows into the subsystem formed by X' and Y. But the growth rate of his subsystem is also given by  $f_Y(r) = r^2 - br + c$ , so that if the prior system died out so eventually will this one. We now have all the groups dying out except X. Lineage X sustains itself if and only if  $no \geq 1$ .

The case of Complete *Sepaade* not only produces potential differences in the growth rates of lineages but also more specific results.

PROPOSITION. With Complete *Sepaade*, we have the following steady state results.

- (i) The total population and the *Teeria* lineage X grow at rate  $r^* = no$ .
- (ii) If  $ny_2 < no$ , the *Teeria* population completely dominates the non-*Teeria* population.
- (iii) If  $no < 1$  all the lineages populations die out. The *Teeria* population survives if  $no \geq 1$  and the non-*Teeria* lineages die out when  $ny_2$  is sufficiently small.

*Proof:* We have  $p_X = 0$  and  $p_X' = p'$  which implies that the characteristic polynomial (\*) reduces to

$$f(r) = [(r - no)(r - ny_2 \cdot p') + (r - ny_2)no \cdot p]^2 \cdot [(r - no)(r - ny_2 \cdot p')]$$

$$= [f_N(r)]^2 [f_X(r)]; \quad f_N(r) = f_Z(r) = f_Y(r)$$

Clearly, the roots of  $f_N(r)$  and  $f_X(r)$  include  $no$  and  $ny_2 \cdot p'$ ;  $no$  is the largest of these two roots since  $ny_2 \cdot p' \leq ny_2 \leq no$  by the Assumption. Solving  $f_N(r) = 0$  yields the other two roots, each with multiplicity two. We are interested in  $r^*$ , the largest root  $r^* = \max(no, r)$ . But  $f_N(no) = no(no - ny_2)p \geq 0$  which means that  $r \leq no$  since  $f_N(r)$  is strictly increasing near its largest root. Thus,  $r^* = no$ .

We associate the roots of  $f(r)$  with the growth rates of each lineage: the roots of  $f_X(r)$  correspond to the *Teeria* lineage while the roots of  $f_N(r)$  correspond to the non-*Teeria* lineages. With  $r^* = no$ ,  $f_X(no) = 0$  and the *Teeria* growth rate is  $no$ . Since  $f_N(no) = no(no - ny_2)p \geq 0$ , the non-*Teeria* grow at a slower rate when  $ny_2 < no$  unless  $p = 0$ .

A necessary and sufficient condition for the non-*Teeria* lineages to die out is:  $f_N(1) = (1 - no)(1 - ny_2 \cdot p') + (1 - ny_2)no \cdot p > 0$ . This condition holds if  $no < 1$ . The condition also holds with  $no \geq 1$  when  $ny_2 < 1$  is sufficiently small and  $p > 0$ . This completes the proof.

The above propositions only describe growth rates in the steady state. When the growth rates of the lineages are different, then growth rates capture which lineages come to completely dominate the population. However, even when lineage growth rates are the same, there can be dramatic differences in the lineage population levels. This is true of both incomplete and complete *Sepaade*. Consider Complete *Sepaade*. There is one special case in which all lineages grow at the same rate. This is when  $ny_2 = no$ . However, whenever  $ny_1 > 0$  the level of *Sepaade* is higher and often by many magnitudes (see example...)

Another way the steady state results are not indicative of dynamics is highlighted by the transition dynamics. Consider Complete *Sepaade*. We know that in the steady state  $r^* = n_0$ . Thus, if  $n_0 < 1$ , all lineages will eventually die out. However, this might take a long time and there might be dramatic growth before this happens. When  $n_y = n_{y1} + n_{y2}$  is large this is exactly what happens (see example ?). In the example, the rate of convergence is particularly slow because complete *Sepaade* has birthing taking place every two periods.

#### 4. Perturbation and simulation analysis (incomplete)

Perturbation analysis allows us to measure the contribution of each vital coefficient to population growth. Growth elasticities with respect to the vital coefficients are calculated and compared to simulation results.

We conjecture the following comparative dynamic that across steady states:  $dr^*/dp_x > 0$ ,  $d(X_n/Y_n)/dp_x > 0$  and  $d(X_n/Z_n)/dp_x > 0$ . The first conjecture is that the population growth rate is unambiguously increasing as the proportion of Terria women-marrying-young increases. The second and third conjectures describe the ratio of the population of lineage X to lineages Y and Z respectively. Our simulation results indicate that lineage X grows proportionately larger when there are more women-marrying-young in that lineage.

Numerical examples

(Ex.1)  $n_{y1} = 2, n_{y2} = 0, n_0 = 2$  Analysis of growth level here.

(Ex. 2)  $n_{y1} = 2, n_{y2} = 1, n_0 = 1$

(Ex. 3)  $n_{y1} = 1.75, n_{y2} = 1, n_0 = 1.5$

(Ex. 4)  $n_{y1} = 1.75, n_{y2} = 1.13, n_0 = 1.76$

In each case, compare  $p' < 1$  versus  $p' = 1$ .]

#### 5. Conclusion

The paper examines a particular age-group society, the Rendille tribe of Northern Kenya, and develops and solves a “lineage” matrix population model representing this society. The Rendille are a particularly interesting case study because their lineage system is integrated with their age-set and generation group organization. Age-sets of similarly aged males are organized into age-set lines along three lines of descent (which we denote X, Y, and Z). The lineage system relates fathers and their children according to genealogical generations. A rotation through the three age-set lines distinguishes the generation group of fathers from the next generation group of their children. The matrix model maps from one genealogical generation to the next to the next and reveals the genealogical dynamics inherent in the Rendille social organization.

We are able to analytically solve the model and prove the existence of a unique globally stable dynamic path that converges to a (periodic) steady-state growth path. The steady state growth path is characterized with necessary and sufficient conditions for growth of the age-set lines. The rules governing marriage as they relate to lineage considerations substantially reduce the size and the growth rate of the population; they also induce periodicity in the demographics, and dramatically favour one of the age-set lines. Specifically, the institution of Sepaade lead to the Teeria (age-set line X) dominating. In the extreme case where Sepaade held back all early-born daughters from marrying young, the other age-set lines quickly disappear leaving only the Teeria line with negative population growth.

More generally, the analysis suggests that matrix population modeling is a powerful tool for analyzing the social dynamics of age-group societies. As these societies incorporate similarly aged individuals into age-groups that transit the lifecycle together, they display more homogeneity than other societies. In our analysis of the Rendille heterogeneity was also limited by clear and simple rules on marriage and lineage. Other societies with straightforward marriage rules should also be amenable to relatively simple matrix population modeling.

We hope our analysis is also of interest to theoretical population science because of the novel way in which we apply the classical Perron-Frobenius methods (e.g. Tuljapurkar & Caswell 1997). In biology, for instance, structured-population models typically introduce population dynamics along a single dimension, usually age or size; similarly, mathematical models have been used in cultural anthropology to study the dynamics of kinship relations or age-group rules but few models can tractably accommodate both kinds of dynamics simultaneously. In contrast, our model tracks reproductive transitions across lineage groups (inter-genealogical transitions) as well as across age cohorts (inter-generational transitions). The work here advances the goal of integrating the systems of socioeconomic, demographic and lineage organization within a coherent dynamic model.

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Table 1:  
Historical Timeline (incomplete)

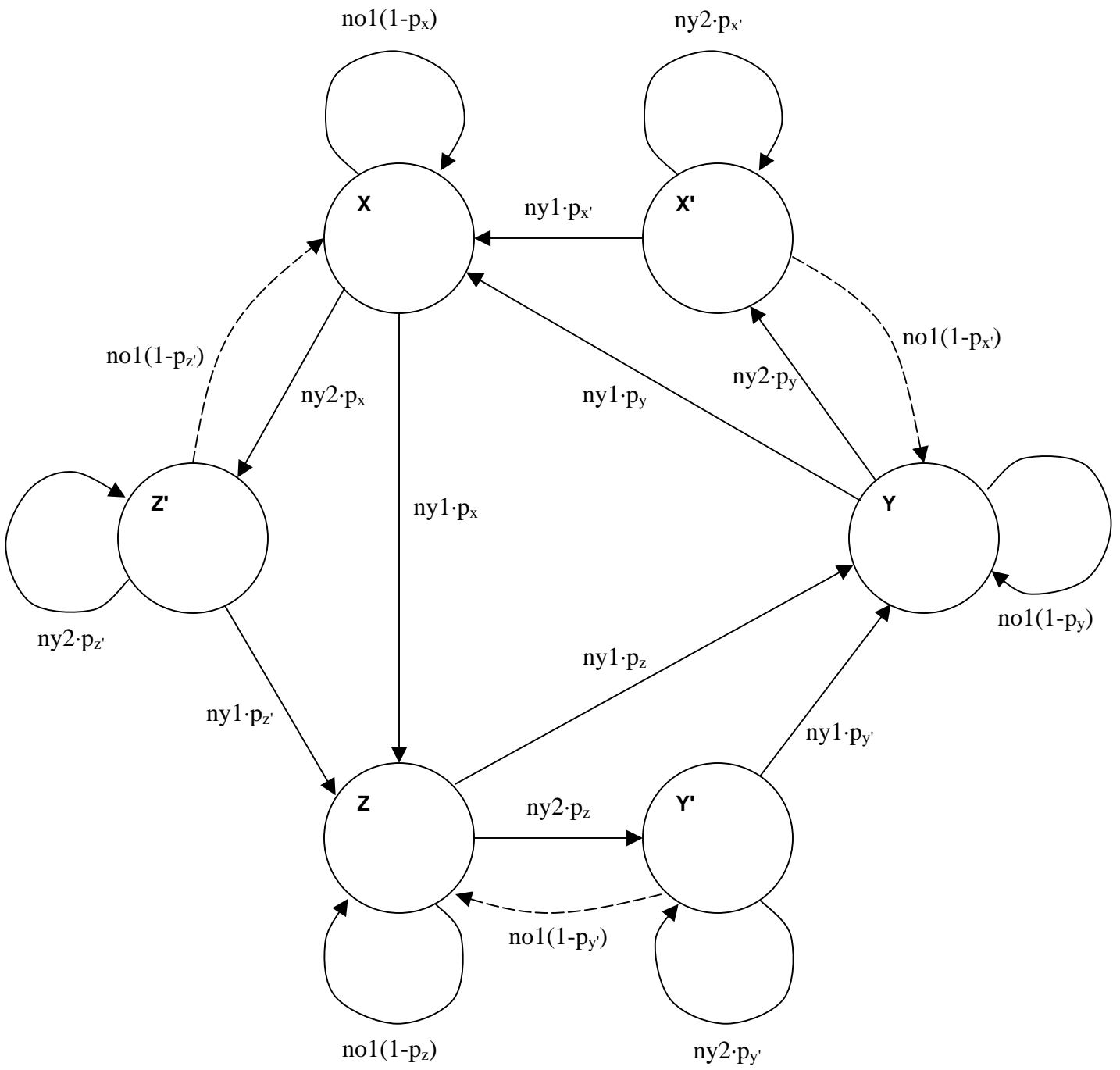
Fahan (n)	Line	Age-set (t)	Name	Circumcision Year	Marriage Year
0	X	0			
0	Y	1		1769	1780
0	Z	2		1783	1794
1	X	3		1797	1808
1	Y	4		1811	1822
1	Z	5	Irbaandf	1825	1836
2	X	6	Ilkibugu	1839	1851
2	Y	7	Libaale	1853	1864
2	Z	8	D'bgudo	1867a	1878a
3	X	9	Dismaala	1881a	1892a
3	Y	10	Irbaangudo	1895a	1908*
3	Z	11	D'fgudo	1909-10*	1920
4	X	12	Irbaalis	1923	1934
4	Y	13	Libaale	1937	1948*
4	Z	14	Irband'if	1951	1962
5	X	15	D'fgudo	1965	1976
5	Y	16	Irbaangudo	1979	1990
5	Z	17		1993	2004
6	X	18		2007	2018
6	Y	19		0	
6	Z	20		0	

Each *fahan* opens with the circumcision of line X (*Teeria*) men and close with the marriage of line Z men 39 years later. The start of *fahan* n corresponds to the initiation of line X men of set-set  $t=3n$ .

*Sepaade* begins in  $t=5$  and end in  $t=17$ . There are 11 intervening periods.

Sources: Roth 1991, 2004, ?

**Figure 1: Life-Cycle Flow Diagram**



## APPENDIX

### A1. The steady state: existence, uniqueness, stability

**PROPOSITION.** The system of maternal equations has a unique and stable steady state characterized by the largest root of the characteristic equation,  $f(r) = 0$ .

*Proof.* As remarked in the text, the proof proceeds in three steps: a transformation of the maternal equations into a first-order system, a characterization of the associated transition matrix, and a direct application of the Perron-Frobenius theorem.

a. *The first-order transformation.* Recall that the maternal equations are given by:

$$\begin{aligned} X_{n+1} &= no(1-p_Z)Z'_{n-1} + no(1-p_X)X_n + ny1 \cdot p_X X'_n + ny1 \cdot p_Y Y_n \\ X'_{n+1} &= ny2 \cdot p_X X'_n + ny2 \cdot p_Y Y_n \\ Y_{n+1} &= no(1-p_X)X'_n + no(1-p_Y)Y_n + ny1 \cdot p_Y Y'_n + ny1 \cdot p_Z Z_n \\ Y'_{n+1} &= ny2 \cdot p_Y Y'_n + ny2 \cdot p_Z Z_n \\ Z_{n+1} &= no(1-p_Y)Y'_n + no(1-p_Z)Z_n + ny1 \cdot p_Z Z'_n + ny1 \cdot p_X X_{n+1} \\ Z'_{n+1} &= ny2 \cdot p_Z Z'_n + ny2 \cdot p_X X_{n+1} \end{aligned}$$

Substituting  $Z'_{n-1} = (ny2 \cdot p_Z)^{-1} Z'_n - (p_X/p_Z)X_n$  in the first equation and expanding  $X_{n+1}$  in the fifth and sixth equations, we obtain:

$$\begin{aligned} X_{n+1} &= [no(p_Z - p_X)/p_Z]X_n + ny1 \cdot p_X X'_n + ny1 \cdot p_Y Y_n + [(no/ny2) \cdot (1-p_Z)/p_Z]Z'_n \\ X'_{n+1} &= ny2 \cdot p_X X'_n + ny2 \cdot p_Y Y_n \\ Y_{n+1} &= no(1-p_X)X'_n + no(1-p_Y)Y_n + ny1 \cdot p_Y Y'_n + ny1 \cdot p_Z Z_n \\ Y'_{n+1} &= ny2 \cdot p_Y Y'_n + ny2 \cdot p_Z Z_n \\ Z_{n+1} &= [ny1 \cdot no(p_Z - p_X)(p_X/p_Z)]X_n + (ny1)^2 \cdot p_X p_X X'_n + (ny1)^2 \cdot p_X p_Y Y_n + no(1-p_Y)Y'_n + no(1-p_Z)Z_n \\ &\quad + [ny1 \cdot p_Z + (ny1 \cdot no/ny2) \cdot (1-p_Z)(p_X/p_Z)]Z'_n \\ Z'_{n+1} &= [ny2 \cdot no(p_Z - p_X)(p_X/p_Z)]X_n + ny2 \cdot ny1 \cdot p_X p_X X'_n + ny2 \cdot ny1 \cdot p_X p_Y Y_n \\ &\quad + [ny2 \cdot p_Z + no(1-p_Z)(p_X/p_Z)]Z'_n \end{aligned}$$

This yields the first-order linear system  $\mathbf{x}_{n+1} = \mathbf{A}\mathbf{x}_n$  where  $\mathbf{x} \equiv (X, X', Y, Y', Z, Z')$  and:

$$\mathbf{A} \equiv \begin{pmatrix} no(p_Z - p_X)/p_Z & ny1 \cdot p_X & ny1 \cdot p_Y & & & (no/ny2)(1-p_Z)/p_Z \\ & ny2 \cdot p_X & ny2 \cdot p_Y & & & \\ & no(1-p_X) & no(1-p_Y) & ny1 \cdot p_Y & ny1 \cdot p_Z & \\ & & & ny2 \cdot p_Y & ny2 \cdot p_Z & \\ ny1 \cdot no(p_Z - p_X)(p_X/p_Z) & (ny1)^2 \cdot p_X p_X & (ny1)^2 \cdot p_X p_Y & no(1-p_Y) & no \cdot (1-p_Z) & ny1 \cdot p_Z + (ny1 \cdot no/ny2)(1-p_Z)(p_X/p_Z) \\ ny2 \cdot no(p_Z - p_X)(p_X/p_Z) & ny2 \cdot ny1 \cdot p_X p_X & ny2 \cdot ny1 \cdot p_X p_Y & & & ny2 \cdot p_Z + no(1-p_Z)(p_X/p_Z) \end{pmatrix}$$

b. *Characterization of A.* To proceed, we impose the following regularity conditions:

**ASSUMPTION.**  $0 < p_X \leq p \leq p_X' = p' \leq 1$

[ **ASSUMPTION.** (weaker)  $p_j \geq p_k$  for  $j = Z, X, Y$  and  $k = X, Y, Z$ . The proportion of late-born women marrying young from one lineage is no smaller than that of early-born women from the subsequent lineage. ]

Notice that the Assumption restricts the parameter space to the case of Incomplete Sepaade ( $p_x > 0$ ). Complete Sepaade ( $p_x = 0$ ) is a singular case that is dealt with separately; see the main text for further discussion. However, we have found in simulations that Complete Sepaade does constitute a limit point of the Incomplete Sepaade case as  $p \rightarrow 0$ . [Expand on this in the text?]

The crux of the proof is the following result:

THEOREM (PERRON-FROBENIUS). Let  $\mathbf{A}$  be an irreducible, aperiodic, nonnegative square matrix. Then there exists an eigenvalue of  $\mathbf{A}$ ,  $r^*$ , satisfying the following:

- i)  $r^*$  is real and positive,
- ii)  $r^* > |r_i|$  for all other eigenvalues  $r_i$ ,
- iii) the left and right eigenvectors  $\mathbf{u}$  and  $\mathbf{v}$  associated with  $r$  are uniquely positive up to scaling,
- iv)  $r^*$  is a simple root of the characteristic equation of  $\mathbf{A}$ .

(Seneta 1973)

DEFINITION. Let  $\mathbf{T}$  be a square matrix and let  $t_{ij}^{(n)}$  denote the entry in the  $i$ th row and  $j$ th column of  $\mathbf{T}^n$  where  $n$  is a positive integer.

- i.  $\mathbf{T}$  is *nonnegative* when  $t_{ij}^{(1)} \geq 0$  for all  $(i,j)$ .
- ii.  $\mathbf{T}$  is *irreducible* when for each  $(i,j)$  there exists  $b$  such that  $t_{ij}^{(b)} > 0$ .
- iii.  $\mathbf{T}$  is *aperiodic* when the greatest common divisor of those  $b$  for which  $t_{ii}^{(b)} > 0$  is 1 for all  $i$ .

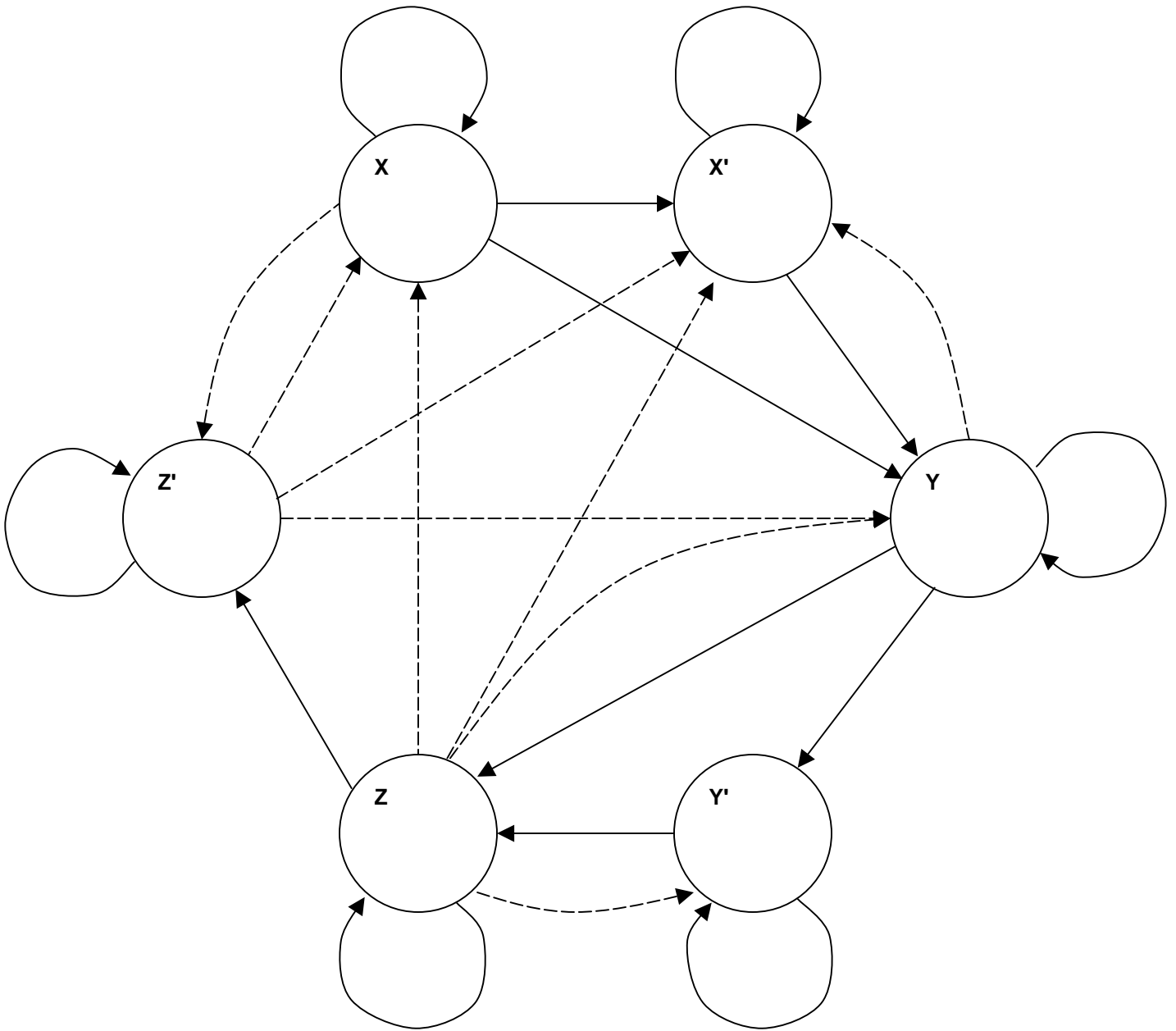
To apply the theorem, we need only verify that the transition matrix  $\mathbf{A}$  from the first-order transformation is nonnegative, irreducible, and aperiodic.

*Nonnegativity*. By the Assumption, it is immediate that all of the entries of  $\mathbf{A}$  are non-negative.

*Irreducibility and aperiodicity*. Consider the *incidence digraph* of  $\mathbf{A}$  illustrated in Figure 3. The vertices and arcs correspond to maternal groups and flows, respectively. Accordingly,  $a_{ij} > 0$  iff there is an arc from vertex  $i$  to vertex  $j$  and  $a_{ij}^{(n)} > 0$  iff there exists a path from vertex  $i$  to vertex  $j$  of length  $n$ . It turns out that  $\mathbf{A}$  is irreducible iff the incidence digraph of  $\mathbf{A}$  is strongly connected (Minc 1988); that is, a path exists between any two vertices in the graph. To verify that  $\mathbf{A}$  is strongly connected under the Assumption is straightforward. [Footnote: With  $p_x = 0$ , the proof fails because the incidence digraph of  $\mathbf{A}$  is no longer strongly connected.] Moreover, the presence of loops (1-cycles) in the graph immediately implies that  $\mathbf{A}$  is aperiodic.

Thus we have shown that  $\mathbf{A}$  satisfies the conditions of the Theorem.

Figure 3: Incidence digraph of the transition matrix A



b. *Identification of the steady state.* The Perron-Frobenius theorem says that  $\mathbf{A}$  has a single dominant eigenvalue  $r^* > 0$  with positive left and right eigenvectors  $\mathbf{u}$  and  $\mathbf{v}$ . We know that  $r^*$ ,  $\mathbf{u}$ , and  $\mathbf{v}$  are jointly determined by  $\mathbf{A}$  and its characteristic equation,  $f(r) = 0$ . When  $\mathbf{u}$  and  $\mathbf{v}$  are normalized so that  $\mathbf{u}^T \mathbf{v} = 1$ , the singular value decomposition (SVD) of  $\mathbf{A}$  yields:

$$\mathbf{A}^n = (r^*)^n \cdot \mathbf{v} \mathbf{u}^T + O(n^{m-1} |r_2|^n)$$

where  $r_2$  is the second-largest eigenvalue of  $\mathbf{A}$  and  $m$  is the multiplicity of  $r_2$ . [Footnote: the term  $O(n^{m-1} |r_2|^n)$  is bounded in the sense that there exist real numbers  $C, D$  such that  $C \cdot n^{m-1} |r_2|^n \leq O(n^{m-1} |r_2|^n) \leq D \cdot n^{m-1} |r_2|^n$  for all  $n$ .]

Since the theorem guarantees that  $r^* > |r_2|$ , it follows that  $(r^*)^n \gg |r_2|^n$  for large  $n$ : as  $n$  increases, the second matrix term in the SVD expression becomes increasingly dominated by the first term so that  $\mathbf{A}^n \rightarrow (r^*)^n \cdot \mathbf{v} \mathbf{u}^T$ . We then have  $\mathbf{x}_n = \mathbf{A} \mathbf{x}_{n-1} = \dots = \mathbf{A}^n \mathbf{x}_0 \rightarrow (r^*)^n \cdot (\mathbf{v} \mathbf{u}^T \mathbf{x}_0)$  or  $\mathbf{x}_{n+1} \rightarrow (r^*) \cdot \mathbf{x}_n$ . Regardless of the initial population  $\mathbf{x}_0$ , the system always converges to a state wherein all maternal groups grow at a constant rate  $r^*$ : it is in this sense that the steady state is globally stable. Furthermore, since  $\mathbf{u}$  and  $\mathbf{v}$  are uniquely positive among normalized eigenvectors, the steady-state group distribution is unique given  $\mathbf{x}_0$ . We conclude that  $(r^*, \mathbf{u}, \mathbf{v}, \mathbf{x}_0)$  completely identifies the steady state.

## A2. Proof of the Lemma

LEMMA.  $f(1) (<, =, >) 0$  iff  $r^* (>, =, <) 1$ .

*Proof:* Our task is to show that  $f(r) (<, =, >) f(r^*) = 0$  when  $r (<, =, >) r^*$  for all values of  $r$  under consideration. First, rewrite the characteristic polynomial as:

$$\begin{aligned} f(r) &= (r^2 - br + c)^2 (r^2 - b_X r + c_X) - r^4 (ny1)^3 \cdot p^2 p_X \\ &= [(r - k_1^N)(r - k_2^N)]^2 \cdot [(r - k_1^X)(r - k_2^X)] - r^4 (ny1)^3 \cdot p^2 p_X \\ &= [f_N(r)]^2 \cdot [f_X(r)] - r^4 (ny1)^3 \cdot p^2 p_X \end{aligned}$$

where the  $k_i^X$ 's and  $k_i^N$ 's are the roots of  $f_X(r)$  and  $f_Y(r) = f_Z(r)$ , resp.; assume  $k_1^j \leq k_2^j$  without loss of generality. Then:

$$\begin{aligned} k_1^j + k_2^j &= b_j = no(1-p_j) + ny2 \cdot p' \\ k_1^j \cdot k_2^j &= c_j = no \cdot ny2(p'-p_j) \end{aligned}$$

$$\rightarrow k_1^j = (b_j - d_j)/2, \quad k_2^j = (b_j + d_j)/2$$

where  $d_j = (b_j^2 - 4c_j)^{1/2}$ . All of the  $k_i^j$ 's are real since:

$$\begin{aligned} b_j^2 - 4c_j &= [no(1-p_j) + ny2 \cdot p']^2 - 4no \cdot ny2(p'-p_j) \\ &= no^2(1-p_j)^2 + 2no(1-p)ny2 \cdot p' + (ny2 \cdot p')^2 - 4no \cdot ny2(p'-p_j) \\ &\geq no^2(1-p_j)^2 + 2no(1-p_j)ny2 \cdot p' + (ny2 \cdot p')^2 - 4no \cdot ny2(1-p_j)p' \\ &\geq [no(1-p_j) - ny2 \cdot p']^2 \\ &\geq 0 \end{aligned}$$

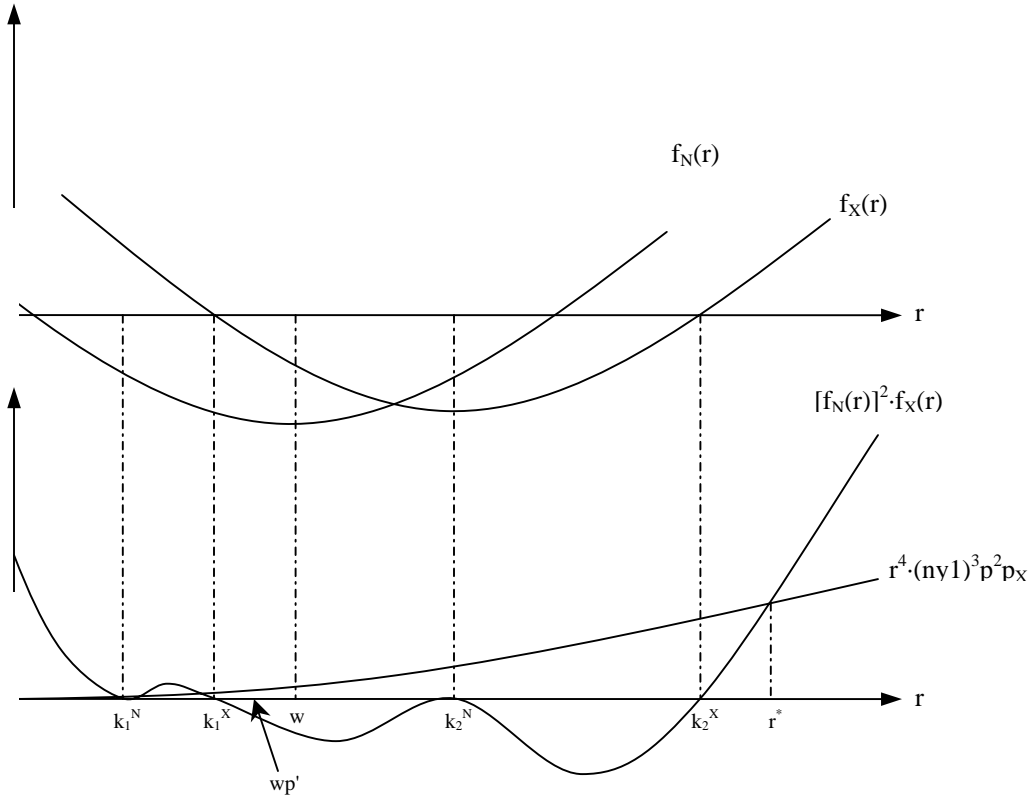
Moreover, the  $k_i^j$ 's must be non-negative since  $b_j \geq 0$  and  $c_j \geq 0$  under the assumption  $p' \geq p_j$ . Now consider the following factorization:

$$f_j(r) = (r - no)(r - ny2 \cdot p') + (r - ny2)no \cdot p_j$$

Note that  $f_N(r) (<, =, >) f_X(r)$  when  $r (<, =, >) ny2$ , given  $p_X \leq p$ . By assumption,  $0 \leq ny2 \cdot p' \leq ny2 \leq no$  and  $p_j \leq p'$  which implies that  $f_j(0) \geq 0$ ,  $f_j(ny2 \cdot p') \leq 0$ ,  $f_j(ny2) \leq 0$ , and  $f_j(no) \geq 0$ . Also,  $f_X(r) (\leq, \geq) 0$

implies  $[f_N(r)]^2 \cdot [f_X(r)] (\leq, \geq) 0$ . Since  $f(r)$  is continuous, we can apply the intermediate value theorem repeatedly to obtain  $0 \leq k_1^N \leq k_1^X \leq ny_2 \cdot p'$  and  $ny_2 \leq k_2^N \leq k_2^X \leq no$ .

Figure 2: Illustration of the Lemma proof



To locate the roots of  $f(r)$  proper, note that  $[f_N(r)]^2 \cdot [f_X(r)] (<, =, >) r^4 (ny_1)^3 \cdot p^2 p_X$  whenever  $f(r) (<, =, >) 0$  by definition and  $[f_N(r)]^2 \cdot [f_X(r)] \leq 0 \leq r^4 (ny_1)^3 \cdot p^2 p_X$  for  $ny_2 \cdot p' \leq r \leq k_2^X$ . The coefficient of the  $r^6$  term in the expansion of  $f(r)$  is positive so  $f(r)$  is strictly increasing near its largest root  $r^*$ ; clearly  $r^* \geq k_2^X$ . It follows that  $f(r) \leq 0$  for  $ny_2 \cdot p' \leq r \leq r^*$  and  $f(r) > 0$  for  $r > r^*$ . Since  $1 \geq ny_2 \cdot p'$  by assumption, we have  $f(1) (<, =, >) 0$  iff  $r^* (>, =, <) 1$ . This completes the proof of the Lemma.

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