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14 Differential Reproduction with Two Sexes

In Chapter 3, we considered a “one-sex” model of intergenerational social mobility with differential reproduction. For simplicity, that model maintained the fiction that each child has only one parent. Of course, in reality, each child has two parents. In the present chapter, we thus develop and analyze a “two-sex” version of the model. While the linearity of the one-sex model guarantees that the population will reach a unique limiting distribution, the non-linearity of the two-sex version creates the potential for more complicated dynamics. In particular, we will see the possibility of multiple equilibria and catastrophes.

14.1 The two-sex model

Conceptually, the one-sex model assumed a two-step process within each generation. First, parents have children according to the reproduction matrix R . Second, each child’s type is selected according to the intergenerational transition matrix P . Once these two steps are completed, the children in the current generation become the parents in the next generation. We thus obtain the equation

$$\mathbf{x}_{t+1} = \mathbf{x}_t R P$$

where \mathbf{x}_t is the frequency distribution for generation t . Letting n denote the number of types of individuals,¹ note that the frequency distribution vector \mathbf{x}_t is $1 \times n$, the reproduction matrix R is $n \times n$, and the transition matrix P is $n \times n$.

Moving to a two-sex version of the model, we now assume a three-step process within each generation. First, individuals form couples in the manner described by a “matching” matrix N_t . (For simplicity, we will assume that all individuals are matched into couples. The rationale for the time subscript on N_t will be addressed in the next section.) Adopting the female perspective, each element $N_t(i, k)$ of this matrix may be interpreted as the probability that a girl of type i forms a couple of type k in generation t . Because each girl or boy can possess any of the n types, there are n^2 types of couples. Consequently, the matching matrix N_t is $n \times n^2$. Letting the vector \mathbf{x}_t (which remains $1 \times n$) denote the frequency distribution of *girls* in generation t , the vector $\mathbf{x}_t N_t$ (which is $1 \times n^2$) gives the frequency distribution of *couples* in generation t .

The final two steps remain reproduction and intergenerational transition. However, each diagonal element $r(k)$ of the reproduction matrix now indicates the average

¹Chapter 3 included examples in which the “types” were based on income or occupation or IQ score. Other applications might include education or religion.

number of girls for each type- k couple.² Thus, the R matrix is $n^2 \times n^2$. Relatedly, because each element $P(k, i)$ of the intergenerational transition matrix now indicates the probability that a child born to type- k parents will acquire type i , the P matrix is $n^2 \times n$. Once these three steps are completed, the children born at the end of generation t become the population at the beginning of generation $t + 1$. We thus obtain the equation

$$\mathbf{x}_{t+1} = \mathbf{x}_t N_t R P$$

where the frequency distribution vector \mathbf{x}_t is $1 \times n$, the matching matrix N_t is $n \times n^2$, the reproduction matrix R is $n^2 \times n^2$, and the transition matrix P is $n^2 \times n$.³

14.2 The matching matrix

Following our treatment of the one-sex model in Chapter 3, we may assume that reproduction rates (the elements of the R matrix) and intergenerational transition probabilities (the elements of the P matrix) are fixed parameters that do not vary over time. In contrast, the matching probabilities (elements of the N_t matrix) will generally depend on the current state of the process (the vector \mathbf{x}_t). This is why we have placed the time subscript on the N_t matrix.

To elaborate, suppose there are $n = 2$ type of individuals. We can then list the $n^2 = 4$ types of couples as

$$11, 12, 21, 22$$

where ij indicates a couple composed of a type- i girl and a type- j boy. Note that a type-1 girl cannot form a couple of type 21 or 22, which would require a type-2 girl. Similarly, a type-2 girl cannot form a couple of type 11 or 12, which would require a type-1 girl. Further, because all girls are matched, all type-1 girls must form a couple of either type 11 or 12. Similarly, all type-2 girls must form a couple of either type 21 or 22. Given these considerations, we might attempt to specify the matching matrix as

$$N = \begin{bmatrix} a & 1-a & 0 & 0 \\ 0 & 0 & b & 1-b \end{bmatrix}$$

²We assume that couples have, on average, equal numbers of boys and girls. Thus, $r(k)$ can also be interpreted as one-half the average number of children for each type- k couple.

³The present chapter draws on Preston & Campbell (1993), who specify the two-sex model in a slightly different way. Maintaining our present assumption on time-indexing (so that matching is the first step in each generation), their specification becomes

$$\mathbf{m}_{t+1} = \mathbf{m}_t R P N_{t+1} \times (1/2)$$

where \mathbf{m}_t denotes the $(1 \times n^2)$ frequency distribution of couples in generation t . In the Preston & Campbell formulation, each diagonal element $r(k)$ of the reproduction matrix indicates the average number of children (not girls) per couple, necessitating the final multiplication by $(1/2)$. To further reconcile the two specifications, note that $\mathbf{x}_{t+1} = \mathbf{m}_t R P$ and that $\mathbf{m}_t = \mathbf{x}_t N_t$. While both specifications produce the same results, ours is more convenient because we need to keep track of only n types of individuals (rather than n^2 types of couples).

where a and b are fixed parameters that do not vary over time.

However, this formulation of the matching matrix ignores an important “accounting constraint” which links the parameters a and b to the current state of the process. In words, this constraint is

$$\begin{aligned} & \text{number of type-11 couples} + \text{number of type-21 couples} \\ & = \text{number of type-1 boys} \end{aligned}$$

which can be expanded as

$$\begin{aligned} & (\text{number of type-1 girls})(\text{probability that a type-1 girl forms a type-11 couple}) \\ & + (\text{number of type-2 girls})(\text{probability that a type-2 girl forms a type-21 couple}) \\ & = \text{number of type-1 boys}. \end{aligned}$$

Because we assume that couples have (on average) equal number of girls and boys, and that intergenerational transition probabilities do not vary by the child’s gender, the number of type-1 boys is equal to the number of type-1 girls. The accounting constraint can thus be written formally as

$$h_t a + (1 - h_t) b = h_t$$

where

$$h_t = \frac{\mathbf{x}_t(1)}{\mathbf{x}_t(1) + \mathbf{x}_t(2)}$$

denotes the proportion of type-1 (or “high” type) individuals in generation t . Rearranging the accounting constraint, we obtain

$$b = (1 - a) \frac{h_t}{1 - h_t}.$$

Thus, if we assume that a does not vary over time, then b is determined by a and h_t . Intuitively, if we first assign boys to the type-1 girls using the matching probability a , then the number of boys of each type that are “left over” for the type-2 girls will determine the matching probability b .⁴ Of course, we could alternatively write the accounting constraint as

$$a = 1 - b \left(\frac{1 - h_t}{h_t} \right)$$

and assume that b is fixed over time while a depends on b and h_t . But the crucial point is that a or b (or both) generally depend on the current state of the process.

⁴To illustrate, suppose $a = 1/2$ and $\mathbf{x}_t = [20 \ 80]$ so that $h_t = 1/5$. After we assign 10 type-1 boys and 10 type-2 boys to the 20 type-1 girls, there are 10 type-1 boys and 70 type-2 boys remaining for the type-2 girls. Thus, $a = 1/2$ and $h_t = 1/5$ implies $b = 1/8$.

Instead of fixing either a or b , we'll adopt an alternative specification of the matching matrix which involves an "endogamy" parameter. This parameter α , which is scaled between 0 and 1, is defined so that

$$a = \alpha + (1 - \alpha)h_t$$

and thus the matching matrix becomes

$$N_t = \begin{bmatrix} \alpha + (1 - \alpha)h_t & (1 - \alpha)(1 - h_t) & 0 & 0 \\ 0 & 0 & (1 - \alpha)h_t & \alpha + (1 - \alpha)(1 - h_t) \end{bmatrix}.$$

This specification incorporates two special cases. Setting $\alpha = 1$, individuals are always matched to partners of their own type. In this "complete endogamy" case, the matching matrix becomes

$$N = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$

Note that a time subscript on N is unnecessary because this matrix does not change over time. In contrast, setting $\alpha = 0$, matching probabilities depend entirely on the proportions of each type in the population. In this "random matching" case, the matching matrix becomes

$$N_t = \begin{bmatrix} h_t & 1 - h_t & 0 & 0 \\ 0 & 0 & h_t & 1 - h_t \end{bmatrix}.$$

In reality, individuals often match with partners of the same type, though the strength of this tendency may depend upon the particular "type" under consideration (whether income or IQ score or religion). Thus, given our specification of the matching matrix, we may set α between 0 and 1 to capture the reflect the strength of the endogamy effect in particular applications.

14.3 Population projection

In the extreme case of complete endogamy ($\alpha = 1$), the matching probabilities do not depend on the current state of the system. Consequently, we may write the matching matrix as N (without the time subscript) and population dynamics are determined by the equation

$$\mathbf{x}_{t+1} = \mathbf{x}_t N R P.$$

Given an initial condition \mathbf{x}_0 ,

$$\begin{aligned} \mathbf{x}_1 &= \mathbf{x}_0 N R P \\ \mathbf{x}_2 &= \mathbf{x}_1 N R P = \mathbf{x}_0 (N R P)^2 \\ \mathbf{x}_3 &= \mathbf{x}_2 N R P = \mathbf{x}_0 (N R P)^3 \end{aligned}$$

and thus by induction we obtain

$$\mathbf{x}_t = \mathbf{x}_0(NRP)^t$$

for any t . In contrast, when endogamy is incomplete ($\alpha < 1$), the matching probabilities are dependent on the current state. Consequently, we write the matching matrix as N_t (with the time subscript) and population dynamics are determined by the equation

$$\mathbf{x}_{t+1} = \mathbf{x}_t N_t R P.$$

Importantly, because we must know \mathbf{x}_t in order to obtain N_t for each generation t , population projections must be computed iteratively.

To illustrate, let's consider a numerical example with the parameter values indicated below.

```
>> alpha = .5    % endogamy parameter

alpha =
    0.5000

>> R = diag([.8 1 1 1.3])    % reproduction matrix

R =
    0.8000         0         0         0
         0    1.0000         0         0
         0         0    1.0000         0
         0         0         0    1.3000

>> P = [.7 .3; .5 .5; .5 .5; .2 .8]    % transition matrix

P =
    0.7000    0.3000
    0.5000    0.5000
    0.5000    0.5000
    0.2000    0.8000
```

For concreteness, suppose that types are based on IQ scores, so that the population is partitioned into those with high IQ (type 1) and low IQ (type 2). Our parameter assumptions then imply that the “high-high” (type-11) couples have the lowest reproduction rate ($r(11) = 0.8$), the “low-low” (type-22) couples have the highest reproduction rate ($r(22) = 1.3$), and the “mixed” (type-12 or type-21) couples have intermediate reproduction rates ($r(12) = r(21) = 1$). We have further assumed that the high-high couples are the most likely to have a high-IQ child ($P(11, 1) = 0.7$), low-low couples are the least likely ($P(22, 1) = 0.2$), and mixed couples have an intermediate probability ($P(12, 1) = P(21, 1) = 0.5$).

Further choosing an initial frequency distribution \mathbf{x}_0 , we can now determine the frequency distribution \mathbf{x}_1 for generation 1. To do so, we first compute the proportion

of high-IQ individuals h_0 , then compute the matching matrix N_0 , and finally compute the new frequency distribution. We can then repeat the same series of steps to obtain the frequency distribution \mathbf{x}_2 for generation 2.

```
>> x = [100 100] % frequency distribution for girls in generation 0

x =
    100    100

>> h = x(1)/sum(x) % proportion of high-IQ individuals

h =
    0.5000

>> N = [alpha+(1-alpha)*h, (1-alpha)*(1-h), 0, 0; 0, 0, (1-alpha)*h, alpha+(1-alpha)*(1-h)]

N =
    0.7500    0.2500         0         0
         0         0    0.2500    0.7500

>> x*N % frequency distribution for couples

ans =

    75    25    25    75

>> x = x*N*R*P % frequency distribution for girls in generation 1

x =
   86.5000  121.0000

>> h = x(1)/sum(x) % proportion of high-IQ individuals

h =
    0.4169

>> N = [alpha+(1-alpha)*h, (1-alpha)*(1-h), 0, 0; 0, 0, (1-alpha)*h, alpha+(1-alpha)*(1-h)]

N =
    0.7084    0.2916         0         0
         0         0    0.2084    0.7916

>> x*N % frequency distribution for couples

ans =
   61.2795   25.2205   25.2205   95.7795

>> x = x*N*R*P % frequency distribution for girls in generation 2

x =
   84.4397  139.5383
```

Note how the decrease in the proportion of high-IQ individuals (from 50% in generation 0 to 41.69% in generation 1) causes the matching matrix to change between generations. The probability of matching with a high-IQ boys drops for both high-IQ girls (from 75% in generation 0 to 70.84% in generation 1) and low-IQ girls (from 25% in generation 0 to 20.84% in generation 1).

To project the population ahead for 15 generations, we can embed the matlab commands within a for loop. Note that the matching matrix is recomputed at each iteration of the loop.

```
>> x = [100 100];
>> popfreq = x;
>> for t = 1:15;
    h = x(1)/sum(x);
    N = [alpha+(1-alpha)*h, (1-alpha)*(1-h), 0, 0; 0, 0, (1-alpha)*h, alpha+(1-alpha)*(1-h)];
    x = x*N*R*P;
    popfreq = [popfreq; x];
end
>> popfreq

popfreq =
 100.0000  100.0000
   86.5000  121.0000
   84.4397  139.5383
   88.3007  158.0205
   95.6319  177.6029
  105.3251  198.9562
  116.9087  222.5510
  130.2303  248.7807
  145.3054  278.0197
  162.2448  310.6536
  181.2193  347.0972
  202.4434  387.8055
  226.1686  433.2828
  252.6820  484.0905
  282.3075  540.8546
  315.4084  604.2742
```

Normalizing by population size to obtain probability distributions for each generation, we find that the population has converged to a stable-growth equilibrium.

```
>> popsize = sum(popfreq,2)

popsize =
 200.0000
 207.5000
 223.9780
 246.3212
 273.2349
 304.2813
```

```

339.4598
379.0110
423.3251
472.8984
528.3165
590.2489
659.4514
736.7725
823.1621
919.6825

>> popdist = diag(popsizes.^-1)*popfreq

popdist =
    0.5000    0.5000
    0.4169    0.5831
    0.3770    0.6230
    0.3585    0.6415
    0.3500    0.6500
    0.3461    0.6539
    0.3444    0.6556
    0.3436    0.6564
    0.3432    0.6568
    0.3431    0.6569
    0.3430    0.6570
    0.3430    0.6570
    0.3430    0.6570
    0.3430    0.6570
    0.3430    0.6570
    0.3430    0.6570

```

Thus, for the present example, we obtain a limiting distribution in which 34.3% of the population has high-IQ while the remaining 65.7% has low-IQ.

14.4 A one-dimensional dynamical system

Following the linear models developed in the first half of this book, the preceding section specified the dynamics of the frequency distribution, which indicates the *number* of individuals of each type in each generation. Of course, as we have just seen, it is possible to normalize the frequency distribution by population size to obtain the *proportions* of individuals of each type in each generation. However, to link to the nonlinear models developed in the second half of the book, we will now specify the dynamics of the probability distribution more directly.

To begin, consider the special case in which all types of couples have (on average) 1 girl each. Because R is the identity matrix, population dynamics are given by

$$\mathbf{x}_{t+1} = \mathbf{x}_t N_t P$$

and population size does not change over time. Thus, if the initial frequency distribution \mathbf{x}_0 is normalized as a probability distribution, then all subsequent distributions are also probability distributions. That is,

$$\mathbf{x}_t(1) + \mathbf{x}_t(2) = 1$$

for all t . Consequently, we obtain

$$\begin{aligned}\mathbf{x}_t(1) &= h_t \\ \mathbf{x}_t(2) &= 1 - h_t\end{aligned}$$

and can rewrite the population dynamics as

$$[h_{t+1} \ 1 - h_{t+1}] = [h_t \ 1 - h_t] N_t P.$$

Having obtained this two-equation system, it is evident that we do not need to keep track of both types of individuals. In particular, given $\mathbf{x}_t(1) = h_t$, we know that $\mathbf{x}_t(2)$ must be equal to $1 - h_t$. Thus, focusing solely on type-1 individuals, we obtain a one-dimensional model with dynamics given by

$$h_{t+1} = [h_t \ 1 - h_t] N_t P(:, 1)$$

where

$$P(:, 1) = \begin{bmatrix} P(11, 1) \\ P(12, 1) \\ P(21, 1) \\ P(22, 1) \end{bmatrix}$$

denotes the first column of the P matrix. Alternatively, to move away from matrix notation, we could write the dynamics in the form

$$h_{t+1} = f(h_t)$$

where

$$\begin{aligned}f(h) &= h [\alpha + (1 - \alpha)h] P(11, 1) \\ &\quad + (1 - \alpha) h (1 - h) [P(12, 1) + P(21, 1)] \\ &\quad + (1 - h) [\alpha + (1 - \alpha)(1 - h)] P(22, 1)\end{aligned}$$

is the generator function.

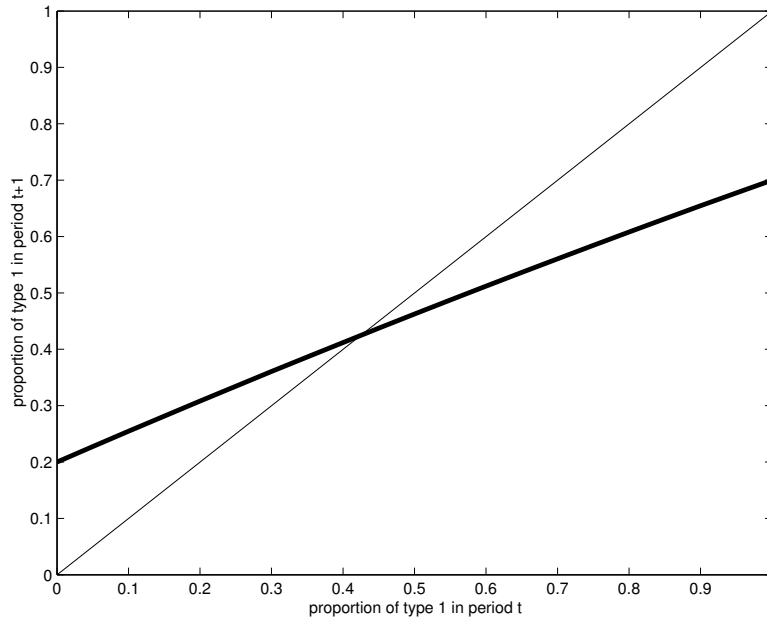
Given numerical assumptions on the parameters, we can plot this generator function against the 45-degree line to determine fixed points and assess their stability. To illustrate, consider the example below (which retains the assumptions on α and P made in the preceding section).

```

>> alpha = .5; P = [.7 .3; .5 .5; .5 .5; .2 .8]; % parameters

>> f = [];
>> for h = 0:.05:1;
    N = [alpha+(1-alpha)*h, (1-alpha)*(1-h), 0, 0; 0, 0, (1-alpha)*h, alpha+(1-alpha)*(1-h)];
    fh = [h 1-h] * N * P(:,1);
    f = [f, fh];
end
>> plot(0:.05:1,f,0:1,0:1) % generator function

```



From this diagram, we see that there is a unique, stable equilibrium. Computing a time path from any initial condition (I'll leave this task to the reader as an exercise), we find that 42.44% of the population is type 1 in equilibrium.

Of course, this solution differs from the equilibrium computed in the preceding section because we have not allowed differential reproduction. Once we do so, the model becomes

$$h_{t+1} = \frac{[h_t \ 1-h_t]N_t R P(:,1)}{\text{sum}([h_t \ 1-h_t]N_t R)}$$

where the summation in the denominator is taken over the ($n^2 = 4$) elements of the input vector. Alternatively, while the generator function becomes rather cumbersome, it remains possible to write these dynamics in the form

$$h_{t+1} = f(h_t)$$

where

$$f(h) = \frac{h[\alpha + (1 - \alpha)h]r(11)P(11, 1) + (1 - \alpha)h(1 - h)[r(12)P(12, 1) + r(21)P(21, 1)] + (1 - h)[\alpha + (1 - \alpha)(1 - h)]r(22)P(22, 1)}{h[\alpha + (1 - \alpha)h]r(11) + (1 - \alpha)h(1 - h)[r(12) + r(21)] + (1 - h)[\alpha + (1 - \alpha)(1 - h)]r(22)}.$$

Intuitively, having normalized population size to 1 in period t , the numerator of the generator function indicates the number of type-1 individuals in period $t + 1$, while the denominator indicates the size of the population in period $t + 1$. Thus, the quotient represents the proportion of type-1 individuals in period $t + 1$.

It may be useful to note that, in the absence of differential reproduction, the generator function simplifies to the equation presented above. To see this, suppose that all types of parents have (on average) r girls. This implies

$$R = rI$$

and hence

$$h_{t+1} = \frac{r [h_t \ 1-h_t]N_t P(:, 1)}{r \text{sum}([h_t \ 1-h_t]N_t)}.$$

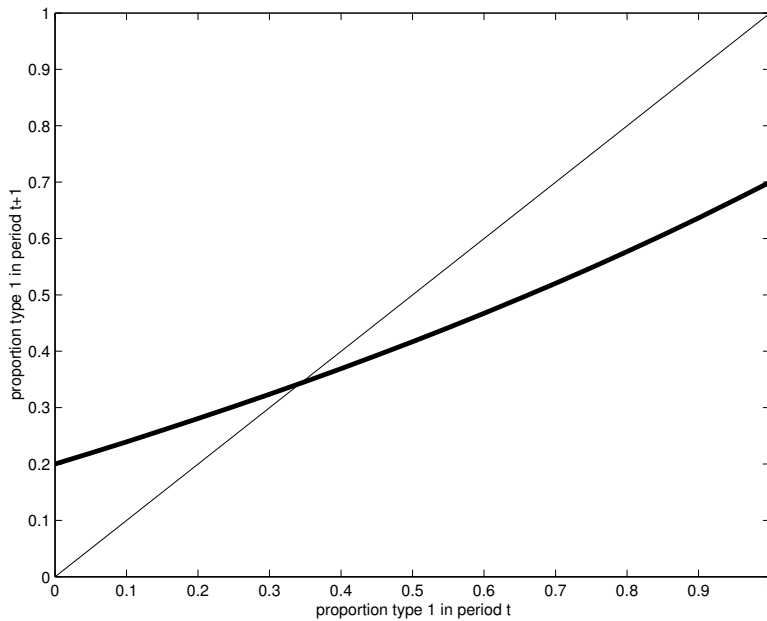
Because $[h_t \ 1-h_t]N_t$ is the probability distribution over couples, the elements of this vector must sum to 1. Further cancelling the rs from the numerator and denominator, we obtain

$$h_{t+1} = [h_t \ 1-h_t]N_t P(:, 1)$$

as before.

Having incorporated differential reproduction into the model, we can now return to the numerical example from the preceding section. We'll first plot the generator function, and then compute a time path starting from the same initial condition ($h_0 = 0.5$) as before.

```
>> alpha = .5; R = diag([.8 1 1 1.3]); P = [.7 .3; .5 .5; .5 .5; .2 .8]; % parameters
>> f = [];
>> for h = 0:.05:1
    N = [alpha+(1-alpha)*h, (1-alpha)*(1-h), 0, 0; 0, 0, (1-alpha)*h, alpha+(1-alpha)*(1-h)];
    fh = ([h 1-h] * N * R * P(:,1)) / sum([h 1-h] * N * R);
    f = [f, fh];
end
>> plot(0:.05:1,f,0:1,0:1) % generator function
```



```

>> h = 0.5;
>> popdist = h;
>> for t = 1:15
    N = [alpha+(1-alpha)*h, (1-alpha)*(1-h), 0, 0; 0, 0, (1-alpha)*h, alpha+(1-alpha)*(1-h)];
    h = ([h 1-h] * N * R * P(:,1)) / sum([h 1-h] * N * R);
    popdist = [popdist; h];
end

>> popdist

popdist =
    0.5000
    0.4169
    0.3770
    0.3585
    0.3500
    0.3461
    0.3444
    0.3436
    0.3432
    0.3431
    0.3430
    0.3430
    0.3430
    0.3430
    0.3430
    0.3430
    0.3430

```

Comparing these results to those obtained earlier, note that our population projections precisely match (the first column of) those shown in the preceding section.

14.5 Uniqueness of the equilibrium

The preceding example featured a unique equilibrium. In fact, for some special cases of the model, it is possible to prove that the equilibrium *must* be unique. In particular, multiple equilibrium cannot arise when endogamy is complete ($\alpha = 1$) or when there is no differential reproduction ($R = rI$).

To establish the first result, we can draw on our knowledge of linear models from Chapter 3. Recall that, for the one-sex version of the model, primitivity of the RP matrix implies that the population will eventually reach a unique stable-growth equilibrium. Given complete endogamy ($\alpha = 1$), the two-sex model essentially reduces to the one-sex model. To see this, note that

$$NRP = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} r(11) & 0 & 0 & 0 \\ 0 & r(12) & 0 & 0 \\ 0 & 0 & r(21) & 0 \\ 0 & 0 & 0 & r(22) \end{bmatrix} \begin{bmatrix} P(11,1) & 1-P(11,1) \\ P(12,1) & 1-P(12,1) \\ P(21,1) & 1-P(21,1) \\ P(22,1) & 1-P(22,1) \end{bmatrix}$$

can be rewritten as

$$NRP = \begin{bmatrix} r(11) & 0 \\ 0 & r(22) \end{bmatrix} \begin{bmatrix} P(11,1) & 1-P(11,1) \\ P(22,1) & 1-P(22,1) \end{bmatrix}.$$

This matrix is primitive when both reproduction rates are positive, so that

$$\begin{aligned} r(11) &> 0 \\ r(22) &> 0 \end{aligned}$$

and intergenerational transitions are not certain, so that

$$\begin{aligned} 0 &< P(11,1) < 1 \\ 0 &< P(22,1) < 1 \end{aligned}$$

Assuming these conditions hold, we know that the unique equilibrium h^* is determined by the condition

$$\lambda[h^* \ 1 - h^*] = [h^* \ 1 - h^*]NRP$$

where λ is the dominant eigenvalue of the $(NRP)'$ matrix. Thus, because the model is linear when endogamy is complete, multiple equilibria cannot arise.

To establish the second result, recall that the generator function can be written

$$\begin{aligned} f(h) &= h [\alpha + (1 - \alpha)h] P(11,1) \\ &\quad + (1 - \alpha) h (1 - h) [P(12,1) + P(21,1)] \\ &\quad + (1 - h) [\alpha + (1 - \alpha)(1 - h)] P(22,1) \end{aligned}$$

when there is no differential reproduction. Using calculus, we obtain

$$f''(h) = 2(1 - \alpha)(P(11, 1) + P(22, 1) - P(12, 1) - P(21, 1))$$

which is a constant (that depends on the model parameters but not h). Thus, the generator function is convex (the slope rises in h) when this constant is positive, concave (the slope falls in h) when this constant is negative, and linear when this constant is zero. Further evaluating this function at $h = 0$ and $h = 1$, we obtain

$$f(0) = P(22, 1) > 0$$

$$f(1) = P(11, 1) < 1$$

where the inequalities follow from primitivity of the P matrix. Graphically, plotting the generator function, it must start above the 45-degree line (for $h = 0$), end below the 45-degree line (for $h = 1$). Obviously, linearity of generator function implies a unique intersection with the 45-degree line. But upon reflection, it should be clear that either convexity or concavity of the generator function also implies a unique intersection. That is, there is a unique fixed point $h^* = f(h^*)$.⁵

14.6 Multiple equilibria

Moving beyond these special cases, it is possible to construct examples with multiple equilibria. In particular, Preston and Campbell (1993) have demonstrated the possibility of multiple equilibria when reproduction is “centrifugal.” This means that reproduction rates are higher for couples in which the partners are more similar to each other. In particular, for our current model (with $n = 2$), reproduction is centrifugal when same-type couples (types 11 and 22) have more children than mixed couples (types 12 and 21).

To illustrate the possibility of multiple equilibria, consider an example with the following parameter values.

```
>> alpha = 0; % assume random matching

>> R = diag([5 1 1 5]) % centrifugal reproduction

R =
     5     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     5

>> P = [.9 .1; .5 .5; .5 .5; .1 .9] % intergenerational transmission
```

⁵Returning to the first example in the preceding section (with no differential reproduction), you can check that $h(0) = P(22, 1) = 0.2$, $h(1) = P(11, 1) = 0.7$, and $P(11, 1) + P(22, 1) - P(12, 1) - P(21, 1) = -0.1$. Thus, the generator function for that example is convex.

```

P =
    0.9000    0.1000
    0.5000    0.5000
    0.5000    0.5000
    0.1000    0.9000

```

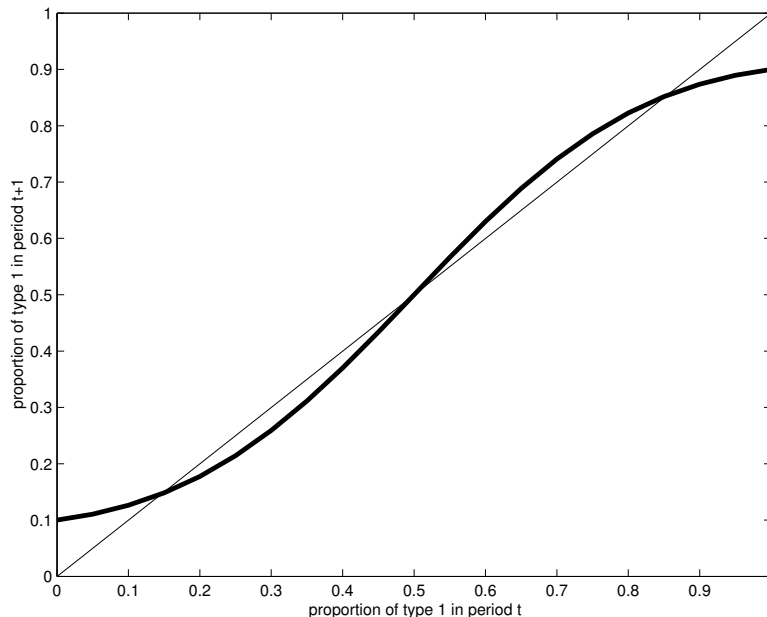
In this (admittedly extreme) example, same-type couples have five times as many children as mixed couples, and intergenerational persistence is very high for same-type couples. Plotting the generator function, we find three different fixed points.

```

>> f = [];
>> for x = 0:.05:1
    N = [alpha+(1-alpha)*x, (1-alpha)*(1-x), 0, 0; 0, 0, (1-alpha)*x, alpha+(1-alpha)*(1-x)];
    fx = [x 1-x]*N*R*P(:,1)/sum([x 1-x]*N*R);
    f = [f; fx];
end

>> plot(0:.05:1,f,0:1,0:1) % generator function

```



Further computation (left to the reader) would show that the stable equilibria occur when 14.64% or 85.35% of the population is type 1.

The possibility of multiple equilibria also raises the possibility of catastrophes. To illustrate, suppose that the population is initially at the stable upper equilibrium, and that the reproduction rate for type-11 couples gradually falls from $r(11) = 5$ to $r(11) = 3$. Graphically, the decline in this parameter causes the generator to shift downwards.

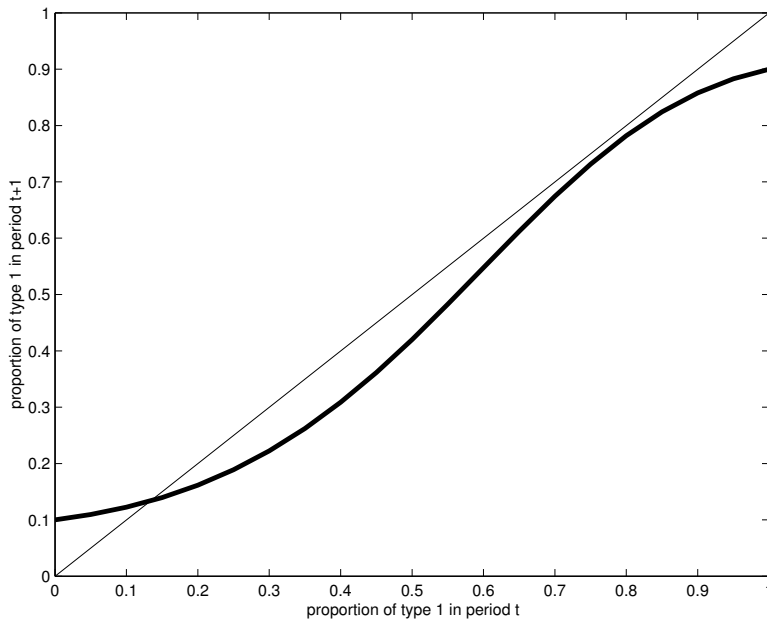
```

>> R(1,1) = 3 % new reproduction rate for type-11 couples

R =
     3     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     5

>> f = []
>> for x = 0:.05:1
    N = [alpha+(1-alpha)*x, (1-alpha)*(1-x), 0, 0; 0, 0, (1-alpha)*x, alpha+(1-alpha)*(1-x)];
    fx = [x 1-x]*N*R*P(:,1)/sum([x 1-x]*N*R);
    f = [f; fx];
end
>> plot(0:.05:1,f,0:1,0:1) % generator function

```



Crucially, once $r(11)$ falls below a critical value (slightly higher than 3), the upper equilibrium no longer exists. In particular, for $r(11) = 3$, there is a unique equilibrium in which 13.35% of the population is type 1. Thus, it is possible for a gradual decline in this parameter to produce a “catastrophic” decrease in the proportion of type-1 individuals.

In light of this example, we might revisit our discussion of the intergenerational dynamics of IQ scores from Chapter 3. As emphasized in that chapter, the linearity of the one-sex model guarantees a unique limiting distribution. Any small changes in parameter values would have a small effect on the generator function, and hence a small effect on the equilibrium. In contrast, the non-linearity of the two-sex model permits multiple equilibria and creates the potential for catastrophes. Arguably, this might provide some theoretical support for commentators concerned about the effect

of differential reproduction on the dynamics of IQ scores. If our society was in fact on the “brink” of a catastrophe, small adverse changes in reproduction rates (or intergenerational transition probabilities) could have a dramatic effect on the equilibrium distribution of IQ scores. On the other hand, it is important to note that we obtained multiple equilibria only by making some extreme assumptions on these parameters. Restricting parameter values to empirical sensible ranges, further numerical examples suggest that there is little scope for multiple equilibria.⁶

14.7 Further reading

Preston and Campbell (Am J Soc, 1993)

⁶In particular, given the (empirically sensible) assumptions that couples with higher IQ have lower reproduction rates ($r(11) < r(12), r(21) < r(22)$) and are more likely to have high-IQ children ($P(11, 1) > P(12, 1), P(21, 1) > P(22, 1)$), I suspect (but have not proven) that the equilibrium must be unique.