Supplementary Material

A classification of structured coalescent processes with migration, conditional on the population pedigree

Sabin Lessard[1,*], Terry Easlick[1,†], and John Wakeley[2,‡]

[1] *Département de mathématiques et de statistique, Université de Montréal, Montréal, QC H3C 3J7, Canada*
[2] *Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA*

[*] *sabin.lessard@umontreal.ca,* [†] *terry.easlick@umontreal.ca,* [‡] *wakeley@fas.harvard.edu*

May 12, 2026

0 Introduction

In this Supplementary Material, we provide further calculations regarding the four limits for coalescence times in structured diploid populations (structured-coalescent, many-demes, low-migration, rare-migration). We also consider monoecious as well as dioecious populations with either migration of haploid gametes or migration of diploid offspring. For reference, Table S1 shows the notation for the main quantities in play both here and in the main text, and Table S2 gives a detailed summary of our main results, corresponding to Table 1 in the main text.

N	Number individuals per deme
D	Number of demes
m	Migration fraction
α	Probability of migration
$\mathcal{A}$	Population pedigree
$\tau^{(\cdot)}$	Coalescence time
$\tau^{(\cdot)} \,\vert\, \mathcal{A}$	Conditional coalescence time
$F_\cdot(t)$	Conditional survival function
$\mathbb{E}(F_\cdot(t))$	Mean of survival function
$\mathrm{Var}(F_\cdot(t))$	Variance of survival function
$\mathcal{F}$	Probability of coalescence before migration for a pair of lines
$\mathcal{U}$	Probability of coalescence before migration for two pairs of lines
Π	Transition matrix for one pair of lines
$\widetilde{\Pi}$	Transition matrix for two pairs of lines
G	Rate matrix for a pair of lines at one locus
$\widetilde{G}$	Rate matrix for two pairs of lines at two loci

Table S1: Notation used with $\cdot$ standing for N, D, m or α as variable. Pairs of lines are in the same deme but at different unlinked loci.

The quantities in Table S2 specifying the limiting variances of the conditional survival functions of coalescence times for all the models are

$$
\begin{aligned}
C_1 &= 1 - \mathcal{U}_1 - (1 - \mathcal{F}_1)^2, \\
C_2 &= 1 - \mathcal{U}_2 - (1 - \mathcal{F}_2)^2, \\
C_3 &= 1 - \mathcal{U}_3 - (1 - \mathcal{F}_3)^2, \\
C_4 &= 1 - \mathcal{U}_4 - (1 - \mathcal{F}_4)^2, \\
C_5 &= \exp\left\{\frac{2t}{N+1}\right\} - 1, \\
C_6 &= \exp\left\{\frac{4t}{N+1}\right\} - 1, \\
C_7 &= \exp\left\{\frac{4t}{N+2}\right\} - 1, \\
C_8 &= \exp\left\{\frac{2t}{N+2}\right\} - 1, \\
C_9 &= \exp\left\{\left[\frac{2}{N+1}m(1-m) + \frac{4N^2}{(N+1)^2}m^2(1-m)^2\right]t\right\} - 1, \\
C_{10} &= \exp\left\{\left[\frac{4}{N+1}m(1-m) + \frac{4(N-1)^2}{(N+1)^2}m^2(1-m)^2\right]t\right\} - 1, \\
C_{11} &= \exp\left\{\left[\frac{2}{N+2}m(1-m) + \frac{4(N+1)^2}{(N+2)^2}m^2(1-m)^2\right]t\right\} - 1, \\
C_{12} &= \exp\left\{\left[\frac{4}{N+2}m(1-m) + \frac{4N^2}{(N+2)^2}m^2(1-m)^2\right]t\right\} - 1
\end{aligned}
$$

with

$$
\begin{aligned}
\mathcal{F}_1 = \mathcal{F}_4 &= \frac{(1-m)^2}{2Nm(2-m) + (1-m)^2}, \\
\mathcal{F}_2 &= \frac{1}{(2N-1)m(2-m) + (1-m)^2}, \\
\mathcal{F}_3 &= \frac{(1-m)^4}{2Nm(2-m) + 2(1-m)^2 - (1-m)^4}.
\end{aligned}
$$

Here, $\mathcal{U}_1$, $\mathcal{U}_2$, $\mathcal{U}_3$, $\mathcal{U}_4$ are probabilities of coalescence at any of two unlinked loci for ancestral lines starting in the same individual in the limit of a large number of demes, while $\mathcal{F}_1$, $\mathcal{F}_2$, $\mathcal{F}_3$, $\mathcal{F}_4$ are probabilities of coalescence for ancestral lines at a single locus under the same assumptions. With $M = 4Mn$ held fixed as $N \to \infty$, the former have the same limit $(1+2M)/(1+M)^2$, and the latter the same limit $1/(1+M)$. Moreover, $C_1, \ldots, C_8$ tend to 0 as $N \to \infty$ and this occurs when the chance that ancestral lines at different loci travel together in the same gamete becomes negligible in the limit of a large deme size so that coalescence times at unlinked loci are independent in this limit. This is not the case in the rare-migration limit, in which even ancestral lines in different individuals can travel together, and $C_9, \ldots, C_{12}$ all tending to $\exp\left\{\left[4m^2(1-m)^2\right]t\right\} - 1 > 0$.

Limit	Initial state	Monoecious population Gametic migration	Monoecious population Diploid migration	Dioecious population Gametic migration	Dioecious population Diploid migration
Structured-coalescent	[••]	0	0	0	0
	[•][•]	0	0	0	0
Many-demes	[••]	$C_1 \exp\left\{-\frac{1-\mathcal{F}_1}{N}\, t\right\}$	$C_2 \exp\left\{-\frac{1-\mathcal{F}_2}{N-1}\, t\right\}$	$C_3 \exp\left\{-\frac{1-\mathcal{F}_3}{N}\, t\right\}$	$C_4 \exp\left\{-\frac{1-\mathcal{F}_4}{N+(1-m)^2}\, t\right\}$
	[•][•]	0	0	0	0
Low-migration	[••]	0	0	0	0
	[•][•]	$C_5 \exp\{-4t\}$	$C_6 \exp\{-4t\}$	$C_7 \exp\{-4t\}$	$C_8 \exp\{-4t\}$
Rare-migration	[••]	0	0	0	0
	[•][•]	$C_9 \exp\{-4m(1-m)t\}$	$C_{10} \exp\{-4m(1-m)t\}$	$C_{11} \exp\{-4m(1-m)t\}$	$C_{12} \exp\{-4m(1-m)t\}$

Table S2: Limiting variance of the conditional survival function given the population pedigree. The exponential functions are the squares of the limiting expectations. In the low- and rare-migration limits with initial state [••], the survival function takes the value 0 with probabilty 1. With diploid migration, the initial states [••] and [•][•] are replaced by [(••)] and [(•)][(•)], respectively.

Moreover, let us recall that the conditions for the four limits are the following: (1) $N \to \infty$ with $M = 4Nm$ fixed for $D = 2$, $\alpha = 1$ and $2N$ generations as unit of time for the structured-coalescent limit; (2) $D \to \infty$ for $\alpha = 1$ and D generations as unit of time for the many-demes limit; (3) $m \to 0$ for $D = 2$, $\alpha = 1$ and $1/m$ generations as unit of time for the low-migration limit; and (4) $\alpha \to 0$ for $D = 2$ and $1/\alpha$ generations as unit of time for the rare-migration limit.

1 Many-demes limit for monoecious populations with gametic migration, additional calculations

1.1 Fast-process absorption probabilities

As in the main text section 'Many-demes limit', let u_i denote the absorption probability in the coalescent state 1 given initial state i for $i = 1, \ldots, 17$. From main text equation (19), we have $u_1 = 1$, $u_3 = u_4 = \mathcal{F}$, and $u_2 = u_5 = u_6 = u_7 = u_8 = u_9 = 0$. Using these and the block structure of the transition matrix for the subsets of states $\tilde{S}_1 = \{1, \ldots, 9\}$ and $\tilde{S}_2 = \{10, \ldots, 17\}$ in main text equation (17) we can solve for the remaining u_i with $i \in \{10, \ldots, 17\}$ in main text equation (20) using first-step analysis.

There are 35 non-zero entries in $\tilde{\mathbf{A}}_{21}$ and 26 non-zero entries in $\tilde{\mathbf{A}}_{22}$. We do not detail these here but they are straightforward to compute. In short: each gamete is a migrant with probability m independently of all other gametes; each gamete traces back to one of the N parental individuals in its deme uniformly and independently of all other gametes; then the gene copy or copies in each gamete trace back to the gene copies in the parent according to Mendel's laws.

For example, consider state 12, or [••][∘∘]. In the process described by $\tilde{\mathbf{A}}$, which recall has transition probabilities of order $O(1)$ in the limit $D \to \infty$, state 12 cannot be reached from any other state. But states 1, 3 and 4 can be reached in one step from state 12. The transition probability from state 12 to state 1 can be written

$$\frac{(1-m)^2}{N} - \left(\frac{(1-m)^2}{2N}\right)^2. \tag{S1}$$

This can be derived by accounting for all possibilities using the rules in the previous paragraph, for example there being zero, one, two, three or four migration events. Alternatively, it can be obtained by noting that the pairs [••] and [∘∘] in state 12 independently coalesce with probability $(1-m)^2/(2N)$, and the transition to state 1 entails the coalescence of at least one pair.

Considering all possible single-step outcomes for state 12, we have

$$u_{12} = \frac{(1-m)^2\big(4N - (1-m)^2\big)}{4N^2} + \frac{m(2-m)(1-m)^2(2N-1)}{N}\mathcal{F} + \frac{(1-m)^4(2N-1)^2}{4N^2}u_{12}, \tag{S2}$$

in which the first term on the right-hand side is another way of writing (S1) and the second term is the one-step transition probability to either state 3 or state 4 times the probability of absorption in state 1 from those states. Solving (S2) gives $u_{12} = 1 - (1-\mathcal{F})^2$.

In the same way, we have

$$\begin{aligned} u_{10} = {} & \frac{(1-m)^2}{2N} + \frac{m(1-m)^2(2N-1)}{2N}\mathcal{F} \\ & + \frac{(1-m)^3(N-1)(2N-1)}{2N^2}u_{10} + \frac{(1-m)^3(2N-1)}{2N^2}u_{14}\,, \end{aligned} \tag{S3}$$

$$u_{14} = \frac{(1-m)^2}{2N} + \frac{(1-m)^2(N-1)}{2N}u_{10} + \frac{(1-m)^2}{2}u_{14}\,, \tag{S4}$$

which give $u_{10} = u_{14} = \mathcal{F}$, and

$$\begin{aligned} u_{11} = {} & \frac{(1-m)^2}{2N} + \frac{m(1-m)^2(2N-1)}{2N}\mathcal{F} \\ & + \frac{(1-m)^3(N-1)(2N-1)}{2N^2}u_{11} + \frac{(1-m)^3(2N-1)}{2N^2}u_{15}\,, \end{aligned} \tag{S5}$$

$$u_{15} = \frac{(1-m)^2}{2N} + \frac{(1-m)^2(N-1)}{2N}u_{11} + \frac{(1-m)^2}{2}u_{15}\,, \tag{S6}$$

which give $u_{11} = u_{15} = \mathcal{F}$.

The absorption probabilities u_{13}, u_{16} and u_{17} for [$\bullet\bullet\circ\circ$], [$\bullet\bullet\circ$], and [$\bullet\bullet$] are considerably more complicated. Using $u_1 = 1$, $u_3 = u_4 = u_{10} = u_{11} = u_{14} = u_{15} = \mathcal{F}$, and $u_2 = u_5 = u_6 = u_7 = u_8 = u_9 = 0$, we have

$$\begin{aligned} u_{13} = {} & \frac{(1-m)^2\big(4N + 8Nm^2 - (1-m)^2\big)}{4N^2} + \frac{m(2-m)(1-m)^2(2N-1)}{N}\mathcal{F} \\ & + \frac{(1-m)^4(N-1)\big(4N^2 - 8N + 3\big)}{4N^3}u_{13} + \frac{(1-m)^4(N-1)(2N-1)}{N^3}u_{16} \\ & + \frac{(1-m)^4(2N-1)}{4N^3}u_{17}\,, \end{aligned} \tag{S7}$$

$$\begin{aligned} u_{16} = {} & \frac{(1-m)^2(4N-1+m)}{4N^2} + \frac{m(1-m)^2(2N-1)}{N}\mathcal{F} \\ & + \frac{(1-m)^3(N-1)(2N-3)}{4N^2}u_{13} + \frac{(1-m)^3\big(N^2-1\big)}{2N^2}u_{16} + \frac{(1-m)^3}{4N}u_{17}\,, \end{aligned} \tag{S8}$$

$$u_{17} = \frac{3(1-m)^2}{4N} + \frac{(1-m)^2(N-1)}{4N}u_{13} + \frac{(1-m)^2(N-1)}{2N}u_{16} + \frac{(1-m)^2}{4}u_{17}\,. \tag{S9}$$

The first term on the right-hand sides of (S7), (S8) and (S9) are the single-step transition probabilities to state 1 from states 13, 16 and 17, respectively. The terms multiplied by $\mathcal{F}$ in (S7) and (S8) are the total single-step probabilities of going from states 13 and 16 to any of the states 3-4, 10-11, or 14-15, from which the probability of eventual absorption in state 1 is equal to $\mathcal{F}$. The remaining terms correspond to transitions among states 13, 16 and 17. Solving (S7), (S8) and (S9) for u_{13}, u_{16}, u_{17} results in unwieldy expressions.

The Mathematica notebook `q17manydemes.nb` displayed in Section 6 gives the expressions for the fixation probabilities u_{13}, u_{16}, u_{17} on the fast time scale in the many-demes limit of a monoecious population with gametic migration, and further displays the structured-coalescent and strong-migration limits of u_{17}, which for convenience of notation we also call $\mathcal{U}$. Using these expressions, confirmation that the quantity $1-\mathcal{U}-(1-\mathcal{F})^2$ is indeed not equal to zero for any finite N is given in Subsection 1.3.

1.2 Adding the structured-coalescent assumption

Here we consider $m = M/(4N)$ as $N \to \infty$ with $M > 0$ kept constant, using Lemma 1 of Möhle (1998). The transition matrix in the limit of an infinite number of demes, that is $\tilde{\mathbf{A}}$ in main text equation (17), can be expressed as

$$\tilde{\mathbf{A}} = \tilde{\tilde{\mathbf{A}}} + \frac{\tilde{\tilde{\mathbf{B}}}_N}{2N},$$

where

$$\tilde{\tilde{\mathbf{A}}} = \begin{pmatrix} \tilde{\tilde{\mathbf{A}}}_{11} & \mathbf{0} \\ \mathbf{0} & \tilde{\tilde{\mathbf{A}}}_{22} \end{pmatrix}$$

is the transition matrix when $N = \infty$ and $m = 0$ with

$$\tilde{\tilde{\mathbf{A}}}_{11} = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1/2 & 1/2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1/2 & 0 & 0 & 1/2 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1/4 & 1/2 & 0 & 1/4 \end{pmatrix}$$

and

$$\tilde{\tilde{\mathbf{A}}}_{22} = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1/2 & 0 & 0 & 0 & 1/2 & 0 & 0 & 0 \\ 0 & 1/2 & 0 & 0 & 0 & 1/2 & 0 & 0 \\ 0 & 0 & 0 & 1/2 & 0 & 0 & 1/2 & 0 \\ 0 & 0 & 0 & 1/4 & 0 & 0 & 1/2 & 1/4 \end{pmatrix}.$$

Moreover, we have

$$\tilde{\tilde{\mathbf{P}}} = \lim_{k\to\infty} \tilde{\tilde{\mathbf{A}}}^k = \begin{pmatrix} \tilde{\tilde{\mathbf{P}}}_{11} & \mathbf{0} \\ \mathbf{0} & \tilde{\tilde{\mathbf{P}}}_{22} \end{pmatrix},$$

where

$$\tilde{\tilde{\mathbf{P}}}_{11} = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \end{pmatrix}$$

and

$$\tilde{\tilde{\mathbf{P}}}_{22} = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \end{pmatrix},$$

while the rows $10, 11, 12, 13$ of

$$\tilde{\tilde{\mathbf{B}}} = \lim_{N\to\infty} \tilde{\tilde{\mathbf{B}}}_N = \begin{pmatrix} \tilde{\tilde{\mathbf{B}}}_{11} & \tilde{\tilde{\mathbf{B}}}_{12} \\ \tilde{\tilde{\mathbf{B}}}_{21} & \tilde{\tilde{\mathbf{B}}}_{22} \end{pmatrix}$$

are given by

$$\begin{pmatrix} 1 & 0 & M/2 & 0 & 0 & M & 0 & 0 & 0 & -1-3M/2 & 0 & 0 & 0 & \mathbf{0} \\ 1 & 0 & 0 & M/2 & 0 & M & 0 & 0 & 0 & 0 & -1-3M/2 & 0 & 0 & \mathbf{0} \\ 2 & 0 & M & M & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -2-2M & 0 & \mathbf{0} \\ 2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & M & M & 0 & -2-2M & \mathbf{0} \end{pmatrix}. \quad \text{(S10)}$$

These are also the rows $10, 11, 12, 13$ of $\tilde{\tilde{\mathbf{G}}} = \tilde{\tilde{\mathbf{P}}}\tilde{\tilde{\mathbf{B}}}\tilde{\tilde{\mathbf{P}}}$. Applying Lemma 1 of Möhle (1998), we have

$$\lim_{N\to\infty} \tilde{\mathbf{A}}^{\lfloor 2Nt \rfloor} = \tilde{\tilde{\mathbf{P}}} \exp\{t\tilde{\tilde{\mathbf{G}}}\}.$$

In the limit as $N \to \infty$ with $2N$ time steps as unit of time, there are instantaneous transitions from states in $\{14, 15, 16, 17\}$ to states in $\{10, 11, 12, 13\}$ from which the rates of change are given in (S10).

Conditioning on the first change of state, the probabilities of fixation into state 1 starting from states in $\{10, 11, 12, 13\}$ in the limit as $N \to \infty$ are given by

$$\begin{aligned} u_{10} &= \frac{1}{1+3M/2}u_1 + \frac{M/2}{1+3M/2}u_3 + \frac{M}{1+3M/2}u_6, \\ u_{11} &= \frac{1}{1+3M/2}u_1 + \frac{M/2}{1+3M/2}u_4 + \frac{M}{1+3M/2}u_6, \\ u_{12} &= \frac{2}{2+2M}u_1 + \frac{M}{2+2M}u_3 + \frac{M}{2+2M}u_4, \\ u_{13} &= \frac{2}{2+2M}u_1 + \frac{M}{2+2M}u_{10} + \frac{M}{2+2M}u_{11}, \end{aligned}$$

where $u_1 = 1$, $u_3 = u_4 = 1/(1+M)$ and $u_6 = 0$. We obtain

$$\begin{aligned} u_{10} = u_{11} &= \frac{1}{1+M}, \\ u_{12} = u_{13} &= \frac{1+2M}{(1+M)^2}. \end{aligned}$$

We conclude that

$$\mathcal{U} = u_{17} = \frac{1+2M}{(1+M)^2} = 1 - \left(\frac{M}{1+M}\right)^2, \quad \text{(S13)}$$

where $M/(1+M) = \lim_{N\to\infty}(1-\mathcal{F})$ with $\mathcal{F}$ given in equation (12) in the main text.

1.3 For all finite N, $1-\mathcal{U}-(1-\mathcal{F})^2$ is not equal to zero

We employ Bernstein polynomial representations to further analyze $1-\mathcal{U}-(1-\mathcal{F})^2$ where $\mathcal{U} = u_{17}$. For a fixed degree d, the Bernstein polynomial basis on $[0,1]$ is given by

$$B_{k,d}(x) = \binom{d}{k} x^k (1-x)^{d-k}, \qquad k = 0, \ldots, d.$$

These basis polynomials span the space of polynomials of degree at most d, and thus any polynomial $p(x)$ with $\deg(p) \le d$ admits the exact representation

$$p(x) = \sum_{k=0}^{d} b_k \, B_{k,d}(x)$$

for suitable coefficients b_k. Although the quantity $1 - u_{17} - (1-\mathcal{F})^2$ depends on N and m, we hereafter apply the Bernstein representation in the variable $0 < m < 1$, treating $N \ge 4$ as a parameter. Hence we may write

$$p(N,m) = \sum_{k=0}^{d} b_k(N) \, B_{k,d}(m),$$

where $B_{k,d}(m) = \binom{d}{k} m^k (1-m)^{d-k}$ and the coefficients $b_k(N)$ depend polynomially on N. The above machinery allows us to write

$$1-\mathcal{U}-(1-\mathcal{F})^2 = \frac{4\,N\,m\,(1-m)^2}{(2Nm(2-m)+(1-m)^2)^2} \cdot \frac{P(N,m)}{Q(N,m)},$$

where

$$P(N,m) = \sum_{i=0}^{10} b_i(N) B_{i,10}(m)$$

is a Bernstein polynomial with coefficients

$$
\begin{aligned}
b_0(N) &= 24N^4 + 9N^3 - 40N^2 + 29N - 6,\\
b_1(N) &= \frac{32}{5}N^5 + \frac{129}{5}N^4 - \frac{143}{5}N^3 + \frac{121}{10}N^2 - \frac{1}{5}N - \frac{3}{10},\\
b_2(N) &= \frac{64}{45}N^6 + \frac{584}{45}N^5 + \frac{64}{15}N^4 - \frac{139}{15}N^3 + \frac{28}{5}N^2 - \frac{3}{5}N,\\
b_3(N) &= \frac{56}{15}N^6 + \frac{371}{30}N^5 - \frac{487}{120}N^4 + \frac{47}{60}N^3 + \frac{101}{120}N^2 - \frac{1}{15}N,\\
b_4(N) &= \frac{88}{15}N^6 + \frac{122}{15}N^5 - \frac{253}{105}N^4 + \frac{124}{105}N^3 + \frac{1}{35}N^2,\\
b_5(N) &= \frac{460}{63}N^6 + \frac{44}{9}N^5 - \frac{1}{2}N^4 + \frac{13}{42}N^3,\\
b_6(N) &= \frac{288}{35}N^6 + \frac{62}{21}N^5 - \frac{1}{105}N^4 + \frac{1}{35}N^3,\\
b_7(N) &= \frac{53}{6}N^6 + \frac{47}{30}N^5,\\
b_8(N) &= \frac{136}{15}N^6 + \frac{8}{15}N^5,\\
b_9(N) &= \frac{44}{5}N^6,\\
b_{10}(N) &= 8N^6,
\end{aligned}
$$

and $B_{i,10}(m) = \binom{10}{i} m^i (1-m)^{10-i}$. Similarly,

$$Q(N,m) = \sum_{j=0}^{9} c_j(N) C_{j,9}(m)$$

is a Bernstein polynomial with coefficients

$$
\begin{aligned}
c_0(N) &= 12N^5 + 41N^4 - 41N^3 + 3N^2 + 13N - 4, \\
c_1(N) &= \frac{2N}{9}\left(24N^5 + 116N^4 + 11N^3 - 88N^2 + 65N - 12\right), \\
c_2(N) &= \frac{N}{18}\left(244N^5 + 392N^4 - 215N^3 + 46N^2 + 31N - 6\right), \\
c_3(N) &= \frac{N^2}{42}\left(896N^4 + 460N^3 - 271N^2 + 120N - 1\right), \\
c_4(N) &= \frac{2N^3}{63}\left(839N^3 + 119N^2 - 50N + 30\right), \\
c_5(N) &= \frac{4N^3}{63}\left(467N^3 + 12N^2 + N + 3\right), \\
c_6(N) &= \frac{2N^4}{21}\left(327N^2 + 2\right), \\
c_7(N) &= \frac{286}{9}N^6, \\
c_8(N) &= 32N^6, \\
c_9(N) &= 32N^6,
\end{aligned}
$$

and $C_{j,9}(m) = \binom{9}{j} m^j (1-m)^{9-j}$.

First note that all of the above Bernstein basis polynomials are positive on $(0, 1)$. Secondly, a direct check shows that $b_i(4) > 0$ for $i = 0, \ldots, 10$ and $c_j(4) > 0$ for $j = 0, \ldots, 9$. Each $b_i(N)$ and $c_j(N)$ is a polynomial in N with positive leading coefficient. Momentarily treating as real-valued polynomials for $x \in \mathbb{R}$, a quick calculation shows that $\frac{d}{dx} b_i(x) > 0$ and $\frac{d}{dx} c_j(x) > 0$ for all $x \in [4, \infty)$. Hence $b_i(x) > 0$ and $c_j(x) > 0$ for all $x \geq 4$, and in particular $b_i(N) > 0$ and $c_j(N) > 0$ for all $N \geq 4$. Thus it follows that $P(N, m) > 0$ and $Q(N, m) > 0$ for all $N \geq 4$ and $0 < m < 1$. Additionally, it is not hard to verify that

$$
\frac{4\,N\,m\,(1-m)^2}{\left(2Nm(2-m) + (1-m)^2\right)^2} > 0, \text{ for } N \geq 4, 0 < m < 1.
$$

Therefore, the quantity $1 - \mathcal{U} - (1 - \mathcal{F})^2$ is not equal to zero. Moreover, these results concretely illustrate that infinite global population yet finite deme size is not sufficient to suppress pedigree effects; namely, such effects disappear only when deme sizes also grow without bound.

1.4 Limiting behaviour of $(1 - \mathcal{U} - (1 - \mathcal{F})^2)$ *as* $N \to \infty$ *with* $4Nm = M$

We analyze the limiting behaviour of the many-demes model under the structured-coalescent assumption. In this regime, pedigree effects vanish at a rate inversely proportional to deme size.

Using the results of the previous subsection, and taking the limit $N \to \infty$ with $4Nm = M$ held fixed, we obtain

$$\lim_{\substack{N\to\infty \\ 4Nm=M}} N\left(1-\mathcal{U}-(1-\mathcal{F})^2\right) = \frac{M(M^2+4M+6)}{3(1+M)^3},$$

which can also be seen in the Mathematica notebook `q17manydemes.nb` displayed in Section 6.

2 Low-migration limit for monoecious populations with gametic migration

In this section, we will consider $D = 2$ demes of fixed size N and let $m \to 0$ for $\alpha = 1$. The possible states for the ancestral lines of a pair of genes at a single locus in an individual are the same as in the main text: [•] for only one in one deme, [••] for two in the same deme, and [•][•] for two in different demes. As for the transition matrix from one generation to the previous one, it can be expressed as

$$\mathbf{\Pi}_m = \mathbf{A} + m\mathbf{B}_m,$$

where

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & 0 \\ \frac{1}{2N} & 1-\frac{1}{2N} & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

and

$$\mathbf{B}_m \to \mathbf{B} = \begin{pmatrix} 0 & 0 & 0 \\ -\frac{2}{2N} & -2+\frac{2}{2N} & 2 \\ \frac{2}{2N} & 2-\frac{2}{2N} & -2 \end{pmatrix}$$

as $m \to 0$. By Lemma 1 of Möhle (1998), we have

$$\mathbf{\Pi}_m^{\lfloor t/m \rfloor} \to \mathbf{P}\exp\{t\mathbf{G}\}$$

as $m \to 0$, where

$$\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix} \tag{S14}$$

and

$$\mathbf{G} = \mathbf{PBP} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 2 & 0 & -2 \end{pmatrix}.$$

Equation (S14) shows that ancestral lines that start in initial state [••] coalesce instantaneously on the new time scale as $m \to 0$ regardless of the details of the pedigree. For ancestral lines that start in initial state [•][•], the conditional survival function $F_m(t) = \mathbb{P}\big(\tau^{(m)} > \lfloor t/m \rfloor \,\big|\, \mathcal{A}\big)$ satisfies

$$\lim_{m \to 0} \mathbb{E}\left(F_m(t)\right) = \exp\{-2t\} \tag{S15}$$

for $t \geq 0$.

Now, considering the ancestral lines that start from two pairs of genes at unlinked loci labeled 1 and 2 in an individual, the possible states for the ancestral sequences are the same as in the previous subsection but they are ordered differently as below:

1. only one • or only one ∘ or only one •
2. [• • ∘∘]
3. [• • ∘][∘]
4. [• ∘ ∘][•]
5. [••][∘∘]
6. [••∘]
7. [••][∘]
8. [•][•∘]
9. [••]
10. [•][•]
11. [•∘][•]
12. [•∘][•∘]

With respect to these states, the transition matrix from one generation to the previous one takes the form

$$\tilde{\mathbf{\Pi}}_m = \tilde{\mathbf{A}} + m\tilde{\mathbf{B}}_m,$$

where $\tilde{\mathbf{A}}$ is the transition matrix in the absence of migration. In this case, there will be absorption into state class $\tilde{S}_0 = \{1\}$ from any initial state in $\tilde{S}_1 = \{2, \ldots, 9\}$ as a result of coalescence events. On the other hand, from any initial state in $\tilde{S}_2 = \{10, 11, 12\}$, the ancestral lines in each deme will follow a Markov chain on the state space $\{(•), (•∘)\}$, independently of the ancestral lines in the other deme, whose probabilities of transition by recombination or coalescence are given by

$$\begin{pmatrix} \frac{1}{2} & \frac{1}{2} \\ \frac{1}{2N} & 1 - \frac{1}{2N} \end{pmatrix}.$$

The stationary distribution of this chain is $(1/(N+1), N/(N+1))$. With respect to the states in $\tilde{S}_2$, the entries of $\tilde{\mathbf{A}}$ are given by

$$\tilde{\mathbf{A}}_{22} = \begin{pmatrix} \frac{1}{4} & \frac{1}{2} & \frac{1}{4} \\ \frac{1}{4N} & \frac{1}{2} & \frac{1}{2}\left(1 - \frac{1}{2N}\right) \\ \left(\frac{1}{2N}\right)^2 & \frac{2}{2N}\left(1 - \frac{1}{2N}\right) & \left(1 - \frac{1}{2N}\right)^2 \end{pmatrix},$$

which satisfies

$$\lim_{k\to\infty} \left(\tilde{\mathbf{A}}_{22}\right)^k = \tilde{\mathbf{P}}_{22} = \begin{pmatrix} \frac{1}{(N+1)^2} & \frac{2N}{(N+1)^2} & \frac{N^2}{(N+1)^2} \\ \frac{1}{(N+1)^2} & \frac{2N}{(N+1)^2} & \frac{N^2}{(N+1)^2} \\ \frac{1}{(N+1)^2} & \frac{2N}{(N+1)^2} & \frac{N^2}{(N+1)^2} \end{pmatrix},$$

owing to the ergodic theorem for discrete-time Markov chains on a finite state space (see, e.g., Karlin and Taylor (1975)). Moreover, with respect to the state sets $\tilde{S}_0, \tilde{S}_1$ and $\tilde{S}_2$, we have

$$\tilde{\mathbf{P}} = \lim_{k\to\infty} \tilde{\mathbf{A}}^k = \begin{pmatrix} 1 & \mathbf{0} & \mathbf{0} \\ \mathbf{1} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \tilde{\mathbf{P}}_{22} \end{pmatrix},$$

where $\mathbf{0}$ and $\mathbf{1}$ are matrices of zeros and ones, respectively. With respect to the same state sets, the rate matrix for changes that involve migration events in the limit as $m \to 0$ takes the form

$$\lim_{m\to 0} \tilde{\mathbf{B}}_m = \tilde{\mathbf{B}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{B}}_{10} & \tilde{\mathbf{B}}_{11} & \tilde{\mathbf{B}}_{12} \\ \tilde{\mathbf{B}}_{20} & \tilde{\mathbf{B}}_{21} & \tilde{\mathbf{B}}_{22} \end{pmatrix},$$

where

$$\tilde{\mathbf{B}}_{22} = \begin{pmatrix} -2 & 0 & 0 \\ 0 & -3 & 0 \\ 0 & 0 & -4 \end{pmatrix} \tilde{\mathbf{A}}_{22}.$$

Lemma 1 of Möhle (1998) guarantees that

$$\lim_{m\to 0} \tilde{\mathbf{\Pi}}_m^{\lfloor t/m \rfloor} = \tilde{\mathbf{P}} \exp\{t\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}}\},$$

where

$$\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{G}}_{20} & \mathbf{0} & \tilde{\mathbf{G}}_{22} \end{pmatrix}$$

with

$$\tilde{\mathbf{G}}_{22} = \tilde{\mathbf{P}}_{22}\tilde{\mathbf{B}}_{22}\tilde{\mathbf{P}}_{22} = \tilde{\mathbf{P}}_{22}\begin{pmatrix} -2 & 0 & 0 \\ 0 & -3 & 0 \\ 0 & 0 & -4 \end{pmatrix}\tilde{\mathbf{P}}_{22} = -\frac{2(2N+1)}{N+1}\tilde{\mathbf{P}}_{22}$$

and

$$\tilde{\mathbf{G}}_{20} = \tilde{\mathbf{P}}_{22}\left(\tilde{\mathbf{B}}_{20} + \tilde{\mathbf{B}}_{21}\mathbf{1}\right) = -\tilde{\mathbf{P}}_{22}\tilde{\mathbf{B}}_{22}\mathbf{1} = \frac{2(2N+1)}{N+1}\mathbf{1}.$$

This uses the fact that the entries on each row of $\tilde{\mathbf{B}}$ must sum up to 0.

We conclude that

$$\lim_{m\to 0}\mathbb{E}\left(F_m(t)^2\right) = \exp\left\{-\frac{2(2N+1)}{N+1}t\right\} = \exp\{-4t\}\exp\left\{\frac{2}{N+1}t\right\} \tag{S16}$$

for $t \geq 0$. Combining this with our previous result yields

$$\lim_{m\to 0}\mathrm{Var}\left(F_m(t)\right) = \exp\{-4t\}\left(\exp\left\{\frac{2}{N+1}t\right\} - 1\right) \tag{S17}$$

for $t \geq 0$, which we note tends to zero as $N \to \infty$.

3 Rare-migration limit for monoecious populations with gametic migration

In this section, we will consider $D = 2$ for fixed N and $m \in (0, 1)$ as $\alpha \to 0$. The possible states for the ancestral lines of a pair of genes at a single locus in an individual are the same as the prior section: [•] for only one in one deme, [••] for two in the same deme, and [•][•] for two in different demes. In similar fashion as before, we can express this transition matrix as

$$\mathbf{\Pi}_\alpha = \mathbf{A} + \alpha\mathbf{B}_\alpha,$$

where

$$\mathbf{A} = \lim_{\alpha\to 0}\mathbf{\Pi}_\alpha = \begin{pmatrix} 1 & 0 & 0 \\ \frac{1}{2N} & 1-\frac{1}{2N} & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

and

$$\mathbf{B}_\alpha = \frac{\mathbf{\Pi}_\alpha - \mathbf{A}}{\alpha} \to \mathbf{B} = 2m(1-m)\begin{pmatrix} 0 & 0 & 0 \\ -\frac{1}{2N} & -\left(1-\frac{1}{2N}\right) & 1 \\ \frac{1}{2N} & 1-\frac{1}{2N} & -1 \end{pmatrix}$$

as $\alpha \to 0$. We again utilise Lemma 1 of Möhle (1998) and obtain

$$\mathbf{\Pi}^{\lfloor t/\alpha \rfloor} \to \mathbf{P} \exp\{t\mathbf{G}\},$$

as $\alpha \to 0$, where

$$\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix} \tag{S18}$$

and

$$\mathbf{G} = \mathbf{PBP} = 2m(1-m) \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 1 & 0 & -1 \end{pmatrix}.$$

Equation (S18) implies that ancestral lines starting in initial state [••] coalesce instantaneously on the new time scale in the limit as $\alpha \to 0$. For ancestral lines that start from initial state [•][•], the survival function $F_\alpha(t) = \mathbb{P}\big(\tau^{(\alpha)} > \lfloor t/\alpha \rfloor \,\big|\, \mathcal{A}\big)$ satisfies

$$\lim_{\alpha\to 0} \mathbb{E}\left(F_\alpha(t)\right) = \exp\{-2m(1-m)t\} \tag{S19}$$

for $t \geq 0$.

We again consider the ancestral lines that start from two pairs of genes at unlinked loci labeled 1 and 2 in an individual, and the same ordering of the possible states for the ancestral sequences as in the previous subsection:

1. only one • or only one ∘ or only one •
2. [• • ∘∘]
3. [• • ∘][∘]
4. [• ∘ ∘][•]
5. [••][∘∘]
6. [••∘]
7. [••][∘]
8. [•][•∘]
9. [••]
10. [•][•]
11. [•∘][•]
12. [•∘][•∘]

With respect to these states, the transition matrix from one generation to the previous one takes the form

$$\tilde{\mathbf{\Pi}}_\alpha = \tilde{\mathbf{A}} + \alpha\tilde{\mathbf{B}}_\alpha,$$

where $\tilde{\mathbf{A}}$ is again the no-migration transition matrix from the low-migration regime. States in $\tilde{S}_1 = \{2, \ldots, 9\}$ absorb into $\tilde{S}_0 = \{1\}$ via coalescence, while in $\tilde{S}_2 = \{10, 11, 12\}$ each deme's ancestral lines evolve independently on $\{(\bullet), (\bullet\circ)\}$ with recombination and coalescence transition probabilities given by

$$\begin{pmatrix} \frac{1}{2} & \frac{1}{2} \\ \frac{1}{2N} & 1 - \frac{1}{2N} \end{pmatrix}.$$

With respect to these subsets of states, we have as previously

$$\tilde{\mathbf{P}} = \lim_{k\to\infty} \tilde{\mathbf{A}}^k = \begin{pmatrix} 1 & \mathbf{0} & \mathbf{0} \\ \mathbf{1} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \tilde{\mathbf{P}}_{22} \end{pmatrix},$$

where

$$\tilde{\mathbf{P}}_{22} = \lim_{k\to\infty} \left(\tilde{\mathbf{A}}_{22}\right)^k = \begin{pmatrix} \frac{1}{(N+1)^2} & \frac{2N}{(N+1)^2} & \frac{N^2}{(N+1)^2} \\ \frac{1}{(N+1)^2} & \frac{2N}{(N+1)^2} & \frac{N^2}{(N+1)^2} \\ \frac{1}{(N+1)^2} & \frac{2N}{(N+1)^2} & \frac{N^2}{(N+1)^2} \end{pmatrix},$$

while $\mathbf{0}$ and $\mathbf{1}$ are matrices of zeros and ones, respectively. With respect to the same state sets, the rate matrix for changes that involve migration events in the limit as $\alpha \to 0$ takes the form

$$\lim_{\alpha\to 0} \tilde{\mathbf{B}}_\alpha = \tilde{\mathbf{B}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{B}}_{10} & \tilde{\mathbf{B}}_{11} & \tilde{\mathbf{B}}_{12} \\ \tilde{\mathbf{B}}_{20} & \tilde{\mathbf{B}}_{21} & \tilde{\mathbf{B}}_{22} \end{pmatrix},$$

where

$$\tilde{\mathbf{B}}_{22} = m(1-m) \begin{pmatrix} -2 & 0 & 0 \\ 0 & -3 & 0 \\ 0 & 0 & -4(1-m+m^2) \end{pmatrix} \tilde{\mathbf{A}}_{22}.$$

Notice that $2m(1-m) = 1 - (1-m)^2 - m^2$, while we have $3m(1-m) = 1 - (1-m)^3 - m^3$ and $4m(1-m)(1-m+m^2) = 1 - (1-m)^4 - m^4 - 2m^2(1-m)^2$.

Lemma 1 of Möhle (1998) guarantees that

$$\lim_{\alpha\to 0} \tilde{\mathbf{\Pi}}_m^{\lfloor t/\alpha \rfloor} = \tilde{\mathbf{P}} \exp\{t\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}}\},$$

where

$$\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{G}}_{20} & \mathbf{0} & \tilde{\mathbf{G}}_{22} \end{pmatrix}$$

with

$$\tilde{\mathbf{G}}_{22} = \tilde{\mathbf{P}}_{22}\tilde{\mathbf{B}}_{22}\tilde{\mathbf{P}}_{22} = \left[-\frac{4N+2}{N+1} m(1-m) + \frac{4N^2}{(N+1)^2} m^2(1-m)^2 \right] \tilde{\mathbf{P}}_{22}$$

and

$$\tilde{\mathbf{G}}_{20} = \tilde{\mathbf{P}}_{22}\left(\tilde{\mathbf{B}}_{20} + \tilde{\mathbf{B}}_{21}\mathbf{1}\right) = -\tilde{\mathbf{P}}_{22}\tilde{\mathbf{B}}_{22}\mathbf{1} = \left[\frac{4N+2}{N+1} m(1-m) - \frac{4N^2}{(N+1)^2} m^2(1-m)^2 \right] \mathbf{1}.$$

Therefore, we obtain

$$\lim_{\alpha \to 0} \mathbb{E}\left(F_\alpha(t)^2\right) = \exp\left\{ \left[-\frac{4N+2}{N+1} m(1-m) + \frac{4N^2}{(N+1)^2} m^2(1-m)^2 \right] t \right\} \tag{S20}$$

for $t \geq 0$. Moreover, combined with the earlier results, $\mathrm{Var}\left(F_\alpha(t)\right)$ tends to

$$\left(\exp\left\{ \left[\frac{2}{N+1} m(1-m) + \frac{4N^2}{(N+1)^2} m^2(1-m)^2 \right] t \right\} - 1 \right) \exp\left\{ -4m(1-m)t \right\}$$

as $\alpha \to 0$ for $t \geq 0$.

4 Monoecious populations with diploid migration

In this section, we consider a monoecious diploid population as in the main text but with migration of offspring instead of migration of gametes. Under this assumption, we have to distinguish between ancestral lines in the same individual and ancestral lines in different individuals in the same deme.

The possible states for two ancestral lines at a single locus are: [(•)] for one in one individual in one deme, [(•)(•)] for two in two individuals in the same deme, [(•)][(•)] for two in two individuals in different demes, and the additional state [(••)] for two in the same individual in one deme. The transition matrix with these states in this order is given by

$$\begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{1}{2N}(1-\alpha\beta) & \left(1-\frac{1}{N}\right)(1-\alpha\beta) & \alpha\beta & \frac{1}{2N}(1-\alpha\beta) \\ \frac{1}{2N}\frac{\alpha\beta}{D-1} & \left(1-\frac{1}{N}\right)\frac{\alpha\beta}{D-1} & 1-\frac{\alpha\beta}{D-1} & \frac{1}{2N}\frac{\alpha\beta}{D-1} \\ \frac{1}{2N} & \left(1-\frac{1}{N}\right) & 0 & \frac{1}{2N} \end{pmatrix}, \tag{S21}$$

in which

$$\beta = 2m(1-m) + m^2\frac{D-2}{D-1}$$

represents the conditional probability for two offspring chosen at random in the same deme to come from two different demes given that migration occurs, and $\beta/(D-1)$ the conditional probability for two offspring in different demes to come from the same deme.

4.1 Structured-coalescent limit

In this subsection, we consider $D = 2$ demes of large size N and a fixed deme-scaled migration fraction $m = M/(4N)$ with probability $\alpha = 1$ in each generation. The transition matrix in (S21) for a pair of ancestral lines at a single locus can be written in the form

$$\mathbf{\Pi}_N = \mathbf{A} + \frac{\mathbf{B}_N}{2N},$$

where

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix}$$

and

$$\mathbf{B}_N \to \mathbf{B} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & -(2+M) & M & 1 \\ 0 & M & -M & 0 \\ 1 & -2 & 0 & 1 \end{pmatrix}$$

as $N \to \infty$. Using Lemma 1 of Möhle (1998), we have

$$\mathbf{\Pi}_N^{\lfloor 2Nt \rfloor} \to \mathbf{P}\exp\{t\mathbf{G}\}$$

as $N \to \infty$, where

$$\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k = \mathbf{A}$$

and

$$\mathbf{G} = \mathbf{PBP} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & -(1+M) & M & 0 \\ 0 & M & -M & 0 \\ 1 & -(1+M) & M & 0 \end{pmatrix}.$$

Therefore, in the limit $N \to \infty$ and starting from state $[(\bullet\bullet)]$, there is an instantaneous transition to state $[(\bullet)(\bullet)]$ and this is followed by a continuous time Markov chain on the states $[(\bullet)]$, $[(\bullet)(\bullet)]$ and $[(\bullet)][(\bullet)]$ with rate matrix $\mathbf{G}$ as given in equation (5) in the main text, i.e., just as in the case of gametic migration.

For two pairs of ancestral lines at two unlinked loci, the state space S can be decomposed into the following subsets: $S_1 = \{1, \ldots, 6\}$ for fewer than four ancestral lines or four ancestral lines in four different individuals, S_2 for four ancestral lines in the same deme except state 2, S_3 for two ancestral lines at locus 1 and one at locus 2 in one deme and another ancestral line at locus 2 in a different deme except state 3, S_4 for two ancestral lines at locus 2 and one at locus 1 in one deme and another ancestral line at locus 1 in a different deme except state 4, S_5 for one ancestral line at locus 1 and one at locus 2 in each of two different demes except state 5, and S_6 for two ancestral lines at locus 1 in one deme and two ancestral lines at locus 2 in a different deme except state 6. The transition matrix with respect to these subsets can be written as

$$\tilde{\mathbf{\Pi}}_N = \tilde{\mathbf{A}} + \frac{\tilde{\mathbf{B}}_N}{2N},$$

where

$$\lim_{k\to\infty} \tilde{\mathbf{A}}^k = \tilde{\mathbf{P}} = \begin{pmatrix} \mathbf{I} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{1}\mathbf{e}_2^\mathsf{T} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{1}\mathbf{e}_3^\mathsf{T} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{1}\mathbf{e}_4^\mathsf{T} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{1}\mathbf{e}_5^\mathsf{T} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{1}\mathbf{e}_6^\mathsf{T} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{pmatrix}$$

with $\mathbf{1}$ representing a column vector of all ones and $\mathbf{e}_i^\mathsf{T}$ being the i-th row vector of the 6-dimensional identity matrix $\mathbf{I}$ for $i = 1, \ldots, 6$. Further, the first 6 rows of $\lim_{N\to\infty} \tilde{\mathbf{B}}_N = \tilde{\mathbf{B}}$ are given by

$$\begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} \\ 2 & -(12+2M) & M & M & 0 & 0 & \mathbf{u}_2^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} \\ 1 & M/2 & -(6+2M) & 0 & M & M/2 & \mathbf{0}^\mathsf{T} & \mathbf{u}_3^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} \\ 1 & M/2 & 0 & -(6+2M) & M & M/2 & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{u}_4^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} \\ 0 & 0 & M & M & -(4+2M) & 0 & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{u}_5^\mathsf{T} & \mathbf{0}^\mathsf{T} \\ 2 & 0 & M & M & 0 & -(2+2M) & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} & \mathbf{0}^\mathsf{T} \end{pmatrix}$$

with $\mathbf{u}_2^\intercal\mathbf{1} = 10$, $\mathbf{u}_3^\intercal\mathbf{1} = \mathbf{u}_4^\intercal\mathbf{1} = 5$ and $\mathbf{u}_5^\intercal\mathbf{1} = 4$. In this case, Lemma 1 of Möhle (1998) yields

$$\lim_{N\to\infty} \tilde{\mathbf{\Pi}}_N^{\lfloor 2Nt\rfloor} = \tilde{\mathbf{P}}\exp\{t\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}}\},$$

where the entries of $\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}}$ corresponding to the states in S_1 are given by

$$\tilde{\mathbf{G}} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 2 & -(2+2M) & M & M & 0 & 0 \\ 1 & M/2 & -(1+2M) & 0 & M & M/2 \\ 1 & M/2 & 0 & -(1+2M) & M & M/2 \\ 0 & 0 & M & M & -2M & 0 \\ 2 & 0 & M & M & 0 & -(2+2M) \end{pmatrix},$$

which is the same as the rate matrix in equation (9) in the main text for the case of gametic migration.

We can conclude that the results in main text section 'Structured-coalescent limit' apply *mutadis mutandis*.

4.2 Many-demes limit

For N and m fixed with $\alpha = 1$ as $D \to \infty$, the transition matrix for a pair of ancestral lines at the same locus denoted by $\mathbf{\Pi}_D$ satisfies

$$\mathbf{A} = \lim_{D\to\infty} \mathbf{\Pi}_D = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{(1-m)^2}{2N} & \left(1-\frac{1}{N}\right)(1-m)^2 & m(2-m) & \frac{(1-m)^2}{2N} \\ 0 & 0 & 1 & 0 \\ \frac{1}{2N} & \left(1-\frac{1}{N}\right) & 0 & \frac{1}{2N} \end{pmatrix},$$

from which

$$\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \tilde{\mathcal{F}} & 0 & 1-\tilde{\mathcal{F}} & 0 \\ 0 & 0 & 1 & 0 \\ \mathcal{F} & 0 & 1-\mathcal{F} & 0 \end{pmatrix},$$

where

$$\mathcal{F} = \frac{\tilde{\mathcal{F}}}{(1-m)^2} = \frac{1}{(2N-1)m(2-m)+(1-m)^2}. \tag{S22}$$

Furthermore,

$$\mathbf{B} = \lim_{D\to\infty} (\mathbf{\Pi}_D - \mathbf{A})\, D = \begin{pmatrix} 0 & 0 & 0 & 0 \\ \frac{m^2}{2N} & m^2\big(1-\frac{1}{N}\big) & -m^2 & \frac{m^2}{2N} \\ \frac{m(2-m)}{2N} & m(2-m)\big(1-\frac{1}{N}\big) & -m(2-m) & \frac{m(2-m)}{2N} \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$\mathbf{G} = \mathbf{PBP} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ (1-\tilde{\mathcal{F}})c & 0 & -(1-\tilde{\mathcal{F}})c & 0 \\ c & 0 & -c & 0 \\ (1-\mathcal{F})c & 0 & -(1-\mathcal{F})c & 0 \end{pmatrix},$$

where

$$c = \frac{m(2-m)}{2N} + m(2-m)\left(1-\frac{1}{N}\right)\tilde{\mathcal{F}} + \frac{m(2-m)}{2N}\mathcal{F} = \frac{1-\mathcal{F}}{2(N-1)}. \tag{S23}$$

This is the rate of coalescence of two ancestral lines starting in individuals in different demes with D generations as unit of time as $D \to \infty$. This differs slightly from the corresponding result $(1-\mathcal{F})/(2N)$ in equation (13) in the main text for the case of gametic migration. Starting from state $[(\bullet\bullet)]$ and owing to Lemma 1 of Möhle (1998), which ensures that $\lim_{D\to\infty} \mathbf{\Pi}_D{}^{\lfloor tD \rfloor} = \mathbf{P}\exp\{t\mathbf{G}\}$, we have

$$\lim_{D\to\infty} \mathbb{E}(F_D(t)) = (1-\mathcal{F})\exp\left\{-\frac{1-\mathcal{F}}{2(N-1)}t\right\}$$

for $t \geq 0$, which differs from the corresponding result in equation (15) in the main text for the case of gametic migration only by the replacement of $2N$ with $2(N-1)$ in the rate of coalescence for $t > 0$.

As for two pairs of ancestral lines at two unlinked loci, the transition matrix from one generation to the previous one can be expressed in the form

$$\tilde{\mathbf{\Pi}}_D = \tilde{\mathbf{A}} + \frac{\tilde{\mathbf{B}}_D}{D},$$

where $\tilde{\mathbf{A}}$ is the transition matrix in the limit of an infinite number of demes. In this limit, all states but two are transient. The state with only one ancestral line at any one of the loci and the state with the four ancestral lines in all different individuals in all different demes are absorbing. Call these states 1 and 2, respectively. Taking D generations as unit of time and letting D go to infinity, there are instantaneous transitions to these states 1 and 2 from any other state. Moreover, once in

state 2, the rate of transition to state 1 is the rate at which two individuals carrying two ancestral lines at the same locus come from the same deme, times the probability that the two ancestral lines come from the same gene in the same parent, plus the probabilities that they come either from the two genes in the same parent or from two genes in different parents, and coalesce before migrating in the limiting process. This gives the rate

$$\lambda = 2m(2-m)\left(\frac{1}{2N} + \frac{\mathcal{F}}{2N} + \left(1 - \frac{1}{N}\right)\hat{\mathcal{F}}\right) = \frac{1-\mathcal{F}}{N-1},$$

which is twice the rate in (S23) and which we note differs slightly from the corresponding result for gametic migration, $(1-\mathcal{F})/N$ in equation (22) in the main text. With diploid migration, therefore, starting with genes at two unlinked loci in two gametes in different demes, represented by [(•)][(•)], there is an instantaneous transition to state 2 and this is followed by a transition to the fixation state 1 at rate $(1-\mathcal{F})/(N-1)$.

Starting with initial state [(••)], so that both pairs of lines start from the same gametes in the same deme, however, there will be an instantaneous transition to either the fixation state 1 with some probability $\mathcal{U}$, or to state 2 with the complementary probability $1-\mathcal{U}$ from which the transition to the fixation state 1 will occur at rate $(1-\mathcal{F})/(N-1)$. This $\mathcal{U}$ corresponds to u_{17} in main text section 'Many-demes limit' and in Subsection 1.1. We do not attempt to derive it here but we anticipate that like u_{17} it will not in general be equal to $1-(1-\mathcal{F})^2$, which would be the value that would make $\lim_{D\to\infty}\mathrm{Var}(F_D(t))$ here equal to zero.

However, in the limit of a large deme size with $M = 4Nm$ kept constant, ancestral lines cannot stay in the same individual with probability one and we have

$$\mathcal{U} = \frac{2}{2+2M} + \frac{2M}{2+2M}\mathcal{F},$$

where here we use

$$\mathcal{F} = \frac{1}{1+M}$$

to represent the limiting $N\to\infty$ value of (S22) with $M = 4Nm$ kept constant. This yields

$$\mathcal{U} = \frac{1+2M}{(1+M)^2}$$

which is identical to the corresponding value for gametic migration (S13) derived in Subsection 1.1. We conclude similarly that, under diploid migration, the effect of conditioning on the pedigree becomes negligible with the addition of the structured-coalescent assumption to the many-demes model.

4.3 Low-migration limit

For $D = 2$ demes and a small migration fraction m with probability $\alpha = 1$ in each generation, the transition matrix in (S21) for a pair of ancestral lines at a single locus can be written in the form

$$\mathbf{\Pi}_m = \mathbf{A} + m\mathbf{B}_m,$$

where

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{1}{2N} & 1-\frac{1}{N} & 0 & \frac{1}{2N} \\ 0 & 0 & 1 & 0 \\ \frac{1}{2N} & 1-\frac{1}{N} & 0 & \frac{1}{2N} \end{pmatrix} \tag{S24}$$

and

$$\mathbf{B}_m \to \mathbf{B} = 2\begin{pmatrix} 0 & 0 & 0 & 0 \\ -\frac{1}{2N} & -(1-\frac{1}{N}) & 1 & -\frac{1}{2N} \\ \frac{1}{2N} & 1-\frac{1}{N} & -1 & \frac{1}{2N} \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

as $m \to 0$. By Lemma 1 of Möhle (1998), we have

$$\mathbf{\Pi}_m^{\lfloor t/m \rfloor} \to \mathbf{P}\exp\{t\mathbf{G}\}$$

as $m \to 0$, where

$$\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix} \tag{S25}$$

and

$$\mathbf{G} = \mathbf{PBP} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 2 & 0 & -2 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

Therefore, starting from the state $[(\bullet)][(\bullet)]$, the survival function satisfies

$$\lim_{m\to 0} \mathbb{E}\left(F_m(t)\right) = \exp\{-2t\}$$

for $t \geq 0$, which is identical to the corresponding result (S15) for gametic migration. On the other hand, starting from the initial state [(••)], there is instantaneous coalescence in the limit as $m \to 0$.

Now, considering the ancestral lines that start from two pairs of genes at unlinked loci labeled 1 and 2, the transition matrix from one generation to the previous one takes the form

$$\tilde{\mathbf{\Pi}}_m = \tilde{\mathbf{A}} + m\tilde{\mathbf{B}}_m,$$

where $\tilde{\mathbf{A}}$ is the transition matrix in the absence of migration. In this case, there will be absorption into $\tilde{S}_0 = \{1\}$, where 1 is the state with only one ancestral line at anyone of the loci, from any initial state with two ancestral lines at each of the loci but at least two in a same deme, which defines the set of states $\tilde{S}_1$. The other states are [(•)][(•)], [(•○)][(•)], [(•)(○)][(•)], [(•○)][(•○)], [(•○)][(•)(○)] or [(•)(○)] [(•)(○)], where •, ○, and • represent sequences ancestral at locus 1 only, at locus 2 only, and at both loci, respectively, while ( ) represents an individual and [ ] a deme. When they are in this set of states, represented by $\tilde{S}_2$, the ancestral lines in each deme will follow a Markov chain on the state space $\{[(\bullet)], [(\bullet\circ)], [(\bullet)(\circ)]\}$, independently of the ancestral lines in the other deme, whose probabilities of transition by recombination or coalescence are given by

$$\begin{pmatrix} \frac{1}{2} & \frac{1}{2} & 0 \\ \frac{1}{2N} & \frac{1}{2N} & 1-\frac{1}{N} \\ \frac{1}{2N} & \frac{1}{2N} & 1-\frac{1}{N} \end{pmatrix}.$$

The stationary distribution of this chain is $(\pi_1, \pi_2, \pi_3) = (1/(N+1), 1/(N+1), (N-1)/(N+1))$. With respect to the state sets $\tilde{S}_0, \tilde{S}_1$ and $\tilde{S}_2$ in this order, we have

$$\tilde{\mathbf{P}} = \lim_{k\to\infty} \tilde{\mathbf{A}}^k = \begin{pmatrix} 1 & \mathbf{0} & \mathbf{0} \\ \mathbf{1} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \tilde{\mathbf{P}}_{22} \end{pmatrix}, \tag{S26}$$

where

$$\tilde{\mathbf{P}}_{22} = \begin{pmatrix} \pi_1^2 & 2\pi_1\pi_2 & 2\pi_1\pi_3 & \pi_2^2 & 2\pi_2\pi_3 & \pi_3^3 \\ \pi_1^2 & 2\pi_1\pi_2 & 2\pi_1\pi_3 & \pi_2^2 & 2\pi_2\pi_3 & \pi_3^3 \\ \pi_1^2 & 2\pi_1\pi_2 & 2\pi_1\pi_3 & \pi_2^2 & 2\pi_2\pi_3 & \pi_3^3 \\ \pi_1^2 & 2\pi_1\pi_2 & 2\pi_1\pi_3 & \pi_2^2 & 2\pi_2\pi_3 & \pi_3^3 \\ \pi_1^2 & 2\pi_1\pi_2 & 2\pi_1\pi_3 & \pi_2^2 & 2\pi_2\pi_3 & \pi_3^3 \\ \pi_1^2 & 2\pi_1\pi_2 & 2\pi_1\pi_3 & \pi_2^2 & 2\pi_2\pi_3 & \pi_3^3 \end{pmatrix},$$

while $\mathbf{0}$ and $\mathbf{1}$ are matrices of zeros and ones, respectively. With respect to the same state sets, the

rate matrix for changes that involve migration events in the limit as $m \to 0$ takes the form

$$\lim_{m\to 0} \tilde{\mathbf{B}}_m = \tilde{\mathbf{B}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{B}}_{10} & \tilde{\mathbf{B}}_{11} & \tilde{\mathbf{B}}_{12} \\ \tilde{\mathbf{B}}_{20} & \tilde{\mathbf{B}}_{21} & \tilde{\mathbf{B}}_{22} \end{pmatrix},$$

where

$$\tilde{\mathbf{B}}_{22} = \begin{pmatrix} -2 & 0 & 0 & 0 & 0 & 0 \\ 0 & -2 & 0 & 0 & 0 & 0 \\ 0 & 0 & -3 & 0 & 0 & 0 \\ 0 & 0 & 0 & -2 & 0 & 0 \\ 0 & 0 & 0 & 0 & -3 & 0 \\ 0 & 0 & 0 & 0 & 0 & -4 \end{pmatrix} \tilde{\mathbf{A}}_{22}$$

with $\tilde{\mathbf{A}}_{22}$ being the submatrix of $\tilde{\mathbf{A}}$ corresponding to the states in $\tilde{S}_2$ in the above order. Lemma 1 of Möhle (1998) guarantees that

$$\lim_{m\to 0} \tilde{\mathbf{\Pi}}_m^{\lfloor t/m \rfloor} = \tilde{\mathbf{P}} \exp\{t\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}}\},$$

where

$$\tilde{\mathbf{P}}\tilde{\mathbf{B}}\tilde{\mathbf{P}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{G}}_{20} & \mathbf{0} & \tilde{\mathbf{G}}_{22} \end{pmatrix}$$

with

$$\tilde{\mathbf{G}}_{22} = \tilde{\mathbf{P}}_{22}\tilde{\mathbf{B}}_{22}\tilde{\mathbf{P}}_{22} = -\frac{4N}{N+1}\tilde{\mathbf{P}}_{22}$$

and

$$\tilde{\mathbf{G}}_{20} = \tilde{\mathbf{P}}_{22}\left(\tilde{\mathbf{B}}_{20} + \tilde{\mathbf{B}}_{21}\mathbf{1}\right) = -\tilde{\mathbf{P}}_{22}\tilde{\mathbf{B}}_{22}\mathbf{1} = \frac{4N}{N+1}\mathbf{1}.$$

This uses the fact that the entries on each row of $\tilde{\mathbf{B}}$ must sum up to 0.

We conclude that, with initial state $[(\bullet)][(\bullet)]$, the survival function satisfies

$$\lim_{m\to 0} \mathbb{E}\left(F_m(t)^2\right) = \exp\left\{-\frac{4N}{N+1}t\right\} = \exp\{-4t\}\exp\left\{\frac{4}{N+1}t\right\}$$

for $t \geq 0$, which differs slightly from the gametic-migration result (S16). Combining this with our

previous result yields

$$\lim_{m\to 0} \mathrm{Var}\left(F_m(t)\right) = \exp\left\{-4t\right\}\left(\exp\left\{\frac{4}{N+1}t\right\} - 1\right)$$

for $t \geq 0$, which vanishes as $N \to \infty$, similar to (S17) in Section 2 under gametic migration.

4.4 Rare-migration limit

With $D = 2$ for fixed N and $m \in (0, 1)$ as $\alpha \to 0$, the possible states for the ancestral lines of a pair of genes at a single locus are the same as in the prior subsection and the transition matrix can be expressed as

$$\mathbf{\Pi}_\alpha = \mathbf{A} + \alpha \mathbf{B}_\alpha,$$

where $\mathbf{A}$ is given in (S24) and

$$\mathbf{B}_\alpha \to \mathbf{B} = 2m(1-m)\begin{pmatrix} 0 & 0 & 0 & 0 \\ -\frac{1}{2N} & -\left(1-\frac{1}{N}\right) & 1 & -\frac{1}{2N} \\ \frac{1}{2N} & 1-\frac{1}{N} & -1 & \frac{1}{2N} \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

as $\alpha \to 0$. Lemma 1 of Möhle (1998) yields

$$\mathbf{\Pi}^{\lfloor t/\alpha \rfloor} \to \mathbf{P}\exp\{t\mathbf{G}\},$$

as $\alpha \to 0$, where $\mathbf{P}$ is given in (S25) and

$$\mathbf{G} = \mathbf{PBP} = 2m(1-m)\begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

Therefore, for the ancestral lines that start from [(•)][(•)], the survival function satisfies

$$\lim_{\alpha\to 0} \mathbb{E}\left(F_\alpha(t)\right) = \exp\{-2m(1-m)t\}$$

for $t \geq 0$, which is identical to the corresponding result (S19) for gametic migration. For ancestral lines that start from the initial state [(••)], there is instantaneous coalescence in the limit as $\alpha \to 0$.

As for the ancestral lines that start from two pairs of genes at two unlinked loci with the same

possible states as in the previous subsection, the transition matrix takes the form

$$\tilde{\mathbf{\Pi}}_\alpha = \tilde{\mathbf{A}} + \alpha \tilde{\mathbf{B}}_\alpha,$$

where $\tilde{\mathbf{A}}$ is the same as in the previous subsection, while

$$\lim_{\alpha \to 0} \tilde{\mathbf{B}}_\alpha = \tilde{\mathbf{B}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{B}}_{10} & \tilde{\mathbf{B}}_{11} & \tilde{\mathbf{B}}_{12} \\ \tilde{\mathbf{B}}_{20} & \tilde{\mathbf{B}}_{21} & \tilde{\mathbf{B}}_{22} \end{pmatrix},$$

where

$$\tilde{\mathbf{B}}_{22} = m(1-m) \begin{pmatrix} -2 & 0 & 0 & 0 & 0 & 0 \\ 0 & -2 & 0 & 0 & 0 & 0 \\ 0 & 0 & -3 & 0 & 0 & 0 \\ 0 & 0 & 0 & -2 & 0 & 0 \\ 0 & 0 & 0 & 0 & -3 & 0 \\ 0 & 0 & 0 & 0 & 0 & -4(1-m+m^2) \end{pmatrix} \tilde{\mathbf{A}}_{22}.$$

Then Lemma 1 of Möhle (1998) guarantees that

$$\lim_{\alpha \to 0} \tilde{\mathbf{\Pi}}_\alpha^{\lfloor t/\alpha \rfloor} = \tilde{\mathbf{P}} \exp\{t \tilde{\mathbf{P}} \tilde{\mathbf{B}} \tilde{\mathbf{P}}\},$$

where $\tilde{\mathbf{P}}$ is given in (S26). Then we find

$$\tilde{\mathbf{P}} \tilde{\mathbf{B}} \tilde{\mathbf{P}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{G}}_{20} & \mathbf{0} & \tilde{\mathbf{G}}_{22} \end{pmatrix}$$

with

$$\tilde{\mathbf{G}}_{22} = \tilde{\mathbf{P}}_{22} \tilde{\mathbf{B}}_{22} \tilde{\mathbf{P}}_{22} = \left[-\frac{4N}{N+1} m(1-m) + \frac{4(N-1)^2}{(N+1)^2} m^2 (1-m)^2 \right] \tilde{\mathbf{P}}_{22}$$

and $\tilde{\mathbf{G}}_{20} = -\tilde{\mathbf{G}}_{22}$. Therefore, with initial state $[(\bullet)][(\bullet)]$, we obtain

$$\lim_{\alpha \to 0} \mathbb{E}\left(F_\alpha(t)^2\right) = \exp\left\{ \left[-\frac{4N}{N+1} m(1-m) + \frac{4(N-1)^2}{(N+1)^2} m^2 (1-m)^2 \right] t \right\},$$

which tends to $\exp\left\{-4m(1-m)(1-m+m^2)t\right\}$ as $N \to \infty$, for $t \geq 0$, and which differs slightly from the gametic-migration result (S20). Overall, although the constants are different, we reach the same conclusion here in the case of diploid migration as we did in Section 3 in the case of gametic

migration, namely that the limiting variance of $F_\alpha(t)$ is not equal to zero in the rare-migration model.

5 Dioecious populations

Here we assume a dioecious diploid population with $N/2$ males and $N/2$ females in each of D demes instaed of a monoecious population. Conditional coalescence times in this model for $D = 1$ were studied in Wakeley et al. (2012), primarily using simulations. For $D \geq 2$, we will assume either gametic migration as in the main text or diploid migration as in the Section 4. As throughout, α is the probability for migration to occur in any given generation. In the case of gametic migration, a proportion m of gametes produced in each deme migrate uniformly to the other demes and this is followed by random pairing of male and female gametes within demes. In the case of diploid migration, m is the proportion of offspring that uniformly migrate to the other demes after random pairing of male and female gametes within demes.

The state space for two distinct ancestral lines at the same locus is the same as in Section 4 for diploid migration in a monoecious population: [(•)] for one in one individual in one deme, [(•)(•)] for two in two individuals in the same deme, [(•)][(•)] for two in two individuals in different demes, and [(••)] for two in the same individual in one deme. The transition matrix is slightly different, being given by

$$\begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{1}{2N}(1-\alpha\beta) & \left(1-\frac{1}{N}\right)(1-\alpha\beta) & \alpha\beta & \frac{1}{2N}(1-\alpha\beta) \\ \frac{1}{2N}\frac{\alpha\beta}{D-1} & \left(1-\frac{1}{N}\right)\frac{\alpha\beta}{D-1} & 1-\frac{\alpha\beta}{D-1} & \frac{1}{2N}\frac{\alpha\beta}{D-1} \\ 0 & 1-\alpha\beta & \alpha\beta & 0 \end{pmatrix} \tag{S27}$$

under gametic migration and

$$\begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{1}{2N}(1-\alpha\beta) & \left(1-\frac{1}{N}\right)(1-\alpha\beta) & \alpha\beta & \frac{1}{2N}(1-\alpha\beta) \\ \frac{1}{2N}\frac{\alpha\beta}{D-1} & \left(1-\frac{1}{N}\right)\frac{\alpha\beta}{D-1} & 1-\frac{\alpha\beta}{D-1} & \frac{1}{2N}\frac{\alpha\beta}{D-1} \\ 0 & 1 & 0 & 0 \end{pmatrix} \tag{S28}$$

under diploid migration. Here,

$$\beta = 2m(1-m) + m^2\frac{D-2}{D-1}$$

represents the conditional probability for two gametes or offspring, respectively, chosen at random in the same deme to come from two different demes given that migration occurs, and $\beta/(D-1)$ the conditional probability for two gametes or offspring, respectively, in different demes to come

from the same deme.

5.1 Structured-coalescent limit

For the structured-coalescent with $D = 2$, $\alpha = 1$ and $m = M/(4N)$, the transition matrix for a pair of ancestral lines at a single locus can be written in the form

$$\mathbf{\Pi}_N = \mathbf{A} + \frac{\mathbf{B}_N}{4N},$$

where $\mathbf{A}$ is the same as in Subsection 4.1, while $\mathbf{B} = \lim_{N\to\infty} \mathbf{B}_N$ is given by

$$\begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & -(2+M) & M & 1 \\ 0 & M & -M & 0 \\ 0 & -M & M & 0 \end{pmatrix}$$

under gametic migration and

$$\begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & -(2+M) & M & 1 \\ 0 & M & -M & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

under diploid migration. In both cases, $\mathbf{PBP}$ where $\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k = \mathbf{A}$ is the same as in Subsection 4.1.

For two pairs of ancestral lines at two unlinked loci, the transition matrix takes the form

$$\tilde{\mathbf{\Pi}}_N = \tilde{\mathbf{A}} + \frac{\tilde{\mathbf{B}}_N}{2N}$$

with the same $\lim_{k\to\infty} \tilde{\mathbf{A}}^k = \tilde{\mathbf{P}}$ and the same first 6 rows of $\lim_{N\to\infty} \tilde{\mathbf{B}}_N = \tilde{\mathbf{B}}$ corresponding to the states with fewer than four ancestral lines or four ancestral lines in four different individuals. The same rate matrix $\tilde{\mathbf{G}}$ as in Subsection 4.1 and in equation (9) the main text section 'Structured-coalescent limit' is obtained, and the same conclusion that the effect of the pedigree becomes negligible ensues because then we have $\lim_{N\to\infty} \mathrm{Var}(F_N(t)) = 0$.

5.2 Many-demes limit

With $D \geq 4$ and $\alpha = 1$, the transition matrix for a pair of ancestral lines at the same locus can be decomposed as

$$\mathbf{\Pi}_D = \mathbf{A} + \frac{\mathbf{B}_D}{D},$$

where

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{(1-m)^2}{2N} & \left(1 - \frac{1}{N}\right)(1-m)^2 & m(2-m) & \frac{(1-m)^2}{2N} \\ 0 & 0 & 1 & 0 \\ 0 & (1-m)^2 & m(2-m) & 0 \end{pmatrix},$$

under gametic migration and

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{(1-m)^2}{2N} & \left(1 - \frac{1}{N}\right)(1-m)^2 & m(2-m) & \frac{(1-m)^2}{2N} \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix},$$

under diploid migration. In both cases, we have

$$\mathbf{P} = \lim_{k \to \infty} \mathbf{A}^k = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \tilde{\mathcal{F}} & 0 & 1 - \tilde{\mathcal{F}} & 0 \\ 0 & 0 & 1 & 0 \\ \mathcal{F} & 0 & 1 - \mathcal{F} & 0 \end{pmatrix}$$

as in Subsection 4.2, but where

$$\mathcal{F} = (1-m)^2 \tilde{\mathcal{F}} = \frac{(1-m)^4}{2Nm(2-m) + 2(1-m)^2 - (1-m)^4}$$

under gametic migration and

$$\mathcal{F} = \tilde{\mathcal{F}} = \frac{(1-m)^2}{2Nm(2-m) + (1-m)^2}$$

under diploid migration. On the other hand,

$$\mathbf{B} = \lim_{D\to\infty} \mathbf{B}_D = \begin{pmatrix} 0 & 0 & 0 & 0 \\ \frac{m^2}{2N} & m^2\left(1-\frac{1}{N}\right) & -m^2 & \frac{m^2}{2N} \\ \frac{m(2-m)}{2N} & m(2-m)\left(1-\frac{1}{N}\right) & -m(2-m) & \frac{m(2-m)}{2N} \\ 0 & m^2 & -m^2 & 0 \end{pmatrix}$$

under gametic migration, while it is the same as in Subsection 4.2 with all zero entries in the last row under diploid migration. This leads to the rate matrix

$$\mathbf{PBP} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ (1-\tilde{\mathcal{F}})c & 0 & -(1-\tilde{\mathcal{F}})c & 0 \\ c & 0 & -c & 0 \\ (1-\mathcal{F})c & 0 & -(1-\mathcal{F})c & 0 \end{pmatrix},$$

where

$$c = \frac{m(2-m)}{2N} + m(2-m)\left(1-\frac{1}{N}\right)\tilde{\mathcal{F}} + \frac{m(2-m)}{2N}\mathcal{F}$$

is the rate of coalescence starting from state $[(\bullet)][(\bullet)]$ as in Subsection 4.2. Here, we have

$$c = \frac{1-\mathcal{F}}{2(N+(1-m)^2)}$$

under gametic migration and

$$c = \frac{1-\mathcal{F}}{2N}$$

under diploid migration. This means that there is instantaneous coalescence from states $[(\bullet)(\bullet)]$ and $[(\bullet\bullet)]$ with probabilities $\tilde{\mathcal{F}}$ and $\mathcal{F}$, respectively, and instantaneous transition to state $[(\bullet)][(\bullet)]$ with the complementary probabilities from which coalescence occurs at rate c.

Similarly, starting from two ancestral lines at each of two unlinked loci in four individuals in different demes, the rate of coalescence is

$$\lambda = 2m(2-m)\left(\frac{1}{2N} + \frac{\mathcal{F}}{2N} + \left(1-\frac{1}{N}\right)\tilde{\mathcal{F}}\right) = 2c.$$

On the other hand, starting from two ancestral lines at each of two unlinked loci in the same individual in the same deme, there will be either instantaneous coalescence with some probability $\mathcal{U}$ or instantaneous transition to all ancestral lines in different individuals in different demes with probability $1-\mathcal{U}$, so that $\lim_{D\to\infty} \mathrm{Var}(F_D(t)) \neq 0$ in general. But in the limit of a large deme size

with $M = 4Nm$ kept constant, we have

$$\mathcal{U} = \frac{1+2M}{(1+M)^2}$$

as in Subsection 4.2, so that the effect of the pedigree does become negligible with the addition of this structured-coalescent assumption.

5.3 Low-migration limit

With $D = 2$, $\alpha = 1$ and considering a small migration fraction m, the transition matrix for a pair of ancestral lines at a single locus takes the form

$$\mathbf{\Pi}_m = \mathbf{A} + m\mathbf{B}_m,$$

where

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ \frac{1}{2N} & 1-\frac{1}{N} & 0 & \frac{1}{2N} \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix}$$

under either gametic migration or diploid migration, while $\mathbf{B} = \lim_{m\to 0} \mathbf{B}_m$ is given by

$$2\begin{pmatrix} 0 & 0 & 0 & 0 \\ -\frac{1}{2N} & -(1-\frac{1}{N}) & 1 & -\frac{1}{2N} \\ \frac{1}{2N} & 1-\frac{1}{N} & -1 & \frac{1}{2N} \\ 0 & -1 & 1 & 0 \end{pmatrix}$$

under gametic migration and the same matrix but with all zero entries in the last row as in Subsection 4.3 under diploid migration. This leads to the same $\mathbf{P} = \lim_{k\to\infty} \mathbf{A}^k$ and the rate matrix $\mathbf{PBP}$ in the limit $m \to 0$ with time measured in units of $1/m$ generations. This means instant coalescence for two ancestral lines at the same locus if they start from the same deme, but coalescence at rate 2 if they start from different demes.

Now, considering the ancestral lines that start from two pairs of genes at two unlinked loci and arranging the states as in Subsection 4.3, the transition matrix from one generation to the previous one takes the same form

$$\tilde{\mathbf{\Pi}}_m = \tilde{\mathbf{A}} + m\tilde{\mathbf{B}}_m,$$

where

$$\tilde{\mathbf{P}} = \lim_{k\to\infty} \tilde{\mathbf{A}}^k = \begin{pmatrix} 1 & \mathbf{0} & \mathbf{0} \\ \mathbf{1} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \tilde{\mathbf{P}}_{22} \end{pmatrix}$$

with each row of $\tilde{\mathbf{P}}_{22}$ given by $(\pi_1^2, 2\pi_1\pi_2, 2\pi_1\pi_3, \pi_2^2, 2\pi_2\pi_3, \pi_3^3)$. Here, the frequency vector $(\pi_1, \pi_2, \pi_3) = (1/(N+2), 1/(N+2), N/(N+2))$ is the stationary distribution of the transition matrix

$$\begin{pmatrix} \frac{1}{2} & \frac{1}{2} & 0 \\ 0 & 0 & 1 \\ \frac{1}{2N} & \frac{1}{2N} & 1 - \frac{1}{N} \end{pmatrix}$$

for two ancestral lines at two unlinked loci in the same gamete, in different gametes in the same individual and in different individuals, respectively, in the same deme in the absence of migration. On the other hand,

$$\lim_{m\to 0} \tilde{\mathbf{B}}_m = \tilde{\mathbf{B}} = \begin{pmatrix} 0 & \mathbf{0} & \mathbf{0} \\ \tilde{\mathbf{B}}_{10} & \tilde{\mathbf{B}}_{11} & \tilde{\mathbf{B}}_{12} \\ \tilde{\mathbf{B}}_{20} & \tilde{\mathbf{B}}_{21} & \tilde{\mathbf{B}}_{22} \end{pmatrix}$$

has

$$\tilde{\mathbf{B}}_{22} = \begin{pmatrix} -2 & 0 & 0 & 0 & 0 & 0 \\ 0 & -3 & 0 & 0 & 0 & 0 \\ 0 & 0 & -3 & 0 & 0 & 0 \\ 0 & 0 & 0 & -4 & 0 & 0 \\ 0 & 0 & 0 & 0 & -4 & 0 \\ 0 & 0 & 0 & 0 & 0 & -4 \end{pmatrix} \tilde{\mathbf{A}}_{22}$$

under gametic migration and the same $\tilde{\mathbf{B}}_{22}$ as in Subsection 4.3 under diploid migration. Starting from two ancestral lines at each of two loci in different demes, this gives a rate of coalescence

$$\lambda = 2\pi_1^2 + 3(2\pi_1\pi_2 + 2\pi_1\pi_3) + 4(\pi_2^2 + 2\pi_2\pi_3 + \pi_3^3) = \frac{2(2N+3)}{(N+2)}$$

under gametic migration and

$$\lambda = 2(\pi_1^2 + 2\pi_1\pi_2 + \pi_2^2) + 3(2\pi_1\pi_3 + 2\pi_2\pi_3) + 4\pi_3^3 = \frac{4(N+1)}{(N+2)}$$

under diploid migration. Otherwise, there is instantaneous coalescence. Notice that $\lambda \to 4$ as $N \to \infty$. This is the same rate as in the diploid, monoecious migration model of Subsection 4.3,

and is twice the rate for the haploid migration model in Section 2. Overall, the same conclusions hold, that there is an effect of the pedigree but that it becomes negligible as the deme size increases.

5.4 Rare-migration limit

In the case of a fixed migration fraction $m \in (0,1)$ with small probability α in each generation for $D = 2$, the transition matrix for a pair of ancestral lines at a single locus takes the form

$$\mathbf{\Pi}_\alpha = \mathbf{A} + \alpha \mathbf{B}_\alpha$$

with the same $\mathbf{A}$ as in the previous subsection but with a multiplicative factor $2m(1-m)$ instead of 2 in $\mathbf{B} = \lim_{\alpha \to 0} \mathbf{B}_\alpha$, which gives the rate of coalescence of two ancestral lines starting from different demes. This is the same constant $2m(1-m)$ that appears in Section 3 and Subsection 4.4.

For two pairs of ancestral lines at two unlinked loci, the decomposition

$$\tilde{\mathbf{\Pi}}_\alpha = \tilde{\mathbf{A}} + \alpha \tilde{\mathbf{B}}_\alpha$$

has the same $\tilde{\mathbf{A}}$ as in the previous subsection, while $\tilde{\mathbf{B}} = \lim_{\alpha \to 0} \tilde{\mathbf{B}}_\alpha$ has

$$\tilde{\mathbf{B}}_{22} = m(1-m) \begin{pmatrix} -2 & 0 & 0 & 0 & 0 & 0 \\ 0 & -3 & 0 & 0 & 0 & 0 \\ 0 & 0 & -3 & 0 & 0 & 0 \\ 0 & 0 & 0 & -4(1-m+m^2) & 0 & 0 \\ 0 & 0 & 0 & 0 & -4(1-m+m^2) & 0 \\ 0 & 0 & 0 & 0 & 0 & -4(1-m+m^2) \end{pmatrix} \tilde{\mathbf{A}}_{22}$$

under gametic migration and the same $\tilde{\mathbf{B}}_{22}$ as in Subsection 4.4 under diploid migration and monoecy. Therefore, there is instantaneous coalescence unless the two ancestral lines at each of the two loci are in different demes, in which case the rate of coalescence is given by

$$\begin{aligned} \lambda &= m(1-m)(2\pi_1^2 + 3(2\pi_1\pi_2 + 2\pi_1\pi_3) + 4(1-m+m^2)(\pi_2^2 + 2\pi_2\pi_3 + \pi_3^2)) \\ &= \frac{2(2N+3)}{(N+2)} m(1-m) - \frac{4(N+1)^2}{(N+2)^2} m^2(1-m)^2 \end{aligned}$$

under gametic migration and

$$\lambda = m(1-m)(2(\pi_1^2 + 2\pi_1\pi_2 + \pi_2^2) + 3(2\pi_1\pi_3 + 2\pi_2\pi_3) + 4(1-m+m^2)\pi_3^2)$$

$$= \frac{4(N+1)}{(N+2)} m(1-m) - \frac{4N^2}{(N+2)^2} m^2(1-m)^2$$

under diploid migration. In both cases, $\lambda \to 4m(1-m)(1-m+m^2)$ as $N \to \infty$. Again, although the constants differ, the conclusion is the same as in Section 3 and Subsection 4.4, that there is a persistent pedigree effect for $m \in (0,1)$.

6 Mathematica notebook on fixation probabilities

The following pages display the Mathematica notebook `q17manydemes.nb` showing the solutions of (S7), (S8) and (S9) for the fixation probabilities u_{13}, u_{16} and u_{17} on the fastest time scale in the many-demes limit of a monoecious population with gametic migration, and also in its structured-coalescent and strong-migration limits. The notebook itself can be downloaded from https://doi.org/10.6084/m9.figshare.32144278.

```
(* Supplementary Mathematica notebook for Lessard, Easlick and Wakeley (2026) *)
(* "A classification of structured coalescent processes
  with migration conditional on the population pedigree" *)
(* specifically for the unwieldy expressions for the terms u13,
u16 and u17 in the many-demes limit. *)
(* Note that N is reserved for the function N[]
 in Mathematica. So we use n for the deme size here. *)
```

In[1]:=
```
(* equation (29) in the main text *)
(* "cal" because it is $\mathcal{F}$ in the .tex file *)
(* this is needed in order to solve for
 u13solve u16solve u17solve in the next cell *)
calF[n_, m_] := ((1 - m) ^ 2 / (2 n m (2 - m) + (1 - m) ^ 2))
```

In[2]:=
```
(* system of first-step equations (A7) (A8) (A9) in Appendix Section 1 *)
Assuming[m > 0 && m < 1 && n ≥ 4, FullSimplify[
  Solve[{((-1 + m)^2 (-1 + 2 m + 4 n + m^2 (-1 + 8 n)))/(4 n^2) + ((-1 + m)^2 m^2 (-1 + 2 n))/n calF[n, m] -
      ((-1 + m)^3 m (-1 + n) (-1 + 2 n) calF[n, m])/n^2 - ((-1 + m)^3 m (-1 + n) (-1 + 2 n) calF[n, m])/n^2 -
      u13solve + ((-1 + m)^4 (-1 + n) (3 - 8 n + 4 n^2) u13solve)/(4 n^3) -
      ((-1 + m)^3 m (-1 + 2 n) calF[n, m])/n^2 - ((-1 + m)^3 m (-1 + 2 n) calF[n, m])/n^2 +
      ((-1 + m)^4 (-1 + n) (-1 + 2 n) u16solve)/n^3 + ((-1 + m)^4 (-1 + 2 n) u17solve)/(4 n^3),
    ((-1 + m)^2 (-1 + m + 4 n))/(4 n^2) + ((-1 + m)^2 m (-1 + n) calF[n, m])/(2 n) +
      ((-1 + m)^2 m (-1 + n) calF[n, m])/(2 n) - ((-1 + m)^3 (-1 + n) (-3 + 2 n) u13solve)/(4 n^2) +
      1/2 (-1 + m)^2 m calF[n, m] + 1/2 (-1 + m)^2 m calF[n, m] - u16solve -
      ((-1 + m)^3 (-1 + n) (1 + n) u16solve)/(2 n^2) - ((-1 + m)^3 u17solve)/(4 n),
    (3 (-1 + m)^2)/(4 n) + ((-1 + m)^2 (-1 + n) u13solve)/(4 n) + ((-1 + m)^2 (-1 + n) u16solve)/(2 n) -
      u17solve + 1/4 (-1 + m)^2 u17solve} == 0, {u13solve, u16solve, u17solve}]]]
```

Out[2]=

$$\{\{\text{u13solve} \to -\big(\big(4\,(-1+m)^2\,(1-2n)\,(1-n)\,\big((-1+m)^6-2\,(-3+m)\,(-1+m)^4\,(1+m)\,n\big)\\ \big((-2+m)\,(-1+m)^3\,m-(-1+m)\,(-3+(-2+m)\,m\,(-2+3\,(-2+m)\,m))\big)\,n+\\ 2\,(-3+m)\,m\,(1+m)\,(3+(-3+m)\,m)\,n^2\big)+\\ \big(3\,(-1+m)^6\,(1-2n)\,\big((-1+m)^2-2\,(-2+m)\,m\,n\big)-(-3+m)\,(-1+m)^2\,(1+m)\\ n^2\,\big((-1+m)^4-2\,(-1+m)^2\,(2+m\,(-6+7\,m))\,n+8\,(-2+m)\,m\,(2+m\,(-2+3\,m))\,n^2\big)\big)\\ \big((-1+m)^5\,(-1+n)-(-3+m)\,(1+m)\,\big(2\,n^2+(-1+m)^3\,\big(-1+n^2\big)\big)\big)\big)\big)\big/\\ \big(\big((-1+m)^2-2\,(-2+m)\,m\,n\big)\,\big(2\,(-1+m)^3\,(4+(-2+m)\,m\,(-2+n)-3\,n)\,(1-2n)\,(-1+n)^2\\ \big((-1+m)^6-2\,(-3+m)\,(-1+m)^4\,(1+m)\,n\big)-\big((-1+m)^6\,(-1+n)\,(-1+2n)+\\ (-3+m)\,(1+m)\,n\,\big(4\,n^3-(-1+m)^4\,(-1+n)\,(3+4\,(-2+n)\,n)\big)\big)\\ \big((-1+m)^5\,(-1+n)-(-3+m)\,(1+m)\,\big(2\,n^2+(-1+m)^3\,\big(-1+n^2\big)\big)\big)\big)\big)\big),\\ \text{u16solve} \to \big((-1+m)^2\,\big(-4\,(-1+m)^9+(-1+m)^7\,(13+27\,(-2+m)\,m)\,n-\\ (-1+m)^5\,(-3+m\,(-116+m\,(356+75\,(-4+m)\,m)))\,n^2+\\ (-1+m)^4\,(41+m\,(-109+m\,(-446+m\,(878+m\,(-507+95\,m)))))\,n^3-\\ (-1+m)^3\,(-41+m\,(382+m\,(-241+m\,(-936+m\,(997+m\,(-334+37\,m))))))\,n^4-\\ 2\,(-1+m)\,\big(-6+m\,\big(-114+m\,\big(461+m\,\big(-300+m\,\big(-449+m\,\big(622-213\,m+7\,m^3\big)\big)\big)\big)\big)\big)\,n^5+\\ 8\,(-3+m)\,(-2+m)\,m\,(1+m)\,\big(-2+(-1+m)^2\,m\,\big(-4+m+m^2\big)\big)\,n^6\big)\big/\\ \big(-4\,(-1+m)^{11}+(-1+m)^9\,(13+33\,(-2+m)\,m)\,n-\\ (-1+m)^7\,(-3+m\,(-170+m\,(536+113\,(-4+m)\,m)))\,n^2+\\ (-1+m)^6\,(41+m\,(-41+m\,(-864+m\,(1680+209\,(-5+m)\,m))))\,n^3-\\ (-1+m)^4\,(41+m\,(-429+m\,(497+m\,(1989+m\,(-4837+m\,(4149+227\,(-7+m)\,m))))))\,n^4+\\ 2\,(-1+m)^3\\ (6+m\,(150+m\,(-741+m\,(582+m\,(1259+m\,(-2516+m\,(1787+73\,(-8+m)\,m)))))))\\ n^5-4\,(-2+m)\,(-1+m)^2\,m\\ (-12+m\,(-90+m\,(205+m\,(-37+m\,(-226+m\,(230+13\,(-7+m)\,m)))))))\,n^6+\\ 8\,(-3+m)\,(-2+m)^2\,m^2\,(1+m)\,(2+(-2+m)\,m)\,(1+m\,(3+(-3+m)\,m))\,n^7\big),\\ \text{u17solve} \to \big(-4\,(-1+m)^{11}+(-1+m)^9\,(13+21\,(-2+m)\,m)\,n-\\ (-1+m)^8\,(3+m\,(57+m\,(-155+73\,m)))\,n^2+\\ (-1+m)^6\,(41+m\,(-201+m\,(4+m\,(540+m\,(-593+173\,m)))))\,n^3-\\ (-1+m)^5\,(-41+m\,(424+m\,(-745+m\,(-46+m\,(1027+3\,m\,(-286+69\,m)))))))\,n^4+\\ 2\,(-1+m)^4\,(-6+m\,(-108+m\,(413+m\,(-333+m\,(-160+m\,(436+m\,(-267+53\,m))))))))\\ n^5-8\,(-2+m)\,(-1+m)^2\,m\,\big(-6+(-1+m)^2\,m\,(-12+m\,(3+m\,(3+2\,(-3+m)\,m)))\big)\,n^6\big)\big/\\ \big(-4\,(-1+m)^{11}+(-1+m)^9\,(13+33\,(-2+m)\,m)\,n-\\ (-1+m)^7\,(-3+m\,(-170+m\,(536+113\,(-4+m)\,m)))\,n^2+\\ (-1+m)^6\,(41+m\,(-41+m\,(-864+m\,(1680+209\,(-5+m)\,m))))\,n^3-\\ (-1+m)^4\,(41+m\,(-429+m\,(497+m\,(1989+m\,(-4837+m\,(4149+227\,(-7+m)\,m))))))\,n^4+\\ 2\,(-1+m)^3\\ (6+m\,(150+m\,(-741+m\,(582+m\,(1259+m\,(-2516+m\,(1787+73\,(-8+m)\,m)))))))\\ n^5-4\,(-2+m)\,(-1+m)^2\,m\\ (-12+m\,(-90+m\,(205+m\,(-37+m\,(-226+m\,(230+13\,(-7+m)\,m)))))))\,n^6+\\ 8\,(-3+m)\,(-2+m)^2\,m^2\,(1+m)\,(2+(-2+m)\,m)\,(1+m\,(3+(-3+m)\,m))\,n^7\big)\}\}$$

In[3]:=

```
(* these are just cut and pasted from solutions above *)
(* u13 and u16 are not considered further but
```

```
 they have the same limits as those for u17 below *)
u13[n_, m_] := -((4 (-1 + m)^2 (1 - 2 n) (1 - n) ((-1 + m)^6 - 2 (-3 + m) (-1 + m)^4 (1 + m) n)
         ((-2 + m) (-1 + m)^3 m - (-1 + m) (-3 + (-2 + m) m (-2 + 3 (-2 + m) m)) n +
            2 (-3 + m) m (1 + m) (3 + (-3 + m) m) n^2) +
        (3 (-1 + m)^6 (1 - 2 n) ((-1 + m)^2 - 2 (-2 + m) m n) - (-3 + m) (-1 + m)^2 (1 + m) n^2
             ((-1 + m)^4 - 2 (-1 + m)^2 (2 + m (-6 + 7 m)) n + 8 (-2 + m) m (2 + m (-2 + 3 m)) n^2))
         ((-1 + m)^5 (-1 + n) - (-3 + m) (1 + m) (2 n^2 + (-1 + m)^3 (-1 + n^2)))))/
     (((-1 + m)^2 - 2 (-2 + m) m n) (2 (-1 + m)^3 (4 + (-2 + m) m (-2 + n) - 3 n) (1 - 2 n)
          (-1 + n)^2 ((-1 + m)^6 - 2 (-3 + m) (-1 + m)^4 (1 + m) n) - ((-1 + m)^6 (-1 + n) (-1 + 2 n) +
             (-3 + m) (1 + m) n (4 n^3 - (-1 + m)^4 (-1 + n) (3 + 4 (-2 + n) n)))
          ((-1 + m)^5 (-1 + n) - (-3 + m) (1 + m) (2 n^2 + (-1 + m)^3 (-1 + n^2))))))
u16[n_, m_] := ((-1 + m)^2 (-4 (-1 + m)^9 + (-1 + m)^7 (13 + 27 (-2 + m) m) n -
        (-1 + m)^5 (-3 + m (-116 + m (356 + 75 (-4 + m) m))) n^2 +
        (-1 + m)^4 (41 + m (-109 + m (-446 + m (878 + m (-507 + 95 m))))) n^3 -
        (-1 + m)^3 (-41 + m (382 + m (-241 + m (-936 + m (997 + m (-334 + 37 m)))))) n^4 -
        2 (-1 + m) (-6 + m (-114 + m (461 + m (-300 + m (-449 + m (622 - 213 m + 7 m^3))))))) n^5 +
        8 (-3 + m) (-2 + m) m (1 + m) (-2 + (-1 + m)^2 m (-4 + m + m^2))) n^6))/
   (-4 (-1 + m)^11 + (-1 + m)^9 (13 + 33 (-2 + m) m) n -
      (-1 + m)^7 (-3 + m (-170 + m (536 + 113 (-4 + m) m))) n^2 +
      (-1 + m)^6 (41 + m (-41 + m (-864 + m (1680 + 209 (-5 + m) m)))) n^3 -
      (-1 + m)^4 (41 + m (-429 + m (497 + m (1989 + m (-4837 + m (4149 + 227 (-7 + m) m)))))) n^4 +
      2 (-1 + m)^3
       (6 + m (150 + m (-741 + m (582 + m (1259 + m (-2516 + m (1787 + 73 (-8 + m) m))))))
       n^5 - 4 (-2 + m) (-1 + m)^2 m
       (-12 + m (-90 + m (205 + m (-37 + m (-226 + m (230 + 13 (-7 + m) m)))))) n^6 +
      8 (-3 + m) (-2 + m)^2 m^2 (1 + m) (2 + (-2 + m) m) (1 + m (3 + (-3 + m) m)) n^7)
u17[n_, m_] :=
  (-4 (-1 + m)^11 + (-1 + m)^9 (13 + 21 (-2 + m) m) n - (-1 + m)^8 (3 + m (57 + m (-155 + 73 m))) n^2 +
      (-1 + m)^6 (41 + m (-201 + m (4 + m (540 + m (-593 + 173 m))))) n^3 -
      (-1 + m)^5 (-41 + m (424 + m (-745 + m (-46 + m (1027 + 3 m (-286 + 69 m)))))) n^4 +
      2 (-1 + m)^4 (-6 + m (-108 + m (413 + m (-333 + m (-160 + m (436 + m (-267 + 53 m))))))) n^5 -
      8 (-2 + m) (-1 + m)^2 m (-6 + (-1 + m)^2 m (-12 + m (3 + m (3 + 2 (-3 + m) m)))) n^6)/
   (-4 (-1 + m)^11 + (-1 + m)^9 (13 + 33 (-2 + m) m) n -
      (-1 + m)^7 (-3 + m (-170 + m (536 + 113 (-4 + m) m))) n^2 +
      (-1 + m)^6 (41 + m (-41 + m (-864 + m (1680 + 209 (-5 + m) m)))) n^3 -
      (-1 + m)^4 (41 + m (-429 + m (497 + m (1989 + m (-4837 + m (4149 + 227 (-7 + m) m)))))) n^4 +
      2 (-1 + m)^3
       (6 + m (150 + m (-741 + m (582 + m (1259 + m (-2516 + m (1787 + 73 (-8 + m) m))))))
       n^5 - 4 (-2 + m) (-1 + m)^2 m
       (-12 + m (-90 + m (205 + m (-37 + m (-226 + m (230 + 13 (-7 + m) m)))))) n^6 +
      8 (-3 + m) (-2 + m)^2 m^2 (1 + m) (2 + (-2 + m) m) (1 + m (3 + (-3 + m) m)) n^7)
```

In[6]:=
```
(* this cell pertains to the end of section Many-demes limit in the main text *)
(* adding the structured-
 coalescent limit assumptions to these many-demes results *)
(* first the limit of calF *)
Assuming[M > 0, FullSimplify[Limit[calF[n, M / (4 n)], n → Infinity]]]
(* the term in parentheses on the right-
 hand-side of equation (51) is 1-u17-(1-F)^2 *)
(* and for this to converge to zero
  u17 has to have the same limit as 1-(1-F)^2 *)
Simplify[1 - (1 - %) ^ 2]
(* next the limit u17 which is the same and the limit of 1-(1-F)^2 above *)
Assuming[M > 0, FullSimplify[Limit[u17[n, M / (4 n)], n → Infinity]]]
```

Out[6]=
$$\frac{1}{1+M}$$

Out[7]=
$$\frac{1+2M}{(1+M)^2}$$

Out[8]=
$$\frac{1+2M}{(1+M)^2}$$

In[17]:=
```
(* this cell pertains to Figure 4 and the equation for g(M) *)
(* which is given by the following limit *)
Assuming[M > 0,
 Simplify[Limit[n (1 - u17[n, M / (4 n)] - (1 - calF[n, M / (4 n)]) ^ 2), n → Infinity]]]
```

Out[17]=
$$\frac{M\left(6+4M+M^2\right)}{3\,(1+M)^3}$$

In[9]:=
```
(* this cell pertains to the Discussion *)
(* now just letting the deme size tend to infinity with m fixed *)
(* i.e. adding the stong-
 migration limit assumptions to these many-demes results *)
(* first the limit of calF *)
Assuming[m > 0 && m < 1, FullSimplify[Limit[calF[n, m], n → Infinity]]]
(* next the limit of u17 *)
Assuming[m > 0 && m < 1, FullSimplify[Limit[u17[n, m], n → Infinity]]]
(* both tend to zero so 1-u17-(1-F)^2 in equation (51) does as well *)
```

Out[9]= 0

Out[10]=
```
0
```

7 Acknowledgements

We thank Yichen Si for helpful calculations and discussions in the initial stages of this project. Terry Easlick and Sabin Lessard were supported in part by Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grant 8833 to Sabin Lessard.

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