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2 **Supplementary Information for**
3 **A Demographic and Evolutionary Analysis of Maternal Effect Senescence**
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7 **This PDF file includes:**

- 8 Supplementary text
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11 Supporting Information Text

12 **A. Fertility model: Coale and Trussell.** The Coale and Trussell model (1), from human demography, represents differences in
13 the fertility schedules of populations by using a ‘natural fertility schedule’ ($\tilde{m}(a)$), an age at which the population-specific
14 schedules can diverge from the natural fertility schedule (a_0), and a parameter that controls how rapidly the schedules diverge
15 (θ). The model is

$$16 \quad m(a) = \tilde{m}(a) \exp[-v(a)], \quad [1]$$

$$17 \quad v(a) = \begin{cases} 0 & a \leq a_0 \\ \theta(a - a_0) & a > a_0. \end{cases} \quad [2]$$

18
19 The Coale and Trussell model is typically fit to each population separately by choosing θ and a_0 to satisfy some statistical
20 criterion (e.g., minimizing the sum of squared deviations between the model and the data).

21 If we had observed the fertility schedules of individuals in every maternal age class, we could have used model [1]–[2] directly.
22 We, however, need to estimate fertility schedules for maternal ages that we did not measure in the laboratory experiment by
23 interpolating among those we did. We therefore amended the Coale and Trussell model to incorporate the effects of maternal
24 age g :

$$25 \quad m(a, g) = \tilde{m}(a) \exp[-v(a, g)], \quad [3]$$

$$26 \quad v(a, g) = \begin{cases} 0 & a \leq a_0 \\ \theta \cdot (g - \tilde{g}) \cdot (a - a_0) & a > a_0. \end{cases} \quad [4]$$

27 We now imagine that the “natural fertility schedule” is associated with a “natural maternal age” which, in model [3]–[4], is the
28 new parameter \tilde{g} .

29 To fit model [3]–[4], we minimized the sum of squared deviations between the model and the data over all of the possible
30 choices of

31 $\tilde{m}(a)$. We assumed that natural fertility schedule $\tilde{m}(a)$ was one of five functions: one of the four observed fertility schedules
32 for mothers with maternal age equal to 3, 5, 7 or 9; or the average fertility schedule over all maternal ages.

33 \tilde{g} . With each of the five candidate natural fertility schedules, we associate exactly one value of \tilde{g} . For the four observed
34 schedules, with maternal ages 3, 5, 7, and 9, we set \tilde{g} equal to the maternal age. For the fifth, average, candidate schedule
35 we set $\tilde{g} = 6$.

36 a_0 . Based on visual inspection of the observed fertility schedules (Fig. 1), we assumed that $a_0 \in \{2, 3, 4, 5\}$.

37 θ . The rate parameter θ was assumed to be a real positive number.

38 The best fit is achieved by the ‘average’ fertility schedule for $\tilde{m}(x)$, with $\tilde{g} = 6$, $a_0 = 4$, and $\theta = 0.0192$. The data, model fits,
39 and extrapolated curves are shown in the main text (Fig. 1A).

40 **B. Mortality model: Weibull.** The Weibull model is a common representation of the time-to-failure in survival probability
41 estimation for living organisms. It is a continuous probability distribution described by two parameters, and the shape of
42 the probability density function (*pdf*) is very flexible. From the individual culture experiments described in (2), we have the
43 time-to-death of many individual rotifers—with maternal ages 3, 5, 7, and 9 days—and we used this data to fit the Weibull
44 distribution:

$$45 \quad f(x|a, b) = \frac{a}{b} \left(\frac{x}{a}\right)^{b-1} e^{-(x/a)^b}. \quad [5]$$

46 The failure time, x , of each rotifer in the dataset is the oldest age (days) at which it was observed alive. The Weibull *pdf* [5]
47 is fit to observed failure times in each maternal age cohort, yielding four Weibull models. Inspection of the parameters from
48 those four models indicates that the parameters a and b vary log-linearly with maternal age group (Fig. S1), such that the
49 Weibull parameters are themselves parametric functions of maternal age group, g . Although a linear model would fit equally
50 well to the four points (Fig. S1), the log-linear form is necessary so that the Weibull parameters will both be non-negative for
51 maternal age groups up to $g = 16$. With this formulation, the time-to-death description of mortality probabilities is a function
52 of a single variable, g , which varies among groups, and four parameters that are defined for the population as a whole (the
53 slope and intercept of the log-linear functions for a and b). The resulting Weibull *pdfs* are shifted towards earlier and more
54 evenly spread times of death as g increases (Fig. S2). The resulting survivorship curves are shown in the main text (Fig. 1B).

55 **C. Birthflow model: fertility and survivorship curves.** Birth and death for the lab-cultured rotifers are continuous processes,
56 and by censusing once per day, information on the age of an individual is limited. Neonates were assigned an age of 0 on the
57 day that they were first counted in the census, but their true ages were between 0 and 1. Therefore, estimates of both fecundity
58 and survival probability represent averages over the census interval (1 day), and a birth-flow model (3) must be used to build
59 up the transition matrix, \mathbf{A} .

60 The survivorship curve (the proportion of neonates that survive to each age) was calculated using $1 - \mathcal{F}(x|a, b)$, where \mathcal{F} is
 61 the cumulative distribution function for the Weibull model [5]. The transition probabilities for the matrix model formulation
 62 are given by

$$63 \quad P_i = \frac{l_i + l_{i+1}}{l_{i-1} + l_i}, \quad [6]$$

64 where P_i is the probability of surviving from age class i to age class $i + 1$, and l_i , the probability of surviving to age i , is the
 65 survivorship curve derived from the Weibull model [5].

66 Likewise, the observed number of offspring produced by an individual in an interval averages over several processes that are
 67 unobserved during the interval. Production of neonates by a given age class, F_i ,

$$68 \quad F_i = \frac{l_0 + l_1}{2} \cdot \frac{m_i + P_i \cdot m_i + 1}{2}, \quad [7]$$

69 is determined by the fertility at that age, the fertility at the next age, the probability that individuals survive to that next age,
 70 and the probability that the offspring survive long enough to be counted. The average offspring must survive 0.5 days to be
 71 counted, and the fertility of the mother is an average, weighted by the probability of surviving to the next age (3). The values
 72 of the m_i in equation [7] come directly from the fertility model described in Section A.

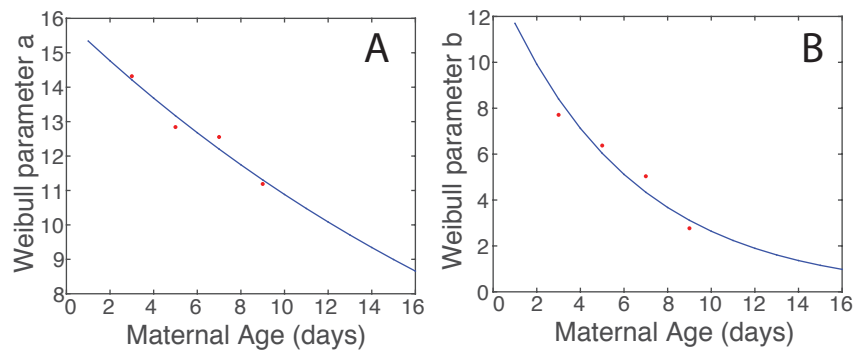


Fig. S1. Weibull model parameters a (panel A) and b (panel B) vary log-linearly with maternal age group. Red points represent the observed Weibull parameters for maternal ages 3, 5, 7, and 9. The blue lines are the log-linear best fits, $a = \exp(-0.038 \cdot g + 2.77)$ and $b = \exp(-0.165 \cdot g + 2.63)$.

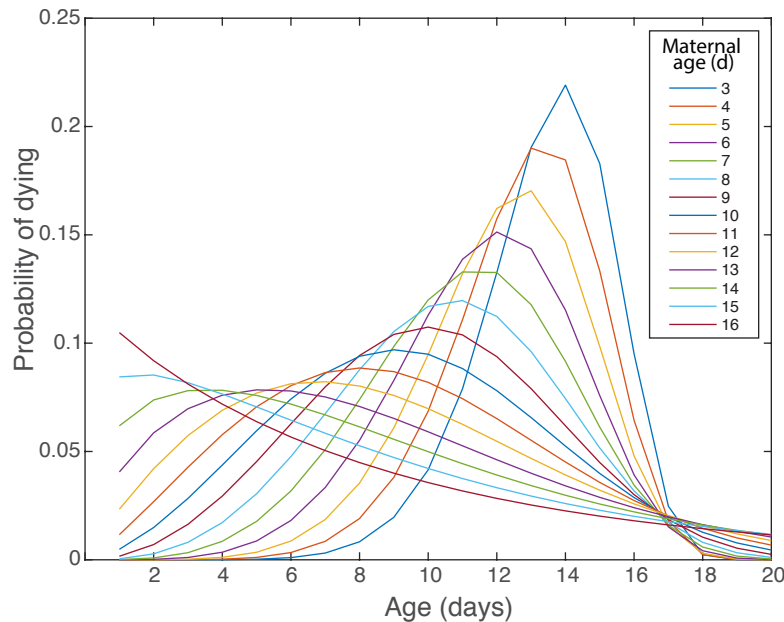


Fig. S2. Weibull probability density functions from the full model that varies with g , for $g \in [3, 4, \dots, 16]$. The blue curve with the highest peak is for maternal age group 3, and the red curve that is highest at age 1 day is for maternal age group 16.

73 **D. Multistate model construction.** In what follows, “stage” refers to maternal age class. The matrix $\mathcal{D}(\mathbf{x})$ contains \mathbf{x} on the
74 diagonal and zeros elsewhere. The transpose of \mathbf{x} is \mathbf{x}^\top . The vector \mathbf{e}_j is the j th unit vector: a vector with a 1 in the j th entry
75 and zeros elsewhere. The symbol \otimes denotes the Kronecker product. The vec operator turns a $m \times n$ matrix into a $mn \times 1$
76 vector by stacking the columns. Subscripts are used to denote the dimension of matrices and vectors; $\mathbf{0}_{m \times n}$ is a $m \times n$ matrix
77 of zeros, and $\mathbf{1}_m$ is a $m \times 1$ vector of ones.

78 The details of construction of age-stage models, using the vec-permutation formulation, are given in (4). In our particular
79 case of maternal age effects, we begin with the vectors \mathbf{p}_j , containing stage-specific survival probabilities at age j and \mathbf{f}_j
80 containing stage-specific fertilities at age j . Define the matrices

$$81 \quad \mathbf{U}_j = \mathcal{D}(\mathbf{p}_j), \quad \text{for } j = 1, \dots, \omega, \quad [8]$$

82 and

$$83 \quad \mathbf{D}_i = \text{subdiag}(\mathbf{1}_{\omega-1}), \quad \text{for } i = 1, \dots, s. \quad [9]$$

84 Let \mathbf{U} and \mathbb{D} be block diagonal matrices with the \mathbf{U}_j and \mathbf{D}_i on the diagonal, and let \mathbf{K} be the vec-permutation matrix. Then

$$85 \quad \tilde{\mathbf{U}} = \mathbf{K}^\top \mathbb{D} \mathbf{K} \mathbf{U}. \quad [10]$$

86 For fertility, define the fertility matrices

$$87 \quad \mathbf{F}_j = \mathbf{e}_j \mathbf{f}_j^\top, \quad j = 1, \dots, \omega \quad [11]$$

88 and the $\omega \times \omega$ age assignment matrices \mathbf{H}_i , which are all identical, with ones in the first row and zeros elsewhere. Create the
89 block diagonal matrices \mathbb{F} and \mathbb{H} . Then

$$90 \quad \tilde{\mathbf{F}} = \mathbf{K}^\top \mathbb{H} \mathbf{K} \mathbb{F}. \quad [12]$$

92 **E. Selection gradients and LTRE calculations.** The selection gradients on the stage-specific survival probability at age j are
93 given by

$$94 \quad \frac{\partial \lambda}{\partial \mathbf{p}_j^\top} = \frac{\partial \lambda}{\partial \text{vec}^\top \tilde{\mathbf{U}}} \frac{\partial \text{vec} \tilde{\mathbf{U}}}{\partial \text{vec}^\top \mathbf{U}_j} \frac{d \text{vec} \mathbf{U}_j}{d \mathbf{p}_j^\top}. \quad [13]$$

95 Without loss of generality, assume that the eigenvectors of $\tilde{\mathbf{A}}$ are scaled so that $\tilde{\mathbf{w}}^\top \tilde{\mathbf{v}} = 1$. Then the first term in [13] is

$$96 \quad \frac{\partial \lambda}{\partial \text{vec}^\top \tilde{\mathbf{U}}} = \tilde{\mathbf{w}}^\top \otimes \tilde{\mathbf{v}}^\top. \quad [14]$$

97 The third term is

$$98 \quad \frac{d \text{vec} \mathbf{U}_j}{d \mathbf{p}_j^\top} = \mathcal{D}(\text{vec} \mathbf{I}_s) (\mathbf{I}_s \otimes \mathbf{1}_s). \quad [15]$$

99 The second term can be expressed in terms of two matrices (5)

$$100 \quad \mathbf{Q}_i = \begin{pmatrix} \mathbf{0}_{s \times (i-1)s} & \mathbf{I}_s & \mathbf{0}_{s \times (\omega-i)} \end{pmatrix} \quad [16]$$

101 and

$$102 \quad \mathbf{R}_i = \begin{pmatrix} \mathbf{0}_{(i-1)s \times s} \\ \mathbf{I}_s \\ \mathbf{0}_{(\omega-i)s \times s} \end{pmatrix}. \quad [17]$$

103 In terms of these matrices,

$$104 \quad \frac{\partial \text{vec} \tilde{\mathbf{U}}}{\partial \text{vec}^\top \mathbf{U}_j} = \mathbf{Q}_{j-1} \otimes \mathbf{R}_j \quad [18]$$

105 (see (5) for proof).

106 The selection gradients on stage-specific fertility at age j are

$$107 \quad \frac{\partial \lambda}{\partial \mathbf{f}_j^\top} = \frac{\partial \lambda}{\partial \text{vec}^\top \tilde{\mathbf{F}}} \frac{\partial \text{vec} \tilde{\mathbf{F}}}{\partial \text{vec}^\top \mathbf{F}_j} \frac{d \text{vec} \mathbf{F}_j}{d \mathbf{f}_j^\top}, \quad [19]$$

108 the terms of which are

$$109 \quad \frac{\partial \lambda}{\partial \text{vec}^\top \tilde{\mathbf{F}}} = \tilde{\mathbf{w}}^\top \otimes \tilde{\mathbf{v}}^\top, \quad [20]$$

$$110 \quad \frac{\partial \text{vec} \tilde{\mathbf{F}}}{\partial \text{vec}^\top \mathbf{F}_j} = \mathbf{Q}_j \otimes \mathbf{R}_1, \quad \text{and} \quad [21]$$

$$111 \quad \frac{d \text{vec} \mathbf{F}_j}{d \mathbf{f}_j^\top} = \mathbf{I}_s \otimes \mathbf{e}_j. \quad [22]$$

112 The derivatives in expressions [13] and [19] provide the material for LTRE decomposition of the differences in λ between the
 113 life histories with and without maternal age senescence. See (3, Chap. 10) for a general discussion of LTRE calculations and
 114 (6) for a presentation in terms of matrix calculus. We use the latter approach here.

115 We use $\tilde{\mathbf{A}}^{(r)}$, $\tilde{\mathbf{B}}^{(r)}$, and $\tilde{\mathbf{C}}^{(r)}$ as reference matrices. The difference $\Delta\lambda$ between the original matrix and the reference matrix
 116 is, to first order,

$$117 \quad \Delta\lambda \approx \sum_{j=1}^{\omega} \frac{\partial\lambda}{\partial p_j^{\top}} \Delta\mathbf{p}_j + \sum_{j=1}^{\omega} \frac{\partial\lambda}{\partial f_j^{\top}} \Delta\mathbf{f}_j, \quad [23]$$

118 where the derivatives are evaluated midway between the two survival and fertility schedules.

119 Define contribution matrices \mathbf{C}_p and \mathbf{C}_f , where the i th row of \mathbf{C}_p , which we write as $\mathbf{C}_p(i, :)$, contains the contributions of
 120 differences in stage-specific survival at age i to $\Delta\lambda$, and similarly for $\mathbf{C}_f(i, :)$. These matrices are given by

$$121 \quad \mathbf{C}_p(i, :) = \frac{\partial\lambda}{\partial \mathbf{p}_i^{\top}} \mathcal{D}(\Delta\mathbf{p}_i), \quad i = 1, \dots, \omega, \quad [24]$$

$$122 \quad \mathbf{C}_f(i, :) = \frac{\partial\lambda}{\partial \mathbf{f}_i^{\top}} \mathcal{D}(\Delta\mathbf{f}_i), \quad i = 1, \dots, \omega. \quad [25]$$

123 The contributions shown in Fig. 5 of the main text are obtained by summing over ages; i.e., as column sums of \mathbf{C}_p and \mathbf{C}_f .

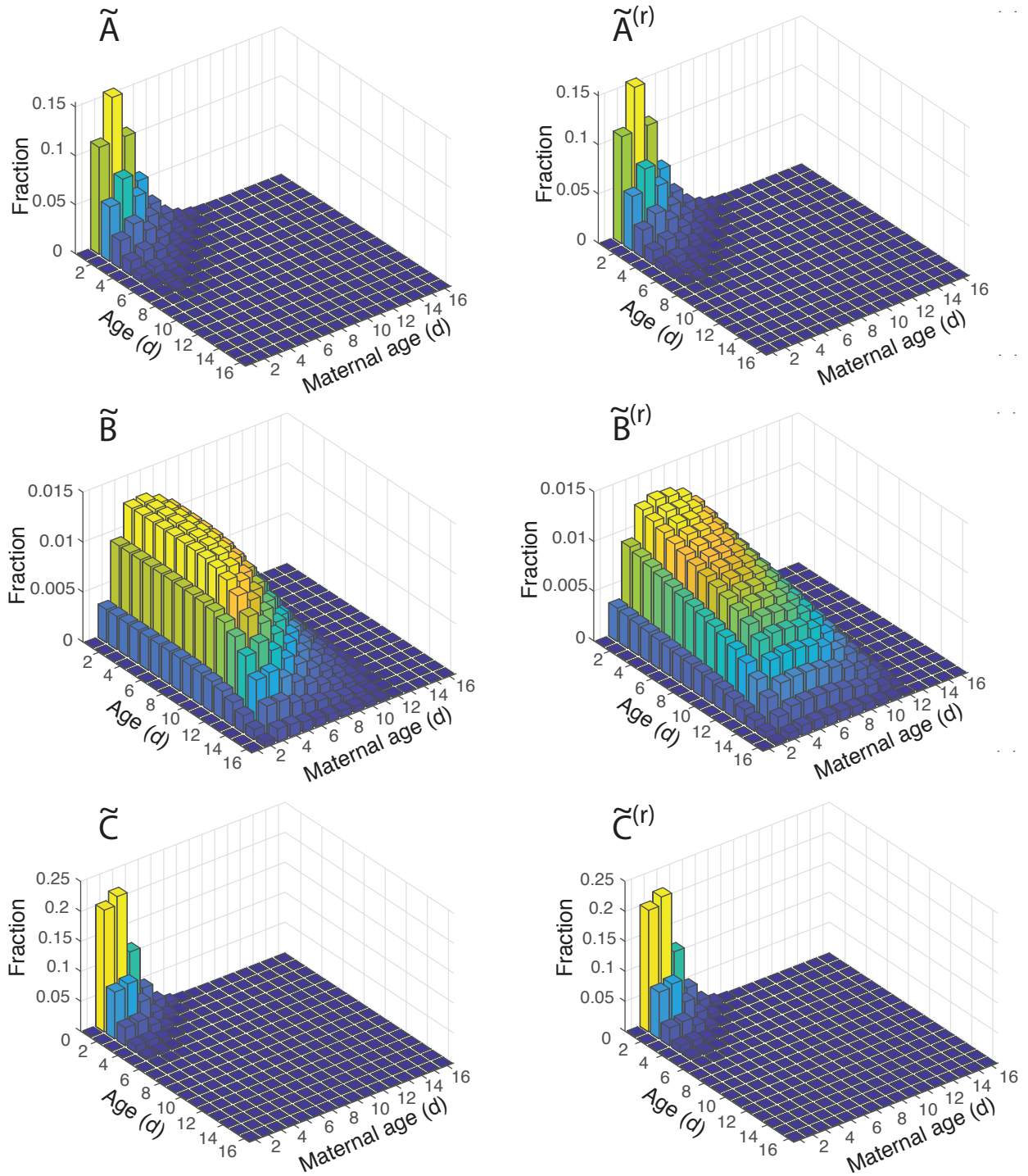


Fig. S3. Stable age-by-maternal-age distributions for all six population models: high-growth population with maternal age effects (\tilde{A} , top left), high-growth population without maternal age effects ($\tilde{A}^{(r)}$, top right), fertility-adjusted low-growth population with maternal age effects (\tilde{B} , center left), fertility-adjusted low-growth population without maternal age effects ($\tilde{B}^{(r)}$, center right), survival-adjusted low-growth population with maternal effects (\tilde{C} , bottom left), and survival-adjusted low-growth population without maternal effects ($\tilde{C}^{(r)}$, bottom right). The height of each bar represents the percent of the stable population that is of that age and maternal age. The bars are colored by their height, corresponding with the values on the z-axis. The colorbars and z-axis are consistent within each row of sub-panels (\tilde{A} and $\tilde{A}^{(r)}$, \tilde{B} and $\tilde{B}^{(r)}$, \tilde{C} and $\tilde{C}^{(r)}$).

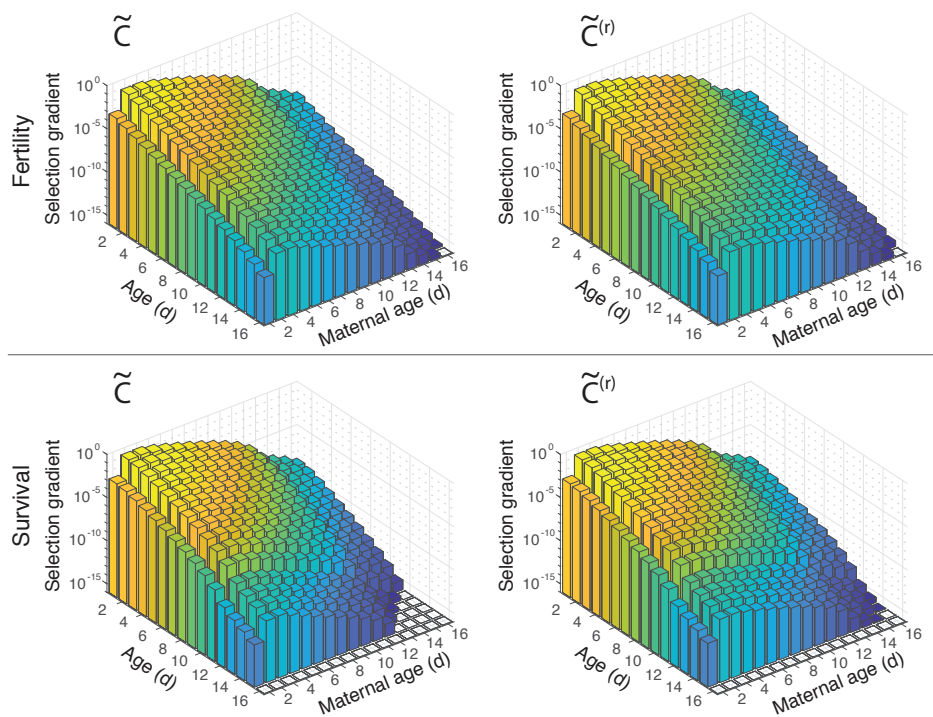


Fig. S4. Selection gradients on survival and fertility in low-growth life histories generated by adjusting survival, with (\tilde{C}) and without ($\tilde{C}^{(r)}$) the presence of maternal age effects. The panels in the top row are the selection gradients on fertility parameters, and the bottom row are for survival parameters. The left column shows the selection gradients with maternal effects, and the right column shows the selection gradients without maternal effects. The height of the bars is on a log-scale, and the bars are colored by their height, corresponding to the z-axis. All subpanels have the same z-axis limits and corresponding color axis.

124 **References**

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